



## RayBiotech, Inc.

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# Certificate of Analysis and Data Sheet Recombinant Human Hexokinase-4

**Catalog No.**  
228-10518

**Source**  
*Escherichia coli*

## Synonyms

Glucokinase, EC 2.7.1.2, Hexokinase-4, Hexokinase type IV, HK IV, HK4, Hexokinase-D, GCK, GK, GLK, HNF3, HKIV, HXKP, MODY2.

## Introduction

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).

## Description

Glucokinase 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 485 amino acids and having a molecular mass of 54.3 kDa.

HK4 is purified by proprietary chromatographic techniques.

## Physical Appearance:

Sterile filtered colorless solution.

## Formulation

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

## Storage Conditions

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 storage it is recommended to add a carrier protein (0.1% HSA or BSA).

**Please avoid freeze-thaw cycles.**

**The products are furnished for LABORATORY RESEARCH USE ONLY.  
Not for diagnostic or therapeutic use.**



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### **Purity**

Greater than 95.0% as determined by:

- (a) Analysis by RP-HPLC.
- (b) Analysis by SDS-PAGE.

### **Amino Acid Sequence**

MGSSHHHHHH SSGLVPRGSH MLDDRARMEA AKKEKVEQIL AEFQLQEEDL  
KKVMRRMQKE MDRGLRLETH EEASVKMLPT YVRSTPEGSE VGDFLSLDLG GTNFRVMLVK  
VGEGEEGQWS VKTKHQMYSI PEDAMTGTA E MLFDYISECI SDFLDKHQMK HKKLPLGFTF  
SFPVRHEDID KGILLNWT KG FKASGAEGNN VVGLLRDAIK RRGDFEMDVV AMVNDTVATM  
ISCYYEDHQC 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.

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