Appendix A.

A.1. Sequences used in alignment to predict TM regions of LPA_2

>sp|Q9HBW0|EDG4_HUMAN Lysophosphatidic acid receptor Edg-4 (LPA receptor 2) (LPA-2) - Homo sapiens (Human).

>sp|Q9UBY5|EDG7_HUMAN Lysophosphatidic acid receptor Edg-7 (LPA receptor 3) (LPA-3) - Homo sapiens (Human).

>sp|Q92633|EDG2_HUMAN Lysophosphatidic acid receptor Edg-2 (LPA receptor 1) (LPA-1) - Homo sapiens (Human).

>sp|Q61130|EDG2_MOUSE Lysophosphatidic acid receptor Edg-2 (LPA receptor 1) (LPA-1) (Rec1.3) (VZG-1) - Mus musculus (Mouse), and Rattus norvegicus (Rat).

>sp|Q9EQ31|EDG7_MOUSE Lysophosphatidic acid receptor Edg-7 (LPA receptor 3) (LPA-3) - Mus musculus (Mouse).

>sp|Q9JL06|EDG4_MOUSE Lysophosphatidic acid receptor Edg-4 (LPA receptor 2) (LPA-2) - Mus musculus (Mouse).

>tr|Q9DC35 Endothelial differentiation sphingolipid G-protein-coupled receptor 1 (Hypothetical protein) - Mus musculus (Mouse).

>sp|P21453|EDG1_HUMAN Probable G protein-coupled receptor Edg-1 - Homo sapiens (Human).

>sp|Q99500|EDG3_HUMAN Sphingosine 1-phosphate receptor Edg-3 (S1P receptor Edg-3) (Endothelial differentiation G-protein-coupled receptor 3) - Homo sapiens (Human).

>tr|Q8BP20 Endothelial differentiation - Mus musculus (Mouse).

>sp|O95136|EDG5_HUMAN Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5) (Endothelial differentiation G-protein coupled receptor 5) - Homo sapiens (Human).

>tr|Q8C3Q7 Endothelial differentiation - Mus musculus (Mouse).

>tr|Q9Z0L1 G protein-coupled receptor precursor - Mus musculus (Mouse).

>sp|P47746|CB1R_MOUSE Cannabinoid receptor 1 (CB1) (CB-R) (Brain-type cannabinoid receptor) - Mus musculus (Mouse).

>sp|P21554|CB1R_HUMAN Cannabinoid receptor 1 (CB1) (CB-R) (CANN6) - Homo sapiens (Human).

>sp|P33032|MC5R_HUMAN Melanocortin-5 receptor (MC5-R) (MC-2) - Homo sapiens (Human).

>tr|Q9EQM7 Melanocortin-4 receptor - Mus musculus (Mouse).

>sp|P32245|MC4R_HUMAN Melanocortin-4 receptor (MC4-R) - Homo sapiens (Human).

>sp|P41968|MC3R_HUMAN Melanocortin-3 receptor (MC3-R) - Homo sapiens (Human).

A.2. Alignment for predicting the TM region of LPA_2

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CLUSTAL W (1.74) multiple sequence alignment

sp|Q9HBW0|EDG4_HUMAN      ------------------------------------------------------------
sp|Q9UBY5|EDG7_HUMAN      ------------------------------------------------------------
sp|Q92633|EDG2_HUMAN      ----------------------------------------------------------MA
sp|Q61130|EDG2_MOUSE      ----------------------------------------------------------MA
sp|Q9EQ31|EDG7_MOUSE      ------------------------------------------------------------
sp|Q9JL06|EDG4_MOUSE      ------------------------------------------------------------
tr|Q9DC35                 ------------------------------------------------------------
sp|P21453|EDG1_HUMAN      ------------------------------------------------------------
sp|Q99500|EDG3_HUMAN      ------------------------------------------------------------
tr|Q8BP20                 ------------------------------------------------------------
sp|O95136|EDG5_HUMAN      ------------------------------------------------------------
tr|Q8C3Q7                 ------------------------------------------------------------
tr|Q9Z0L1                 ------------------------------------------------------------
sp|P47746|CB1R_MOUSE      MKSILDGLADTTFRTITTDLLYVGSNDIQYEDIKGDMASKLGYFPQKFPLTSFRGSPFQE
sp|P21554|CB1R_HUMAN      MKSILDGLADTTFRTITTDLLYVGSNDIQYEDIKGDMASKLGYFPQKFPLTSFRGSPFQE
sp|P33032|MC5R_HUMAN      ------------------------------------------------------------
tr|Q9EQM7                 ------------------------------------------------------------
sp|P32245|MC4R_HUMAN      ------------------------------------------------------------
sp|P41968|MC3R_HUMAN      ---------------------------------------MSIQKTYLEGDFVFPVSSSSF


sp|Q9HBW0|EDG4_HUMAN      -------------MVIMG--QCYYNETIGFFYNNSGKEL---------SSHWR-----PK
sp|Q9UBY5|EDG7_HUMAN      ----------------MN--ECHYDKHMDFFYNRSNTDT---------VDDWTG----TK
sp|Q92633|EDG2_HUMAN      AISTSIPVISQPQFTAMNEPQCFYNESIAFFYNRSGKHL---------ATEWN-----TV
sp|Q61130|EDG2_MOUSE      AASTSSPVISQPQFTAMNEQQCFYNESIAFFYNRSGKYL---------ATEWN-----TV
sp|Q9EQ31|EDG7_MOUSE      ----------------MN--ECHYDKRMDFFYNRSNTDT---------ADEWTG----TK
sp|Q9JL06|EDG4_MOUSE      ----------------MG--QCYYNETIGFFYNNSGKEL---------SLHWR-----PK
tr|Q9DC35                 -MVSTSIPEVKALRSSVS--DYGNYDIIVRHYNYTGKLN---------IGAEKD----HG
sp|P21453|EDG1_HUMAN      -MGPTSVPLVKAHRSSVS--DYVNYDIIVRHYNYTGKLN---------ISADKE----NS
sp|Q99500|EDG3_HUMAN      --------MATALPPRLQ--PVRGNETLREHYQYVGKLAGR-------LKEASE----G-
tr|Q8BP20                 --------MATTHAQGHQ--PVLGNDTLREHYDYVGKLAGR-------LRDPPE----GG
sp|O95136|EDG5_HUMAN      ------------MGSLYS--EYLNPNKVQEHYNYTKETL----------ETQET----TS
tr|Q8C3Q7                 ------------MGGLYS--EYLNPEKVLEHYNYTKETL----------DMQET----TS
tr|Q9Z0L1                 -MNISTWSTLVTPESCHRLAASGHSLLIVLHYNHSGRLASR-------GGSEDG----GG
sp|P47746|CB1R_MOUSE      KMTAGDNSPLVPAGDTTNITEFYNKSLSSFKENEDNIQCGENFMDMECFMILNP----SQ
sp|P21554|CB1R_HUMAN      KMTAGDNPQLVPA-DQVNITEFYNKSLSSFKENEENIQCGENFMDIECFMVLNP----SQ
sp|P33032|MC5R_HUMAN      ----------------MNSSFHLHFLDLNLNATEGNLSGP-------NVKNKSS--PCED
tr|Q9EQM7                 --------MNSTHHHGMYTSLHLWNRSSYGLHSNASESLG-------KGHPDGG--CYEQ
sp|P32245|MC4R_HUMAN      --------MVNSTHRGMHTSLHLWNRSSYRLHSNASESLG-------KGYSDGG--CYEQ
sp|P41968|MC3R_HUMAN      LRTLLEPQLGSALLTAMNASCCLPSVQPTLPNGSEHLQAP-------FFSNQSSSAFCEQ


sp|Q9HBW0|EDG4_HUMAN      DVVVVALGLTVSVLVLLTNLLVIAAIASNRRFHQ-PIYYLLGNLAAADLFAGVAYLFLMF
sp|Q9UBY5|EDG7_HUMAN      LVIVLCVGTFFCLFIFFSNSLVIAAVIKNRKFHF-PFYYLLANLAAADFFAGIAYVFLMF
sp|Q92633|EDG2_HUMAN      SKLVMGLGITVCIFIMLANLLVMVAIYVNRRFHF-PIYYLMANLAAADFFAGLAYFYLMF
sp|Q61130|EDG2_MOUSE      SKLVMGLGITVCVFIMLANLLVMVAIYVNRRFHF-PIYYLMANLAAADFFAGLAYFYLMF
sp|Q9EQ31|EDG7_MOUSE      LVIVLCVGTFFCLFIFFSNSLVIAAVITNRKFHF-PFYYLLANLAAADFFAGIAYVFLMF
sp|Q9JL06|EDG4_MOUSE      DVVVVALGLTVSVLVLLTNLLVIAAIASNRRFHQ-PIYYLLGNLAAADLFAGMAYLFLMF
tr|Q9DC35                 IKLTSVVFILICCFIILENIFVLLTIWKTKKFHR-PMYYFIGNLALSDLLAGVAYTANLL
sp|P21453|EDG1_HUMAN      IKLTSVVFILICCFIILENIFVLLTIWKTKKFHR-PMYYFIGNLALSDLLAGVAYTANLL
sp|Q99500|EDG3_HUMAN      STLTTVLFLVICSFIVLENLMVLIAIWKNNKFHN-RMYFFIGNLALCDLLAGIAYKVNIL
tr|Q8BP20                 TLITTILFLVTCSFIVLENLMVLIAIWKNNKFHN-RMYFFIGNLALCDLLAGIAYKVNIL
sp|O95136|EDG5_HUMAN      RQVASAFIVILCCAIVVENLLVLIAVARNSKFHS-AMYLFLGNLAASDLLAGVAFVANTL
tr|Q8C3Q7                 RKVASAFIIILCCAIVVENLLVLIAVARNSKFHS-AMYLFLGNLAASDLLAGVAFVANTL
tr|Q9Z0L1                 LGMLRGPSVAAGCLVVLENAMVLAAIAIYMRSRR-WVYYCLLNITLSDLLTGLAYVVNVL
sp|P47746|CB1R_MOUSE      QLAIAVLSLTLGTFTVLENLLVLCVILHSRSLRCRPSYHFIGSLAVADLLGSVIFVYSFV
sp|P21554|CB1R_HUMAN      QLAIAVLSLTLGTFTVLENLLVLCVILHSRSLRCRPSYHFIGSLAVADLLGSVIFVYSFI
sp|P33032|MC5R_HUMAN      MGIAVEVFLTLGVISLLENILVIGAIVKNKNLHS-PMYFFVCSLAVADMLVSMSSAWETI
tr|Q9EQM7                 LFVSPEVFVTLGVISLLENILVIVAIAKNKNLHS-PMYFFICSLAVADMLVSVSNGSETI
sp|P32245|MC4R_HUMAN      LFVSPEVFVTLGVISLLENILVIVAIAKNKNLHS-PMYFFICSLAVADMLVSVSNGSETI
sp|P41968|MC3R_HUMAN      VFIKPEVFLSLGIVSLLENILVILAVVRNGNLHS-PMYFFLCSLAVADMLVSVSNALETI
                                         .. * :*: .:      :    *  : .:: .*:: .:      .
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sp|Q9HBW0|EDG4_HUMAN      HTGPRT-------ARLSLEGWFLRQGLLDTSLTASVATLLAIAVERHRSVMA-VQLHSRL
sp|Q9UBY5|EDG7_HUMAN      NTGPVS-------KTLTVNRWFLRQGLLDSSLTASLTNLLVIAVERHMSIMR-MRVHSNL
sp|Q92633|EDG2_HUMAN      NTGPNT-------RRLTVSTWLLRQGLIDTSLTASVANLLAIAIERHITVFR-MQLHTRM
sp|Q61130|EDG2_MOUSE      NTGPNT-------RRLTVSTWLLRQGLIDTSLTASVANLLAIAIERHITVFR-MQLHTRM
sp|Q9EQ31|EDG7_MOUSE      NTGPVS-------KTLTVNRWFLRQGLLDTSLTASLANLLVIAVERHMSIMR-MRVHSNL
sp|Q9JL06|EDG4_MOUSE      HTGPPH-------CQALHQRLVPATGPAGHQPHGVSGHTAGIAVERHRSVMA-VQLHSRL
tr|Q9DC35                 LSGATT-------YKLTPAQWFLREGSMFVALSASVFSLLAIAIERYITMLK-MKLHNGS
sp|P21453|EDG1_HUMAN      LSGATT-------YKLTPAQWFLREGSMFVALSASVFSLLAIAIERYITMLK-MKLHNGS
sp|Q99500|EDG3_HUMAN      MSGKKT-------FSLSPTVWFLREGSMFVALGASTCSLLAIAIERHLTMIK-MRPYDAN
tr|Q8BP20                 MSGRKT-------FRLSPTVWFLREGSMFVALGASTCSLLAIAIERHLTMIK-MRPYDAN
sp|O95136|EDG5_HUMAN      LSGSVT-------LRLTPVQWFAREGSAFITLSASVFSLLAIAIERHVAIAK-VKLYGSD
tr|Q8C3Q7                 LSGHVT-------LSLTPVQWFAREGSAFITLSASVFSLLAIAIERQVALAK-VKLYGSD
tr|Q9Z0L1                 LSGTRT-------FQLSPVHWFLREGLLFMALAASTFSLLFTAGERFATMVR-VAESGAT
sp|P47746|CB1R_MOUSE      DFHVFH-------RKDSPNVFLFKLGGVTASFTASVGSLFLTAIDRYISIHRPLAYKRIV
sp|P21554|CB1R_HUMAN      DFHVFH-------RKDSRNVFLFKLGGVTASFTASVGSLFLTAIDRYISIHRPLAYKRIV
sp|P33032|MC5R_HUMAN      TIYLLNNKHLVIADAFVRHIDNVFDSMICISVVASMCSLLAIAVDRYVTIFYALRYHHIM
tr|Q9EQM7                 VITLLN-STDTDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIM
sp|P32245|MC4R_HUMAN      IITLLN-STDTDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIM
sp|P41968|MC3R_HUMAN      MIAIVHSDYLTFEDQFIQHMDNIFDSMICISLVASICNLLAIAVDRYVTIFYALRYHSIM
                                                   .       .        * :*  ::   :

sp|Q9HBW0|EDG4_HUMAN      PRGRVVMLIVGVWVAALGLGLLPAHSWHCLCALDRCSRMAPLLSRSYLAVWALSSLLVFL
sp|Q9UBY5|EDG7_HUMAN      TKKRVTLLILLVWAIAIFMGAVPTLGWNCLCNISACSSLAPIYSRSYLVFWTVSNLMAFL
sp|Q92633|EDG2_HUMAN      SNRRVVVVIVVIWTMAIVMGAIPSVGWNCICDIENCSNMAPLYSDSYLVFWAIFNLVTFV
sp|Q61130|EDG2_MOUSE      SNRRVVVVIVVIWTMAIVMGAIPSVGWNCICDIDHCSNMAPLYSDSYLVFWAIFNLVTFV
sp|Q9EQ31|EDG7_MOUSE      TKKRVTLLILLVWAIAIFMGAVPTLGWNCLCNISACSSLAPIYSRSYLIFWTVSNLLAFF
sp|Q9JL06|EDG4_MOUSE      PRGRVVTLIVGVWAAALGLGLLPAHFWHCLCDLDSCSRMVPLFSRSYLAAWALSSLLVFL
tr|Q9DC35                 NSSRSFLLISACWVISLILGGLPIMGWNCISSLSSCSTVLPLYHKHYILFCTTVFTLLLL
sp|P21453|EDG1_HUMAN      NNFRLFLLISACWVISLILGGLPIMGWNCISALSSCSTVLPLYHKHYILFCTTVFTLLLL
sp|Q99500|EDG3_HUMAN      KRHRVFLLIGMCWLIAFTLGALPILGWNCLHNLPDCSTILPLYSKKYIAFCISIFTAILV
tr|Q8BP20                 KKHRVFLLIGMCWLIAFSLGALPILGWNCLENFPDCSTILPLYSKKYIAFLISIFTAILV
sp|O95136|EDG5_HUMAN      KSCRMLLLIGASWLISLVLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSIILL
tr|Q8C3Q7                 KSCRMLMLIGASWLISLILGGLPILGWNCLNQLEACSTVLPLYAKHYVLCVVTIFSVILL
tr|Q9Z0L1                 KTSRVYGCIGLCWLLAAILGLLPLLGWNCVCAFPRCSSLLPLYSKGYVLFCVVVFALILV
sp|P47746|CB1R_MOUSE      TRPKAVVAFCLMWTIAIVIAVLPLLGWNCKKLQSVCSDIFPLIDETYLMFWIGVTSVLLL
sp|P21554|CB1R_HUMAN      TRPKAVVAFCLMWTIAIVIAVLPLLGWNCEKLQSVCSDIFPHIDETYLMFWIGVTSVLLL
sp|P33032|MC5R_HUMAN      TARRSGAIIAGIWAFCTGCGIVFILYS---------------ESTYVILCLISMFFAMLF
tr|Q9EQM7                 TVRRVGIIISCIWAACTVSGVLFIIYS---------------DSSAVIICLISMFFTMLV
sp|P32245|MC4R_HUMAN      TVKRVGIIISCIWAACTVSGILFIIYS---------------DSSAVIICLITMFFTMLA
sp|P41968|MC3R_HUMAN      TVRKALTLIVAIWVCCGVCGVVFIVYS---------------ESKMVIVCLITMFFAMML
                             :    :   *  .   . :                         :          :

sp|Q9HBW0|EDG4_HUMAN      LMVAVYTRIFFYVRRRVQRMAEHVSCH--------------P--RYRETTLSLVKTVVII
sp|Q9UBY5|EDG7_HUMAN      IMVVVYLRIYVYVKRKTNVLSPHTSGS--------------I--SRRRTPMKLMKTVMTV
sp|Q92633|EDG2_HUMAN      VMVVLYAHIFGYVRQRTMRMSRHSSGP--------------R--RNRDTMMSLLKTVVIV
sp|Q61130|EDG2_MOUSE      VMVVLYAHIFGYVRQRTMRMSRHSSGP--------------R--RNRDTMMSLLKTVVIV
sp|Q9EQ31|EDG7_MOUSE      IMVAVYVRIYMYVKRKTNVLSPHTSGS--------------I--SRRRAPMKLMKTVMTV
sp|Q9JL06|EDG4_MOUSE      LMVAVYTRIFFYVRRRVERMAEHVSCH--------------P--RYRETTLSLVKTVVII
tr|Q9DC35                 SIVILYCRIYSLVRTRSRRLTFRKNIS--------------KASRSSEKSLALLKTVIIV
sp|P21453|EDG1_HUMAN      SIVILYCRIYSLVRTRSRRLTFRKNIS--------------KASRSSE-NVALLKTVIIV
sp|Q99500|EDG3_HUMAN      TIVILYARIYFLVKSSSRKVANHNN---------------------SERSMALLRTVVIV
tr|Q8BP20                 TIVILYARIYCLVKSSSRRVANHN----------------------SERSMALLRTVVIV
sp|O95136|EDG5_HUMAN      AIVALYVRIYCVVRSSHADMAAPQ-------------------------TLALLKTVTIV
tr|Q8C3Q7                 AIVALYVRIYFVVRSSHADVAGPQ-------------------------TLALLKTVTIV
tr|Q9Z0L1                 AILSLYGAIFRVVRANGQKSPRPP--------------------ARRKSRRLLNTVLMI
sp|P47746|CB1R_MOUSE      FIVYAYMYILWKAHSHAVRMIQRGTQKSIIIHTSEDGKVQVTRPDQARMDIRLAKTLVLI
sp|P21554|CB1R_HUMAN      FIVYAYMYILWKAHSHAVRMIQRGTQKSIIIHTSEDGKVQVTRPDQARMDIRLAKTLVLI
sp|P33032|MC5R_HUMAN      LLVSLYIHMFLLARTHVKRIAALPGAS----------------SARQRTSMQGAVTVTML
tr|Q9EQM7                 LMASLYVHMFLMARLHIKRIAVLPGTG----------------TIRQGTNMKGAITLTIL
sp|P32245|MC4R_HUMAN      LMASLYVHMFLMARLHIKRIAVLPGTG----------------AIRQGANMKGAITLTIL
sp|P41968|MC3R_HUMAN      LMGTLYVHMFLFARLHVKRIAALPPADG--------------VAPQQHSCMKGAVTITIL
                           :   *  :   .:                                          *:  :
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sp|Q9HBW0|EDG4_HUMAN      LGAFVVCWTPGQVVLLLDGLGCES----CNVLAVEKYFLLLAEANSLVNAAVYSCRDAEM
sp|Q9UBY5|EDG7_HUMAN      LGAFVVCWTPGLVVLLLDGLNCRQ----CGVQHVKRWFLLLALLNSVVNPIIYSYKDEDM
sp|Q92633|EDG2_HUMAN      LGAFIICWTPGLVLLLLD-VCCPQ----CDVLAYEKFFLLLAEFNSAMNPIIYSYRDKEM
sp|Q61130|EDG2_MOUSE      LGAFIVCWTPGLVLLLLD-VCCPQ----CDVLAYEKFFLLLAEFNSAMNPIIYSYRDKEM
sp|Q9EQ31|EDG7_MOUSE      LGAFVVCWTPGLVVLLLDGLNCKQ----CNVQHVKRWFLLLALLNSVMNPIIYSYKDEDM
sp|Q9JL06|EDG4_MOUSE      LGAFVVCWTPGQVVLLLDGLDCKT----CNVLAVEKYFLLLAEANSLVNAVVYSCRDAEM
tr|Q9DC35                 LSVFIACWAPLFILLLLD-VGCKAK--TCDILYKAEYFLVLAVLNSGTNPIIYTLTNKEM
sp|P21453|EDG1_HUMAN      LSVFIACWAPLFILLLLD-VGCKVK--TCDILFRAEYFLVLAVLNSGTNPIIYTLTNKEM
sp|Q99500|EDG3_HUMAN      VSVFIACWSPLFILFLID-VACRVQ--ACPILFKAQWFIVLAVLNSAMNPVIYTLASKEM
tr|Q8BP20                 VSVFIACWSPLFILFLID-VACRAK--ECSILFKSQWFIMLAVLNSAMNPVIYTLASKEM
sp|O95136|EDG5_HUMAN      LGVFIVCWLPAFSILLLD-YACPVH--SCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDL
tr|Q8C3Q7                 LGVFIICWLPAFSILLLD-STCPVR--ACPVLYKAHYFFAFATLNSLLNPVIYTWRSRDL
tr|Q9Z0L1                 LVAFVVCWGPLFGLLLADIFGSNVW--AQEYLRGMDWILALAVFNSAINPLIYSFRSREV
sp|P47746|CB1R_MOUSE      LVVLIICWGPLLAIMVYDVFGKMN----KLIKTVFAFCSMLCLLNSTVNPIIYALRSKDL
sp|P21554|CB1R_HUMAN      LVVLIICWGPLLAIMVYDVFGKMN----KLIKTVFAFCSMLCLLNSTVNPIIYALRSKDL
sp|P33032|MC5R_HUMAN      LGVFTVCWAPFFLHLTLM-LSCPQNLYCSRFMSHFNMYLILIMCNSVMDPLIYAFRSQEM
tr|Q9EQM7                 IGVFVVCWAPFFLHLLFY-ISCPQNPYCVCFMSHFNLYLILIMCNAVIDPLIYALRSQEL
sp|P32245|MC4R_HUMAN      IGVFVVCWAPFFLHLIFY-ISCPQNPYCVCFMSHFNLYLILIMCNSIIDPLIYALRSQEL
sp|P41968|MC3R_HUMAN      LGVFIFCWAPFFLHLVLI-ITCPTNPYCICYTAHFNTYLVLIMCNSVIDPLIYAFRSLEL
                          : .:  ** *    :                         .   *:  :. :*:  . ::

sp|Q9HBW0|EDG4_HUMAN      -RRTFRRLLC-CACLR-------QSTR----ESVHYTSSAQ----GGASTRIMLPENGHP
sp|Q9UBY5|EDG7_HUMAN      -YGTMKKMIC-CFSQE-NPER-RPSRI----PSTVLSRSDT----GSQYIEDSISQGAVC
sp|Q92633|EDG2_HUMAN      -SATFRQILC-CQ----------RSEN----PTGPTEGSDR----SASSLNHTILAGVHS
sp|Q61130|EDG2_MOUSE      -SATFRQILC-CQ----------RNEN----PNGPTEGSDR----SASSLNHTILAGVHS
sp|Q9EQ31|EDG7_MOUSE      -YNTMRKMIC-CALQDSNTER-RPSRN----PSTIHSRSET----GSQYLEDSISQGPVC
sp|Q9JL06|EDG4_MOUSE      -RRTFRRLLC-CMCLR-------WSSH----KSARYSASAQ----TGASTRIMLPENGRP
tr|Q9DC35                 RRAFIRIVSC-CKCPNGDSAG-KFKRP--IIPGMEFSRSKS---DNSSHPQKDDGDNPET
sp|P21453|EDG1_HUMAN      RRAFIRIMSC-CKCPSGDSAG-KFKRP--IIAGMEFSRSKS---DNSSHPQKDEGDNPET
sp|Q99500|EDG3_HUMAN      RRAFFRLV---CNCLVR-GRG-ARASP--IQPALDPSRSKSSSSNNSSHSPKVKEDLPHT
tr|Q8BP20                 RRAFFRLV---CGCLVK-GKG-TQASP--MQPALDPSRSKSSSSNNSSHSPKVKEDLPRV
sp|O95136|EDG5_HUMAN      RREVLRPL----QCWRP-GVG-VQGRRRGGTPGHHLLPLRS---SSSLERGMHMPTSPTF
tr|Q8C3Q7                 RREVLRPL----QCWRR-GKG-VTGRR-GGNPGHRLLPLRS---SSSLERGMHMPTSPTF
tr|Q9Z0L1                 QRAVLAFLCCGCLWLGLRGPGDCLTRITEAHSGASTTDSSLRPRDSFRTSRSLSFRMREP
sp|P47746|CB1R_MOUSE      RHAFRSMFPS-CEGTAQPLDN-SMGDSDCLHKHANNTASMHR--AAESCIKSTVKIAKVT
sp|P21554|CB1R_HUMAN      RHAFRSMFPS-CEGTAQPLDN-SMGDSDCLHKHANNAASVHR--AAESCIKSTVKIAKVT
sp|P33032|MC5R_HUMAN      RKTFKEIIC--CRGFRIACSF-PRRD----------------------------------
tr|Q9EQM7                 RKTFKEIIC--FYPLGGICEL-SSRY----------------------------------
sp|P32245|MC4R_HUMAN      RKTFKEIIC--CYPLGGLCDL-SSRY----------------------------------
sp|P41968|MC3R_HUMAN      RNTFREILCG-CNGMNLG------------------------------------------
                                 .

sp|Q9HBW0|EDG4_HUMAN      LMDSTL--------------
sp|Q9UBY5|EDG7_HUMAN      NKSTS---------------
sp|Q92633|EDG2_HUMAN      NDHSVV--------------
sp|Q61130|EDG2_MOUSE      NDHSVV--------------
sp|Q9EQ31|EDG7_MOUSE      NKNGS---------------
sp|Q9JL06|EDG4_MOUSE      LMDSTL--------------
tr|Q9DC35                 IMSSGNVNSSS---------
sp|P21453|EDG1_HUMAN      IMSSGNVNSSS---------
sp|Q99500|EDG3_HUMAN      DPSSCIMDKNAALQNGIFCN
tr|Q8BP20                 ATSSCIIDKNRSFQNGVLCK
sp|O95136|EDG5_HUMAN      LEGNTVV-------------
tr|Q8C3Q7                 LEGNTVV-------------
tr|Q9Z0L1                 LSSISSVRST----------
sp|P47746|CB1R_MOUSE      MSVSTDTSAEAL--------
sp|P21554|CB1R_HUMAN      MSVSTDTSAEAL--------
sp|P33032|MC5R_HUMAN      --------------------
tr|Q9EQM7                 --------------------
sp|P32245|MC4R_HUMAN      --------------------
sp|P41968|MC3R_HUMAN      --------------------
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Appendix B.

B.1. Sequences used in alignment to predict TM regions of $S1P_1$

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>sp|O08530|EDG1_MOUSE Sphingosine 1-phosphate receptor Edg-
1 (Lysophospholipid receptor B1) - Mus musculus (Mouse).

>sp|Q99500|EDG3_HUMAN Sphingosine 1-phosphate receptor Edg-
3 (S1P receptor Edg-3) (Endothelial differentiation G-
protein-coupled receptor 3) - Homo sapiens (Human).

>sp|Q9Z0U9|EDG3_MOUSE Sphingosine 1-phosphate receptor Edg-
3 (S1P receptor Edg-3) (Endothelial differentiation G-
protein-coupled receptor 3) (Lysophospholipid receptor B3)
- Mus musculus (Mouse).

>sp|O95136|EDG5_HUMAN Sphingosine 1-phosphate receptor Edg-
5 (S1P receptor Edg-5) (Endothelial differentiation G-
protein coupled receptor 5) - Homo sapiens (Human).

>sp|O95977|EDG6_HUMAN Sphingosine 1-phosphate receptor Edg-
6 (S1P receptor Edg-6) (Endothelial differentiation G-
protein coupled receptor 6) - Homo sapiens (Human).

>sp|Q9Z0L1|EDG6_MOUSE Sphingosine 1-phosphate receptor Edg-
6 (S1P receptor Edg-6) (Endothelial differentiation G-
protein coupled receptor 6) (Lysophospholipid receptor C1)
- Mus musculus (Mouse).

>sp|Q92633|EDG2_HUMAN Lysophosphatidic acid receptor Edg-2
(LPA receptor 1) (LPA-1) - Homo sapiens (Human).

>sp|Q8K5E0|EDG7_RAT Lysophosphatidic acid receptor Edg-7
(LPA receptor 3) (LPA-3) (snGPCR32) - Rattus norvegicus
(Rat).

>sp|Q95KH4|EDG4_MACFA Lysophosphatidic acid receptor Edg-4
(LPA receptor 2) (LPA-2) - Macaca fascicularis (Crab eating
macaque) (Cynomolgus monkey).

>sp|Q98894|CB1A_FUGRU Cannabinoid receptor type 1A - Fugu
rubripes (Japanese pufferfish) (Takifugu rubripes).

>sp|P21554|CB1R_HUMAN Cannabinoid receptor 1 (CB1) (CB-R)
(CANN6) - Homo sapiens (Human).
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>sp|P46089|GPR3_HUMAN Probable G protein-coupled receptor
GPR3 (ACCA orphan receptor) - Homo sapiens (Human).

>sp|P51651|GPR6_RAT Probable G protein-coupled receptor
GPR6 (CNL3) - Rattus norvegicus (Rat).

>sp|P46095|GPR6_HUMAN Probable G protein-coupled receptor
GPR6 - Homo sapiens (Human).

>sp|P34972|CB2R_HUMAN Cannabinoid receptor 2 (CB2) (CB-2)
(CX5) - Homo sapiens (Human).
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B.2. Alignment for predicting the TM region of S1P$_1$

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CLUSTAL W (1.74) multiple sequence alignment

unk|VIRT9968|Blast_submission      --------------------------------------------------
sp|O08530|EDG1_MOUSE               --------------------------------------------------
sp|Q99500|EDG3_HUMAN               --------------------------------------------------
sp|Q9Z0U9|EDG3_MOUSE               --------------------------------------------------
sp|O95136|EDG5_HUMAN               --------------------------------------------------
sp|O95977|EDG6_HUMAN               --------------------------------------------------
sp|Q9Z0L1|EDG6_MOUSE               --------------------------------------------------
sp|Q92633|EDG2_HUMAN               --------------------------------------------------
sp|Q8K5E0|EDG7_RAT                 --------------------------------------------------
sp|Q95KH4|EDG4_MACFA               --------------------------------------------------
sp|Q98894|CB1A_FUGRU               MKSVLDGVADTTFRTITSGLQYLGSNDANYDDPLNDAAFKTGFSLQK-PL
sp|P21554|CB1R_HUMAN               MKSILDGLADTTFRTITTDLLYVGSNDIQYEDIKGDMASKLGYFPQKFPL
sp|P46089|GPR3_HUMAN               --------------------------------------------------
sp|P51651|GPR6_RAT                 --------------------------------------MNASAAALNESQ
sp|P46095|GPR6_HUMAN               --------------------------------------MNASAASLNDSQ
sp|P34972|CB2R_HUMAN               --------------------------------------------------


unk|VIRT9968|Blast_submission      ------------MGPT--SVPLVKAHRSSVSDYVNYDIIVRHYN------
sp|O08530|EDG1_MOUSE               ------------MVST--SIPEVKALRSSVSDYGNYDIIVRHYN------
sp|Q99500|EDG3_HUMAN               ---------------------MATALPPRLQPVRGNETLREHYQ------
sp|Q9Z0U9|EDG3_MOUSE               ---------------------MATTHAQGHQPVLGNDTLREHYD------
sp|O95136|EDG5_HUMAN               -------------------------MGSLYSEYLNPNKVQEHYN------
sp|O95977|EDG6_HUMAN               ------------MNAT--GTPVAPESCQQLAAGGHSRLIVLHYN------
sp|Q9Z0L1|EDG6_MOUSE               ------------MNISTWSTLVTPESCHRLAASGHSLLIVLHYN------
sp|Q92633|EDG2_HUMAN               ---------MAAISTSIPVISQPQFTAMNEPQCFYNESIAFFYN------
sp|Q8K5E0|EDG7_RAT                 ---------------------------MN--ECHYDKRMDFFYN------
sp|Q95KH4|EDG4_MACFA               ------------------------MVTMG--HCYYNETIGFFYN------
sp|Q98894|CB1A_FUGRU               SAFRSNSFPNKVPADEELIFKGIPFFPTNSTDLFGNRNTTRDEN--SIQC
sp|P21554|CB1R_HUMAN               TSFRGSPFQEKMTAGDNP--QLVPADQVNITEFYNKSLSSFKENEENIQC
sp|P46089|GPR3_HUMAN               ---------------------MMWGAGSPLAWLSAGSGNVNVSS------
sp|P51651|GPR6_RAT                 VVAVAAEGAAAAATAAGTPDTSEWGPPAASAALGGGGGPNGSLE------
sp|P46095|GPR6_HUMAN               VVVVAAEGAAAAATAAGGPDTGEWGPPAA-AALGAGGGANGSLE------
sp|P34972|CB2R_HUMAN               -----------------------------MEECWVTEIANGSKD------
                                                                              .

unk|VIRT9968|Blast_submission      -YTGKLN--ISADKENSIKLTSVVFILICCFIILENIFVLLTIWKTKKFH
sp|O08530|EDG1_MOUSE               -YTGKLN--IGAEKDHGIKLTSVVFILICCFIILENIFVLLTIWKTKKFH
sp|Q99500|EDG3_HUMAN               -YVGKLAGRLKEASEG-STLTTVLFLVICSFIVLENLMVLIAIWKNNKFH
sp|Q9Z0U9|EDG3_MOUSE               -YVGKLAGRLRDPPEGGTLITTILFLVTCSFIVLENLMVLIAIWKNNKFH
sp|O95136|EDG5_HUMAN               -YTKETL---ETQETTSRQVASAFIVILCCAIVVENLLVLIAVARNSKFH
sp|O95977|EDG6_HUMAN               -HSGRLAGRGGPEDGG-LGALRGLSVAASCLVVLENLLVLAAITSHMRSR
sp|Q9Z0L1|EDG6_MOUSE               -HSGRLASRGGSEDGGGLGMLRGPSVAAGCLVVLENAMVLAAIAIYMRSR
sp|Q92633|EDG2_HUMAN               -RSGKHL--ATEWN-TVSKLVMGLGITVCIFIMLANLLVMVAIYVNRRFH
sp|Q8K5E0|EDG7_RAT                 -RSNTDT--ADEWTGTKLVIVLCVGTFFCLFIFFSNSLVIAAVITNRKFH
sp|Q95KH4|EDG4_MACFA               -NSGKEL--SSHWR-PKDVVVVALGLTVSVLVLLTNLLVIAAIASNRRFH
sp|Q98894|CB1A_FUGRU               GENFMDMECFMILTPSQQLAVAVLSLTLGTFTVLENLVVLCVIFQSRTLR
sp|P21554|CB1R_HUMAN               GENFMDIECFMVLNPSQQLAIAVLSLTLGTFTVLENLLVLCVILHSRSLR
sp|P46089|GPR3_HUMAN               -VGPAEGPTGPAAPLPSPKAWDVVLCISGTLVSCENALVVAIIVGTPAFR
sp|P51651|GPR6_RAT                 -LSSQLPAGPSGLLLSAVNPWDVLLCVSGTVIAGENALVVALIASTPALR
sp|P46095|GPR6_HUMAN               -LSSQLSAGPPGLLLPAVNPWDVLLCVSGTVIAGENALVVALIASTPALR
sp|P34972|CB2R_HUMAN               GLDSNPMKDYMILSGPQKTAVAVLCTLLGLLSALENVAVLYLILSSHQLR
                                                                      *  *:  :      :

unk|VIRT9968|Blast_submission      R-PMYYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLREGSMFV
sp|O08530|EDG1_MOUSE               R-PMYYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLREGSMFV
sp|Q99500|EDG3_HUMAN               N-RMYFFIGNLALCDLLAGIAYKVNILMSGKKTFSLSPTVWFLREGSMFV
sp|Q9Z0U9|EDG3_MOUSE               N-RMYFFIGNLALCDLLAGIAYKVNILMSGRKTFSLSPTVWFLREGSMFV
sp|O95136|EDG5_HUMAN               S-AMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFI
sp|O95977|EDG6_HUMAN               R-WVYYCLVNITLSDLLTGAAYLANVLLSGARTFRLAPAQWFLREGLLFT
sp|Q9Z0L1|EDG6_MOUSE               R-WVYYCLLNITLSDLLTGLAYVVNVLLSGTRTFQLSPVHWFLREGLLFM
sp|Q92633|EDG2_HUMAN               F-PIYYLMANLAAADFFAGLAYFYLMFNTGPNTRRLTVSTWLLRQGLIDT
sp|Q8K5E0|EDG7_RAT                 F-PFYYLLANLAAADFFAGIAYVFLMFNTGPVSKTLTVNRWLLRQGLLDT
sp|Q95KH4|EDG4_MACFA               Q-PIYYLLGNLAAADLFAGVAYLFLMFHTGPRTARLSLEGWFLRQGLLDT
sp|Q98894|CB1A_FUGRU               CRPSYHFIGSLAVADLLGSVIFVYSFLDFHVFHKKDSPNVFLFKLGGVTA
sp|P21554|CB1R_HUMAN               CRPSYHFIGSLAVADLLGSVIFVYSFIDFHVFHRKDSRNVFLFKLGGVTA
sp|P46089|GPR3_HUMAN               A-PMFLLVGSLAVADLLAGLG---LVLHFAAVFCIGSAEMSLVLVGVLAM
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sp|P51651|GPR6_RAT                 T-PMFVLVGSLATADLLAGCG---LILHFVFQYVVPSETVSLLMVGFLVA
sp|P46095|GPR6_HUMAN               T-PMFVLVGSLATADLLAGCG---LILHFVFQYLVPSETVSLLTVGFLVA
sp|P34972|CB2R_HUMAN               RKPSYLFIGSLAGADFLASVVFACSFVNFHVFHGVDSKAVFLLKIGSVTM
                                       :  : .:: .*:: .       .         :    :   *

unk|VIRT9968|Blast_submission      ALSASVFSLLAIAIERYITMLK-MKLHNGSNNFRLFLLISACWVISLILG
sp|O08530|EDG1_MOUSE               ALSASVFSLLAIAIERYITMLK-MKLHNGSNSSRSFLLISACWVISLILG
sp|Q99500|EDG3_HUMAN               ALGASTCSLLAIAIERHLTMIK-MRPYDANKRHRVFLLIGMCWLIAFTLG
sp|Q9Z0U9|EDG3_MOUSE               ALGASTCSLLAIAIERHLTMIK-MRPYDANKKHRVFLLIGMCWLIAFSLG
sp|O95136|EDG5_HUMAN               TLSASVFSLLAIAIERHVAIAK-VKLYGSDKSCRMLLLIGASWLISLVLG
sp|O95977|EDG6_HUMAN               ALAASTFSLLFTAGERFATMVRPVAESGATKTSRVYGFIGLCWLLAALLG
sp|Q9Z0L1|EDG6_MOUSE               ALAASTFSLLFTAGERFATMVR-VAESGATKTSRVYGCIGLCWLLAAILG
sp|Q92633|EDG2_HUMAN               SLTASVANLLAIAIERHITVFR-MQLHTRMSNRRVVVVIVVIWTMAIVMG
sp|Q8K5E0|EDG7_RAT                 SLTASLANLLVIAVERHMSIMR-MRIHSNLTKKRVTLLILLVWAIAIFMG
sp|Q95KH4|EDG4_MACFA               SLTASVATLLAIAVERRRSVMA-VQLHSRLPRGRVVMLIVGVWVAALGLG
sp|Q98894|CB1A_FUGRU               SFTASVGSLFLTAIDRYISIHRPLAYRRIVTRTKAVIAFCMMWTISIIIA
sp|P21554|CB1R_HUMAN               SFTASVGSLFLTAIDRYISIHRPLAYKRIVTRPKAVVAFCLMWTIAIVIA
sp|P46089|GPR3_HUMAN               AFTASIGSLLAITVDRYLSLYNALTYYSETTVTRTYVMLALVWGGALGLG
sp|P51651|GPR6_RAT                 SFAASVSSLLAITVDRYLSLYNALTYYSRRTLLGVHLLLAATWTVSLGLG
sp|P46095|GPR6_HUMAN               SFAASVSSLLAITVDRYLSLYNALTYYSRRTLLGVHLLLAATWTVSLGLG
sp|P34972|CB2R_HUMAN               TFTASVGSLLLTAIDRYLCLRYPPSYKALLTRGRALVTLGIMWVLSALVS
                                   :: **  .*:  : :*   :                  :   *  :  :.

unk|VIRT9968|Blast_submission      GLPIMGWNCISALSSCSTVLPLYHKHYILFCTTVFTLLLLSIVILYCRIY
sp|O08530|EDG1_MOUSE               GLPSMGWNCISSLSSCSTVLPLYHKHYILFCTTVFTLLLLSIVILYCRIY
sp|Q99500|EDG3_HUMAN               ALPILGWNCLHNLPDCSTILPLYSKKYIAFCISIFTAILVTIVILYARIY
sp|Q9Z0U9|EDG3_MOUSE               ALPILGWNCLENFPDCSTILPLYSKKYIAFLISIFTAILVTIVILYARIY
sp|O95136|EDG5_HUMAN               GLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSIILLAIVALYVRIY
sp|O95977|EDG6_HUMAN               MLPLLGWNCLCAFDRCSSLLPLYSKRYILFCLVIFAGVLATIMGLYGAIF
sp|Q9Z0L1|EDG6_MOUSE               LLPLLGWNCVCAFPRCSSLLPLYSKGYVLFCVVVFALILVAILSLYGAIF
sp|Q92633|EDG2_HUMAN               AIPSVGWNCICDIENCSNMAPLYSDSYLVFWAIFNLVTFVVMVVLYAHIF
sp|Q8K5E0|EDG7_RAT                 AVPTLGWNCLCNISACSSLAPIYSRSYLIFWTVSNLLAFFIMVVVYVRIY
sp|Q95KH4|EDG4_MACFA               LLPAHSWHCLCALDRCSRMAPLLSRSYLAVWALSSLLVFLLMVAVYTRIF
sp|Q98894|CB1A_FUGRU               VLPLLGWNCKRLNSVCSDIFPLIDENYLMFWIGVTSVLVLFIIYAYIYIL
sp|P21554|CB1R_HUMAN               VLPLLGWNCEKLQSVCSDIFPHIDETYLMFWIGVTSVLLLFIVYAYMYIL
sp|P46089|GPR3_HUMAN               LLPVLAWNCLDGLTTCGVVYP-LSKNHLVVLAIAFFMVFGIMLQLYAQIC
sp|P51651|GPR6_RAT                 LLPVLGWNCLADRASCSVVRP-LTRSHVALLSTSFFVVFGIMLHLYVRIC
sp|P46095|GPR6_HUMAN               LLPVLGWNCLAERAACSVVRP-LARSHVALLSAAFFMVFGIMLHLYVRIC
sp|P34972|CB2R_HUMAN               YLPLMGWTCCP--RPCSELFPLIPNDYLLSWLLFIAFLFSGIIYTYGHVL
                                    :*  .* *      *. : *     ::          .  ::  *  :

unk|VIRT9968|Blast_submission      SLVRTRSRRLTFRKNIS--------------KASRSSE-NVALLKTVIIV
sp|O08530|EDG1_MOUSE               SLVRTRSRRLTFRKNIS--------------KASRSSEKSLALLKTVIIV
sp|Q99500|EDG3_HUMAN               FLVKSSSRKVANHNN---------------------SERSMALLRTVVIV
sp|Q9Z0U9|EDG3_MOUSE               CLVKSSSRRVANHN----------------------SERSMALLRTVVIV
sp|O95136|EDG5_HUMAN               CVVRSSHADMAAPQ-------------------------TLALLKTVTIV
sp|O95977|EDG6_HUMAN               RLVQASGQKAPRPA---------------------ARRKARRLLKTVLMI
sp|Q9Z0L1|EDG6_MOUSE               RVVRANGQKSPRPP---------------------ARRKSRRLLNTVLMI
sp|Q92633|EDG2_HUMAN               GYVRQRTMRMSRHSSGP--------------R--RNRDTMMSLLKTVVIV
sp|Q8K5E0|EDG7_RAT                 MYVKRKTNVLSPHTSGS--------------I--SRRRAPMKLMKTVMTV
sp|Q95KH4|EDG4_MACFA               FYVRRRVQRMAEHVSCH--------------P--RYRETTLSLVKTVVII
sp|Q98894|CB1A_FUGRU               WKAHHHAVRMLSRTSQKSLVVYSAEGTKVQTTRPEQTRMDIRLAKTLVLI
sp|P21554|CB1R_HUMAN               WKAHSHAVRMIQRGTQKSIIIHTSEDGKVQVTRPDQARMDIRLAKTLVLI
sp|P46089|GPR3_HUMAN               RIVCRHAQQIALQRHLL--------------PA-SHYVATRKGIATLAVV
sp|P51651|GPR6_RAT                 QVVWRHAHQIALQQHCL--------------AP-PHLAATRKGVGTLAVV
sp|P46095|GPR6_HUMAN               QVVWRHAHQIALQQHCL--------------AP-PHLAATRKGVGTLAVV
sp|P34972|CB2R_HUMAN               WKAHQHVASLSGHQDRQ-------------VPGMARMRLDVRLAKTLGLV
                                     .                                          *:  :

unk|VIRT9968|Blast_submission      LSVFIACWAPLFILLLLDVG-CKVKTCDILFRAEYFLVLAVLNSGTNPII
sp|O08530|EDG1_MOUSE               LSVFIACWAPLFILLLLDVG-CKAKTCDILYKAEYFLVLAVLNSGTNPII
sp|Q99500|EDG3_HUMAN               VSVFIACWSPLFILFLIDVA-CRVQACPILFKAQWFIVLAVLNSAMNPVI
sp|Q9Z0U9|EDG3_MOUSE               VSVFIACWSPLFILFLIDVA-CRAKECSILFKSQWFIMLAVLNSAMNPVI
sp|O95136|EDG5_HUMAN               LGVFIVCWLPAFSILLLDYA-CPVHSCPILYKAHYFFAVSTLNSLLNPVI
sp|O95977|EDG6_HUMAN               LLAFLVCWGPLFGLLLADVFGSNLWAQEYLRGMDWILALAVLNSAVNPII
sp|Q9Z0L1|EDG6_MOUSE               LVAFVVCWGPLFGLLLADIFGSNVWAQEYLRGMDWILALAVFNSAINPLI
sp|Q92633|EDG2_HUMAN               LGAFIICWTPGLVLLLLD---VCCPQCDVLAYEKFFLLLAEFNSAMNPII
sp|Q8K5E0|EDG7_RAT                 LGAFVVCWTPGLVVLLLDG--LNCKQCNVQHVKRWFLLLALLNSVMNPII
sp|Q95KH4|EDG4_MACFA               LGAFVVCWTPGQVVLLLDG--LGCKSCNVLAVEKYFLLLAEANSLVNAAV
sp|Q98894|CB1A_FUGRU               LAVLVICWGPLLAIMVYDL--FWKMDDNIKTVFAFCSMLCLLNSTVNPII
sp|P21554|CB1R_HUMAN               LVVLIICWGPLLAIMVYDV--FGKMNKLIKTVFAFCSMLCLLNSTVNPII
sp|P46089|GPR3_HUMAN               LGAFAACWLPFTVYCLLG------DAHSPPLYTYLTLLPATYNSMINPII
sp|P51651|GPR6_RAT                 LGTFGASWLPFAIYCVVG------SQEDPAIYTYATLLPATYNSMINPII
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sp|P46095|GPR6_HUMAN               LGTFGASWLPFAIYCVVG------SHEDPAVYTYATLLPATYNSMINPII
sp|P34972|CB2R_HUMAN               LAVLLICWFPVLALMAHSLA--TTLSDQVKKAFAFCSMLCLINSMVNPVI
                                   : .:  .* *       .                     .  **  *. :

unk|VIRT9968|Blast_submission      YTLTNKEMRRAFIRIM---SCCKCPSGDSAGKFKRPIIA-GMEFSRSKS-
sp|O08530|EDG1_MOUSE               YTLTNKEMRRAFIRIV---SCCKCPNGDSAGKFKRPIIP-GMEFSRSKS-
sp|Q99500|EDG3_HUMAN               YTLASKEMRRAFFRLV---CNCLVRG---RGARASPIQP-ALDPSRSKSS
sp|Q9Z0U9|EDG3_MOUSE               YTLASKEMRRAFFRLV---CGCLVKG---KGTQASPMQP-ALDPSRSKSS
sp|O95136|EDG5_HUMAN               YTWRSRDLRREVLRP----LQCWRPGVGVQGRRRGGTPGHHLLPLRSSSS
sp|O95977|EDG6_HUMAN               YSFRSREVCRAVLSFLC--CGCLRLGMRGPGDCLARAVEAHSGASTTDSS
sp|Q9Z0L1|EDG6_MOUSE               YSFRSREVQRAVLAFLC--CGCLWLGLRGPGDCLTRITEAHSGASTTDSS
sp|Q92633|EDG2_HUMAN               YSYRDKEMSATFRQILC--CQRSEN-------------PTGPTEGSDRSA
sp|Q8K5E0|EDG7_RAT                 YSYKDEDMYNTMRKMIC--CAPHDSN----AERHPSRIPSTIHSRSDTGS
sp|Q95KH4|EDG4_MACFA               YSCRDAEMRRTFRRLLC--CACLRRS----TR------ESAHYTSSAQGG
sp|Q98894|CB1A_FUGRU               YALRSRDLRHAFLSSC---HACRGSAQQLDNSL--ESDCQNRNVN--ISA
sp|P21554|CB1R_HUMAN               YALRSKDLRHAFRSMF---PSCEGTAQPLDNSMG-DSDCLHKHANNAASV
sp|P46089|GPR3_HUMAN               YAFRNQDVQKVLWAVC---CCCSSS-------------KIPFRSRSPSDV
sp|P51651|GPR6_RAT                 YAFRNQEIQRALWLLF---CGCFQS-------------KVPFRSRSPSEV
sp|P46095|GPR6_HUMAN               YAFRNQEIQRALWLLL---CGCFQS-------------KVPFRSRSPSEV
sp|P34972|CB2R_HUMAN               YALRSGEIRSSAHHCLAHWKKCVRG------------LGSEAKEEAPRSS
                                   *:  . ::

unk|VIRT9968|Blast_submission      --DNSSHPQKDEGDNPETIMSSGNVNSSS---------
sp|O08530|EDG1_MOUSE               --DNSSHPQKDDGDNPETIMSSGNVNSSS---------
sp|Q99500|EDG3_HUMAN               SSNNSSHSPKVKEDLPHTAPSSCIMDKNAALQNGIFCN
sp|Q9Z0U9|EDG3_MOUSE               SSNNSSHSPKVKEDLPRVATSSCIIDKNRSFQNGVLCK
sp|O95136|EDG5_HUMAN               -LERGMHMPTS----PTFLEGNTVV-------------
sp|O95977|EDG6_HUMAN               LRPRDSFRGSRSLSFRMREPLSSISSVRSI--------
sp|Q9Z0L1|EDG6_MOUSE               LRPRDSFRTSRSLSFRMREPLSSISSVRST--------
sp|Q92633|EDG2_HUMAN               SSLNHTILAGV-----HSNDHSVV--------------
sp|Q8K5E0|EDG7_RAT                 QYLEDSISQGQ-----VCNKSSS---------------
sp|Q95KH4|EDG4_MACFA               ASTRIMLPENG-----HPLMDSTL--------------
sp|Q98894|CB1A_FUGRU               NRAAESCVKTTVKIAKVTMSVSTETSAEAV--------
sp|P21554|CB1R_HUMAN               HRAAESCIKSTVKIAKVTMSVSTDTSAEAL--------
sp|P46089|GPR3_HUMAN               --------------------------------------
sp|P51651|GPR6_RAT                 --------------------------------------
sp|P46095|GPR6_HUMAN               --------------------------------------
sp|P34972|CB2R_HUMAN               VTETEADGKITPWPDSRDLDLSDC--------------
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