

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q8NG31	KNL1_HUMAN	Homo sapiens	Kinetochorescaffold 1	2.364213	T158;T714;S716;S720;S731	S32;S60;T539;S578;S584;T586;S767;S956;S1039;S1076;S1088;S1448;S1675;S1773;S1831;S1845;S1860	34019948;37217939;28510447;35254053;30059200;35132862;30379171	MDGVSSSEANEENDNIERPVRRRHS SILKPPRSPLQDLRGGNERVQESNA LRNKKNSRRVFSADTIKVFQTESHM KIVRKSEMEGCSAMVPSQLQLLPPG FKRFSCLSLPETETGENLLLIQNKKL EDNYCEITGMNTLLSAPIHTQMQQK EFSIIHTREKRHANDQTIVFSDENQ MDLTSSHTVMITKGLLDNPISEKSTK IDTTSFLANLKLHTEDSRMKKEVNF SVDQNTSSENKIDFNDFIKRLKTGK CSAFPDPDPKENFEIPIYSKEPNAS STHQMHVSLKEDENNSNITRLFREK DDGMNFTQCHTANIQTLIPTSSETN SRESKGN DITYGND FMDLTFNHTL QILPATGNFSEIENQTNAMDVTTG YGTKASGNKTVFKSKQNTAFQDLSI NSADKIHITRSHIMGAETHIVSQCNC QDARILAMTPEIYSNPSIQGCKTVF YSSCNDAMEMTKCLSNMREEKNLL KHDSNYAKMYCNP DAMSSLTEKTIY SGEENMDITKSHTVAIDNQIFKQDQ SNVQIAAAPTPEKEMMLQNLMTTSE DGKMNVCNSVPHVSKERIQQSLS NPLSISLTD RKT ELLSGENMDLTES HTSNLGSQVPLAAYNLAPESSESH SQSKSSSDECEITKSRNEPFORSDI IAKNSLTD TWNKDKDWVLKILPYLD KDSPQSADCNQEIATSHNIVYCGGV LDKQITNRNTVSWEQSLFSTTKPLF SSGQFSMKNHDTAISSHTVKSVLGQ NSKLAEPLRKSLSNPTPDYCHDKMII CSEEEQNMDLTKSHTVVIGFGPSEL QELGKTNLEHTTGQLTTMNRQIAVK VEKCGKSPIEKSGVLKSNCIMDVLE DESVQKPKFPKEKQNVKIWGRKSVG GPKIDKTIVFSEDDKNDMDITKSYTI EINHRP LLEKRDCHLVPLAGTSETIL YTCRQDDMEITRSHTTALECKTVSP DEITTRPMDKT VV FVDNHVELEMTE SHTVFIDYQEKERTDRPNFELSQRK SLGTPTVICTPTEESVFFPGNGESDR LVANDSQLTPLEEWSNNRGPVEVA DNMELSKSATCKNIKDVQSPGFLNE PLSSKSQRRKSLKLNKDKTIVFSEN HKNDMDITQSCMVEIDNESALEDK EDFHLAGASKTILYSCGQDDMEITRS HTTALECKTLLPNEIAIRPMDKTVLF TDNYS DLEV TDSHTVFIDCQATEKIL EENPKFGIGKGNLGVSF PKDN S CV QEIAEKQALAVGNKIVLHTEQKQQL FAATNR TTNEIIFHSAAMDEKVIGK VVDQACTLEKAQVESCQLNRRDRR NVDFTSSHATAVCGSSDNYSCLPNV ISCTDNLEGSAMLLCDKDEEKANYC PVQNDLAYANDFASEYYLESEGQPL SAPCPLEKEEVIQTSTKGQLDCVIT LHKDQDLIKDPRNLLANQTLVYSQD LGEMTKLNSKRVSFKLPKDQMKVY VDDIYVIPQPHFSTDQPPLPKKGQSS INKEEVILSKAGNKS LNIIENSSAPIC

ENKPKILNSEEWFAAACKKELKENI
QTTNYNTALDFHNSDVTKQVIQTH
VNAGEAPDPVITSNVPCFHSIKPNLN
NLNGKTGEFLAFQTVHLPPLPEQLL
ELGNKAHNDMHIVQATEIHNINIIS
NAKDSRDEENKSSHNGAETTSPPK
TVFKDKVRRCSLGFILPRLPNKRNC
VTGIDDLEQIPADTTDINHLETQPV
SKDSGIGSVAGKLNLSPSQYINEENL
PVYPDEINSSDSINIETEEKALIETY
KEISPYENKMGKTCNSQKRTWVQE
EEDIHKEKKIRKNEIKFSDTTQDREI
FDHHTTEEDIDKSANSVLIKNLSRTP
SCSSSLDSIKADGTSLDFSTYRSSQM
ESQFLRDTICEESLREKLQDGRITIR
EFFILLQVHILIQKPRQSNLPGNFTV
NTPPTPEDLMLSQYVYRPKIQIYRED
CEARRQKIEELKLSASNQDKLLVDIN
KNLWEKMRHCSDKELKAFGIYLNKI
KSCFTKMTKVFTHQGKVALYGKLVQ
SAQNEREKLQIKIDEMDKILKKIDNC
LTEMETETKNLEDEEKNNPVEEWD
SEMRAAEKELEQLKTEEEELQRNLL
ELEVQKEQTLAQIDFMQKQRNRTEE
LLDQLSLEWDVVEWSDDQAVFTFV
YDTIQLTITFEESVVGFPFLDKRYRKI
VDVNFQSLLEDQAPPSSLLVHKLIF
QYVEEKESWKKCTTQHQLPKMLE
EFSLVVHHCRLLGEEIEYLKRWGPN
YNLMNIDINNELRLLFSSSAFAK
FEITLFLSAYYPSVPLSTIQNHVGNT
SQDDIATILSKVPLENNYLKNVVKQI
YQDLFQDCHFYH