

UniprotKB ID	Entry name	organism	full name	oglcnaescore	oglcnae sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	en re
P18583	SON_HUMAN	Homo sapiens	Protein SON	32.235711	S94;S244;T252;T253;T254;S260;T265;S267;S354;T534;T702;S763;S1091;S1094;S1095;S1097;S1102;T1615;S1644;S1821;S1841;T2172	S94;S142;S152;S154;S160;S283;T400;T959;S998;S1035;S1043;S1060;S1068;S1082;S1556;S1651;S1697;S1701;S1747;S1759;S1766;S1769;S1782;S1783;S1948;S1950;S1952;S2009;S2011;S2013;S2029;S2031;S2129;T2163;S2238	40136647;30379171;35289036;35132862;30059200;41350704;28657654;36240223;40307207;23301498;38665916;20068230;37217939;35254053;29249144;33214551;40596516;34019948;31492838;29237092;30620550;39534244;22661428;37340703;29351928;39531497;34105348;34725712;32119511;27114449	MATNIEQIFRSFVVSFKFREIQQLSSGRNEGQLNGETNTPIEIGNQAGDAAASARSLPNEEIVQKIEEVLGSLDTE LRYKPDLLKEGSRKSRCSVQTDPTD EIPTKKSCKKHKHKNKKKKKKEKE KKYKRQPEEESKTKSHDDGNIDLE SDSFLKFDSEPSAVALLEPTRAFGPS ETNESPAVVLEPPVVSMEVSEPHILE TLKPATKTAELSVVTSVISEQSEQS VAVMPEPSMTKILDSFAAAPVPTTTL VLKSSPEPVVTMSVEYQMKSVLKSVE STSPEPSKIMLVEPPVAKVLEPSETL VVSSETPTEVYPEPSTSTTMDFPES AIEALRLPEQPVDVPSAIEADSSMTRP QELPELPKTTALELQESSVASAMELP GPPATSMPELQPPVTPVLELPGPSA TPVPELPGPLSTPVPELPGPPATAVP ELPGPSVTPVPQLSQELPLPAPSM GLEPPQEVPEPPVMAQELPGLPLVT AAVELPEQPAVTVAMELTEQPVITTT ELEQPVGMTTVEHPGHPEVTTATGL LGQPEATMVLELPGQPVATTALELP GQPSVTGVPELPGPLSATRALELSGQ PVATGALELPGPLMAAGALEFSGQS GAAGALELLGQPLATGVLELPGQPG APELPGQPVAIVALEISVQSVTTTSE LSTMTVSQSLEVPSTTALESYNTVAQ ELPTTLVGETSVTVGVDPMLMAPESHI LASNTMETHILASNTMDSQMLASN TMSQMLASNTMDSQMLASSTMD SQMLATSSMDSQMLATSSMDSQML ATSTMSQMLATSSMDSQMLATSS MDSQMLATSSMDSQMLATSSMDS QMLATSTMSQMLATSTMSQMLA TSSMDSQMLASGTMSQMLASGT MDAQMLASGTMDAQMLASSTQDS AMLGSKSPDPYRLAQDPYRLAQDPY RLGHDHPYRLGHDAYRLGQDPYRLG HDPYRLTPDPYRMSRPRYRIAPRSYR IAPRPYRLAPRPLMLASRRSMMSY AAERSMMSYERSMMSYERSMMS PMAERSMMSAYERSMMSAYERSM MSPMAERSMMSAYERSMMSAYER SMMSPMADRSMMMSGADRSMMS SYSAADRSMMSSYSAADRSMMSSY TADRSMMMSMAADSYTDSYTDYTEA YMVPPLPPEEPPPTMPLPPEEPPMT PPLPPEEPPPEPALPTEQSALTAENT WPTEVPSSPEESVSQPEPPVQSEI SEPSAVPTDYSVSADSPSVLVSEAAV TVPEPPPEPESSITLTPVESAVVAEEH EVVPERPVTCMVSETPAMSAEPTVL ASEPPVMSETAETFDMSMRASGHVAS EVSTSLLPVAVTTPVLAESILEPPAM AAPESSAMAVLESSAVTVLESSTVTV LESSTVTVLEPSVVTVPEPPVVAEPD YVTIPVPSVALEPSVPLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTV SEQTQVIPTVEAIESTPMILESSMSS HVMKGINLSSGDQNLAPEIGMQEIA LHSGEPPHAEHLKGFYEEHGIN IDLNINNHILIAKEMEHNVTCAAGTS PVGEIGEEKILPTSETKQRTVLDTYP GVSEADAGETLSSGTFPALEPDATGT SKGIEFTTASTLSLVNKYDVLDSLTT QDTEHDMVISTSPSGGSEADIEGPLP AKDIHLDPNNSNLLVSKDTEEPLPV KESDQTLAALLSPKESGGGEKVPVP PKETLPDSGFSANIEDINEADLVRPL LPKDMERLTSRAGIEGPLLASDVGR DRSAASPVVSSMPERASESSSEEKD DYEIVKVKDTHEKSKKNRDKGE KEKKRDSLSRSRKRKSKSEHKSRK RTSERSRARKRSKSKSHRSQTRS RRSRRRRRSRSRKRKRRRSVSK EKRRRSPKHRKSRERKRKRSSRD NRKTVRARSRTPSRRSRSHTPSRRR RRSRVGRRRSFSISPSRRSRTPSRRS RTPSRRSRTPSRRSRTPSRRSRTPSR RSRTPSRRRRSRVRRRSFSISPV	True	False	2.218	4.979	0.997	0.

