

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|------------|--------------|-------------|--------------|--|---|---|---|
| P18583 | SON_HUMAN | Homo sapiens | Protein SON | 31.577381 | S244;T252;T253;T254;S260;T265;S354;T702;S763;S1091;S1097;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 | 30059200;30379171;33214551;34105348;20068230;31492838;32119511;22661428;29249144;28657654;27114449;29351928;29237092;34019948;30620550;23301498 | MATNIEQIFRSFVVSKFREIQEQLSSGRNEGQLNGETNTPIEGNQAGDAAASARSLPNEEIVQKIEEVLSGVLDTE LRYKPDLEKESRKSRCVSVQTDPTD EIPTKKS KKKKKHKNKKKKKKEKE KKYKRQPEEESKTKSHDDGNIDLE SDSFLKFDSEPSAVALPTRAFIGPS ETNESPAVVLEPPVVSMEVSEPHILE TLKPATKTAELSVVSTSVISEQSEQS VAVMPEPSMTKILDSFAAAPVPTTTL VLKSSEPVTMSVEYQMKSVLKSVE STSPEPSKIMLVPEPPVAKVLEPSETL VVSSETPTEVYPEPSTSTTMDFPES AIEALRLPEQPVDVPEIADSSMTRP QELPELPKTTALELQESSVASAMELP GPPATSMPELQGPVTPVLELPGPSA TPVPELPGPLSTPVPELPGPPATAVP ELPGPSVTPVPQLSQELPGLPAPSM GLEPPQEVPEPPVMAQELPGLPLVT AAVELPEQPAVTVAMELTEQPVTIT ELEQPVGMTTVEHPGHPEVTTATGL LGQPEATMVLELPGQPVATTALELP GQPSVTGVPELPGPLSATRALELSGQ PVATGALELPGPLMAAGALEFSGQS GAAGALELLGQPLATGVLELPGQFG APPELPGQPVATVALEISVQSVTTSE LSTMTVVSQSLEVPSTTALESYNTVAQ ELPTTLVGETSVTVGVDPLMAPESHI LASNTMETHILASNTMDSQMLASN TMDSQMLASNTMDSQMLASSTMD SQMLATSSMDSQMLATSSMDSQML ATSTMDSQMLATSSMDSQMLATSS MDSQMLATSSMDSQMLATSSMDS QMLATSTMDSQMLATSTMDSQMLA TSSMDSQMLASGTMDSQMLASGT MDAQMLASGTMDAQMLASSTQDS AMLGKSPDPYRLAQDPYRLAQDPY RLGHDYRLGHDAYRLGQDPYRLG HDYRLTPDPYRMSRPRYRIAPRSYR IAPRYRLAPRPLMLASRRSMMMSY AAERSMMSYERSMMSYERSMMS PMAERSMMSAYERSMMSAYERSM MSPMAERSMMSAYERSMMSAYER SMMSPMADRSMMSMGADRSMMS SYSAADRSMMSYSAADRSMMSY TADRSMMSMAADSYTDSYTDYTEA YMVPLPPEEPPTMPPLPPEEPPMT PPLPPEEPPEGPALPTEQSALTAENT WPTEVPSSPSEESVSQPEPPVSQSEI SEPSAVPTDYSVASDPSVLVSEAAV TVPEPPPEPESSITLTPVESAVVAEEH EVVPERPVTMCMVSETPAMSAEPTVL ASEPPVMSETAETFDSMRASGHVAS EVSTSLVPAVTTPLAESILEPPAM AAPESSAMAVLESSAVTVLESSTVTV LESSTVTVLEPSVTVPEPPVVAEPD YVTIPVVSVALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTV SEQTQVIPTEVAIESTPMILESSIMSS HVMKGINLSSGDQNLAPEIGMQEIA LHSGEEPHAEHLKGFYSEHGIN |

IDLNINNHLLIAKEMEHTVCAAGTS
PVGEIGEEKILPTSETKQRTVLDTYP
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