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	acgctttgtacatggagaaaataaagtgaaacaaagcactattgcactggcactcttaccgctcttatttacccctgtggca aaagcccaggtgaagcttcagcagtccggggctgagctggtgaggcctgggtcctcagtgaagatttcctgcaaggctt ctggctacgcattcagtaactcctggataaactgggtgaagcagaggcctggacagggtcttgagtggattggacagatt tatcctggagattatgatactaactacaatggaaaattcaagggtaaagccacactgactgcagactacctcctccagcac agcctacatgcagctcaacagcctaacatctgaggactctgcggtctatttctgtgcaagggggggatcgatctactatggt aacctcgggttcttcgatgtctgggggcgcagggaccacggtcaccgtctcctcagccaaaacgacacccccatctgtcta tccactggcccctggatctgctgcccaaactaactccatggtgaccctgggatgcctggtcaagggctatttcccgagcc

		agtgacagtgaccttggaacctctggatccatgtccagcgggtgtcacaccttccagtgtcctgcagctgtgacctacact ctgagcagctcagtgactgtccctccagcacctggcccagcgagaccgtcacctgcaacgttgcccaccggccagc agcaccaagggtggacaagaaaattgtgcccagggattgtggttgtaagccttgcatatgtacagtccttatcgtc atcgct
6	nt VH_A2	atggactggacctggaggttcctctttgtggcagcagcaacaggtgcccactcccaggtccagctggtacagtctggg gctgaggtgaagaagcctgggtcctcagtgaaggtctcctgcaaggcttctggatacaccttcaccagctatgat atcagctgggtgcgacaggcccctggacaagggcttgagtggatgggatggatcaacgctggcaatggtaacaca aaatatgcacagaagttccagggcagagtcaccattaccagggacacatccgcgagcacagcctacatggagctg agcagcctgagatctgaggacacggccgtgtattactgtgcgagaggcctacgg ggattttcctatggtatggacgtctggggccaagggaccctggtcaccgtctcctcagcctccaccaagggcc catcggtcttccccctggcaccctcctccaagagcacctctgggggcacagcggccctgggctgcctggtcaag gactacttccccgaaccggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccggct gtcctacagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggcacccagac ctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagaaagttgagcccaaatcttgtgacaa aactcacacatgcccaccgtgcccagcacctgaactcctggggggaccgtcagtcttcctcttccccccaaaacc caaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctg aggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtac aacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtg caaggtctccaacaaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgagaacc acaggtgtacaccctgcccccatcccgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaag gcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcct cccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggg gaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctc cgggtaaatga
7	nt VK_A1	atgaagttgcctgttaggctgctggtgctgatgttctggattcctgcttccagcagtgatgttgtgatgacccaaac tccactctccctgcccgtcacccttggacagccggcctccatctcctgcaggtctagtcaaagcctcgtatacagtg atggaaacacctacttgaattggtttcagcagaggccaggccaatctccaaggcgcctaatttataaggtttcta actgggactctggggtccctgacagattcagtggcagcgggtcaggcactgatttcacactgaaaatcagccggg tggaggctgaggatgttggggtttattactgcatgcaaggtacacactggcctcggacgttcggccaagggacc aaggtggaaatcaaacgaactgtggctgcaccatctgtcttcatcttcccgccatctgatgagcagttgaaatct ggaactgcctctgttgtgtgcctgctgaataacttctatcccagagaggccaaagtacagtggaaggtggataa cgccctccaatcgggtaactcccaggagagtgtcacagagcaggacagcaaggacagcacctacagcctcagca gcaccctgacgctgagcaaagcagactacgagaaacacaaagtctacgcctgcgaagtcacccatcagggcctg agctcgccgtcacaaagagcttcaacaggggagagtgttag
8	nt VK_A2	atgaagttgcctgttaggctgctggtgctgatgttctggattcctgcttccagcagtgatgttgtgatgacccaaac tccactctccctgcccgtcacccttggacagccggcctccatctcctgcaggtctagtcaaagcctcgtatacagtg atggaaacacctacttgaattggtttcagcagaggccaggccaatctccaaggcgcctaatttataaggtttcta actgggactctggggtccctgacagattcagtggcagcgggtcaggcactgatttcacactgaaaatcagccggg tggaggctgaggatgttggggtttattactgcatgcaaggtacacactggcctcggacgttcggccaagggacc aaggtggaaatcaaacgaactgtggctgcaccatctgtcttcatcttcccgccatctgatgagcagttgaaatct ggaactgcctctgttgtgtgcctgctgaataacttctatcccagagaggccaaagtacagtggaaggtggataa cgccctccaatcgggtaactcccaggagagtgtcacagagcaggacagcaaggacagcacctacagcctcagca gcaccctgacgctgagcaaagcagactacgagaaacacaaagtctacgcctgcgaagtcacccatcagggcctg agctcgccgtcacaaagagcttcaacaggggagagtgttag
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	STSNLAS
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	ggttactcattcattgagtacaccatagactgg
23	nt VH_CDR2_A1	ggacagattttatcctggagattatgatactaactacaatggaaagttcaag
24	nt VH_CDR2_A2	ggaaatattggatccttattatggaacaaccgattacaatcagatgttcacg

25	nt VH_CDR3_A1	gcaagggggggatcgactactatggttacccgggttttcgatgtc
26	nt VH_CDR3_A2	gcaagagggtccgcctggttttctac
27	nt VK_CDR1_A1	actgccagtcaagtgtaagttccagttactgcac
28	nt VK_CDR1_A2	agtgccagctcaagtgtaacttacatgtac
29	nt VK_CDR2_A1	aggacatccaacctggcttct
30	nt VK_CDR2_A2	gacacatccaacctggcttct
31	nt VK_CDR3_A1	caccagtatcatcgttcccgtacacg
32	nt VK_CDR3_A2	cagcagtggagtaattacccactcacg
33	IGHV1-80*01 (Genebank AC160990 Musmus) nt 138392-138424	ggctacgcattcagtagctactggatgaactgg
34	IGHV1-80*01 (Genebank AC160990 Musmus) nt 138461-138511	ggacagattatcctggagatggtgatactaactacaacggaaagttcaag
35	IGHV1-39*01 (Genebank AC079181 Musmus) nt 153382-153394	ggttacgcattcactgactacgaacatgaactgg
36	IGHV1-39*01 (Genebank AC079181 Musmus) nt 153431-153461	ggagttattaatcctaactatggtactactacctacaatcagaagttcaag
37	IGKV4-74*01 (Genebank: AJ231217 Musmus) nt 496-531	actgccagtcaagtgtaagtccagttactgtac
38	IGKV4-74*01 (Genebank: AJ231217 Musmus) nt 577-597	agcaatccaacctggctct
39	IGKV4-74*01 (Genebank: AJ231217 Musmus) nt 681-718	caccagtatcatcgttcccacca
40	IGKV4-55*01 (Genebank: AJ231225 Musmus) nt 523-552	agtgccagctcaagtgtaagttacatgtac
41	IGKV4-55*01 (Genebank: AJ231225 Musmus) nt 588-618	gacacatccaacctggcttct
42	IGKV4-55*01 (Genebank: AJ231225 Musmus) nt 715-739	cagcagtggagtagttacccacca
43	ADP-ribosyl cyclase 2 (CD157, BST1)	MAAQGCAASRLLQLLLQLLLLLLLAAGGAHARVWHGEGTSAHLHDIFLGRCAEYHALL SPEQRNKNCTAIWEAFKVALDKDPCSVLPSDYDLFINLSRHSIPRDKSLFWENSHLLV NSFADNTRRFMPLSDVLYGRVADFLSWCRQKNDSGLDYQSCPTSEDCENNPVDSF WKRASIQYSKDSSGVIHVMLNGSEPTGAYPIKGFFADYEIPNLQKEKITRIEIWVMHEIG GPNVESCGEGSMKVLEKRLKDMGFQYSCINDYRPVKLLQCVDHSTHPDCALKSAAA ATQRKAPSLYTEQHAGLIIPLFLVLASRTQL
44	aa 29 - 292 of ADP-ribosyl cyclase 2 (CD157; BST1)	GARARWRGEGTSAHLRDIFLGRCAEYRALLSPEQRNKNCTAIWEAFKVALDKDPCSV LPSDYDLFINLSRHSIPRDKSLFWENSHLLVNSFADNTRRFMPLSDVLYGRVADFLSW CRQKNDSGLDYQSCPTSEDCENNPVDSFWKRASIQYSKDSSGVIHVMLNGSEPTGA YPIKGFFADYEIPNLQKEKITRIEIWVMHEIGGPNVESCGEGSMKVLEKRLKDMGFQYS CINDYRPVKLLQCVDHSTHPDCALKSAAAATQRK
45	A2 VH (amino acids 21-137	QAYLQQSGPELVKAGASVKMSCKASGYSFIEYTINWVKQSHGKSLEWIGNIDPYYGT

	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 XXXXXXXXXX XXXXXRVTL 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 SLSASVGDHV TITCXXXXXX XXXXXWYQQKPGKAPKLLIY XXXXXXXGVP SRFSGSGSGT DFTLTISSLQPEDFATYYCX XXXXXXXXFG QGTKVEIK
51	VH1_CDR2	NIDPYYGTTYYNQMFQ
52	aa VH_A3	MKQSTIALALLPLLFTPVAKAQVQLQQSRAELVMPGASVKMSCKTSGYTFSDYWVHW VRQRPGQGLEWIGAIDGSDTFNDYSQKFKGRATLTVDESSSTVYMQLSSLTSEDSAV YYCARGQLLQYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFP EPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASST KVDKKIVPRDCmmmHHHH
53	aa VK_A3	MKYLLPTAAAGLLLLAAQPAMADIQLTQSPASLSASVGETVTITCRASENIYSYLAWYQ QKQGKSPQLLVYNTKTLGEGVPSRFSGSGSGTQFSLKINSLQPEDFGSYYCQHHYGT PFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGS ERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFN RNES
54	nt VH_A3	gtgaaacaaagcactattgcactggcactcttaccgctcttattacccctgtgctgcaaaagcccaggtccagctgcagcag tctaggactgaactggtgatgcctggggcttcagtgaagatgtcctgcaagacttctggctacacattcactgactactggt acactgggtgaggcagaggcctggacaagggcttgagtggatcggagcgattgatggttctgatacttttaatgactaca gtcagaagttcaaggacagggccacattgactgtagacgaatcctccagcacagtctacatgcaactcagcagcctgac atctgaggactctgcggtctattactgtgcaagggggggtcgcttctacagtactggggccaaggcaccactctcacagtctc ctcagccaccaccgaaggcccatctgtctatccactggcccctggatctgctgcccaaactaactccatggtgaccctgg gatgcctggtcaagggctatttccctgagccagtgacagtgacctggaactctggatccctgtccagcggtgtgcacacct tcccagctgtcctgcagtctgacctctacactctgagcagctcagtgactgtcccctccagcacctggcccagcgagacc gtcacctgcaacgttgcccacccggccagcagcaccaaggtggacaagaaaattgtgcccagggattgtggttcatcatcac catcaccatcactaa
55	nt VK_A3	atgaaatacctattgcctacggcagccgctggattgttattactcgctgcccaaccagccatggccgacatccagctgacc cagtctccagcctccctatctgcatctgtgggagaaactgtcaccatcacatgtcgagcaagtgaaaacatttacagttatt agcatggtatcagcagaaacagggaaatctcctcagctcctggtctataatactaaaaccttagcagaaggtgtgccca tcaaggttcagtggcagtggatcagggacacaatttctctgaagatcaacagcctgcagcctgaagattttgggagttatt actgtcaacatcattatggtactccattcacgttcggctcggggacaaagttggaaataaacgggctgatgctgcaccca actgtatccatctcccaccatccagtgagcagttaacatctggaggtgcctcagtcgtgtgcttcttgaacaacttctaccc caaagacatcaatgtcaagtggaagattgatggcagtgaacgacaaaatggcgtcctgaacagttggactgatcaggac agcaaagacagcacctacagcatgagcagcaccctcacgttgaccaaggacgagtatgaacgacataacagctata cctgtgaggccactcacaagacatcaacttcacccattgtcaagagcttcaacaggaatgagtgttaa
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	ggctacacattcactgactactggctacactgg
63	nt VH_CDR2_A3	ggagcgattgatggttctgatactttaaatgactacagtcagaagttcaag
64	nt VH_CDR3_A3	gcaaggggggcctttctacggtac
65	nt VK_CDR1_A3	cgagcaagtgaaaacatttacagttatttagca
66	nt VK_CDR2_A3	aatacaaaaaccttaggagaa
67	nt VK_CDR3_A3	caacatcattatggtactccattcacg
68	IGHV1-69*01 (AC073333)	ggctacacctttaccagctactggatgcactgg
69	IGHV1-69*01 (AC073333)	ggagcgatgatcctttgatagtttatactaactacaatcagaagttcaag
70	IGKV12-44*01 (AJ235955)	cgagcaagtgagaatatttacagttatttagca
71	IGKV12-44*01 (AJ235955)	aatgcaaaaaccttagcgaga
72	IGKV12-44*01 (AJ235955)	caacatcattatggtactccttc