



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 7, 2020 – 04:07 am BST

PDB ID : 6NLW
Title : The crystal structure of class D carbapenem-hydrolyzing beta-lactamase BlaA from *Shewanella oneidensis* MR-1
Authors : Tan, K.; Tesar, C.; Endres, M.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2019-01-09
Resolution : 1.85 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

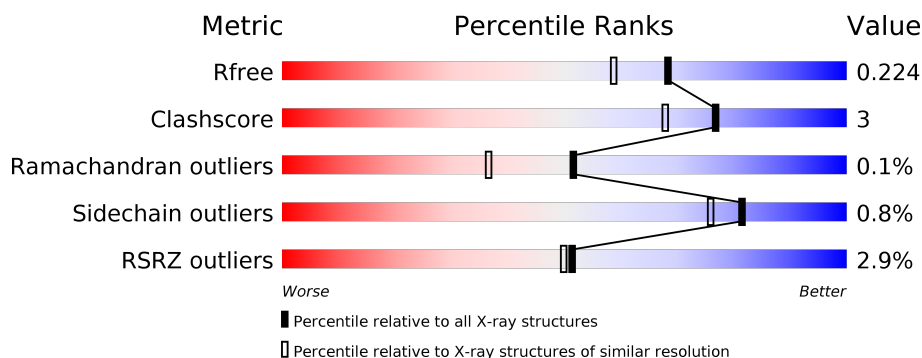
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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 on 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	246	<div> <div>2%</div> <div> <div></div> <div>92%</div> <div>7%</div> </div> </div>
1	B	246	<div> <div>3%</div> <div> <div></div> <div>91%</div> <div>7%</div> </div> </div>
1	C	246	<div> <div>3%</div> <div> <div></div> <div>91%</div> <div>8%</div> </div> </div>
1	D	246	<div> <div>4%</div> <div> <div></div> <div>94%</div> <div></div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	B	305	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 8674 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 Beta-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	243	Total	C	N	O	S	0	2	0
			1997	1274	351	365	7			
1	B	242	Total	C	N	O	S	0	0	0
			1978	1262	348	361	7			
1	C	243	Total	C	N	O	S	0	0	0
			1975	1259	347	362	7			
1	D	242	Total	C	N	O	S	0	2	0
			1982	1265	348	362	7			

There are 12 discrepancies between the modelled and reference sequences:

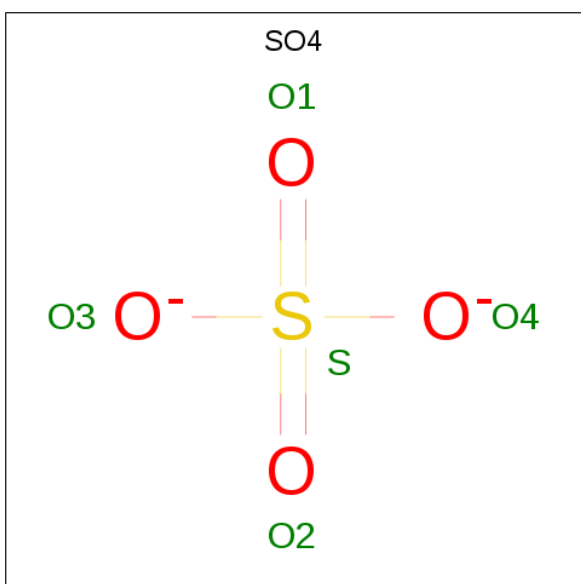
Chain	Residue	Modelled	Actual	Comment	Reference
A	20	SER	-	expression tag	UNP Q6RFZ0
A	21	ASN	-	expression tag	UNP Q6RFZ0
A	22	ALA	-	expression tag	UNP Q6RFZ0
B	20	SER	-	expression tag	UNP Q6RFZ0
B	21	ASN	-	expression tag	UNP Q6RFZ0
B	22	ALA	-	expression tag	UNP Q6RFZ0
C	20	SER	-	expression tag	UNP Q6RFZ0
C	21	ASN	-	expression tag	UNP Q6RFZ0
C	22	ALA	-	expression tag	UNP Q6RFZ0
D	20	SER	-	expression tag	UNP Q6RFZ0
D	21	ASN	-	expression tag	UNP Q6RFZ0
D	22	ALA	-	expression tag	UNP Q6RFZ0

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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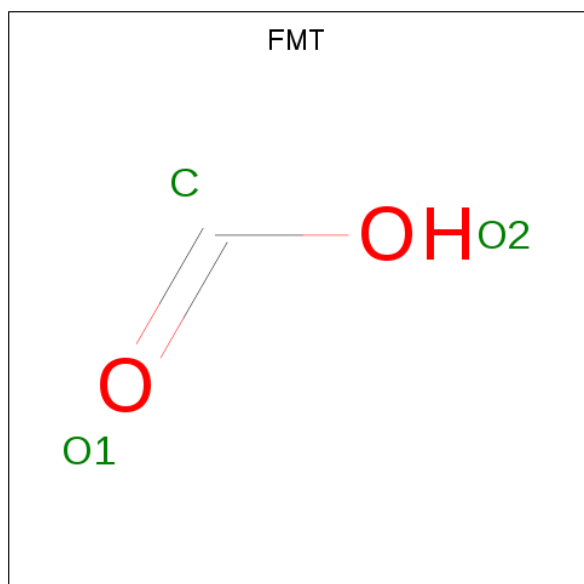
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Cl	0	0
			2	2		
4	A	1	Total	Cl	0	0
			1	1		
4	D	1	Total	Cl	0	0
			1	1		
4	C	2	Total	Cl	0	0
			2	2		

- Molecule 5 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



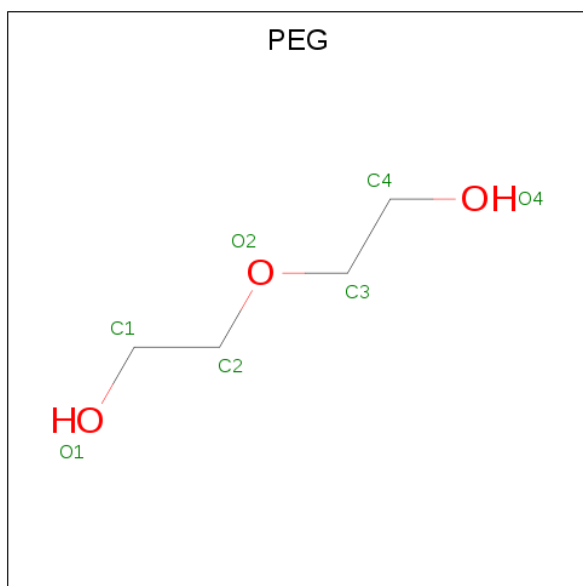
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			3	1	2		

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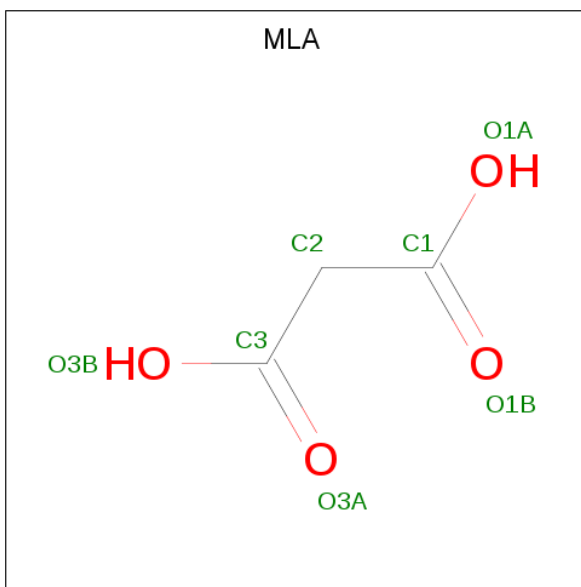
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		
5	B	1	Total	C	O	0	0
			3	1	2		
5	B	1	Total	C	O	0	0
			3	1	2		
5	C	1	Total	C	O	0	0
			3	1	2		
5	C	1	Total	C	O	0	0
			3	1	2		
5	D	1	Total	C	O	0	0
			3	1	2		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is MALONIC ACID (three-letter code: MLA) (formula: $C_3H_4O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	D	1	Total	C	O	0	0
			7	3	4		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	157	Total	O	0	1
			158	158		
8	B	112	Total	O	0	0
			112	112		
8	C	126	Total	O	0	0
			126	126		
8	D	139	Total	O	0	0
			139	139		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

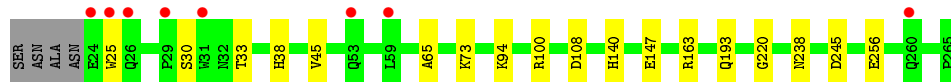
- Molecule 1: Beta-lactamase

Chain A: 



- Molecule 1: Beta-lactamase

Chain B: 



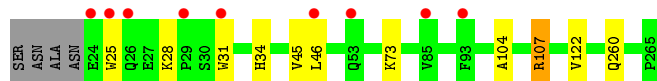
- Molecule 1: Beta-lactamase

Chain C: 



- Molecule 1: Beta-lactamase

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	174.33Å 61.39Å 122.80Å 90.00° 119.53° 90.00°	Depositor
Resolution (Å)	39.03 – 1.85 39.47 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.03-1.85) 99.7 (39.47-1.85)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 1.84Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.183 , 0.225 0.183 , 0.224	Depositor DCC
R_{free} test set	4831 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	22.8	Xtriage
Anisotropy	0.434	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 53.9	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	0.95	EDS
Total number of atoms	8674	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.78 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.2446e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: GOL, MLA, CL, FMT, SO4, PEG

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	0.52	0/2053	0.61	1/2778 (0.0%)
1	B	0.47	0/2028	0.59	0/2745
1	C	0.47	0/2025	0.57	0/2744
1	D	0.48	0/2038	0.59	0/2759
All	All	0.48	0/8144	0.59	1/11026 (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	221	TRP	CA-CB-CG	5.06	123.32	113.70

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	1997	0	1955	7	0
1	B	1978	0	1932	12	0
1	C	1975	0	1912	17	0
1	D	1982	0	1937	11	0
2	A	12	0	16	0	0
2	B	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	6	0	7	1	0
2	D	6	0	8	1	0
3	A	35	0	0	0	0
3	B	35	0	0	3	0
3	C	20	0	0	0	0
3	D	40	0	0	0	0
4	A	1	0	0	0	0
4	B	2	0	0	1	0
4	C	2	0	0	2	0
4	D	1	0	0	1	0
5	A	12	0	4	0	0
5	B	6	0	2	0	0
5	C	6	0	2	1	0
5	D	3	0	1	0	0
6	B	7	0	10	1	0
7	D	7	0	2	0	0
8	A	158	0	0	0	0
8	B	112	0	0	0	0
8	C	126	0	0	0	0
8	D	139	0	0	0	0
All	All	8674	0	7796	47	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 3.

All (47) 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:44:ILE:HD12	1:C:237:MET:HB3	1.38	1.03
1:D:104:ALA:HA	1:D:107:ARG:NH1	1.86	0.91
1:B:73:LYS:NZ	4:B:309:CL:CL	2.46	0.84
1:A:25:TRP:CZ3	1:A:45:VAL:HG13	2.26	0.71
1:C:237:MET:CE	1:C:239:MET:HE3	2.29	0.63
1:C:44:ILE:CD1	1:C:237:MET:HB3	2.24	0.61
1:C:239:MET:HE2	1:C:253:ILE:HD12	1.82	0.60
1:D:107:ARG:HD2	1:D:107:ARG:N	2.16	0.60
1:C:44:ILE:HD12	1:C:237:MET:CB	2.22	0.60
1:C:25:TRP:CZ3	1:C:45:VAL:HG13	2.38	0.59
1:C:239:MET:CE	1:C:253:ILE:HD12	2.32	0.59
1:B:140:HIS:HD2	1:B:147:GLU:OE1	1.88	0.56
1:B:100:ARG:HD3	6:B:313:PEG:H12	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:SER:O	1:B:33:THR:HG22	2.07	0.54
1:D:104:ALA:HA	1:D:107:ARG:HH11	1.69	0.53
1:C:23:ASN:HA	1:C:47:TRP:HH2	1.75	0.51
1:C:242:PRO:HD2	4:C:307:CL:CL	2.47	0.51
1:A:23:ASN:HB3	1:A:47:TRP:CH2	2.46	0.51
1:D:25:TRP:CZ3	1:D:45:VAL:HG13	2.45	0.51
1:D:104:ALA:O	1:D:107:ARG:HD3	2.12	0.50
1:B:25:TRP:CZ3	1:B:45:VAL:HG13	2.47	0.50
1:C:30:SER:O	1:C:33:THR:HG22	2.13	0.49
1:C:237:MET:HE3	1:C:239:MET:HE3	1.94	0.48
1:D:107:ARG:CD	1:D:107:ARG:N	2.78	0.47
1:B:65:ALA:HB1	1:B:163:ARG:HB3	1.96	0.47
1:C:168:GLU:O	5:C:309:FMT:H	2.14	0.47
1:A:25:TRP:CE3	1:A:54:GLY:HA3	2.50	0.47
1:C:237:MET:HE1	1:C:239:MET:HE3	1.96	0.47
1:B:30:SER:OG	3:B:307:SO4:O3	2.27	0.46
1:B:193:GLN:HG3	3:B:305:SO4:O3	2.15	0.46
1:D:73:LYS:NZ	4:D:310:CL:CL	2.74	0.45
1:B:94:LYS:HD2	1:B:108:ASP:CG	2.38	0.45
1:B:220:GLY:O	1:B:238:ASN:HA	2.18	0.44
1:D:34:HIS:NE2	1:D:260:GLN:OE1	2.42	0.44
1:D:31:TRP:CH2	1:D:46:LEU:HD12	2.52	0.44
1:C:73:LYS:HE3	1:C:123:TYR:CD1	2.53	0.43
1:B:193:GLN:HA	3:B:305:SO4:O3	2.18	0.43
1:C:73:LYS:NZ	4:C:306:CL:CL	2.74	0.42
1:D:122:VAL:HA	2:D:301:GOL:C1	2.49	0.42
1:D:28:LYS:HB3	1:D:28:LYS:HE3	1.85	0.42
1:A:65:ALA:HB1	1:A:163:ARG:HB3	2.02	0.42
1:B:38:HIS:NE2	1:B:256:GLU:OE2	2.46	0.42
1:A:134:ARG:O	1:A:138:MET:HG2	2.20	0.42
1:C:220:GLY:O	1:C:238:ASN:HA	2.19	0.42
1:A:124:GLN:HG2	1:A:154:ASP:O	2.20	0.41
1:A:47:TRP:HB3	1:A:234:PHE:HB2	2.03	0.40
1:C:121:PRO:HB2	2:C:301:GOL:H31	2.03	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	
1	A	243/246 (99%)	239 (98%)	3 (1%)	1 (0%)	34	19
1	B	240/246 (98%)	235 (98%)	5 (2%)	0	100	100
1	C	241/246 (98%)	238 (99%)	3 (1%)	0	100	100
1	D	242/246 (98%)	238 (98%)	4 (2%)	0	100	100
All	All	966/984 (98%)	950 (98%)	15 (2%)	1 (0%)	51	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	24	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	
1	A	212/212 (100%)	209 (99%)	3 (1%)	67	55
1	B	209/212 (99%)	208 (100%)	1 (0%)	88	86
1	C	207/212 (98%)	205 (99%)	2 (1%)	76	69
1	D	210/212 (99%)	209 (100%)	1 (0%)	88	86
All	All	838/848 (99%)	831 (99%)	7 (1%)	81	76

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53(A)	GLN
1	A	82	ASP
1	A	118	SER
1	B	245	ASP
1	C	60	LYS
1	C	107	ARG
1	D	107	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	53	GLN
1	B	140	HIS
1	C	260	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 48 ligands modelled in this entry, 6 are monoatomic - leaving 42 for Mogul analysis.

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
5	FMT	B	311	-	0,2,2	0.00	-	0,1,1	0.00	-
3	SO4	A	303	-	4,4,4	0.08	0	6,6,6	0.43	0
2	GOL	C	301	-	5,5,5	1.32	1 (20%)	5,5,5	0.71	0
3	SO4	B	306	-	4,4,4	0.13	0	6,6,6	0.22	0
3	SO4	D	302	-	4,4,4	0.22	0	6,6,6	0.42	0
7	MLA	D	312	-	0,6,6	0.00	-	0,7,7	0.00	-
3	SO4	A	309	-	4,4,4	0.14	0	6,6,6	0.22	0
3	SO4	C	305	-	4,4,4	0.18	0	6,6,6	0.13	0
3	SO4	C	302	-	4,4,4	0.13	0	6,6,6	0.29	0
3	SO4	A	306	-	4,4,4	0.13	0	6,6,6	0.25	0
3	SO4	B	304	-	4,4,4	0.15	0	6,6,6	0.20	0
3	SO4	D	308	-	4,4,4	0.12	0	6,6,6	0.12	0
2	GOL	D	301	-	5,5,5	0.99	0	5,5,5	1.04	0
3	SO4	D	304	-	4,4,4	0.13	0	6,6,6	0.10	0
3	SO4	A	307	-	4,4,4	0.15	0	6,6,6	0.07	0
5	FMT	D	311	-	0,2,2	0.00	-	0,1,1	0.00	-
2	GOL	A	301	-	5,5,5	1.04	0	5,5,5	0.75	0
3	SO4	A	304	-	4,4,4	0.12	0	6,6,6	0.22	0
3	SO4	B	305	-	4,4,4	0.74	0	6,6,6	1.19	1 (16%)
6	PEG	B	313	-	6,6,6	0.48	0	5,5,5	0.29	0
3	SO4	D	309	-	4,4,4	0.15	0	6,6,6	0.10	0
3	SO4	C	304	-	4,4,4	0.16	0	6,6,6	0.11	0
3	SO4	D	307	-	4,4,4	0.14	0	6,6,6	0.07	0
3	SO4	A	308	-	4,4,4	0.14	0	6,6,6	0.10	0
3	SO4	B	303	-	4,4,4	0.15	0	6,6,6	0.29	0
3	SO4	D	306	-	4,4,4	0.16	0	6,6,6	0.08	0
2	GOL	A	302	-	5,5,5	0.76	0	5,5,5	0.94	0
3	SO4	C	303	-	4,4,4	0.16	0	6,6,6	0.16	0
3	SO4	D	303	-	4,4,4	0.44	0	6,6,6	1.20	1 (16%)
3	SO4	A	305	-	4,4,4	0.16	0	6,6,6	0.10	0
3	SO4	D	305	-	4,4,4	0.14	0	6,6,6	0.10	0
5	FMT	A	314	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	311	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	B	312	-	0,2,2	0.00	-	0,1,1	0.00	-
3	SO4	B	308	-	4,4,4	0.12	0	6,6,6	0.10	0
2	GOL	B	301	-	5,5,5	0.80	0	5,5,5	1.18	0
3	SO4	B	307	-	4,4,4	0.13	0	6,6,6	0.13	0
5	FMT	A	313	-	0,2,2	0.00	-	0,1,1	0.00	-
3	SO4	B	302	-	4,4,4	0.14	0	6,6,6	0.07	0
5	FMT	A	312	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	C	309	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	C	308	-	0,2,2	0.00	-	0,1,1	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	D	301	-	-	4/4/4/4	-
2	GOL	B	301	-	-	2/4/4/4	-
2	GOL	C	301	-	-	2/4/4/4	-
2	GOL	A	301	-	-	0/4/4/4	-
2	GOL	A	302	-	-	1/4/4/4	-
7	MLA	D	312	-	-	0/0/4/4	-
6	PEG	B	313	-	-	1/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	GOL	O2-C2	-2.13	1.37	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	305	SO4	O3-S-O1	-2.38	96.87	109.31
3	D	303	SO4	O3-S-O1	-2.28	97.39	109.31

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	301	GOL	C1-C2-C3-O3
2	B	301	GOL	C1-C2-C3-O3
2	D	301	GOL	O1-C1-C2-O2
2	D	301	GOL	O1-C1-C2-C3
2	D	301	GOL	O2-C2-C3-O3
2	C	301	GOL	O1-C1-C2-O2
2	B	301	GOL	O2-C2-C3-O3
6	B	313	PEG	C1-C2-O2-C3
2	A	302	GOL	O2-C2-C3-O3
2	C	301	GOL	O1-C1-C2-C3

There are no ring outliers.

6 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	301	GOL	1	0
2	D	301	GOL	1	0
3	B	305	SO4	2	0
6	B	313	PEG	1	0
3	B	307	SO4	1	0
5	C	309	FMT	1	0

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	243/246 (98%)	-0.04	4 (1%) 72 72	16, 24, 37, 80	0
1	B	242/246 (98%)	0.20	8 (3%) 46 44	17, 27, 51, 77	0
1	C	243/246 (98%)	0.11	7 (2%) 51 50	17, 28, 45, 86	0
1	D	242/246 (98%)	0.18	9 (3%) 41 39	16, 25, 42, 84	0
All	All	970/984 (98%)	0.11	28 (2%) 51 50	16, 26, 45, 86	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	25	TRP	5.2
1	D	24	GLU	5.2
1	D	26	GLN	3.9
1	C	23	ASN	3.8
1	B	29	PRO	3.4
1	B	26	GLN	3.4
1	D	25	TRP	3.2
1	A	23	ASN	3.2
1	C	140	HIS	3.2
1	B	31	TRP	3.1
1	D	31	TRP	3.0
1	B	53	GLN	3.0
1	B	24	GLU	2.9
1	D	93	PHE	2.8
1	D	29	PRO	2.8
1	C	133	ALA	2.7
1	C	194	ALA	2.7
1	D	46	LEU	2.6
1	D	85	VAL	2.6
1	A	190	ILE	2.6
1	A	243	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	260	GLN	2.3
1	C	245	ASP	2.3
1	C	101	ASP	2.3
1	B	59	LEU	2.3
1	C	24	GLU	2.2
1	D	53	GLN	2.2
1	A	194	ALA	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 carbohydrates 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
5	FMT	D	311	3/3	0.45	0.19	53,53,57,60	0
2	GOL	A	302	6/6	0.71	0.17	56,58,59,60	0
5	FMT	A	313	3/3	0.75	0.16	46,46,46,51	0
5	FMT	C	309	3/3	0.76	0.22	61,61,62,64	0
5	FMT	B	311	3/3	0.77	0.14	49,49,53,53	0
6	PEG	B	313	7/7	0.81	0.17	46,54,57,58	0
3	SO4	D	307	5/5	0.83	0.15	89,90,91,93	5
3	SO4	B	307	5/5	0.83	0.20	86,93,93,97	0
3	SO4	B	306	5/5	0.85	0.17	74,80,83,84	0
3	SO4	C	304	5/5	0.86	0.24	88,90,93,94	0
2	GOL	C	301	6/6	0.86	0.20	33,43,49,55	0
4	CL	C	307	1/1	0.86	0.06	69,69,69,69	0
5	FMT	A	312	3/3	0.87	0.14	53,53,53,54	0
3	SO4	A	305	5/5	0.87	0.15	71,73,76,79	0
5	FMT	B	312	3/3	0.88	0.12	61,61,62,62	0
3	SO4	D	305	5/5	0.89	0.23	89,89,93,95	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SO4	A	307	5/5	0.89	0.14	95,96,98,98	0
3	SO4	A	309	5/5	0.90	0.36	78,82,85,87	0
3	SO4	D	308	5/5	0.90	0.21	84,88,90,92	0
5	FMT	C	308	3/3	0.90	0.13	43,43,49,51	0
3	SO4	A	308	5/5	0.91	0.28	86,88,90,91	0
3	SO4	A	304	5/5	0.91	0.20	58,65,67,69	0
2	GOL	B	301	6/6	0.91	0.11	32,35,41,43	0
3	SO4	D	309	5/5	0.91	0.20	62,70,73,76	0
3	SO4	B	308	5/5	0.92	0.27	79,81,83,84	0
3	SO4	D	306	5/5	0.92	0.27	84,86,89,92	0
2	GOL	D	301	6/6	0.92	0.18	24,34,39,48	0
3	SO4	D	303	5/5	0.92	0.19	27,31,40,46	5
7	MLA	D	312	7/7	0.92	0.11	49,51,56,57	0
3	SO4	B	305	5/5	0.92	0.19	17,35,41,48	5
5	FMT	A	314	3/3	0.92	0.14	64,64,66,66	0
3	SO4	B	302	5/5	0.93	0.24	85,88,90,90	0
3	SO4	C	305	5/5	0.93	0.14	46,48,52,56	5
5	FMT	A	311	3/3	0.93	0.12	31,31,35,39	0
3	SO4	B	304	5/5	0.93	0.10	42,51,61,64	0
3	SO4	A	306	5/5	0.94	0.16	66,75,83,85	0
2	GOL	A	301	6/6	0.94	0.13	30,41,45,45	0
4	CL	B	310	1/1	0.94	0.13	60,60,60,60	0
3	SO4	C	303	5/5	0.96	0.14	62,64,67,70	0
3	SO4	D	304	5/5	0.96	0.21	78,79,83,84	0
4	CL	D	310	1/1	0.97	0.08	27,27,27,27	0
4	CL	C	306	1/1	0.97	0.07	33,33,33,33	0
3	SO4	C	302	5/5	0.98	0.07	29,33,35,36	0
4	CL	B	309	1/1	0.98	0.07	38,38,38,38	0
3	SO4	D	302	5/5	0.98	0.12	25,30,33,35	0
3	SO4	B	303	5/5	0.98	0.14	30,41,48,49	0
4	CL	A	310	1/1	0.99	0.06	28,28,28,28	0
3	SO4	A	303	5/5	0.99	0.06	27,29,31,35	0

6.5 Other polymers ⓘ

There are no such residues in this entry.