



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 03:05 PM UTC

PDB ID : 6NFP / pdb_00006nfp
Title : 1.7 Angstrom Resolution Crystal Structure of Arginase from Bacillus subtilis subsp. subtilis str. 168
Authors : Minasov, G.; Wawrzak, Z.; Evdokimova, E.; Grimshaw, S.; Kwon, K.; Savchenko, A.; Satchell, K.J.F.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2018-12-20
Resolution : 1.70 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

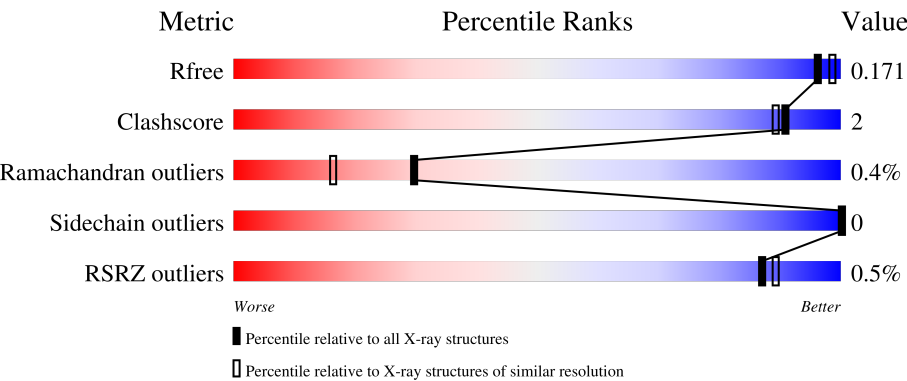
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	299	93%5%.
1	B	299	% 94%. .
1	C	299	92%. .
1	D	299	91%6%.

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Mol	Chain	Length	Quality of chain
1	E	299	%  93% • •
1	F	299	%  93% • •

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	GOA	C	315	-	X	-	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 15539 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 Arginase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	11	0
			2310	1454	391	454	11			
1	B	290	Total	C	N	O	S	0	4	0
			2231	1402	377	440	12			
1	C	290	Total	C	N	O	S	0	7	0
			2260	1420	380	449	11			
1	D	289	Total	C	N	O	S	0	8	0
			2257	1420	378	447	12			
1	E	287	Total	C	N	O	S	0	6	0
			2229	1404	373	441	11			
1	F	289	Total	C	N	O	S	0	5	0
			2237	1406	377	443	11			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP P39138
A	-1	ASN	-	expression tag	UNP P39138
A	0	ALA	-	expression tag	UNP P39138
B	-2	SER	-	expression tag	UNP P39138
B	-1	ASN	-	expression tag	UNP P39138
B	0	ALA	-	expression tag	UNP P39138
C	-2	SER	-	expression tag	UNP P39138
C	-1	ASN	-	expression tag	UNP P39138
C	0	ALA	-	expression tag	UNP P39138
D	-2	SER	-	expression tag	UNP P39138
D	-1	ASN	-	expression tag	UNP P39138
D	0	ALA	-	expression tag	UNP P39138
E	-2	SER	-	expression tag	UNP P39138
E	-1	ASN	-	expression tag	UNP P39138
E	0	ALA	-	expression tag	UNP P39138
F	-2	SER	-	expression tag	UNP P39138
F	-1	ASN	-	expression tag	UNP P39138

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Chain	Residue	Modelled	Actual	Comment	Reference
F	0	ALA	-	expression tag	UNP P39138

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total Cl 4 4	0	0
2	B	1	Total Cl 1 1	0	0
2	C	3	Total Cl 3 3	0	0
2	D	1	Total Cl 1 1	0	0
2	E	1	Total Cl 1 1	0	0

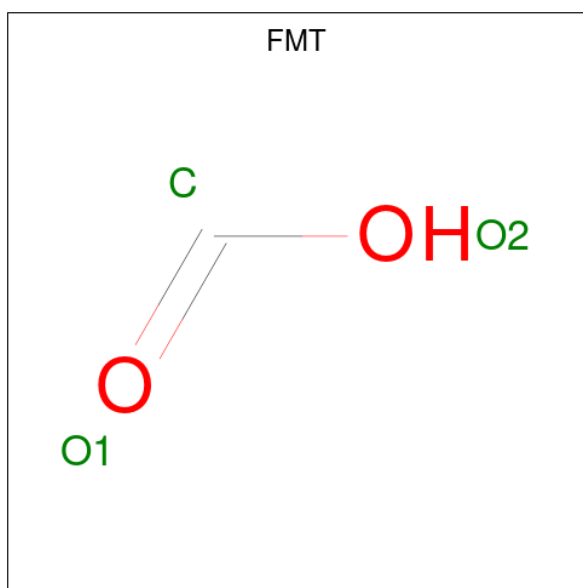
- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Na 1 1	0	0
3	B	1	Total Na 1 1	0	0
3	E	1	Total Na 1 1	0	0

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Mg 2 2	0	0
4	B	2	Total Mg 2 2	0	0
4	C	2	Total Mg 2 2	0	0
4	D	2	Total Mg 2 2	0	0
4	E	2	Total Mg 2 2	0	0
4	F	2	Total Mg 2 2	0	0

- Molecule 5 is FORMIC ACID (CCD ID: FMT) (formula: CH_2O_2).



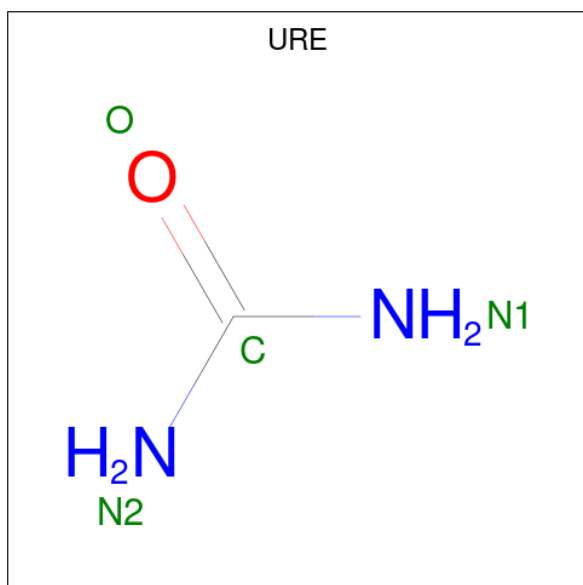
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		
5	B	1	Total	C	O	0	0
			3	1	2		
5	B	1	Total	C	O	0	0
			3	1	2		
5	B	1	Total	C	O	0	0
			3	1	2		
5	D	1	Total	C	O	0	0
			3	1	2		
5	D	1	Total	C	O	0	0
			3	1	2		
5	D	1	Total	C	O	0	0
			3	1	2		
5	E	1	Total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

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

- Molecule 6 is UREA (CCD ID: URE) (formula: CH₄N₂O).



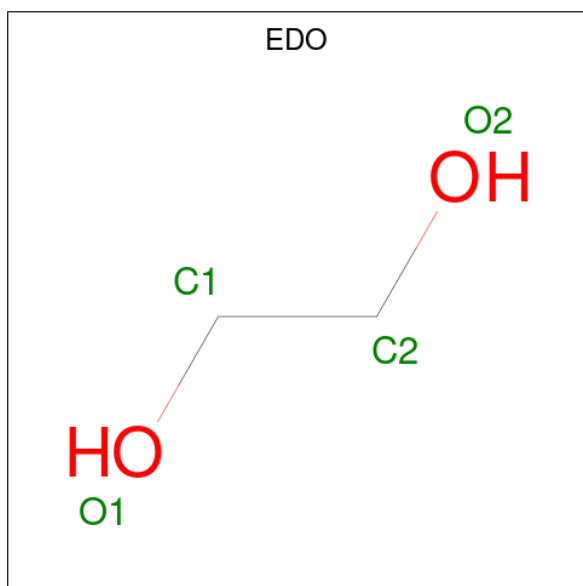
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			4	1	2	1		
6	A	1	Total	C	N	O	0	0
			4	1	2	1		
6	A	1	Total	C	N	O	0	0
			4	1	2	1		
6	B	1	Total	C	N	O	0	0
			4	1	2	1		
6	B	1	Total	C	N	O	0	0
			4	1	2	1		
6	B	1	Total	C	N	O	0	0
			4	1	2	1		
6	C	1	Total	C	N	O	0	0
			4	1	2	1		
6	C	1	Total	C	N	O	0	0
			4	1	2	1		
6	C	1	Total	C	N	O	0	0
			4	1	2	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total 4	C 1	N 2	O 1	0	0
6	C	1	Total 4	C 1	N 2	O 1	0	0
6	C	1	Total 4	C 1	N 2	O 1	0	0
6	E	1	Total 4	C 1	N 2	O 1	0	0
6	E	1	Total 4	C 1	N 2	O 1	0	0
6	F	1	Total 4	C 1	N 2	O 1	0	0
6	F	1	Total 4	C 1	N 2	O 1	0	0

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



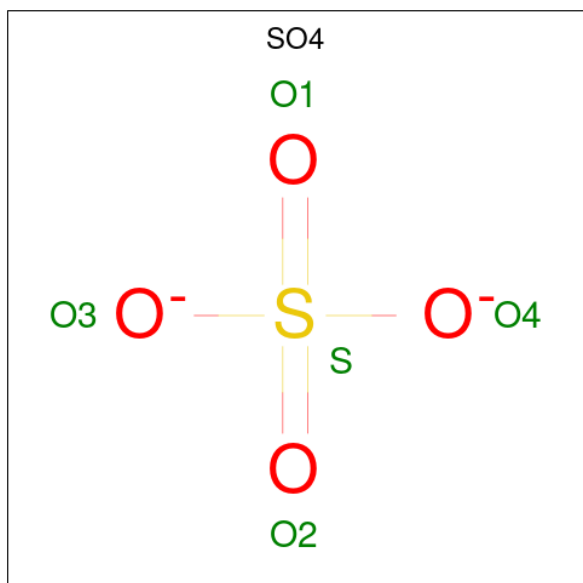
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total 4	C 2	O 2	0	0
7	A	1	Total 4	C 2	O 2	0	0
7	A	1	Total 4	C 2	O 2	0	0
7	A	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	C	1	Total	C	O	0	0
			4	2	2		
7	C	1	Total	C	O	0	0
			4	2	2		
7	C	1	Total	C	O	0	0
			4	2	2		
7	D	1	Total	C	O	0	0
			4	2	2		
7	E	1	Total	C	O	0	0
			4	2	2		
7	F	1	Total	C	O	0	0
			4	2	2		
7	F	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



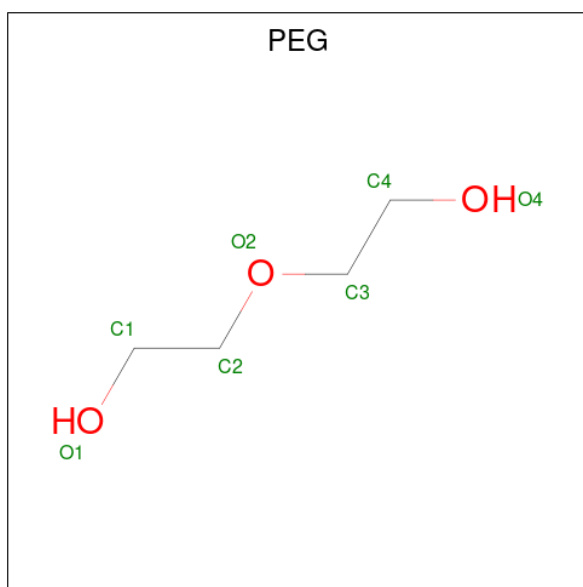
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	S	0	0
			5	4	1		

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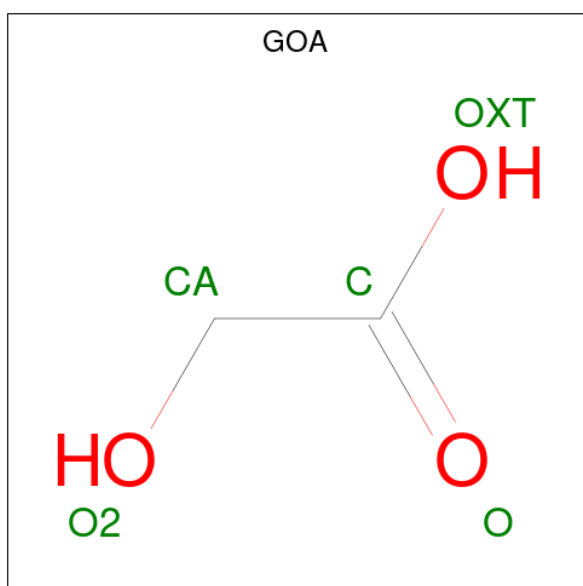
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	S	0	0
			5	4	1		
8	B	1	Total	O	S	0	0
			5	4	1		
8	B	1	Total	O	S	0	0
			5	4	1		
8	B	1	Total	O	S	0	0
			5	4	1		
8	B	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	D	1	Total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

- Molecule 9 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



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

- Molecule 10 is GLYCOLIC ACID (CCD ID: GOA) (formula: $C_2H_4O_3$).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	D	1	Total	C	O	0	0
			5	2	3		
10	F	1	Total	C	O	0	0
			5	2	3		

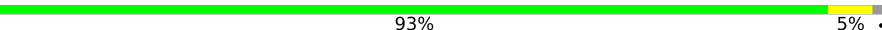
- Molecule 11 is water.

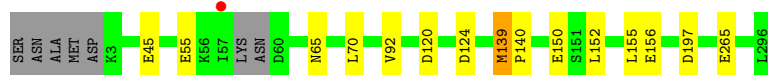
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	294	Total	O	0	23
			311	311		
11	B	273	Total	O	0	21
			291	291		
11	C	291	Total	O	0	12
			301	301		
11	D	275	Total	O	0	15
			287	287		
11	E	243	Total	O	0	11
			253	253		
11	F	247	Total	O	0	13
			258	258		

3 Residue-property plots [i](#)

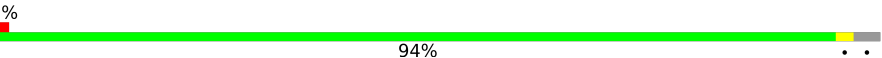
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Arginase

Chain A:  93% 5% .



- Molecule 1: Arginase

Chain B:  94% . .



- Molecule 1: Arginase

Chain C:  92% . .



- Molecule 1: Arginase

Chain D:  91% 6% .

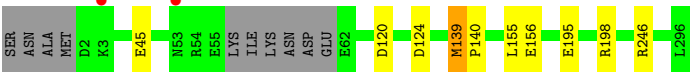
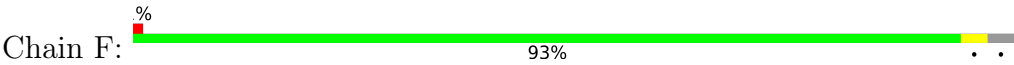


- Molecule 1: Arginase

Chain E:  93% . .



- Molecule 1: Arginase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.41Å 143.99Å 85.52Å 90.00° 109.35° 90.00°	Depositor
Resolution (Å)	29.99 – 1.70 29.99 – 1.70	Depositor EDS
% Data completeness (in resolution range)	94.3 (29.99-1.70) 94.3 (29.99-1.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.139 , 0.166 0.148 , 0.171	Depositor DCC
R_{free} test set	9706 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	26.1	Xtriage
Anisotropy	0.249	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.024 for l,-k,h	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	15539	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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: GOA, CL, NA, EDO, PEG, URE, FMT, MG, 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	1.00	0/2344	1.14	2/3162 (0.1%)
1	B	1.02	0/2266	1.16	1/3063 (0.0%)
1	C	1.02	0/2294	1.13	2/3100 (0.1%)
1	D	1.01	0/2291	1.18	1/3096 (0.0%)
1	E	1.00	0/2264	1.16	2/3061 (0.1%)
1	F	1.01	0/2271	1.16	1/3069 (0.0%)
All	All	1.01	0/13730	1.15	9/18551 (0.0%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	120	ASP	CA-CB-CG	6.53	119.13	112.60
1	C	120	ASP	CA-CB-CG	5.72	118.32	112.60
1	F	120	ASP	CA-CB-CG	5.62	118.22	112.60
1	A	197	ASP	CA-CB-CG	5.54	118.14	112.60
1	D	120	ASP	CA-CB-CG	5.50	118.10	112.60
1	A	120	ASP	CA-CB-CG	5.26	117.86	112.60
1	B	120	ASP	CA-CB-CG	5.17	117.77	112.60
1	E	197	ASP	CA-CB-CG	5.15	117.75	112.60
1	C	197	ASP	CA-CB-CG	5.05	117.66	112.60

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	2310	0	2334	8	0
1	B	2231	0	2237	6	0
1	C	2260	0	2263	8	0
1	D	2257	0	2264	10	0
1	E	2229	0	2233	7	0
1	F	2237	0	2242	8	0
2	A	4	0	0	0	0
2	B	1	0	0	0	0
2	C	3	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
5	A	6	0	2	0	0
5	B	9	0	3	0	0
5	D	12	0	4	0	0
5	E	12	0	4	0	0
5	F	6	0	2	0	0
6	A	12	0	12	1	0
6	B	12	0	12	0	0
6	C	24	0	24	2	0
6	E	8	0	8	0	0
6	F	8	0	8	0	0
7	A	20	0	30	0	0
7	B	8	0	12	0	0
7	C	12	0	18	1	0
7	D	4	0	6	0	0
7	E	4	0	6	1	0
7	F	8	0	12	0	0
8	A	10	0	0	0	0
8	B	20	0	0	0	0
8	C	15	0	0	0	0
8	D	20	0	0	0	0
8	E	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	F	10	0	0	0	0
9	B	14	0	20	0	0
10	C	10	0	0	0	0
10	D	5	0	0	0	0
10	F	5	0	0	0	0
11	A	311	0	0	2	0
11	B	291	0	0	0	0
11	C	301	0	0	0	0
11	D	287	0	0	1	0
11	E	253	0	0	1	0
11	F	258	0	0	0	0
All	All	15539	0	13756	48	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 (48) 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:E:177:GLU:H	1:E:177:GLU:CD	1.94	0.75
1:C:203:LYS:HE3	1:C:207:GLU:OE2	1.96	0.65
1:B:124:ASP:HB3	1:B:140:PRO:HD2	1.83	0.60
1:E:177:GLU:CD	1:E:177:GLU:N	2.60	0.60
1:A:55[B]:GLU:OE2	1:A:65:ASN:HA	2.01	0.59
1:F:139:MET:N	1:F:140:PRO:CD	2.65	0.59
7:C:313:EDO:H11	1:F:246:ARG:HG2	1.83	0.58
1:D:150:GLU:H	1:D:150:GLU:CD	2.12	0.57
1:C:124:ASP:HB3	1:C:140:PRO:HD2	1.87	0.55
1:C:139:MET:N	1:C:140:PRO:CD	2.70	0.55
1:F:139:MET:N	1:F:140:PRO:HD2	2.22	0.54
1:C:5[B]:ILE:HD13	1:C:291[B]:LEU:HD13	1.88	0.54
1:A:70[B]:LEU:CD2	1:A:152:LEU:HD23	2.37	0.54
1:D:124:ASP:HB3	1:D:140:PRO:HD2	1.90	0.54
1:E:139:MET:N	1:E:140:PRO:CD	2.73	0.52
1:B:139:MET:N	1:B:140:PRO:CD	2.72	0.52
1:C:155:LEU:HG	1:C:156:GLU:HG2	1.91	0.52
1:A:139:MET:N	1:A:140:PRO:CD	2.73	0.51
1:D:139:MET:N	1:D:140:PRO:CD	2.73	0.51
1:F:139:MET:H	1:F:140:PRO:CD	2.23	0.51
1:A:124:ASP:HB3	1:A:140:PRO:HD2	1.93	0.50
1:A:155:LEU:HG	1:A:156:GLU:HG2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:288:GLU:OE1	6:C:307:URE:N2	2.45	0.50
1:F:45[B]:GLU:O	1:F:45[B]:GLU:HG3	2.14	0.48
6:A:312:URE:N2	11:A:403:HOH:O	2.35	0.48
1:B:246:ARG:HG2	7:E:311:EDO:H22	1.96	0.48
1:B:74:GLU:HG2	1:B:155:LEU:HD11	1.96	0.47
1:E:139:MET:N	1:E:140:PRO:HD2	2.30	0.46
1:F:124:ASP:HB3	1:F:140:PRO:HD2	1.98	0.45
1:D:1:MET:CE	1:D:5:ILE:HD11	2.47	0.44
1:D:203:LYS:O	1:D:207:GLU:HG3	2.18	0.44
1:F:155:LEU:HG	1:F:156:GLU:HG2	1.99	0.44
1:A:45[B]:GLU:O	1:A:45[B]:GLU:HG3	2.17	0.43
1:D:74[A]:GLU:HG2	1:D:155:LEU:HD11	2.00	0.43
1:D:10:MET:HG3	1:D:76:LEU:HD22	1.99	0.43
1:F:195:GLU:OE1	1:F:198:ARG:NH2	2.51	0.43
1:A:150:GLU:HG2	11:A:610:HOH:O	2.19	0.42
1:E:3:LYS:HD2	11:E:631:HOH:O	2.20	0.42
1:B:45[A]:GLU:O	1:B:45[A]:GLU:HG3	2.18	0.42
1:A:92:VAL:O	1:A:265:GLU:HA	2.20	0.42
1:D:92:VAL:O	1:D:265:GLU:HA	2.19	0.41
1:C:86:GLU:OE1	6:C:311:URE:N1	2.53	0.41
1:D:206:GLU:OE1	11:D:401:HOH:O	2.22	0.41
1:E:146:GLY:HA2	1:E:153:VAL:HG13	2.00	0.41
1:D:146:GLY:HA2	1:D:153:VAL:HG13	2.01	0.41
1:E:92:VAL:O	1:E:265:GLU:HA	2.20	0.40
1:B:74:GLU:CG	1:B:155:LEU:HD11	2.52	0.40
1:C:74:GLU:HG2	1:C:155:LEU:HD11	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	298/299 (100%)	288 (97%)	9 (3%)	1 (0%)	36	22
1	B	290/299 (97%)	282 (97%)	7 (2%)	1 (0%)	36	22
1	C	293/299 (98%)	286 (98%)	6 (2%)	1 (0%)	36	22
1	D	293/299 (98%)	284 (97%)	8 (3%)	1 (0%)	36	22
1	E	289/299 (97%)	284 (98%)	4 (1%)	1 (0%)	36	22
1	F	290/299 (97%)	283 (98%)	6 (2%)	1 (0%)	36	22
All	All	1753/1794 (98%)	1707 (97%)	40 (2%)	6 (0%)	30	22

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	139	MET
1	F	139	MET
1	A	139	MET
1	C	139	MET
1	D	139	MET
1	E	139	MET

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	254/249 (102%)	254 (100%)	0	100	100
1	B	244/249 (98%)	244 (100%)	0	100	100
1	C	248/249 (100%)	248 (100%)	0	100	100
1	D	247/249 (99%)	247 (100%)	0	100	100
1	E	244/249 (98%)	244 (100%)	0	100	100
1	F	245/249 (98%)	245 (100%)	0	100	100
All	All	1482/1494 (99%)	1482 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	HIS
1	B	149	HIS
1	C	149	HIS
1	E	32	HIS
1	E	149	HIS
1	F	32	HIS

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 94 ligands modelled in this entry, 25 are monoatomic - leaving 69 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	$\# Z > 2$
6	URE	B	309	-	3,3,3	0.14	0	3,3,3	0.04	0
8	SO4	F	310	4	4,4,4	0.32	0	6,6,6	0.09	0
10	GOA	D	309	-	4,4,4	1.05	0	4,4,4	2.06	1 (25%)
6	URE	C	308	-	3,3,3	0.14	0	3,3,3	0.04	0
6	URE	B	310	-	3,3,3	0.14	0	3,3,3	0.03	0
8	SO4	D	310	4	4,4,4	0.32	0	6,6,6	0.09	0
7	EDO	F	308	-	3,3,3	0.06	0	2,2,2	0.17	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	FMT	F	304	-	2,2,2	0.29	0	1,1,1	0.14	0
6	URE	F	305	-	3,3,3	0.11	0	3,3,3	0.04	0
7	EDO	D	308	-	3,3,3	0.11	0	2,2,2	0.23	0
8	SO4	E	312	4	4,4,4	0.35	0	6,6,6	0.08	0
5	FMT	D	307	-	2,2,2	0.28	0	1,1,1	0.14	0
7	EDO	C	312	-	3,3,3	0.11	0	2,2,2	0.07	0
5	FMT	E	308	-	2,2,2	0.24	0	1,1,1	0.16	0
7	EDO	A	315	-	3,3,3	0.08	0	2,2,2	0.13	0
8	SO4	B	313	4	4,4,4	0.34	0	6,6,6	0.07	0
7	EDO	A	314	-	3,3,3	0.08	0	2,2,2	0.12	0
8	SO4	B	314	-	4,4,4	0.34	0	6,6,6	0.08	0
8	SO4	B	315	-	4,4,4	0.35	0	6,6,6	0.09	0
8	SO4	C	319	-	4,4,4	0.33	0	6,6,6	0.07	0
9	PEG	B	318	-	6,6,6	0.15	0	5,5,5	0.10	0
5	FMT	F	303	-	2,2,2	0.27	0	1,1,1	0.16	0
7	EDO	A	316	-	3,3,3	0.12	0	2,2,2	0.24	0
5	FMT	E	305	-	2,2,2	0.43	0	1,1,1	0.13	0
5	FMT	B	305	-	2,2,2	0.40	0	1,1,1	0.15	0
5	FMT	B	307	-	2,2,2	0.26	0	1,1,1	0.16	0
5	FMT	D	304	-	2,2,2	0.34	0	1,1,1	0.16	0
5	FMT	D	306	-	2,2,2	0.27	0	1,1,1	0.16	0
8	SO4	C	318	4	4,4,4	0.33	0	6,6,6	0.08	0
6	URE	A	310	-	3,3,3	0.29	0	3,3,3	0.15	0
10	GOA	C	315	-	4,4,4	1.01	0	4,4,4	2.43	2 (50%)
6	URE	A	312	-	3,3,3	0.20	0	3,3,3	0.08	0
7	EDO	B	312	-	3,3,3	0.08	0	2,2,2	0.07	0
6	URE	C	310	-	3,3,3	0.16	0	3,3,3	0.05	0
7	EDO	C	314	-	3,3,3	0.15	0	2,2,2	0.12	0
8	SO4	A	319	-	4,4,4	0.34	0	6,6,6	0.08	0
7	EDO	E	311	-	3,3,3	0.10	0	2,2,2	0.23	0
8	SO4	A	318	4	4,4,4	0.32	0	6,6,6	0.09	0
7	EDO	C	313	-	3,3,3	0.07	0	2,2,2	0.22	0
10	GOA	F	309	-	4,4,4	1.14	0	4,4,4	2.21	1 (25%)
6	URE	C	309	-	3,3,3	0.18	0	3,3,3	0.03	0
8	SO4	D	311	-	4,4,4	0.35	0	6,6,6	0.08	0
8	SO4	B	316	-	4,4,4	0.36	0	6,6,6	0.09	0
6	URE	C	307	-	3,3,3	0.12	0	3,3,3	0.15	0
9	PEG	B	317	-	6,6,6	0.16	0	5,5,5	0.08	0
6	URE	C	311	-	3,3,3	0.12	0	3,3,3	0.05	0
7	EDO	F	307	-	3,3,3	0.08	0	2,2,2	0.13	0
7	EDO	A	317	-	3,3,3	0.11	0	2,2,2	0.22	0
10	GOA	C	316	-	4,4,4	0.98	0	4,4,4	2.27	1 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	URE	E	310	-	3,3,3	0.22	0	3,3,3	0.04	0
7	EDO	B	311	-	3,3,3	0.10	0	2,2,2	0.19	0
6	URE	C	306	-	3,3,3	0.18	0	3,3,3	0.09	0
8	SO4	F	311	-	4,4,4	0.33	0	6,6,6	0.07	0
5	FMT	A	308	-	2,2,2	0.43	0	1,1,1	0.11	0
8	SO4	D	312	-	4,4,4	0.36	0	6,6,6	0.07	0
5	FMT	A	309	-	2,2,2	0.34	0	1,1,1	0.13	0
6	URE	A	311	-	3,3,3	0.13	0	3,3,3	0.04	0
5	FMT	B	306	-	2,2,2	0.23	0	1,1,1	0.16	0
6	URE	E	309	-	3,3,3	0.21	0	3,3,3	0.06	0
5	FMT	E	306	-	2,2,2	0.22	0	1,1,1	0.17	0
8	SO4	D	313	-	4,4,4	0.34	0	6,6,6	0.10	0
6	URE	B	308	-	3,3,3	0.17	0	3,3,3	0.04	0
8	SO4	C	317	-	4,4,4	0.36	0	6,6,6	0.08	0
8	SO4	E	313	-	4,4,4	0.34	0	6,6,6	0.07	0
5	FMT	D	305	-	2,2,2	0.30	0	1,1,1	0.14	0
7	EDO	A	313	-	3,3,3	0.12	0	2,2,2	0.24	0
8	SO4	E	314	-	4,4,4	0.34	0	6,6,6	0.07	0
5	FMT	E	307[A]	-	2,2,2	0.30	0	1,1,1	0.14	0
6	URE	F	306	-	3,3,3	0.13	0	3,3,3	0.03	0

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
10	GOA	D	309	-	-	2/2/2/2	-
7	EDO	F	308	-	-	1/1/1/1	-
7	EDO	D	308	-	-	1/1/1/1	-
7	EDO	C	312	-	-	0/1/1/1	-
7	EDO	A	315	-	-	1/1/1/1	-
7	EDO	A	314	-	-	1/1/1/1	-
9	PEG	B	318	-	-	1/4/4/4	-
7	EDO	A	316	-	-	1/1/1/1	-
10	GOA	C	315	-	-	2/2/2/2	-
7	EDO	B	312	-	-	0/1/1/1	-
7	EDO	C	314	-	-	1/1/1/1	-
7	EDO	E	311	-	-	1/1/1/1	-
10	GOA	F	309	-	-	0/2/2/2	-
9	PEG	B	317	-	-	2/4/4/4	-
10	GOA	C	316	-	-	2/2/2/2	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	F	307	-	-	0/1/1/1	-
7	EDO	A	317	-	-	1/1/1/1	-
7	EDO	B	311	-	-	1/1/1/1	-
7	EDO	A	313	-	-	1/1/1/1	-
7	EDO	C	313	-	-	1/1/1/1	-

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	C	315	GOA	OXT-C-CA	4.13	119.40	111.90
10	C	316	GOA	OXT-C-CA	4.09	119.33	111.90
10	F	309	GOA	OXT-C-CA	4.04	119.24	111.90
10	D	309	GOA	OXT-C-CA	3.65	118.54	111.90
10	C	315	GOA	O-C-CA	-2.07	117.49	123.48

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	C	315	GOA	O-C-CA-O2
10	C	315	GOA	OXT-C-CA-O2
10	C	316	GOA	OXT-C-CA-O2
10	D	309	GOA	O-C-CA-O2
10	D	309	GOA	OXT-C-CA-O2
9	B	317	PEG	O1-C1-C2-O2
9	B	318	PEG	O2-C3-C4-O4
7	A	313	EDO	O1-C1-C2-O2
7	A	317	EDO	O1-C1-C2-O2
7	E	311	EDO	O1-C1-C2-O2
7	A	315	EDO	O1-C1-C2-O2
7	B	311	EDO	O1-C1-C2-O2
7	C	313	EDO	O1-C1-C2-O2
7	A	314	EDO	O1-C1-C2-O2
7	D	308	EDO	O1-C1-C2-O2
10	C	316	GOA	O-C-CA-O2
7	A	316	EDO	O1-C1-C2-O2
7	F	308	EDO	O1-C1-C2-O2
7	C	314	EDO	O1-C1-C2-O2
9	B	317	PEG	C1-C2-O2-C3

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	312	URE	1	0
7	E	311	EDO	1	0
7	C	313	EDO	1	0
6	C	307	URE	1	0
6	C	311	URE	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	292/299 (97%)	-0.41	1 (0%)	90 91	11, 26, 38, 96	11 (3%)
1	B	290/299 (96%)	-0.38	2 (0%)	84 86	14, 26, 42, 72	4 (1%)
1	C	290/299 (96%)	-0.40	1 (0%)	90 91	13, 27, 40, 83	7 (2%)
1	D	289/299 (96%)	-0.36	0	100 100	12, 27, 42, 68	8 (2%)
1	E	287/299 (95%)	-0.29	2 (0%)	84 86	14, 28, 44, 84	6 (2%)
1	F	289/299 (96%)	-0.26	2 (0%)	84 86	13, 30, 46, 97	5 (1%)
All	All	1737/1794 (96%)	-0.35	8 (0%)	87 89	11, 27, 43, 97	41 (2%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	57	ILE	5.5
1	C	132	PRO	2.6
1	B	0	ALA	2.4
1	E	53	ASN	2.4
1	E	132	PRO	2.1
1	F	53	ASN	2.1
1	B	132	PRO	2.0
1	F	3	LYS	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

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
6	URE	C	307	4/4	0.70	0.13	40,47,55,58	0
4	MG	D	303	1/1	0.73	0.16	35,35,35,35	1
4	MG	F	302	1/1	0.75	0.12	37,37,37,37	1
7	EDO	A	315	4/4	0.76	0.13	62,69,70,71	0
4	MG	B	304	1/1	0.77	0.14	32,32,32,32	1
6	URE	C	308	4/4	0.78	0.10	67,68,69,70	0
9	PEG	B	317	7/7	0.78	0.14	60,67,74,75	0
4	MG	E	304	1/1	0.79	0.11	35,35,35,35	1
5	FMT	D	307	3/3	0.80	0.16	64,64,67,69	0
8	SO4	A	318	5/5	0.80	0.14	48,66,80,92	0
6	URE	E	310	4/4	0.80	0.13	61,62,64,66	0
4	MG	C	305	1/1	0.81	0.11	33,33,33,33	1
7	EDO	A	316	4/4	0.81	0.18	47,54,60,61	0
7	EDO	A	314	4/4	0.83	0.14	53,55,57,58	0
5	FMT	E	305	3/3	0.83	0.14	38,38,44,45	0
5	FMT	D	306	3/3	0.83	0.12	42,42,56,62	0
6	URE	F	305	4/4	0.83	0.10	68,69,71,72	0
8	SO4	D	310	5/5	0.83	0.21	43,50,57,64	5
7	EDO	A	313	4/4	0.83	0.16	51,52,56,60	0
2	CL	E	301	1/1	0.84	0.18	80,80,80,80	0
5	FMT	B	305	3/3	0.84	0.12	33,33,43,47	0
4	MG	A	307	1/1	0.84	0.12	34,34,34,34	1
2	CL	C	303	1/1	0.84	0.17	83,83,83,83	0
5	FMT	F	304	3/3	0.85	0.11	62,62,63,66	0
8	SO4	C	318	5/5	0.85	0.20	40,52,55,59	5
6	URE	C	309	4/4	0.85	0.12	68,70,70,71	0
8	SO4	E	314	5/5	0.85	0.09	81,89,92,93	0
6	URE	C	311	4/4	0.85	0.11	64,66,68,69	0
7	EDO	C	312	4/4	0.86	0.13	39,39,41,44	0
5	FMT	A	308	3/3	0.86	0.12	36,36,42,45	0
4	MG	F	301	1/1	0.86	0.10	32,32,32,32	1
5	FMT	D	304	3/3	0.86	0.12	38,38,47,54	0
5	FMT	D	305	3/3	0.86	0.13	41,41,55,56	0
6	URE	A	311	4/4	0.86	0.11	55,61,66,71	0
9	PEG	B	318	7/7	0.86	0.14	49,55,59,60	0
10	GOA	D	309	5/5	0.86	0.12	54,55,61,62	0
6	URE	B	309	4/4	0.87	0.10	68,69,73,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	EDO	D	308	4/4	0.87	0.14	53,55,57,58	0
10	GOA	C	316	5/5	0.87	0.11	59,61,64,66	0
8	SO4	F	310	5/5	0.87	0.17	44,51,53,59	5
7	EDO	B	311	4/4	0.88	0.11	49,56,58,58	0
8	SO4	B	313	5/5	0.88	0.15	37,44,49,56	5
8	SO4	B	314	5/5	0.88	0.17	51,51,54,56	5
8	SO4	B	315	5/5	0.88	0.15	49,50,55,56	5
6	URE	C	310	4/4	0.88	0.12	71,75,77,78	0
6	URE	B	310	4/4	0.88	0.09	64,67,68,68	0
5	FMT	B	307	3/3	0.89	0.16	68,68,69,69	0
7	EDO	B	312	4/4	0.89	0.12	45,53,54,64	0
5	FMT	B	306	3/3	0.89	0.12	42,42,52,59	0
8	SO4	C	317	5/5	0.89	0.18	51,56,57,57	5
5	FMT	E	307[A]	3/3	0.89	0.16	45,45,48,50	3
7	EDO	A	317	4/4	0.89	0.12	56,61,62,63	0
2	CL	A	304	1/1	0.90	0.16	80,80,80,80	0
6	URE	F	306	4/4	0.90	0.08	58,58,60,65	0
6	URE	B	308	4/4	0.90	0.12	56,59,63,67	0
7	EDO	C	313	4/4	0.90	0.11	38,49,49,51	0
8	SO4	D	313	5/5	0.90	0.10	63,64,68,76	0
8	SO4	E	312	5/5	0.90	0.17	41,48,52,57	5
5	FMT	E	306	3/3	0.90	0.09	45,45,51,60	0
7	EDO	E	311	4/4	0.90	0.11	39,46,48,51	0
2	CL	A	303	1/1	0.90	0.12	76,76,76,76	0
8	SO4	A	319	5/5	0.90	0.14	53,55,56,58	5
6	URE	E	309	4/4	0.90	0.12	65,68,69,72	0
4	MG	D	302	1/1	0.90	0.08	31,31,31,31	1
2	CL	C	302	1/1	0.91	0.07	74,74,74,74	0
5	FMT	A	309	3/3	0.91	0.12	40,40,47,49	0
8	SO4	C	319	5/5	0.91	0.10	58,60,64,74	0
8	SO4	D	312	5/5	0.92	0.13	52,56,57,59	5
5	FMT	F	303	3/3	0.92	0.12	65,65,66,69	0
4	MG	E	303	1/1	0.92	0.09	34,34,34,34	1
10	GOA	C	315	5/5	0.92	0.09	33,38,40,49	0
8	SO4	E	313	5/5	0.92	0.11	61,64,71,73	0
7	EDO	F	308	4/4	0.92	0.09	49,53,54,56	0
6	URE	A	312	4/4	0.93	0.10	52,55,61,63	0
8	SO4	D	311	5/5	0.93	0.12	60,63,64,66	5
6	URE	A	310	4/4	0.93	0.12	34,39,41,44	0
5	FMT	E	308	3/3	0.93	0.09	47,47,52,58	0
8	SO4	F	311	5/5	0.93	0.10	60,62,68,74	0
4	MG	A	306	1/1	0.94	0.06	30,30,30,30	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MG	B	303	1/1	0.94	0.08	30,30,30,30	1
7	EDO	F	307	4/4	0.95	0.09	36,40,40,43	0
6	URE	C	306	4/4	0.95	0.07	42,48,53,53	0
7	EDO	C	314	4/4	0.95	0.10	35,38,40,42	0
10	GOA	F	309	5/5	0.95	0.07	37,40,49,56	0
8	SO4	B	316	5/5	0.96	0.07	55,60,63,73	0
2	CL	B	301	1/1	0.97	0.11	43,43,43,43	0
3	NA	B	302	1/1	0.97	0.05	24,24,24,24	0
2	CL	D	301	1/1	0.97	0.12	43,43,43,43	0
4	MG	C	304	1/1	0.97	0.04	29,29,29,29	1
2	CL	A	302	1/1	0.98	0.13	45,45,45,45	0
3	NA	A	305	1/1	0.98	0.03	24,24,24,24	0
2	CL	A	301	1/1	0.99	0.10	38,38,38,38	0
2	CL	C	301	1/1	0.99	0.11	42,42,42,42	0
3	NA	E	302	1/1	0.99	0.05	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.