

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q8C0T5	S11L1_MOUSE	Mus musculus	Signal-induced proliferation-associated 1-like protein 1	33.049824	T14;S1114;S1391;T1402;S1403	S162;S187;S193;S208;S255;S288;S1078;S1087;S1116;S1127;S1149;S1170;S1181;S1234;S1249;S1305;T1309;S1328;S1345;S1369;S1370;S1391;S1410;S1412;S1507;S1528;T1530;S1533;S1544;S1547;S1564;S1567;S1582;S1624;S1626;S1629;S1687;S1690;S1707;S1708;S1712	22645316;22517741;36852467;33300544;34887587;35822049;34678516	MTSLKRSQTERPVTADRASVVSTDG APKVHTDDDFYMRRFRSQNSLGS VMAAVGPPRSEGPHHITSTPGVPKM GVRARIADWPPRKENVKESSRSSQE IETSSCLELSSKGSFVSGSSVSLN SNDSAMLSIQNTLKNKTGPAESM DSRFLMPEAYPSSPRKALRRIRQRS NSDITISELDVDSFDECISPTYKSGPS LHREYGSTSSIDKQGTSGDSFFDLLK GYKDDRSRDRGPTTKLSDFLITGGGK GSGFSLDVIDGPISQRENLRFLKERE KPLKRRSKSETGDSIFRKLRLNAKGE ELGKSSDLEDNRSEDSVRPWTCPKC FAHYDVQSILFDLNEAIMNRHNVIK RRNTTGGASAAVASLVSGPLSHSAS FSSPMGSTEDLNSKGS LGMDQGDD KSNELVMSCPYFRNEIGGEGERKIS LSKSNSGSFGCESTSFESALSSHCT NAGVAVLEVPKESLMLHLDRVKRYT VEHVDLGAYYYRKFYQKEHWNYP GADENLGPVAVSIRREKPEDMKENG SPYNYRIIFRTSELMTLRGSVLEDAIP STAKHSTARGPLKEVLEHVIPELNV QCLRLAFNTPKVTEQLMKLDEQGL NYQQKVGIMYCKAGQSTEEEMYN ESAGPAFEFLQLLGERVRLKGF YRAQLDTKTDSTGTHSLYTTYKDY MFHVSTMLPYTPNNKQQLLRKRI GNDIVTIVFQEPGAQPFSPKNIRSHF QHVIVVRAHNPCTESVCYSVAVTR SRDVPSFGPPIPKGVTFPKSNVFRDF LLAKVINAENAAHKSEKFRAMATRT RQEYLKDLAEKNVTNTPIDPSGKFPF ISLASKKKEKSKYPGAELSSMGAIV WAVRAKDYNKAMEFDCLLGISSEFI VLIEQETKSVAFNCSCRDVIGWTSSD TSLKIFYERGEVSVESFISGEDIKEI VRRQLQFVSKGCESVEMTLRRNLG QLGFHVNYEGIVADVEPYGYAWQAG LRQGSRLVEICKVAVATLSHEQMIDL LRTSVTVKVVIIPPHDDCTPRRSCSE TYRMPVMEYQMNEGISYEFKFPFR NNNKWQRNASKGAHSPQVPSQLQS PMTSRLNAGKGDGKMPPPERAANIP RSISSDGRPLERRLSPGSDIYVTVSS MALARSQCRNPSNLSSSSETGSGG GTYRQKSMPEGFVSVRRSPASIDRQ NTQSDISGSGKSTPSWQRSEDSLAD QMEPTCHLPAVSKVLPAFRESPPSGR LMRQDPVVHLSPNKQGHSDSHYSS HSSSNTLSSNASSAHSDEKWDGDD RTESDLNSYNLQGTSAADSGIDTASY GPSHGSTASLGASTSSPRSGPGKEK VAPLWHSSSEVLADRTLETEGHG MDRKAESSLSLDIHSKSGGSSPLS RENSTFSINDAASHTSTMSSRHSAS PVVFSSARSSPKEELHPTASSQLAPS FSSSSSSSGPRTFYPRQATSKYLI GWKKPEGTINSVGFMDTRKRHSQSD GNEIAHTRLRASTRDLQASPKPTSKS TIEEDLKKLIDLESPTPESQNFKFH

ALSSPQSPFPTTPTSRRALHRTLSD
SIYSSQREHFFTSRASLLDQALPNDV
LFSSTYPSLPKSLPLRRPSYTLGMKS
LHGFEFSASDSSLTDIQETRQPIPD
GLMPLPDAASDLWNSLVDAKAY
EVQRASFFAASDENHRPLSAASNSD
QLEEQALVQMKSYSKDPSPTLASK
VDQLEGMLKMLREDLKKEKEDKAQ
LQAEVEHLREDNLRQEEESQNASD
KLKKFTEWVFNTIDMS