

agrin_triad_fs1 CSEIVCRMGATCSNEIQEG.....QCS..IDCHNLTKSE....P
agrin_triad_fs2 CNNITCENYSICRLESNGITDNNPTCRCPNVC.....SLYYNP
agrin_caeel_fs1 CEQSLCPFGSKC.....GLKTGVCEC.KARCRVVDV.....
agrin_caeel_fs2 CEDLRGPGEDCVVNQINGILLA.KVCVCP.TQCPNYGDSVE.SSP
agrin_apime_fs1 CEKTYCSWGATC..VVSENGK.P.LCQCP.TDCPS.....TSEP
agrin_apime_fs2 CTKLNCSQGSQCVRSR.DG.SEA.SCECL.ESCPSLGDHEG.SSP
agrin_strpu_fs1 CDMVLCIFGAVCEEN..EQGR.P.QCICDRQ.CPD.....MMA
agrin_strpu_fs2 CEGVQCSFGSEC..MI.EGDR.A.TCECP.NACPL.....IYSP
agrin_cioin_fs1 COEVLGCGYGASCQAV..DEDT.T.TCVCPVSCSASPPTEDILAP
agrin_cioin_fs2 CSTVTCDFNAACVVRPSDDGSLAPECECP..TCENVA.....VEP
agrin_chick_fs1 CRGMLCGFGAVCERSPTDPSQ.A.SCVCKKTACPV.....VVAP
agrin_chick_fs2 CAEVTCSFGSTCVRSA.DG.QTA.GCVCEP.ASCSGVAE.....SI
agrin_rat_fs1 CRGMLCGFGAVCEPSVEDPGR.A.SCVCKKNACPA.....TVAP
agrin_rat_fs2 CANVTCSEFGSTCVPSA.DG.QTA.SCLCP.TTCFGAPD.....GT

agrin_triad_fs1 VCASDLKVVYSNTCOLERQSCLTGT...QLNILPRDNC
agrin_triad_fs2 ICGNNNKTYYTQCHMIQDSC...QNNITVIKSYGGECE
agrin_caeel_fs1 VCGSDHVSYSYSSFCCHLSVRSCVLAKNGVRLRVATKGPC
agrin_caeel_fs2 VCGSSHGVYQSSCHLRHHACESKT...NITVKFFGRC
agrin_apime_fs1 VCGSDNVTYTNYCHLRKSSCLERK...STRVKNQGAC
agrin_apime_fs2 VCGTDGTDYPSLCEMNRAACAKGA...NITMAFQGKC
agrin_strpu_fs1 VCGSDGTTYLSECFLDKASCEQKK...RVYVASQGSCE
agrin_strpu_fs2 ICGSDGVSYGNTCEMEAASCROQK...EITLVNEGMC
agrin_cioin_fs1 ICGSDGVTYPNECRLRAAECMAQH...RIKIKATTSC
agrin_cioin_fs2 VCGSDQRSHRSSCDLRRASCVEGR...VITVVRNSAC
agrin_chick_fs1 VCGSDYSTYSNECELEKAQCNOQR...RIKVISKGPC
agrin_chick_fs2 VCGSDGKDYRSECDLNKHACDKQE...NVFKKFDGAC
agrin_rat_fs1 VCGSDASTYSNECELQRAQCNOQR...RIRLLRQGPC
agrin_rat_fs2 VCGSDGVDPSECCQLLSHACASQE...HIFKKFNGPC