

PRMT6

PDB:4QPP

Revision

Revision Type:created

Revised by:created

Revision Date:created

Entry Clone Accession:GI:227908866

Entry Clone Source:MGC

SGC Clone Accession:

Tag:N-terminal: His-tag with integrated TEV protease site: MHHHHHHSSGRENL^YFQ*G

Host:Sf9

Construct

Prelude:

Sequence:

gMSQPKRRKLESGGGGGEGEGTEEEEDGAEREAALEPRRTKRERDQLYYECYSDVSVHEEMIADRVRTDAYRLGILRNWAALRGKTV
LDVGAGTGILSIFCAQAGARRVYAVEASAIWQQAREVVRFNGLEDRVHVLPGPVETVELPEQVDAIVSEWMGYGLLHESMLSSVLHA
RTKWLKEGGLLLPASAE^LFIAPISDQMLEWRLGFWSQVKQHYGVDMSCLEGFATRC^LMGHSEIVVQGLSGEDVLARPQRFAQLELSR
AGLEQELEAGVGGRFRCSCYGSAPMHGFAIW^FQVTFPGGESEKPLVLSTSPFHPATHWKQALLYLNEPVQVEQD^TDVSGEITLLPSR
DNP^RRLRVLLRYKVGDQEEKTKDFAMED

Vector:pFBOH-MHL

Growth

Medium:

Antibiotics:

Procedure:HRMT1L6 was expressed in Sf9 cells

Purification

Procedure

For purification the cell paste was thawed and resuspended in lysis buffer containing 20 mM Tris-HCl, pH 8.0, 500 mM NaCl, 5 mM imidazol, 2 mM β -mercaptoethanol, 5% glycerol, 0.6% NP-40, protease inhibitor cocktail (Roche), 3000 U of benzonase (Novagen). Cells were lyzed by brief sonication. The clarified lysate was loaded onto a 2 mL TALON column (Clontech). The column was washed with 50 column volumes of 20 mM Tris-HCl buffer, pH 8.0, containing 500 mM NaCl, 5% cglycerol and 5 mM imidazole, and the protein was eluted with elution buffer (20 mM Tris-HCl, pH 8.0, 250 mM NaCl, 5% glycerol, 250 mM imidazole). The eluted protein was loaded on a Superdex200 column (GE Healthcare), equilibrated with 20 mM Tris-HCl buffer, pH 8.0, and 150 mM NaCl. Pooled fractions containing HRMT1L6 were subjected to TEV treatment

to remove His-tag. The protein was further purified to homogeneity by ion-exchange chromatography.

Extraction

Procedure

Cells were harvested by centrifugation at 5,000 rpm. The cell pellets were frozen in liquid nitrogen and stored at -80°C.

Concentration: 16 mg/ml - Enzymatic treatment: TEV

Ligand

MassSpec: expected mass is 42022.6 Da, measured mass is 42132.48 Da.

Crystallization: Purified HRMT1L6 (4.9 mg/ml) was complexed with S-adenosyl-L-homocysteine (SAH, Sigma) and DS-421 at 1:5 molar ratio of protein:compound and crystallized using the hanging drop vapor diffusion method at 20 °C by mixing 1 µl of the protein solution with 1 µl of the reservoir solution containing 2.0 M sodium formate, 0.1 M sodium acetate, pH 4.6.

NMR Spectroscopy:

Data Collection:

Data Processing: