

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 :	MGSSHHHHHH SSGLVPRGSH MDSIGSSGLR QGEETLSCSE EGLPGPSDSSE LVQECLQQFKVTRAQLQIQI QASLLGSM EQ ALRGQASPAP AVRMLPTYVG STPHGTEQGD FVVLELGATG ASLRVLWVTL TGIEGHRVPEP RSQEFVIPQE VMLGAGQQLF DFAAHCLSEF LDAQPVNKQGLQLGFSFSFP CHQTGLDRST LISWTKGFRC SGVEGQDVVQ LLRD AIRRQG AYNIDVVAVV NDTVGTMMGC EPGVRPCEVG LVDVTGTNAC YMEEARHVAV LDEDRGRVCV SVEWGSFSDD GALGPVLTTF DHTLDHESLN PGAQRFEKMI GGLYLGE LVR LVL AHLARCG VLFGGCTSPA LLSQGSILLE HVAEMEDPST GAARVHAILQ DLGLSPGASD VELVQHVCAA VCTRAAQLCA AALAAVLSCL QHSREQTLQ VAVATGGRVC ERHPRFCSVL QGTVMLLAPE CDVSLIPSDVGGGRGVAMVT AVAARLAAHR RLLEETLAPF RLNHDQLAAV QAQMRKAMAK GLRGEASSLR MLPTFVRATP DG SERGDFLA LDLGGTNFRV LLVRVTTGVQ ITSEIYSIPE TVAQGSQQQL FDHIVDCIVD FQKQGLSGQ SLPLGFTFSF PCRQLGLDQG ILLNWTGKFK ASDCEGQDVV SLLREAITRR QAVELNVVAI VNDTVGTMMMS CGYEDPRCEI GLIVGTGTNA CYMEELRN VAGVPGDSGRMC INMEWGAFGD DGSLAMLSTR FDASVDQASI NPGKQRFKEM ISGMYLGEIV RHILLHLTSL GVLFRGQQIQ RLQTRDIFKT KFLSEIESDS LALRQVRAIL EDLGLPLTSDDALMVLEVCQ AVSQRAAQLC GAGVAAVVEK IRENRGLEEL AVSVGVDGTL YKLHPRFSSL VAATVRELAP RCVVTFLOQE DGSGKGAALV TAVACRLAQL TRV.

