	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extrac region
0	Q7Z3U7	MON2_HUMAN	Homo sapiens	Protein MON2 homolog	18.134238	NaN	S205;S537	35008409;23301498;37217939;38665916	MSGTSSPEAVKKLLENMQSDLRALS LECKKKFPPVKEAAESGIIKVKTIAAR NTEILAALKENSSEVVQPFLMGCGT KEPKITQLCLAAIQRLMSHEVVSETA AGNIINMLWQLMENSLEELKLLQTV LVLLTTNTVVHDEALSKAIVLCFRLH FTKDNITNNTAAATVRQVVTVVFER MVAEDERHRDIIEQPVLVQGNSNRR SVSTLKPCAKDAYMLFQDLCQLVNA DAPYWLVGMTEMTRTFGLELLESVL NDFPQVFLQHQEFSFLLKERVCPLVI KLFSPNIKFRQGSSTSSSPAPVEKPY FPICMRLLRVVSVLIKQFYSLLVTEC EIFLSLLVKFLDADKPQWLRAVAVES IHRFCVQPQLLRSFCQSYDMKQHST KVFRDIVNALGSFIQSLFLVPPTGNP ATSNQAGNNNLGGSVSAPANSGMV GIGGGVTLLPAFEYRGTWIPILTITVQ GSAKATYLEMLDKVEPPTIPEGYAM SVAFHCLLDLVRGITSMIEGELGELE TECQTTTEEGSSPTQSTEQQDLQST SDQMDKEIVSRAVWEEMVNACWC GLLAALSLLLDASTDEAATENILKAE LTMAALCGRLGLVTSRDAFITAICKG SLPPHYALTVLNTTTAATLSNKSYSV QGQSVMMISPSSESHQQVVAVGQP LAVQPQGTVMLTSKNIQCMRTLLNL AHCHGAVLGTSWQLVLATLQHLVWI LGLKPSSGGALKPGRAVEGPSTVLTT AVMTDLPVISNILSRLFESSQYLDDV SLHHLINALCSLSLEAMDMAYGNN KEPSLFAVAKLLETGLVNMHRIEILW RPLTGHLLEVCQHPNSRMREWGAE ALTSLIKAGLTFNHDPPLSQNQRLQL LLLNPLKEMSNINHPDIRLKQLECV LQILQSQGDSLGPGWPLVLGVMGAI RNDQGESLIRTAFQCLQLVVTDFLPT MPCTCLQIVVDVAGSFGLHNQELNI SLTSIGLLWNISDYFFQRGETIEKEL NKEEAAQQKQAEEKGVVLNRPFHP APPFDCLWLCLYAKLGELCVDPRPA VRKSAGQTLFSTIGAHGTLLQHSTW HTVIWKVLFHLLDRVRESSTTADKE KIESGGGNILIHHSRDTAEKQWAET WVLTLAGVARIFNTRRYLLQPLGDFS RAWDVLLDHIQSAALSKNNEVSLAA LKSFQEILQIVSPVRDSDKPETPPVV NVPVPVLIGPISGMSRPFVRTDSIGE KLGRYSSSEPPIVTDELEDLNLWWA AWNTWYRIGSESTKPPITFDKLTFIP SQPFLTALIQIFPALYQHIKTGFNMD DLQKLGVILHSAISVPISSDASPFILP SYTEAVLTSLQEAVLTALDVLQKAIC VGPENMQIMYPAIFDQLLAFVEFSC KPPQYGQLETKHIANAKYNQIQLFAP AEWVALNYVPFAERSLEVVVDLYQK TACHKAVVNEKVLQNIIKTLRVPLSL KYSCPSESTWKLAVSSLLRVLSIGLP VARQHASSGKFDSMWPELANTFED FLFTKSIPPDNLSIQEFQRNENIDVE VVQLISNEILPYANFIPKEFVGQIMT MLNKGSIHSQSSSFTEAEIDIRLREE FSKMCFETLLQFSFSNKVTTPQEGYI SRMALSVLLKRSQDVLHRYIEDERL SGKCPLPRQQVTEIIFVLKAVSTLIDS LKKTQPENVDGNTWAQVIALYPTLV ECITCSSSEVCSALKEALVPFKDFMQ PPASRVQNGES	None	None	None	None	None	None	None	None	None