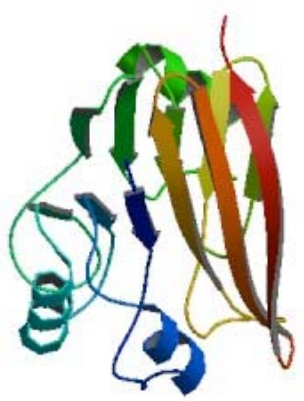
Vacuolar Protein Sorting Protein 29

Human, VPS29
Expressed in *E.Coli*
Cat. No. CBCRY38
Lot. No. (See product label)

BACKGROUND

VPS29 belongs to a group of genes coding for vacuolar protein sorting (VPS) proteins that, when functionally impaired, disrupt the efficient delivery of vacuolar hydrolases. The protein encoded by this gene, Vps29, is a component of a large multimeric complex, termed the retromer complex, which is involved in retrograde transport of proteins from endosomes to the trans-Golgi network. Vps29 may be involved in the formation of the inner shell of the retromer coat for retrograde vesicles leaving the prevacuolar compartment.

CRYSTAL STRUCTURE



MOLECULAR DESCRIPTION

***Protein classification*:** cytoplasmic protein

Structure Weight: 20531.90 Da

***Polymer*:** 1

Molecule: Vacuolar Protein Sorting Protein 29
***Chains*:** A

Type: polypeptide (L)

***Chain Length*:** 182 amino acids

GENE INFORMATION

Gene Name: VPS29
Synonyms: DC15; DC7; DKFZp564F0223; FLJ20492; PEP11; retromer protein; vacuolar protein sorting 29; vacuolar sorting protein VPS29/PEP11; x 007 protein; EC 3.1.3.3; hVPS29; vesicle protein sorting 29

UniProt ID: Q9UBQ0

GeneID: 51699

Chromosome Location: 12q24

Function: zinc ion binding; hydrolase activity; metal ion binding

CRYSTAL INFORMATION

PDB ID: 1W24

MMDB ID: 32322

Source: E.Coli

Method: X-Ray Diffraction

Resolution: 2.10 Å

PRIMARY CITATION

Wang, D., Guo, M., Liang, Z., Fan, J., Zhu, Z., Zang, J., Zhu, Z., Li, X., Teng, M., Niu, L., Dong, Y., Liu, P. (2005) Crystal Structure of Human Vacuolar Protein Sorting Protein 29 Reveals a Phosphodiesterase/Nuclease-Like Fold and Two Protein-Protein Interaction Sites. J.Biol.Chem. 280: 22962

FOR RESEARCH USE ONLY

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