

## 32-3026: GCK Recombinant Protein

**Alternative Name :** Glucokinase, EC 2.7.1.2, Hexokinase-4, Hexokinase type IV, HK IV, HK4, Hexokinase-D, GCK, GK, GLK, HHF3, HKIV, HXKP, MODY2.

### Description

Source : Escherichia Coli. Glucokinase Human Recombinant produced in E.Coli is a single, non-glycosylated, polypeptide chain (aa 1-465) fused to a 20aa His tag at the N-terminal encoding the sequence of 485 amino acids and having a molecular mass of 54.3 kDa. HK4 is purified by proprietary chromatographic techniques. Hexokinases phosphorylate glucose to produce glucose-6-phosphate, thus committing glucose to the glycolytic pathway. Alternative splicing of Glucokinase results in three tissue-specific forms of glucokinase, one found in pancreatic islet beta cells and two found in liver. The protein localizes to the outer membrane of mitochondria. In contrast to other forms of hexokinase, HK4 is not inhibited by its product glucose-6-phosphate but remains active while glucose is abundant. Mutations in this gene have been associated with non-insulin dependent diabetes mellitus (NIDDM), maturity onset diabetes of the young, type 2 (MODY2) and persistent hyperinsulinemic hypoglycemia of infancy (PHHI).

### Product Info

**Amount :** 10 µg  
**Purification :** Greater than 95.0% as determined by SDS-PAGE.  
**Content :** The protein (1mg/ml) contains 20mM Tris-HCl 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 SGLVPRGSH MLDDRARMEA AKKEKVEQIL AEFQLQEEDL KKVMRRMQKE MDRGLRLETH EEASVKMLPT YVRSTPEGSE VGDFLSLDLG GTNFRVMLVK VGEEGEQWS VKTKHQMYSI PEDAMTGTAELMLFDYISECI SDFLDKHQMK HKKLPLGFTF SFPVRHEDID KGILLNWTGK FKASGAEGNN VVGLLRDAIK RRGDFEMDVV AMVNDTVATM ISCYEDHQC EVGMIVGTGC NACYMEEMQN VELVEGDEGR MCVNTEWGAF GDSGELDEFL LEYDRLVDES SANPGQQLYE KLIGGKYMGE LVRLVLLRLV DENLLFHGEA SEQLRTRGAF ETRFVSQVES DTGDRKQIYN ILSTLGLRPS TTDCDIVRRA CESVSTRAAH MCSAGLAGVI NRMRESRSED VMRITVGVDG SVYKLHPSFK ERFHASVRRL TPSCEITFIE SEEGSGRGAA LVSAVACKKA CMLGQ.

