9853 Pacific Heights Blvd.
Suite D. San Diego,
CA 92121, USA
Tel: 858-263-4982
Email: info@abeomics.com

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

Alternative Name :	78 kDa glucose-regulated protein,GRP-78,Endoplasmic reticulum lumenal 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 RVEIIANDQG NRITPSYVAF TPEGERLIGD AAKNQLTSNP ENTVFDAKRL IGRTWNDPSV QQDIKFLPFK VVEKKTKPYI QVDIGGGQTK TFAPEEISAM VLTKMKETAE AYLGKKVTHA VVTVPAYFND AQRQATKDAG TIAGLNVMRI INEPTAAAIA YGLDKREGEK NILVFDLGGG TFDVSLLTID NGVFEVVATN GDTHLGGEDF DQRVMEHFIK LYKKKTGKDV RKDNRAVQKL RREVEKAKRA LSSQHQARIE IESFYEGEDF SETLTRAKFE ELNMDLFRST MKPVQKVLED SDLKKSDIDE IVLVGGSTRI PKIQQLVKEF FNGKEPSRGI NPDEAVAYGA AVQAGVLSGD QDTGDLVLLD VCPLTLGIET VGGVMTKLIP RNTVVPTKKS QIFSTASDNQ PTVTIKVYEG ERPLTKDNHL LGTFDLTGIP PAPRGVPQIE VTFEIDVNGI LRVTAEDKGT GNKNKITITN DQNRLTPEEI ERMVNDAEKF AEEDKKLKER IDTRNELESY AYSLKNQIGD KEKLGGKLSS EDKETMEKAV EEKIEWLESH QDADIEDFKA KKKELEEIVQ PIISKLYGSA GPPPTGEEDT AELEHHHHHH.