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agrin_triad_lamg1  AIPSFHDGSYIRFKNTSTWDR....EVNLTIEFMPSVFDGLILIGGNLVSS
agrin_triad_lamg2  FSPYFGGQSYLEYTD.KTSDYFAASSVTINLKVKPLKPNGLIFYGSQREDN
agrin_triad_lamg3  PSVAFDGGNVYTLRNNISADEKEFNFNTIELQLKTFNLHGLILWSGPRNYS
agrin_triad_lamg4  PSLAFDGRSAYPYLNNVDNRLTVSSIQSFQLSFKTLSSNGLILWHG.....
agrin_triad_lamg5  PAYWFTPTSYITLLSAVTEKKNSFSSNRYEFLVRGYH.NGLLLWLGQSQPN
agrin_triad_lamg6  PPVSFSGSKAVRYLSDVNRGLRAFRQNSLRLTFKTRKSTAVLFWLG..NDN
agrin_apime_lamg1  EVASFDGKSYVRMNRLKAY.....HKFSVEVEFKTYADNGIILYNQQKSDG
agrin_apime_lamg2  LIPEMSGDGFLELPCLEGVAKA....FSIELWFLTHASDGLLLYNGQLNNG
agrin_apime_lamg3  RPVRFKGDNFLQFRHRNGRRRKGQQSNKFELRLRTTHPDGLIAWIG.....
agrin_strpu_lamg1  TTPSFAGDSYLAYPEMDAF.....MEVEIVIEFQPGATEGVLLYEAQTAEG
agrin_strpu_lamg2  VVPGFAGNSYMQLPSLM.MPDD....SVIDVEFLTSSPDGVIFYNGQTADG
agrin_strpu_lamg3  DPLRFDGQTSIQYYNGVSKKQRALRTHQIQLSFKTAEPNGALFWNG..VGN
agrin_human_lamg1  PVPAFEGRSFLAFPTLRAY.....HTLRLALEFRALEPQGLLLYNG.NARG
agrin_human_lamg2  FLADFNGFSHLELRGLHTFARDLGEKMALEVVFLARGPSGLLLYNGQKTDG
agrin_human_lamg3  DTLAFDGRTFVEYLNAVTESEKALQSNHFELSLRTEATQGLVLWSGKATER

agrin_triad_lamg1  ....NGDYFALSLRSRYIE.........ASFELGSGKGTA.SSKIAVEVNR
agrin_triad_lamg2  ....RGDFILLNLVEGYLEFR.........FDLGSGT.AVIRSASPLTLNN
agrin_triad_lamg3  QNQR.RPFIALAVTNGNIQLR.........FNLGTQDNHIT.STVRINDGN
agrin_triad_lamg4  .NQKPGDFISVGIRNKFVELN.........YNLGSGTKTLTGGWQQVNDDK
agrin_triad_lamg5  PNR...DYLGVAIVNNRVQLR.........FNVGSGKIEIVVDVI.VTDGY
agrin_triad_lamg6  DPRLRSDYMSAAVEAGYFKIR.........YNLGGGATSSTILTLRVDDNQ
agrin_apime_lamg1  ....TGDFVSLAIVDGHVQFR.........YNLGNG.PVILTSPERVTMKT
agrin_apime_lamg2  ....RGDFISLNLVQAKLEFR.........FNLGSGI.ANITSPDPVTLDT
agrin_apime_lamg3  ..RGKVEHLILSLHGGQVLLTYKSKNEQIS..........LRSRERVDDGV
agrin_strpu_lamg1  ....NGDFISLAIVNNQVEFRFLATDQSNGFDLGSAEPVVITSTVDLQLMT
agrin_strpu_lamg2  ....RGDFISLNMRDGYLEFR.........YDLGSSI.AEIKSVDRLALNE
agrin_strpu_lamg3  .....ADFQAVGVSDGYVEYA.........YNLGRGITRI.RTTQKVDNNK
agrin_human_lamg1  ....K.DFLALALLDGRVQLR.........FDTGSG.PAVLTSAVPVEPGQ
agrin_human_lamg2  ....KGDFVSLALRDRRLEFR.........YDLGKGA.AVIRSREPVTLGA
agrin_human_lamg3  .....ADYVALAIVDGHLQLS.........YNLGSQPVVL.RSTVPVNTNR

agrin_triad_lamg1  WYRATVKRSGRDFTIQVNEEPPVVGKVPGSLSELNSLTDIYLGTLPSGLST
agrin_triad_lamg2  SHDINITRNGRYGTMRIDQQPEVRGIASGSFVLLSLFAPFYFGGH..P.NF
agrin_triad_lamg3  WHTIKAYRIGRQANLTVDTEF.RSTTVSTGSPQIAVDGDLFLGGLNTTPKK
agrin_triad_lamg4  WHKVLVDRQSRYGNLTVDGRS.ITGFANPSATELNAADYLYLGGVENIAAK
agrin_triad_lamg5  WHKVKIERNGSSGTLTVDGVSQKSN.PREGASVLNVDGNILIGGTPNIATT
agrin_triad_lamg6  WHTVYINRNLTNALLYVD.HLETSAISLQFQQELNVASYFYLGGVPE....
agrin_apime_lamg1  FHSVAAKRYHKDGVLIFNDGEDVVGQSQGMLKSLDLNQDTFVG.NMPT.NY
agrin_apime_lamg2  WHCVRISRLGREGVLQLDDGTVARGLSGSPLTELNLEMPLYVGGL..K.HW
agrin_apime_lamg3  FHQIRASRRRRTSMIQVDDSAPVKVSTE..MTLLTTNGKLFVGGKPG....
agrin_strpu_lamg1  WHRLRAYRSRREGSLSVDGEPEVTGTSEGVSGALNLGEDLFIGYAVPP.E.
agrin_strpu_lamg2  WHAVRVIRMGKSGEMILNDLPPVKGTSPPGASQLNLRQPLFIGGV..R.SY
agrin_strpu_lamg3  WHTVIITRNLIDASLQVDNEEPVMGQSRAGASQLDTDGFLYLGQGVNVP..
agrin_human_lamg1  WHRLELSRHWRRGTLSVDGETPVLGESPSGTDGLNLDTDLFVG.GVPE.DQ
agrin_human_lamg2  WTRVSLERNGRKGALRVGDGPRVLGESPVPHTVLNLKEPLYVGGA..P.DF
agrin_human_lamg3  WLRVVAHREQREGSLQVGNEAPVTGSSPLGATQLDTDGALWLGGLPELPVG

agrin_triad_lamg1  SNQFRSRIQMNQNFGGCIRSLDINNIEYNLNVPSSNKPDNVVSYYQLTRCV
agrin_triad_lamg2  AAMN.SKTKIKTGLVGCIESVTINGQEKQL......VKD.AIYGAGVSSCN
agrin_triad_lamg3  NW..NL...YRYNYVGCIRNIQIQHHKVNI......VTDLKVPQ.QHTTCE
agrin_triad_lamg4  TS..NL...YYSFYEGCVKEVKLSGVSLNM......QRDIQIRQ.RLYTCQ
agrin_triad_lamg5  TS..NK...YLENYRGCLKNFVIDGFVVNL......QL.MATESVNTKSCP
agrin_triad_lamg6  NNIDYT...SNDNFIGCMANVEVNGKIVQL......SDDAVDPNISLPRCQ
agrin_apime_lamg1  SKV.YENIGTNHGFLGCIRLKINRIHVDLHV...GRDKEILETYRVKECG
agrin_apime_lamg2  REIH.RLAGARTGLVGAIQRLMVNGKTYQN......LA.VNVTQHNTEIYD
agrin_apime_lamg3  .........HRGIKGCVSDFVVDKRRLQLGRR...........RIEYCH
agrin_strpu_lamg1  ..VGLRLANTNQGFVGCIRYVEINSQELDISS...S.GSSVEYGANVGECG
agrin_strpu_lamg2  GEVS.RRAAITDGLNGAVRRFVVNEVDYST......LKDFAEAKVNVEEFR
agrin_strpu_lamg3  GSMESS...Y.TYYTGCIQDVLLDEVPLHL......YENAQGEKPSLF.CS
agrin_human_lamg1  AAVALERTFVGAGLRGCIRLLDVNNQRLELGI...G.PGAATRGSGVGECG
agrin_human_lamg2  SKLA.RAAAVSSGFDGAIQLVSLGGRQLLT......PEHV.LRQVDVTSFA
agrin_human_lamg3  PALPKA...YGTGFVGCLRDVVVGRHPLHL......LEDAV.TKPELRPCP
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