Full wwPDB X-ray Structure Validation Report (i)

Oct 2, 2023 – 03:17 PM EDT

PDB ID	:	6NIF
Title	:	crystal structure of human REV7-RAN complex
Authors	:	Wang, X.; Pertz, L.; Hua, D.P.; Zhang, T.Q.; Listovsky, T.; Xie, W.
Deposited on	:	2018-12-27
Resolution	:	2.00 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 (i)) 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 2.00 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 2 unique types of molecules in this entry. The entry contains 1859 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 hREV7, GTP-binding nuclear protein Ran, hREV3 fusion.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	212	1712	1110	287	304	11	0	1	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q9UI95
A	124	ALA	ARG	engineered mutation	UNP Q9UI95
A	472	GLY	-	linker	UNP Q9UI95
A	473	SER	-	linker	UNP Q9UI95
A	474	GLY	-	linker	UNP Q9UI95
A	475	SER	-	linker	UNP Q9UI95
A	476	GLY	-	linker	UNP Q9UI95
A	477	SER	-	linker	UNP Q9UI95
A	478	GLY	-	linker	UNP Q9UI95
A	479	SER	-	linker	UNP Q9UI95
A	480	GLY	-	linker	UNP Q9UI95
A	481	SER	-	linker	UNP Q9UI95
A	482	GLY	-	linker	UNP Q9UI95
A	483	SER	-	linker	UNP Q9UI95
A	484	GLY	-	linker	UNP Q9UI95
A	485	SER	-	linker	UNP Q9UI95
A	486	GLY	-	linker	UNP Q9UI95
A	487	SER	-	linker	UNP Q9UI95
A	488	GLY	-	linker	UNP Q9UI95
A	489	SER	-	linker	UNP Q9UI95
A	490	GLY	-	linker	UNP Q9UI95
A	491	SER	-	linker	UNP Q9UI95
A	511	ALA	-	linker	UNP F5H018
A	512	SER	-	linker	UNP F5H018

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	147	Total O 147 147	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 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	64.57Å 64.57Å 113.78Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.28 – 2.00	Depositor
% Data completeness (in resolution range)	99.2 (32.28-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.31 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155)	Depositor
R, R_{free}	0.226 , 0.266	Depositor
Wilson B-factor (Å^2)	34.0	Xtriage
Anisotropy	0.386	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
Total number of atoms	1859	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.27% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

4 Model quality

4.1 Standard geometry

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

4.2 Too-close contacts

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

4.3 Torsion angles

4.3.1 Protein backbone

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

4.3.2 Protein sidechains

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

4.3.3 RNA

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

4.4 Non-standard residues in protein, DNA, RNA chains

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

4.5 Carbohydrates

There are no monosaccharides in this entry.

4.6 Ligand geometry

There are no ligands in this entry.

4.7 Other polymers

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

5.1 Protein, DNA and RNA chains

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

5.2 Non-standard residues in protein, DNA, RNA chains

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

5.3 Carbohydrates

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

5.4 Ligands

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

5.5 Other polymers

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