



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 7Q72 / pdb_00007q72
Title : Structure of Pla1 in complex with Red1
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Deposited on : 2021-11-09
Resolution : 2.80 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

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
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

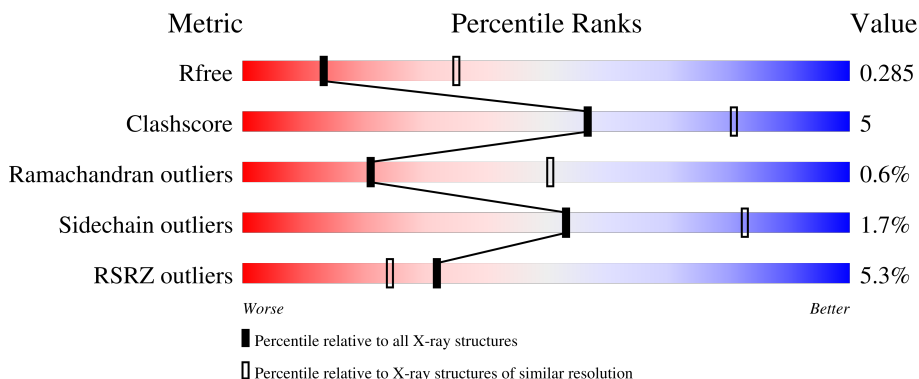
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 ≥ 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	575	74% 14% 11%
1	B	575	7% 75% 12% 13%
2	C	70	9% 41% 9% 50%
2	D	70	6% 23% .. 74%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8531 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 Poly(A) polymerase pla1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	511	Total	C	N	O	S	0	0	0
			4097	2638	699	744	16			
1	B	502	Total	C	N	O	S	0	0	0
			4027	2593	686	732	16			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q10295
A	2	LYS	-	expression tag	UNP Q10295
A	3	HIS	-	expression tag	UNP Q10295
A	4	HIS	-	expression tag	UNP Q10295
A	5	HIS	-	expression tag	UNP Q10295
A	6	HIS	-	expression tag	UNP Q10295
A	7	HIS	-	expression tag	UNP Q10295
A	8	HIS	-	expression tag	UNP Q10295
A	9	PRO	-	expression tag	UNP Q10295
B	1	MET	-	initiating methionine	UNP Q10295
B	2	LYS	-	expression tag	UNP Q10295
B	3	HIS	-	expression tag	UNP Q10295
B	4	HIS	-	expression tag	UNP Q10295
B	5	HIS	-	expression tag	UNP Q10295
B	6	HIS	-	expression tag	UNP Q10295
B	7	HIS	-	expression tag	UNP Q10295
B	8	HIS	-	expression tag	UNP Q10295
B	9	PRO	-	expression tag	UNP Q10295

- Molecule 2 is a protein called NURS complex subunit red1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	35	Total	C	N	O	0	0	0
			268	169	40	59			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	18	Total	C	N	O	0	0	0
			136	88	21	27			

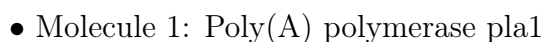
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	284	GLY	-	expression tag	UNP Q9UTR8
C	285	ALA	-	expression tag	UNP Q9UTR8
C	286	MET	-	expression tag	UNP Q9UTR8
C	287	GLY	-	expression tag	UNP Q9UTR8
C	346	GLY	-	expression tag	UNP Q9UTR8
C	347	SER	-	expression tag	UNP Q9UTR8
C	348	HIS	-	expression tag	UNP Q9UTR8
C	349	HIS	-	expression tag	UNP Q9UTR8
C	350	HIS	-	expression tag	UNP Q9UTR8
C	351	HIS	-	expression tag	UNP Q9UTR8
C	352	HIS	-	expression tag	UNP Q9UTR8
C	353	HIS	-	expression tag	UNP Q9UTR8
D	284	GLY	-	expression tag	UNP Q9UTR8
D	285	ALA	-	expression tag	UNP Q9UTR8
D	286	MET	-	expression tag	UNP Q9UTR8
D	287	GLY	-	expression tag	UNP Q9UTR8
D	346	GLY	-	expression tag	UNP Q9UTR8
D	347	SER	-	expression tag	UNP Q9UTR8
D	348	HIS	-	expression tag	UNP Q9UTR8
D	349	HIS	-	expression tag	UNP Q9UTR8
D	350	HIS	-	expression tag	UNP Q9UTR8
D	351	HIS	-	expression tag	UNP Q9UTR8
D	352	HIS	-	expression tag	UNP Q9UTR8
D	353	HIS	-	expression tag	UNP Q9UTR8

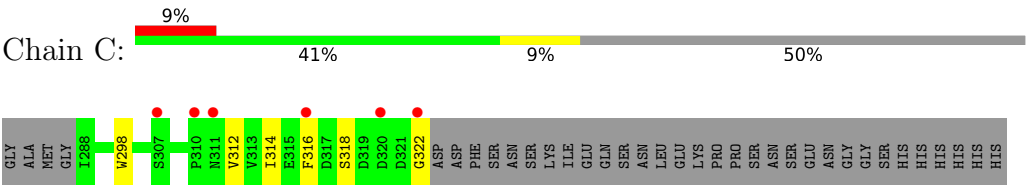
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	O	0	0
			1	1		
3	B	2	Total	O	0	0
			2	2		

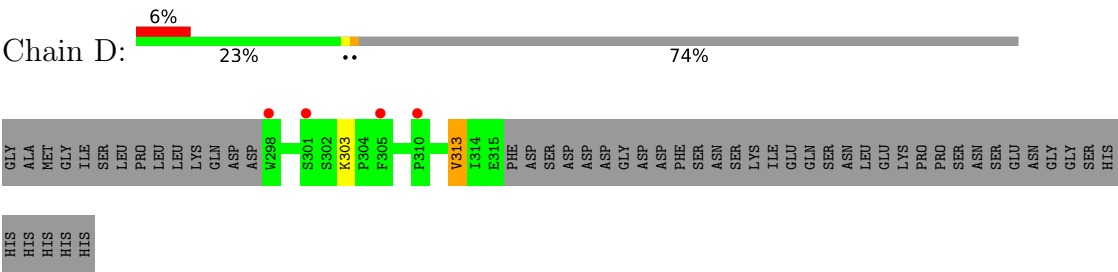
- Molecule 1: Poly(A) polymerase pla1



● Molecule 2: NURS complex subunit red1



● Molecule 2: NURS complex subunit red1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	128.64Å 151.34Å 65.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	98.02 – 2.80 98.02 – 2.81	Depositor EDS
% Data completeness (in resolution range)	64.0 (98.02-2.80) 64.0 (98.02-2.81)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.82Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158+SVN	Depositor
R, R_{free}	0.241 , 0.283 0.241 , 0.285	Depositor DCC
R_{free} test set	2000 reflections (6.23%)	wwPDB-VP
Wilson B-factor (Å ²)	51.1	Xtriage
Anisotropy	0.159	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 35.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	8531	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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](#)

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	0.08	0/4194	0.23	0/5697
1	B	0.10	0/4124	0.25	0/5604
2	C	0.11	0/274	0.29	0/373
2	D	0.09	0/140	0.26	0/191
All	All	0.09	0/8732	0.24	0/11865

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
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	404	ASP	Peptide
1	B	404	ASP	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	4097	0	4139	44	0
1	B	4027	0	4053	35	0
2	C	268	0	250	3	0
2	D	136	0	132	2	0
3	A	1	0	0	1	0
3	B	2	0	0	0	0
All	All	8531	0	8574	79	0

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 5.

The worst 5 of 79 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:B:78:LYS:NZ	1:B:118:HIS:O	2.22	0.71
1:A:407:ALA:HB2	1:A:491:GLU:HG2	1.74	0.68
1:A:397:VAL:HG11	1:A:411:PRO:HG3	1.77	0.67
1:B:501:LEU:HB3	2:D:313:VAL:HG22	1.76	0.67
1:B:102:VAL:HG13	1:B:220:ARG:HG2	1.75	0.67

There are no symmetry-related clashes.

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	505/575 (88%)	480 (95%)	22 (4%)	3 (1%)	21	51
1	B	496/575 (86%)	461 (93%)	32 (6%)	3 (1%)	21	51
2	C	33/70 (47%)	30 (91%)	3 (9%)	0	100	100
2	D	16/70 (23%)	13 (81%)	3 (19%)	0	100	100
All	All	1050/1290 (81%)	984 (94%)	60 (6%)	6 (1%)	21	51

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	289	PRO
1	A	210	PRO
1	B	146	ASP
1	B	116	PRO
1	A	150	PRO

5.3.2 Protein sidechains ⓘ

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	446/502 (89%)	440 (99%)	6 (1%)	61	86
1	B	438/502 (87%)	431 (98%)	7 (2%)	55	83
2	C	33/63 (52%)	31 (94%)	2 (6%)	17	46
2	D	17/63 (27%)	16 (94%)	1 (6%)	18	48
All	All	934/1130 (83%)	918 (98%)	16 (2%)	53	83

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	491	GLU
1	B	490	LEU
1	B	144	VAL
1	B	489	GLU
2	C	314	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	430	GLN
1	B	272	HIS
1	B	368	HIS
1	A	257	ASN
1	A	79	HIS

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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, 95th 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 ²)	Q<0.9
1	A	511/575 (88%)	0.12	7 (1%) 73 64	7, 34, 72, 89	0
1	B	502/575 (87%)	0.58	39 (7%) 19 14	16, 52, 100, 134	0
2	C	35/70 (50%)	0.73	6 (17%) 4 3	23, 44, 88, 89	0
2	D	18/70 (25%)	1.40	4 (22%) 2 1	52, 87, 111, 114	0
All	All	1066/1290 (82%)	0.38	56 (5%) 32 24	7, 43, 95, 134	0

The worst 5 of 56 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	80	MET	4.6
1	B	147	ALA	4.0
1	B	132	LEU	3.9
1	B	375	ALA	3.5
1	B	145	PRO	3.5

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.