Product Datasheet

Product Name	DnaK ATPase Binding Domain E.Coli Recombinant
Cata No	CB500760
Source	*Escherichia Coli.*
Synonyms	HSP-70, HSP70, DnaK, Chaperone protein dnaK, Heat shock protein 70, Heat shock 70 kDa protein, groP, grpF, seg, b0014, JW0013.

Description

DnaK, originally identified for its DNA replication by bacteriophage l 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.

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.

Physical Appearance

Sterile filtered colorless solution.

Purity

Greater than 95.0% as determined by:
(a) Analysis by RP-HPLC.
(b) Analysis by SDS-PAGE.

Formulation

The DnaK protein contains 25mM Tris-HCl, pH7.5, 100mM NaCl, 5mM DTT and 10%Glycerol.

Stability

Store at 4℃ if entire vial will be used within 2-4 weeks.
Store, frozen at -20℃ 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.

Sequence

MGKIIGIDLG TTNSCVAIMD GTTPRVLENA
EGDRTTPSII AYTQDGETLV
GQPAKRQAVTNPQNTLFAIK RLIGRRFQDE
EVQRDVSIMP FKIIAADNGD AWVEVKGQKM
APPQISAEVLKKMKKTAEDY LGEPVTEAVI
TVPAYFNDAQ RQATKDAGRI AGLEVKRIIN
EPTAAALAYGLDKGTGNRTI AVYDLGGGTF
DISIIEIDEV DGEKTFEVLA TNGDTHLGGE
DFDSRLINYLVEEFKKDQGI DLRNDPLAMQ
RLKEAAEKAK IELSSAQQTD VNLPYITADA
TGPKHMNIKV TRAKLESLVE DLVNRSIEPL
KVALQDAGLS VSDIDDVILV GGQTRMPMVQ
KKVAEFFGKEPRKDVNPDEA VAIGAAVQGG
VLTG.

Applications