

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
D3YZU1	SHAN1_MOUSE	Mus musculus	SH3 and multiple ankyrin repeat domains protein 1	23.096634	NaN	T186;S540;S671;S791;S898;S1291;S1442	22645316;34678516;35822049;22826440	MTHSPATSEDEERHSASECPEGGSE SDSSPDGPGRGPQGRGRGSGAPG NLASTRGLQGRSMSVPDDAHFSMM VFRIGIPDLHQTKCLRFNPDATIWTA KQQVLCALSES LQDVLNYGLFQPAT SGRDANFLEEEERLLREYPQSFKEGV PYLEFRYKTRVYKQTNLDEKQLAKL HTKTGLKKFLEYVQLGTSDKVARLL DKGLDPNYHSDSDGETPLTLAAQTE GSVEVIRTLCLGGAHIDFRARDGMT ALHKAACARHCLALTALLDLGGSPN YKDRRGLTPLFHTAMVGGDPRCCEL LLYNRAQLGIADENGWQEIHQACQR GHSQHLEHLLFYGAEPGAQNASGN TALHICALYNKETCARILLYRGANKD VKNNNGQTPPFQVAVIAGNFELGELI RNHREQDVVPPQESPKYAARRRGPP GAGLTVPPALLRANS DTSMALPDW MVFSAPGASSSGTPGPTSGSQGQSQ PSAPSTKLSSGTLRSASSPRGARARS PSRGRHPEDAKRQPRGRPSSSGTPR DGPAGGTGGSGGPGGSLGSRGRRR KLYSAVPGRSFMVAVKSYQAQGEI SLSKGEKIKVLSIGEGGFWEQVKG RVGWFPSCLEEVANRSQEGRQES RSDKAKRLFRHYTVGSYDSFDAPSLI DGIDSGSDYIIEKKTVLLQKKDSEGF GFVLRGAKAQTPIEEFTPTPAFPALQ YLESVDEGGVAWRAGLRMGDFLIEV NGQNVVKVGHRRQVVMIRQGGNTL MVKVVMVTRHPDMDEAVHKKASQ QAKRLPPAISLRKSMTSELEEMVS PWKKKIEYEQQPAAVPSMEKKRTVY QMALNKLDEILAAAQQTISASESPGP GGLASLGKHRPKGFFATES SFDPHH RSQPSYDRPSFLPPGGLMLRQKSIG AAEDDRPYLAPPAMKFSRSLVPGS EDIPPPPTTSPPEPPYSTPPAPSSSGR LTPSPRGGPFNPGSGGGLPASSPSSF DGPSPDPRSGGREKSLYHSGALPP AHHHPPHHHHHHAPPQPHHHHA HPPHPPEMETGGSPDDPPRLALGP QPSLRGWRGGGPSPTSGAPSPSHHS SSGGSSGPAQAPALRYFQLPPRAASA AMYVPARSGRGRKGPLVKQTKVEGE PQKGS LPPASSPTSPALPRSEPPAG PSEKNSIPIPTIIKAPSTSSSGRSSQ SSTEAEPPPTQPDGAGGGGSSPSPAP ATSPVPPSPSPVPTPASPSGPATLDFT SQFGAALVGAARREGGWQNEARRR STLFLSTDAGDEDGGDSGLGPGAPP GPRLRHKSIDEGMFSAEPYLRLES GGSSGGYGAYAAGSRAYGGSGSSA FTSFLPPRPLVHPLTGKALDPASPLG

LALAAERALKESSEGGVTPQPPRP
PSPRYDAPPPTLHHHSPHSPHSPA
RHEPVLRLWGDPARRELGYRAGLGS
QEKALTASPPAARRSLHRLPPTAPG
VGPLLLQLGPEPPTPHPGVSKAWRT
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AGTRGSSTEDGPGVPPSPRRVLPTS
PTSPRGNEENGLPLLVLPPPAPSVDV
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PLTPGPPHPLPDPPSPATPLPAAPP
AVAAAPPTLDSTASSLTSYDSEVATL
TQGAPAAPGDPPAPGPPAPAAPAPPA
PQGPDPPTGDSGIEEVDSSSSDH
PLETISSASTLSSLSAEGGGNTGGVA
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GGSGTPGPPYPPQLMTPSKLRGRAL
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GATSPSASSASASTRHLQGVFEMR
PPLRRAPSPSLLPASDHKVSAPAPRP
SSLPILPSGPLYPGLFDIRSSPTGGAG
GSADPFAPVFVPPHPGISGGLGGALS
GASRSLSPTRLLSLPPDKPFGAKPLG
FWTKFDVADWLEWLGLSEHRAQFL
DHEIDGSHLPALTKEDYVDLGVTRV
GHRMNIDRALKFFLER