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5OYL

VSV G CR2

PDB DOI: https://doi.org/10.2210/pdb5OYL/pdb

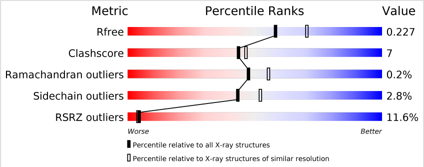
Classification: VIRAL PROTEIN
Organism(s): Recombinant vesicular stomatitis Indiana virus rVSV-G/GFP, Homo sapiens
Expression System: Escherichia coli
Mutation(s): No

Deposited: 2017-09-11 **Released:** 2018-03-21
Deposition Author(s): Albertini, A.A., Belot, L., Legrand, P., Gaudin, Y.
Funding Organization(s): French National Research Agency

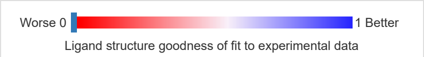
Experimental Data Snapshot

Method: X-RAY DIFFRACTION
Resolution: 2.25 Å
R-Value Free: 0.224
R-Value Work: 0.188
R-Value Observed: 0.190

wwPDB Validation 3D Report Full Report



Ligand Structure Quality Assessment



This is version 1.2 of the entry. See complete history.

Literature

Structural basis for the recognition of LDL-receptor family members by VSV glycoprotein.

Nikolic, J., **Belot, L.**, **Raux, H.**, **Legrand, P.**, **Gaudin, Y.**, **A Albertini, A.**
(2018) Nat Commun **9**: 1029-1029

PubMed: **29531262**
DOI: https://doi.org/10.1038/s41467-018-03432-4
Primary Citation of Related Structures:
5OY9, 5OYL

PubMed Abstract:

Biological Assembly 1

3D View: Structure | 1D-3D View | Electron Density | Validation Report | Ligand Interaction

Global Symmetry: Asymmetric - C1
Global Stoichiometry: Hetero 2-mer - A1B1

Find Similar Assemblies

Biological assembly 1 assigned by authors and generated by PISA (software)

Macromolecules

Find similar proteins by: Sequence ▾ (by identity cutoff) | 3D Structure

Entity ID: 1

Molecule	**Chains**	**Sequence Length**	**Organism**
Glycoprotein	A	410	**Recombinant vesic stomatitis Indiana v rVSV-G/GFP**

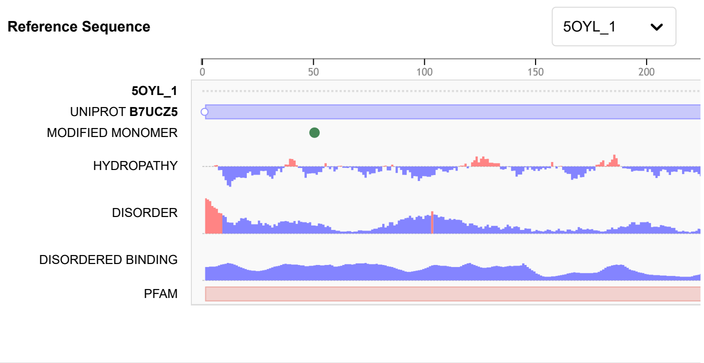
UniProt

Find proteins for **B7UCZ5** *(Recombinant vesicular stomatitis Indiana virus rVSV-G/GFP)*
Explore B7UCZ5

Entity Groups

Sequence Clusters	30% Identity 50% Identity 70% Identity 90% Identity 95% Identity 1
UniProt Group	B7UCZ5

Protein Feature View



Find similar proteins by: Sequence ▾ (by identity cutoff) | 3D Structure

Molecule	Chains	Sequence Length	Organism
Low-density lipoprotein receptor	B [auth D]	46	**Homo sapiens**

UniProt & NIH Common Fund Data Resources

Find proteins for **P01130** *(Homo sapiens)*
Explore **P01130**

PHAROS: P01130

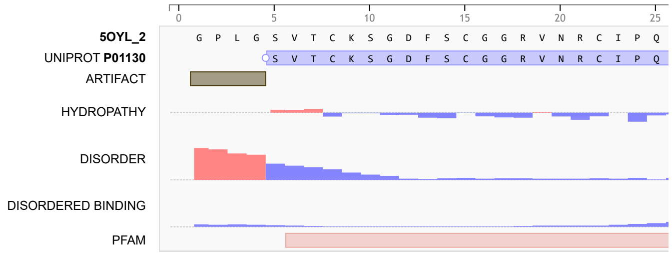
Entity Groups

Sequence Clusters	**30% Identity** **50% Identity** **70% Identity** **90% Identity** **95% Identity** **1**
UniProt Group	**P01130**

Protein Feature View

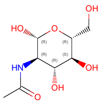
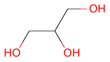
Reference Sequence

5OYL_2

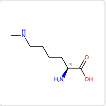


Small Molecules

Ligands **3 Unique**

ID	Chains	Name / Formula / InChI Key	2D Diagram	3D Interactions
NAG Download Instance Coordinates	C [auth A], D [auth A], E [auth A]	**2-acetamido-2-deoxy-beta-D-glucopyranose** $C_8 H_{15} N O_6$ OVRNDRQMDRJTHS-FMDGEEDCSA-N		Ligand Interaction
GOL Download Instance Coordinates		**GLYCEROL** $C_3 H_8 O_3$ PEDCQBHIVMGVHV-UHFFFAOYSA-N		Ligand Interaction
CA Download Instance Coordinates	F [auth A], N [auth D]	**CALCIUM ION** Ca BHPQYMZQTOCNFJ-UHFFFAOYSA-N	Ca^{+2}	Ligand Interaction

Modified Residues **1 Unique**

ID	Chains	Type	Formula	2D Diagram	Parent
MLZ	A	L-PEPTIDE LINKING	$C_7 H_{16} N_2 O_2$		LYS

Experimental Data & Validation

Experimental Data

R-Value Free: 0.224
R-Value Work: 0.188
R-Value Observed: 0.190
Space Group: H 3 2

Unit Cell:

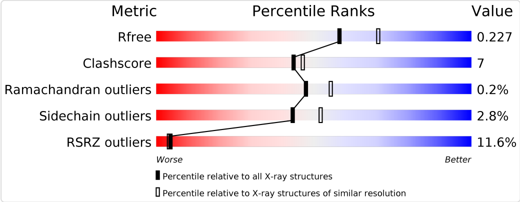
Length (Å)	Angle (˚)
a = 90.04	α = 90
b = 90.04	β = 90
c = 515.78	γ = 120

Software Package:

Software Name	Purpose
REFMAC	refinement
PDB_EXTRACT	data extraction
XDS	data reduction
XSCALE	data scaling
MOLREP	phasing

Structure Validation

View Full Validation Report



Ligand Structure Quality Assessment

Entry History & Funding Information

Deposition Data

Released Date: 2018-03-21
Deposition Author(s): Albertini, A.A., Belot, L., Legrand, P., Gaudin, Y.

Funding Organization	Location	Grant Number
French National Research Agency	France	ANR-15-CE11-0020

Revision History (Full details and data files)

- **Version 1.0: 2018-03-21**
  Type: Initial release
- **Version 1.1: 2018-04-18**
  Changes: Data collection, Database references
- **Version 1.2: 2020-07-29**
  Type: Remediation
  Reason: Carbohydrate remediation
  Changes: Data collection, Derived calculations, Structure summary

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