

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q9JLC8	SACS_MOUSE	Mus musculus	Sacsin	25.685855	NaN	S1781;S2513;T2518;S3437;T4263;S4266	39627609	METKFKRWRVTVLVRGCVGCRITVA VPATATGRDLKERIFAETSFPVAEQR LWRGDREVPDWIKIGDLSKTCHLF VNLQSKGLKGGGRFGQTPPLVDFL KDILRRYPEGGQILKELIQNAEDAGA TEVKFLYDETYGTETLWSKDMAQY QGSALYVYNNAVFTPEDWHGQIEIA RSRKDDPLKVGFRFCIGFNSVYHITD VPCIFSGDQIGMLDPHQTLFGPHES GQCWNLKDDIKEINELPDQFAPFIG VFGSTKETFTNGSFPGTFFRFRPLRLQ PSQLSNNLYTKQKVFLEFDSFRADA DTVLLFLKSVQAVSLHVREADGTEK LVFRVTAASENKALKHERPNSIKILGT AISNYCKKIPNSVTCVYHINIVLED ESTKDAQKTSWLVCNSVGGRGISSK LDLADDELKFPPIGLAMPLSGKDEE NGAISDFSGKAFCLPLPPGEEERTG LPVHISGFFGLTDNRRRSIKWRELDQ WRDPAALWNEYLIVNVVPKTYATLIL DSIKRLETEKSSDFPLSVDTIYKLWP EASKVKAHWHPVLGPLFSELFQHAV IYSIGGEWVKLEQVHFSELDGSLEST RSVLNLYQSSGKQIAKVPGNLAAAV QLSAASATSSASPVKRVTPAWVRQV LRKCAHLGSAEEKLHLEFVLSDAQ YSELLGLELLPLQSGAFVPPFSSVSD QDVVYITSEFFRSLFPLEARLILE NLKPHLLAALKEAAQTRGRPCTQLQ LLNPERFARLIKEVMNTFWPGRELV VQWYPFSEDKRHPSLSWLKMVWKN LYHFSEDLTFDEMPILPRTLLED QTCVELIRLRIPSVVILDDTEAQLPE FLADIVQKLGIVLRLDTSIQHPLV KKYIHSPLPSAILQIMEKIPLOKLCNQ IASLLPTHKDALRKFASLTDTSEKE KRRIQELTIFKRINHSSDQGISSYTKL KGCKVLDHTAKLPTDLRLSVSVIDSS DEATIRLANMLKIEKLTTSCLKFVL KDIGNAFYTQEEVTQLMLWILENLS SLKNENSNVLDWMLPLKFHMSQG HVVAAGDLDFDPIEVLRLDFYNEEE ACFPPTFTSPDILHSLRQIGLKNES LKEKDVVQVARKIEALQVSSCQNQD VLMKKAKTLLLVLNKNQTLLOSSEG KMALKKIKWVPACKERPPNPGSLV WKGDLNLCAPPDMCDAAHAVLVG SSLPLVESVHVNLEQALSIFTKPTIN AVLKHFKTVVDWYTSKTFSEDEYYQ FQHILLEIYGFMDHDLSEGKDSFKA LKFPWVWTGKNFCPLAQAVIKPTHD LDLQPYLYNVPKTMAKFHQLFKACG SIEELTSDHISMVIQKVYLKSDQELS EESKQNLHMLNMRWLYSNQIP ASPNTVPYIHSRNPSKLVKMPIHEC CYCDIKVDDLNDLLEDSEPIILVHE DIPMKTAEWLKVPCSTRLINPENM GFEQSGQREPLTVRIKNILEEYPSV DIFKELLQNADDANATECSFMIDMR RNMDIRENLLDPGMAACHGALWS FNNSEFSDSDFLNITRLGESLKRGE VDKVGKFGGLGFNSVYHITDIPIMSR EFMIMFDPNINHISKHIKDRSNPGIK INWSKQKRLRKFPPNQKPFIDVFG CQLPLAVEAPYSYNGTLFRLSFRTQQ EAKVSEVSSTCYNTADIYSLVDEFSL CGHRLIIFTQVSNMYLKYLKIEETN PSLAQDTIIKKKVCPSKALNAPVLSV LKEAAKLMKTCSSSNKKLPTDVPKS SCILQITVEEFHHVFRRIADLQSPFL RGPDDDPATLFEMAKSGQSKKPSDE LPQKTVDCTTWLICTMDTGALKF SLNESGRRRLGLVPCGAVGVLLHETO EQKWTVKPHIGEVFCYLPLRIKTGLP IHINGFAVTSNRKEIWKTDTKGRW NTTFMRHVIVKAYLQALSVLRLDLAIG GELTDYTYAVVWDPDLVHDDFSVI CKGFYEDIAHGKGLTRVFSDGSM WVSMKNVRLDDSIQRKDVGSAAF	False	False	2.266	3.14	3.762	1.115	0.76	1.418	1.167

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 GFEEAGCKQILLENFSEKOFFSEVF  
 FPNIQEIEAELRDPLMNFVLEKLD  
 EFSGILRVTPCPCVCSLEGHPLVPSR  
 LIHPEGRVAKLFDTKDGRFFPYGSTQ  
 DYLNPIILIKLVQLGMAKDDILWDDM  
 LERAESVAEINKSDHAAACLRSILL  
 SLIDEKLIKIDPRAKDFAAKYQTIFFL  
 PFLTKPAGFSLEWKGNFSPKPMFA  
 ATDIYTAEYQDIVCLLQPIILNENSHS  
 FRGCGSVSLAVKEFLGLLKKTVDLV  
 INQLKQVAKSVDDGITLYQENITNAC  
 YKYLHEAVLQNE MAKATHEKLPFC  
 FILVENVYVESEKVSFHLNFEAAPYL  
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 YRLKHLLEIGFNLVYNCDETANLY  
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TLKSATDNLISDTSYLIAMLCNDIY  
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