

Display Files Download Files Data API

5OYL

VSV G CR2

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

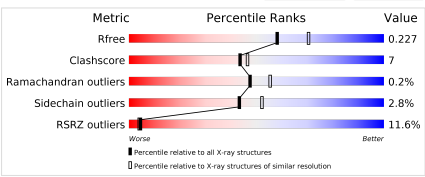
Classification: VIRAL PROTEIN
Organism(s): Recombinant vesicular stomatitis Indiana virus rVSV-G/GFP, Homo sapiens
Expression System: Escherichia coli
Mutation(s): No

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

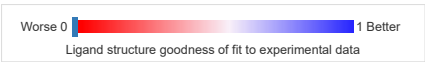
Experimental Data Snapshot

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



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., AAlbertini, 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 vesicular stomatitis Indiana virus rVSV-G/GFP

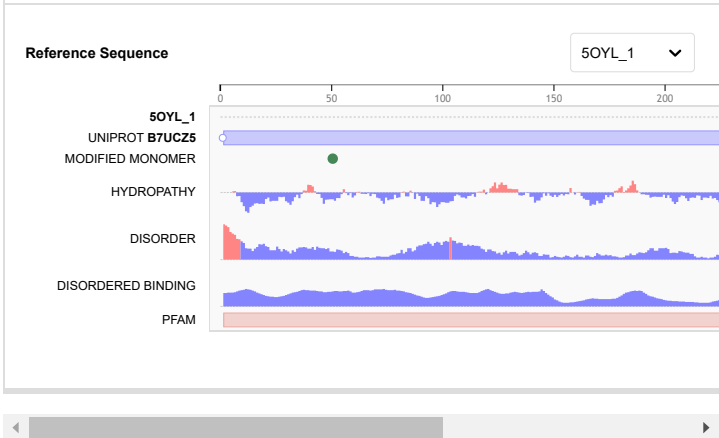
UniProt

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

Entity ID: 2

Molecule

Low-density lipoprotein receptor

Chains

B [auth D]

Sequence Length

46

Organism

[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

5OYL_2

UNIPROT P01130

ARTIFACT

HYDROPATHY

DISORDER

DISORDERED BINDING

PFAM

0

5

10

15

20

25

G

P

L

G

S

V

T

C

K

S

G

D

F

S

C

G

G

R

V

N

R

C

I

P

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N

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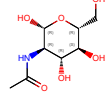
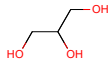
I

P

Q

Small Molecules

Ligands 3 Unique

ID	Chains	Name / Formula / InChI Key	2D Diagram	3D Interactions
NAG	C [auth A], D [auth A], E [auth A]	2-acetamido-2-deoxy-beta-D-glucopyranose C ₈ H ₁₅ N O ₆ OVRNDRQMDRJTHS-EMDGEEDCSA-N		<div>Ligand Interaction</div>
GOL		GLYCEROL C ₃ H ₈ O ₃ PEDCQBHIVMGVHV-UHFFFAOYSA-N		<div>Ligand Interaction</div>
CA	F [auth A], N [auth D]	CALCIUM ION Ca BHPQYMZQTOCNFJ-UHFFFAOYSA-N	<div>Ca⁺²</div>	<div>Ligand Interaction</div>

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

Method: X-RAY DIFFRACTION

Resolution: 2.25 Å

https://www.rcsb.org/structure/5oyl
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R-Value Free: 0.224
R-Value Work: 0.188
R-Value Observed: 0.190
Space Group: **H 3 2**

Unit Cell:

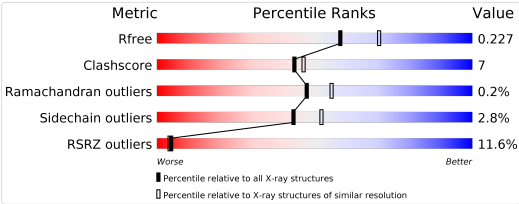
Length (Å)	Angle (°)
a = 90.04	α = 90
b = 90.04	β = 90
c = 515.78	γ = 120

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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