

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
O75165	DJC13_HUMAN	Homo sapiens	DnaJ homolog subfamily C member 13	10.241892	T2167	NaN	37217939;30379171	MNIIRENKDLACFYTTKHSWRGKYK RVFSVGTTHAITTYNPNTLEVTNQWP YGDICISISPVGKQGTEFNLTFRKGS GKKSETLKFSTEHRTELLTEALRFRT DFSEGKITGRRYNCYKHHWSDSRKP VILEVTPGGFDQINPATNRVLCSDYD RNIEGFVDLSDYQGGFCILYGGFSRL HLFASEQREEIIKSAIDHAGNYIGISL RIRKEPLEFEQYLNLRFGKYSTDESI TSLAEFVVQKISPRHSEPVKRVLALT ETCLVERDPATYNIATLKPLGEVFAL VCDSNPQLFTIEFIKQVRKYSSTE RDSLLASLLDGVRASGNRDVCVKMT PTHKGQRWGLLSMPVDEEVESLHL RFLATPPNGNFADAVFRFNANISYS GVLHAVTQDGLFSENKEKLINNAIT ALLSQEGDVVASNAELESQFQAVRR LVASKAGFLAFTQLPKFRERLGVKVV KALKRSNNGIHA AVDMLCALMCP MHDDYDLRQEQLNKASLLSSKKFLE NLEKFNSHVDHGTGALVISSLLDF LTFALCAPYSETTEGQQFDMLEMV ASNGRTLKLFQHPMAIKGAGLV MKAIEEGDKEIATKMQELALSEGAL PRHLHTAMFTISSDQRMLTNRQLSR HLVGLWTADNATATNLLKRILPPGL LAYLESSDLVPEKADARMHVRDNVK IAMDQYGKFNKVP EWQRLAGKAAK EVEKFAKEKVDLVL MHWRDRMGIA QKENINQKPVVLRKRRQRIKIEANW DLFYRFGQDHARSNLIWNFKTREE LKDTLESEMRAFNI DRELGSANVIS WNHHEFEVKYECLAEI KIGDYLLR LLEEDENEESGSIKRSYEFFNELYH RFL LTPKVN MKCLCLQALAI VYGR HEEIGPFTDTRYIIGMLERCTDKLER DRLILFLNKLILNKNV KDLMD SNGI RILVDLLTLAHLHVS RATVPLQSNVI EAAPDMKRESEKEWYFGNADKERS GPYGFHEMQELWTKGMLNAKTRC WAQGM DGWRPLQSIPQLKWCLLAS GQAVLNETDLATLILNMLITMCGYF PSRDQDNAIIRPLPKVKRLLSDSTCL PHIIQLLLTFDPILVEKVAILLYHIMQ DNPQLPRLYLSGVFFFIMMYTGSNV LPVARFLKYTHTKQAFKSEETKGQDI FORSILGHILPEAMVCYLENYEPK SEIFLGEFDTPEAIWSSEMRRMIEK IAAHLADFTPR LQSNTRALYQYCP IPI

INYPQLENEFCNIYYLKQLCDTLRF
PDWPIKDPVKLLKDTLDAWKKEVEK
KPPMMSIDDAYEVLNLPQGQPHD
ESKIRKAYFRLAQKYHPDKNPEGRD
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GYPMLIRTITMETSDDLLFSKESPLL
PAATELAFHTVNC SALNAEELRREN
GLEVLQEAFSRCVAVLTRASKPSDM
SVQVCGYISKCYSVAAQFECKREKIT
EMPSIIKDLCRVLYFGKSIPRVAALG
VECVSSFAVDFWLQTHLFQAGILWY
LLGFLFNYYDYLEESGIQKSEETNQQ
EVANSLAKLSVHALSRLGGYLAEQ
ATPENPTIRKSLAGMLTPYVARKLAV
ASVTEILKMLNSNTESPYLIWNNST
RAELLEFLSQENMIKKGDCDKTY
GSEFVYSDHAKELIVGEIFVRVYNEV
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HTFMAITHAAKVESEQHGDRLPRVE
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LIFSLLRVHGAGQVQQLALEVNVNIVT
SNQDCVNNIAESMVLSSLLALLHSL
PSSRQLVLETLYALTSSTKIIKEAMAK
GALIYLLDMFCNSTHPQVRAQTAEL
FAKMTADKLIGPKVRITLTKFLPSVF
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WNDNSRDKVSTTVREMMLEHFKN
QQDNPEANWKLPEDFAVVFGAEAG
ELAVGGVFLRIFIAQPAWVLRKPREF
LIALLEKLTELLEKNNPHGETLETLT
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VIQAMNHRNNAIPKSAIRVIHALSEN
ELCVRAMASLETIGPLMNGMKKRA
DTVGLACEAINRMFQKEQSELVAQA
LKADLVPYLLKLEGGIGLENLDSPAA
TKAQIVKALKAMTRSLQYGEQVNEIL
CRSSVWSAFKDQKHDLFISESQTAG
YLTGPGVAGYLTAGTSTSVMSNLPPP
VDHEAGDLGYQT