



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 16, 2024 – 02:17 PM EST

PDB ID : 4FC2
Title : Crystal structure of mouse poly(ADP-ribose) glycohydrolase (PARG) catalytic domain
Authors : Wang, Z.; Cheng, Z.; Xu, W.
Deposited on : 2012-05-23
Resolution : 1.91 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

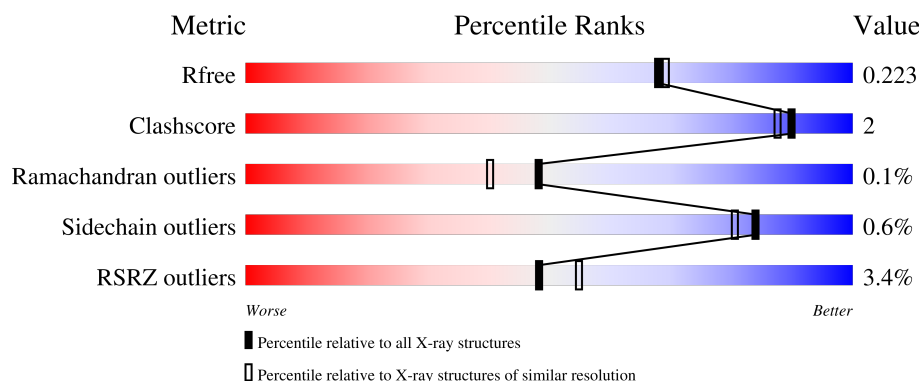
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.91 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}	164625	1028 (1.92-1.92)
Clashscore	180529	1100 (1.92-1.92)
Ramachandran outliers	177936	1087 (1.92-1.92)
Sidechain outliers	177891	1087 (1.92-1.92)
RSRZ outliers	164620	1028 (1.92-1.92)

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	521	<div> <div>4%</div> <div>95%</div> <div>..</div> </div>
1	B	521	<div> <div>3%</div> <div>93%</div> <div>..</div> </div>
1	C	521	<div> <div>3%</div> <div>93%</div> <div>..</div> </div>
1	D	521	<div> <div>3%</div> <div>93%</div> <div>5% .</div> </div>

2 Entry composition [i](#)

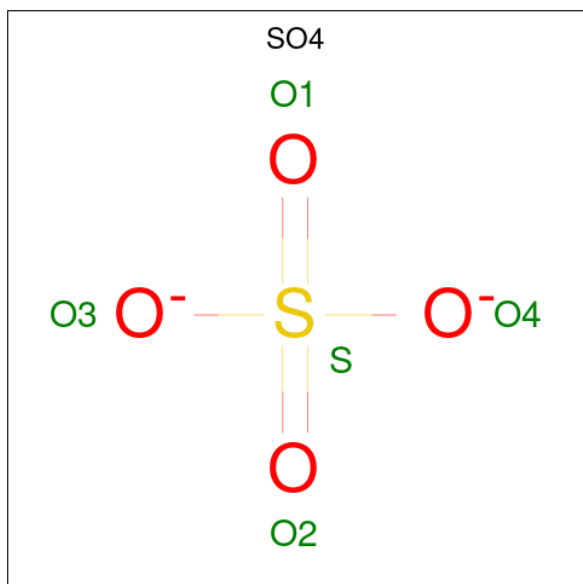
There are 3 unique types of molecules in this entry. The entry contains 18082 atoms, of which 0 are hydrogens and 0 are deuteriums.

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(ADP-ribose) glycohydrolase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	508	Total	C	N	O	S	Se	0	0	0
			4122	2632	717	750	14	9			
1	B	507	Total	C	N	O	S	Se	0	0	0
			4115	2628	716	748	14	9			
1	C	508	Total	C	N	O	S	Se	0	0	0
			4122	2632	717	750	14	9			
1	D	508	Total	C	N	O	S	Se	0	0	0
			4122	2633	717	749	14	9			

- Molecule 2 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

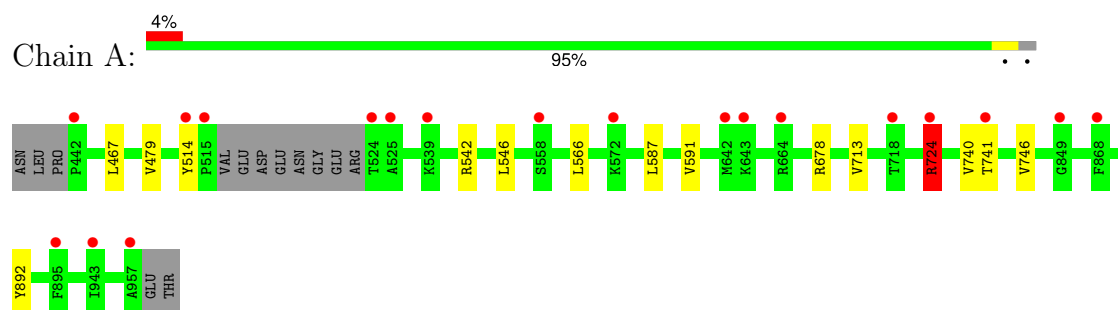
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	378	Total	O	0	0
			378	378		
3	B	354	Total	O	0	0
			354	354		
3	C	391	Total	O	0	0
			391	391		
3	D	338	Total	O	0	0
			338	338		

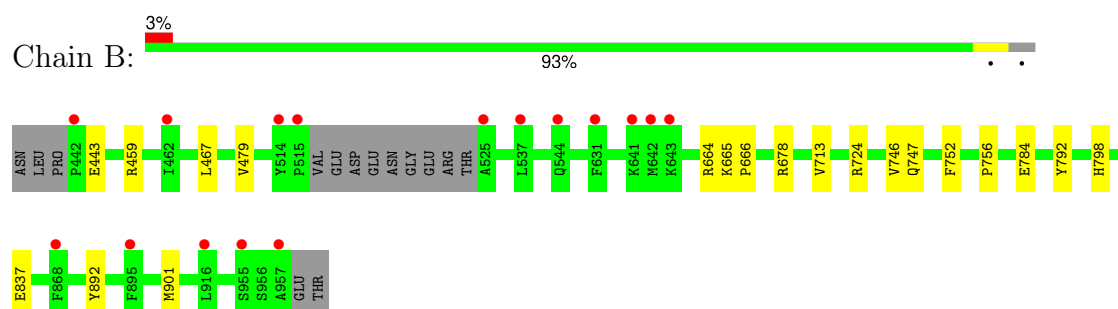
3 Residue-property plots [i](#)

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.

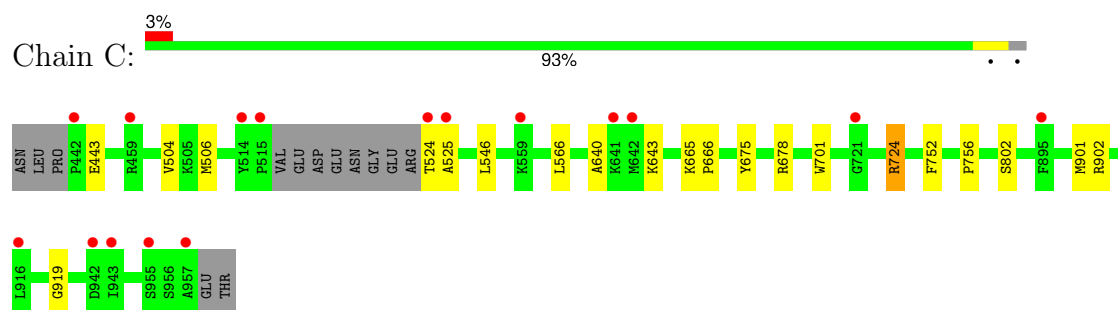
- Molecule 1: Poly(ADP-ribose) glycohydrolase



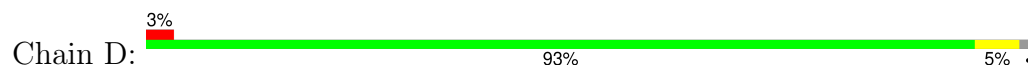
- Molecule 1: Poly(ADP-ribose) glycohydrolase

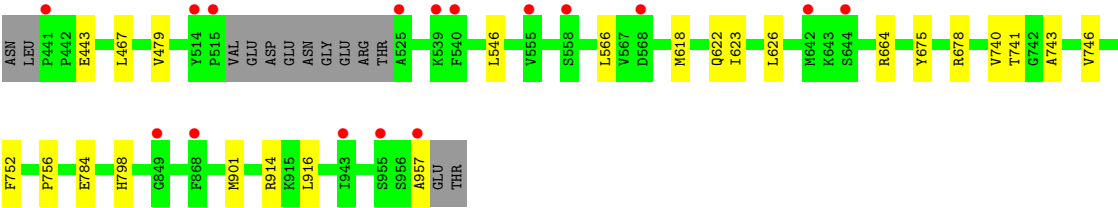


- Molecule 1: Poly(ADP-ribose) glycohydrolase



- Molecule 1: Poly(ADP-ribose) glycohydrolase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	67.14Å 90.40Å 104.70Å 81.64° 88.41° 89.36°	Depositor
Resolution (Å)	50.00 – 1.91 50.00 – 1.91	Depositor EDS
% Data completeness (in resolution range)	92.1 (50.00-1.91) 92.1 (50.00-1.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.174 , 0.214 0.182 , 0.223	Depositor DCC
R_{free} test set	8659 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	24.3	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 32.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.105 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18082	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.62% 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: SO4

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	0.44	0/4216	0.57	1/5691 (0.0%)
1	B	0.43	0/4209	0.58	0/5681
1	C	0.45	0/4216	0.57	0/5691
1	D	0.42	0/4217	0.56	0/5693
All	All	0.43	0/16858	0.57	1/22756 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	724	ARG	NE-CZ-NH1	5.90	123.25	120.30

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	4122	0	4087	7	0
1	B	4115	0	4080	12	0
1	C	4122	0	4087	19	0
1	D	4122	0	4087	17	0
2	A	35	0	0	0	0
2	B	35	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	35	0	0	0	0
2	D	35	0	0	0	0
3	A	378	0	0	0	0
3	B	354	0	0	0	0
3	C	391	0	0	0	0
3	D	338	0	0	2	0
All	All	18082	0	16341	55	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 2.

All (55) 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:C:504:VAL:CG1	1:C:506:MSE:HE3	1.72	1.18
1:C:504:VAL:CG1	1:C:506:MSE:CE	2.25	1.15
1:C:504:VAL:HG12	1:C:506:MSE:CE	1.78	1.13
1:C:504:VAL:HG12	1:C:506:MSE:HE3	1.27	1.07
1:D:618:MSE:HE1	1:D:626:LEU:HD12	1.42	0.99
1:C:504:VAL:HG11	1:C:506:MSE:CE	1.97	0.94
1:C:504:VAL:HG11	1:C:506:MSE:HE1	1.55	0.88
1:D:618:MSE:HE1	1:D:626:LEU:CD1	2.15	0.77
1:A:724:ARG:HG3	1:A:724:ARG:HH11	1.57	0.68
1:B:664:ARG:NH2	1:B:792:TYR:O	2.27	0.67
1:C:524:THR:HG22	1:C:525:ALA:H	1.62	0.64
1:D:618:MSE:HE3	1:D:622:GLN:HB3	1.80	0.62
1:D:546:LEU:HD23	1:D:566:LEU:HD21	1.83	0.59
1:D:618:MSE:HE2	1:D:623:ILE:HG13	1.85	0.58
1:C:506:MSE:HA	1:C:506:MSE:HE2	1.86	0.57
1:D:957:ALA:HB3	3:D:1203:HOH:O	2.05	0.56
1:C:504:VAL:HG12	1:C:506:MSE:HE2	1.80	0.54
1:B:746:VAL:CG1	1:B:747:GLN:H	2.19	0.54
1:D:443:GLU:HG3	1:D:901:MSE:HE1	1.89	0.54
1:C:504:VAL:CB	1:C:506:MSE:HE3	2.34	0.54
1:C:546:LEU:HD23	1:C:566:LEU:HD21	1.91	0.52
1:D:467:LEU:O	1:D:479:VAL:HG11	2.09	0.51
1:B:443:GLU:HG3	1:B:901:MSE:HE1	1.92	0.51
1:C:640:ALA:O	1:C:643:LYS:HG3	2.11	0.50
1:C:443:GLU:HG3	1:C:901:MSE:HE1	1.94	0.49
1:B:746:VAL:CG1	1:B:747:GLN:N	2.75	0.49
1:A:724:ARG:HH11	1:A:724:ARG:CG	2.24	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:467:LEU:O	1:A:479:VAL:HG11	2.14	0.47
1:D:664:ARG:NH1	3:D:1139:HOH:O	2.47	0.47
1:D:752:PHE:O	1:D:756:PRO:HA	2.15	0.46
1:D:618:MSE:HE2	1:D:623:ILE:CG1	2.46	0.46
1:C:752:PHE:O	1:C:756:PRO:HA	2.15	0.46
1:D:675:TYR:CG	1:D:756:PRO:HG2	2.51	0.45
1:C:724:ARG:HH21	1:C:802:SER:HA	1.82	0.45
1:B:752:PHE:O	1:B:756:PRO:HA	2.17	0.44
1:A:740:VAL:HG13	1:A:741:THR:HG23	1.98	0.44
1:D:740:VAL:HG13	1:D:741:THR:HG23	2.01	0.43
1:A:587:LEU:O	1:A:591:VAL:HG23	2.19	0.43
1:D:618:MSE:HE3	1:D:622:GLN:CB	2.46	0.42
1:D:664:ARG:NH1	1:D:743:ALA:O	2.52	0.42
1:C:701:TRP:O	1:C:919:GLY:HA2	2.19	0.42
1:B:746:VAL:HG12	1:B:747:GLN:N	2.34	0.42
1:B:837:GLU:HA	1:B:837:GLU:OE1	2.20	0.42
1:C:665:LYS:N	1:C:666:PRO:HD2	2.34	0.42
1:C:675:TYR:CD1	1:C:756:PRO:HG2	2.55	0.42
1:B:746:VAL:HG13	1:B:747:GLN:H	1.83	0.42
1:B:467:LEU:O	1:B:479:VAL:HG11	2.20	0.41
1:D:784:GLU:HG3	1:D:798:HIS:HB2	2.02	0.41
1:B:784:GLU:HG3	1:B:798:HIS:HB2	2.03	0.41
1:C:443:GLU:OE2	1:C:902:ARG:HD3	2.21	0.41
1:A:546:LEU:HD23	1:A:566:LEU:HD21	2.03	0.41
1:A:713:VAL:HG23	1:A:892:TYR:HB3	2.03	0.40
1:B:665:LYS:N	1:B:666:PRO:HD2	2.37	0.40
1:B:713:VAL:HG23	1:B:892:TYR:HB3	2.04	0.40
1:D:914:ARG:HB2	1:D:916:LEU:HD13	2.04	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	504/521 (97%)	489 (97%)	14 (3%)	1 (0%)	44	34
1	B	503/521 (96%)	492 (98%)	11 (2%)	0	100	100
1	C	504/521 (97%)	492 (98%)	12 (2%)	0	100	100
1	D	504/521 (97%)	489 (97%)	14 (3%)	1 (0%)	44	34
All	All	2015/2084 (97%)	1962 (97%)	51 (2%)	2 (0%)	48	40

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	746	VAL
1	A	746	VAL

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	447/450 (99%)	443 (99%)	4 (1%)	75	70
1	B	446/450 (99%)	443 (99%)	3 (1%)	81	77
1	C	447/450 (99%)	445 (100%)	2 (0%)	89	88
1	D	447/450 (99%)	446 (100%)	1 (0%)	92	92
All	All	1787/1800 (99%)	1777 (99%)	10 (1%)	84	80

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	514	TYR
1	A	542	ARG
1	A	678	ARG
1	A	724	ARG
1	B	459	ARG
1	B	678	ARG
1	B	724	ARG
1	C	678	ARG
1	C	724	ARG

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Mol	Chain	Res	Type
1	D	678	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

28 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	C	1004	-	4,4,4	0.25	0	6,6,6	0.07	0
2	SO4	A	1005	-	4,4,4	0.29	0	6,6,6	0.15	0
2	SO4	C	1007	-	4,4,4	0.24	0	6,6,6	0.11	0
2	SO4	B	1005	-	4,4,4	0.21	0	6,6,6	0.18	0
2	SO4	A	1001	-	4,4,4	0.24	0	6,6,6	0.17	0
2	SO4	D	1005	-	4,4,4	0.28	0	6,6,6	0.29	0
2	SO4	A	1002	-	4,4,4	0.28	0	6,6,6	0.27	0
2	SO4	D	1001	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	D	1006	-	4,4,4	0.23	0	6,6,6	0.14	0
2	SO4	B	1002	-	4,4,4	0.19	0	6,6,6	0.17	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	C	1003	-	4,4,4	0.29	0	6,6,6	0.08	0
2	SO4	A	1007	-	4,4,4	0.24	0	6,6,6	0.12	0
2	SO4	A	1004	-	4,4,4	0.26	0	6,6,6	0.09	0
2	SO4	D	1007	-	4,4,4	0.24	0	6,6,6	0.16	0
2	SO4	B	1004	-	4,4,4	0.27	0	6,6,6	0.18	0
2	SO4	A	1006	-	4,4,4	0.22	0	6,6,6	0.21	0
2	SO4	C	1006	-	4,4,4	0.26	0	6,6,6	0.06	0
2	SO4	A	1003	-	4,4,4	0.26	0	6,6,6	0.14	0
2	SO4	D	1004	-	4,4,4	0.26	0	6,6,6	0.13	0
2	SO4	B	1003	-	4,4,4	0.32	0	6,6,6	0.16	0
2	SO4	D	1002	-	4,4,4	0.26	0	6,6,6	0.12	0
2	SO4	B	1001	-	4,4,4	0.23	0	6,6,6	0.17	0
2	SO4	C	1001	-	4,4,4	0.20	0	6,6,6	0.16	0
2	SO4	C	1002	-	4,4,4	0.24	0	6,6,6	0.17	0
2	SO4	C	1005	-	4,4,4	0.24	0	6,6,6	0.11	0
2	SO4	D	1003	-	4,4,4	0.25	0	6,6,6	0.16	0
2	SO4	B	1007	-	4,4,4	0.23	0	6,6,6	0.26	0
2	SO4	B	1006	-	4,4,4	0.24	0	6,6,6	0.16	0

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 ⓘ

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(Å ²)	Q<0.9
1	A	499/521 (95%)	0.27	19 (3%)	44 50	25, 36, 55, 74	0
1	B	498/521 (95%)	0.24	16 (3%)	50 56	24, 36, 54, 76	0
1	C	499/521 (95%)	0.19	16 (3%)	50 56	25, 35, 51, 71	0
1	D	499/521 (95%)	0.29	16 (3%)	50 56	25, 37, 57, 73	0
All	All	1995/2084 (95%)	0.25	67 (3%)	48 55	24, 36, 54, 76	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	957	ALA	6.8
1	C	514	TYR	4.6
1	D	441	PRO	4.1
1	A	515	PRO	3.7
1	A	514	TYR	3.6
1	B	957	ALA	3.5
1	C	515	PRO	3.4
1	B	642	MET	3.3
1	C	524	THR	3.3
1	B	515	PRO	3.3
1	A	943	ILE	3.3
1	D	515	PRO	3.3
1	A	642	MET	3.2
1	D	525	ALA	3.2
1	D	514	TYR	3.0
1	B	955	SER	3.0
1	D	955	SER	3.0
1	C	957	ALA	3.0
1	A	524	THR	3.0
1	B	544	GLN	2.9
1	D	642	MET	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	642	MET	2.9
1	C	641	LYS	2.9
1	B	514	TYR	2.8
1	A	895	PHE	2.8
1	C	525	ALA	2.8
1	B	442	PRO	2.7
1	B	462	ILE	2.7
1	C	895	PHE	2.6
1	B	895	PHE	2.6
1	C	442	PRO	2.6
1	A	849	GLY	2.6
1	A	957	ALA	2.6
1	B	525	ALA	2.5
1	D	555	VAL	2.5
1	B	641	LYS	2.5
1	A	643	LYS	2.4
1	A	525	ALA	2.4
1	C	459	ARG	2.4
1	D	568	ASP	2.4
1	A	741	THR	2.4
1	B	631	PHE	2.4
1	B	868	PHE	2.4
1	D	540	PHE	2.4
1	C	559	LYS	2.3
1	A	724	ARG	2.3
1	D	539	LYS	2.3
1	D	868	PHE	2.2
1	C	721	GLY	2.2
1	C	943	ILE	2.2
1	D	849	GLY	2.2
1	D	558	SER	2.2
1	B	643	LYS	2.2
1	A	442	PRO	2.2
1	B	537	LEU	2.2
1	A	664	ARG	2.1
1	A	539	LYS	2.1
1	C	942	ASP	2.0
1	C	955	SER	2.0
1	D	644	SER	2.0
1	A	718	THR	2.0
1	D	943	ILE	2.0
1	A	572	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	558	SER	2.0
1	B	916	LEU	2.0
1	C	916	LEU	2.0
1	A	868	PHE	2.0

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
2	SO4	D	1003	5/5	0.69	0.16	76,77,77,81	0
2	SO4	A	1003	5/5	0.75	0.14	77,78,79,80	0
2	SO4	B	1003	5/5	0.76	0.15	67,68,69,73	0
2	SO4	C	1003	5/5	0.77	0.14	75,75,76,77	0
2	SO4	B	1004	5/5	0.78	0.15	71,73,75,76	0
2	SO4	C	1004	5/5	0.79	0.14	69,73,75,76	0
2	SO4	B	1006	5/5	0.81	0.12	86,86,88,88	0
2	SO4	A	1004	5/5	0.81	0.13	74,78,79,82	0
2	SO4	D	1004	5/5	0.81	0.14	84,85,87,88	0
2	SO4	C	1006	5/5	0.82	0.13	80,80,83,84	0
2	SO4	B	1007	5/5	0.83	0.12	68,73,74,78	0
2	SO4	A	1007	5/5	0.84	0.11	79,79,80,82	0
2	SO4	D	1006	5/5	0.84	0.14	86,86,88,89	0
2	SO4	D	1007	5/5	0.84	0.11	66,69,73,74	0
2	SO4	A	1006	5/5	0.86	0.11	81,82,84,85	0
2	SO4	C	1007	5/5	0.87	0.10	63,70,70,71	0
2	SO4	B	1001	5/5	0.88	0.14	80,81,84,85	0
2	SO4	C	1005	5/5	0.90	0.15	50,53,56,59	0
2	SO4	A	1002	5/5	0.90	0.16	65,66,75,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	B	1005	5/5	0.90	0.18	54,58,59,62	0
2	SO4	D	1001	5/5	0.90	0.12	73,76,80,83	0
2	SO4	A	1001	5/5	0.91	0.13	75,75,77,80	0
2	SO4	D	1005	5/5	0.92	0.14	55,57,58,61	0
2	SO4	A	1005	5/5	0.92	0.14	57,58,59,60	0
2	SO4	C	1001	5/5	0.92	0.12	74,75,78,80	0
2	SO4	D	1002	5/5	0.93	0.12	69,69,71,73	0
2	SO4	C	1002	5/5	0.94	0.14	60,62,63,64	0
2	SO4	B	1002	5/5	0.95	0.12	63,64,66,69	0

6.5 Other polymers [i](#)

There are no such residues in this entry.