

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondr
Q8C0T5	SI1L1_MOUSE	Mus musculus	Signal-induced proliferation-associated 1-like protein 1	53.0869	T14;S114;S1114;S1127;S1391;S1400;T1402;S1403;T1404;S1438	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	22517741;22645316;33300544;40885482;34887587;36852467;35822049;40021952;34678516	MTSLKRSQTERPVTADRASVSTDG APKVHTDDFYMRRFRSQNGSLGSS VMAAVGPPRSEGPHHITSTPGVPKM GVRARIADWPPRKENVKSSRSQ IETSSCLELSSKSGSPVSGSSVSLN SNDSAMLKSIQNTLNKKTGPAESM DSRFLMPEAYPSSPRKALRRIRORS NSDITISELDVDSFDECISPTYKSGPS LHREYGTSSIDKQGTSGDSFFDLLK GYKDRSDRGPTPKLSDFLITGGGK GSGFSLDVIDGPISQRENRLFKERE KPLKRRSKSETGDSIFRKLRNAKGE ELGKSSDLEDNRSEDSVRPWTCPKC FAHYDVQSILFDLNEAIMNRHNVIK RRNTTGGASAAVASLVSGPLSHSAS FSSPMGSTEDLNSKGSGLMDQGDD KSNELVMSCPYFRNEIGGGERKIS LSKSNSGSFGCESTSFESALSSHCT NAGVAVLEVPEKSLMLHLDRVKRYT VEHVDLGAYYRKFYQKEHWNYF GADENLGPVAVSIRREKPEDMKENG SPYNYRIIFRTSELMTRLGVSLEDAIP STAKHSTARGLPLKEVLEHVIPELNV QCLRLAFNTPKVTEQLMKLDEQGL NYQQKVGIMYCKAGQSTEEEMYNN ESAGPAFEFELQLLGERVRLKGFKE YRAQLDTKTDSTGTHSLYTYKDYEI MFHVSTMLPYTPNNKQQLLRKRHI GNDIVTIVFQEPGAQPFSPKNIRSHF QHVFVIVRAHNPCTESVCYSVAVTR SRDVPSPGPPKGVTFPKSNVFRDF LLAKVINAENAANKSEKFRAMATRT ROEYLKDLAEKNVTNTPIDPSGKFPF ISLASKKKEKSKPYPGAELSSMGAIV WAVRAKDYNKAMEFDCLLGISSEFI VLIEQETKSVAFNCSCRDVIGWTSSD TSLKIFYERGECVSVESFISGEDIKEI VRLQFVSKGCESEVMTLRRNGLG QLGFHVNVEGIVADVEPYGYAWQAG LRQGSRLVEICKVAVATLSHEQMIDL LRTSVTVKVIIPPHDDCTPRRSCSE TYRMPVMEYOMNEGYSYEFKFPFR NNNKWQRNASKGAHSPQVPSQLQS PMTSRLNAGKGDGKMPPPERAANIP RSISSDGRPLERLSPGSDIYVTVSS MALARSQCRNSPSNLSSSSETGSGG GTYROKSMPEFGVSRSPASIDRQ NTQSDISGSGKSTPSWQRSEDSLAD QMEPTCHLPAVSKVLPAFRESPSGR LMRQDPVHLSPNKQGHSDSHYSS HSSNTLSSNASSAHSDEKWDGD RTESDLNSYNYLQGTSDSGIDTASY GPSHGSTASLGASTSSPRSGPGKEK VAPLWHSSSEVLSLADRTLETGHHG MDRKAESSLSLDIHSKSGGSSPLS RENSTFSINDAASHTSTMSSRHSAS PVVFSSARSSPKEELHPTASSQLAPS FSSSSSSSGPRTFYPRQGATSKYLI GWKKPEGTINSVGFMDTRKRHQSD GNEIAHTRLRASTRDLQASPKPTS TIEEDLKKLIDLESPTPESQKNFKFH ALSSPQSPFPTTPTSRRALHRTLSD SIYSSQREHFFTSRASLLDQALPNDV LFSSTYPSLPKSLPLRRPSYTLGMKS LHGEFASDSSLTDIQETRRQPIPD GLMPLPDAASDLWNSLVDAAKAY EVQRASFFAASDENHRPLSAASNSD QLEEQALVQMKSYSKDPSPTLASK VDQLEGMLKMLREDLKKEKEDKAQ LQAEVEHLREDNLRQEEQNASD KLKKFTEWVFNTIDMS	False	False	2.496	2.919	0.641