



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 1, 2021 – 02:14 pm GMT

PDB ID : 7OSS
Title : PARP15 catalytic domain in complex with OUL194
Authors : Maksimainen, M.M.; Lehtio, L.
Deposited on : 2021-06-09
Resolution : 1.50 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.4 (270009), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

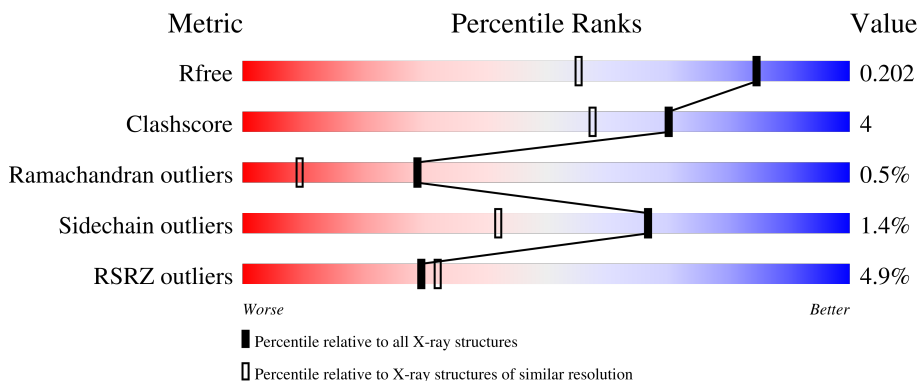
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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}	130704	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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	221	
1	B	221	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3522 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 Protein mono-ADP-ribosyltransferase PARP15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	194	1634	1033	287	306	8	0	8	0
1	B	197	1635	1038	285	303	9	0	8	0

There are 46 discrepancies between the modelled and reference sequences:

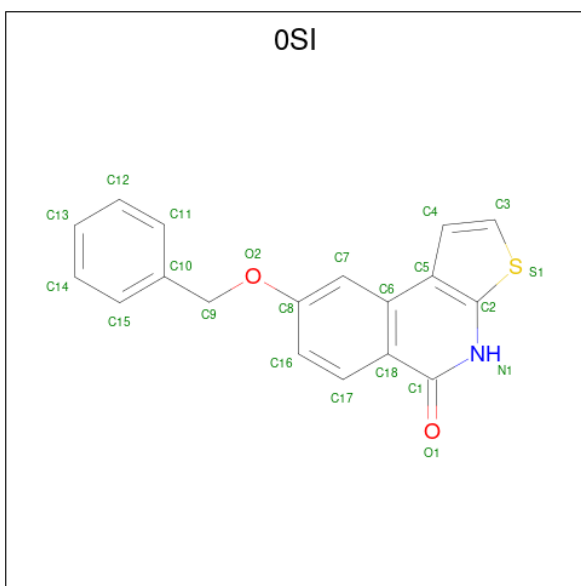
Chain	Residue	Modelled	Actual	Comment	Reference
A	458	MET	-	initiating methionine	UNP Q460N3
A	459	HIS	-	expression tag	UNP Q460N3
A	460	HIS	-	expression tag	UNP Q460N3
A	461	HIS	-	expression tag	UNP Q460N3
A	462	HIS	-	expression tag	UNP Q460N3
A	463	HIS	-	expression tag	UNP Q460N3
A	464	HIS	-	expression tag	UNP Q460N3
A	465	SER	-	expression tag	UNP Q460N3
A	466	SER	-	expression tag	UNP Q460N3
A	467	GLY	-	expression tag	UNP Q460N3
A	468	VAL	-	expression tag	UNP Q460N3
A	469	ASP	-	expression tag	UNP Q460N3
A	470	LEU	-	expression tag	UNP Q460N3
A	471	GLY	-	expression tag	UNP Q460N3
A	472	THR	-	expression tag	UNP Q460N3
A	473	GLU	-	expression tag	UNP Q460N3
A	474	ASN	-	expression tag	UNP Q460N3
A	475	LEU	-	expression tag	UNP Q460N3
A	476	TYR	-	expression tag	UNP Q460N3
A	477	PHE	-	expression tag	UNP Q460N3
A	478	GLN	-	expression tag	UNP Q460N3
A	479	SER	-	expression tag	UNP Q460N3
A	480	MET	-	expression tag	UNP Q460N3
B	458	MET	-	initiating methionine	UNP Q460N3
B	459	HIS	-	expression tag	UNP Q460N3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	460	HIS	-	expression tag	UNP Q460N3
B	461	HIS	-	expression tag	UNP Q460N3
B	462	HIS	-	expression tag	UNP Q460N3
B	463	HIS	-	expression tag	UNP Q460N3
B	464	HIS	-	expression tag	UNP Q460N3
B	465	SER	-	expression tag	UNP Q460N3
B	466	SER	-	expression tag	UNP Q460N3
B	467	GLY	-	expression tag	UNP Q460N3
B	468	VAL	-	expression tag	UNP Q460N3
B	469	ASP	-	expression tag	UNP Q460N3
B	470	LEU	-	expression tag	UNP Q460N3
B	471	GLY	-	expression tag	UNP Q460N3
B	472	THR	-	expression tag	UNP Q460N3
B	473	GLU	-	expression tag	UNP Q460N3
B	474	ASN	-	expression tag	UNP Q460N3
B	475	LEU	-	expression tag	UNP Q460N3
B	476	TYR	-	expression tag	UNP Q460N3
B	477	PHE	-	expression tag	UNP Q460N3
B	478	GLN	-	expression tag	UNP Q460N3
B	479	SER	-	expression tag	UNP Q460N3
B	480	MET	-	expression tag	UNP Q460N3

- Molecule 2 is 8-phenylmethoxy-4 {H}-thieno[2,3-c]isoquinolin-5-one (three-letter code: OSI) (formula: C₁₈H₁₃NO₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	22	18	1	2	1	0	0

- Molecule 3 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
3	B	1	4	2	1	1	0	0

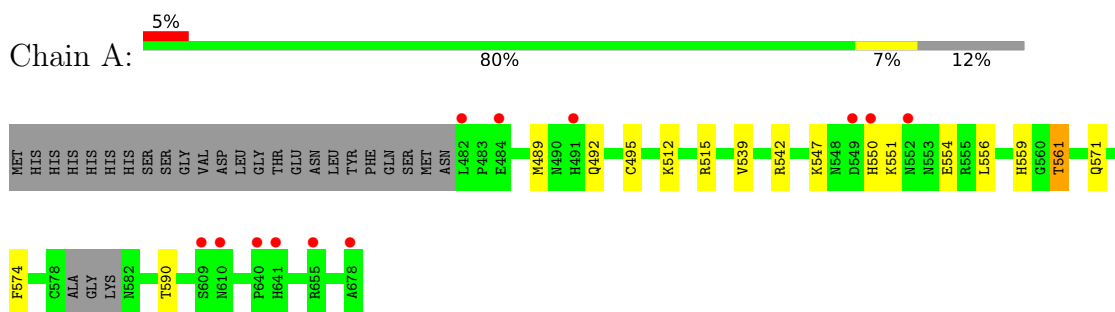
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	94	Total O 94 94	0	0
4	B	133	Total O 133 133	0	0

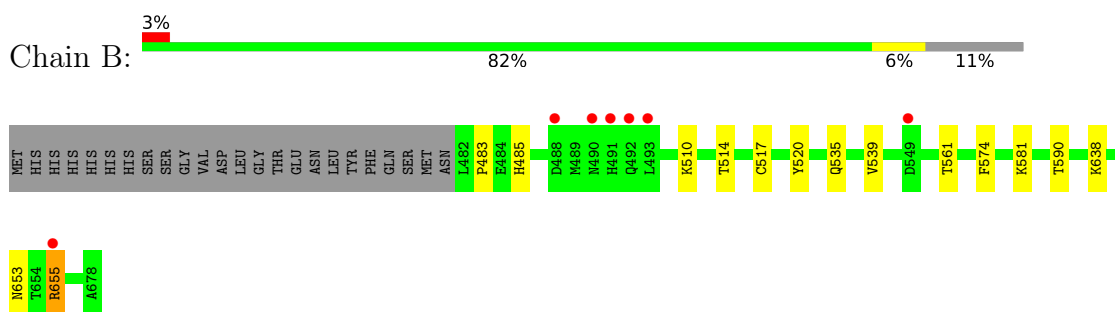
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Protein mono-ADP-ribosyltransferase PARP15



- Molecule 1: Protein mono-ADP-ribosyltransferase PARP15



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	45.46Å 68.74Å 160.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.78 – 1.50 43.74 – 1.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.78-1.50) 100.0 (43.74-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.153 , 0.192 0.163 , 0.202	Depositor DCC
R_{free} test set	4078 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	21.9	Xtriage
Anisotropy	0.385	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3522	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.76% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: DMS, OSI

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	0.64	1/1692 (0.1%)	0.74	0/2290
1	B	0.62	0/1704	0.74	0/2309
All	All	0.63	1/3396 (0.0%)	0.74	0/4599

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	554	GLU	CD-OE2	-5.29	1.19	1.25

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1634	0	1572	14	0
1	B	1635	0	1594	13	0
2	A	22	0	0	0	0
3	B	4	0	6	0	0
4	A	94	0	0	2	0
4	B	133	0	0	2	0
All	All	3522	0	3172	23	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 4.

All (23) 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:517[B]:CYS:HG	1:B:520:TYR:HD2	0.99	0.93
1:B:517[B]:CYS:SG	1:B:520:TYR:HD2	1.97	0.87
1:B:517[B]:CYS:SG	1:B:520:TYR:CD2	2.68	0.86
1:A:542[B]:ARG:NE	1:B:535[B]:GLN:HE22	1.88	0.72
1:A:542[B]:ARG:HG2	1:A:542[B]:ARG:HH21	1.58	0.69
1:A:542[B]:ARG:HE	1:B:535[B]:GLN:HE22	1.41	0.67
1:A:559:HIS:CD2	1:A:561:THR:HG22	2.33	0.64
1:A:559:HIS:HD2	1:A:561:THR:HG22	1.65	0.62
1:B:561[B]:THR:HG22	4:B:908:HOH:O	2.01	0.59
1:B:653:ASN:OD1	1:B:655:ARG:HG3	2.04	0.57
1:B:510:LYS:O	1:B:514:THR:HG23	2.05	0.56
1:A:539:VAL:HG21	1:B:539:VAL:HG21	1.89	0.55
1:A:489:MET:SD	1:A:495[A]:CYS:SG	2.98	0.51
1:A:542[B]:ARG:HG2	1:A:542[B]:ARG:NH2	2.24	0.49
1:B:574:PHE:HB3	1:B:590:THR:HG21	1.98	0.46
1:B:483:PRO:HB3	1:B:485[B]:HIS:NE2	2.31	0.45
1:A:574:PHE:HB3	1:A:590:THR:HG21	1.98	0.45
1:A:571[A]:GLN:HG3	4:A:866:HOH:O	2.17	0.44
1:B:638:LYS:CE	4:B:843:HOH:O	2.67	0.42
1:A:547:LYS:HD2	4:A:838:HOH:O	2.19	0.42
1:A:512:LYS:HD3	1:A:556:LEU:HD23	2.02	0.41
1:A:559:HIS:HD2	1:A:561:THR:CG2	2.32	0.41
1:A:542[B]:ARG:CZ	1:B:535[B]:GLN:HE22	1.98	0.40

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	198/221 (90%)	191 (96%)	5 (2%)	2 (1%)	15	3
1	B	203/221 (92%)	202 (100%)	1 (0%)	0	100	100
All	All	401/442 (91%)	393 (98%)	6 (2%)	2 (0%)	29	9

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	550	HIS
1	A	551	LYS

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	183/198 (92%)	180 (98%)	3 (2%)	62	36
1	B	184/198 (93%)	182 (99%)	2 (1%)	73	53
All	All	367/396 (93%)	362 (99%)	5 (1%)	67	42

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	492	GLN
1	A	515	ARG
1	A	561	THR
1	B	581	LYS
1	B	655	ARG

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	492	GLN
1	A	543	GLN
1	B	492	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	194/221 (87%)	0.06	12 (6%) 20 22	18, 27, 58, 86	0
1	B	197/221 (89%)	-0.22	7 (3%) 42 47	16, 24, 40, 75	0
All	All	391/442 (88%)	-0.08	19 (4%) 29 32	16, 25, 52, 86	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	550	HIS	10.0
1	B	490	ASN	6.4
1	B	491	HIS	5.7
1	B	492	GLN	4.1
1	A	484	GLU	3.9
1	A	549	ASP	3.5
1	A	482	LEU	3.3
1	A	655	ARG	2.8
1	B	488	ASP	2.8
1	A	640	PRO	2.8
1	A	609	SER	2.6
1	A	610	ASN	2.6
1	A	491	HIS	2.4
1	B	655	ARG	2.3
1	A	552	ASN	2.2
1	A	678	ALA	2.2
1	A	641	HIS	2.2
1	B	549	ASP	2.1
1	B	493	LEU	2.1

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 monosaccharides 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, 95th 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 ²)	Q<0.9
3	DMS	B	701	4/4	0.91	0.15	23,43,48,52	0
2	0SI	A	701	22/22	0.94	0.09	22,27,34,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.