

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q5S003	SPG17_MOUSE	Mus musculus	Sperm-associated antigen 17	25.875327	T154;S156	NaN	30059200	MAPKKEKPTGSANYKIWEPSLIAAH LNQNDWKASIAFVVGNRVEDDLLIH ALDLAVRLPQRKLFISIVSWEDILQQ MDEIQSLAESASAKKGGKPTSVNLP LHYEVFLAAKIIIMESGEKLTPLIGKL LKCQLLHIKSKDQQRRENEKMMVEE RTKSEKDKGKGSPEKKVASAKPG KGKSKDQPEATVTVRKTTLQKRRGE DDEAKSYIDDEPDDGAQYIIVVGFN NPQLLAIMTELGIPITSVIKISSENYE PLQTHLAAVRQQEAVLPEDIEAE KLKRKNSIKELEVFWKYLEPILNNEK LEIHFLDVARLQYVMKATYFSPDWS DNEQMLALGTEIFENIACLMYDSL WKROHHHYLQSMQLINVPQVVSEK TVLEAITPEPPPSTAPAPTGGKKAQY EESHAPPTVAFIITTEVDMRYNDLL NPIPEEFISVSLILHCMVEQVATEE DLIPPSLVEPAPRADGLDYRIAAHIVS ILPSLCLSEKKNLREIFLTEGESES KALPKGPLLLNYHDAHAKKYALKD QKNFDPVQVEQEMQSKPLWFLQ FPLPPPWNSTKRLATIHLMHFCTN EVLSWNEVERAFKVFTEFSLKLESEV DEEGRKPTETTSDDTVENFNIPWD NPARFAKLIRQRYIHRMSMQKAPPV VVEIENTERTLFFVNKNFAKAEQDAQ GDENSPNSDEPDASVTGSTSNSTK PWNSSNRQFSEKETS GSMWQPES MDQTMDEIKDDAATKDDSPKPKPK KMVVEADIEDIKKTQQRSLMDWSFT EYFQPKVLLQVLQEAHQYRCVDSY YHTQDNSLLVFNPMNLQRLQCE HWNIALHSNVGFRNYLELVAKSIED WVTQEEAKYQEAKMAEELNRIRIEL ELKATVKTSAKIPGPKRSKTNKVSS KTELSDOEKDKEKEKDKIPFVLEGSL KAWKEEQERLAEERLKEEKKAEEK GKDTGKKGKDKADKDDAKALKKK SSSKEKPKEPAKTLEVIEETAPLPVP EVVYPPFRGYNMGDIPQISGTNYLY PSDGGQIEVEKTRFERGSTFIKVKVK KDKHNFIHLKDPKEIVKKEKEEKNS EEEEEEEEKEEVEEKKPKGEEEEK VKQKVEMKRAQIEKEAVSKFGSFA TLENGICLSISYYGSGNMAPEVINSE LEAMMNIPSAMTATVVPVAVVTPQG KGKAKPKGKEKHKDSIKEEELPKEE EKKNHIEEVEPEVIVQESPPYVPTF QNLNVSCPSGLLLTFIGQESTDYSIV DEEPTRNLMIRQSYRQLKHFEFYK AVMPPLEQEAASRVVTSQGTVIKYML DGSTQILFADGAVSSSPDSGPVYTSP ELPTSPHNGDLVDSASQPKSETGPEI IITKKGKGHKNQTVANKSETHDIPE VPPPTPVESHIGTWFTTTPDGRIGT KGLEKIEDLKPYLFFQATDPINGTVM TTREDKVIIVEKKDGTTRVVDHADGTR ITTFYQVYEDHITPSNDEETTEGPR VTRQVKCMRIESSHYATIITNCESS CCATFGDGTSIIAKPQGSYQVLPNT GCLYIDKDCSATYCHESSNLYHPF QKREQLRASRYMKHTSEVICEVQD PEGNTFQVMADGSVSTTLPKKLED DFNVQMEGYESLSSLHLEKNHMQUI YGEHVPRFFVYTDGSGVELLRSDI EEYLSLAYGESTTVLQEPVQYEPGA LSITVLRPFHEASQWIMKKELDTIVP PNLQSRSWERFSPVEKKTGPPFGT QIWKGLSIGSKQLTNIPAPILEGPKVL QMRQFIQHEVIKNEVKLQISLKDY INHILKKEDELQEMTVKDSRTEEER GNAADLLKLVMSFPMEEETTKSHM TKVAAHLTVLFKQSMASAPKCSPTS YSKEFLEKKWRSLSQGTSWKEKLEQ QRNNIKKTQSYLMQIKTEVTPYFKS	None	None	None	None	None	None	None		

ELSSLFKSKYDYLEKFSKSLPPFVKK
NEAKLMTAVPDLYSDSTLTVDTKEKE
ASNTHPLLNQEVAENIQESPKEKET
EYVNKSLQTSSSQNOYENVTISPKEK
VYQSQTEIETKDTKESAIQNFTEKFK
KYTKKSASQNEIEDLIKSTKESVSQR
QTENVTRPPTTEEPDIYMPIKIPTQSLL
QDVTGQARKEKVRLLPYMMSSKPKS
QPYAKVEDPVGGRVNTSSIASAAMY
NPNASPFGFHLLPPSVKFGVLKEGH
TYATIVKLNKVGVDFCRFRVKQPPPS
TGLKVITYKPGPVAAGLQAEKVELFA
MAVGEDGAKGSAHISHNIEIMTEHD
VLFPLVEATVLTSSNYDNRPNLPO
GKENPMVFRTSTISSSSLGVMMSQK
ATHH