

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q9NZJ4	SACS_HUMAN	Homo sapiens	Sacsin	10.778112	T2858;S3197	S1779;S2511;T2516;S3435;T4261;S4264	28411811;35254053;30379171	METKENRWVPVTVLPGCVGCRTVA ALASWTVRDVKERIFAETGFPVSEQ RLWRGGRELSDWIKIGDLTSKNCHL FVNLSKGLKGGGRFGQTPPLVDF LKDILRRYPEGGQILKELIQNAEDAG ATEVKFLYDETQYGTETLWSKDMAP YQGPALYVYNNNAVFTPEDWHGIEI ARSRKKDDPLKVGFRFGIGFNSVYHIT DVPCIFSGDQIGMLDPHQTLFGPHE SGQCWNLKDDSKSEISLSDQFAPFV GIFGSTKETFINGNFPGTFFRFPLRL QPSQLSSNLYNKQKVLELFESFRAD ADTVLLFLKSVQDVSLYVREADGTE KLVFRVTSSESKALKHERPNSIKILG TAISNYCKKTPSNITCVTYHVNIVL EEESTKDAQTSWLVCNSVGGRGIS SKLDSLADLKFVPIIGIAMPLSSRD DEAKGATSDFSGKAFCLPLPPGEE SSTGLPVHISGFFGLTDNRRSIKWRE LDQWRDPAALWNEFLVMNVVPKAY ATLILDSIKRLEMEKSSDFPLSVDVIY KLWPEASKVKVHWQPVLEPLFSELL QNAVIYSISCDWVRLEQVYFSELDE NLEYTKTVLNYLQSSGKQIAKVPGN VDAAVQLTAASGTPVRKVTPAWVR QVLRKCAHLGCAEEKLHLEFVLSLSD QAYSELLGLELLPLQNGNFVPFSSSV SDQDVIIYITSAEYPRSLFPSLEGRFIL DNLKPHLVAALKEAAQTRGRPCTQL QLLNPERFARLIKEVMNTFWPGREL IVQWYFPDENRNHPSVSWLKMVWK NLYIHFSEDLTLFDEMPLIPRTILEE GQTCVELIRLRIPSLVILDDSEEAQLP EFLADIVQKLGGFVLKKLDASIQHPL IKKYIHSPLPSAVLQIMEKMPLQKLC NQITSLLPHTKDALRKFASLTDSSSE KEKRIIQELAIFKRINHSSDQGISSYT KLKGCKVLHHTAKLPADLRLSISVID SSDEATIRLANMLKIEQLKTTSCCLKL VLKDIENAFYSHEEVTQLMLWVLEN LSSLKNENPNVLEWLTPLKFIQISQE QMVSAGELFDPDIEVLKDLFCNEEG TYFPPSVFTSPDILHSLRQIGLKNEA SLKEKDVVQVAKKIEALQVGACPDQ DVLLKKAKTLLLVLNKNHTLLQSSE GKMTLKKIKWVPACKERPPNYPGSL VWKGDLNLCAPPDMCDVGHAILIG SSLPLVESIHVNLEKALGIFTKPSLSA VLKHFKIVVDWYSSKTFSEDEYYQF QHILLEIYGFMDHDLNEGKDSFRAL KFPWVWTGKKFCPLAQAVIKPIHDL DLQPYLHNVPKTMKAFHQLFKVCG

SIEELTSDHISMVIQKIYKSDQDLSE
QESKQNLHMLNIRWLYSNQIPAS
PNTVPVPIHHSKNPSKLIMKPIHECCY
CDIKVDDLNDLLEDVPEIILVHEDIP
MKTAEWLKVPCLSTRLINPENMGFE
QSGQREPLTVRIKNILEEYPSVDIFK
ELLQNADDANATECSFLIDMRRNM
DIRENLDPGMAACHGPALWSFN
SQFSDSDFVNITRLGESLKRGEVDK
VGKFGGLGFNSVYHITDIPIMSREFM
IMFDPNINHISKHIKDKSNPGIKINW
SKQKRLRKFNPQFKPFIDVFGCQL
PLTVEAPYSYNGTLFRLSFRTQQEAK
VSEVSSTCYNTADIYSLVDEFSLCGH
RLIIFTQSVKSMYLYKIEETNPSLA
QDTVVIKKKSCSSKALNTPVLSVLKE
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DDPAALFEMAKSGQSKKPSDELSQK
TVECTTWLLCTCMDTGEALKFSLSE
SGRRLGLVPCGAVGVQLSEIQDQKW
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GCAVTSNRKEIWKTDTKGRWNTTF
MRHVIVKAYLQVLSVLRDLATSGEL
MDYTYAVWPDPLVHDDFSVICQG
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SVSLAVKEFLGLLKKPTVDLVINQLK
EVAKSVDGKITLYQENITNACYKYLH
EALMQNEITKMSIIDKLPFSFILVE
NAYVDSEKVSFHLNFEAAPYLYQLP
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PDTNMLLPAKSLCYNDPCWIKVKD
TTVKYCHADIPREVAVKLGAVPKRH
KALERYASNVCFTTLGTEFGQKEKL
TSRIKSILNAYPSEKEMLKELLQNAD
DAKATEICFVFDPRQHPVDRIFDDK
WAPLQGPALCVYNNQPFTEDDVRGI
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YHITDCPSFISGNDILCIFDPHARYAP
GATSISPRMFRDLADFRTOFSDV
LDLYLGTHFKLDNCTMFRFPLRNAE
MAKVSEISSVPASDRMVQNLLDKLR

SDGAELLMFLNHMEKISICEIDKST
GALNVLYSVKGKITDGDRLKRKQFH
ASVIDSVTKKRQLKDIPVQOITYTMD
TEDSEGNLTTWLICNRSGFSSMEKV
SKSVISAHKNQDITLFPRTGGVAACIT
HNYKPHRAFCLPLSLETGLPFHV
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DWNNSLMTALIAPAYVELLIQLKKRY
FPGSDPTLSVLQNTPIHVVKDTLKKF
LSFFPVNRLDLQPDLYCLVKALYNCI
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IITWINMSTSNKTRPFFDNLLQDEL
QHLKNADYNITTRKTVAENVYRLKH
LLEIGFNLVYNCDEANLYHCLIDA
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HIGKLPCRLQQTNLKLFHSLKLLVD
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NTLYLKYSNILLNCKVAKVFDISSFA
DLLSSVLPREYKTKSCTKWKDNFAS
ESWLKNAWHFISESVSVKEDQEETK
PTFDIVVDTLKD WALLPGTKFTVSAN
QLVVPEGDVLLPLSLMHIAVFPNAQ
SDKV FHALMKAGCIQLALNKICSKD
SAFVPLLSCHTANIESPTSILKALHY
MVQTSFRAEKL VENDORFEALLMYFN
CNLNHLMSQDDIKILKSLPCYKSISG
RYVSIGKFGTCYVLTKSIPSAEVEKW
TQSSSAFLEEKIHLKELYEVIGCVP
VDDLEVYKHL PKIENLSYDAKLEH
LIIHDANSRLKQAKHFYDRTVRVFE
VMLPEKLFIPNDFFKLEQLIKPKNH
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QFAKEISVRANTENWSKETLQNTVD
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LIKFNQAQVNP KFKQCDVLQLLWTS
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VSGLFRSLQND SVKVRSDLENVRDL
ALYLP SQDGRLVKSSILVFDDAPHYK
SRIQGNIGVQMLVDLSQCYLGKDHG
FHTKLIMLFPQKLRPRLSSILEEQL
DEETPKVCQFGALCSLQGRLLLS
SEQFITGLIRIMKHENDNAFLANEE
KAIRLCKALREGLKVSCFEKLQTTLR
VKGFNPIPHSRSETFAFLKRFGNAVI
LLYIQHSDSKDINFLALAMTLKSAT
DNLISDTSYLIAMLCNDIYRIGEKL

