	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	Q8TF72	SHRM3_HUMAN	Homo sapiens	Protein Shroom3	19.994096	NaN	S213;S439;S443;S816;S890;S910;S913;S970;S1069;S1072;S1221;S1441	37217939	MMRTTEDFHKPSATLNSNTATKGR YIYLEAFLEGGAPWGFTLKGGLEHG EPLIISKVEEGGKADTLSSKLQAGDE VVHINEVTLSSSRKEAVSLVKGSYKT LRLVVRRDVCTDPGHADTGASNFVS PEHLTSGPQHRKAAWSGGVKLRLK HRRSEPAGRPHSWHTTKSGEKQPD ASMMQISQGMIGPPWHQSYHSSSS TSDLSNYDHAYLRRSPDQCSSQGSM ESLEPSGAYPPCHLSPAKSTGSIDQL SHFHNKRDSAYSSFSTSSSILEYPHP GISGRERSGSMDNTSARGGLLEGM RQADIRYVKTVYDTRRGVSAEYEVNS SALLLQGREARASANGQGYDKWSNI PRGKGVPPPSWSQQCPSSLETATDN LPPKVGAPLPPARSDSYAAFRHRERP SSWSSLDQKRLCRPQANSLGSLKSP FIEEQLHTVLEKSPENSPPVKPKHNY TQKAQPGQPLLPTSIYPVPSLEPHFA QVPQPSVSSNGMLYPALAKESGYIAP QGACNKMATIDENGNQNGSGRPGF AFCQPLEHDLLSPVEKKPEATAKYVP SKVHFCSVPENEEDASLKRHLTPPQ GNSPHSNERKSTHSNKPSSHPHSL KCPQAQAWQAGEDKRSSRLSEPWE GDFQEDHNANLWRRLEREGLGQSL SGNFGKTKSAFSSLQNIPESLRRHSS LELGRGTQEGYPGGRPTCAVNTKAE DPGRKAAPDLGSHLDRQVSYPRPEG RTGASASFNSTDPSPEEPPAPSHPH TSSLGRRGPGPGSASALQGFQYGKP HCSVLEKVSKFEQREQGSQRPSVGG SGFGHNYRPHRTVSTSSTSGNDFEE TKAHIRFSESAEPLGNGEQHFKNGE LKLEEASRQPCGQQLSGGASDSGRG PQRPDARLLRSQSTFQLSSEPEREPE WRDRPGSPESPLLDAPFSRAYRNSIK DAQSRVLGATSFRRRDLELGAPVAS RSWRPRPSSAHVGLRSPEASASASP HTPRERHSVTPAEGDLARPVPPAAR RGARRRLTPEQKKRSYSEPEKMNEV GIVEEAEPAPLGPQRNGMRFPESSV ADRRRLFERDGKACSTLSLSGPELK QFQQSALADYIQRKTGKRPTSAAGC SLQEPGPLRERAQSAYLQPGPAALE GSGLASASSLSSLREPSLQPRREATL LPATVAETQQAPRDRSSSFAGGRRL GERRRGDLLSGANGGTRGTQRGDE TPREPSSWGARAGKSMSAEDLLERS DVLAGPVHVRSRSSPATADKRQDVL LGQDSGFGLVKDPCYLAGPGSRSLS CSERGQEEMLPLFHHLTPRWGGSG CKAIGDSSVPSECPGTLDHQRQASR TPCPRPPLAGTQGLVTDTRAAPLTPI GTPLPSAIPSGYCSQDGQTGRQPLPP YTPAMMHRSNGHTLTQPPGPRGCE GDGPEHGVEEGTRKRVSLPQWPPPS RAKWAHAAREDSLPEESSAPDFANL KHYQKQQSLPSLCSTSDPDTPLGAP STPGRISLRISESVLRDSPPPHEDYE DEVFVRDPHPKATSSPTFEPLPPPPP PPPSQETPVYSMDDFPPPPPHTVCE AQLDSEDPEGPRPSFNKLSKVTIARE RHMPGAAHVVGSQTLASRLQTSIKG SEAESTPPSFMSVHAQLAGSLGGQP APIQTQSLSHDPVSGTQGLEKKVSPD PQKSSEDIRTEALAKEIVHQDKSLAD ILDPDSRLKTTMDLMEGLFPRDVNL LKENSVKRKAIQRTVSSSGCEGKRN EDKEAVSMLVNCPAYYSVSAPKAEL LNKIKEMPAEVNEEEEQADVNEKKA ELIGSLTHKLETLQEAKGSLLTDIKL NNALGEEVEALISELCKPNEFDKYR MFIGDLDKVVNLLLSLSGRLARVEN VLSGLGEDASNEERSSLYEKRKILAG QHEDARELKENLDRRERVVLGILAN YLSEEQLQDYQHFVKMKSTLLIEQR KLDDKIKLGQEQVKCLLESLPSDFIP KAGALALPPNLTSEPIPAGGCTFSGI FPTLTSPL	None	None	None	None	None	None	None	None	None