



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:45 PM UTC

PDB ID : 3WSX / pdb\_00003wsx  
Title : SorLA Vps10p domain in ligand-free form  
Authors : Kitago, Y.; Nakata, Z.; Nagae, M.; Nogi, T.; Takagi, J.  
Deposited on : 2014-03-30  
Resolution : 2.35 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

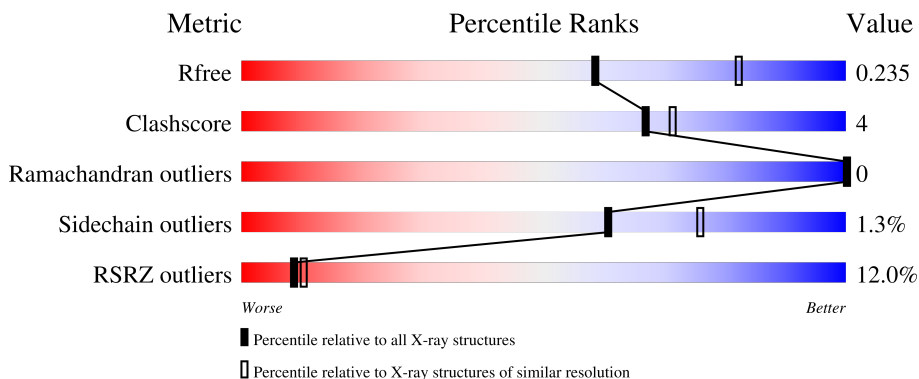
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	734	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PO4	A	804	-	X	-	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5066 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Sortilin-related receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	606	4830	3075	818	918	19	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

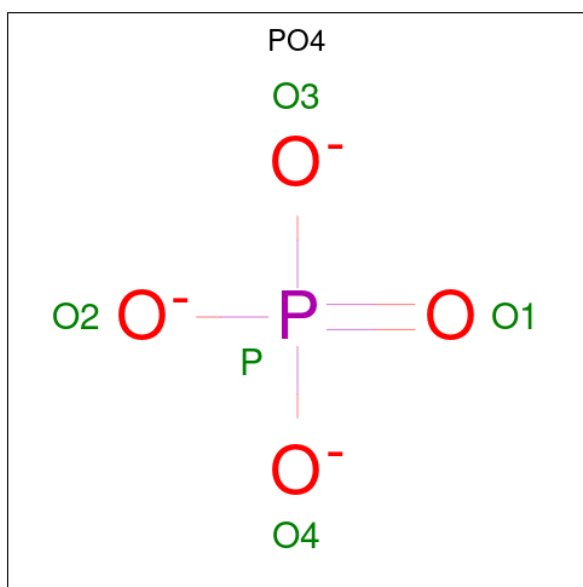
Chain	Residue	Modelled	Actual	Comment	Reference
A	754	SER	-	expression tag	UNP Q92673
A	755	ARG	-	expression tag	UNP Q92673
A	756	LEU	-	expression tag	UNP Q92673
A	757	GLU	-	expression tag	UNP Q92673
A	758	ASN	-	expression tag	UNP Q92673
A	759	LEU	-	expression tag	UNP Q92673
A	760	TYR	-	expression tag	UNP Q92673
A	761	PHE	-	expression tag	UNP Q92673
A	762	GLN	-	expression tag	UNP Q92673

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O<sub>4</sub>P).



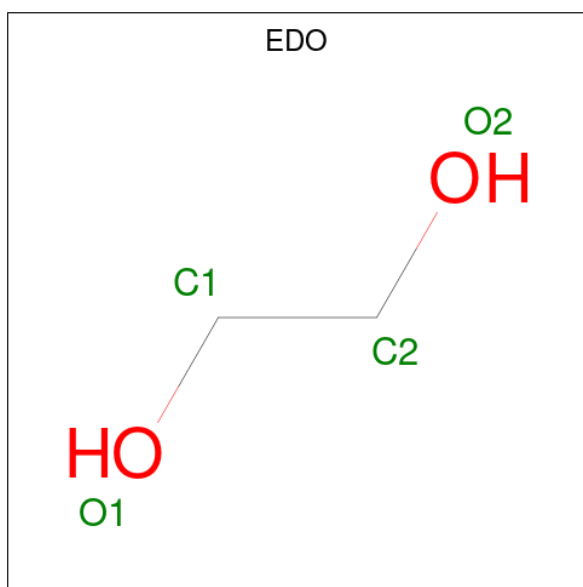
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P 5 4 1	0	0
3	A	1	Total O P 5 4 1	0	0
3	A	1	Total O P 5 4 1	0	0

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0

- Molecule 5 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	A	150	Total 150	O 150	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	126.37Å 126.37Å 290.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.63 – 2.35 47.63 – 2.35	Depositor EDS
% Data completeness (in resolution range)	97.6 (47.63-2.35) 97.6 (47.63-2.35)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.70 (at 2.34Å)	Xtrriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.208 , 0.238 0.205 , 0.235	Depositor DCC
$R_{free}$ test set	2849 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.0	Xtrriage
Anisotropy	0.087	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 46.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5066	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, PO4, EDO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.84	0/4954	0.92	5/6705 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	642	GLU	N-CA-C	-7.10	104.55	112.57
1	A	719	GLY	N-CA-C	6.73	121.24	110.87
1	A	720	SER	CA-C-N	-5.21	115.20	123.12
1	A	720	SER	C-N-CA	-5.21	115.20	123.12
1	A	112	GLU	N-CA-C	5.12	116.86	111.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	744	ARG	Peptide

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4830	0	4608	34	1
2	A	42	0	39	0	0
3	A	20	0	0	2	0
4	A	24	0	36	3	0
5	A	150	0	0	0	0
All	All	5066	0	4683	35	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 35 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:718:VAL:HG12	1:A:718:VAL:O	1.72	0.90
1:A:255:ILE:CD1	1:A:302:LEU:CD2	2.66	0.74
1:A:654:ARG:HD3	1:A:658:ALA:HB3	1.79	0.64
1:A:329:SER:HB2	1:A:335:MET:HG2	1.81	0.62
1:A:473:CYS:CB	1:A:510:VAL:HG13	2.31	0.60

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:ASP:O	1:A:726:ARG:NH2[6_665]	2.05	0.15

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	588/734 (80%)	569 (97%)	19 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	526/633 (83%)	519 (99%)	7 (1%)	61	76

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	300	PHE
1	A	409	GLU
1	A	654	ARG
1	A	451	GLU
1	A	266	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	104	GLN
1	A	289	ASN
1	A	301	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

13 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	EDO	A	811	-	3,3,3	0.50	0	2,2,2	0.32	0
4	EDO	A	812	-	3,3,3	0.77	0	2,2,2	0.51	0
3	PO4	A	804	-	4,4,4	1.43	1 (25%)	6,6,6	1.92	3 (50%)
2	NAG	A	802	1	14,14,15	0.46	0	17,19,21	1.23	2 (11%)
4	EDO	A	810	-	3,3,3	0.50	0	2,2,2	0.33	0
3	PO4	A	805	-	4,4,4	0.90	0	6,6,6	0.53	0
3	PO4	A	807	-	4,4,4	0.66	0	6,6,6	0.41	0
3	PO4	A	806	-	4,4,4	0.65	0	6,6,6	0.51	0
4	EDO	A	808	-	3,3,3	0.44	0	2,2,2	0.85	0
4	EDO	A	809	-	3,3,3	0.52	0	2,2,2	0.41	0
2	NAG	A	803	1	14,14,15	0.49	0	17,19,21	1.29	3 (17%)
2	NAG	A	801	1	14,14,15	0.79	1 (7%)	17,19,21	1.52	3 (17%)
4	EDO	A	813	-	3,3,3	0.57	0	2,2,2	0.41	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	811	-	-	0/1/1/1	-
4	EDO	A	812	-	-	1/1/1/1	-
2	NAG	A	802	1	-	2/6/23/26	0/1/1/1
2	NAG	A	801	1	-	0/6/23/26	0/1/1/1
4	EDO	A	810	-	-	1/1/1/1	-
4	EDO	A	808	-	-	0/1/1/1	-

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	803	1	-	0/6/23/26	0/1/1/1
4	EDO	A	809	-	-	1/1/1/1	-
4	EDO	A	813	-	-	1/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	NAG	C1-C2	2.33	1.55	1.52
3	A	804	PO4	P-O3	-2.22	1.48	1.54

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	NAG	C1-C2-N2	3.10	115.32	110.43
3	A	804	PO4	O4-P-O2	3.08	117.50	107.91
2	A	803	NAG	C1-O5-C5	2.74	115.86	112.19
2	A	802	NAG	C3-C4-C5	-2.48	105.74	110.23
3	A	804	PO4	O4-P-O3	-2.24	100.96	107.91

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	809	EDO	O1-C1-C2-O2
4	A	810	EDO	O1-C1-C2-O2
4	A	812	EDO	O1-C1-C2-O2
2	A	802	NAG	C4-C5-C6-O6
4	A	813	EDO	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	812	EDO	2	0
3	A	804	PO4	1	0
3	A	805	PO4	1	0
4	A	808	EDO	1	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	606/734 (82%)	0.47	73 (12%) <b>9</b> <b>10</b>	25, 43, 84, 123	0

The worst 5 of 73 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	478	ALA	8.6
1	A	718	VAL	8.2
1	A	89	PRO	7.3
1	A	130	PRO	6.7
1	A	712	PRO	5.9

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	PO4	A	806	5/5	0.76	0.15	77,77,84,84	0
4	EDO	A	809	4/4	0.77	0.32	66,67,69,77	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	A	801	14/15	0.85	0.18	70,79,89,90	0
4	EDO	A	811	4/4	0.86	0.20	51,56,60,60	0
4	EDO	A	812	4/4	0.86	0.17	49,50,53,53	0
3	PO4	A	804	5/5	0.87	0.15	47,47,56,65	0
3	PO4	A	805	5/5	0.89	0.13	84,84,93,94	0
2	NAG	A	803	14/15	0.90	0.13	66,76,86,87	0
3	PO4	A	807	5/5	0.91	0.21	53,67,71,74	0
4	EDO	A	808	4/4	0.92	0.14	48,50,51,52	0
2	NAG	A	802	14/15	0.93	0.09	51,57,64,68	0
4	EDO	A	810	4/4	0.93	0.15	43,57,58,58	0
4	EDO	A	813	4/4	0.94	0.13	38,38,38,39	0

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.