

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence |
|--------------|-------------|--------------|-----------------------------|--------------|---------------|--|-------------------|---|
| Q9H1H9 | KI13A_HUMAN | Homo sapiens | Kinesin-like protein KIF13A | 12.251566 | S636;S1587 | S636;S1287;S1454;S1490;S1529;S1572;S1648;S1698;S1494;S1481;S1481 | 35254053;30620550 | MSDTKVKVAVRVRPMNRRELELNT KCVVEMEGNQTVLHPPPSNTKQGE RKPPKVFAFDYCFWSMDESNTTKYA GQEVVFKCLGEGILEKAFQYNACIF AYGQTGSGKSFSMMGHAEQLGLIPR LCCALFKRISLEQNESQTFKVEVSY MEIYNEKVRDLLDPKGSRQSLKVRE HKVLGPYVDGLSQLAVTSFEDIESL MSEGKNSRTVAATNMNEESSRSHA VFNIITQTLYDLQSGNSGEKVSQVS LVDLAGSERVSKTGAAGERLKEGSN INKSLTTLGLVISSLADQAAGKGKSK FVPYRDSVLTWLLKDNLGGNSQTS MIATISPAADNYEETLSTLRYADRAK RIVNHAVVNEDPNAKVIRELREEVE KLREQLSQAEAMKAPELKEKLEESE KLIKELTVTWEEKLRKTEEIAQERQR QLESMGISLEMSGIKVGGDDKCYLVN LNADPALNELLVYYLKDHTRVGADT SQDIQLFGIGIQPHCEIDIASDGDVT LTPKENARSCVNGTLVCSTTQLWHG DRILWGNHFFRINLPKRKRRDWL KDFEKETGPPEHDLDAASEASSEPD YNYEFAQMEVIMKTLNSNDPVQNV VQVLEKQYLEEKRSALÉEORLMYER ELEQLRQQLSPDRQPQSSGPDRLAY SSQTAQQKVTQWAEERDELFRQSLA KLREQLVKANTLVREANFLAEEMSK LTDYQVTLQIPAAANLSANRKRGAIVS EPAIQVRRKGKSTQVWTIEKLENKLI DMRDLYQEWKEKVPEAKRLYGKRG DPFYEAQENHNLIGVANVFLECLFC DVKLQYAVPIISQQGEVAGRLHVEV MRVTGAVPERVVEDDSSSENSSES LEVVDSSGEIHRVKKLTCRVKIKEAT GLPLNLSNFVFCQYTFWDQCESTVA APVVDPEVSPQSKDAQYTVTFSHC KDYVVNVTEEFLEFISDGALAEVWG HRCAGNGSSIWEVDSLHAKTRTLHD RWNEVTRRIEMWISILELNEGEYA AVELHQAKDVNTGGIFQLRQGHSSR VQVTVKPVQHSGLPLMVEAILSFSI GCVTARSTKLQRGLDSYQRDDEDGD DMDSYQEEDLNCVRERWSDALIKR REYLDEQIKKVSNKTEKTEDDVERE AQLVEQWVGLTEERNAVLVPAPGSG IPGAPADWIPPPGMETHIPVFLDLN ADDLSANEQLVGPASGVNSILPKE HGSQFFYLPPIKHSDDDEVSATASWDS |

SVHDSVHLNRVTPQNERIYLIVKTTV
QLSHPAAMELVLRKRIAANIYNKQS
FTQSLKRRISLKNIFYSCGVTYEIVSN
IPKATEEIEDRETLALLAARSENEG
SDGETYIEKYTRGVLQVENILSLERL
RQAVTVKEALSTKARHIRRSLSTPNV
HNVSSRPDLSGFDEDDKGWPENQ
LDMSDYSSSYQDVACYGTLPRDSPR
RNKEGCTSETPHALTVSPFKAFSPQ
PPKFFKPLMPVKEEHKKRIALEARPL
LSQESMPPPQAHNPGCIVPSGSNGS
SMPVEHNSKREKKIDSEEEENELEA
INRKLISQPYVPVEFADFSVYNASL
ENREWFSSKVDLSNSRVLEKEVSR
PTTSSITSGYFSHSASNATLSDMVVP
SSDSSQLAIQTKDADSTEHSSTPSLV
HDFRPSSNKELTEVEKGLVKDKIIVV
PLKENSALAKGSPSSQSIPEKNSKSL
CRTGSCSELDACPSKISQPARGFCPR
EVTVEHTTNILEDHSFTEFMGVSEG
KDFDGLTDSSAGELSSRRSLPNKTG
GKTVSDGLHHPSQLHSKLENDQVII
PEAAFWVLCCQ