

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membr
G3X9J0	SI1L3_MOUSE	Mus musculus	Signal-induced proliferation-associated 1-like protein 3	38.119336	S1563;T1568	S94;S140;S394;S1358;T1381;S1538;S1541;S1614;S1617;S1672;T1694;T1698	34887587;40885482	MTTYRPLPNDGVDLAASCGARSTDI LPGPHPGDYTPMGFWAQNCGSMPOP LGESPAATTTTRSPPTPAMPKMGVR ARVADWPPKRDALREQSNPSPSQDT DGVKTTKVAHSMRNLQNGQLPSST PASSGSRAFHRLSRRRSKDVEFQDG WPRSPGRAFLPLRHRSSSEITLSECD VEEPGDPGRTRHPGVLPFLFREYGST SSIDVQGVPEQSFDDILNEFRSEQPE ARGSQNLRELLQVDPGALSGGSGCGT KGDPRNGOPTKDSLQSLQPLKEKEK SRKKPVRLGSGDVTVDSSIFRKLRS KPEGEVGRPLGETEESRSPPEASRP WVCQKSAHFHFDVQSMFLDLNEAAA NRVSAQRRNTTTCASAASAASAMV TLTASRAHSLGTLDPFTSTEDLNCK ENLEQDLGDDNSNDLLSCLPHFRN EIGGERERNVFSRASVGSPPGGSSE AHMAEPTLSTHRTNASISVLEVPKE QQRTOQSRPROYSIEHVDLGARYYQD YFVGKEHANYFGVDEKLGPAVAVSIK REKLEDHKDHGPOYQYRIIFRTRELI TLRGSILEDATPTATKHGTGRGLPLK DALEYVPELNIHCLRLALNTPKVTE QLLKLDEQGLCRKHKVGILYCKAGQ SSEEMYNNEEAGPAFEFLDLLGD KVCLKGFTKYAAQLDVKTDSTGTHS LYTTYQDYEIMFHVSTLLPYTPNNRQ QLLRKRHIGNDIVTIIFQEPGALPFTP KNIRSHFQHVFIIVRVHNPCTENVCY SMAVTRSKDAPPPGPPINGTFRKS DVFRDFLLAKVINAENAAHKSDFKH TMASTRQEYLDLAENCVSNTPID SSGKFNLSLTSKKKEKTKARAGAEQ HSAGAIAWRVAADYQSEIDCILG ISNEFVLLDLRTKEVVFNCYCGDVI GWTDPSSTIKIFYGRGDHIFLQAAEG SVEDIRDIVRQLKVMNMGWETVDMT LRRNGLGQLGFHVKYDGTVAEVEDY GFAWQAGLRQGSRLVEICKVAVVTL SHDQMIDLLRTSVTVKVVIIPPFEDG TPRRGWPEYDMNASEPKTESETTT PGGRPPYRSNAPWQWSPASHNSL PATKWTTPATPGHAQSLRSLPKQTP VVPFRESQPLHSKRPVSPFETPFAAS PAGADRVPYRQPSGSFSTPGSATYA RYKPSPERYAAAPHLLSFDPHFMH DGMSSGDSSGGGLTSQESTMERPK PEPLWHVPAQARLSAMTSGSIGSKHP SRQDAAGKDSPNRHSKGEFQYSSHS SSNTLSSNASSSHSDDRWFDPDPL EPEQDPFSGKGSSDSGIDTTLTYTSSP SCMSLAKAPRPTKPHKPPGNIGLGG GGRESAGRPHPVDRRREVSAPAVVA GQNKGYRPKLYSSGCTPPGLVGGG RDPFRQPSDMGSRAGYPTQVYKTAS AETPRPSQLSQSPFQLSTSVPKSFF SKQPAHNKHSTGWKRTDEPPPRPLP FTDSKKQVDTNAKNVFGQPRLRASL RDLRSPRKNYKSTIEDDLKKLIVMD NLGPEQERDTGQSPQKSLQRTLSDE SLCSGRREPSFASPASLEPGLPSDVL FTSTCTFPSTLPARRQHQAHPSPS GAPSTTPATGNGFPEKKSASASELS LADGRDRPLRRLDPGMMPLPDAA GLEWSSLVNAAKAYEVQRAVSLFSL NDPALSPEIPPAHSPVHSHLSLSE QTPRATPTMSEESPLDLTGKVVYQLE VMLKQLHTDLQKEKQDKVVLQSEV ASLRQNNQRLQEESSQAASEQLRKFA ELFSREKKELE	False	False	2.633	3.74	False	False	2.0	3.0