

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi appar
O43149	ZZEF1_HUMAN	Homo sapiens	Zinc finger ZZ-type and EF-hand domain-containing protein 1	27.163227	T66;S1509;T1512	S240;S1475;S1488;S1509;T1512;S1518;T1521;T1523;S1537;S1540;S2444	29351928;30379171;40307207	MGNAPSHSSEDEAAAAGGEGWGP HQDWAAVSGTTPGPGVAAPALPAAA LLEPARLREAAAALPTPPCESLVSR HRGALFRWLEERLGRGEESVTLQF RELLEARGAGCSSEQFEEAFAQFDA EGDGTVDAENMLEALKNSSGANLQ GELSHIIRQLQACSLVPGFTDIFSEK EGLDIHSSMILRFLHRNRLSSAVMP YPMLEHCNNMCTMRSSVLKESLDQ LVQKEKESPGDLTRSPMDKLSVA KCYAYIETSSNSADIDKMTNGETSSY WQSDGSACSHWIRLKMKPDVLRH LSIAVAATDQSYMPQOQVTVAVGRNA SDLQEVDRDVHIPSNTVGYVTLLENA NVSQLYVQINIKRCLSDGCDTRI HGL RAVGFQRVKKSGVSVSDASAIWYWS LLTSLVTASMETNPAFVQTVLHNTQ KALRHMPPPLSLSPGSTDFSTFLSPN VLEEVDSFLIRITSCCSTPEVELTLLA FALARGSVAKVMSLCTITDHLDTQ YDASSLLSMASVRQNLKYGKPLQ LTLQACDVKGEDKSGPENLLVEPW TRDGFLETGKTRASTIFSTGTESAF QVTQIRIMVRRGGIGAQCGLVFAYNS SSDKFCAEEHFKRFEKYDKWKLQEL RQFVKSRIIGCSSDDLGEDDPGWFE LEEEWDEADV KLVQQRVAKYLMVK FLCTRQESAERLGVQLTISGYLRPA RAEAEQSVTCAHCRKDTESVCGGAT LLLRRLQFIQQLAHDLVQKESGLKY KSFLLDFAGLDLQIFWNFYSKLKQNP REECVSAQTLQLLQSCFVLOGD VLAASEEEKAPIQSPKGVAAKELYT HLCDDVVDKVDGDSVPMELKQEV R NTLNNGAAIFFPNRQTRRNHLFTM MNVTEQEHKQSLQLTFRSLCTYFSD KDPGGLLLLPEKNLAKMNISEVLA VMDTLVSAARECELLMLSGAPGEV GSVLFLFWSVQGSLLSWCYLQLKS TDGAKDLAVDLIEKYVGOFLASMR AILESLSFSQYSGKTIVERLCNSVFSM AARQLVIFLLDFCTLDIPHCVLLREF SVLTELKLCGSGPEGGLRKL DVET WQQEQPVVLTHTWKESAHNYENN CHEVSVFVSPGATYFEVEFDDRCET EKRYDYLEFTDARGRKRTRYDTKVGT DKWPVKVTFKAGPRLQFLFHS DSSH NEWGYKFTVTACGLPDVAVSWGLD LQLLVSRMLMGRASOCMALKSVRQL GSNMVPQAKMALVSSPLWKPVF RHQVCPELELEASWPHPHRNSKE VKNIPDDPCRHFLLDFAQSEPAQNF CGPYSELFKGFIQACRQAPKTDIVA GSTIDQAVNATFAALVYRTPDLYEKL QKYVNSGGKIALSEFAQVYSLADGI RIWMLEMKQKSLMSLGNEAEEKHS SEATEVNPESLAKECIEKSLLLKFL PTGISSKESCEKLETADETSHLQPLN KRQRTSSVVEEHFQASVSPTEAAPP ATGDQSPGLGTQPKLPSSSGLPAAD VSPATAEEPLSPSTPTRRPPFTRGRL RLLSFRSMEEARLVPTVKEKYPVLK DVMDFIKDQSLSHRSVVKVLSLRKA QAQSILEVLKITQHCAESLQPHCF HPPFILFLELLTCQKDFNTYFGHLE GCGADLHKEIRDYTYQLVFLVAVK GFSLLNDRSLLPALSCVQTALLHLLD MGWEPNDLAFVDIQLPDLMLKMS QENISVHDSVISQWSEDELADAKO NSEWMDECQDGMFEAWYEKIAQE DPEKQRKMHMFIARYCDLLNVDISC DGCDEIAPWHRYRCLQCSMDLCK TCFLGGVKGPEGHGDDHEMVNMEFT CDHCQGLIIGRRMNCNVCDDFDLC YGCYAAKYSYGHLPHTSITAHPMV TIRISDRQLIQPYIHNSWLLFAALA LYSAHLASAEDVDGEKLDPOTRSSA TTLRSQCMQLVGDCLMKAHQGKGL KALALLGVLPDGDSSLEDQALPVTVP TGASEEQLEKAVQGAELSEAGNGK	False	False	2.678	1.592	1.532	False	False

RAVHEEIRPVDFKQRNKADKGVLSL
KDPSCQTQISDSPADASPTGLPDAE
DSEVSSQKPIEEKAVTPSPEQVFAEC
SQKRILGLLAAMLPLKSGPTVPLID
LEHVLPLMFQVVISNAGHLNETYHL
TLGLLGQLIRLLPAEVDAAVIVLSA
KHNLFAGDSSIVPDGWTTHLLFS
LGAVCLDSRVGLDWACSMAEILRSL
NSAPLWRDVIATFTDHCIKQLPFQLK
HTNIFLLVLVGFPOVLVCGTRCVY
MDNANEPHNVIILKHFTEKNRAVIV
DVKTRKRKTVDYQLVQKGGGQEC
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SGPAHMTYILDMFMQLEEKHEWEK
ILQKVLQGCREDMLGTMALAAQCF
MEEPGMEVQVRESKHPYNNNTNFE
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ERVVPHLPLAKIWEWLVGACRQTG
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QDYLLALTTDDHLLRCAAQALQNTA
AISLAINYPNKATRLWNVEC