

HSPC150 protein

PDB:1YH2

Revision

Revision Type:created

Revised by:created

Revision Date:created

Entry Clone Accession:gi:33872714

Entry Clone Source:MGC

SGC Clone Accession:ubc44.001.167; plate SDC005:H6

Tag:N-terminal His-tag with integrated thrombin-cleavage site MGSSHHHHHSSGLVPRGS.

Host:E.coli BL21 (DE3)

Construct

Prelude:

Sequence:

gsSGLVPRGSMQRASRLKRELHMLATEPPPGITCWQDKDQMDDLRAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTPIYHP
NIDSAGRICLDVLKLPPKGAWRPSLNIATVLTSQLLMSEPNPDDPLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEEEMLD
NLP

Vector:p28a-LIC

Growth

Medium:TB

Antibiotics:

Procedure:HSPC150 was expressed in E. coli BL21 (DE3) grown in Terrific Broth (TB) in the presence of 50 µg/ml of kanamycin at 37°C to an OD600 of 5.5. Cells were then induced by isopropyl-1-thio-D-galactopyranoside (IPTG), final concentration 0.05 mM, and incubated overnight at 15°C. The culture was centrifuged and the cell pellets were collected and stored at -80°C.

Purification

Procedure

The cleared lysate was loaded onto a TALON metal-affinity resin column from BD Biosciences at 4°C. The column was washed with wash buffer A (10mM Tris-HCl pH 8.0, 0.5 M NaCl, 5% glycerol, 10 mM imidazole, 1 mM β -mercaptoethanol), wash buffer B (same as wash buffer A but containing 0.05% Tween 20) and again wash buffer A, and the protein was eluted with 10 mM Tris-HCl, pH 8.0, 0.5 M NaCl, 5% glycerol, 200 mM imidazole, 1 mM β -mercaptoethanol. The protein was further purified by gel filtration on a HighLoad 16/60 Superdex 200 column (GE Healthcare) equilibrated with 20 mM Tris-HCl, pH 8.0, 0.5 M NaCl, 5% glycerol, 2mM dithiothreitol and concentrated by ultrafiltration.

Extraction

Procedure

The cell pellet was resuspended in lysis buffer (10 mM Tris-HCl, pH 8.0, 0.5 M NaCl, 5% glycerol, 2 mM imidazole, 1 mM β -mercaptoethanol) with protease inhibitor (0.1mM phenylmethyl sulfonyl fluoride, PMSF) and lysed using Microfluidizer. The lysate was cleared by centrifugation.

Concentration: 17 mg/mL

Ligand

MassSpec:

Crystallization: Purified HSPC150 was crystallized using the sitting drop vapor diffusion method. Crystals grew when the protein (17mg/mL) was mixed with the reservoir solution in a 1:1 volume ratio, and the drop was equilibrated against a reservoir solution containing 4 M sodium formate.

NMR Spectroscopy:

Data Collection:

Data Processing: