```
mGM1110/1-635     1 - - MVVAFLGRPE - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - CILCLSSAL - - CAMA   22
mGLB1L2/1-676     1 MPKWSLRRRPGRTLGLLLLLLVLSFLVLRSPRVFMLNVVVSVLFLAAASACSSPAVGPSPGS   60
mGLB1L3/1-649     1 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - MAIFFLPTV - - - - - - LSGFAPHS   17

mGM1110/1-635    23 LLSNNEFSRLNQTHLTPLLLINRKVGLQVKD - - - - - SQFTLEGFPFRIISGTIDYFRIPR   77
mGLB1L2/1-676    61 SAEESHLSRLNWSTLVPLWLQHQRLGLRTKG - - - - - PDFILEDSIFQILGGSIHYFRVPR  115
mGLB1L3/1-649    18 EEVFKSPARFSWSNLTPSELKNRFVGLSTKTNALGKAYFTLEGHKFMIVGGSIHYFRVPR   77

mGM1110/1-635    78 NSWRLSLRKMQAGGFNTLTTHIPWNLHEPAVGQFYFTENTDLIAFITMASQSGLWWILCP  137
mGLB1L2/1-676   116 EYWRDRLLKLKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFIQLAAKIGLWWILRP  175
mGLB1L3/1-649    78 EYWKDRLLKLQACGFNTVTTYIPWNLHEQERGKFDFSEILDLEAYVLLAKTIGLWWILRP  137

mGM1110/1-635   138 GPYIGSDLDLGGLPSWLLKDPKMKLRTTYKGFTKAMNRYFDNLIPKIAKFQYKKGGPIIA  197
mGLB1L2/1-676   176 GPYICSEIDLGGLPSWLLQDPDMKLRTTYHGFTKAVDLYFDHLMSRVVPLQYKHGGPIIA  235
mGLB1L3/1-649   138 GPYICAEVDLGGLPSWLLRNPVTDLRTTNKGFIEAVDKYFDHLIPKILPLQYRHGGPVIA  197

mGM1110/1-635   198 VQVENEYGSYYMDKKYMAYVKTALVSRGIDELLMTADDGVSLRKGHLENVLATVHMKNIK  257
mGLB1L2/1-676   236 VQVENEYGSYNKDRAYMPYIKKALEDRGIIEMLLTSDNKDGLEKGVVDGVLATINLQSQQ  295
mGLB1L3/1-649   198 VQVENEYGSFQKDRNYMNYLKKALLKRGIVELLLTSDDKDGIQIGSVNGALTTINMNSFT  257

mGM1110/1-635   258 KETF - - GDLRSIQGKSPILMMVYTTKSFDTWGTLHQTGDAQMLLKDVHEMFHLGFSLNFY  315
mGLB1L2/1-676   296 ELMALNTVLLSIQGIQPKMVMEYWTGWFDSWGGSHNILDSSEVLQTVSAIIKDGSSINLY  355
mGLB1L3/1-649   258 KDSF - - IKLHKMQSDKPIMIMEYWTGWYDSWGSKHIEKSAEEIRHTVYKFISYGLSFNMY  315

mGM1110/1-635   316 MFQGGTNFGLIGGAQSSEGYKPVVTSYDYNALVSEGGEYTVQYREFQRFFHSVTDSHLTV  375
mGLB1L2/1-676   356 MFHGGTNFGFINGAMHFNDYKADVTSYDYDAILTEAGDYTAKYTKLRELFGTVSGIPPPP  415
mGLB1L3/1-649   316 MFHGGTNFGFINGGRYENHHISVVTSYDYDAVLSEAGDYTEKYFKLRKLFASGSARPLPP  375

mGM1110/1-635   376 QPKTTQMFAYQPVTLLYFMTLWEFLPNLVKTTKSSKPLSMEQLRVNERSGQSFGYILYET  435
mGLB1L2/1-676   416 PPELTAKMVYEPMSPALYLSLWDAIQYMDKPVTSETPINMENLPVNNGNGQAFGYVLYET  475
mGLB1L3/1-649   376 LPPLIPKAIYPSVNLSFYLPLFDILPYLNQPVMLHTPVTMENLPINNGSGQPFGLVLYET  435

mGM1110/1-635   436 VIFSGGLITSRGHIRDRGQVFLDNIYIGLLDQSNSELLLYKDVSKKSQILRILVENQGRL  495
mGLB1L2/1-676   476 TIFSSGVLS - - GLVRDRGQVFLNRVSIGFLDYKTTKITI - - PLTQGYTILRILVENRGRV  531
mGLB1L3/1-649   436 SICSGGSLF - - ASVHDSAQVFLNDQSIGILDENHEVLQI - - PKIQGCQLLRILVENQGRI  491

mGM1110/1-635   496 TSGQDINKERKGLTGDIYLDKSPLRPFKIYSLEMNNIFIQREFPNSWQRVTSQVQGPAFF  555
mGLB1L2/1-676   532 NYGNNIDSQRKGLIGNLYLNNKALKNFKIYSLDMTKFLQRFDMDNWSVIPKELTFPAFF  591
mGLB1L3/1-649   492 NYSWRIQSEQKGLKEVVSIDGLLLTNFTIYSLDMKMSFFKRLRSASWRLAPKTYNGPAFY  551

mGM1110/1-635   556 LSYLKAGDPPQDTFMKIQGWGKGVISINGRSLGRYWNIGPQETVFVPGSWLQPGVNKIIM  615
mGLB1L2/1-676   592 LGALSVGIYPSDTFLKLEGWVKGVVFVNGHNLGRYWNVGPQETLYLPGVWLDKGINKVII  651
mGLB1L3/1-649   552 WGILNAGSSPTDTFLHLPNWHYGFVFINGRNLGRYWDIGPQRTLYLPGPWLHPEDNEVIV  611

mGM1110/1-635   616 FEELKGDEKIHFSTKAQLGH - - - - - - - - - - - - - - - - - -                              635
mGLB1L2/1-676   652 FEETMSGSMVQSTDIPHLGRNQYIN - - - - - - - - - - - - -                              676
mGLB1L3/1-649   612 FEKIEKGFDIQTRKKPQLQECYETGSGLPDAAGDADPC                                     649
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