

## 32-5304: Recombinant E.Coli DnaK ATPase Binding Domain

**Alternative Name :** HSP-70,HSP70,DnaK,Chaperone protein dnaK,Heat shock protein 70,Heat shock 70 kDa protein,groP,grpF,seg,b0014,JW0013.

### Description

Source : Escherichia Coli. Recombinant DnaK Substrate Binding Domain produced in E.Coli is a single, non-glycosylated polypeptide chain containing 384 amino acids and having a molecular mass of 48.1 kDa. DnaK, originally identified for its DNA replication by bacteriophage I in E. coli is the bacterial HSP-70 chaperone. This protein is involved in the folding and assembly of newly synthesized polypeptide chains and in preventing the aggregation of stress-denatured proteins. DnaK(amino acids1-384) is N-terminal ATPase domain and ATP bound to the ATPase domain induces a conformational change in the substrate binding domain (residues 385-638). The protein coding region of the ATPase domain of DNAK (amino acids 1-384) was amplified by PCR and cloned into an E. coli expression vector. The ATPase domain of DNAK was purified to apparent homogeneity by using conventional column chromatography techniques.

### Product Info

**Amount :** 50 µg  
**Purification :** Greater than 95.0% as determined by:(a) Analysis by RP-HPLC.(b) Analysis by SDS-PAGE.  
**Content :** The DnaK protein contains 25mM Tris-HCl, pH7.5, 100mM NaCl, 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 :** MGKIIIGIDLG TTNSCVAIMD GTTPRVLENA EGDRTTPSII AYTQDGETLV GQPAKRQAVTNPQNTLFAIK  
RLIGRRFQDE EVQRDVSIMP FKIIAADNGD AWVEVKGQKM APPQISAEVLKMKKTAEDY LGPEVTEAVI  
TVPAYFNDAQ RQATKDAGRI AGLEVKRIIN EPTAAALAYGLDKGTGNRTI AVYDLGGGTF DISIIEIDEV  
DGEKTFEVLA TNGDTHLGGE DFDSRLINYLVEEFKKDQGI DLRNDPLAMQ RLKEAAEKAK IELSSAQQTD  
VNLPIYITADA TGPKHMNIKV TRAKLESLVE DLVNRSIEPL KVALQDAGLS VSDIDDVILV GGQTRMPMVQ  
KKVAEFFGKEPRKDVNPDEA VAIGAAVQGG VLTG.