



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2FAO / pdb_00002fao
Title : Crystal Structure of Pseudomonas aeruginosa LigD polymerase domain
Authors : Zhu, H.; Nandakumar, J.; Aniukwu, J.; Wang, L.K.; Glickman, M.S.; Lima, C.D.; Shuman, S.
Deposited on : 2005-12-07
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 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
Mogul : 2022.3.0, CSD as543be (2022)
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

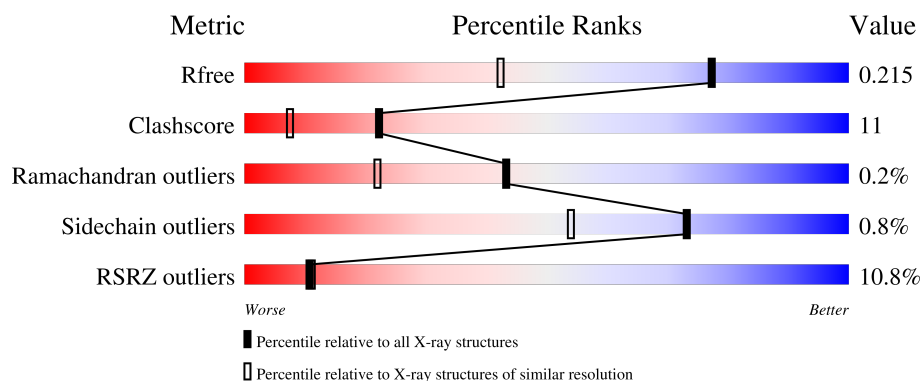
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (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	309	 10% 78% 17% • 5%
1	B	309	 10% 75% 20% • 5%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5165 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.

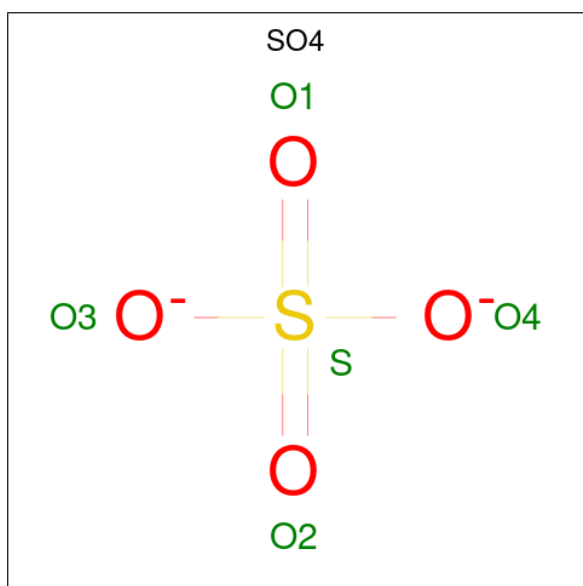
- Molecule 1 is a protein called probable ATP-dependent DNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2321	1464	437	415	5			
1	B	295	Total	C	N	O	S	0	0	0
			2321	1464	437	415	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	532	MET	-	initiating methionine	UNP Q9I1X7
B	532	MET	-	initiating methionine	UNP Q9I1X7

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

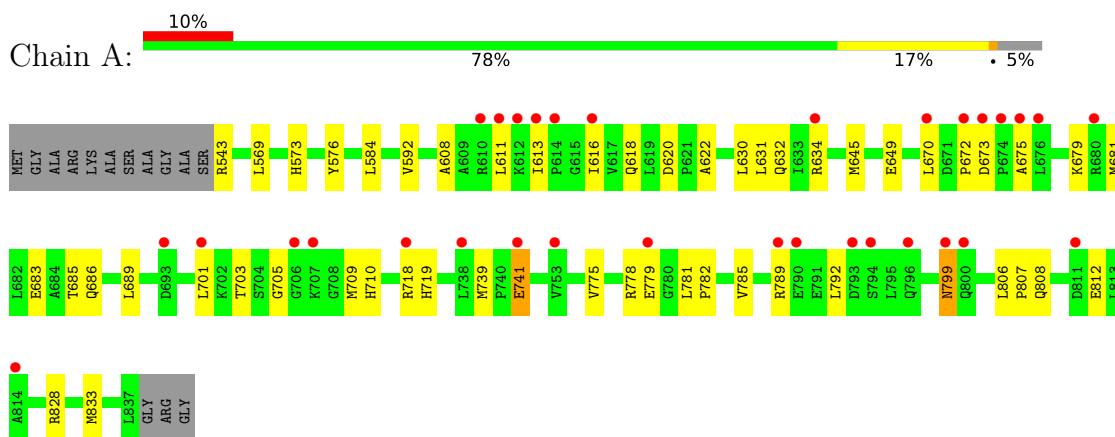
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	272	Total	O	0	0
			272	272		
3	B	226	Total	O	0	0
			226	226		

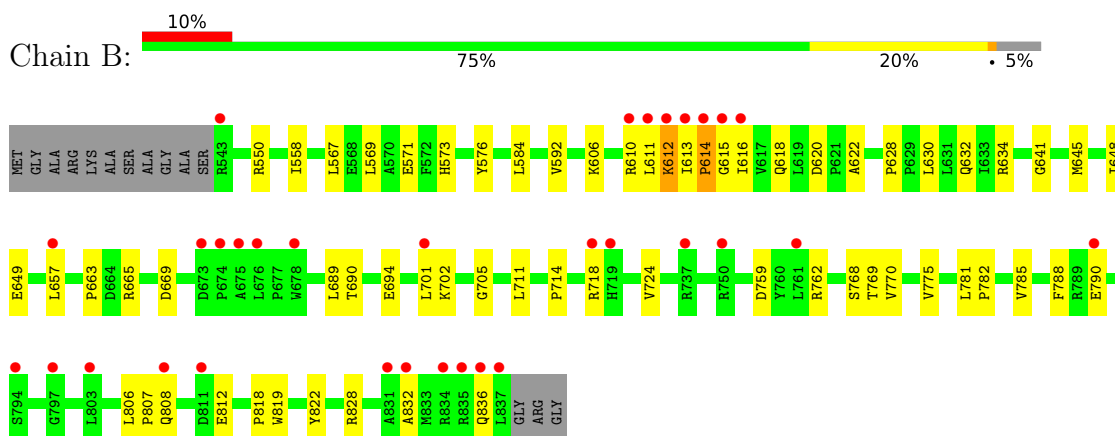
3 Residue-property plots

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: probable ATP-dependent DNA ligase



- Molecule 1: probable ATP-dependent DNA ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	71.75Å 203.58Å 44.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.54 – 1.50 40.54 – 1.50	Depositor EDS
% Data completeness (in resolution range)	95.8 (40.54-1.50) 96.0 (40.54-1.50)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.97 (at 1.50Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.206 , 0.214 0.206 , 0.215	Depositor DCC
R_{free} test set	5073 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	11.8	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 36.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5165	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.47% 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: 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	0.39	0/2372	0.88	5/3215 (0.2%)
1	B	0.35	0/2372	0.88	8/3215 (0.2%)
All	All	0.37	0/4744	0.88	13/6430 (0.2%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	785	VAL	N-CA-C	11.16	120.46	107.73
1	A	584	LEU	N-CA-C	7.91	120.99	111.82
1	A	785	VAL	N-CA-C	7.55	119.64	107.71
1	B	584	LEU	N-CA-C	6.54	119.41	111.82
1	B	705	GLY	N-CA-C	-6.30	106.62	115.32
1	A	705	GLY	N-CA-C	-5.92	107.15	115.32
1	B	628	PRO	N-CA-C	-5.46	104.03	110.70
1	B	630	LEU	N-CA-C	-5.36	103.61	110.53
1	A	703	THR	N-CA-C	-5.34	102.98	110.50
1	B	558	ILE	N-CA-C	-5.30	105.23	111.00
1	B	612	LYS	N-CA-C	-5.25	105.87	113.21
1	A	630	LEU	N-CA-C	-5.11	104.12	110.41
1	B	648	ILE	N-CA-C	-5.09	107.84	112.12

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	A	2321	0	2346	49	0
1	B	2321	0	2346	50	0
2	A	15	0	0	0	0
2	B	10	0	0	0	0
3	A	272	0	0	8	0
3	B	226	0	0	8	0
All	All	5165	0	4692	99	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 11.

All (99) 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:A:645:MET:HG3	3:A:442:HOH:O	1.43	1.18
1:B:645:MET:HG3	3:B:476:HOH:O	1.42	1.17
1:A:670:LEU:HD22	1:A:681:MET:HE1	1.57	0.87
1:B:611:LEU:HD11	1:B:618:GLN:HG3	1.64	0.80
1:B:613:ILE:HG13	3:B:476:HOH:O	1.82	0.78
1:B:616:ILE:HG22	3:B:222:HOH:O	1.86	0.73
1:B:613:ILE:HG23	1:B:641:GLY:HA3	1.71	0.70
1:A:592:VAL:HB	1:A:649:GLU:HB2	1.79	0.65
1:A:681:MET:CE	1:A:685:THR:OG1	2.44	0.65
1:A:779:GLU:HG2	3:A:460:HOH:O	1.96	0.65
1:A:632:GLN:CD	1:A:634:ARG:HE	2.07	0.63
1:A:778:ARG:HG2	1:A:778:ARG:HH11	1.65	0.62
1:A:808:GLN:O	1:A:812:GLU:HG3	2.00	0.61
1:B:576:TYR:OH	1:B:807:PRO:HG3	2.00	0.61
1:A:613:ILE:HG13	3:A:442:HOH:O	2.01	0.60
1:B:832:ALA:O	1:B:836:GLN:HG3	2.01	0.59
1:A:611:LEU:HD22	1:A:616:ILE:HD13	1.85	0.58
1:A:739:MET:HB3	1:A:741:GLU:OE2	2.04	0.58
1:A:679:LYS:HG2	3:A:210:HOH:O	2.03	0.58
1:B:592:VAL:HB	1:B:649:GLU:HB2	1.87	0.57
1:A:611:LEU:HD13	1:A:616:ILE:CG2	2.36	0.56
1:A:681:MET:HE2	1:A:685:THR:OG1	2.05	0.56
1:A:681:MET:HE3	1:A:685:THR:OG1	2.06	0.55
1:B:620:ASP:OD2	1:B:622:ALA:HB3	2.07	0.55
1:A:611:LEU:HD11	1:A:631:LEU:CD2	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:669:ASP:HB3	1:B:759:ASP:HB3	1.89	0.55
1:A:681:MET:HE3	1:A:681:MET:O	2.07	0.54
1:A:618:GLN:HG2	3:A:324:HOH:O	2.08	0.54
1:A:670:LEU:CD2	1:A:681:MET:HE1	2.32	0.54
1:B:611:LEU:HD13	1:B:616:ILE:CG2	2.39	0.53
1:B:611:LEU:HD11	1:B:618:GLN:CG	2.35	0.53
1:B:569:LEU:O	1:B:573:HIS:HD2	1.91	0.53
1:B:690:THR:O	1:B:694:GLU:HG3	2.09	0.52
1:B:808:GLN:HB3	3:B:443:HOH:O	2.09	0.52
1:A:718:ARG:HB3	1:A:718:ARG:NH2	2.25	0.51
1:A:620:ASP:OD2	1:A:622:ALA:HB3	2.11	0.51
1:A:569:LEU:O	1:A:573:HIS:HD2	1.93	0.51
1:A:778:ARG:HG2	1:A:778:ARG:NH1	2.25	0.51
1:B:663:PRO:HG2	1:B:724:VAL:HG21	1.92	0.51
1:A:611:LEU:HD13	1:A:616:ILE:HG23	1.91	0.50
1:B:611:LEU:HD13	1:B:616:ILE:HG23	1.93	0.50
1:B:612:LYS:C	1:B:614:PRO:HD3	2.36	0.50
1:A:543:ARG:N	3:A:282:HOH:O	2.44	0.50
1:A:576:TYR:OH	1:A:807:PRO:HG3	2.11	0.49
1:B:701:LEU:HG	1:B:711:LEU:CD2	2.42	0.49
1:B:808:GLN:O	1:B:812:GLU:HG3	2.12	0.49
1:B:665:ARG:HD3	1:B:822:TYR:OH	2.12	0.49
1:A:685:THR:HB	1:A:792:LEU:HD21	1.95	0.49
1:B:632:GLN:HE22	1:B:657:LEU:HD12	1.78	0.48
1:A:613:ILE:O	1:A:616:ILE:HG22	2.14	0.48
1:B:612:LYS:O	1:B:614:PRO:HD3	2.14	0.48
1:B:632:GLN:CD	1:B:634:ARG:HD2	2.38	0.48
1:B:762:ARG:HH21	1:B:769:THR:HG23	1.79	0.47
1:A:781:LEU:N	1:A:782:PRO:HD3	2.30	0.47
1:A:689:LEU:HD13	1:A:789:ARG:HG3	1.97	0.47
1:B:573:HIS:HE1	3:B:2:HOH:O	1.98	0.47
1:A:679:LYS:O	1:A:683:GLU:HG3	2.15	0.46
1:A:573:HIS:HE1	3:A:1:HOH:O	1.98	0.46
1:A:799:ASN:HD22	1:A:799:ASN:H	1.63	0.46
1:B:613:ILE:HG22	1:B:613:ILE:O	2.15	0.46
1:A:611:LEU:HD12	1:A:618:GLN:CG	2.47	0.45
1:A:741:GLU:CD	1:A:741:GLU:H	2.24	0.45
1:B:689:LEU:HD11	1:B:701:LEU:CD1	2.47	0.45
1:B:550:ARG:HG2	1:B:550:ARG:HH11	1.81	0.45
1:B:781:LEU:N	1:B:782:PRO:HD3	2.31	0.45
1:B:770:VAL:HG23	3:B:168:HOH:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:828:ARG:O	1:A:833:MET:HE1	2.18	0.44
1:B:567:LEU:O	1:B:571:GLU:HG3	2.18	0.44
1:B:613:ILE:HG23	1:B:641:GLY:CA	2.44	0.44
1:A:718:ARG:HH21	1:A:718:ARG:CB	2.31	0.44
1:B:689:LEU:HD11	1:B:701:LEU:HD11	1.99	0.44
1:B:613:ILE:O	1:B:614:PRO:C	2.61	0.44
1:A:806:LEU:N	1:A:807:PRO:CD	2.81	0.43
3:A:488:HOH:O	1:B:610:ARG:HD2	2.18	0.43
1:B:649:GLU:HG2	1:B:775:VAL:O	2.19	0.43
1:B:762:ARG:HD2	1:B:768:SER:O	2.19	0.43
1:B:612:LYS:HD2	1:B:612:LYS:HA	1.88	0.42
1:B:788:PHE:CE1	1:B:818:PRO:HA	2.55	0.42
1:B:718:ARG:HE	1:B:828:ARG:NH2	2.17	0.42
1:A:701:LEU:HD12	1:A:710:HIS:O	2.19	0.42
1:A:670:LEU:N	1:A:670:LEU:HD12	2.35	0.42
1:B:606:LYS:HE3	3:B:107:HOH:O	2.20	0.42
1:B:613:ILE:O	1:B:615:GLY:N	2.53	0.41
1:A:673:ASP:C	1:A:675:ALA:H	2.27	0.41
1:B:790:GLU:H	1:B:790:GLU:CD	2.28	0.41
1:A:799:ASN:HD22	1:A:799:ASN:C	2.28	0.41
1:A:686:GLN:CD	1:A:792:LEU:HD23	2.46	0.41
1:A:701:LEU:HD11	1:A:709:MET:HB3	2.02	0.41
1:A:701:LEU:HD21	1:A:792:LEU:HD13	2.02	0.41
1:A:718:ARG:NH2	1:A:718:ARG:CB	2.83	0.41
1:B:702:LYS:HD3	1:B:819:TRP:CH2	2.56	0.41
1:A:608:ALA:HB3	1:A:631:LEU:HD21	2.02	0.41
1:B:701:LEU:HG	1:B:711:LEU:HD23	2.02	0.41
1:B:714:PRO:HG3	1:B:822:TYR:CE1	2.55	0.41
1:A:649:GLU:HG2	1:A:775:VAL:O	2.21	0.41
1:B:806:LEU:N	1:B:807:PRO:CD	2.84	0.41
1:B:808:GLN:HG2	3:B:148:HOH:O	2.20	0.41
1:A:686:GLN:HA	1:A:686:GLN:HE21	1.86	0.40
1:B:632:GLN:NE2	1:B:657:LEU:HD12	2.36	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	293/309 (95%)	283 (97%)	10 (3%)	0	100	100
1	B	293/309 (95%)	284 (97%)	8 (3%)	1 (0%)	36	17
All	All	586/618 (95%)	567 (97%)	18 (3%)	1 (0%)	43	22

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	614	PRO

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	242/248 (98%)	238 (98%)	4 (2%)	53	26
1	B	242/248 (98%)	242 (100%)	0	100	100
All	All	484/496 (98%)	480 (99%)	4 (1%)	73	54

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	672	PRO
1	A	719	HIS
1	A	741	GLU
1	A	799	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	563	GLN
1	A	573	HIS
1	A	686	GLN
1	A	751	ASN
1	A	799	ASN
1	B	573	HIS
1	B	654	ASN
1	B	686	GLN
1	B	751	ASN

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](#)

5 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	A	1303	-	4,4,4	0.37	0	6,6,6	0.07	0
2	SO4	B	1306	-	4,4,4	0.37	0	6,6,6	0.08	0
2	SO4	A	1302	-	4,4,4	0.34	0	6,6,6	0.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	B	1301	-	4,4,4	0.36	0	6,6,6	0.12	0
2	SO4	A	1305	-	4,4,4	0.38	0	6,6,6	0.09	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	295/309 (95%)	0.47	32 (10%) 11 11	6, 12, 24, 31	0
1	B	295/309 (95%)	0.62	32 (10%) 11 11	6, 14, 26, 32	0
All	All	590/618 (95%)	0.55	64 (10%) 11 11	6, 13, 24, 32	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	611	LEU	11.2
1	B	613	ILE	9.8
1	B	614	PRO	7.6
1	B	611	LEU	6.4
1	A	674	PRO	6.4
1	B	612	LYS	6.1
1	B	674	PRO	5.4
1	A	612	LYS	5.0
1	A	675	ALA	4.9
1	A	614	PRO	4.8
1	A	613	ILE	4.5
1	A	610	ARG	4.1
1	B	835	ARG	3.8
1	B	675	ALA	3.7
1	A	706	GLY	3.7
1	A	707	LYS	3.6
1	B	701	LEU	3.4
1	B	837	LEU	3.4
1	A	673	ASP	3.4
1	B	811	ASP	3.4
1	B	808	GLN	3.2
1	B	831	ALA	3.2
1	A	718	ARG	3.1
1	B	750	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	610	ARG	3.1
1	A	800	GLN	3.0
1	B	797	GLY	3.0
1	B	719	HIS	3.0
1	A	799	ASN	2.9
1	A	794	SER	2.8
1	B	676	LEU	2.7
1	A	814	ALA	2.6
1	A	701	LEU	2.6
1	A	738	LEU	2.6
1	B	803	LEU	2.5
1	B	678	TRP	2.5
1	B	615	GLY	2.5
1	A	634	ARG	2.5
1	B	794	SER	2.4
1	B	657	LEU	2.4
1	B	832	ALA	2.4
1	A	670	LEU	2.4
1	A	616	ILE	2.4
1	A	741	GLU	2.4
1	A	789	ARG	2.3
1	B	718	ARG	2.3
1	B	616	ILE	2.3
1	A	676	LEU	2.3
1	B	761	LEU	2.3
1	B	737	ARG	2.3
1	B	673	ASP	2.2
1	B	836	GLN	2.2
1	A	753	VAL	2.2
1	A	796	GLN	2.2
1	A	779	GLU	2.1
1	A	790	GLU	2.1
1	A	672	PRO	2.1
1	B	543	ARG	2.1
1	B	834	ARG	2.1
1	A	680	ARG	2.0
1	B	790	GLU	2.0
1	A	811	ASP	2.0
1	A	693	ASP	2.0
1	A	793	ASP	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 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
2	SO4	B	1306	5/5	0.67	0.17	39,40,41,41	0
2	SO4	A	1305	5/5	0.75	0.17	37,37,39,39	0
2	SO4	A	1303	5/5	0.88	0.12	34,34,35,35	0
2	SO4	B	1301	5/5	0.96	0.09	16,17,20,21	0
2	SO4	A	1302	5/5	0.97	0.08	15,16,18,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.