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32-5313: Recombinant Human GroEL (HSP60) (27-573 a.a.)

Alternative Name :	CPN60,GROEL,HLD4,HSP-60,HSP60,HSP65,HuCHA60,SPG13,Chaperonin 60,60 kDa chaperonin,P60 lymphocyte protein,60 kDa heat shock protein,mitochondrial.

Description

Source : Escherichia Coli. GROEL Human Recombinant produced in E.Coli is a single, non-glycosylated polypeptide chain containing 572 amino acids (27-573 a.a.) and having a molecular mass of 60kDa.GROEL is fused to a 25 amino acid His-tag at N-terminus & purified by proprietary chromatographic techniques. GroEL, HSP60 is a chaperonin located in the mitochondria which is responsible for the transportation & refolding of proteins from the cytoplasm directly into the mitochondrial matrix. GroEL is regulated by the HSP10 cochaperonin, which is a single heptameric protein ring having a molecular mass of 10 kDa which form a unique complex with HSP60. HSP10, GroES coordinates the ATPase activity of the HSP60 subunits in order to allow the release of bound polypeptide in a manner that is productive for its correct folding.

Product Info

Amount :	10 µg
Purification :	Greater than 90.0% as determined by SDS-PAGE.
Content :	GROEL protein solution (0.5mg/ml) contains 20mM Tris-HCl buffer, (pH 8.0) 0.1M NaCl 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 MGSHMAKDVK FGADARALML QGVDLLADAV AVTMGPKGRT VIIEQSWGSP KVTKDGVTVA KSIDLKDKYK NIGAKLVQDV ANNTNEEAGD GTTTATVLAR SIAKEGFEKI SKGANPVEIR RGVMLAVDAV IAELKKQSKP VTTPEEIAQV ATISANGDKE IGNIISDAMK KVGRKGVITV KDGKTLNDEL EIIEGMKFDR GYISPYFINT SKGQKCEFQD AYVLLSEKKI SSIQSIVPAL EIANAHRKPL VIIAEDVDGE ALSTLVLNRL KVGLQVVAVK APGFGDNRKN QLKDMAIATG GAVFGEEGLT LNLEDVQPHD LGKVGEVIVT KDDAMLLKGK GDKAQIEKRI QEIIEQLDVT TSEYEKEKLN ERLAKLSDGV AVLKVGGTSD VEVNEKKDRV TDALNATRAA VEEGIVLGGG CALLRCIPAL DSLTPANEDQ KIGIEIIKRT LKIPAMTIAK NAGVEGSLIV EKIMQSSSEV GYDAMAGDFV NMVEKGIIDP TKVVRTALLD AAGVASLLTT AEVVVTEIPK EEKDPGMGAM GGMGGGMGGG MF.