

AXL Antibody Nucleotide sequence:**Seq. #1: Rat-11B7-VLkappa-clone 33:**

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

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

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

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

1	GACATCCAGATGACCCAGTCTCCATCCTCCATGTCTACATCTCTGGGAG	50
51	ACAGAGTCACTATTACTTGCCGGGCAAGTCAAGACATTGGAAATTATTT	100
101	AAGCTGGTTCCAACAGAAAGTAGGGGAAATCTCCTAGGCGTATGATTTAT	150
151	GGTGCAATCAAGTTGGCAGTTGGGGTCCCATCAAGGTTCAAGTGGAAAGTA	200
201	GGTCTGGATCAGATTATTCTCTGACCATCAGCAGCCTGGAGTCTGAAGA	250
251	TATGGCGATCTATTACTGTCTACAGTATATACAGTTTCCGCTCACGTTT	300
301	GGTTCT GGGACCAAGCTGGAGCTGAAACGG	350

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

1	GAGGTGCAACTTCAGGAGTCAGGACCTGGCCTTGTGAAACCCCTCACAGT	50
51	CACTCTCCCTCACCTGTTCTGTCACTGGTTATTCCATCACTAGTAATTA	100
101	CTGGGGCTGGATCCGGAAGTTCCCAGGAAATAAAATGGAGTGGATTGGA	150
151	CACATAACCAACAGTGGTAACACTACCTACAATCCATCTCTCAAAAGTC	200
201	GAATCTCCATTAGTAGAGACACATCGAGGAATCAGTTCTTCCTGCAGTT	250
251	GAACCTCTGTGACTACTGAGGACACAGCCACATATTACTGTGCAAAAGGA	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	GATNLAAGVPSRFSGSRSGSDYSLTISSELESEDMADYYCLQSKESPWTF	100
101	GGGTKLELKR	150

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

1	EVQLQESGPGLVKPSQSLSLTCSVTGYSITSNYWGWIRKFPQDKMEWMG	50
51	YITYSGSTSYNPSLKSRIISITRDTSKNQFFLQLNSVTSEDATATYYCAIT	100
101	TFYYWGQGVMVTVSS	150

11D5:

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

1	DIQMTQSPSSMSTSLGDRVTITCRASQDIGNYLSWFQQKVGKSPRRMIY	50
51	GAIKLAVGVPSRFSGSRSGSDYSLTISSELESEDMAIYYCLQYIQFPLTF	100
101	GSGTKLELKR	150

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

1	EVQLQESGPGLVKPSQSLSLTCSVTGYSITSNYWGWIRKFPQGNKMEWIG	50
51	HITNSGNTTYNPSLKSRIISIRDTSRNQFFLQLNSVTTEDATATYYCAKG	100
101	AFDYWGQGVMVTVSS	150

10D12:

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

1	DIQMTQAPSSLPASLGDRVTIACRASQDIGNYLRWFQQKPGKSPRLMIS	50
51	GATNLAAGVPSRFSGSRSGSDYSRTISSELESEDMADYYCLQSKESPWTF	100
101	GGGTKLELKR	150

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

1	EVQLQESGPGLVKPSQSLTCSVTGYSITSNYWGWIRKFPGNKMEWMG	50
51	YITNSGGTAYNPSLKSRI SITRDTSKNQFFLQLNSVIPEDSATYFCSRT	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	GGTGCAACCAACTTGGCAGCTGGGGTCCCATCAAGGTTCAAGTGGCAGTA	200
201	GGTCTGGGTCAGATTATTCTCTGACCATCAGCAGCCTGGAGTCTGAAGA	250
251	TATG	300
301	GCAGACTATTACTGTCTACAGTCTAAAGAGTCCCCTTGGACGTTTCGGTG	350
351	GAGGCACCAAGCTGGAGCTGAAACGTACGGTGGCTGCACCATCTGTCTT	400
401	CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTT	450
451	GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGA	500
500	AGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGA	550
551	GCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTG	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	AGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGG	450
451	GGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG	500
500	GTGACGGTGTTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCT	550
551	TCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT	600
601	GACCGTGCCTTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG	650
651	AATCAC	700
701	AAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTG	750
751	ACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGG	800
800	ACCGTCAGTCTTCCTCTTCCCCCCTAAAACCAAGGACACCCCTCATGATC	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	GCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGC	
	TCCTTC	
	TTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGA	
	ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC	
	GCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA	

Seq. #33: ch11B7g2

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

Seq. #34: ch11D5k

1	GACATCCAGATGACCCAGTCTCCATCCTCCATGTCTACATCTCTGGGAG	50
51	ACAGAGTCACCATTACTTGCCGGGCAAGTCAAGACATTGGAAATTATTT	100

101	AAGCTGGTTCCAACAGAAAGTAGGGAAATCTCCTAGGCGTATGATTTAT	150
151	GGTGCAATCAAGTTGGCAGTTGGGGTCCCATCAAGGTTTCAGTGGAAGTA	200
201	GGTCTGGATCAGATTATTCTCTGACCATCAGCAGCCTGGAGTCTGAAGA	250
251	TATG	300
301	GCGATCTATTACTGTCTACAGTATATACAGTTTCCGCTCACGTTTCGGTT	350
351	CTGGGACCAAGCTGGAGCTGAAACGTACGGTGGCTGCACCATCTGTCTT	400
401	CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTT	450
451	GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGA	500
500	AGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGA	550
551	GCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTG	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	GAATCTGTGACTACTGAGGACACAGCCACATATTACTGTGCAAAAGGA	300
301	GCGTTT	350
351	GATTACTGGGGCCAAGGAGTCATGGTCACTGTCAGCTCAGCGTCCACCA	400
401	AGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGG	450
451	GGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG	500
500	GTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCT	550
551	TCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT	600
601	GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG	650
651	AATCAC	700
701	AAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTG	750
751	ACAAAACCTACACATGCCACCGTGCCAGCACCTGAATCCTGGGGGG	800
800	ACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATC	850
851	TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG	900
901	ACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGCATAA	950
951	TGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTG	1000
1001	GTCAGC	1050
1051	GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGT	1100
1101	GCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC	1150
1151	CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA	1200
1200	TCCCGGGATGAGCTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCA	1250
1251	AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA	1300
1301	GCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGC	
	TCCTTC	
	TTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGA	
	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	GTGACGGTGTCGTGGAACCTCAGGCGCTCTGACCAGCGGCGTGCACACCT	550
551	TCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT	600
601	GACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTA	650
651	GATCAC	700
701	AAGCCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTG	750
751	TCGAGTGCCACCGTGCCAGCACCACTGTGGCAGGACCGTCAGTCTT	800
800	CCTCTTCCCCCCTCAAGGACACCCCTCATGATCTCCCGGACCCCT	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 sequeces

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 Sequences

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 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 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	AATTA AAAAGCTAGCAAGCTTGCCACCATGGATATGCGTGTA CCTGCACA	50
51	GCTGT TAGGACTGCTTCTGCTCTGGCTTAGGGGAGCAAGATGCGACATC	100
101	CAGATGACTCAGAGCCCAAGCTCCTTGTCTGCCAGTGTGGGTGATAGGG	150
151	TCACCATAACCTGTCGAGCTTCACAGGATATCGGCAACTACCTACGCTG	200
201	GTATCAGCAGAAACCGGGCAAAGCCCCAAAGCTGCTGATCTATGGCGCC	250
251	ACCAATCTGGCTGCTGGTGTTCCTCTCGGTTCA GTGGGTCTGGATCAG	300
301	GCACAGACTTCACACTCACCATTTCAGCCTCCAACCCGAGGACTTTGC	350
351	GACGTACTACTGCTTGCAGTCCAAGGAATCCCCTTGGACATTTGGGCAA	400
401	GGGACTAAGGTGGAGATTAAGCGTACGAATTAAAA	

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

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

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

1	AATTA AAAAGCTAGCAAGC TTGCCACCATGGATATGCGCGTCTTAGCCCA	50
51	ACTACTCGGTCTGCTTCTGTTGTGCTTTCCAGGAGCCAGGTGTGACATC	100
101	CAGATGACACAGTCCCCCTAGTAGCCTGTCTGCGTCTGTAGGCGATCGAG	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	TGCTTGTGGCTGCTCCTAGGTGGGTGTTAAGCCAGGTTTCAGCTCCAGGA	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 Sequence

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	AGAAAGTCCTTTTCGTGGGTAACCCAGGGAATATCACAGGTGCCCGGGGA	150
151	CTCACGGGCACCCCTTCGGTGTGAGCTCCAGGTTTCAGGGAGAGCCCCCG	200
201	AGGTACACTGGCTTCGGGACGGACAGATCCTGGAGCTCGCGGACAGTAC	250
251	CCAGACCCAGGTGCCCCCTGGGTGAAGATGAGCAGGATGACTGGATAGTG	300
301	GTCAGCCAGCTCAGAATCGCCTCCCTACAGCTTTCGACGCGGGACAGT	350
351	ACCAGTGTTCGGTGTTCCTGGGACATCAGAACTTCGTGTCCCAGCCTGG	400
401	CTACGTAGGGCTGGAGGGCTTACCTTACTTCCTGGAGGAGCCTGAGGAC	450
451	AGGACTGTGGCCGCCAACACCCCCCTTCAACCTGAGCTGCCAAGCCAGG	500
501	GACCCCCAGAGCCCGTGGACCTACTCTGGCTCCAGGATGCTGTCCCCCT	550
551	GGCCACAGCTCCAGGTCATGGTCCCCAGCGCAACCTGCATGTTCCAGGG	600
601	CTGAACAAGACATCCTCTTTCTCCTGCGAAGCCCATAACGCCAAGGGAG	650
651	TCACCACATCCCGCACGGCCACCATCACAGTGCTCCCCCAGCAGCCCCG	700
701	TAACCTCCATCTGGTCTCCCGCCAACCCACGGAGCTGGAGGTGGCTTGG	750
751	ACTCCAGGCCTGAGCGGCATCTACCCCTGACCCACTGCACCCTGCAGG	800
801	CTGTGCTGTGACAGATGGGATGGGCATCCAGGCGGGAGAACCAGACCC	850
851	CCCAGAGGAGCCCCCTCACCTTGCAAGCATCTGTGCCCCCCCCACCAGCTT	900
901	CGGCTGGGCAGCCTCCATCCTCACACCCCTTATCACATCCGTGTGGCAT	950
951	GCACCAGCAGCCAGGGCCCCCTCATCCTGGACACACTGGCTTCCTGTGGA	1000
1001	GACGCCGGAGGGAGTGCCCCCTGGGCCCCCTGAGAACATTAGTGCCACG	1050
1051	CGGAATGGGAGCCAGGCCTTCGTGCATTGGCAGGAGCCCCGGGCGCCCC	1100
1101	TGCAGGGTACCCTGTAGGGTACCGGCTGGCGTATCAAGGCCAGGACAC	1150
1151	CCCAGAGGTGCTAATGGACATAGGGCTAAGGCAAGAGGTGACCCTGGAG	1200
1201	CTGCAGGGGGACGGGTCTGTGTCCAATCTGACAGTGTGTGTGGCAGCCT	1250
1251	AACTGCTGCTGGGGATGGACCCTGGAGCCTCCCAGTACCCCTGGAGGC	1300
1301	CTGGCGCCCAGGGCAAGCACAGCCAGTCCACCAGCTGGTGAAGGAACT	1350
1351	TCAGCTCCTGCCTTCTCGTGGCCCTGGTGGTATATACTGCTAGGAGCAG	1400
1401	TCGTGGCCGCTGCCTGTGTCTCATCTTGGCTCTCTTCTTGTCCACCG	1450
1451	GCGAAAGAAGGAGACCCGTTATGGAGAAGTGTTTCGAGCCAACAGTGGA	1500
1501	AGAGGTGAACTGGTAGTCAGGTACCGCGTGCAGCAAGTCCTACAGTCGCC	1550
1551	GGACCACTGAAGCTACCTTGAACAGCCTGGGCATCAGTGAAGAGCTGAA	1600
1601	GGAGAAGCTGCGGGATGTGATGGTGGACCGGCACAAGGTGGCCCTGGGG	1650
1651	AAGACTCTGGGAGAAGGAGAGTTTGGAGCCGTGATGGAAGGCCAGCTCA	1700
1701	ACCAGGACGACTCCATCCTCAAGGTGGCTGTGAAGACAATGAAGATTGC	1750
1751	CATCTGCACAAGGTGAGAGCTGGAGGATTTCTGAGTGAAGCAGCTGTC	1800
1801	ATGAAGGAATTCGACCATCCCAATGTCATGAGGCTCATCGGTGTCTGTT	1850
1851	TCCAGGGTTCTGAACGAGAGAGCTTCCAGCACCTGTGGTCATCTTACC	1900
1901	TTTCATGAAGCATGGAGACCTACACAGCTTCCTCCTCTATTCCCGGCTT	1950
1951	GGGGACCAGCCAGTGTACCTGCCCACTCAGATGCTAGTGAAGTTCATGG	2000
2001	CGGACATCGCCAGTGGCATGGAATATCTGAGTACCAAGAGATTTCATACA	2050
2051	CCGGGACCTGGCGGCCAGGAAGTGCATGCTGAATGAGAACATGTCCGTG	2100
2101	TGTGTGGCGGACTTCGGGCTCTCCAAGAAGATCTACAACGGGGACTACT	2150
2151	ACCGCCAGGGACGTATCGCCAAGATGCCAGTCAAGTGGATTGCCATTGA	2200
2201	GAGTCTAGCTGACCGTGTCTACACGAGCAAGAGTGATGTGTGGTCTTTC	2250
2251	GGGGTGACAATGTGGGAGATTGCCACAAGAGGCCAAACCCCATATCCAG	2300
2301	GCGTGGAGAACAGCGAGATTTATGACTATCTGCGCCAGGGAAATCGCCT	2350
2351	GAAGCAGCCTGCGGACTGTCTGGATGGACTGTATGCCTTGATGTCGCGG	2400

2401	TGCTGGGAGCTAAATCCCCAGGACCGGCCAAGTTTTACAGAGCTGCGGG	2450
2451	AAGATTTGGAGAACACACTGAAGGCCTTGCCTCCTGCCCAGGAGCCTGA	2500
2501	CGAAATCCTCTATGTCAACATGGATGAAGGTGGAGGTTATCCTGAACCT	2550
2551	CCCGGCGCTGCTGGAGGAGCTGACCCCCCAACCCAGCTAGACCCTAAGG	2600
2601	ATTCTGTAGCTGCCTCACTTCGGCTGAGGTCCATCCTGCTGGACGCTA	2650
2651	TGTCCTCTGCCCTTCCACAGCCCCCTAGCCCCGCTCAGCCTGCTGATAGG	
	GGCTCCCCAGCAGCCCCAGGGCAGGAGGATGGTGCC	

Seq #84: Cyno AXL amino acid sequence

1	MAWRCPRMGRVPLAWCLALCGWVCMAPRGTAEESEPFVGNPGNITGARG	50
51	LTGTLRCQLQVQGEPPVHWLRDQILELADSTQTQVPLGEDEQDDWIV	100
101	VSQRLIASLQLSDAGQYQCLVFLGHQNFVSQPGYVGLEGLPYFLEPED	150
151	RTVAANTPFNLSCQAQGPPEPVDLLWLQDAVPLATAPGHGPQRNLHVP	200
201	LNKTSSFSCAHNAGVTTSRATITVLPQQPRNLHLVSRQPTELEVAW	250
251	TPGLSGIYPLTHCTLQAVLSDDGMGIQAGEPDPPPEEPLTLQASVPPHQL	300
301	RLGSLHPHTPYHIRVACTSSQGPSSWTHWLPVETPEGVPLGPPENISAT	350
351	RNGSQAFVHWQEPRAPLQGTLLGYRLAYQGQDTPEVLMDIGLRQEVTL	400
401	LQGDGSVSNLTVCVAAAYTAAGDGPWSLPVPLEAWRPGQAQPVHQLVKET	450
451	SAPAFSWPWWYILLGAVVAAACVLILALFLVHRRKKETRYGEVFEPTE	500
501	RGELVVRYRVRKSYSRRTTEATLNSLGISEELKEKLRDVMVDRHKVALG	550
551	KTLGEGEFGAVMEGQLNQDDSSILKVAVKTMKIAICTRSELEDFLSEAVC	600
601	MKEFDHPNVMRLIGVCFQGSERESFPAPVVILPFMKHGDLSFLLYSRL	650
651	GDQPVYLPTQMLVKFMADIASGMEYLSTKRFIHRDLAARNCMLNENMSV	700
701	CVADFGLSKKIYNGDYRQGRIAKMPVKWIAIESLADRVYTSKSDVWSF	750
751	GVTMWEIATRGTPTYPGVENSEIYDYLRQGNRLKQPADCLDGLYALMSR	800
801	CWELNPQDRPSFTELREDLENTLKALEPPAQEPDEILYVNMDEGGGYPEP	850
851	PGAAGGADPPTQLDPKDSCLTSAEVHPAGRYVLCSTAPSPAQPADR	900
	GSPAAPGQEDGA	