

| UniprotKB ID | Entry name | organism | full name | oglcnacscore | oglcnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus | plasma membrane | extracel region |
|--------------|------------|--------------|-----------------------|--------------|---------------|-----------------------|-------------------------------------|---|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|-----------------|-----------------|
| Q61768 | KINH_MOUSE | Mus musculus | Kinesin-1 heavy chain | 29.368587 | NaN | S933;S945 | 39627609;33300544;36288343;34887587 | MADPAECNIKVMCRFRPLNESEVN RGDKYYAKFQGEDTVMIASKPYAFD RVFQSSTSQEQVYNDCAKKIVKDVL EGYNGTIFAYGQTSSGKTHMEGKL HDPEGMGIHPRIVQDIFNYIYSMDEN LEFHIKVSYPFEIYLDKIRDLLDVSKTN LSVHEDKNRVYPYVKGCTERFVCSFD EVMDTIDEGKSNRHVAVTNMNEHS SRSHSIFLINVKQENTQTTEQKLSGKL YLVDLAGSEKVSKTGAEGAVLDEAK NINKSLSALGNVISALAEGSTYVPYR DSKMTRILQDSLGGNCRRTTIVICCSF SSYNESETKSTLLFGQRAKTIKNTVC VNVELTAEQWKKYKEKEKNKTLR NTIQWLENELNRRWRNGETVPIDEQ FDKEKANLEAFTADKDIATSDKPAA AVGMAGSFTDAERRKCEELAKLYK QLDDKDEEINQQSQLVEKLTQML DQEELLASTRRDQDNMQAELNRLQ AENDASKEEVKEVLQALELAVNYD QKSQEVEDKTKEYELLSDELNQKSA TLASIDAEIQKLEMTNHQKKRAAE MMASLLKDLAEIGIAGVNNQVQKPE GTGMIDEEFTVARLYSKMKSEVKT MVKRCKQLESTQTESNKKMEENEK ELAACQLRISQHEAKIKSLTEYLQNV EQKKRQLEESVDSLGEELVQLRAQE KVHEMEKEHLLNKVQTANEVQAVE QQIQSHRETHQKQISSLRDEVEAKE KLITDLQDQNKQMVLEQERLRVEHE RLKATDQEKSRKLHELTVMQDRRE QARQDLKGLEETVAKELQTLHNLRK LFVQDLATRVKKSAEVSDDTGGSA AQKQKISFLENNLEQLTKVHKQLVR DNADLRCELPKLEKRLRATAERVKA LESALKEAKENASDRKRYQVEVDR IKEAVRSKNMARRGHSQAIAKPIRPG QHPAASPTHPTVIRGGGSFVQNNQ PVGLRGGGGKQS | True | False | 4.754 | 2.993 | 5.0 | 1.923 | 2.573 | 2.174 | 1.814 |