



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:50 PM UTC

PDB ID : 7S81 / pdb_00007s81
Title : Structure of human PARP1 domains (Zn1, Zn3, WGR, HD) bound to a DNA double strand break.
Authors : Rouleau-Turcotte, E.; Pascal, J.M.
Deposited on : 2021-09-17
Resolution : 3.60 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 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

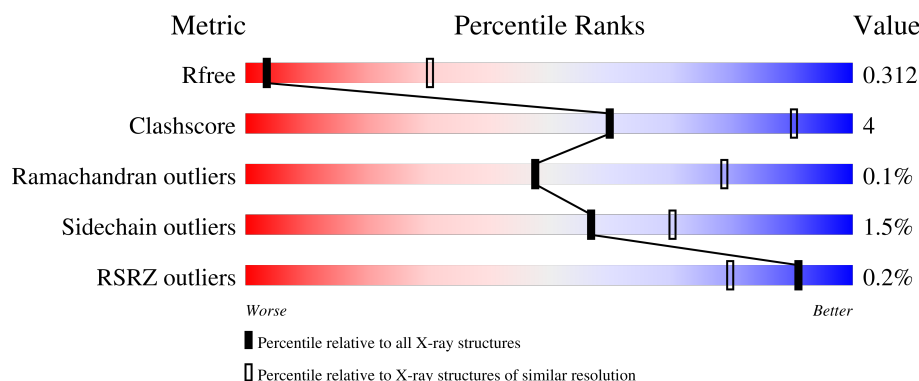
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)

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	D	12	83% 17%
1	E	12	83% 17%
1	L	12	83% 17%
1	M	12	75% 25%
2	C	266	68% 12% 20%

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Mol	Chain	Length	Quality of chain
2	H	266	
2	K	266	
2	P	266	
3	A	116	
3	F	116	
3	I	116	
3	N	116	
4	B	160	
4	G	160	
4	J	160	
4	O	160	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 28252 atoms, of which 13765 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 DNA chain called DNA (5'-D(*AP*TP*GP*CP*GP*GP*CP*CP*GP*CP*AP*T)-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	M	12	Total	C	H	N	O	P	0	0	0
			379	116	136	46	70	11			
1	L	12	Total	C	H	N	O	P	0	0	0
			379	116	136	46	70	11			
1	E	12	Total	C	H	N	O	P	0	0	0
			379	116	136	46	70	11			
1	D	12	Total	C	H	N	O	P	0	0	0
			379	116	136	46	70	11			

- Molecule 2 is a protein called Poly [ADP-ribose] polymerase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	213	Total	C	H	N	O	S	0	0	0
			3386	1083	1686	281	329	7			
2	K	203	Total	C	H	N	O	S	0	0	0
			3220	1033	1601	269	312	5			
2	P	196	Total	C	H	N	O	S	0	0	0
			3125	1001	1558	262	299	5			
2	H	200	Total	C	H	N	O	S	0	0	0
			3172	1017	1577	267	306	5			

There are 140 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	507	MET	-	initiating methionine	UNP P09874
C	508	GLY	-	expression tag	UNP P09874
C	509	SER	-	expression tag	UNP P09874
C	510	SER	-	expression tag	UNP P09874
C	511	HIS	-	expression tag	UNP P09874
C	512	HIS	-	expression tag	UNP P09874
C	513	HIS	-	expression tag	UNP P09874

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Chain	Residue	Modelled	Actual	Comment	Reference
C	514	HIS	-	expression tag	UNP P09874
C	515	HIS	-	expression tag	UNP P09874
C	516	HIS	-	expression tag	UNP P09874
C	517	SER	-	expression tag	UNP P09874
C	518	SER	-	expression tag	UNP P09874
C	519	GLY	-	expression tag	UNP P09874
C	520	LEU	-	expression tag	UNP P09874
C	521	VAL	-	expression tag	UNP P09874
C	522	PRO	-	expression tag	UNP P09874
C	523	ARG	-	expression tag	UNP P09874
C	524	GLY	-	expression tag	UNP P09874
C	525	SER	-	expression tag	UNP P09874
C	526	HIS	-	expression tag	UNP P09874
C	?	-	SER	deletion	UNP P09874
C	?	-	LYS	deletion	UNP P09874
C	?	-	LEU	deletion	UNP P09874
C	?	-	PRO	deletion	UNP P09874
C	?	-	LYS	deletion	UNP P09874
C	?	-	PRO	deletion	UNP P09874
C	?	-	VAL	deletion	UNP P09874
C	?	-	GLN	deletion	UNP P09874
C	?	-	ASP	deletion	UNP P09874
C	?	-	LEU	deletion	UNP P09874
C	?	-	ILE	deletion	UNP P09874
C	?	-	LYS	deletion	UNP P09874
C	?	-	MET	deletion	UNP P09874
C	?	-	ILE	deletion	UNP P09874
C	762	ALA	VAL	variant	UNP P09874
K	507	MET	-	initiating methionine	UNP P09874
K	508	GLY	-	expression tag	UNP P09874
K	509	SER	-	expression tag	UNP P09874
K	510	SER	-	expression tag	UNP P09874
K	511	HIS	-	expression tag	UNP P09874
K	512	HIS	-	expression tag	UNP P09874
K	513	HIS	-	expression tag	UNP P09874
K	514	HIS	-	expression tag	UNP P09874
K	515	HIS	-	expression tag	UNP P09874
K	516	HIS	-	expression tag	UNP P09874
K	517	SER	-	expression tag	UNP P09874
K	518	SER	-	expression tag	UNP P09874
K	519	GLY	-	expression tag	UNP P09874
K	520	LEU	-	expression tag	UNP P09874

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Chain	Residue	Modelled	Actual	Comment	Reference
K	521	VAL	-	expression tag	UNP P09874
K	522	PRO	-	expression tag	UNP P09874
K	523	ARG	-	expression tag	UNP P09874
K	524	GLY	-	expression tag	UNP P09874
K	525	SER	-	expression tag	UNP P09874
K	526	HIS	-	expression tag	UNP P09874
K	?	-	SER	deletion	UNP P09874
K	?	-	LYS	deletion	UNP P09874
K	?	-	LEU	deletion	UNP P09874
K	?	-	PRO	deletion	UNP P09874
K	?	-	LYS	deletion	UNP P09874
K	?	-	PRO	deletion	UNP P09874
K	?	-	VAL	deletion	UNP P09874
K	?	-	GLN	deletion	UNP P09874
K	?	-	ASP	deletion	UNP P09874
K	?	-	LEU	deletion	UNP P09874
K	?	-	ILE	deletion	UNP P09874
K	?	-	LYS	deletion	UNP P09874
K	?	-	MET	deletion	UNP P09874
K	?	-	ILE	deletion	UNP P09874
K	762	ALA	VAL	variant	UNP P09874
P	507	MET	-	initiating methionine	UNP P09874
P	508	GLY	-	expression tag	UNP P09874
P	509	SER	-	expression tag	UNP P09874
P	510	SER	-	expression tag	UNP P09874
P	511	HIS	-	expression tag	UNP P09874
P	512	HIS	-	expression tag	UNP P09874
P	513	HIS	-	expression tag	UNP P09874
P	514	HIS	-	expression tag	UNP P09874
P	515	HIS	-	expression tag	UNP P09874
P	516	HIS	-	expression tag	UNP P09874
P	517	SER	-	expression tag	UNP P09874
P	518	SER	-	expression tag	UNP P09874
P	519	GLY	-	expression tag	UNP P09874
P	520	LEU	-	expression tag	UNP P09874
P	521	VAL	-	expression tag	UNP P09874
P	522	PRO	-	expression tag	UNP P09874
P	523	ARG	-	expression tag	UNP P09874
P	524	GLY	-	expression tag	UNP P09874
P	525	SER	-	expression tag	UNP P09874
P	526	HIS	-	expression tag	UNP P09874
P	?	-	SER	deletion	UNP P09874

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Chain	Residue	Modelled	Actual	Comment	Reference
P	?	-	LYS	deletion	UNP P09874
P	?	-	LEU	deletion	UNP P09874
P	?	-	PRO	deletion	UNP P09874
P	?	-	LYS	deletion	UNP P09874
P	?	-	PRO	deletion	UNP P09874
P	?	-	VAL	deletion	UNP P09874
P	?	-	GLN	deletion	UNP P09874
P	?	-	ASP	deletion	UNP P09874
P	?	-	LEU	deletion	UNP P09874
P	?	-	ILE	deletion	UNP P09874
P	?	-	LYS	deletion	UNP P09874
P	?	-	MET	deletion	UNP P09874
P	?	-	ILE	deletion	UNP P09874
P	762	ALA	VAL	variant	UNP P09874
H	507	MET	-	initiating methionine	UNP P09874
H	508	GLY	-	expression tag	UNP P09874
H	509	SER	-	expression tag	UNP P09874
H	510	SER	-	expression tag	UNP P09874
H	511	HIS	-	expression tag	UNP P09874
H	512	HIS	-	expression tag	UNP P09874
H	513	HIS	-	expression tag	UNP P09874
H	514	HIS	-	expression tag	UNP P09874
H	515	HIS	-	expression tag	UNP P09874
H	516	HIS	-	expression tag	UNP P09874
H	517	SER	-	expression tag	UNP P09874
H	518	SER	-	expression tag	UNP P09874
H	519	GLY	-	expression tag	UNP P09874
H	520	LEU	-	expression tag	UNP P09874
H	521	VAL	-	expression tag	UNP P09874
H	522	PRO	-	expression tag	UNP P09874
H	523	ARG	-	expression tag	UNP P09874
H	524	GLY	-	expression tag	UNP P09874
H	525	SER	-	expression tag	UNP P09874
H	526	HIS	-	expression tag	UNP P09874
H	?	-	SER	deletion	UNP P09874
H	?	-	LYS	deletion	UNP P09874
H	?	-	LEU	deletion	UNP P09874
H	?	-	PRO	deletion	UNP P09874
H	?	-	LYS	deletion	UNP P09874
H	?	-	PRO	deletion	UNP P09874
H	?	-	VAL	deletion	UNP P09874
H	?	-	GLN	deletion	UNP P09874

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Chain	Residue	Modelled	Actual	Comment	Reference
H	?	-	ASP	deletion	UNP P09874
H	?	-	LEU	deletion	UNP P09874
H	?	-	ILE	deletion	UNP P09874
H	?	-	LYS	deletion	UNP P09874
H	?	-	MET	deletion	UNP P09874
H	?	-	ILE	deletion	UNP P09874
H	762	ALA	VAL	variant	UNP P09874

- Molecule 3 is a protein called Poly [ADP-ribose] polymerase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	N	89	Total	C	H	N	O	S	0	1	0
			1437	461	710	131	129	6			
3	I	87	Total	C	H	N	O	S	0	0	0
			1397	450	687	126	128	6			
3	A	91	Total	C	H	N	O	S	0	0	0
			1441	463	709	130	133	6			
3	F	85	Total	C	H	N	O	S	0	0	0
			1376	444	677	124	125	6			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	-19	MET	-	initiating methionine	UNP P09874
N	-18	GLY	-	expression tag	UNP P09874
N	-17	SER	-	expression tag	UNP P09874
N	-16	SER	-	expression tag	UNP P09874
N	-15	HIS	-	expression tag	UNP P09874
N	-14	HIS	-	expression tag	UNP P09874
N	-13	HIS	-	expression tag	UNP P09874
N	-12	HIS	-	expression tag	UNP P09874
N	-11	HIS	-	expression tag	UNP P09874
N	-10	HIS	-	expression tag	UNP P09874
N	-9	SER	-	expression tag	UNP P09874
N	-8	SER	-	expression tag	UNP P09874
N	-7	GLY	-	expression tag	UNP P09874
N	-6	LEU	-	expression tag	UNP P09874
N	-5	VAL	-	expression tag	UNP P09874
N	-4	PRO	-	expression tag	UNP P09874
N	-3	ARG	-	expression tag	UNP P09874
N	-2	GLY	-	expression tag	UNP P09874
N	-1	SER	-	expression tag	UNP P09874

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Chain	Residue	Modelled	Actual	Comment	Reference
N	0	HIS	-	expression tag	UNP P09874
I	-19	MET	-	initiating methionine	UNP P09874
I	-18	GLY	-	expression tag	UNP P09874
I	-17	SER	-	expression tag	UNP P09874
I	-16	SER	-	expression tag	UNP P09874
I	-15	HIS	-	expression tag	UNP P09874
I	-14	HIS	-	expression tag	UNP P09874
I	-13	HIS	-	expression tag	UNP P09874
I	-12	HIS	-	expression tag	UNP P09874
I	-11	HIS	-	expression tag	UNP P09874
I	-10	HIS	-	expression tag	UNP P09874
I	-9	SER	-	expression tag	UNP P09874
I	-8	SER	-	expression tag	UNP P09874
I	-7	GLY	-	expression tag	UNP P09874
I	-6	LEU	-	expression tag	UNP P09874
I	-5	VAL	-	expression tag	UNP P09874
I	-4	PRO	-	expression tag	UNP P09874
I	-3	ARG	-	expression tag	UNP P09874
I	-2	GLY	-	expression tag	UNP P09874
I	-1	SER	-	expression tag	UNP P09874
I	0	HIS	-	expression tag	UNP P09874
A	-19	MET	-	initiating methionine	UNP P09874
A	-18	GLY	-	expression tag	UNP P09874
A	-17	SER	-	expression tag	UNP P09874
A	-16	SER	-	expression tag	UNP P09874
A	-15	HIS	-	expression tag	UNP P09874
A	-14	HIS	-	expression tag	UNP P09874
A	-13	HIS	-	expression tag	UNP P09874
A	-12	HIS	-	expression tag	UNP P09874
A	-11	HIS	-	expression tag	UNP P09874
A	-10	HIS	-	expression tag	UNP P09874
A	-9	SER	-	expression tag	UNP P09874
A	-8	SER	-	expression tag	UNP P09874
A	-7	GLY	-	expression tag	UNP P09874
A	-6	LEU	-	expression tag	UNP P09874
A	-5	VAL	-	expression tag	UNP P09874
A	-4	PRO	-	expression tag	UNP P09874
A	-3	ARG	-	expression tag	UNP P09874
A	-2	GLY	-	expression tag	UNP P09874
A	-1	SER	-	expression tag	UNP P09874
A	0	HIS	-	expression tag	UNP P09874
F	-19	MET	-	initiating methionine	UNP P09874

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-18	GLY	-	expression tag	UNP P09874
F	-17	SER	-	expression tag	UNP P09874
F	-16	SER	-	expression tag	UNP P09874
F	-15	HIS	-	expression tag	UNP P09874
F	-14	HIS	-	expression tag	UNP P09874
F	-13	HIS	-	expression tag	UNP P09874
F	-12	HIS	-	expression tag	UNP P09874
F	-11	HIS	-	expression tag	UNP P09874
F	-10	HIS	-	expression tag	UNP P09874
F	-9	SER	-	expression tag	UNP P09874
F	-8	SER	-	expression tag	UNP P09874
F	-7	GLY	-	expression tag	UNP P09874
F	-6	LEU	-	expression tag	UNP P09874
F	-5	VAL	-	expression tag	UNP P09874
F	-4	PRO	-	expression tag	UNP P09874
F	-3	ARG	-	expression tag	UNP P09874
F	-2	GLY	-	expression tag	UNP P09874
F	-1	SER	-	expression tag	UNP P09874
F	0	HIS	-	expression tag	UNP P09874

- Molecule 4 is a protein called Poly [ADP-ribose] polymerase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	G	135	Total 2034	C 654	H 1000	N 174	O 199	S 7	0	0	0
4	O	138	Total 2092	C 671	H 1033	N 179	O 202	S 7	0	0	0
4	J	139	Total 2099	C 674	H 1033	N 179	O 206	S 7	0	0	0
4	B	130	Total 1942	C 628	H 950	N 166	O 191	S 7	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	215	MET	-	initiating methionine	UNP P09874
G	367	LEU	-	expression tag	UNP P09874
G	368	GLU	-	expression tag	UNP P09874
G	369	HIS	-	expression tag	UNP P09874
G	370	HIS	-	expression tag	UNP P09874
G	371	HIS	-	expression tag	UNP P09874
G	372	HIS	-	expression tag	UNP P09874

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Chain	Residue	Modelled	Actual	Comment	Reference
G	373	HIS	-	expression tag	UNP P09874
G	374	HIS	-	expression tag	UNP P09874
O	215	MET	-	initiating methionine	UNP P09874
O	367	LEU	-	expression tag	UNP P09874
O	368	GLU	-	expression tag	UNP P09874
O	369	HIS	-	expression tag	UNP P09874
O	370	HIS	-	expression tag	UNP P09874
O	371	HIS	-	expression tag	UNP P09874
O	372	HIS	-	expression tag	UNP P09874
O	373	HIS	-	expression tag	UNP P09874
O	374	HIS	-	expression tag	UNP P09874
J	215	MET	-	initiating methionine	UNP P09874
J	367	LEU	-	expression tag	UNP P09874
J	368	GLU	-	expression tag	UNP P09874
J	369	HIS	-	expression tag	UNP P09874
J	370	HIS	-	expression tag	UNP P09874
J	371	HIS	-	expression tag	UNP P09874
J	372	HIS	-	expression tag	UNP P09874
J	373	HIS	-	expression tag	UNP P09874
J	374	HIS	-	expression tag	UNP P09874
B	215	MET	-	initiating methionine	UNP P09874
B	367	LEU	-	expression tag	UNP P09874
B	368	GLU	-	expression tag	UNP P09874
B	369	HIS	-	expression tag	UNP P09874
B	370	HIS	-	expression tag	UNP P09874
B	371	HIS	-	expression tag	UNP P09874
B	372	HIS	-	expression tag	UNP P09874
B	373	HIS	-	expression tag	UNP P09874
B	374	HIS	-	expression tag	UNP P09874

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	N	1	Total Zn 1 1	0	0
5	I	1	Total Zn 1 1	0	0
5	A	1	Total Zn 1 1	0	0
5	G	1	Total Zn 1 1	0	0
5	O	1	Total Zn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	J	1	Total 1	Zn 1	0	0
5	F	1	Total 1	Zn 1	0	0
5	B	1	Total 1	Zn 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	M	1	Total 1	O 1	0	0
6	L	3	Total 3	O 3	0	0
6	E	1	Total 1	O 1	0	0
6	N	1	Total 1	O 1	0	0
6	A	1	Total 1	O 1	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.

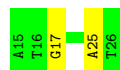
- Molecule 1: DNA (5'-D(*AP*TP*GP*CP*GP*GP*CP*CP*GP*CP*AP*T)-3')

Chain M: 



- Molecule 1: DNA (5'-D(*AP*TP*GP*CP*GP*GP*CP*CP*GP*CP*AP*T)-3')

Chain L: 



- Molecule 1: DNA (5'-D(*AP*TP*GP*CP*GP*GP*CP*CP*GP*CP*AP*T)-3')

Chain E: 



- Molecule 1: DNA (5'-D(*AP*TP*GP*CP*GP*GP*CP*CP*GP*CP*AP*T)-3')

Chain D: 

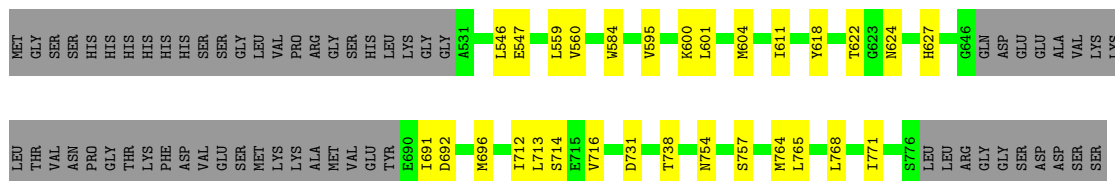


- Molecule 2: Poly [ADP-ribose] polymerase 1

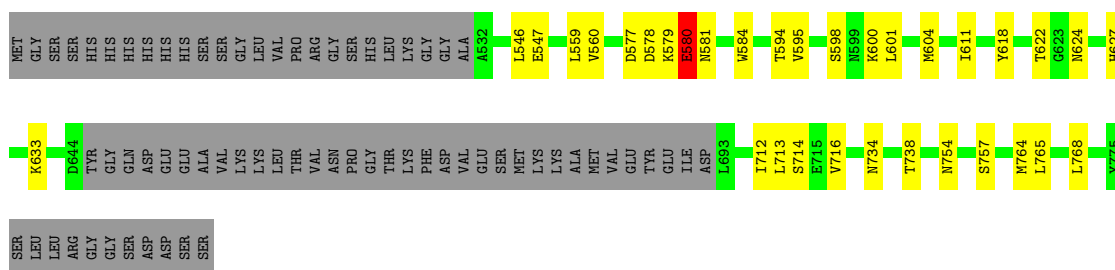
Chain C: 



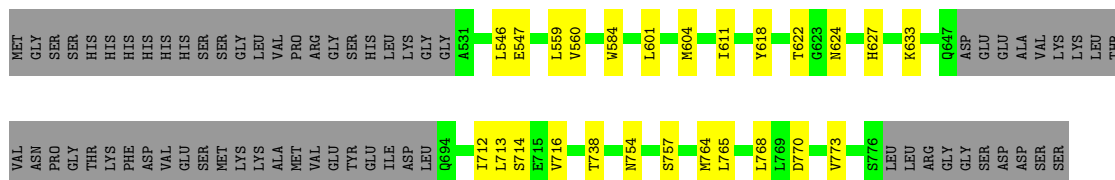
- Molecule 2: Poly [ADP-ribose] polymerase 1



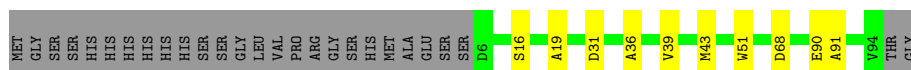
- Molecule 2: Poly [ADP-ribose] polymerase 1



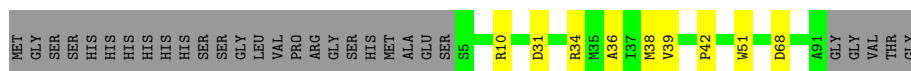
- Molecule 2: Poly [ADP-ribose] polymerase 1



- Molecule 3: Poly [ADP-ribose] polymerase 1

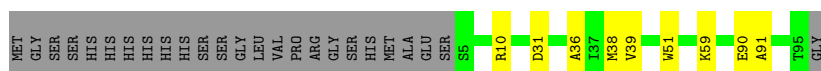


- Molecule 3: Poly [ADP-ribose] polymerase 1

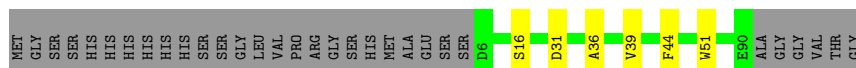


- Molecule 3: Poly [ADP-ribose] polymerase 1

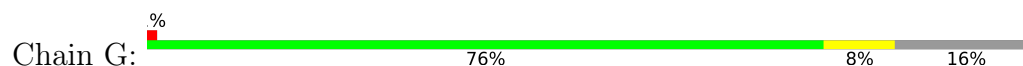




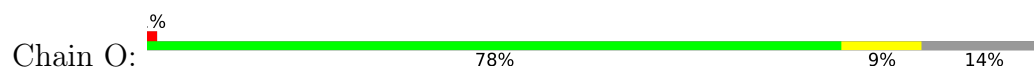
- Molecule 3: Poly [ADP-ribose] polymerase 1



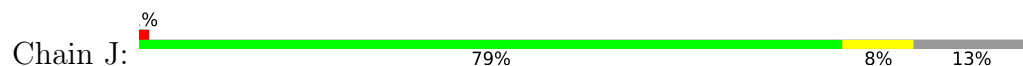
- Molecule 4: Poly [ADP-ribose] polymerase 1



- Molecule 4: Poly [ADP-ribose] polymerase 1



- Molecule 4: Poly [ADP-ribose] polymerase 1



- Molecule 4: Poly [ADP-ribose] polymerase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.76Å 128.55Å 227.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.35 – 3.60 49.35 – 3.60	Depositor EDS
% Data completeness (in resolution range)	98.5 (49.35-3.60) 98.4 (49.35-3.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.28 (at 3.57Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.252 , 0.312 0.274 , 0.312	Depositor DCC
R_{free} test set	1849 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	131.3	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 154.0	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	0.94	EDS
Total number of atoms	28252	wwPDB-VP
Average B, all atoms (Å ²)	219.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.50% 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

5.1 Standard geometry

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

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	D	0.16	0/272	0.42	0/418
1	E	0.16	0/272	0.42	0/418
1	L	0.16	0/272	0.42	0/418
1	M	0.16	0/272	0.42	0/418
2	C	0.12	0/1734	0.29	0/2336
2	H	0.10	0/1629	0.27	0/2196
2	K	0.10	0/1653	0.26	0/2229
2	P	0.12	0/1600	0.37	2/2157 (0.1%)
3	A	0.11	0/752	0.27	0/1010
3	F	0.11	0/719	0.28	0/965
3	I	0.11	0/730	0.27	0/980
3	N	0.11	0/750	0.28	0/1006
4	B	0.11	0/1009	0.28	0/1365
4	G	0.10	0/1051	0.28	0/1418
4	J	0.11	0/1084	0.29	0/1463
4	O	0.12	0/1077	0.29	0/1452
All	All	0.11	0/14876	0.30	2/20249 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	580	GLU	CA-C-N	-7.43	110.93	122.37
2	P	580	GLU	C-N-CA	-7.43	110.93	122.37

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	D	243	136	136	2	0
1	E	243	136	136	5	0
1	L	243	136	136	2	0
1	M	243	136	136	3	0
2	C	1700	1686	1686	18	0
2	H	1595	1577	1577	14	0
2	K	1619	1601	1601	21	0
2	P	1567	1558	1558	22	0
3	A	732	709	709	6	0
3	F	699	677	677	5	0
3	I	710	687	687	5	0
3	N	727	710	710	6	0
4	B	992	950	950	11	0
4	G	1034	1000	1000	8	0
4	J	1066	1033	1033	9	0
4	O	1059	1033	1033	9	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
5	I	1	0	0	0	0
5	J	1	0	0	0	0
5	N	1	0	0	0	0
5	O	1	0	0	0	0
6	A	1	0	0	0	0
6	E	1	0	0	0	0
6	L	3	0	0	0	0
6	M	1	0	0	0	0
6	N	1	0	0	0	0
All	All	14487	13765	13765	119	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 (119) 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)
2:K:595:VAL:O	3:A:59:LYS:NZ	1.93	1.02
1:L:17:DG:OP1	2:P:600:LYS:NZ	2.08	0.85
2:K:618:TYR:O	2:K:622:THR:HG22	1.88	0.73
2:C:618:TYR:O	2:C:622:THR:HG22	1.88	0.73
2:P:618:TYR:O	2:P:622:THR:HG22	1.89	0.71
2:H:618:TYR:O	2:H:622:THR:HG22	1.89	0.71
1:E:23:DG:O5'	4:B:274:SER:OG	2.11	0.68
2:K:622:THR:HG23	2:K:624:ASN:H	1.62	0.65
2:H:622:THR:HG23	2:H:624:ASN:H	1.62	0.65
2:C:622:THR:HG23	2:C:624:ASN:H	1.62	0.64
1:E:15:DA:HI'	3:F:44:PHE:CB	2.28	0.64
2:P:622:THR:HG23	2:P:624:ASN:H	1.62	0.63
1:E:15:DA:HI'	3:F:44:PHE:HB3	1.81	0.63
2:K:731:ASP:HA	4:J:319:THR:HG21	1.83	0.60
2:C:691:ILE:HG21	2:C:771:ILE:CD1	2.33	0.58
1:E:23:DG:C5'	4:B:274:SER:HG	2.16	0.58
2:P:560:VAL:HG12	2:P:738:THR:OG1	2.04	0.58
2:K:560:VAL:HG12	2:K:738:THR:OG1	2.03	0.57
2:K:731:ASP:OD1	4:J:316:THR:HG21	2.04	0.57
2:C:560:VAL:HG12	2:C:738:THR:OG1	2.04	0.57
2:P:633:LYS:NZ	4:O:317:ALA:O	2.29	0.57
2:H:560:VAL:HG12	2:H:738:THR:OG1	2.04	0.57
4:O:305:LYS:O	4:O:307:ASP:N	2.38	0.57
4:J:305:LYS:O	4:J:307:ASP:N	2.38	0.56
4:G:263:GLU:HG2	4:B:266:ILE:HG23	1.87	0.56
1:L:25:DA:OP1	3:I:34:ARG:NH2	2.37	0.56
3:N:43:MET:HE3	2:P:598:SER:HB2	1.88	0.56
4:B:305:LYS:O	4:B:307:ASP:N	2.38	0.55
3:A:90:GLU:O	3:A:91:ALA:HB3	2.05	0.54
2:K:691:ILE:HG21	2:K:771:ILE:CD1	2.37	0.53
2:K:713:LEU:HD12	2:K:765:LEU:HD12	1.91	0.53
2:P:738:THR:HG21	4:O:318:TRP:HZ3	1.74	0.53
4:G:305:LYS:O	4:G:307:ASP:N	2.38	0.52
2:H:713:LEU:HD12	2:H:765:LEU:HD12	1.91	0.52
2:P:579:LYS:O	2:P:580:GLU:CB	2.58	0.52
2:C:713:LEU:HD12	2:C:765:LEU:HD12	1.91	0.52
2:C:643:ILE:HG22	2:C:644:ASP:N	2.26	0.51
4:B:321:CYS:SG	4:B:323:VAL:HG23	2.51	0.51
4:J:321:CYS:SG	4:J:323:VAL:HG23	2.51	0.51
1:M:3:DG:OP1	2:K:600:LYS:NZ	2.35	0.50
3:A:10:ARG:HD2	3:A:38:MET:HE2	1.93	0.50
2:P:713:LEU:HD12	2:P:765:LEU:HD12	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:604:MET:HE2	2:C:604:MET:HA	1.94	0.50
2:P:754:ASN:OD1	2:P:757:SER:N	2.44	0.50
4:O:321:CYS:SG	4:O:323:VAL:HG23	2.51	0.49
2:H:604:MET:HA	2:H:604:MET:HE2	1.94	0.49
2:C:754:ASN:OD1	2:C:757:SER:N	2.44	0.49
2:K:604:MET:HE2	2:K:604:MET:HA	1.94	0.49
2:C:692:ASP:HA	2:C:696:MET:HE3	1.94	0.49
2:P:604:MET:HA	2:P:604:MET:HE2	1.95	0.49
2:H:754:ASN:OD1	2:H:757:SER:N	2.44	0.49
4:O:339:PHE:O	4:O:343:SER:N	2.46	0.48
4:J:339:PHE:O	4:J:343:SER:N	2.46	0.48
2:K:754:ASN:OD1	2:K:757:SER:N	2.44	0.48
4:G:321:CYS:SG	4:G:323:VAL:HG23	2.53	0.48
3:A:36:ALA:HB2	3:A:51:TRP:CE3	2.49	0.47
2:C:731:ASP:HA	4:B:319:THR:HG21	1.95	0.47
4:B:339:PHE:O	4:B:343:SER:N	2.46	0.47
2:K:738:THR:HG21	4:J:318:TRP:HZ3	1.79	0.47
3:I:36:ALA:HB2	3:I:51:TRP:CE3	2.50	0.47
2:P:577:ASP:OD1	2:P:578:ASP:N	2.47	0.47
1:E:23:DG:P	4:B:274:SER:HG	2.36	0.47
3:F:36:ALA:HB2	3:F:51:TRP:CE3	2.50	0.47
2:H:611:ILE:HD12	2:H:611:ILE:N	2.31	0.46
4:J:295:CYS:SG	4:J:296:GLU:N	2.88	0.46
1:D:11:DA:OP1	3:F:16:SER:HB3	2.15	0.46
3:N:36:ALA:HB2	3:N:51:TRP:CE3	2.50	0.46
4:G:263:GLU:HG2	4:B:266:ILE:CG2	2.46	0.46
4:B:295:CYS:SG	4:B:296:GLU:N	2.88	0.46
2:C:611:ILE:HD12	2:C:611:ILE:N	2.31	0.46
2:K:611:ILE:HD12	2:K:611:ILE:N	2.30	0.46
2:K:584:TRP:HB3	2:K:601:LEU:HD11	1.98	0.46
1:M:11:DA:O3'	3:N:19:ALA:HA	2.15	0.46
2:K:691:ILE:HG21	2:K:771:ILE:HD13	1.98	0.46
2:P:611:ILE:HD12	2:P:611:ILE:N	2.31	0.45
4:G:339:PHE:O	4:G:343:SER:N	2.46	0.45
2:P:734:ASN:ND2	4:O:319:THR:HG22	2.32	0.45
4:G:318:TRP:CE2	2:H:633:LYS:HG2	2.52	0.45
2:P:584:TRP:HB3	2:P:601:LEU:HD11	1.99	0.45
4:J:316:THR:HG23	4:J:319:THR:H	1.82	0.44
4:B:316:THR:HG23	4:B:319:THR:H	1.82	0.44
4:G:295:CYS:SG	4:G:296:GLU:N	2.91	0.44
2:C:584:TRP:HB3	2:C:601:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:10:DC:O3'	3:F:16:SER:HB3	2.18	0.44
4:G:316:THR:HG23	4:G:319:THR:H	1.83	0.44
4:O:295:CYS:SG	4:O:296:GLU:N	2.91	0.44
4:O:316:THR:HG23	4:O:319:THR:H	1.83	0.43
2:H:584:TRP:HB3	2:H:601:LEU:HD11	1.99	0.43
2:K:712:ILE:O	2:K:716:VAL:HG23	2.19	0.43
2:H:712:ILE:O	2:H:716:VAL:HG23	2.19	0.43
3:I:10:ARG:HD2	3:I:38:MET:HE2	1.99	0.42
2:C:712:ILE:O	2:C:716:VAL:HG23	2.19	0.42
3:A:90:GLU:O	3:A:91:ALA:CB	2.67	0.42
2:P:580:GLU:C	2:P:581:ASN:OD1	2.62	0.42
2:P:712:ILE:O	2:P:716:VAL:HG23	2.19	0.42
2:C:559:LEU:C	2:C:559:LEU:HD23	2.45	0.42
2:C:546:LEU:HD23	2:C:547:GLU:N	2.35	0.42
2:P:559:LEU:C	2:P:559:LEU:HD23	2.45	0.42
2:K:546:LEU:HD23	2:K:547:GLU:N	2.35	0.42
2:P:633:LYS:HG3	4:O:317:ALA:HB1	2.02	0.41
2:H:559:LEU:C	2:H:559:LEU:HD23	2.45	0.41
2:P:546:LEU:HD23	2:P:547:GLU:N	2.35	0.41
2:H:764:MET:O	2:H:768:LEU:HD13	2.21	0.41
2:C:764:MET:O	2:C:768:LEU:HD13	2.21	0.41
3:I:42:PRO:HD3	3:A:91:ALA:HB1	2.02	0.41
2:K:559:LEU:C	2:K:559:LEU:HD23	2.46	0.41
2:H:770:ASP:HA	2:H:773:VAL:HG22	2.03	0.41
2:K:692:ASP:HA	2:K:696:MET:HE3	2.02	0.41
2:C:594:THR:HG22	2:C:595:VAL:N	2.36	0.41
2:C:770:ASP:HA	2:C:773:VAL:HG22	2.03	0.41
2:K:764:MET:O	2:K:768:LEU:HD13	2.21	0.41
3:N:68:ASP:OD1	3:N:68:ASP:N	2.54	0.41
3:I:68:ASP:OD1	3:I:68:ASP:N	2.54	0.41
2:P:594:THR:HG22	2:P:595:VAL:N	2.36	0.41
2:P:764:MET:O	2:P:768:LEU:HD13	2.21	0.41
3:N:90:GLU:O	3:N:91:ALA:HB3	2.20	0.40
2:H:546:LEU:HD23	2:H:547:GLU:N	2.36	0.40
1:M:10:DC:O3'	3:N:16:SER:HB3	2.21	0.40
2:K:731:ASP:HA	4:J:319:THR:CG2	2.50	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	
2	C	209/266 (79%)	197 (94%)	12 (6%)	0	100	100
2	H	196/266 (74%)	184 (94%)	12 (6%)	0	100	100
2	K	199/266 (75%)	188 (94%)	11 (6%)	0	100	100
2	P	192/266 (72%)	182 (95%)	9 (5%)	1 (0%)	24	57
3	A	89/116 (77%)	83 (93%)	6 (7%)	0	100	100
3	F	83/116 (72%)	78 (94%)	5 (6%)	0	100	100
3	I	85/116 (73%)	81 (95%)	4 (5%)	0	100	100
3	N	88/116 (76%)	82 (93%)	6 (7%)	0	100	100
4	B	128/160 (80%)	121 (94%)	7 (6%)	0	100	100
4	G	133/160 (83%)	125 (94%)	8 (6%)	0	100	100
4	J	137/160 (86%)	128 (93%)	9 (7%)	0	100	100
4	O	136/160 (85%)	126 (93%)	10 (7%)	0	100	100
All	All	1675/2168 (77%)	1575 (94%)	99 (6%)	1 (0%)	48	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	P	580	GLU

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	
2	C	187/230 (81%)	185 (99%)	2 (1%)	65	74
2	H	174/230 (76%)	172 (99%)	2 (1%)	65	74
2	K	177/230 (77%)	175 (99%)	2 (1%)	65	74
2	P	172/230 (75%)	170 (99%)	2 (1%)	63	73
3	A	80/100 (80%)	78 (98%)	2 (2%)	42	63
3	F	77/100 (77%)	75 (97%)	2 (3%)	40	62
3	I	78/100 (78%)	76 (97%)	2 (3%)	40	62
3	N	79/100 (79%)	77 (98%)	2 (2%)	42	63
4	B	104/145 (72%)	103 (99%)	1 (1%)	68	75
4	G	109/145 (75%)	108 (99%)	1 (1%)	70	76
4	J	113/145 (78%)	111 (98%)	2 (2%)	51	68
4	O	112/145 (77%)	110 (98%)	2 (2%)	51	68
All	All	1462/1900 (77%)	1440 (98%)	22 (2%)	57	70

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	627	HIS
2	C	714	SER
2	K	627	HIS
2	K	714	SER
3	N	31	ASP
3	N	39	VAL
3	I	31	ASP
3	I	39	VAL
3	A	31	ASP
3	A	39	VAL
4	G	280	LEU
2	P	627	HIS
2	P	714	SER
2	H	627	HIS
2	H	714	SER
4	O	226	LYS
4	O	280	LEU
4	J	227	GLU
4	J	280	LEU
3	F	31	ASP
3	F	39	VAL
4	B	280	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	753	ASN
2	K	694	GLN
2	K	753	ASN
4	G	242	ASN
2	P	753	ASN
2	H	717	GLN
2	H	753	ASN
4	O	242	ASN
4	J	242	ASN
4	B	242	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

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

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

6.1 Protein, DNA and RNA chains

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(Å²)	Q<0.9	
1	D	12/12 (100%)	-0.37	0	100	100	177, 213, 244, 247	0
1	E	12/12 (100%)	-0.25	0	100	100	195, 259, 278, 279	0
1	L	12/12 (100%)	-0.50	0	100	100	142, 166, 175, 184	0
1	M	12/12 (100%)	-0.52	0	100	100	155, 164, 190, 190	0
2	C	213/266 (80%)	-0.69	0	100	100	134, 216, 281, 321	0
2	H	200/266 (75%)	-0.65	0	100	100	172, 235, 318, 361	0
2	K	203/266 (76%)	-0.70	0	100	100	140, 217, 288, 359	0
2	P	196/266 (73%)	-0.46	0	100	100	164, 224, 309, 362	0
3	A	91/116 (78%)	-0.57	0	100	100	143, 183, 242, 261	0
3	F	85/116 (73%)	-0.55	0	100	100	204, 258, 313, 350	0
3	I	87/116 (75%)	-0.63	0	100	100	139, 185, 241, 276	0
3	N	89/116 (76%)	-0.64	0	100	100	87, 186, 222, 275	1 (1%)
4	B	130/160 (81%)	-0.62	0	100	100	151, 214, 318, 370	0
4	G	135/160 (84%)	-0.60	1 (0%)	84	61	202, 255, 333, 361	0
4	J	139/160 (86%)	-0.51	1 (0%)	84	61	139, 197, 291, 348	0
4	O	138/160 (86%)	-0.42	2 (1%)	73	46	134, 188, 259, 328	0
All	All	1754/2216 (79%)	-0.59	4 (0%)	91	80	87, 215, 306, 370	1 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	J	315	VAL	2.8
4	G	358	PRO	2.7
4	O	343	SER	2.3
4	O	353	GLN	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 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, 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($\text{\AA}^2$)	Q<0.9
5	ZN	G	400	1/1	0.96	0.05	224,224,224,224	0
5	ZN	F	200	1/1	0.96	0.04	246,246,246,246	0
5	ZN	O	400	1/1	0.98	0.09	267,267,267,267	0
5	ZN	J	400	1/1	0.99	0.02	143,143,143,143	0
5	ZN	N	200	1/1	0.99	0.07	161,161,161,161	0
5	ZN	B	400	1/1	0.99	0.04	198,198,198,198	0
5	ZN	A	200	1/1	1.00	0.01	154,154,154,154	0
5	ZN	I	200	1/1	1.00	0.06	227,227,227,227	0

6.5 Other polymers [i](#)

There are no such residues in this entry.