AXL Antibody Nucleotide sequence:

Seq. #1: Rat-11B7-VLkappa-clone 33:

```
1     GACATCCAGATGACCCAGGCTCCATCTTCCCTGCCTGCATCTCTGGGAG    50
51    ACAGAGTCACTATTACTTGCCGGGCAAGCCAAGACATTGGAAATTATTT   100
101   AAGATGGTTCCAGCAGAAACCGGGGAAATCTCCTAGGCTTATGATTTCT   150
151   GGTGCAACCAACTTGGCAGCTGGGGTCCCATCAAGGTTCAGTGGCAGTA   200
201   GGTCTGGGTCAGATTATTCTCTGACCATCAGCAGCCTGGAGTCTGAAGA   250
251   TATGGCAGACTATTACTGTCTACAGTCTAAAGAGTCCCCTTGGACGTTC   300
301   GGTGGA GGCACCAAGCTGGAGCTGAAACGG                     350
```

Seq. #2. Rat-11B7-VH-clone 20:

```
1     GAGGTGCAGCTTCAGGAGTCAGGACCTGGCCTTGTGAAACCCTCACAGT    50
51    CACTCTCCCTCACTGTTCTGTCACTGGTTACTCCATCACTAGTAATTAC   100
101   TGGGGCTGGATCCGGAAGTTCCCAGGAGATAAAATGGAGTGGATGGGAT   150
151   ACATAACCTACAGTGGTAGCACTAGCTACAACCCATCTCTCAAAAGTCG   200
201   AATCTCCATTACTAGAGACACATCGAAGAATCAGTTCTTCCTGCAGTTG   250
251   AACTCTGTAACTTCTGAGGACACAGCCACATATTACTGTGCTATAACAA   300
301   CCTTTT ATTACTGGGGCCAAGGAGTCATGGTCACTGTCTCCTCA       350
```

Seq. #3: Rat-11D5-VLkappa-clone 10:

```
1     GACATCCAGATGACCCAGTCTCCATCCTCCATGTCTACATCTCTGGGAG    50
51    ACAGAGTCACTATTACTTGCCGGGCAAGTCAAGACATTGGAAATTATTT   100
101   AAGCTGGTTCCAACAGAAAGTAGGGAAATCTCCTAGGCGTATGATTTAT   150
151   GGTGCAATCAAGTTGGCAGTTGGGGTCCCATCAAGGTTCAGTGGAAGTA   200
201   GGTCTGGATCAGATTATTCTCTGACCATCAGCAGCCTGGAGTCTGAAGA   250
251   TATGGCGATCTATTACTGTCTACAGTATATACAGTTTCCGCTCACGTTC   300
301   GGTTCT GGGACCAAGCTGGAGCTGAAACGG                     350
```

Seq. #4: Rat-11D5-VH-clone 66:

```
1     GAGGTGCAACTTCAGGAGTCAGGACCTGGCCTTGTGAAACCCTCACAGT    50
51    CACTCTCCCTCACCTGTTCTGTCACTGGTTATTCCATCACTAGTAATTA   100
101   CTGGGGCTGGATCCGGAAGTTCCCAGGAAATAAAATGGAGTGGATTGGA   150
151   CACATAACCAACAGTGGTAACACTACCTACAATCCATCTCTCAAAAGTC   200
201   GAATCTCCATTAGTAGAGACACATCGAGGAATCAGTTCTTCCTGCAGTT   250
251   GAACTCTGTGACTACTGAGGACACAGCCACATATTACTGTGCAAAAGGA   300
301   GCGTTT GATTACTGGGGCCAAGGAGTCATGGTCACAGTCTCGTCA      350
```

Seq. #5: Rat-10D12-VLkappa-clone 8:

```
1     GACATCCAGATGACCCAGGCTCCATCTTCCCTGCCTGCATCTCTGGGAG    50
51    ACAGAGTCACTATTGCTTGCCGGGCAAGCCAAGACATTGGAAATTATTT   100
101   AAGATGGTTCCAGCAGAAACCGGGGAAATCTCCTAGGCTTATGATTTCT   150
151   GGTGCAACCAACTTGGCAGCTGGGGTCCCATCAAGGTTCAGTGGCAGTA   200
201   GGTCTGGGTCAGATTATTCTCGGACCATCAGCAGCCTGGAGTCTGAAGA   250
251   TATGGCAGACTATTACTGTCTACAGTCTAAAGAGTCCCCTTGGACGTTC   300
301   GGTGGA GGCACCAAGCTGGAGCTGAAACGG                     350
```

Seq. #6: Rat-10D12-VH-clone 5:

```
1     GAGGTGCAGCTTCAGGAGTCAGGACCTGGCCTTGTGAAGCCCTCACAGT    50
51    CACTCTCCCTCACCTGCTCTGTCACCGGTTACTCCATCACTAGTAATTA   100
101   CTGGGGCTGGATCCGGAAGTTCCCAGGAAATAAAATGGAGTGGATGGGA   150
151   TACATAACCAACAGTGGTGGCACTGCCTACAACCCATCTCTCAAAAGTC   200
201   GAATCTCCATTACTAGAGACACATCGAAGAATCAGTTCTTCCTGCAATT   250
251   GAACTCTGTAATTCCTGAGGACTCAGCCACATACTTCTGTTCAAGAACC   300
301   CCCTGG GACTGGGGCCAAGGAGTCATGGTCACAGTCTCCTCA 336     350
```

AXL Antibody Amino acid sequence:

11B7:

Seq. #7: Rat-11B7-VLkappa-clone 33:

```
1     DIQMTQAPSSLPASLGDRVTITCRASQDIGNYLRWFQQKPGKSPRLMIS    50
51    GATNLAAGVPSRFSGSRSGSDYSLTISSLESEDMADYYCLQSKESPWTF   100
101   GGGTKLELKR                                          150
```

Seq. #8: Rat-11B7-VH-clone 20:

```
1     EVQLQESGPGLVKPSQSLSLTCSVTGYSITSNYWGWIRKFPGDKMEWMG    50
51    YITYSGSTSYNPSLKSRISITRDTSKNQFFLQLNSVTSEDTATYYCAIT   100
101   TFYYWGQGVMVTVSS                                     150
```

11D5:

Seq. #9: Rat-11D5-VLkappa-clone 10:

```
1     DIQMTQSPSSMSTSLGDRVTITCRASQDIGNYLSWFQQKVGKSPRRMIY    50
51    GAIKLAVGVPSRFSGSRSGSDYSLTISSLESEDMAIYYCLQYIQFPLTF   100
101   GSGTKLELKR                                          150
```

Seq. #10: Rat-11D5-VH-clone 66:

```
1     EVQLQESGPGLVKPSQSLSLTCSVTGYSITSNYWGWIRKFPGNKMEWIG    50
51    HITNSGNTTYNPSLKSRISISRDTSRNQFFLQLNSVTTEDTATYYCAKG   100
101   AFDYWGQGVMVTVSS                                     150
```

10D12:

Seq. #11: Rat-10D12-VLkappa-clone 8:

```
1     DIQMTQAPSSLPASLGDRVTIACRASQDIGNYLRWFQQKPGKSPRLMIS    50
51    GATNLAAGVPSRFSGSRSGSDYSRTISSLESEDMADYYCLQSKESPWTF   100
101   GGGTKLELKR                                          150
```

Seq. #712: Rat-10D12-VH-clone 5:

```
1     EVQLQESGPGLVKPSQSLSLTCSVTGYSITSNYWGWIRKFPGNKMEWMG    50
51    YITNSGGTAYNPSLKSRISITRDTSKNQFFLQLNSVIPEDSATYFCSRT   100
101   PWDWGQGVMVTVSS                                      150
```

CDR Sequences

SeqID No:	Antibody	CDR	Sequence
#13	11B7 Light chain	1	RASQDIGNYLR
#14	11B7 Light chain	2	GATNLAA
#15	11B7 Light chain	3	LQSKESPWT
#16	11B7 Heavy Chain	1	SNYWG
#17	11B7 Heavy Chain	2	YITYSGSTSYNPSLKS
#18	11B7 Heavy Chain	3	----TTFYY
#19	11D5 Light Chain	1	RASQDIGNYLS
#20	11D5 Light Chain	2	GAIKLAV
#21	11D5 Light Chain	3	LQYIQFPLT
#22	11D5 Heavy Chain	1	SNYWG
#23	11D5 Heavy Chain	2	HITNSGNTTYNPSLKS
#24	11D5 Heavy Chain	3	----GAFDY
#25	10D12 Light Chain	1	RASQDIGNYLR
#26	10D12 Light Chain	2	GATNLAA
#27	10D12 Light Chain	3	LQSKESPWT
#28	10D12 Heavy Chain	1	SNYWG
#29	10D12 Heavy Chain	2	YITNSGGTAYNPSLKS
#30	10D12 Heavy Chain	3	----TPWD-

Chimerization nucleotide sequences

Seq. #31: ch11B7k

```
1     GACATCCAGATGACCCAGGCTCCATCTTCCCTGCCTGCATCTCTGGGAG    50
51    ACAGAGTCACTATTACTTGCCGGGCAAGCCAAGACATTGGAAATTATTT   100
101   AAGATGGTTCCAGCAGAAACCGGGGAAATCTCCTAGGCTTATGATTTCT   150
151   GGTGCAACCAACTTGGCAGCTGGGGTCCCATCAAGGTTCAGTGGCAGTA   200
201   GGTCTGGGTCAGATTATTCTCTGACCATCAGCAGCCTGGAGTCTGAAGA   250
251   TATG                                                300
301   GCAGACTATTACTGTCTACAGTCTAAAGAGTCCCCTTGGACGTTCGGTG   350
351   GAGGCACCAAGCTGGAGCTGAAACGTACGGTGGCTGCACCATCTGTCTT   400
401   CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTT   450
451   GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGA   500
500   AGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGA   550
551   GCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTG   600
601   AGCAAA                                              650
      GCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGG
      GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG
```

Seq. #32: ch11B7g1

```
1     GAGGTGCAGCTTCAGGAGTCAGGACCTGGCCTTGTGAAACCCTCACAGT   50
51    CACTCTCCCTCACCTGTTCTGTCACTGGTTACTCCATCACTAGTAATTA   100
101   CTGGGGCTGGATCCGGAAGTTCCCAGGAGATAAAATGGAGTGGATGGGA   150
151   TACATAACCTACAGTGGTAGCACTAGCTACAACCCATCTCTCAAAAGTC   200
201   GAATCTCCATTACTAGAGACACATCGAAGAATCAGTTCTTCCTGCAGTT   250
251   GAACTCTGTAACTTCTGAGGACACAGCCACATATTACTGTGCTATAACA   300
301   ACCTTT                                              350
351   TATTACTGGGGCCAAGGAGTCATGGTCACTGTCAGCTCAGCGTCCACCA   400
401   AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGG   450
451   GGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG   500
500   GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCT   550
551   TCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT   600
601   GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG   650
651   AATCAC                                              700
701   AAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTG   750
751   ACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGG   800
800   ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC   850
851   TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG   900
901   ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAA   950
951   TGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTG   1000
1001  GTCAGT                                              1050
1051  CGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG   1100
1101  GCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC   1150
1151  CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA   1200
1200  TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA   1250
1251  AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA   1300
1301  GCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGC
      TCCTTC
      TTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
      ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC
      GCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
```

Seq. #33: ch11B7g2

```
1     GAGGTGCAGCTTCAGGAGTCAGGACCTGGCCTTGTGAAACCCTCACAGT   50
51    CACTCTCCCTCACCTGTTCTGTCACTGGTTACTCCATCACTAGTAATTA   100
101   CTGGGGCTGGATCCGGAAGTTCCCAGGAGATAAAATGGAGTGGATGGGA   150
151   TACATAACCTACAGTGGTAGCACTAGCTACAACCCATCTCTCAAAAGTC   200
201   GAATCTCCATTACTAGAGACACATCGAAGAATCAGTTCTTCCTGCAGTT   250
251   GAACTCTGTAACTTCTGAGGACACAGCCACATATTACTGTGCTATAACA   300
301   ACCTTT                                              350
351   TATTACTGGGGCCAAGGAGTCATGGTCACTGTCAGCTCAGCGTCCACCA   400
401   AGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGA   450
451   GAGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG   500
500   GTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCT   550
551   TCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT   600
601   GACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTA   650
651   GATCAC                                              700
701   AAGCCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTG   750
751   TCGAGTGCCCACCGTGCCCAGCACCACCTGTGGCAGGACCGTCAGTCTT   800
800   CCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT   850
851   GAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCC   900
901   AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA   950
951   GCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTC   1000
1001  ACCGTT                                              1050
1051  GTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCA   1100
1101  ACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGG   1150
1151  GCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAG   1200
1200  ATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACC   1250
1251  CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAA   1300
1301  CTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTC
      TACAGC
      AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT
      GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCT
      CTCCCTGTCTCCGGGTAAATGA
```

Seq. #34: ch11D5k

```
1     GACATCCAGATGACCCAGTCTCCATCCTCCATGTCTACATCTCTGGGAG    50
51    ACAGAGTCACCATTACTTGCCGGGCAAGTCAAGACATTGGAAATTATTT   100
```

```
101   AAGCTGGTTCCAACAGAAAGTAGGGAAATCTCCTAGGCGTATGATTTAT   150
151   GGTGCAATCAAGTTGGCAGTTGGGGTCCCATCAAGGTTCAGTGGAAGTA   200
201   GGTCTGGATCAGATTATTCTCTGACCATCAGCAGCCTGGAGTCTGAAGA   250
251   TATG                                                300
301   GCGATCTATTACTGTCTACAGTATATACAGTTTCCGCTCACGTTCGGTT   350
351   CTGGGACCAAGCTGGAGCTGAAACGTACGGTGGCTGCACCATCTGTCTT   400
401   CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTT   450
451   GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGA   500
500   AGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGA   550
551   GCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTG   600
601   AGCAAA                                              650
      GCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGG
      GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG
```

Seq. #35: ch11D5g1

```
1     GAGGTGCAACTTCAGGAGTCAGGACCTGGCCTTGTGAAACCCTCACAGT   50
51    CACTCTCCCTCACCTGTTCTGTCACTGGTTATTCCATCACTAGTAATTA   100
101   CTGGGGCTGGATCCGGAAGTTCCCAGGAAATAAAATGGAGTGGATTGGA   150
151   CACATAACCAACAGTGGTAACACTACCTACAATCCATCTCTCAAAAGTC   200
201   GAATCTCCATTAGTAGAGACACATCGAGGAATCAGTTCTTCCTGCAGTT   250
251   GAACTCTGTGACTACTGAGGACACAGCCACATATTACTGTGCAAAAGGA   300
301   GCGTTT                                              350
351   GATTACTGGGGCCAAGGAGTCATGGTCACTGTCAGCTCAGCGTCCACCA   400
401   AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGG   450
451   GGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG   500
500   GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCT   550
551   TCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT   600
601   GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG   650
651   AATCAC                                              700
701   AAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTG   750
751   ACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGG   800
800   ACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC   850
851   TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG   900
901   ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAA   950
951   TGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTG   1000
1001  GTCAGC                                              1050
1051  GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGT   1100
1101  GCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC   1150
1151  CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA   1200
1200  TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA   1250
1251  AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA   1300
1301  GCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGC
      TCCTTC
      TTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
      ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC
      GCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
```

Seq. #36: ch11D5g2

```
1       GAGGTGCAACTTCAGGAGTCAGGACCTGGCCTTGTGAAACCCTCACAGT   50
51      CACTCTCCCTCACCTGTTCTGTCACTGGTTATTCCATCACTAGTAATTA   100
101     CTGGGGCTGGATCCGGAAGTTCCCAGGAAATAAAATGGAGTGGATTGGA   150
151     CACATAACCAACAGTGGTAACACTACCTACAATCCATCTCTCAAAAGTC   200
201     GAATCTCCATTAGTAGAGACACATCGAGGAATCAGTTCTTCCTGCAGTT   250
251     GAACTCTGTGACTACTGAGGACACAGCCACATATTACTGTGCAAAAGGA   300
301     GCGTTT                                              350
351     GATTACTGGGGCCAAGGAGTCATGGTCACTGTCAGCTCAGCGTCCACCA   400
401     AGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGA   450
451     GAGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG   500
500     GTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCT   550
551     TCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT   600
601     GACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTA   650
651     GATCAC                                              700
701     AAGCCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTG   750
751     TCGAGTGCCCACCGTGCCCAGCACCACCTGTGGCAGGACCGTCAGTCTT   800
800     CCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT   850
851     GAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCC   900
901     AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA   950
951     GCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTC   1000
1001    ACCGTT                                              1050
1051    GTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCA   1100
1101    ACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGG   1150
```

```
1151  GCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAG   1200
1200  ATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACC   1250
1251  CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAA   1300
1301  CTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTC
      TACAGC
      AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT
      GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCT
      CTCCCTGTCTCCGGGTAAATGA
```

Chimerizaion Amino acid segunces

Seq. #37: 11B7 LC kappa

```
1    D I Q M T Q A P S S L P A S L G D R V T I T C R A   25
25   S Q D I G N Y L R W F Q Q K P G K S P R L M I S G   50
51   A T N L A A G V P S R F S G S R S G S D Y S L T I   75
76   S S L E S E D M A D Y Y C L Q S K E S P W T F G G  100
101  G T K L E L K R T V A A P S V F I F P P S D E Q L  125
126  K S G T A S V V C L L N N F Y P R E A K V Q W K V  150
151  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  200
176  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  225
201  L S S P V T K S F N R G E C                       250
```

Seq. #38: 11B7-HCgamma1

```
1    E V Q L Q E S G P G L V K P S Q S L S L T C S V T   25
25   G Y S I T S N Y W G W I R K F P G D K M E W M G Y   50
51   I T Y S G S T S Y N P S L K S R I S I T R D T S K   75
76   N Q F F L Q L N S V T S E D T A T Y Y C A I T T F  100
101  Y Y W G Q G V M V T V S S A S T K G P S V F P L A  125
126  P S S K S T S G G T A A L G C L V K D Y F P E P V  150
151  T V S W N S G A L T S G V H T F P A V L Q S S G L  200
176  Y S L S S V V T V P S S S L G T Q T Y I C N V N H  225
201  K P S N T K V D K K V E P K S C D K T H T C P P C  250
226  P A P E L L G G P S V F L F P P K P K D T L M I S  275
251  R T P E V T C V V V D V S H E D P E V K F N W Y V  300
301  D G V E V H N A K T K P R E E Q Y N S T Y R V V S  325
326  V L T V L H Q D W L N G K E Y K C K V S N K A L P  350
350  A P I E K T I S K A K G Q P R E P Q V Y T L P P S  375
376  R D E L T K N Q V S L T C L V K G F Y P S D I A V  400
401  E W E S N G Q P E N N Y K T T P P V L D S D G S F  425
426  F L Y S K L T V D K S R W Q Q G N V F S C S V M H  450
451  E A L H N H Y T Q K S L S L S P G K
```

Seq. #39: 11B7 HC gamma2

```
1    E V Q L Q E S G P G L V K P S Q S L S L T C S V T   25
25   G Y S I T S N Y W G W I R K F P G D K M E W M G Y   50
51   I T Y S G S T S Y N P S L K S R I S I T R D T S K   75
76   N Q F F L Q L N S V T S E D T A T Y Y C A I T T F  100
101  Y Y W G Q G V M V T V S S A S T K G P S V F P L A  125
126  P C S R S T S E S T A A L G C L V K D Y F P E P V  150
151  T V S W N S G A L T S G V H T F P A V L Q S S G L  200
176  Y S L S S V V T V P S S N F G T Q T Y T C N V D H  225
201  K P S N T K V D K T V E R K C C V E C P P C P A P  250
226  P V A G P S V F L F P P K P K D T L M I S R T P E  275
251  V T C V V V D V S H E D P E V Q F N W Y V D G V E  300
301  V H N A K T K P R E E Q F N S T F R V V S V L T V  325
326  V H Q D W L N G K E Y K C K V S N K G L P A P I E  350
350  K T I S K T K G Q P R E P Q V Y T L P P S R E E M  375
376  T K N Q V S L T C L V K G F Y P S D I A V E W E S  400
401  N G Q P E N N Y K T T P P M L D S D G S F F L Y S  425
426  K L T V D K S R W Q Q G N V F S C S V M H E A L H  450
451  N H Y T Q K S L S L S P G K
```

Seq. #40: 11D5 LC kappa

```
1    D I Q M T Q S P S S M S T S L G D R V T I T C R A   25
25   S Q D I G N Y L S W F Q Q K V G K S P R R M I Y G   50
51   A I K L A V G V P S R F S G S R S G S D Y S L T I   75
76   S S L E S E D M A I Y Y C L Q Y I Q F P L T F G S  100
101  G T K L E L K R T V A A P S V F I F P P S D E Q L  125
126  K S G T A S V V C L L N N F Y P R E A K V Q W K V  150
151  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  200
176  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  225
201  L S S P V T K S F N R G E C                       250
```

Seq. #41: 11D5 HC gamma1

```
1    E V Q L Q E S G P G L V K P S Q S L S L T C S V T   25
25   G Y S I T S N Y W G W I R K F P G N K M E W I G H   50
51   I T N S G N T T Y N P S L K S R I S I S R D T S R   75
76   N Q F F L Q L N S V T T E D T A T Y Y C A K G A F  100
101  D Y W G Q G V M V T V S S A S T K G P S V F P L A  125
126  P S S K S T S G G T A A L G C L V K D Y F P E P V  150
151  T V S W N S G A L T S G V H T F P A V L Q S S G L  175
176  Y S L S S V V T V P S S S L G T Q T Y I C N V N H  200
201  K P S N T K V D K K V E P K S C D K T H T C P P C  225
226  P A P E L L G G P S V F L F P P K P K D T L M I S  250
251  R T P E V T C V V V D V S H E D P E V K F N W Y V  275
276  D G V E V H N A K T K P R E E Q Y N S T Y R V V S  300
301  V L T V L H Q D W L N G K E Y K C K V S N K A L P  325
326  A P I E K T I S K A K G Q P R E P Q V Y T L P P S  350
350  R D E L T K N Q V S L T C L V K G F Y P S D I A V  375
376  E W E S N G Q P E N N Y K T T P P V L D S D G S F  400
401  F L Y S K L T V D K S R W Q Q G N V F S C S V M H  425
426  E A L H N H Y T Q K S L S L S P G K               450
```

Seq. #42: 11D5 HC gamma2

```
1    E V Q L Q E S G P G L V K P S Q S L S L T C S V T   25
25   G Y S I T S N Y W G W I R K F P G N K M E W I G H   50
51   I T N S G N T T Y N P S L K S R I S I S R D T S R   75
76   N Q F F L Q L N S V T T E D T A T Y Y C A K G A F  100
101  D Y W G Q G V M V T V S S A S T K G P S V F P L A  125
126  P C S R S T S E S T A A L G C L V K D Y F P E P V  150
151  T V S W N S G A L T S G V H T F P A V L Q S S G L  200
176  Y S L S S V V T V P S S N F G T Q T Y T C N V D H  225
201  K P S N T K V D K T V E R K C C V E C P P C P A P  250
226  P V A G P S V F L F P P K P K D T L M I S R T P E  275
251  V T C V V V D V S H E D P E V Q F N W Y V D G V E  300
301  V H N A K T K P R E E Q F N S T F R V V S V L T V  325
326  V H Q D W L N G K E Y K C K V S N K G L P A P I E  350
350  K T I S K T K G Q P R E P Q V Y T L P P S R E E M  375
376  T K N Q V S L T C L V K G F Y P S D I A V E W E S  400
401  N G Q P E N N Y K T T P P M L D S D G S F F L Y S  425
426  K L T V D K S R W Q Q G N V F S C S V M H E A L H  450
451  N H Y T Q K S L S L S P G K
```

Humanization Amino Acid Sequnces

Seq. #43: Hum11B7-VLk:

```
1    M D M R V P A Q L L G L L L L W L R G A R C D I Q   25
25   M T Q S P S S L S A S V G D R V T I T C R A S Q D   50
51   I G N L R W Y Q Q K P G K A P K L L I Y G A T N L   75
76   A A G V P S R F S G S G S G T D F T L T I S S L Q  100
101  P E D F A T Y Y C L Q S K E S P W T F G Q G T K V  125
126  E I K                                             150
```

Seq. #44: Hum11B7-VH:

```
1    M K H L W F F L L L V A A P R W V L S Q V Q L Q E   25
25   S G P G L V K P S E T L S L T C T V S G G S I S S   50
51   N Y W G W I R Q P P G K G L E W I G Y I T Y S G S   75
76   T S Y N P S L K S R V T I S V D T S K N Q F S L K  100
101  L S S V T A A D T A V Y Y C A R T T F Y Y W G Q G  125
126  T L V T V S S                                     150
```

Seq. #46: Hum11D5-VLk:

```
1    M D M R V L A Q L L G L L L L C F P G A R C D I Q   25
25   M T Q S P S S L S A S V G D R V T I T C R A S Q D   50
51   I G N Y L S W F Q Q K P G K A P K S L I Y G A I K   75
76   L A V G V P S R F S G S G S G T D F T L T I S S L  100
101  Q P E D F A T Y Y C L Q Y I Q F P L T F G G G T K  125
126  V E I K                                           150
```

Seq. #45: Hum11D5-VH:

```
1    M K H L W F F L L L V A A P R W V L S Q V Q L Q E   25
25   S G P G L V K P S E T L S L T C T V S G G S I S S   50
51   N Y W G W I R Q P P G K G L E W I G H I T N S G N   75
76   T T Y N P S L K S RV T I S V D T S K N Q F S L K  100
101  L S S V T A A D T A V Y Y C A R G A F D Y W G Q G  125
126  T L V T V S S                                     150
```

Humanization nucleotide sequences

Seq. #47: Hum11B7-VLk (427 bp)

```
1    AATTAAAAGCTAGCAAGCTTGCCACCATGGATATGCGTGTACCTGCACA   50
51   GCTGTTAGGACTGCTTCTGCTCTGGCTTAGGGGAGCAAGATGCGACATC  100
101  CAGATGACTCAGAGCCCAAGCTCCTTGTCTGCCAGTGTGGGTGATAGGG  150
151  TCACCATAACCTGTCGAGCTTCACAGGATATCGGCAACTACCTACGCTG  200
201  GTATCAGCAGAAACCGGGCAAAGCCCCAAAGCTGCTGATCTATGGCGCC  250
251  ACCAATCTGGCTGCTGGTGTTCCCTCTCGGTTCAGTGGGTCTGGATCAG  300
301  GCACAGACTTCACACTCACCATTTCCAGCCTCCAACCCGAGGACTTTGC  350
351  GACGTACTACTGCTTGCAGTCCAAGGAATCCCCTTGGACATTTGGGCAA  400
401  GGGACTAAGGTGGAGATTAAGCGTACGAATTAAAA
```

Seq. #48: Hum11B7-VH (429 bp)

```
1    AATTAAGGTACCAAGCTTGCCACCATGAAGCACCTCTGGTTCTTTCTCC   50
51   TGCTAGTGGCTGCTCCTCGCTGGGTGTTGAGCCAGGTTCAGTTGCAGGA  100
101  ATCTGGACCAGGACTGGTCAAACCCTCTGAGACACTGTCACTGACATGC  150
151  ACT                                                200
201  GTGTCAGGTGGCTCCATTTCCTCCAACTATTGGGGCTGGATTCGGCAAC  250
251  CTCCGGGAAAAGGGCTTGAGTGGATAGGCTACATCACCTATTCTGGGAG  300
301  TACCTCCTACAATCCCAGTCTTAAGAGCAGGGTGACTATCAGCGTAGAC  350
351  ACC                                                400
401  TCCAAGAACCAGTTTAGCCTCAAGCTGAGTTCTGTGACTGCAGCGGATA
     CAGCCGTCTACTATTGTGCCAGAACCACGTTCTACTATTGGGGTCAGGG
     CACATTAGTCACCGTTAGCTCAGCGAATTAA
```

Seq. #49: Hum11D5-VLk (427 bp)

```
1    AATTAAAAGCTAGCAAGCTTGCCACCATGGATATGCGCGTCTTAGCCCA   50
51   ACTACTCGGTCTGCTTCTGTTGTGCTTTCCAGGAGCCAGGTGTGACATC  100
101  CAGATGACACAGTCCCCTAGTAGCCTGTCTGCGTCTGTAGGCGATCGAG  150
151  TGA                                                200
```

```
201   CCATTACCTGCAGAGCTTCCCAGGATATTGGCAACTATCTGAGCTGGTT   250
251   TCAGCAGAAACCAGGCAAAGCACCCAAGAGTCTCATCTATGGGGCCATC   300
301   AAGCTCGCTGTTGGTGTGCCTTCACGGTTTTCCGGATCTGGGTCAGGCA   350
351   CAG                                                 400
401   ACTTCACTCTGACCATTTCCAGCCTTCAACCGGAAGACTTCGCAACGTA
      CTACTGTCTGCAGTACATCCAGTTCCCCTTGACTTTCGGTGGAGGGACA
      AAGGTGGAGATAAAGCGTACGAATTAAAA
```

Seq. #50: Hum11D5-VH (429 bp)

```
1     AATTAAGGTACCAAGCTTGCCACCATGAAGCATCTGTGGTTCTTTCTGC    50
51    TGCTTGTGGCTGCTCCTAGGTGGGTGTTAAGCCAGGTTCAGCTCCAGGA   100
101   ATCTGGTCCCGGATTGGTGAAACCGAGTGAGACTCTATCCCTGACATGC   150
151   ACC                                                 200
201   GTTAGTGGAGGCAGTATCTCTAGCAACTATTGGGGCTGGATTCGGCAAC   250
251   CACCTGGTAAGGGCCTTGAGTGGATTGGGCACATCACCAACTCTGGGAA   300
301   TACCACCTACAATCCCTCCCTGAAATCACGCGTCACGATAAGCGTGGAC   350
351   ACT                                                 400
401   TCCAAGAACCAGTTCTCCCTCAAGCTCTCAAGCGTCACAGCAGCGGATA
      CAGCCGTATACTACTGTGCAAGAGGGGCCTTTGACTATTGGGGACAGGG
      CACATTGGTGACTGTCAGCTCAGCGAATTAA
```

Primer

SeqID No	Primer:	Sequence
#51	kappa_GSP1	GATGGATGCATTGGTGCAGC
#52	new_kappa_GSP1	ATAGATACAGTTGGTGCAGC
#53	heavy_GSP1	CAGGGTCACCATGGAGTTA
#54	XhoI-hGSP2	CCGCTCGAGCGGGCCAGTGGATAGACAGATGG
#55	XhoI-kGSP2	CCGCTCGAGCGGCCGTTTCAGCTCCAGCTTGG
#56	RT-gamma:	GCG TGT AGT GGT TGT GCA GAG
#57	RT-gamma2	GGG CTT GCC GGC CGT G
#58	RT-kappa	TGG AAC TGA GGA GCA GGT GG
#59	5´Blp	AGA TAA GCT TTG CTC AGC GTC CAC CAA GGG CCC ATC GGT
#60	3´Bam(GAG):	AGA TGG ATC CTC ATT TAC CCG GAG ACA GGG AGA G
#61	5´Bsi:	AGA TAA GCT TCG TAC GGT GGC TGC ACC ATC TGT CTT CAT
#62	3´Bam(CTT):	AGA TGG ATC CCT AAC ACT CTC CCC TGT TGA AGC TCT
#63	VL-11B7-5´:	AGA TAA GCT TGT GCA TTC CGA CAT CCA GAT GAC CCA GGC TCC
#64	VL-11B7-3´:	AGA TCG TAC GTT TCA GCT CCA GCT TGG TGC CTC
#65	VL-11D5-5´:	AGA TAA GCT TGT GCA TTC CGA CAT CCA GAT GAC CCA GTC TCC ATC
#66	VL-11D5-3´:	AGA TCG TAC GTT TCA GCT TGG TCC CAG
#67	VH-11B7/ 11D5-5´:	AGA TAA GCT TGT GCA TTC CGA GGT GCA GCT TCA GGA GTC AGG
#68	VH-11B7/ 11D5-3´:	AGA TGC TGA GCT GAC AGT GAC CAT GAC TCC TTG GCC
#69	MOUSE1	GCG AAT TCG CCA CCA TGG GCA GGG TCC CGC TGG CCT G
#70	MOUSE2	CAG CCG AGG TAT AGG CTG TCA CAG ACA CAG TCA G
#71	MOUSE3	GCA CCC TGT TAG GGT ACC GGC TGG CAT ATC
#72	MOUSE4	ATA AGA ATG CGG CCG CTC AGG CTC CGT CCT CCT GCC CTG
#73	CYNO1	AAT TCG CCA CCA TGG CGT GGC GGT GCC CCA G
#74	CYNO2	CTC TGA CCT CGT GCA GAT GGC AAT CTT CAT C
#75	CYNO3	GTG GCC GCT GCC TGT GTC CTC ATC
#76	CYNO4	ATA AGA ATG C GG CCG CTC AGG CAC CAT CCT CCT GCC CTG

#77	MER1	CGG AAT TCG CCA CCA TGG GGC CGG CCC CGC TGC CGC
#78	MER2	TCG GCT GCC ATT CTG GCC AAC TTC C
#79	SKY1	CGG AAT TCG CCA CCA TGG CGC TGA GGC GGA GC
#80	SKY2	GCC CTC GAG CTA ACA GCT ACT GTG TGG CAG TAG

Leader Squence

Nucleotide Sequence

Seq #81: 1 ATGGGTGACAATGACATCCACTTTGCCTTTCTCTCCACAGG TGTGCATTCC 52

Amino Acid Sequence

Seq #82: 1 M G D N D I H F A F L S T G V H S 17

Mouse and Cyno AXL

Seq #83: Cyno AXL nucleotide sequence

```
1     ATGGCGTGGCGGTGCCCCAGGATGGGCAGGGTCCCGCTGGCCTGGTGCT   50
51    TGGCGCTGTGCGGCTGGGTGTGCATGGCCCCCAGGGGCACACAGGCTGA  100
101   AGAAAGTCCTTTCGTGGGTAACCCAGGGAATATCACAGGTGCCCGGGGA  150
151   CTCACGGGCACCCTTCGGTGTCAGCTCCAGGTTCAGGGAGAGCCCCCCG  200
201   AGGTACACTGGCTTCGGGACGGACAGATCCTGGAGCTCGCGGACAGTAC  250
251   CCAGACCCAGGTGCCCCTGGGTGAAGATGAGCAGGATGACTGGATAGTG  300
301   GTCAGCCAGCTCAGAATCGCCTCCCTACAGCTTTCCGACGCGGGACAGT  350
351   ACCAGTGTTTGGTGTTTCTGGGACATCAGAACTTCGTGTCCCAGCCTGG  400
401   CTACGTAGGGCTGGAGGGCTTACCTTACTTCCTGGAGGAGCCTGAGGAC  450
451   AGGACTGTGGCCGCCAACACCCCCTTCAACCTGAGCTGCCAAGCCCAGG  500
501   GACCCCCAGAGCCCGTGGACCTACTCTGGCTCCAGGATGCTGTCCCCCT  550
551   GGCCACAGCTCCAGGTCATGGTCCCCAGCGCAACCTGCATGTTCCAGGG  600
601   CTGAACAAGACATCCTCTTTCTCCTGCGAAGCCCATAACGCCAAGGGAG  650
651   TCACCACATCCCGCACGGCCACCATCACAGTGCTCCCCCAGCAGCCCCG  700
701   TAACCTCCATCTGGTCTCCCGCCAACCCACGGAGCTGGAGGTGGCTTGG  750
751   ACTCCAGGCCTGAGCGGCATCTACCCCCTGACCCACTGCACCCTGCAGG  800
801   CTGTGCTGTCAGACGATGGGATGGGCATCCAGGCGGGAGAACCAGACCC  850
851   CCCAGAGGAGCCCCTCACCTTGCAAGCATCTGTGCCCCCCCACCAGCTT  900
901   CGGCTGGGCAGCCTCCATCCTCACACCCCTTATCACATCCGTGTGGCAT  950
951   GCACCAGCAGCCAGGGCCCCTCATCCTGGACACACTGGCTTCCTGTGGA 1000
1001  GACGCCGGAGGGAGTGCCCCTGGGCCCCCCTGAGAACATTAGTGCCACG 1050
1051  CGGAATGGGAGCCAGGCCTTCGTGCATTGGCAGGAGCCCCGGGCGCCCC 1100
1101  TGCAGGGTACCCTGTTAGGGTACCGGCTGGCGTATCAAGGCCAGGACAC 1150
1151  CCCAGAGGTGCTAATGGACATAGGGCTAAGGCAAGAGGTGACCCTGGAG 1200
1201  CTGCAGGGGGACGGGTCTGTGTCCAATCTGACAGTGTGTGTGGCAGCCT 1250
1251  ACACTGCTGCTGGGGATGGACCCTGGAGCCTCCCAGTACCCCTGGAGGC 1300
1301  CTGGCGCCCAGGGCAAGCACAGCCAGTCCACCAGCTGGTGAAGGAAACT 1350
1351  TCAGCTCCTGCCTTCTCGTGGCCCTGGTGGTATATACTGCTAGGAGCAG 1400
1401  TCGTGGCCGCTGCCTGTGTCCTCATCTTGGCTCTCTTCCTTGTCCACCG 1450
1451  GCGAAAGAAGGAGACCCGTTATGGAGAAGTGTTCGAGCCAACAGTGGAA 1500
1501  AGAGGTGAACTGGTAGTCAGGTACCGCGTGCGCAAGTCCTACAGTCGCC 1550
1551  GGACCACTGAAGCTACCTTGAACAGCCTGGGCATCAGTGAAGAGCTGAA 1600
1601  GGAGAAGCTGCGGGATGTGATGGTGGACCGGCACAAGGTGGCCCTGGGG 1650
1651  AAGACTCTGGGAGAAGGAGAGTTTGGAGCCGTGATGGAAGGCCAGCTCA 1700
1701  ACCAGGACGACTCCATCCTCAAGGTGGCTGTGAAGACAATGAAGATTGC 1750
1751  CATCTGCACAAGGTCAGAGCTGGAGGATTTCCTGAGTGAAGCAGTCTGC 1800
1801  ATGAAGGAATTCGACCATCCCAATGTCATGAGGCTCATCGGTGTCTGTT 1850
1851  TCCAGGGTTCTGAACGAGAGAGCTTTCCAGCACCTGTGGTCATCTTACC 1900
1901  TTTCATGAAGCATGGAGACCTACACAGCTTCCTCCTCTATTCCCGGCTT 1950
1951  GGGGACCAGCCAGTGTACCTGCCCACTCAGATGCTAGTGAAGTTCATGG 2000
2001  CGGACATCGCCAGTGGCATGGAATATCTGAGTACCAAGAGATTCATACA 2050
2051  CCGGGACCTGGCGGCCAGGAACTGCATGCTGAATGAGAACATGTCCGTG 2100
2101  TGTGTGGCGGACTTCGGGCTCTCCAAGAAGATCTACAACGGGGACTACT 2150
2151  ACCGCCAGGGACGTATCGCCAAGATGCCAGTCAAGTGGATTGCCATTGA 2200
2201  GAGTCTAGCTGACCGTGTCTACACGAGCAAGAGTGATGTGTGGTCCTTC 2250
2251  GGGGTGACAATGTGGGAGATTGCCACAAGAGGCCAAACCCCATATCCAG 2300
2301  GCGTGGAGAACAGCGAGATTTATGACTATCTGCGCCAGGGAAATCGCCT 2350
2351  GAAGCAGCCTGCGGACTGTCTGGATGGACTGTATGCCTTGATGTCGCGG 2400
```

```
2401  TGCTGGGAGCTAAATCCCCAGGACCGGCCAAGTTTTACAGAGCTGCGGG   2450
2451  AAGATTTGGAGAACACACTGAAGGCCTTGCCTCCTGCCCAGGAGCCTGA   2500
2501  CGAAATCCTCTATGTCAACATGGATGAAGGTGGAGGTTATCCTGAACCT   2550
2551  CCCGGCGCTGCTGGAGGAGCTGACCCCCCAACCCAGCTAGACCCTAAGG   2600
2601  ATTCCTGTAGCTGCCTCACTTCGGCTGAGGTCCATCCTGCTGGACGCTA   2650
2651  TGTCCTCTGCCCTTCCACAGCCCCTAGCCCCGCTCAGCCTGCTGATAGG
      GGCTCCCCAGCAGCCCCAGGGCAGGAGGATGGTGCC
```

Seq #84: Cyno AXL amino acid sequence

```
1     MAWRCPRMGRVPLAWCLALCGWVCMAPRGTQAEESPFVGNPGNITGARG    50
51    LTGTLRCQLQVQGEPPEVHWLRDGQILELADSTQTQVPLGEDEQDDWIV   100
101   VSQLRIASLQLSDAGQYQCLVFLGHQNFVSQPGYVGLEGLPYFLEEPED   150
151   RTVAANTPFNLSCQAQGPPEPVDLLWLQDAVPLATAPGHGPQRNLHVPG   200
201   LNKTSSFSCEAHNAKGVTTSRTATITVLPQQPRNLHLVSRQPTELEVAW   250
251   TPGLSGIYPLTHCTLQAVLSDDGMGIQAGEPDPPEEPLTLQASVPPHQL   300
301   RLGSLHPHTPYHIRVACTSSQGPSSWTHWLPVETPEGVPLGPPENISAT   350
351   RNGSQAFVHWQEPRAPLQGTLLGYRLAYQGQDTPEVLMDIGLRQEVTLE   400
401   LQGDGSVSNLTVCVAAYTAAGDGPWSLPVPLEAWRPGQAQPVHQLVKET   450
451   SAPAFSWPWWYILLGAVVAAACVLILALFLVHRRKKETRYGEVFEPTVE   500
501   RGELVVRYRVRKSYSRRTTEATLNSLGISEELKEKLRDVMVDRHKVALG   550
551   KTLGEGEFGAVMEGQLNQDDSILKVAVKTMKIAICTRSELEDFLSEAVC   600
601   MKEFDHPNVMRLIGVCFQGSERESFPAPVVILPFMKHGDLHSFLLYSRL   650
651   GDQPVYLPTQMLVKFMADIASGMEYLSTKRFIHRDLAARNCMLNENMSV   700
701   CVADFGLSKKIYNGDYYRQGRIAKMPVKWIAIESLADRVYTSKSDVWSF   750
751   GVTMWEIATRGQTPYPGVENSEIYDYLRQGNRLKQPADCLDGLYALMSR   800
801   CWELNPQDRPSFTELREDLENTLKALPPAQEPDEILYVNMDEGGGYPEP   850
851   PGAAGGADPPTQLDPKDSCSCLTSAEVHPAGRYVLCPSTAPSPAQPADR   900
      GSPAAPGQEDGA
```

SEQUENCE LISTING

<110> U3 Pharma AG

<120> AXL antibodies

<130> 41800P WO

<140> PCT/EP2008/009548
<141> 2008-11-12

<160> 84

<170> PatentIn version 3.3

<210> 1
<211> 324
<212> DNA
<213> Artificial

<220>
<223> Rat-11B7-VLkappa-clone 33

<400> 1
gacatccaga tgacccaggc tccatcttcc ctgcctgcat ctctgggaga cagagtcact 60

attacttgcc gggcaagcca agacattgga aattatttaa gatggttcca gcagaaaccg 120

gggaaatctc ctaggcttat gatttctggt gcaaccaact tggcagctgg ggtcccatca 180

aggttcagtg gcagtaggtc tgggtcagat tattctctga ccatcagcag cctggagtct 240

gaagatatgg cagactatta ctgtctacag tctaaagagt ccccttggac gttcggtgga 300

ggcaccaagc tggagctgaa acgg 324

<210> 2
<211> 338
<212> DNA
<213> Artificial

<220>
<223> Rat-11B7-VH-clone 20

<400> 2
gaggtgcagc ttcaggagtc aggacctggc cttgtgaaac cctcacagtc actctccctc 60

actgttctgt cactggttac tccatcacta gtaattactg gggctggatc cggaagttcc 120

caggagataa aatggagtgg atgggataca taacctacag tggtagcact agctacaacc 180

catctctcaa aagtcgaatc tccattacta gagacacatc gaagaatcag ttcttcctgc 240

agttgaactc tgtaacttct gaggacacag ccacatatta ctgtgctata acaacctttt 300

attactgggg ccaaggagtc atggtcactg tctcctca 338

<210> 3
<211> 324

<212> DNA
<213> Artificial

<220>
<223> Rat-11D5-VLkappa-clone 10

<400> 3
gacatccaga tgacccagtc tccatcctcc atgtctacat ctctgggaga cagagtcact 60

attacttgcc gggcaagtca agacattgga aattatttaa gctggttcca acagaaagta 120

gggaaatctc ctaggcgtat gatttatggt gcaatcaagt tggcagttgg ggtcccatca 180

aggttcagtg gaagtaggtc tggatcagat tattctctga ccatcagcag cctggagtct 240

gaagatatgg cgatctatta ctgtctacag tatatacagt ttccgctcac gttcggttct 300

gggaccaagc tggagctgaa acgg 324

<210> 4
<211> 339
<212> DNA
<213> Artificial

<220>
<223> Rat-11D5-VH-clone 66

<400> 4
gaggtgcaac ttcaggagtc aggacctggc cttgtgaaac cctcacagtc actctccctc 60

acctgttctg tcactggtta ttccatcact agtaattact ggggctggat ccggaagttc 120

ccaggaaata aaatggagtg gattggacac ataaccaaca gtggtaacac tacctacaat 180

ccatctctca aaagtcgaat ctccattagt agagacacat cgaggaatca gttcttcctg 240

cagttgaact ctgtgactac tgaggacaca gccacatatt actgtgcaaa aggagcgttt 300

gattactggg gccaaggagt catggtcaca gtctcgtca 339

<210> 5
<211> 324
<212> DNA
<213> Artificial

<220>
<223> Rat-10D12-VLkappa-clone 8

<400> 5
gacatccaga tgacccaggc tccatcttcc ctgcctgcat ctctgggaga cagagtcact 60

attgcttgcc gggcaagcca agacattgga aattatttaa gatggttcca gcagaaaccg 120

gggaaatctc ctaggcttat gatttctggt gcaaccaact tggcagctgg ggtcccatca 180

aggttcagtg gcagtaggtc tgggtcagat tattctcgga ccatcagcag cctggagtct 240

gaagatatgg cagactatta ctgtctacag tctaaagagt ccccttggac gttcggtgga 300

ggcaccaagc tggagctgaa acgg 324

<210> 6
<211> 336
<212> DNA
<213> Artificial

<220>
<223> Rat-10D12-VH-clone 5

<400> 6
gaggtgcagc ttcaggagtc aggacctggc cttgtgaagc cctcacagtc actctccctc 60

acctgctctg tcaccggtta ctccatcact agtaattact ggggctggat ccggaagttc 120

ccaggaaata aaatggagtg gatgggatac ataaccaaca gtggtggcac tgcctacaac 180

ccatctctca aaagtcgaat ctccattact agagacacat cgaagaatca gttcttcctg 240

caattgaact ctgtaattcc tgaggactca gccacatact tctgttcaag aacccccctgg 300

gactggggcc aaggagtcat ggtcacagtc tcctca 336

<210> 7
<211> 108
<212> PRT
<213> Artificial

<220>
<223> AXL antibody amino acid sequence Rat-11B7-VLkappa-clone 33

<400> 7

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr
20 25 30

Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Met Ile
35 40 45

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

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

Glu Asp Met Ala Asp Tyr Tyr Cys Leu Gln Ser Lys Glu Ser Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg
100 105

<210> 8
<211> 113
<212> PRT
<213> Artificial

<220>
<223> AXL amino acid sequence Rat-11B7-VH-clone 20

<400> 8

Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asn
20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asp Lys Met Glu Trp Met
35 40 45

Gly Tyr Ile Thr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu Lys
50 55 60

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

Gln Leu Asn Ser Val Thr Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Ile Thr Thr Phe Tyr Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110

Ser

<210> 9
<211> 108
<212> PRT
<213> Artificial

<220>
<223> AXL antibody amino acid sequence Rat-11D5-VLkappa-clone 10

<400> 9

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr
20 25 30

Leu Ser Trp Phe Gln Gln Lys Val Gly Lys Ser Pro Arg Arg Met Ile
35 40 45

Tyr Gly Ala Ile Lys Leu Ala Val Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

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

Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Arg
100 105

<210> 10
<211> 113
<212> PRT
<213> Artificial

<220>
<223> AXL antibody amino acid sequence Rat-11D5-VH-clone 66

<400> 10

Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asn
20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met Glu Trp Ile
35 40 45

Gly His Ile Thr Asn Ser Gly Asn Thr Thr Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Ile Ser Ile Ser Arg Asp Thr Ser Arg Asn Gln Phe Phe Leu
65 70 75 80

Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Lys Gly Ala Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110

Ser

<210> 11
<211> 108
<212> PRT
<213> Artificial

<220>
<223> AXL antibody amino acid sequence Rat-10D12-VLkappa-clone 8

<400> 11

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

Asp Arg Val Thr Ile Ala Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr
20 25 30

Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Met Ile
35 40 45

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

Ser Arg Ser Gly Ser Asp Tyr Ser Arg Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

Glu Asp Met Ala Asp Tyr Tyr Cys Leu Gln Ser Lys Glu Ser Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg
100 105

<210> 12
<211> 112
<212> PRT
<213> Artificial

<220>
<223> AXL antibody amino acid sequence Rat-10D12-VH-clone 5

<400> 12

Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asn
20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met Glu Trp Met
35 40 45

Gly Tyr Ile Thr Asn Ser Gly Gly Thr Ala Tyr Asn Pro Ser Leu Lys
50 55 60

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

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

Arg Thr Pro Trp Asp Trp Gly Gln Gly Val Met Val Thr Val Ser Ser
100 105 110

<210> 13
<211> 11
<212> PRT
<213> Artificial

<220>
<223> 11B7 light chain CDR 1

<400> 13

Arg Ala Ser Gln Asp Ile Gly Asn Tyr Leu Arg
1 5 10

<210> 14
<211> 7
<212> PRT
<213> Artificial

<220>
<223> 11B7 light chain CDR 2

<400> 14

Gly Ala Thr Asn Leu Ala Ala
1 5

<210> 15
<211> 9
<212> PRT
<213> Artificial

<220>
<223> 11B7 light chain CDR 3

<400> 15

Leu Gln Ser Lys Glu Ser Pro Trp Thr
1 5

<210> 16
<211> 5

<212> PRT
<213> Artificial

<220>
<223> 11B7 heavy chain CDR 1

<400> 16

Ser Asn Tyr Trp Gly
1 5

<210> 17
<211> 16
<212> PRT
<213> Artificial

<220>
<223> 11B7 heavy chain CDR 2

<400> 17

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

<210> 18
<211> 5
<212> PRT
<213> Artificial

<220>
<223> 11B7 heavy chain CDR 3

<400> 18

Thr Thr Phe Tyr Tyr
1 5

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

<220>
<223> 11D5 light chain CDR 1

<400> 19

Arg Ala Ser Gln Asp Ile Gly Asn Tyr Leu Ser
1 5 10

<210> 20
<211> 7
<212> PRT
<213> Artificial

<220>
<223> 11D5 light chain CDR 2

<400> 20

Gly Ala Ile Lys Leu Ala Val
1 5

<210> 21
<211> 9
<212> PRT
<213> Artificial

<220>
<223> 11D5 light chain CDR 3

<400> 21

Leu Gln Tyr Ile Gln Phe Pro Leu Thr
1 5

<210> 22
<211> 5
<212> PRT
<213> Artificial

<220>
<223> 11D5 heavy chain CDR 1

<400> 22

Ser Asn Tyr Trp Gly
1 5

<210> 23
<211> 16
<212> PRT
<213> Artificial

<220>
<223> 11D5 heavy chain CDR 2

<400> 23

His Ile Thr Asn Ser Gly Asn Thr Thr Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 24
<211> 5
<212> PRT
<213> Artificial

<220>
<223> 11D5 heavy chain CDR 3

<400> 24

Gly Ala Phe Asp Tyr
1 5

<210> 25
<211> 11
<212> PRT
<213> Artificial

<220>
<223> 10D12 light chain CDR 1

<400> 25

Arg Ala Ser Gln Asp Ile Gly Asn Tyr Leu Arg
1 5 10

<210> 26
<211> 7
<212> PRT
<213> Artificial

<220>
<223> 10D12 light chain CDR2

<400> 26

Gly Ala Thr Asn Leu Ala Ala
1 5

<210> 27
<211> 9
<212> PRT
<213> Artificial

<220>
<223> 10D12 light chain CDR3

<400> 27

Leu Gln Ser Lys Glu Ser Pro Trp Thr
1 5

<210> 28
<211> 5
<212> PRT
<213> Artificial

<220>
<223> 10D12 heavy chain CDR1

<400> 28

Ser Asn Tyr Trp Gly
1 5

<210> 29
<211> 16
<212> PRT

<213> Artificial

<220>
<223> 10D12 heavy chain CDR2

<400> 29

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

<210> 30
<211> 4
<212> PRT
<213> Artificial

<220>
<223> 10D12 heavy chain CDR3

<400> 30

Thr Pro Trp Asp
1

<210> 31
<211> 645
<212> DNA
<213> Artificial

<220>
<223> ch11B7k

<400> 31
gacatccaga tgacccaggc tccatcttcc ctgcctgcat ctctgggaga cagagtcact 60

attacttgcc gggcaagcca agacattgga aattatttaa gatggttcca gcagaaaccg 120

gggaaatctc ctaggcttat gatttctggt gcaaccaact tggcagctgg ggtcccatca 180

aggttcagtg gcagtaggtc tgggtcagat tattctctga ccatcagcag cctggagtct 240

gaagatatgg cagactatta ctgtctacag tctaaagagt ccccttggac gttcggtgga 300

ggcaccaagc tggagctgaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 645

<210> 32
<211> 1332
<212> DNA
<213> Artificial

<220>
<223> ch11B7g1

<400> 32
gaggtgcagc ttcaggagtc aggacctggc cttgtgaaac cctcacagtc actctccctc 60

acctgttctg tcactggtta ctccatcact agtaattact ggggctggat ccggaagttc 120

ccaggagata aaatggagtg gatgggatac ataacctaca gtggtagcac tagctacaac 180

ccatctctca aaagtcgaat ctccattact agagacacat cgaagaatca gttcttcctg 240

cagttgaact ctgtaacttc tgaggacaca gccacatatt actgtgctat aacaaccttt 300

tattactggg gccaaggagt catggtcact gtcagctcag cgtccaccaa gggcccatcg 360

gtcttccccc tggcaccctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 420

ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc 480

agcggcgtgc acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc 540

gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 600

aagcccagca acaccaaggt ggacaagaaa gttgagccca aatcttgtga caaaactcac 660

acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtctt cctcttcccc 720

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 780

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg ggtggtcagt 900

cgtcctcacc gtcctgcacc aggactggct gaatggcaag gagtacaagg caaggtctcc 960

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1260

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1320

ccgggtaaat ga 1332

<210> 33
<211> 1320
<212> DNA
<213> Artificial

<220>
<223> ch11B7g2

<400> 33

gaggtgcagc ttcaggagtc aggacctggc cttgtgaaac cctcacagtc actctccctc 60

acctgttctg tcactggtta ctccatcact agtaattact ggggctggat ccggaagttc 120

ccaggagata aaatggagtg gatgggatac ataacctaca gtggtagcac tagctacaac 180

ccatctctca aaagtcgaat ctccattact agagacacat cgaagaatca gttcttcctg 240

cagttgaact ctgtaacttc tgaggacaca gccacatatt actgtgctat aacaaccttt 300

tattactggg gccaaggagt catggtcact gtcagctcag cgtccaccaa gggcccatcg 360

gtcttccccc tggcgccctg ctccaggagc acctccgaga gcacagccgc cctgggctgc 420

ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgctctgacc 480

agcggcgtgc acaccttccc agctgtccta cagtcctcag gactctactc cctcagcagc 540

gtggtgaccg tgccctccag caacttcggc acccagacct acacctgcaa cgtagatcac 600

aagcccagca acaccaaggt ggacaagaca gttgagcgca aatgttgtgt cgagtgccca 660

ccgtgcccag caccacctgt ggcaggaccg tcagtcttcc tcttcccccc aaaacccaag 720

gacaccctca tgatctcccg gacccctgag gtcacgtgcg tggtggtgga cgtgagccac 780

gaagaccccg aggtccagtt caactggtac gtggacggcg tggaggtgca taatgccaag 840

acaaagccac gggaggagca gttcaacagc acgttccgtg tggtcagcgt cctcaccgtt 900

gtgcaccagg actggctgaa cggcaaggag tacaagtgca aggtctccaa caaaggcctc 960

ccagccccca tcgagaaaac catctccaaa accaaagggc agccccgaga accacaggtg 1020

tacaccctgc ccccatcccg ggaggagatg accaagaacc aggtcagcct gacctgcctg 1080

gtcaaaggct tctaccccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1140

aacaactaca agaccacacc tcccatgctg gactccgacg gctccttctt cctctacagc 1200

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1260

catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaatga 1320

<210> 34
<211> 645
<212> DNA
<213> Artificial

<220>
<223> ch11D5k

<400> 34
gacatccaga tgacccagtc tccatcctcc atgtctacat ctctgggaga cagagtcacc 60

attacttgcc gggcaagtca agacattgga aattatttaa gctggttcca acagaaagta 120

gggaaatctc ctaggcgtat gatttatggt gcaatcaagt tggcagttgg ggtcccatca 180

aggttcagtg gaagtaggtc tggatcagat tattctctga ccatcagcag cctggagtct 240

gaagatatgg cgatctatta ctgtctacag tatatacagt ttccgctcac gttcggttct 300

gggaccaagc tggagctgaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag 645

<210> 35
<211> 1332
<212> DNA
<213> Artificial

<220>
<223> ch11D5g1

<400> 35
gaggtgcaac ttcaggagtc aggacctggc cttgtgaaac cctcacagtc actctccctc 60

acctgttctg tcactggtta ttccatcact agtaattact ggggctggat ccggaagttc 120

ccaggaaata aaatggagtg gattggacac ataaccaaca gtggtaacac tacctacaat 180

ccatctctca aaagtcgaat ctccattagt agagacacat cgaggaatca gttcttcctg 240

cagttgaact ctgtgactac tgaggacaca gccacatatt actgtgcaaa aggagcgttt 300

gattactggg gccaaggagt catggtcact gtcagctcag cgtccaccaa gggcccatcg 360

gtcttccccc tggcaccctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 420

ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc 480

agcggcgtgc acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc 540

gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 600

aagcccagca acaccaaggt ggacaagaaa gttgagccca aatcttgtga caaaactcac 660

acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtctt cctcttcccc 720

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 780

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg ggtggtcagc 900

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 960

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1260

tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1320

ccgggtaaat ga 1332

<210> 36
<211> 1320
<212> DNA
<213> Artificial

<220>
<223> ch11D5g2

<400> 36
gaggtgcaac ttcaggagtc aggacctggc cttgtgaaac cctcacagtc actctccctc 60

acctgttctg tcactggtta ttccatcact agtaattact ggggctggat ccggaagttc 120

ccaggaaata aaatggagtg gattggacac ataaccaaca gtggtaacac tacctacaat 180

ccatctctca aaagtcgaat ctccattagt agagacacat cgaggaatca gttcttcctg 240

cagttgaact ctgtgactac tgaggacaca gccacatatt actgtgcaaa aggagcgttt 300

gattactggg gccaaggagt catggtcact gtcagctcag cgtccaccaa gggcccatcg 360

gtcttccccc tggcgccctg ctccaggagc acctccgaga gcacagccgc cctgggctgc 420

ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgctctgacc 480

agcggcgtgc acaccttccc agctgtccta cagtcctcag gactctactc cctcagcagc 540

gtggtgaccg tgccctccag caacttcggc acccagacct acacctgcaa cgtagatcac 600

aagcccagca acaccaaggt ggacaagaca gttgagcgca aatgttgtgt cgagtgccca 660

ccgtgcccag caccacctgt ggcaggaccg tcagtcttcc tcttcccccc aaaacccaag 720

gacaccctca tgatctcccg gacccctgag gtcacgtgcg tggtggtgga cgtgagccac 780

gaagaccccg aggtccagtt caactggtac gtggacggcg tggaggtgca taatgccaag 840

acaaagccac gggaggagca gttcaacagc acgttccgtg tggtcagcgt cctcaccgtt 900

gtgcaccagg actggctgaa cggcaaggag tacaagtgca aggtctccaa caaaggcctc 960

ccagccccca tcgagaaaac catctccaaa accaaagggc agccccgaga accacaggtg 1020

tacaccctgc ccccatcccg ggaggagatg accaagaacc aggtcagcct gacctgcctg 1080

gtcaaaggct tctaccccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag 1140

aacaactaca agaccacacc tcccatgctg gactccgacg gctccttctt cctctacagc 1200

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1260

catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaatga 1320

<210> 37
<211> 214
<212> PRT
<213> Artificial

<220>
<223> 11B7 LC kappa

<400> 37

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr
20 25 30

Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Met Ile
35 40 45

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

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

Glu Asp Met Ala Asp Tyr Tyr Cys Leu Gln Ser Lys Glu Ser Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 38
<211> 443
<212> PRT
<213> Artificial

<220>
<223> 11B7-HCgamma1

<400> 38

Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asn
20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asp Lys Met Glu Trp Met
35 40 45

Gly Tyr Ile Thr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu Lys
50 55 60

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

Gln Leu Asn Ser Val Thr Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Ile Thr Thr Phe Tyr Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
115 120 125

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
165 170 175

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
180 185 190

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
195 200 205

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
210 215 220

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
245 250 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305 310 315 320

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
340 345 350

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 39
<211> 439
<212> PRT
<213> Artificial

<220>
<223> 11B7 HC gamma2

<400> 39

Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asn
20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asp Lys Met Glu Trp Met
35 40 45

Gly Tyr Ile Thr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu Lys
50 55 60

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

Gln Leu Asn Ser Val Thr Ser Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Ile Thr Thr Phe Tyr Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser
115 120 125

Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
165 170 175

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln
180 185 190

Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp
195 200 205

Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala
210 215 220

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
245 250 255

Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
260 265 270

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
275 280 285

Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp
290 295 300

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
305 310 315 320

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg
325 330 335

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
340 345 350

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
355 360 365

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
370 375 380

Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
385 390 395 400

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
405 410 415

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
420 425 430

Leu Ser Leu Ser Pro Gly Lys
435

<210> 40
<211> 214
<212> PRT
<213> Artificial

<220>
<223> 11D5 LC kappa

<400> 40

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr
20 25 30

Leu Ser Trp Phe Gln Gln Lys Val Gly Lys Ser Pro Arg Arg Met Ile
35 40 45

Tyr Gly Ala Ile Lys Leu Ala Val Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

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

Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

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

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 41
<211> 443
<212> PRT
<213> Artificial

<220>
<223> 11D5 HC gamma1

<400> 41

Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asn
20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met Glu Trp Ile
35 40 45

Gly His Ile Thr Asn Ser Gly Asn Thr Thr Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Ile Ser Ile Ser Arg Asp Thr Ser Arg Asn Gln Phe Phe Leu
65 70 75 80

Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Lys Gly Ala Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
115 120 125

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr

145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
165 170 175

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
180 185 190

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
195 200 205

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
210 215 220

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
245 250 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305 310 315 320

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
340 345 350

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 42
<211> 439
<212> PRT
<213> Artificial

<220>
<223> 11D5 HC gamma2

<400> 42

Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Asn
20 25 30

Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met Glu Trp Ile
35 40 45

Gly His Ile Thr Asn Ser Gly Asn Thr Thr Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Ile Ser Ile Ser Arg Asp Thr Ser Arg Asn Gln Phe Phe Leu
65 70 75 80

Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Lys Gly Ala Phe Asp Tyr Trp Gly Gln Gly Val Met Val Thr Val Ser
100 105 110

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser
115 120 125

Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr

145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
165 170 175

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln
180 185 190

Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp
195 200 205

Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala
210 215 220

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

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
245 250 255

Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
260 265 270

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
275 280 285

Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp
290 295 300

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
305 310 315 320

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg
325 330 335

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
340 345 350

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
355 360 365

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
370 375 380

Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
385 390 395 400

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
405 410 415

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
420 425 430

Leu Ser Leu Ser Pro Gly Lys
435

<210> 43
<211> 128
<212> PRT
<213> Artificial

<220>
<223> Hum11B7-VLk

<400> 43

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

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

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

Gln Asp Ile Gly Asn Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50 55 60

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

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

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

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

<210> 44
<211> 132
<212> PRT
<213> Artificial

<220>
<223> Hum11B7-VH

<400> 44

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

Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
35 40 45

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

Glu Trp Ile Gly Tyr Ile Thr Tyr Ser Gly Ser Thr Ser Tyr Asn Pro
65 70 75 80

Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
85 90 95

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
100 105 110

Tyr Cys Ala Arg Thr Thr Phe Tyr Tyr Trp Gly Gln Gly Thr Leu Val
115 120 125

Thr Val Ser Ser
130

<210> 45
<211> 132
<212> PRT
<213> Artificial

<220>
<223> Hum11D5-VH

<400> 45

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

Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
35 40 45

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

Glu Trp Ile Gly His Ile Thr Asn Ser Gly Asn Thr Thr Tyr Asn Pro
65 70 75 80

Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
85 90 95

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
100 105 110

Tyr Cys Ala Arg Gly Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
115 120 125

Thr Val Ser Ser
130

<210> 46
<211> 129
<212> PRT
<213> Artificial

<220>
<223> Hum11D5-VLk

<400> 46

Met Asp Met Arg Val Leu Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys
1 5 10 15

Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

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

Gln Asp Ile Gly Asn Tyr Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Ser Leu Ile Tyr Gly Ala Ile Lys Leu Ala Val Gly Val
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln

100 105 110

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

Lys

<210> 47
<211> 427
<212> DNA
<213> Artificial

<220>
<223> Hum11B7-VLk

<400> 47
aattaaaagc tagcaagctt gccaccatgg atatgcgtgt acctgcacag ctgttaggac 60

tgcttctgct ctggcttagg ggagcaagat gcgacatcca gatgactcag agcccaagct 120

ccttgtctgc cagtgtgggt gatagggtca ccataacctg tcgagcttca caggatatcg 180

gcaactacct acgctggtat cagcagaaac cgggcaaagc cccaaagctg ctgatctatg 240

gcgccaccaa tctggctgct ggtgttccct ctcggttcag tgggtctgga tcaggcacag 300

acttcacact caccatttcc agcctccaac ccgaggactt tgcgacgtac tactgcttgc 360

agtccaagga atccccttgg acatttgggc aagggactaa ggtggagatt aagcgtacga 420

attaaaa 427

<210> 48
<211> 429
<212> DNA
<213> Artificial

<220>
<223> Hum11B7-VH

<400> 48
aattaaggta ccaagcttgc caccatgaag cacctctggt tctttctcct gctagtggct 60

gctcctcgct gggtgttgag ccaggttcag ttgcaggaat ctggaccagg actggtcaaa 120

ccctctgaga cactgtcact gacatgcact gtgtcaggtg gctccatttc ctccaactat 180

tggggctgga ttcggcaacc tccgggaaaa gggcttgagt ggataggcta catcacctat 240

tctgggagta cctcctacaa tcccagtctt aagagcaggg tgactatcag cgtagacacc 300

tccaagaacc agtttagcct caagctgagt tctgtgactg cagcggatac agccgtctac 360

tattgtgcca gaaccacgtt ctactattgg ggtcagggca cattagtcac cgttagctca 420

gcgaattaa 429

<210> 49
<211> 427
<212> DNA
<213> Artificial

<220>
<223> Hum11D5-VLk

<400> 49
aattaaaagc tagcaagctt gccaccatgg atatgcgcgt cttagcccaa ctactcggtc 60

tgcttctgtt gtgctttcca ggagccaggt gtgacatcca gatgacacag tcccctagta 120

gcctgtctgc gtctgtaggc gatcgagtga ccattacctg cagagcttcc caggatattg 180

gcaactatct gagctggttt cagcagaaac caggcaaagc acccaagagt ctcatctatg 240

gggccatcaa gctcgctgtt ggtgtgcctt cacggttttc cggatctggg tcaggcacag 300

acttcactct gaccatttcc agccttcaac cggaagactt cgcaacgtac tactgtctgc 360

agtacatcca gttccccttg actttcggtg gagggacaaa ggtggagata aagcgtacga 420

attaaaa 427

<210> 50
<211> 429
<212> DNA
<213> Artificial

<220>
<223> Hum11D5-VH

<400> 50
aattaaggta ccaagcttgc caccatgaag catctgtggt tctttctgct gcttgtggct 60

gctcctaggt gggtgttaag ccaggttcag ctccaggaat ctggtcccgg attggtgaaa 120

ccgagtgaga ctctatccct gacatgcacc gttagtggag gcagtatctc tagcaactat 180

tggggctgga ttcggcaacc acctggtaag ggccttgagt ggattgggca catcaccaac 240

tctgggaata ccacctacaa tccctccctg aaatcacgcg tcacgataag cgtggacact 300

tccaagaacc agttctccct caagctctca agcgtcacag cagcggatac agccgtatac 360

tactgtgcaa gaggggcctt tgactattgg ggacagggca cattggtgac tgtcagctca 420

gcgaattaa 429

<210> 51
<211> 20
<212> DNA
<213> Artificial

<220>
<223> primer kappa_GSP1

<400> 51
gatggatgca ttggtgcagc 20

<210> 52
<211> 20
<212> DNA
<213> Artificial

<220>
<223> primer new_kappa_GSP1

<400> 52
atagatacag ttggtgcagc 20

<210> 53
<211> 19
<212> DNA
<213> Artificial

<220>
<223> primer heavy_GSP1

<400> 53
cagggtcacc atggagtta 19

<210> 54
<211> 32
<212> DNA
<213> Artificial

<220>
<223> primer XhoI-hGSP2

<400> 54
ccgctcgagc ggccgtttca gctccagctt gg 32

<210> 55
<211> 32
<212> DNA
<213> Artificial

<220>
<223> primer XhoI-hGSP2

<400> 55
ccgctcgagc gggccagtgg atagacagat gg 32

<210> 56
<211> 21
<212> DNA
<213> Artificial

<220>
<223> primer RT-gamma

<400> 56
gcgtgtagtg gttgtgcaga g 21

<210> 57
<211> 16
<212> DNA
<213> Artificial

<220>
<223> primer RT-gamma2

<400> 57
gggcttgccg gccgtg 16

<210> 58
<211> 20
<212> DNA
<213> Artificial

<220>
<223> primer RT-kappa

<400> 58
tggaactgag gagcaggtgg 20

<210> 59
<211> 39
<212> DNA
<213> Artificial

<220>
<223> primer 5' Blp

<400> 59
agataagctt tgctcagcgt ccaccaaggg cccatcggt 39

<210> 60
<211> 34
<212> DNA
<213> Artificial

<220>
<223> primer 3' Bam(GAG)

<400> 60
agatggatcc tcatttaccc ggagacaggg agag 34

<210> 61
<211> 39
<212> DNA
<213> Artificial

<220>
<223> primer 5' Bsi:

<400> 61

agataagctt cgtacggtgg ctgcaccatc tgtcttcat 39

<210> 62
<211> 36
<212> DNA
<213> Artificial

<220>
<223> primer 3' Bam(CTT)

<400> 62
agatggatcc ctaacactct cccctgttga agctct 36

<210> 63
<211> 42
<212> DNA
<213> Artificial

<220>
<223> primer VL-11B7-5'

<400> 63
agataagctt gtgcattccg acatccagat gacccaggct cc 42

<210> 64
<211> 33
<212> DNA
<213> Artificial

<220>
<223> primer VL-11B7-3'

<400> 64
agatcgtacg tttcagctcc agcttggtgc ctc 33

<210> 65
<211> 45
<212> DNA
<213> Artificial

<220>
<223> primer VL-11D5-5'

<400> 65
agataagctt gtgcattccg acatccagat gacccagtct ccatc 45

<210> 66
<211> 27
<212> DNA
<213> Artificial

<220>
<223> primer VL-11D5-3'

<400> 66
agatcgtacg tttcagcttg gtcccag 27

<210> 67
<211> 42
<212> DNA
<213> Artificial

<220>
<223> primer VH-11B7/11D5-5'

<400> 67
agataagctt gtgcattccg aggtgcagct tcaggagtca gg 42

<210> 68
<211> 36
<212> DNA
<213> Artificial

<220>
<223> primer VH-11B7/11D5-3'

<400> 68
agatgctgag ctgacagtga ccatgactcc ttggcc 36

<210> 69
<211> 37
<212> DNA
<213> Artificial

<220>
<223> primer MOUSE1

<400> 69
gcgaattcgc caccatgggc agggtcccgc tggcctg 37

<210> 70
<211> 34
<212> DNA
<213> Artificial

<220>
<223> primer MOUSE2

<400> 70
cagccgaggt ataggctgtc acagacacag tcag 34

<210> 71
<211> 30
<212> DNA
<213> Artificial

<220>
<223> primer MOUSE3

<400> 71
gcaccctgtt agggtaccgg ctggcatatc 30

<210> 72
<211> 39
<212> DNA
<213> Artificial

<220>
<223> primer MOUSE4

<400> 72
ataagaatgc ggccgctcag gctccgtcct cctgccctg 39

<210> 73
<211> 31
<212> DNA
<213> Artificial

<220>
<223> primer CYNO1

<400> 73
aattcgccac catggcgtgg cggtgcccca g 31

<210> 74
<211> 31
<212> DNA
<213> Artificial

<220>
<223> primer CYNO2

<400> 74
ctctgacctc gtgcagatgg caatcttcat c 31

<210> 75
<211> 24
<212> DNA
<213> Artificial

<220>
<223> primer CYNO3

<400> 75
gtggccgctg cctgtgtcct catc 24

<210> 76
<211> 39
<212> DNA
<213> Artificial

<220>
<223> primer CYNO4

<400> 76
ataagaatgc ggccgctcag gcaccatcct cctgccctg 39

<210> 77
<211> 36
<212> DNA
<213> Artificial

<220>
<223> primer MER1

<400> 77
cggaattcgc caccatgggg ccggccccgc tgccgc 36

<210> 78
<211> 25
<212> DNA
<213> Artificial

<220>
<223> MER2

<400> 78
tcggctgcca ttctggccaa cttcc 25

<210> 79
<211> 32
<212> DNA
<213> Artificial

<220>
<223> primer SKY1

<400> 79
cggaattcgc caccatggcg ctgaggcgga gc 32

<210> 80
<211> 33
<212> DNA
<213> Artificial

<220>
<223> primer SKY2

<400> 80
gccctcgagc taacagctac tgtgtggcag tag 33

<210> 81
<211> 51
<212> DNA
<213> Artificial

<220>
<223> leader sequence

<400> 81
atgggtgaca atgacatcca ctttgccttt ctctccacag gtgtgcattc c 51

<210> 82

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

<220>
<223> leader sequence

<400> 82

Met Gly Asp Asn Asp Ile His Phe Ala Phe Leu Ser Thr Gly Val His
1 5 10 15

Ser

<210> 83
<211> 2682
<212> DNA
<213> Macaca fascicularis

<400> 83
atggcgtggc ggtgccccag gatgggcagg gtcccgctgg cctggtgctt ggcgctgtgc 60

ggctgggtgt gcatggcccc caggggcaca caggctgaag aaagtccttt cgtgggtaac 120

ccagggaata tcacaggtgc ccggggactc acgggcaccc ttcggtgtca gctccaggtt 180

cagggagagc cccccgaggt acactggctt cgggacggac agatcctgga gctcgcggac 240

agtacccaga cccaggtgcc cctgggtgaa gatgagcagg atgactggat agtggtcagc 300

cagctcagaa tcgcctccct acagctttcc gacgcgggac agtaccagtg tttggtgttt 360

ctgggacatc agaacttcgt gtcccagcct ggctacgtag ggctggaggg cttaccttac 420

ttcctggagg agcctgagga caggactgtg gccgccaaca ccccccttcaa cctgagctgc 480

caagcccagg gacccccaga gcccgtggac ctactctggc tccaggatgc tgtcccccctg 540

gccacagctc caggtcatgg tccccagcgc aacctgcatg ttccagggct gaacaagaca 600

tcctctttct cctgcgaagc ccataacgcc aagggagtca ccacatcccg cacggccacc 660

atcacagtgc tcccccagca gccccgtaac ctccatctgg tctcccgcca acccacggag 720

ctggaggtgg cttggactcc aggcctgagc ggcatctacc ccctgaccca ctgcaccctg 780

caggctgtgc tgtcagacga tgggatgggc atccaggcgg gagaaccaga ccccccagag 840

gagcccctca ccttgcaagc atctgtgccc ccccaccagc ttcggctggg cagcctccat 900

cctcacaccc cttatcacat ccgtgtggca tgcaccagca gccagggccc ctcatcctgg 960

acacactggc ttcctgtgga gacgccggag ggagtgcccc tgggcccccc tgagaacatt 1020

agtgccacgc ggaatgggag ccaggccttc gtgcattggc aggagccccg ggcgcccctg 1080

cagggtaccc tgttagggta ccggctggcg tatcaaggcc aggacacccc agaggtgcta 1140

atggacatag ggctaaggca agaggtgacc ctggagctgc agggggacgg gtctgtgtcc 1200

aatctgacag tgtgtgtggc agcctacact gctgctgggg atggaccctg gagcctccca 1260

gtacccctgg aggcctggcg cccagggcaa gcacagccag tccaccagct ggtgaaggaa 1320

acttcagctc ctgccttctc gtggccctgg tggtatatac tgctaggagc agtcgtggcc 1380

gctgcctgtg tcctcatctt ggctctcttc cttgtccacc ggcgaaagaa ggagacccgt 1440

tatggagaag tgttcgagcc aacagtggaa agaggtgaac tggtagtcag gtaccgcgtg 1500

cgcaagtcct acagtcgccg gaccactgaa gctaccttga acagcctggg catcagtgaa 1560

gagctgaagg agaagctgcg ggatgtgatg gtggaccggc acaaggtggc cctggggaag 1620

actctgggag aaggagagtt tggagccgtg atggaaggcc agctcaacca ggacgactcc 1680

atcctcaagg tggctgtgaa gacaatgaag attgccatct gcacaaggtc agagctggag 1740

gatttcctga gtgaagcagt ctgcatgaag gaattcgacc atcccaatgt catgaggctc 1800

atcggtgtct gtttccaggg ttctgaacga gagagctttc cagcacctgt ggtcatctta 1860

cctttcatga agcatggaga cctacacagc ttcctcctct attcccggct tggggaccag 1920

ccagtgtacc tgcccactca gatgctagtg aagttcatgg cggacatcgc cagtggcatg 1980

gaatatctga gtaccaagag attcatacac cgggacctgg cggccaggaa ctgcatgctg 2040

aatgagaaca tgtccgtgtg tgtggcggac ttcgggctct ccaagaagat ctacaacggg 2100

gactactacc gccagggacg tatcgccaag atgccagtca agtggattgc cattgagagt 2160

ctagctgacc gtgtctacac gagcaagagt gatgtgtggt ccttcggggt gacaatgtgg 2220

gagattgcca caagaggcca aaccccatat ccaggcgtgg agaacagcga gatttatgac 2280

tatctgcgcc agggaaatcg cctgaagcag cctgcggact gtctggatgg actgtatgcc 2340

ttgatgtcgc ggtgctggga gctaaatccc caggaccggc caagttttac agagctgcgg 2400

gaagatttgg agaacacact gaaggccttg cctcctgccc aggagcctga cgaaatcctc 2460

tatgtcaaca tggatgaagg tggaggttat cctgaacctc ccggcgctgc tggaggagct 2520

gacccccaa cccagctaga ccctaaggat tcctgtagct gcctcacttc ggctgaggtc 2580

catcctgctg gacgctatgt cctctgccct tccacagccc ctagccccgc tcagcctgct 2640

gataggggct ccccagcagc cccagggcag gaggatggtg cc 2682

<210> 84
<211> 894
<212> PRT
<213> Macaca fascicularis

<400> 84

Met Ala Trp Arg Cys Pro Arg Met Gly Arg Val Pro Leu Ala Trp Cys

1 5 10 15

Leu Ala Leu Cys Gly Trp Val Cys Met Ala Pro Arg Gly Thr Gln Ala
20 25 30

Glu Glu Ser Pro Phe Val Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg
35 40 45

Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln Val Gln Gly Glu Pro
50 55 60

Pro Glu Val His Trp Leu Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp
65 70 75 80

Ser Thr Gln Thr Gln Val Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp
85 90 95

Ile Val Val Ser Gln Leu Arg Ile Ala Ser Leu Gln Leu Ser Asp Ala
100 105 110

Gly Gln Tyr Gln Cys Leu Val Phe Leu Gly His Gln Asn Phe Val Ser
115 120 125

Gln Pro Gly Tyr Val Gly Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu
130 135 140

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

Gln Ala Gln Gly Pro Pro Glu Pro Val Asp Leu Leu Trp Leu Gln Asp
165 170 175

Ala Val Pro Leu Ala Thr Ala Pro Gly His Gly Pro Gln Arg Asn Leu
180 185 190

His Val Pro Gly Leu Asn Lys Thr Ser Ser Phe Ser Cys Glu Ala His
195 200 205

Asn Ala Lys Gly Val Thr Thr Ser Arg Thr Ala Thr Ile Thr Val Leu
210 215 220

Pro Gln Gln Pro Arg Asn Leu His Leu Val Ser Arg Gln Pro Thr Glu
225 230 235 240

Leu Glu Val Ala Trp Thr Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr
245 250 255

His Cys Thr Leu Gln Ala Val Leu Ser Asp Asp Gly Met Gly Ile Gln
260 265 270

Ala Gly Glu Pro Asp Pro Pro Glu Glu Pro Leu Thr Leu Gln Ala Ser
275 280 285

Val Pro Pro His Gln Leu Arg Leu Gly Ser Leu His Pro His Thr Pro
290 295 300

Tyr His Ile Arg Val Ala Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp
305 310 315 320

Thr His Trp Leu Pro Val Glu Thr Pro Glu Gly Val Pro Leu Gly Pro
325 330 335

Pro Glu Asn Ile Ser Ala Thr Arg Asn Gly Ser Gln Ala Phe Val His
340 345 350

Trp Gln Glu Pro Arg Ala Pro Leu Gln Gly Thr Leu Leu Gly Tyr Arg
355 360 365

Leu Ala Tyr Gln Gly Gln Asp Thr Pro Glu Val Leu Met Asp Ile Gly
370 375 380

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

Asn Leu Thr Val Cys Val Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro
405 410 415

Trp Ser Leu Pro Val Pro Leu Glu Ala Trp Arg Pro Gly Gln Ala Gln
420 425 430

Pro Val His Gln Leu Val Lys Glu Thr Ser Ala Pro Ala Phe Ser Trp
435 440 445

Pro Trp Trp Tyr Ile Leu Leu Gly Ala Val Val Ala Ala Ala Cys Val
450 455 460

Leu Ile Leu Ala Leu Phe Leu Val His Arg Arg Lys Lys Glu Thr Arg
465 470 475 480

Tyr Gly Glu Val Phe Glu Pro Thr Val Glu Arg Gly Glu Leu Val Val
485 490 495

Arg Tyr Arg Val Arg Lys Ser Tyr Ser Arg Arg Thr Thr Glu Ala Thr
500 505 510

Leu Asn Ser Leu Gly Ile Ser Glu Glu Leu Lys Glu Lys Leu Arg Asp
515 520 525

Val Met Val Asp Arg His Lys Val Ala Leu Gly Lys Thr Leu Gly Glu
530 535 540

Gly Glu Phe Gly Ala Val Met Glu Gly Gln Leu Asn Gln Asp Asp Ser
545 550 555 560

Ile Leu Lys Val Ala Val Lys Thr Met Lys Ile Ala Ile Cys Thr Arg
565 570 575

Ser Glu Leu Glu Asp Phe Leu Ser Glu Ala Val Cys Met Lys Glu Phe
580 585 590

Asp His Pro Asn Val Met Arg Leu Ile Gly Val Cys Phe Gln Gly Ser
595 600 605

Glu Arg Glu Ser Phe Pro Ala Pro Val Val Ile Leu Pro Phe Met Lys
610 615 620

His Gly Asp Leu His Ser Phe Leu Leu Tyr Ser Arg Leu Gly Asp Gln
625 630 635 640

Pro Val Tyr Leu Pro Thr Gln Met Leu Val Lys Phe Met Ala Asp Ile
645 650 655

Ala Ser Gly Met Glu Tyr Leu Ser Thr Lys Arg Phe Ile His Arg Asp
660 665 670

Leu Ala Ala Arg Asn Cys Met Leu Asn Glu Asn Met Ser Val Cys Val
675 680 685

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

Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala Ile Glu Ser
705 710 715 720

Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp Ser Phe Gly
725 730 735

Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly
740 745 750

Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu
755 760 765

Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg
770 775 780

Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg
785 790 795 800

Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro Ala Gln Glu Pro
805 810 815

Asp Glu Ile Leu Tyr Val Asn Met Asp Glu Gly Gly Gly Tyr Pro Glu
820 825 830

Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr Gln Leu Asp Pro
835 840 845

Lys Asp Ser Cys Ser Cys Leu Thr Ser Ala Glu Val His Pro Ala Gly
850 855 860

Arg Tyr Val Leu Cys Pro Ser Thr Ala Pro Ser Pro Ala Gln Pro Ala
865 870 875 880

Asp Arg Gly Ser Pro Ala Ala Pro Gly Gln Glu Asp Gly Ala
885 890