

TGGT1_294860	MGRSDLIETCCRLQRSCKDLQCSLDELREDEGARLGAEKADLEREVAQTELLERLHRDDGVVGNFFKDIGIHQISDFIQHVRTQTPEAAAAAAAAAAAAAAAAAFGSSASALMKETQKHQFG	120
NCLIV_001740	MGRHDLIETCCRLQRSCKDLQCSLDELHDEDARLRAERTDLERQVAETQVLLERLHRDDGVVGNFFKDIGIHQISDFIQVVRTQTPEAAAAAAAAAAAAAAAAAFGSSASALMKETQKHQFG	120
TGGT1_294860	IRREPVLDSLRRQAAGLREQQG-PVFQATQRKGEALLSSAERAASD-SIFTASSSSLAGKTPTEAAKEIARAMTEAATEAWHRTSSQRLGLAGAGEKKAKHEEAKASPLLESEEKQE	238
NCLIV_001740	VRRDALPDRHGRLEAGGFPCGKDQDRNPVNTTGDALNSRERVADVPEAQTGSSSLSGKTPAEAAKEIARAMTEAATEAWHRTSSQRLGLAGAGEKTEVEGKQTH-QEGEEKKEKE	239
TGGT1_294860	ERSRQDPFSDLVMRVAVGQGGSSVRALLQRKQTEERLQRQIAQWLDASSLSIEEVPSPQAFVPSLASGLTPALSTVTSYSSSGASLAVTPGVSLPVDPPRESEAVRGEPCGEAGAN	358
NCLIV_001740	GRNWQDPFSDLVMKAVGQGGSSVRALLQRKQTEERLQRQIAQWLDASSLSIEEVPSPQAFPLPLGLASGLTAAPPSPVFSSSSLAASGVSPGVCMDAQPTDSQAGSGESVCAEGDG	359
TGGT1_294860	SEKATQEGPAEVFEVPEAGADVPLSTHEERQARQLCDARLLAMQVEKALGMLDIGRFAPQYLPSAACSAPADAYSTQKKDGSAPGEGDS-RAEGKRDGDACSGFIDGSSLDDLCARVFG	477
NCLIV_001740	GKAAQDTASNLQAGGQGDGPSTLSAEERQARQLCDARLLAMQVEKALGMFDIGRFAPQYVAAA--PAASYLLKGDASARPHGERAPDRTRDRDASGFADG-SLDDL CARVFG	475
TGGT1_294860	EQRNDTPVQIEAPQREKLRPQERQDSKADSDKDAVEMKELHKGRTASCVDAGSRGG-GGVLETSSKENDEGEQESERSPLCEGAASPAESQAEQQ--PSDANGLSQPSSQEDGGFYA	594
NCLIV_001740	GNAQTKKAPGS-QQKKQSPETGGLRSKA--DAETVEE---AQETGGAN-SDAMSRGDAPSLLEAKSNRAGVESDSSLPSRLCQAGLTSQAQSPAPSQKLPREDFPSPQPREEEARASP	588
TGGT1_294860	ASSELREDGDLETSSP--E--KTKIVFEREKPREEGREPASVPPAEQAEETPSAVHALAPASVWTEGPPALGARGKKEAEIETGRLEEAHGDTTGGAPGASKSRNETASLPASSSPF	709
NCLIV_001740	--APIRSREGEACVQATRSSCCMQLSECESSQEEAAETASVPHTQAAGPTKALDALAQTHSPHQDPLGVKGEVEVAKEESSLK-ETLADTAPQVGVCDSPKSNATSQAQSAKSCF	705
TGGT1_294860	SPASAMTECQLLPDGAFLSWKFGPEPRALVAAAPAGTCRQLEQVSVLDTAQFEAASLKVSSSKTASPSGLLAPMQKTRAAATLLDLSQLEREYHLTLIARCMQLTFSTGVEEDCGE	829
NCLIV_001740	SPSPMPTVTKLLPDGAVFLSWQFGPEPRTLASAPPACRQLEQVMSLDLTAQFEAATMRS---AAAPSGIQPMPQKTRASTLLLESQGREYHLTLIVRCLFETFTGVEEDCGA	821
TGGT1_294860	PVCGVTVHFRHLHADGLRSLRMRPVSLSTLAF-FPT--RRHAAPLPASTPHNAPAPTSYHSPSLNNGNGSSAVTDQEYCSASSPPASSSLASSSSSVASSFARASAVRQKAGQPQVQ	946
NCLIV_001740	PVCGVTVHFRHLHADGLRSLRMRPVSLSTLAFPPATRQVAAPLPAANTPTATLAPPAH-PSVCKEENATFLAGLD---PSSPAAPDRVS-----AASASPGRDASAPPAL	927
TGGT1_294860	PPCAHVDEIVRADELRGVAACLPEMKTFFSQQAVFSPSSARAESDVPRS-AEERVQSEAPKAPVGCIEIETPT--NCVPAEATSSLSQWTSDESPCWRASSPNEFFSPIPTDAGCTNA	1063
NCLIV_001740	TPCAALGGAGRARERESECGDLSRGLRAPTQVNCVSSSRADREVDQKDAQERDGGSLGRSTCSCTDVEAGQGRSVP-NGGSSSLAVSTPAGTPWRACPGDDFLVRPVPGRAGHGPE	1046
TGGT1_294860	RTQ--VAGFASHPTPETTAFHVAARPLSAASDTRGLLT-----VAFQSPGEGERVGVGKEGGTRSFSPSGSEEV---TLSTGRSEVGVEARPRTLGVSPGLGRENISR	1163
NCLIV_001740	ERSRRAVEAALTTKLQAESAPFLSVAARPLCGPTGGLVGPAPPAASDPLTVAASVAPQPEAEIRG-----GGPAESVPPGSAALGSVELLSSSGKAGAVRCRRVLGVAGGERPVCS	1160
TGGT1_294860	SAPFHSSFGVRSRSPQLEPTSH-APSVGLPVGASAGGTLGSLVLPVQAPGYPVSGVRDNLPSPLHPSSVSAVSSSVLFFPQPAQGNLVPHATRLRARASPPQSAP---TVCLDSAPESL	1278
NCLIV_001740	VSRHAADERFTR-VSGMEPSSLSSRLLGQPAVASA--ACPGSRPLSQASPAYAGVGRDLPSFASPLSAVSSSALF-PHTWQSSLSQSASP-ESSPGPQSGSATHEGRGLDPAAPETR	1275
TGGT1_294860	PLARSTAALSDVVEESLKSFE--ASAWQLARGGARAHQATLDGGEAS-----SPSRLRGRGL-TSLGCLYTRT-DTEQGEAEERSDASAFRTSQEPGDACAAPGVSGCRLGGS	1381
NCLIV_001740	PVAGASVLSSEAVVSLKNLVDVSDAAWALVRGVAQASQAALESAESLGGIGGCGRHATQGVRRGRGLHESLGLCHARRTDAEGPEAETDERSLS-----ARLPAPGESTSHLGAS	1389
TGGT1_294860	LGSAAKASS--LGAEGGGRV-RSSSFRREQQVQCRKQLWAMPESVVRALSSSTSKTLSAGEAHPAATPALQPNADFAAQGTVESRLPGSPVPAVQSGSSDADSLASGLPCGSPS	1498
NCLIV_001740	LGSAAPARGPCGNAPDGRVRRSSLSRREQKHQKCRKQLWAMPDSIRVLAALNPSAGT-VASGEATQPSVREQPV-----GRRP-AVSAPVGSVSA--QSCLPN-IDASRSSSFGSPS	1498

