

## 32-5336: Recombinant Human Heat Shock 70kDa protein 5, Hi-5

### Alternative Name :

78 kDa glucose-regulated protein,GRP-78,Endoplasmic reticulum luminal Ca(2+)-binding protein grp78,Heat shock 70 kDa protein 5,Immunoglobulin heavy chain-binding protein,BiP,HSPA5,GRP78,MIF2,FLJ26106.

### Description

Source : Hi-5 Cells. HSPA5 produced in Hi-5 cells is a single, glycosylated polypeptide chain containing 640 amino acids (20-650 a.a.) and having a molecular mass of 71kDa. HSPA5 is fused to an 8 amino acid His Tag at C-Terminus and purified by proprietary chromatographic techniques. Binding immunoglobulin protein (BiP or HSPA5) is a member of the family of ~70kDa heat shock proteins (HSP 70). HSPA5 is a stress response protein which is induced by agents or conditions that adversely affect endoplasmic reticulum (ER) function. HSPA5 is crucial for the proper glycosylation, folding as well as for the maintenance of cell homeostasis and the prevention of apoptosis.

### Product Info

#### Amount :

20 µg

#### Purification :

Greater than 90.0% as determined by SDS-PAGE.

#### Content :

The HSPA5 protein solution (1mg/ml) 20mM Tris-HCl buffer (pH8.0), 10% glycerol, 2mM DTT and 200mM NaCl.

#### 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 :

MEEDKKEDVG TVVGIDLGTT YSCVGVFKNG RVEIANDQG NRITPSYVAF TPEGERLIGD AAKNQLTSNP  
ENTVFDKRL IGRTWNDPSV QQDIKFLPFK VVEKTKPYI QVDIGGGQTK TFAPEEISAM VLTKMKETAE  
AYLGKKVTHA VVTVPAYFND AQRQATKDAG TIAGLNMVRI INEPTAAIA YGLDKREGEK NILVFDLGGG  
TFDVSLTID NGVFEVVATN GDTHLGGEDF DQRVMEHFIK LYKKTGKDV RKNRAVQKL RREVEKAKRA  
LSSQHARIE IESFYEGEDF SETLTRAKFE ELNMDLFRST MKPVQKVLED SDLKSDIDE IVLVGGSTRI  
PKIQQLVKEF FNGKEPSRGI NPDEAVAYGA AVQAGVLSGD QDTGDLVLLD VCPLTLGIET VGGVMTKLIP  
RNTVVPTKKS QIFSTASDNQ PVTIKVYEG ERPLTKDNHL LGTFDLTGIP PARGVPQIE VTFEIDVNGI  
LRVTAEDKGT GNKNKITN DQNRLTPEEI ERMVNDAEKF AEEDKCLKER IDTRNELESY AYSLKNQIGD  
KEKLGGLSS EDKETMEKAV EEKIEWLESH QDADIEDFKA KKKELEEIVQ PIISKLYGSA GPPPTGEEDT  
AELEHHHHHH.

