

32-2987: CKMT2 Recombinant Protein

Alternative Name : Creatine kinase mitochondrial 2 (sarcomeric), Basic-type mitochondrial creatine kinase, Sarcomeric mitochondrial creatine kinase, creatine kinase S-type, mitochondrial, SMTCK, Mib-CK, EC 2.7.3.2.

Description

Source : E.coli. CKMT2 Human Recombinant produced in E. coli is a single polypeptide chain containing 405 amino acids (40-419) and having a molecular mass of 46.1 kDa. CKMT2 is fused to a 25 amino acid His-tag at N-terminus & purified by proprietary chromatographic techniques. Creatine Kinase, Mitochondrial 2 (CKMT2) is a member of the ATP:guanido phosphotransferase family. CKMT2 is responsible for the transfer of high energy phosphate from mitochondria to the cytosolic carrier, creatine. CKMT2 reversibly catalyzes the transfer of phosphate between ATP and various phosphogens (e.g. creatine phosphate). Creatine kinase isoenzymes have a principal role in energy transduction in tissues with large, variable energy demands, such as skeletal muscle, heart, brain and spermatozoa. Mitochondrial creatine kinase occurs in 2 different oligomeric forms: dimers and octamers, contrary to the exclusively dimeric cytosolic creatine kinase isoenzymes. The CKMT2 gene contains sequences homologous to a number of motifs which are shared among some nuclear genes encoding mitochondrial proteins and therefore may be crucial for the coordinated activation of these genes during mitochondrial biogenesis.

Product Info

Amount :	20 µg
Purification :	Greater than 90% as determined by SDS-PAGE.
Content :	The CKMT2 solution (1mg/ml) contains 20mM Tris-HCl buffer (pH 8.0), 0.1M NaCl, 1mM DTT 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 storage it is recommended to add a carrier protein (0.1% HSA or BSA). Avoid multiple freeze-thaw cycles.
Amino Acid :	MGSSHHHHHH SSGLVPRGSH MGSHEVREQ PRLFPPSADY PDLRKHNNCM AECLTPAIYA KLRNKVTPNG YTLQCIQTG VDNPGHPFIK TVGMVAGDEE SYEVFADLFD PVIKLRHNGY DPRVMKHTTD LDASKITQGQ FDEHYVLSSR VRTGRSIRGL SLPPACTRAE RREVENVAIT ALEGLKGDLA GRYYKLSEMT EQDQQRLLDD HFLQDKPVSP LLTCAGMARD WPDARGIWHN YDKTFLIWIN EEDHTRVISM EKGGMKRVF ERFCRGLKEV ERLIQRGWE FMWNERLGYI LTCPSNLGTG LRAGVHVRIP KLSKDPFRFSK ILENLRLQKR GTGGVDAAV ADVYDISNID RIGRSEVELV QIVIDGVNYL VDCEKKLERG QDIKVPPLP QFGKK

