

## 32-5312: Recombinant Human GroEL (HSP60)

**Alternative Name :** CPN60,GROEL,HSP60,HSP65,SPG13,CHA60,GROL,crpA,mopA,60 kDa heat shock protein mitochondrial,Heat shock protein 60,HSP-60,60 kDa chaperonin,Chaperonin 60,Mitochondrial matrix protein P1,P60 lymphocyte protein,HuCHA60,HSPD1.

### Description

Source : Escherichia Coli. Recombinant Human GroEL, HSP60 produced in E.Coli is a single, non-glycosylated polypeptide chain fused to a 20 a.a. His tag at N-terminus containing 593 amino acids (1-573 a.a.) and having a molecular mass of 63kDa.The HSP60 is 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 :** 20 µg  
**Purification :** Greater than 95.0% as determined by SDS-PAGE.  
**Content :** The GroEL protein contains 20mM Tris-HCl buffer pH-8.0, 5mM 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 MLRLPTVFRQ MRPVSRVLAP HLTRAYAKDV  
KFGADARALMLQGVDLLADA VAVTMGPKGR TVIIEQSWGS PKVTKDGVTV AKSIDLKDKY  
KNIGAKLVQDVANNTNEEAG DGTTTATVLA RSIKEGFEK ISKGANPVEI RRGVMLAVDA  
VIAELKKQSKPVTTPEEIAQ VATISANGDK EIGNIISDAM KKVGRKGVIT VKDGKTLNDE LEIIEGMKFD  
RGYISPYFIN TSKGQKCEFQ DAYVLLSEKK ISSIQSIVPA LEIANHRKP LVIIAEDVDG EALSTLVLNR  
LKVGLQVVAV KAPGFGDNRK NQLKDMAIAT GGAVFGEEGL TLNLEDVQPH DLGKVGIVV  
TKDDAMLLKG KGDKAQIEKR IQEIIQLDV TTSEYEKEKL NERLAKLSDG VAVLKVGGTS DVEVNEKKDR  
VTDALNATRA AVEEGIVLGG GCALLRCIPA LDSLTPANED QKIGIEIIR TLKIPAMTIA KNAGVEGSLI  
VEKIMQSSSE VGYDAMAGDF VNMVEKGIID PTKVVRTALL DAAGVASLLT TAEVVVTEIP KEEKDPGMGA  
MGGMGGMGG GMF.