

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	en ret
A2AQ25	SKT_MOUSE	Mus musculus	Sickle tail protein	59.407704	S353;S357;S359;S361;S1060;T1070;T1340;T1348;S1819;T1833;S1836;T1894;S1895	S169;T244;S361;S365;T393;T470;S474;S809;S1032;S1035;S1038;S1049;S1466;S1741;S1843;S1899;S1902;S1905	22517741;22645316;16452088;40885482;36852467;35822049;40021952	<p>MEESEGQKCEPNLPPSGDSRQMPQ QGRSNLHVTSQEDAACRRPRERLSN GNARAQVSKPARNIPRRHTLGGPRS SKEILGMQPEMDRKRKAEFLHLKQ KYPHHATAIMGHQERLDRQTKSPKL SHSPQPPNLGDPVEHLETSQDLSLE AMSEGEVPSPFARGSRTRASLPVVR SANQTKERSLGVLYLQYGDQTKQLR MPNEVTSTDITRALFVSAFPQQLTM KMLESPSVAIYKDDSRNVYELNDV RNIQDRSLLKVYNKDP SHAFNHMT KAVNGDMRMRQREIVYARGDGLVAP RPGSVAHPHVPINSPSTPVPHSLP PSPSRIPYGGSRPMAIPGNATIPRDR LSSLPVSRSISPSAISLERRDVKPDE DMSSKNLVMFRNEGFYADPYLYHE GRMSIASSHGGHPLDVPDHVIAYHR TAIRSASAYCPSLQAEHMHEQSLY RQKSRKYPDSLPTLGSKTPPASP RVGDLRMDLHPLHNTHGPPHTLQP DRASPSRQSFKKEPGLTVYIEKPRNT SGLSSLVDLGPPLVEKQGFAYSTTTI PKDRETRERMQAMEKQIASLTGLVQ SALFKGPITSSSKEASSEKMVKATAN RNQADGAGTAHVSAKVLGSEVFSL PPSQPLPAGTSPHITSLDMRRNVAE LRLQLQMRQLQLQNEILRAMMK KAELEISNKVKETMKRLEDPVQRQR TLVEQERQKYLHEEERIVKKLCELE DFVEDLKKDSSSTGRVVTLKDVEDG AFLLRQVGEAVATLKGEFPTLQNKM RAVLRIEVEAVRFLKEEPKLDLSLLK RVRSMTDVLTMLRRHVTDGLLKGT DASQAAQYVAMEKATAAEVLKHQEE TAHAPGQPLHCSTGSPGDVKSEVVP LSTMTVHHVQSSPVMQPSQHSSA LMNPAQNLPGGTRPHTASPPAITQE VTSAQAPGPQSPQTPVNGSSMQSL FIEEIHVS SAKNRAVSIEKAEEKWEE KRQNL EHYNGKEFEKLEEAQANI MKSIPNLEMPPASSPVSKGDAAGDK LELSEDPNSEQELDKIGGKSPPPP PPRRSYLPGSGLTTTRSGDVVYTR SMSKVSSDPGPTPQTRATKCPPEE PASAWAPSPVPAPSSKEEEEEEEEE GDKIMAE LQAFQKCSFMDVNPNSH AEQSRANSHLKDTRAGATAPPKEKK NLEFYHEDVRKSDVECENGPOVES QKVTAGALRPSGPKWERVMVDSIS DTSRTSECRADTFTEENATPNKSLF RDSRNYSQKNVPKVSFSSSGLNSLE GEINKGPNVSLQCAIPDLENQKLN FGKTKIEIGQQQENADKSHIPLPTR SAEFSIHDVKTQDQDVPVTGYGOVV LRSKVGRHANMNMNEDGESTPSSP SEEHTATDNIAFMITKTAVQVLSGGE VHDIVSQKGQDVQTVNIDGRKETAS QHEGTEGEEPPVCLDKKPVIHFDEP MDIRSAYKRLSTIFEECDEELERMLT EKEIEEEEDENEDSGVRTSSQMSC EQVDSRSDRMGQKAEQSQPHVLS AELLTPGVOGVRKAEORKLSSADSP DSGNKCGMVDDQFESPKKFKFKF PKKQLAALTQAIRTGKTGKKTQV VYEEEEEDGTLKQKAEAKRFEITRS QPEDALKT MARRQEQLSPEGTLPAS RTDEIRKSTYRTLDSLEQTIKOLENTI SEMSPRALVDTSCSSNRDCGASLPH MAQEVSPRSLVLDEVPPAPEPPTSI SPASRKGSTTPQTSRMPVPMTSKN RPGSLDKASKQSKLQDPRQYRQANG SAKKAGGDCKPTSPSLPASKIPALSP SSGKSSSLPASGDSNNLPNAPATKP SIASSTPLSPQAGRSASASLIPSVSN GSLKFQSPPHAGKGHHSFALQTO NGRAAPTSSSSPPSPASPTSLNQG ARGIRTIHTPSLASYKAQNGSSSKAT PSTAKETS</p>	False	False	1.899	2.695	1.757	Fal