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agrin_triad_nta    CSPSPLQQRI.....SNADYVITAKVLN...INRNQQQPTYSSNVEV
agrin_caeel_nta    CLKPRPTRSYIHSLFENSDVIIAGVITGISY....RVDSLYIENITV
agrin_strpu_nta    CQEYPVEKRE.....EIANVVISGYIH..RIMR.KPRTIMYDCDIEV
agrin_cioin_nta    CLDRTTTEKN.....STSTVILTGTVQYCDVIRAG....SYKCNIKI
agrin_danre_nta    CSEKELEKRE.....EEANVVLTGTVE..EILNMDPVHNTYSCKVRV
agrin_chicken_nta  CPERELQRRE.....EEANVVLTGTVE..EIMNVDPVHHTYSCKVRV
agrin_mouse_nta    CPERALERRE.....EEANVVLTGTVE..EILNVDPVQHTYSCKVRV
agrin_human_nta    CPERALERRE.....EEANVVLTGTVE..EILNVDPVQHTYSCKVRV

agrin_triad_nta    I..EVFKPPRLSLPL................SITIDNFGNTRICRSN
agrin_caeel_nta    IPRRIYKGREYV...............EENKNIVIGNILETEPCAHR
agrin_strpu_nta    V..RVFKGSEAL.......YSNVVPPMD.GNTIQIGGFGDPAICDNA
agrin_cioin_nta    W..RVMKGNSLAMNLITIQKQGILTSMYKKKYVDVYGLGNSAFCKSN
agrin_danre_nta    W..RYLKGKTMV.......NGEVL..LDGGNKVMIGGFGDPHICDNQ
agrin_chicken_nta  W..RYLKGKDIV.......THEIL..LDGGNKVVIGGFGDPLICDNQ
agrin_mouse_nta    W..RYLKGKDVV.......AQESL..LDGGNKVVIGGFGDPLICDNQ
agrin_human_nta    W..RYLKGKDLV.......ARESL..LDGGNKVVISGFGDPLICDNQ

agrin_triad_nta    VNTNDTRILLFN........GSSQKYVLSTSFEYVTEERLKLIRTA
agrin_caeel_nta    LLASDVRIFSLT........NQQGVFLLDAPMIRLTGNEEERNKVA
agrin_strpu_nta    VTPGETRIFMMN.......KNGNGHLMLNSSVIRITLNNLVQAEAA
agrin_cioin_nta    VERADTRIFFLNKL.........NNRLVVSASLDRITLKNLENTQKV
agrin_danre_nta    VATGDTRIFFVNLAPEYMWPNHKNELMLNSSLMRITLRNLEEVEHC
agrin_chicken_nta  VSTGDTRIFFVNPAPQYMWPAHRNELMLNSSLMRITLRNLEEVEHC
agrin_mouse_nta    VSTGDTRIFFVNPAPPYLWPAHKNELMLNSSLMRITLRNLEEVEFC
agrin_human_nta    VSTGDTRIFFVNPAPPYLWPAHKNELMLNSSLMRITLRNLEEVEFC
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