

| 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 | extracellular region |
|--------------|------------|--------------|--------------|--------------|---------------|-----------------------|----------|--|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|-----------------|----------------------|
| 008528 | HXK2_MOUSE | Mus musculus | Hexokinase-2 | 29.185005 | NaN | NaN | 22645316 | MIASHMIACLFTELNQNVQKVDQY LYHMRLSDETLLEISRRFRKEMKKG LGATTHPTAAVKMLPTFVVRSTPDGT EHGEFLALDLGGTNFRVLRVVRTDN GLQRVEMENQIYAIPEIDIMRSGSTQ LFDHIAECLANFMDKLIKEKKLPL GFTFSFPCHQTKLDESFLVSWTKGF KSSGVEGRDVEDLIRKAIQRRGDFDI DIVAVVNDTVGTMTCGYDDQNCIEI GLIVGTGSNACYMEEMRHIDMVEG DEGRMCINMEWGAFGDDGTLNDIR TEFDREIDMGSLNPGKQLFEKMISG MYMGELVRLILVKMAKAELLFOGKL SPELLTTSFETKDVSDIEDDKDGIQ KAYQILVRLGLSPLQEDCVATHRICQ IVSTRSASLCAATLAAVLWRIKENKG EERLRSTIGVDGVSYYKHPHFAKRL HKAVRRLVPCDVRFLRSEDGSGKG AAMVTAVAYRLADQHRARQKTLESL KLSHEQLLEVRRMKVEMEQGLSK ETHEAAPVKMLPTYVCATPDGTEKG DFLALDLGGTNFRVLLVRRVNRGKRR GVEMHNKIYSIPQEVMHGTGEELFD HIVQCIADFLEYMGMKGVSLPLGFT FSFPCQNSLDQSILLKWTGFKAS GCEGEDVVTLLKEAIRRREEFDLDV VAVVNDTVGTMTCGYEDPHCEVG LIVGTGSNACYMEEMRNVELVDGE EGRMCVNMEWGAFGDNGCLDDLRL TVFDVAVDELNPGKQRFKEMISG MYLGEIVRNILDFTKRGLLFRGRISE RLKTRGIFETKFLSQIESDCLALLQV RAILRHGLESTCDDSIIVKEVCTVVA RRAAQLCGAGMAAVVDKIRENRGLD NLKVTVGVDGTYKLPHPHAKVMH ETVRDLAPKCDVSFLESEDGSGKGA ALITAVACRIREAGQR | True | True | 4.605 | 2.964 | 4.739 | 4.517 | 1.803 | 2.838 | 2.995 |