

Full wwPDB X-ray Structure Validation Report (i)

Oct 5, 2023 – 07:55 AM EDT

PDB ID : 6V7P

Title: Crystal structure of SUMO1 in complex with PIAS-SIM2

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Deposited on : 2019-12-09

Resolution : 1.40 Å(reported)

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

We welcome your comments at 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 (i) 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 (1)) were used in the production of this report:

MolProbity : FAILED Xtriage (Phenix) : 1.13 EDS : FAILED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

Validation Pipeline (wwPDB-VP) : 2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3070 atoms, of which 1439 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 Small ubiquitin-related modifier 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	С	76	Total 1287			N 110	O 123	S 3	0	2	0
1	A	74	Total 1250	C 396			O 118	S 3	0	2	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	15	GLY	-	expression tag	UNP P63165
С	16	SER	-	expression tag	UNP P63165
С	52	ALA	CYS	engineered mutation	UNP P63165
A	15	GLY	-	expression tag	UNP P63165
A	16	SER	-	expression tag	UNP P63165
A	52	ALA	CYS	engineered mutation	UNP P63165

• Molecule 2 is a protein called Protein PIAS.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
9	2 D	9	Total	С	Н	N	О	0	1	0
			153	46	77	12	18			
9	D	В 11	Total	С	Н	N	О	0	1	0
2	Б		181	56	90	14	21	U		

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	С	83	Total O 83 83	0	0
3	D	16	Total O 16 16	0	0
3	A	87	Total O 87 87	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	13	Total O 13 13	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.



3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source	
Space group	P 1 21 1	Depositor	
Cell constants	34.35Å 38.47Å 62.74Å	Depositor	
a, b, c, α , β , γ	90.00° 102.71° 90.00°	Depositor	
Resolution (Å)	30.60 - 1.40	Depositor	
% Data completeness	95.3 (30.60-1.40)	Depositor	
(in resolution range)	,		
R_{merge}	(Not available)	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	1.20 (at 1.39Å)	Xtriage	
Refinement program	PHENIX 1.13-2998_1496	Depositor	
R, R_{free}	0.152 , 0.184	Depositor	
Wilson B-factor (\mathring{A}^2)	21.3	Xtriage	
Anisotropy	0.219	Xtriage	
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.33$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	3070	wwPDB-VP	
Average B, all atoms (Å ²)	26.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.38% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

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

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

There are no ligands in this entry.

4.7 Other polymers (i)

There are no such residues in this entry.



4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

