

32-3031: HK-3 Recombinant Protein

Alternative Name : Hexokinase-3, EC 2.7.1.1, Hexokinase type III, HK III, HXK3, HK3.

Description

Source : Escherichia Coli. HK-3 Human Recombinant produced in E.Coli is a single, non-glycosylated, polypeptide chain fused to His tag at the N-terminal encoding the sequence of 943 amino acids and having a molecular mass of 101.1 kDa. HXK3 is purified by proprietary chromatographic techniques. Hexokinases phosphorylate glucose to produce glucose-6-phosphate, thus committing glucose to the glycolytic pathway. HK3 encodes hexokinase 3. Similar to hexokinases 1 and 2, this allosteric enzyme is inhibited by its product glucose-6-phosphate. Hexokinase3 lacks the hydrophobic N-terminal sequence critical for targeting to mitochondria. Hexokinase3 may have anabolic functions, providing H6P for glycogen or lipid synthesis.

Product Info

Amount : 10 µg

Purification : Greater than 95.0% as determined by (a) Analysis by RP-HPLC. (b) Analysis by SDS-PAGE.

Content : The protein (1mg/ml) contains 20mM Tris pH 8.0 and 10% glycerol.

Storage condition : Store at 4°C if entire vial will be used within 2-4 weeks. Store, frozen at -20°C for longer periods of time. For long term it is recommended to add a carrier protein (0.1% HSA or BSA). Please avoid freeze-thaw cycles.

Amino Acid : MGSSHHHHH SSSLVPRGSH MDSIGSSGLR QGEETLSCSE EGLPGSPDSSE
LVQECLQQFKVTRAQLQQI QASLLGSMEQ ALRGQASPAP AVRMLPTYVG STPHGTEQGD
FVVLELGATG ASLRVLWVTL TGIEGHRVPEP RSQEFVIPQE VMLGAGQQLF DFAAHLSEF
LDAQPVNKQGLQLGFSFSFP CHQTGLDRST LISWTKGFRC SGVEGQDVVQ LLRDAIRRQG
AYNIDVVAVV NDTVGTMMGC EPGVRPCEVG LVVDTGTNAC YMEEARHVAV LDEDGRVCV
SVEWGSFSDD GALGPVLTTF DHTLDHESLN PGAQRFEKMI GGLYLDELVR LVLHLARCG
VLFGGCTSPA LLSQGSILLE HVAEMEDPST GAARVHAILQ DLGLSPGASD VELVQHVCAA
VCTRAAQLCA AALAAVLSCL QHSREQQLTQ VAVATGGRVC ERHPRFCSVL QGTMMLAPE
CDVSLIPSDGGGRGVAMVT AVAARLAAHR RLLEETLAPF RLNHDQLAAV QAQMRKAMAK
GLRGEASSLR MLPTFVRATP DGSEKDFLA DLGGTNFRV LLVRVTTGVQ ITSEIYSIPE
TVAQGSQQQL FDHIVDCIVD FQKQGLSGQ SLPLGFTFSF PCRQLGLDQG ILLNWTGKFK
ASDCEGQDVV SLLREAITRR QAVELNVVAI VNDTVGTMMS CGYEDPRCEI GLIVGTGTNA
CYMEELRNAGVPGDSGRMC INMEWGAFGD DGSLAMLSTR FDASVDQASI NPGKQRFKEM
ISGMYLGEIV RHILLHLTSL GVLFRGQQIQ RLQTRDIFKT KFLSEIESDS LALRQVRAIL
EDLGLPLTSDALMVLEVCQ AVSQRAAQLC GAGVAAVVEK IRENRGLEEL AVSVGVDGTL
YKLHPRFSSL VAATVRELAP RCVVTFLLQSE DSGKGAALV TAVACRLAQL TRV.

