

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	end reti
Q9QX47	SON_MOUSE	Mus musculus	Protein SON	46.036015	S241;S250;T251;S256;T262;T1605	S94;S142;S150;S152;S158;T395;T954;S993;S1030;S1038;S1055;S1063;S1077;S1678;S1723;S1727;S1772;S1784;S1791;S1794;S1807;S1808;S1973;S1975;S1977;S2027;S2029;S2031;S2047;S2049;S2147;T2181;S2256	22826440;36852467;22645316;22517741;30059200;29187734;35822049	MAADIEQVFRSFVSKFREIQEQLSSGRSEGLNGETNPPIEGNQAGDTAA SARSLPNEEIVQKIEEVLSGVLDTEL RYKPDLKEASRKRRCVSVQTDPTDE VPTKSKKKKKKKKKKKKKKKKEKE KKYKRQPEESESCLKSHHDGNLESD SFLKFDSEPSAAALEHPVRAFLSEA SETALVLEPPVVSMEVQESHVLETL KPATKAAELSVVSTSVISEQEQMP GMLEPSMTKILDSFTAAPVPMSTAA LKSPPEVVTMSVEYQKSVLKSLETM PPETSKTTLVELPIAKVVEPSETLTIV SETPTEVHPEPSPSTMDPFESSTDDV QRLPEQPVEAPSEIADSSMTRPQESL ELPKTTAVELQESTVASALELPGPPA TSILELQGGPPVTPVPELPGSATPVPE LSGPLSTPVPELPGPPATVVPPELPG SVTPVPQLSQELPGPPAPSMGLEPP QEVPEPPVMAQELSGVPAVSAAIELT GQPAVTVAMELTEQPVTTFEQPV AMTTVEHPGHPEVTTATGLLGOPEA AMVLELPGQPVATTALELSGQPSVT GVPELSGLPSATRALELSGQSVATGA LELPGQLMATGALEFSGQSGAAGAL ELLGQPLATGVLELPGQGAPELPG QPVATVALEISVQSVVTTSELSTMTV SQSLEVPSTTALESYNTVAQELPTTL VGETSVTVGVDPLMAQESHMLASN TMETHMLASNTMDSQMLASNTMD SQMLASNTMDSQMLASNTMDSQM LASSTMDSQMLATSTMDSQMLATS SMDSQMLATSSMDSQMLATSSMDS QMLATSSMDSQMLATSSMDSQML ATSSMDSQMLATSSMDSQMLATSS MDSQMLASGAMDSQMLASGTM DA QMLASGTMDAQMLASSTQDSAMM GSKSPDPYRLAQDPYRLAQDPYRLG HDPYRLGHDAYRLGQDPYRLGHDPY RLTPDPYRVSPRPYRIAPRSYRIAPR YRLAPRPLMLASRRSMMSYAAER SMMSSYERSMMSYERSMMSPMAE RSMMSAYERSMMSAYERSMMSPM AERSMMSAYERSMMSAYERSMMS PMADRSMMSGADRSMMSYSAA DRSMMSYSAADRSMMSYTD RSM MSMAADSYTDSYTDYTEAYMV PPL PPEEPPTMPPLPPEEPPMTPPLPEE PPEGPALSTEQSALTADNTWSTEV T LSTGESLSQPEPPVSQSEISEPMAVP ANYSMSESETSMLASEAVMTVPEPA REPESVTSAPVESAVVAEHEMVPE RPMTYMVSETTMSVEPAVLTSEASV ISETSETYDSMRPFGHAISEVTMSLL EPAVTISQPAENSLELPSMTVPAPST MTTTESPVVAVTEIPPVAVPEPPIMA VPPELPTMAVVKTPAVAVPEPLVAPE PPTMATPELCSLSVSEPPVAVSELPA LADPEHAITAVSGVSSLEPSVPILEPA VSVLQPVMIVSEPSVVPQVPTVAVSE PAVIVSEHTOITSPEMAVESSPVIVDS SVMSSQIMKGMNLLGGDENLGPVEV GMQETLLHPGEEPRDGGHLKSDLY ENEYDRNADLTVNSHLIVKDAEHNT VCATTVGPVGEASEEKILPISETKEIT ELATCAAVSEADIGRSLSSQALELD TVGTSGGFVFTASALISESKYDVEV SVTTQDTEHDMVISTSPSGGSEADIE GPLPAKDIHLDLPSTNFVCKDVEDSL PIKESAAQAVAVALSPKESSEDTEVPL PNKEIVPESGYSASIDEINEADLVRPL LPKDMERLTSLRAGIEGPLLASEVER DKSAAASPVISIPERASESSSEKDD YEIFVKVDTHEKSKKNKNRDKGEK EKKRDSLSRKRKRKSKSEHKSRKR TSESRSRARKRSKSKSHRSQTRSR SRSRRRRRSRSRKSRGRRSVSKE KKRSPKHRSKRERKRKRSSRDN RKAARARSRTPSRRRSHTPSRRR RRSVGRRRSFSISPSRRSRTPSRRR TPSRRSRTPSRRSRTPSRRSRTPSRR	None	None	None	None	None	Non

RRRS AVRRRSFSISPVLRRTPL
RRRFSRSPIRRKRSSERGRSPKRL
TDLDKAQLEIAKANAAMCAKAGV
PLPPNLKPAPPTIEEKVAKKGGATI
EELTECKQIAQSKEDDDVIVNKP
VSDEEEEPFYHHPFKLSEPKPIFF
NLNIAAKPTPKSQVTLTKEFPVSS
GSQHRKKEADSVYGEWVPVEKNGE
ESKDDDNVFSSSLPSEPVDISTAMS
ERALAQRKRLSENAFDLEAMSLNR
AQERIDAWAQLNSIPGQFTGTVQ
VLTQEQ LANTGAQAWIKKQFLRAA
PVTGGMGAVLMRKMGWREGEGLG
KNKEGNKEPILVDFKTRKGLVAVG
ERAQKRSNGFSAAMKDLGKHPVS
ALMEICNRRWQPPEFLLVHDSGPD
HRKHFLFRVLRNGSPYQPNCMFFL
NRY