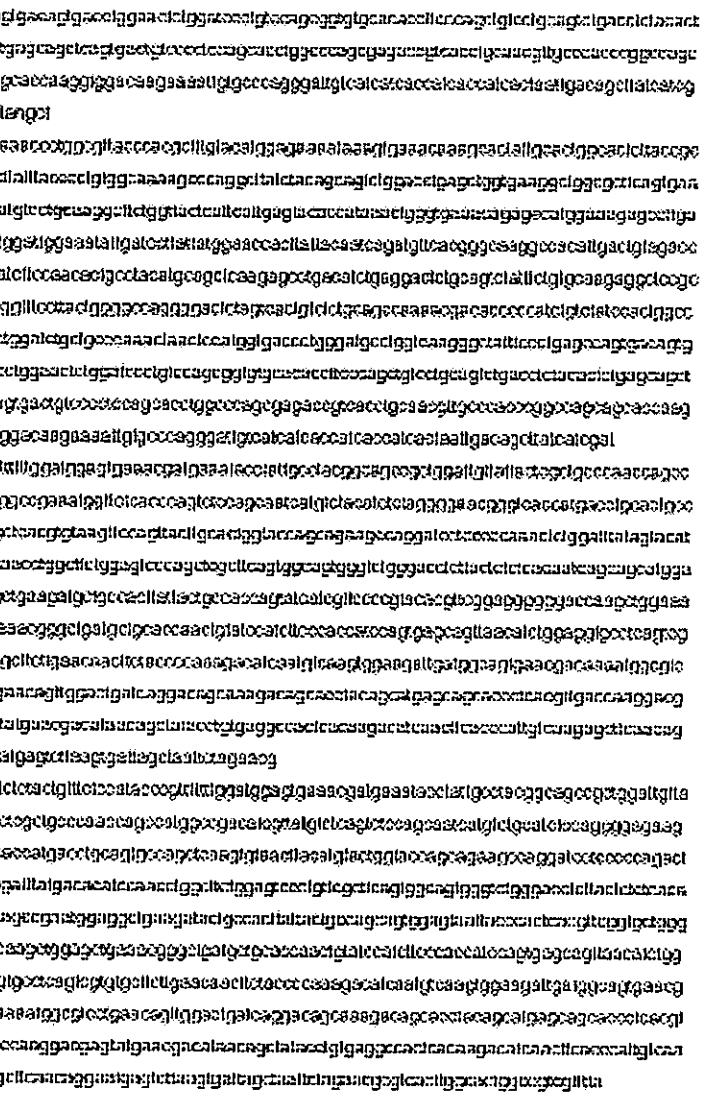
SEQUENCE LIST

SEQ ID No	Description	Sequence
1	aa VH_A1	MKQSTIALALLPLLFTPVAKAQVKLQQSGAELVRPGSSVKISCKASGYAFSNSWINWV KQRPGQGLEWIGQIYPGDYDTNYNGKFKGKATLTADYSSSTAYMQLNSLTSEDSAVY FCARGGSIYYGNLGFFDVWGAGTTVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCL VKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVA HPASSTKVDKKIVPRDCHHHHHHH
2	aa VH_A2	MKQSTIALALLPLLFTPVAKAQAYLQQSGPELVKAGASVKMSCKASGYSFIEYTINWVK QSHGKSLEWIGNIDPYYGTTYYNQMFTGKATLTVDQSSNTAYMQLKSLTSEDSAVYF CARGSAWFPYWGQGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPE PVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTK VDKKIVPRDCHHHHHHH
3	aa VK_A1	MKYLLPTAAAGLLLLAAQPAMAEMVLTQSPAIMSTSLGERVTMTCTASSRVSSSYLH WYQQKPGSSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQY HRSPYTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKI DGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVK SFNRNES
4	aa VK_A2	MKYLLPTAAAGLLLLAAQPAMADIVMSQSPAIMSASPGEKVTMTCSASSSVTYMYWY QQKPGSSPRLLIYDTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDTATYYCQQWSN YPLTFGAGTKLELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDG SERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNES
5	nt VH_A1	acgcttgtacatggagaaaataaagtgaaacaaagcactattgcactggcactcttaccgctcttatttacccctgtggca aaagcccaggtgaagcttcagcagtccggggctgagctggtgaggcctgggtcctcagtgaagatttcctgcaaggctt ctggctacgcattcagtaactcctggataaactgggtgaagcagaggcctggacagggtcttgagtggattggacagatt tatcctggagattatgatactaactacaatggaaaattcaagggtaaagccacactgactgcagactcctccagcac agcctacatgcagctcaacagcctaacatctgaggactctgcggtctatttctgtgcaagggggggatcgatctactatggt aacctcgggttcttcgatgtctgggcgcagggaccacggtcaccgtctcctcagccaaaacgacacccccatctgtcta tccactggcccctggatctgctgcccaaactaactccatggtgaccctgggatgcctggtcaagggctatttcctgagcc

6	nt VH_A2	
7	nt VK_A1	
8	nt VK_A2	
9	aa VH_CDR1_A1	GYAFSNSWINW
10	aa VH_CDR1_A2	GYSFIEYTINW
11	aa VH_CDR2_A1	GQIYPGDYDTNYNGKFK
12	aa VH_CDR2_A2	GNIDPYYGTTYYNQMFT
13	aa VH_CDR3_A1	ARGGSIYYGNLGFFDV
14	aa VH_CDR3_A2	ARGSAWFPY
15	aa VK_CDR1_A1	TASSRVSSSYLH
16	aa VK_CDR1_A2	SASSSVTYMY
17	aa VK_CDR2_A1	ST5NLAS
18	aa VK_CDR2_A2	DTSNLAS
19	aa VK_CDR3_A1	HQYHRSPYT
20	aa VK_CDR3_A2	QQWSNYPLT
21	nt VH_CDR1_A1	ggctacgcattcagtaactcctggataaactgg
22	nt VH_CDR1_A2	ggttactcattcattgaatacaccatcaactgg
23	nt VH_CDR2_A1	ggacagattttatcctggagattatgatactaactacaatgggaaattcaag
24	nt VH_CDR2_A2	ggaaatattgatccttattatggtaccacttatttcaatcagatgttcacg

25	nt VH_CDR3_A1	gcaagggagggatcgactactatggttacccctggttttgctgatgtc
26	nt VH_CDR3_A2	gcaatgaggctatcgactggttttttac
27	nt VK_CDR1_A1	actgccagtcaaagtgtaagttccagttactgcac
28	nt VK_CDR1_A2	agtgccagctcaagtgtaacttacatgtac
29	nt VK_CDR2_A1	agtacatccaacctggcttct
30	nt VK_CDR2_A2	gaccacatccaacctggctct
31	nt VK_CDR3_A1	cagcagtatcatagttccccgtacacg
32	nt VK_CDR3_A2	cagcaggggaggtaattaccctctcacg
33	IGHV1-80*01 (Genebank AC160990 Musmus) nt 136382-136424	ggctacgccatcagtagctacgatggtgatagcagc
34	IGHV1-69*01 (Genebank AC160990 Musmus) nt 136461-136511	ggacagatttatcctggagatggtgatactaactacaacggaaagttcaag
35	IGHV1-39*01 (Genebank AC079181 Musmus) nt 153352-153394	ggttacattcactgactacaacatgaactgt
36	IGHV1-39*01 (Genebank AC079181 Musmus) nt 153431-153481	ggagatattaatcctaactatggtactactcgctacaatcagaagttcaag
37	IGKV4-74*01 (Genebank: AJ231217 Musmus) nt 486-531	actgcaagctcaagtgtaagttccagttactgcac
38	IGKV4-74*01 (Genebank: AJ231217 Musmus) nt 577-597	agcacatccaacctggctct
39	IGKV4-74*01 (Genebank: AJ231217 Musmus) nt 681-718	cagcagtatcatggttccccacca
40	IGKV4-55*01 (Genebank: AJ231225 Musmus) nt 523-552	agtgccagctcaagtgtaagttacatgtac
41	IGKV4-55*01 (Genebank: AJ231225 Musmus) nt 598-618	gacacatccaacctggcttct
42	IGKV4-55*01 (Genebank: AJ231225 Musmus) nt 715-739	cagcaggggaggtacccacca
43	ADP-ribosyl cyclase 2 (CD157; BST1)	MAAQGCAASRLLQLLLQLLLLLLLAAGGARARVVRGEGTSAHLRDIFLGRCAEYRALL SPEQRNKNCTAIVEAFKVALDKDPCSVLPSDYDLFINLSRHSIPRDKSLFWENSHLLV NSFADNTRRFMPLSDVLYGRVADFLSWCRQKNDSGLDYQSCPTSEDCENNPVDSF WKRASIQYSKDSSGVTHVMLNGSEPTGAYPIKGFFADYEIPNLQKEKITRIEIWVMHEIG GPNVESCGEGSMKVLEKRLKDMGFQYSCINDYRPVKLLQCVDHSTHPDCALKSAAA ATQRKAPSLYTEQHAGLIIPLFLVLASRTQL
44	aa 29 - 292 of ADP-ribosyl cyclase 2 (CD157; BST1)	GARARVVRGEGTSAHLRDIFLGRCAEYRALLSPEQRNKNCTAIVEAFKVALDKDPCSV LPSDYDLFINLSRHSIPRDKSLFWENSHLLVNSFADNTRRFMPLSDVLYGRVADFLSW CRQKNDSGLDYQSCPTSEDCENNPVDSFWKRASIQYSKDSSGVTHVMLNGSEPTGA YPIKGFFADYEIPNLQKEKITRIEIWVMHEIGGPNVESCGEGSMKVLEKRLKDMGFQYS CINDYRPVKLLQCVDHSTHPDCALKSAAAATQRK
45	A2 VH (amino acids 21-137	QAYLQQSGPELVKAGASVKMSCKASGYSFIEYTINWVKQSHGKSLEWIGNIQPYYGT

	SEQ ID No:2)	TYYNQMFTGKATLTVDQSSNTAYMQLKSLTSEDSAVYFCARGSAWFPYWGQGTLVT VSA
46	VH1 - Humanised VH_A2	QVQLVQSGA EVKKPGASVK VSCKASGYSF IEYTINWVRQ APGQGLEWIGNIDPYYGTTYY NQMFTGRATL TVDTSISTAY MELSRLRSDDTAVYYCARGSAWF PYWGQGTLV TVSS
47	BF238102 VH	QVQLVQSGA EVKKPGASVK VSCKASGYSF TXXXXXWVRQ APGQGLEWMG XXXXXXXXXXX XXXXXXRVTL TRDTSISTAY MELSRLRSDDTAVYYCARXXXXX XXXWGQGTLV PVSS
48	A2 VL (amino acids 22-128 SEQ ID No:4)	DIVMSQSPA IMSASPGEKV TMTCSAS-SS VTYMYWYQQKPGSSPRLLIY DTSNLASGVP VRFSGSGSGT SYSLTISRMEAEDTATYYCQ QWSNYPLTFG AGTKLELK
49	VL1 - Humanised VK_A2	DIQMTQSPS SLSASVGDRV TITCSAS-SS VTYMYWYQQKPGKAPKLLIY DTSNLASGVP SRFSGSGSGT DYTLTISSLQPEDFATYYCQ QWSNYPLTFG QGTKVEIK
50	X72441 VL	DIQMTQSPS SLSASVGDRV TITCXXXXXX XXXXXWYQQKPGKAPKLLIY XXXXXXXGVP SRFSGSGSGT DFTLTISSLQPEDFATYYCX XXXXXXXXFG QGTKVEIK
51	VH1_CDR2	NIDPYYGTTYYNQMFQ
52	aa VH_A3	MKQSTIALALLPLLFTPVAKAQVQLQQSRAELVMPGASVKMSCKTSGYTFSDYWVHW VRQRPGQGLEWIGAIDGSDTFNDYSQKFKGRATLTVDESSSTVYMQLSSLTSEDSAV YYCARGGLLQYWGQGTTLTVSSAKTTFPSVYPLAPGSAAQTNSMVTLGCLVKGYFP EPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASST KVDKKIVPRDCHHHHHHH
53	aa VK_A3	MKYLLPTAAAGLLLLAAQPAMADIQLTQSPASLSASVGETVTITCRASENIYSYLAWYQ QKQGKSPQLLVYNTKTLGEGVPSRFSGSGSGTQFSLKINSLQPEDFGSYYCQHHYGT PFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGS ERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNES
54	nt VH_A3	gtggaacaaagcacactgtcgctggcactgctcctcttcgcagctcaggcagccatggccCAGGTCCAGCTGCAGCAG TCTGGGGCTGAACTGATGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTACTGGCTACACATTTAGTGACTACTGGGT AGCATGGGTGAGGCAGAGGCCTGGACATGGCCTTGAGTGGATTGGAGCGATTGATGGTTCTGATACTTTTAATGACTACGA GTCGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACGAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCCTGACA ATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGGGGGCTCCTGCAGTACTGGGGCCAAGGCACCACTCTCACAGTC TCCTGCGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCCTGGATCTGCTGCCCAAACTAACTCCATGGTGACCCTG GGATGCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACACC TTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACC GTCACCTGCAACGTTGCCCACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCCAGGGATTGTGGTTGTAAGCCT TGCATATGTACAGTCCCAGAAGTATCATCTGTCTTCATCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTT GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTCGATAACGCCCTCCAATCGGGTAACTCC CAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTAC GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAG TGTTAG
55	nt VK_A3	atgaaatacctattgcctacggcagccgctggattgttattactcgcggcccagccggccatggccGACATCCAGCTGACCC AGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGAAAACATTTACAGTTATT TAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATACAAAAACCTTACCAGATGGTGTCCCA TCAAGGTTCAGTGGCAGTGGATCAGGCACACAATTTTCTCTGAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTAT ACTGTCAACATCATTATGGTGGTCTCCATTCACGTTCGGCTCGGGGACAGAGTGGAAATAAAACGGGTGGATCTGATGCTA ACTGTATCCATCTCCCACCATCCAGTTGATCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTAC CCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGAC AGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGT GAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAA
56	aa VH_CDR1_A3	GYTFSDYWVHW
57	aa VH_CDR2_A3	GAIDGSDTFNDYSQKFK
58	aa VH_CDR3_A3	ARGGLLQY

59	aa VK_CDR1_A3	RASENIYSYLA
60	aa VK_CDR2_A3	NTKTLGE
61	aa VK_CDR3_A3	QHHYGTPFT
62	nt VH_CDR1_A3	ggctacaccatcactgactatggtgtaagctgg
63	nt VH_CDR2_A3	tggatgggatggaaggataccaatgctacactaaatatgctcagaagttccag
64	nt VH_CDR3_A3	gcgagggggggcctactacggtac
65	nt VK_CDR1_A3	cgagcgaagtgaaaatcttacagttatttagca
66	nt VK_CDR2_A3	aatactaaaacccttggagaa
67	nt VK_CDR3_A3	caacatcattatggtactccattcacg
68	IGHV1-69*01 (AC073389)	ggctacaccatcaccagctatggtatcagctg
69	IGHV1-69*01 (AC073389)	tggatgggatggatcatcgatggtatagttatactaactacgcacagaagttccag
70	IGKV12-44*01 (AJ235955)	cgagcgaagtgaaaatcttacagtttatttagca
71	IGKV12-44*01 (AJ235955)	aatgctaaaacccttggcgaa
72	IGKV12-44*01 (AJ235955)	caacatcattatggtactccctcc