



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 12:11 AM UTC

PDB ID : 3ZNJ / pdb_00003znj
Title : Crystal structure of unliganded ClcF from R.opacus 1CP in crystal form 1.
Authors : Roth, C.; Groening, J.A.D.; Kaschabek, S.R.; Schloemann, M.; Straeter, N.
Deposited on : 2013-02-14
Resolution : 2.10 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 : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.48.1

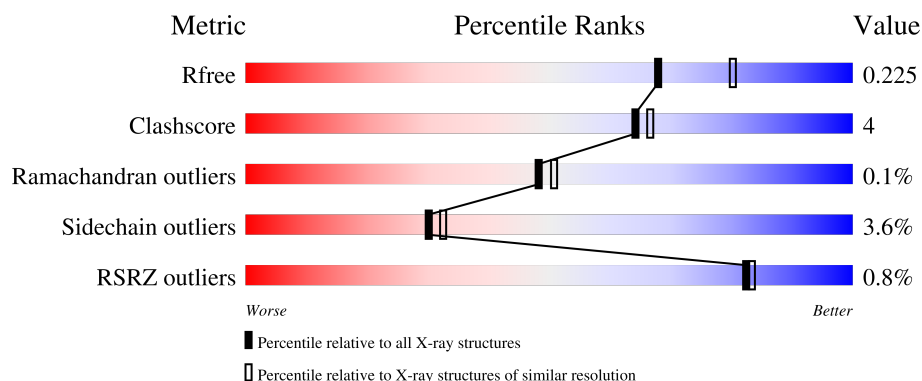
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6234 (2.10-2.10)
Clashscore	180529	6893 (2.10-2.10)
Ramachandran outliers	177936	6839 (2.10-2.10)
Sidechain outliers	177891	6840 (2.10-2.10)
RSRZ outliers	164620	6234 (2.10-2.10)

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	1	94	84% 15% .
1	2	94	83% 14% ..
1	3	94	2% 88% 6% ..
1	4	94	85% 15%
1	5	94	87% 9% ..

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Mol	Chain	Length	Quality of chain
1	6	94	% 83% 16% .
1	7	94	% 88% 10% .
1	8	94	83% 15% .
1	9	94	% 84% 12% ..
1	A	94	89% 11%
1	B	94	% 91% 6% .
1	C	94	96% .
1	D	94	96% .
1	E	94	% 90% 10%
1	F	94	% 86% 12% .
1	G	94	98% .
1	H	94	2% 96% ..
1	I	94	% 91% 9%
1	J	94	94% 6%
1	K	94	94% 5% .
1	L	94	% 94% 5% .
1	M	94	91% 9%
1	N	94	94% 6%
1	O	94	89% 11%
1	P	94	85% 14% .
1	R	94	97% ..
1	S	94	90% 10%
1	T	94	91% 5% .
1	U	94	3% 86% 11% .
1	V	94	% 79% 20% .

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Mol	Chain	Length	Quality of chain
1	W	94	4% 81% 18%
1	X	94	94% 6%
1	Y	94	5% 82% 13%
1	Z	94	% 93% 6%
1	a	94	85% 14%
1	b	94	85% 13%
1	c	94	93% 7%
1	d	94	79% 20%
1	e	94	84% 12%
1	f	94	90% 10%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 66372 atoms, of which 31697 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 5-CHLOROMUCONOLACTONE DEHALOGENASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	1	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	2	93	Total	C	H	N	O	S	0	0	0
			1562	500	779	142	139	2			
1	3	92	Total	C	H	N	O	S	0	0	0
			1544	494	768	141	139	2			
1	4	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	5	92	Total	C	H	N	O	S	0	0	0
			1540	494	766	140	138	2			
1	6	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	7	92	Total	C	H	N	O	S	0	0	0
			1540	494	766	140	138	2			
1	8	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	9	91	Total	C	H	N	O	S	0	0	0
			1523	490	759	136	136	2			
1	A	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	B	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	C	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	D	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	E	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	F	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	G	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	H	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	I	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	J	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	K	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	L	94	Total	C	H	N	O	S	0	1	0
			1587	508	789	143	145	2			
1	M	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	N	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	O	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	P	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	R	94	Total	C	H	N	O	S	0	1	0
			1591	509	794	143	143	2			
1	S	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	T	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	U	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	V	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	W	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	X	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	Y	91	Total	C	H	N	O	S	0	1	0
			1545	496	769	139	139	2			
1	Z	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	a	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	b	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	c	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	d	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			
1	e	92	Total	C	H	N	O	S	0	0	0
			1540	494	766	140	138	2			
1	f	94	Total	C	H	N	O	S	0	0	0
			1575	504	783	143	143	2			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	1	1	Total	Cl	0	0
			1	1		
2	2	1	Total	Cl	0	0
			1	1		
2	3	1	Total	Cl	0	0
			1	1		
2	4	1	Total	Cl	0	0
			1	1		
2	5	1	Total	Cl	0	0
			1	1		
2	6	1	Total	Cl	0	0
			1	1		
2	7	1	Total	Cl	0	0
			1	1		
2	8	1	Total	Cl	0	0
			1	1		
2	9	1	Total	Cl	0	0
			1	1		
2	A	1	Total	Cl	0	0
			1	1		
2	B	1	Total	Cl	0	0
			1	1		
2	C	1	Total	Cl	0	0
			1	1		
2	D	1	Total	Cl	0	0
			1	1		
2	E	1	Total	Cl	0	0
			1	1		
2	F	1	Total	Cl	0	0
			1	1		
2	G	1	Total	Cl	0	0
			1	1		

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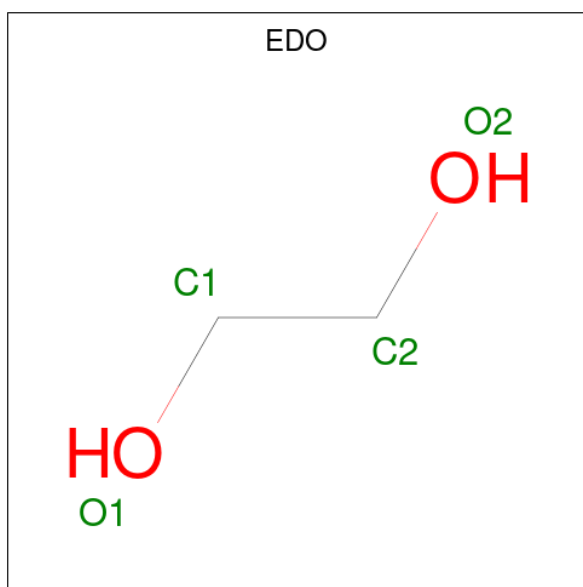
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	H	1	Total 1	Cl 1	0	0
2	I	1	Total 1	Cl 1	0	0
2	J	1	Total 1	Cl 1	0	0
2	K	1	Total 1	Cl 1	0	0
2	L	1	Total 1	Cl 1	0	0
2	M	1	Total 1	Cl 1	0	0
2	N	1	Total 1	Cl 1	0	0
2	O	1	Total 1	Cl 1	0	0
2	P	1	Total 1	Cl 1	0	0
2	R	1	Total 1	Cl 1	0	0
2	S	1	Total 1	Cl 1	0	0
2	T	1	Total 1	Cl 1	0	0
2	U	1	Total 1	Cl 1	0	0
2	V	1	Total 1	Cl 1	0	0
2	W	1	Total 1	Cl 1	0	0
2	X	1	Total 1	Cl 1	0	0
2	Y	1	Total 1	Cl 1	0	0
2	Z	1	Total 1	Cl 1	0	0
2	a	1	Total 1	Cl 1	0	0
2	b	1	Total 1	Cl 1	0	0
2	c	1	Total 1	Cl 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	d	1	Total	Cl	0	0
			1	1		
2	e	1	Total	Cl	0	0
			1	1		
2	f	1	Total	Cl	0	0
			1	1		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	1	1	Total	C	H	O	0	0
			10	2	6	2		
3	1	1	Total	C	H	O	0	0
			10	2	6	2		
3	2	1	Total	C	H	O	0	0
			10	2	6	2		
3	2	1	Total	C	H	O	0	0
			10	2	6	2		
3	3	1	Total	C	H	O	0	0
			10	2	6	2		
3	3	1	Total	C	H	O	0	0
			10	2	6	2		
3	4	1	Total	C	H	O	0	0
			10	2	6	2		
3	4	1	Total	C	H	O	0	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	5	1	Total	C	H	O	0	0
			10	2	6	2		
3	5	1	Total	C	H	O	0	0
			10	2	6	2		
3	6	1	Total	C	H	O	0	0
			10	2	6	2		
3	6	1	Total	C	H	O	0	0
			10	2	6	2		
3	7	1	Total	C	H	O	0	0
			10	2	6	2		
3	7	1	Total	C	H	O	0	0
			10	2	6	2		
3	8	1	Total	C	H	O	0	0
			10	2	6	2		
3	8	1	Total	C	H	O	0	0
			10	2	6	2		
3	9	1	Total	C	H	O	0	0
			10	2	6	2		
3	9	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	B	1	Total	C	H	O	0	0
			10	2	6	2		
3	B	1	Total	C	H	O	0	0
			10	2	6	2		
3	C	1	Total	C	H	O	0	0
			10	2	6	2		
3	C	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	1	Total	C	H	O	0	0
			10	2	6	2		
3	E	1	Total	C	H	O	0	0
			10	2	6	2		
3	E	1	Total	C	H	O	0	0
			10	2	6	2		
3	F	1	Total	C	H	O	0	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	F	1	Total	C	H	O	0	0
			10	2	6	2		
3	G	1	Total	C	H	O	0	0
			10	2	6	2		
3	G	1	Total	C	H	O	0	0
			10	2	6	2		
3	H	1	Total	C	H	O	0	0
			10	2	6	2		
3	H	1	Total	C	H	O	0	0
			10	2	6	2		
3	I	1	Total	C	H	O	0	0
			10	2	6	2		
3	I	1	Total	C	H	O	0	0
			10	2	6	2		
3	J	1	Total	C	H	O	0	0
			10	2	6	2		
3	J	1	Total	C	H	O	0	0
			10	2	6	2		
3	K	1	Total	C	H	O	0	0
			10	2	6	2		
3	K	1	Total	C	H	O	0	0
			10	2	6	2		
3	L	1	Total	C	H	O	0	0
			10	2	6	2		
3	L	1	Total	C	H	O	0	0
			10	2	6	2		
3	M	1	Total	C	H	O	0	0
			10	2	6	2		
3	M	1	Total	C	H	O	0	0
			10	2	6	2		
3	N	1	Total	C	H	O	0	0
			10	2	6	2		
3	N	1	Total	C	H	O	0	0
			10	2	6	2		
3	O	1	Total	C	H	O	0	0
			10	2	6	2		
3	O	1	Total	C	H	O	0	0
			10	2	6	2		
3	P	1	Total	C	H	O	0	0
			10	2	6	2		
3	P	1	Total	C	H	O	0	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	R	1	Total	C	H	O	0	0
			10	2	6	2		
3	R	1	Total	C	H	O	0	0
			10	2	6	2		
3	S	1	Total	C	H	O	0	0
			10	2	6	2		
3	S	1	Total	C	H	O	0	0
			10	2	6	2		
3	T	1	Total	C	H	O	0	0
			10	2	6	2		
3	T	1	Total	C	H	O	0	0
			10	2	6	2		
3	U	1	Total	C	H	O	0	0
			10	2	6	2		
3	V	1	Total	C	H	O	0	0
			10	2	6	2		
3	V	1	Total	C	H	O	0	0
			10	2	6	2		
3	W	1	Total	C	H	O	0	0
			10	2	6	2		
3	W	1	Total	C	H	O	0	0
			10	2	6	2		
3	X	1	Total	C	H	O	0	0
			10	2	6	2		
3	X	1	Total	C	H	O	0	0
			10	2	6	2		
3	Y	1	Total	C	H	O	0	0
			10	2	6	2		
3	Y	1	Total	C	H	O	0	0
			10	2	6	2		
3	Z	1	Total	C	H	O	0	0
			10	2	6	2		
3	a	1	Total	C	H	O	0	0
			10	2	6	2		
3	a	1	Total	C	H	O	0	0
			10	2	6	2		
3	b	1	Total	C	H	O	0	0
			10	2	6	2		
3	b	1	Total	C	H	O	0	0
			10	2	6	2		
3	c	1	Total	C	H	O	0	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	c	1	Total	C	H	O	0	0
			10	2	6	2		
3	d	1	Total	C	H	O	0	0
			10	2	6	2		
3	d	1	Total	C	H	O	0	0
			10	2	6	2		
3	e	1	Total	C	H	O	0	0
			10	2	6	2		
3	e	1	Total	C	H	O	0	0
			10	2	6	2		
3	f	1	Total	C	H	O	0	0
			10	2	6	2		
3	f	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	1	57	Total	O	0	0
			57	57		
4	2	59	Total	O	0	0
			59	59		
4	3	68	Total	O	0	0
			68	68		
4	4	38	Total	O	0	0
			38	38		
4	5	47	Total	O	0	0
			47	47		
4	6	46	Total	O	0	0
			46	46		
4	7	41	Total	O	0	0
			41	41		
4	8	56	Total	O	0	0
			56	56		
4	9	50	Total	O	0	0
			50	50		
4	A	155	Total	O	0	0
			155	155		
4	B	143	Total	O	0	0
			143	143		
4	C	169	Total	O	0	0
			169	169		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	147	Total 147	O 147	0	0
4	E	161	Total 161	O 161	0	0
4	F	122	Total 122	O 122	0	0
4	G	138	Total 138	O 138	0	0
4	H	93	Total 93	O 93	0	0
4	I	75	Total 75	O 75	0	0
4	J	90	Total 90	O 90	0	0
4	K	103	Total 103	O 103	0	0
4	L	87	Total 87	O 87	0	0
4	M	84	Total 84	O 84	0	0
4	N	78	Total 78	O 78	0	0
4	O	64	Total 64	O 64	0	0
4	P	67	Total 67	O 67	0	0
4	R	95	Total 95	O 95	0	0
4	S	88	Total 88	O 88	0	0
4	T	82	Total 82	O 82	0	0
4	U	54	Total 54	O 54	0	0
4	V	46	Total 46	O 46	0	0
4	W	37	Total 37	O 37	0	0
4	X	42	Total 42	O 42	0	0
4	Y	29	Total 29	O 29	0	0

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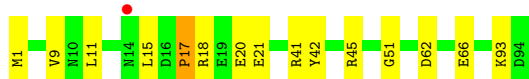
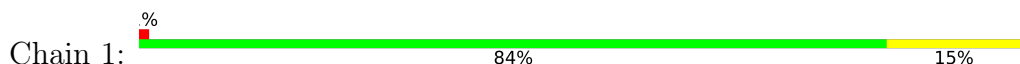
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	Z	44	Total	O	0	0
			44	44		

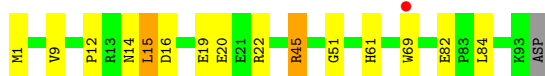
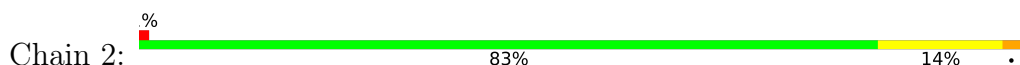
3 Residue-property plots [i](#)

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: 5-CHLOROMUCONOLACTONE DEHALOGENASE



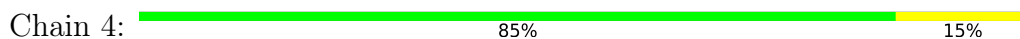
- Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE



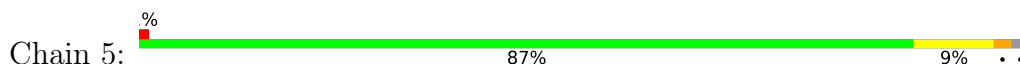
- Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE



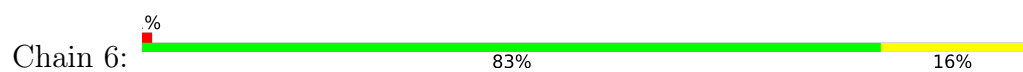
- Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE



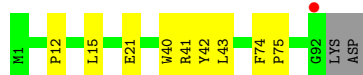
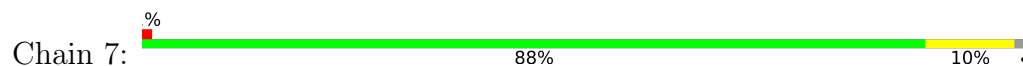
- Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE



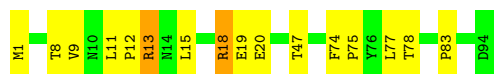
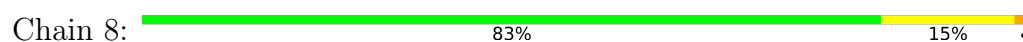
- Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE



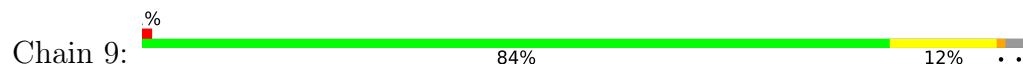
• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE



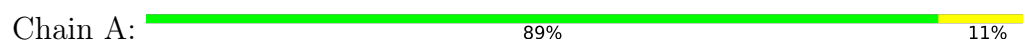
• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE



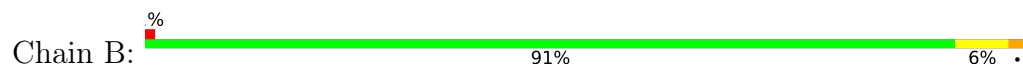
• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE



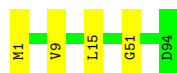
• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE



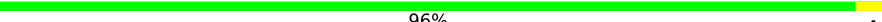
• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain D:  96% .



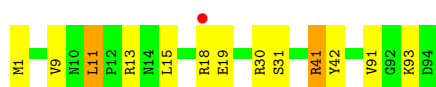
• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain E:  90% 10% .

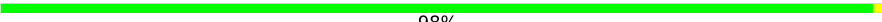


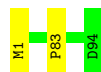
• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain F:  86% 12% .



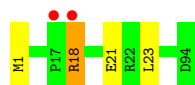
• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain G:  98% .



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain H:  96% .



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain I:  91% 9% .

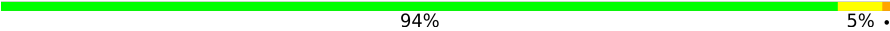


• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain J:  94% 6% .

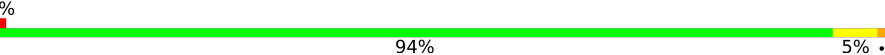


• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain K:  94% 5%



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain L:  94% 5%

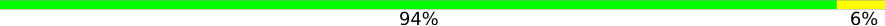


• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain M:  91% 9%



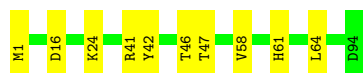
• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain N:  94% 6%



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain O:  89% 11%

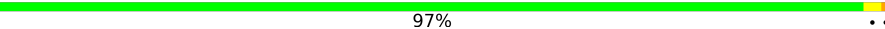


• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain P:  85% 14%



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain R:  97%



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain S:  90% 10%



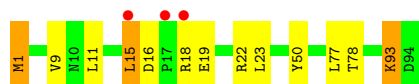
- Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain T:  91% 5% .



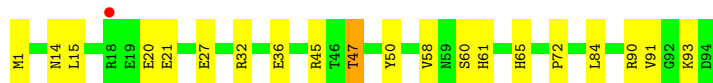
- Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain U:  3% 86% 11% .



- Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain V:  % 79% 20% .

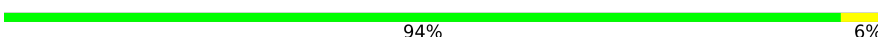


- Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain W:  4% 81% 18% .



- Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain X:  94% 6%

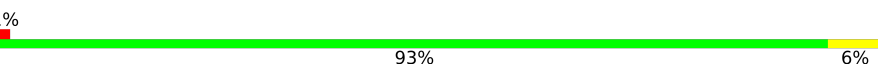


- Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain Y:  5% 82% 13% . .



- Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain Z:  % 93% 6% .



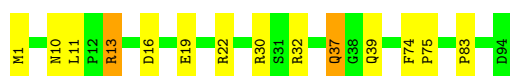
• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain a:  85% 14% .



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain b:  85% 13% .



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain c:  93% 7%



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain d:  79% 20% .



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain e:  84% 12% . .



• Molecule 1: 5-CHLOROMUCONOLACTONE DEHALOGENASE

Chain f:  90% 10%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	151.14Å 79.43Å 198.97Å 90.00° 93.41° 90.00°	Depositor
Resolution (Å)	19.90 – 2.10 19.90 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.3 (19.90-2.10) 95.1 (19.90-2.10)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.33 (at 2.09Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: DEV_1172)	Depositor
R, R_{free}	0.164 , 0.224 0.167 , 0.225	Depositor DCC
R_{free} test set	1340 reflections (0.51%)	wwPDB-VP
Wilson B-factor (Å ²)	25.7	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 52.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	66372	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.69% 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: CL, EDO

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	1	0.29	0/814	0.68	0/1103
1	2	0.29	0/805	0.63	0/1092
1	3	0.29	0/797	0.65	1/1077 (0.1%)
1	4	0.29	0/814	0.66	0/1103
1	5	0.28	0/796	0.61	0/1081
1	6	0.29	0/814	0.63	0/1103
1	7	0.28	0/796	0.65	0/1081
1	8	0.30	0/814	0.63	0/1103
1	9	0.27	0/785	0.63	0/1064
1	A	0.30	0/814	0.61	0/1103
1	B	0.31	0/814	0.62	0/1103
1	C	0.29	0/814	0.60	0/1103
1	D	0.31	0/814	0.61	0/1103
1	E	0.30	0/814	0.64	0/1103
1	F	0.30	0/814	0.63	0/1103
1	G	0.32	0/814	0.60	0/1103
1	H	0.30	0/814	0.66	0/1103
1	I	0.30	0/814	0.63	0/1103
1	J	0.31	0/814	0.63	0/1103
1	K	0.30	0/814	0.64	0/1103
1	L	0.31	0/823	0.63	0/1115
1	M	0.29	0/814	0.60	0/1103
1	N	0.29	0/814	0.61	0/1103
1	O	0.31	0/814	0.65	0/1103
1	P	0.31	0/814	0.64	0/1103
1	R	0.29	0/822	0.63	0/1114
1	S	0.30	0/814	0.63	0/1103
1	T	0.31	0/814	0.61	0/1103
1	U	0.30	0/814	0.67	0/1103
1	V	0.29	0/814	0.66	0/1103
1	W	0.30	0/814	0.67	0/1103
1	X	0.29	0/814	0.62	0/1103

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Y	0.30	0/801	0.67	0/1088
1	Z	0.31	0/814	0.67	0/1103
1	a	0.28	0/814	0.64	0/1103
1	b	0.29	0/814	0.61	0/1103
1	c	0.29	0/814	0.61	0/1103
1	d	0.30	0/814	0.65	0/1103
1	e	0.32	0/796	0.71	0/1081
1	f	0.31	0/814	0.64	0/1103
All	All	0.30	0/32455	0.64	1/43986 (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	3	19	GLU	N-CA-C	-5.33	105.58	111.71

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	1	792	783	779	11	0
1	2	783	779	775	8	0
1	3	776	768	764	6	0
1	4	792	783	779	14	0
1	5	774	766	762	7	0
1	6	792	783	779	9	0
1	7	774	766	762	6	0
1	8	792	783	779	9	0
1	9	764	759	755	6	0
1	A	792	783	779	5	0
1	B	792	783	779	5	0
1	C	792	783	779	3	0
1	D	792	783	779	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	792	783	779	7	0
1	F	792	783	779	9	0
1	G	792	783	779	2	0
1	H	792	783	779	6	0
1	I	792	783	779	6	0
1	J	792	783	779	3	0
1	K	792	783	779	4	0
1	L	798	789	785	4	0
1	M	792	783	779	8	0
1	N	792	783	779	5	0
1	O	792	783	779	7	0
1	P	792	783	779	11	0
1	R	797	794	790	3	0
1	S	792	783	779	9	0
1	T	792	783	779	6	0
1	U	792	783	779	18	0
1	V	792	783	779	16	0
1	W	792	783	779	14	0
1	X	792	783	779	6	0
1	Y	776	769	765	9	0
1	Z	792	783	779	5	0
1	a	792	783	779	8	0
1	b	792	783	779	10	0
1	c	792	783	779	7	0
1	d	792	783	779	10	0
1	e	774	766	762	14	0
1	f	792	783	779	11	0
2	1	1	0	0	0	0
2	2	1	0	0	0	0
2	3	1	0	0	0	0
2	4	1	0	0	0	0
2	5	1	0	0	0	0
2	6	1	0	0	0	0
2	7	1	0	0	0	0
2	8	1	0	0	0	0
2	9	1	0	0	0	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	1	0
2	M	1	0	0	0	0
2	N	1	0	0	0	0
2	O	1	0	0	0	0
2	P	1	0	0	0	0
2	R	1	0	0	0	0
2	S	1	0	0	0	0
2	T	1	0	0	0	0
2	U	1	0	0	0	0
2	V	1	0	0	0	0
2	W	1	0	0	0	0
2	X	1	0	0	1	0
2	Y	1	0	0	0	0
2	Z	1	0	0	0	0
2	a	1	0	0	0	0
2	b	1	0	0	0	0
2	c	1	0	0	0	0
2	d	1	0	0	0	0
2	e	1	0	0	0	0
2	f	1	0	0	0	0
3	1	8	12	12	0	0
3	2	8	12	12	0	0
3	3	8	12	12	1	0
3	4	8	12	12	0	0
3	5	8	12	12	0	0
3	6	8	12	12	1	0
3	7	8	12	12	0	0
3	8	8	12	12	0	0
3	9	8	12	12	0	0
3	A	8	12	12	1	0
3	B	8	12	12	0	0
3	C	8	12	12	0	0
3	D	8	12	12	0	0
3	E	8	12	12	0	0
3	F	8	12	12	1	0
3	G	8	12	12	0	0
3	H	8	12	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	I	8	12	12	0	0
3	J	8	12	12	0	0
3	K	8	12	12	0	0
3	L	8	12	12	1	0
3	M	8	12	12	0	0
3	N	8	12	12	0	0
3	O	8	12	12	0	0
3	P	8	12	12	1	0
3	R	8	12	12	0	0
3	S	8	12	12	0	0
3	T	8	12	12	0	0
3	U	4	6	6	0	0
3	V	8	12	12	0	0
3	W	8	12	12	0	0
3	X	8	12	12	0	0
3	Y	8	12	12	1	0
3	Z	4	6	6	0	0
3	a	8	12	12	0	0
3	b	8	12	12	0	0
3	c	8	12	12	0	0
3	d	8	12	12	0	0
3	e	8	12	12	1	0
3	f	8	12	12	0	0
4	1	57	0	0	1	0
4	2	59	0	0	0	0
4	3	68	0	0	0	0
4	4	38	0	0	1	0
4	5	47	0	0	0	0
4	6	46	0	0	0	0
4	7	41	0	0	0	0
4	8	56	0	0	0	0
4	9	50	0	0	0	0
4	A	155	0	0	0	0
4	B	143	0	0	1	0
4	C	169	0	0	0	0
4	D	147	0	0	1	0
4	E	161	0	0	1	0
4	F	122	0	0	1	0
4	G	138	0	0	0	0
4	H	93	0	0	0	0
4	I	75	0	0	0	0
4	J	90	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	K	103	0	0	0	0
4	L	87	0	0	1	0
4	M	84	0	0	1	0
4	N	78	0	0	0	0
4	O	64	0	0	0	0
4	P	67	0	0	0	0
4	R	95	0	0	0	0
4	S	88	0	0	0	0
4	T	82	0	0	1	0
4	U	54	0	0	0	0
4	V	46	0	0	1	0
4	W	37	0	0	2	0
4	X	42	0	0	0	0
4	Y	29	0	0	0	0
4	Z	44	0	0	1	0
All	All	34675	31697	31537	243	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (243) 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:O:1:MET:SD	1:S:1:MET:HE1	2.26	0.75
1:d:41:ARG:NH1	1:d:94:ASP:O	2.21	0.74
1:B:1:MET:HE1	1:I:1:MET:SD	2.27	0.74
1:M:93:LYS:O	1:M:94:ASP:HB2	1.88	0.72
1:V:50:TYR:OH	4:V:2029:HOH:O	2.07	0.71
1:6:41:ARG:NH2	1:6:94:ASP:O	2.24	0.70
1:F:41:ARG:NH2	4:F:2080:HOH:O	2.25	0.70
1:4:65:HIS:CE1	1:V:45:ARG:HD3	2.27	0.69
1:9:1:MET:N	1:9:58:VAL:O	2.27	0.68
1:O:61:HIS:CE1	1:S:1:MET:HE3	2.28	0.68
1:e:41:ARG:HD3	1:e:42:TYR:CE2	2.29	0.67
1:a:1:MET:HE1	1:d:1:MET:SD	2.34	0.66
1:a:1:MET:SD	1:d:1:MET:HE1	2.36	0.66
1:e:12:PRO:HG2	1:e:15:LEU:HD13	1.79	0.65
1:c:1:MET:SD	1:f:1:MET:HE1	2.38	0.64
1:S:93:LYS:O	1:S:94:ASP:HB2	1.97	0.64
1:L:37:GLN:NE2	4:L:2044:HOH:O	2.31	0.64
1:G:1:MET:HE1	1:J:1:MET:HE1	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:9:VAL:CG2	1:U:50:TYR:CD2	2.82	0.62
1:V:1:MET:HE1	1:Y:1:MET:SD	2.39	0.62
1:V:14:ASN:O	1:V:14:ASN:ND2	2.32	0.62
1:L:1:MET:SD	1:T:1:MET:HE1	2.41	0.61
1:E:1:MET:HE1	1:H:1:MET:SD	2.41	0.61
1:V:65:HIS:CE1	1:X:45:ARG:HD3	2.35	0.61
1:T:41:ARG:NH2	1:T:94:ASP:O	2.34	0.61
1:1:1:MET:SD	1:X:1:MET:HE1	2.40	0.61
1:8:18:ARG:CG	1:8:18:ARG:HH11	2.15	0.59
1:4:41:ARG:HD3	1:4:42:TYR:CE2	2.36	0.59
1:U:9:VAL:HG21	1:U:50:TYR:CD2	2.37	0.59
1:c:1:MET:HE1	1:f:1:MET:SD	2.43	0.59
1:1:17:PRO:O	1:1:20:GLU:N	2.35	0.59
1:U:9:VAL:HG21	1:U:50:TYR:CG	2.38	0.59
1:1:45:ARG:NH2	4:1:2029:HOH:O	2.35	0.58
1:V:61:HIS:CE1	1:Y:1:MET:HG2	2.39	0.58
1:1:93:LYS:HD2	1:1:93:LYS:N	2.19	0.58
1:6:82:GLU:OE1	3:6:1097:EDO:H21	2.05	0.57
1:E:1:MET:SD	1:H:1:MET:HE1	2.45	0.56
1:8:1:MET:SD	1:b:1:MET:HE1	2.45	0.56
1:K:1:MET:SD	1:N:1:MET:HE1	2.45	0.56
1:U:9:VAL:HG12	1:U:77:LEU:CD2	2.35	0.56
1:W:41:ARG:NH2	1:W:94:ASP:O	2.39	0.56
1:O:1:MET:SD	1:S:1:MET:CE	2.94	0.56
1:E:61:HIS:CE1	1:H:1:MET:HE3	2.41	0.55
1:F:31:SER:HB3	3:F:1097:EDO:H22	1.89	0.54
1:P:45:ARG:HD2	1:S:65:HIS:CE1	2.42	0.54
1:3:1:MET:SD	1:Z:1:MET:HE1	2.47	0.54
1:8:18:ARG:HH11	1:8:18:ARG:HG3	1.72	0.54
1:6:9:VAL:HG12	1:6:11:LEU:HD22	1.88	0.54
1:8:83:PRO:HG3	1:b:83:PRO:HG3	1.90	0.54
1:R:46:THR:CG2	1:R:53[A]:ILE:HD12	2.38	0.54
1:9:9:VAL:HG23	1:9:51:GLY:HA2	1.90	0.54
1:4:41:ARG:NH1	4:4:2018:HOH:O	2.40	0.53
1:F:18:ARG:HD3	1:F:19:GLU:N	2.22	0.53
1:F:41:ARG:HD2	1:F:42:TYR:CE2	2.43	0.53
1:T:37:GLN:NE2	4:T:2045:HOH:O	2.41	0.53
1:W:32:ARG:NH1	4:W:2015:HOH:O	2.41	0.53
1:G:83:PRO:HG3	1:J:83:PRO:HG3	1.90	0.52
1:U:9:VAL:HG23	1:U:50:TYR:CD2	2.43	0.52
1:A:15:LEU:HD12	1:A:16:ASP:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:7:12:PRO:HB3	1:f:13:ARG:NH1	2.24	0.52
1:U:9:VAL:CG2	1:U:50:TYR:CG	2.92	0.52
1:U:19:GLU:OE1	1:U:22:ARG:CZ	2.58	0.52
1:L:1:MET:HE1	1:T:1:MET:SD	2.50	0.51
1:C:1:MET:SD	1:F:1:MET:HE1	2.51	0.51
1:F:18:ARG:HD3	1:F:18:ARG:C	2.35	0.50
1:c:65:HIS:CE1	1:e:45:ARG:HD2	2.46	0.50
1:f:90:ARG:NH2	1:f:93:LYS:O	2.44	0.50
1:C:1:MET:HE1	1:F:1:MET:SD	2.51	0.50
1:P:47:THR:HG21	1:S:61:HIS:HB3	1.94	0.50
1:I:22:ARG:HG3	1:I:23:LEU:N	2.27	0.50
2:L:1095:CL:CL	3:L:1097:EDO:C1	2.97	0.50
1:3:1:MET:HE1	1:Z:1:MET:SD	2.52	0.49
1:U:93:LYS:HD3	1:U:93:LYS:N	2.27	0.49
1:7:12:PRO:HB3	1:f:13:ARG:CZ	2.43	0.49
1:5:46:THR:HG23	1:5:53:ILE:HD13	1.94	0.49
1:S:37:GLN:NE2	1:S:39:GLN:OE1	2.46	0.49
1:b:13:ARG:HD3	1:b:13:ARG:N	2.27	0.49
1:O:46:THR:HG22	1:P:82:GLU:OE2	2.13	0.49
1:T:46:THR:HG22	1:T:53:ILE:HD12	1.94	0.49
1:4:1:MET:HE1	1:W:1:MET:CE	2.43	0.48
1:U:15:LEU:HD13	1:U:15:LEU:H	1.79	0.48
1:d:12:PRO:HG2	1:d:15:LEU:HG	1.94	0.48
1:2:61:HIS:CE1	1:5:1:MET:CE	2.95	0.48
1:A:6:ARG:CZ	1:A:53:ILE:HD11	2.42	0.48
1:M:46:THR:HG23	1:M:53:ILE:HD12	1.94	0.48
1:P:19:GLU:HA	1:P:22:ARG:HB3	1.96	0.48
1:Z:18:ARG:HG2	1:Z:19:GLU:N	2.28	0.48
1:9:45:ARG:HD3	1:9:51:GLY:O	2.14	0.48
1:B:9:VAL:HG23	1:B:51:GLY:HA2	1.95	0.48
1:R:46:THR:HG23	1:R:53[A]:ILE:HD12	1.96	0.48
1:b:16:ASP:O	1:b:19:GLU:HG2	2.12	0.48
1:7:12:PRO:HG2	1:7:15:LEU:HD13	1.96	0.48
1:U:9:VAL:HG12	1:U:77:LEU:HD21	1.95	0.48
1:1:41:ARG:HD3	1:1:42:TYR:CZ	2.49	0.47
1:a:16:ASP:HB3	1:a:19:GLU:HB3	1.95	0.47
1:A:82:GLU:OE1	3:A:1096:EDO:H12	2.14	0.47
1:V:14:ASN:O	1:V:14:ASN:CG	2.56	0.47
1:R:1:MET:HE3	1:U:1:MET:SD	2.54	0.47
4:B:2074:HOH:O	1:b:32:ARG:NH1	2.47	0.47
1:2:19:GLU:HA	1:2:22:ARG:CZ	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:37:GLN:HB3	1:b:39:GLN:OE1	2.14	0.47
1:4:41:ARG:CD	1:4:42:TYR:CE2	2.98	0.47
1:E:1:MET:CE	1:H:1:MET:SD	3.03	0.47
1:6:14:ASN:OD1	1:8:13:ARG:NH2	2.48	0.47
1:M:63:GLU:OE2	4:M:2054:HOH:O	2.20	0.46
1:M:46:THR:CG2	1:M:53:ILE:HD12	2.46	0.46
1:c:61:HIS:HB3	1:e:47:THR:HG21	1.96	0.46
1:4:16:ASP:O	1:4:19:GLU:N	2.48	0.46
1:5:6:ARG:NH1	1:5:53:ILE:HD11	2.30	0.46
1:E:17:PRO:O	1:E:21:GLU:HB2	2.16	0.46
1:V:15:LEU:HD13	1:V:20:GLU:HB2	1.97	0.46
1:b:74:PHE:N	1:b:75:PRO:HD2	2.31	0.46
1:M:93:LYS:O	1:M:94:ASP:CB	2.62	0.46
1:4:65:HIS:NE2	1:V:45:ARG:HD3	2.31	0.45
1:6:19:GLU:HG2	1:6:22:ARG:NH2	2.31	0.45
1:B:13:ARG:NH2	1:D:14:ASN:OD1	2.49	0.45
4:E:2073:HOH:O	1:e:32:ARG:NE	2.46	0.45
1:2:45:ARG:HG2	1:2:51:GLY:O	2.17	0.45
1:4:12:PRO:C	1:4:14:ASN:H	2.24	0.45
1:A:87:HIS:CD2	1:B:45:ARG:HG3	2.51	0.45
1:d:1:MET:HE1	1:d:60:SER:HA	1.98	0.45
1:8:12:PRO:HB2	1:8:15:LEU:HD13	1.98	0.45
1:K:45:ARG:HD3	1:K:51:GLY:O	2.17	0.45
1:U:19:GLU:O	1:U:22:ARG:HG2	2.16	0.45
1:P:45:ARG:HD3	1:P:49:LYS:O	2.16	0.45
1:S:90:ARG:HG2	1:S:94:ASP:OXT	2.16	0.45
1:2:9:VAL:HG23	1:2:51:GLY:HA2	1.98	0.45
1:1:62:ASP:O	1:1:66:GLU:HG2	2.17	0.45
1:5:45:ARG:HD3	1:W:65:HIS:CE1	2.52	0.45
1:8:8:THR:HB	1:8:78:THR:OG1	2.16	0.45
1:D:6:ARG:CZ	1:D:53:ILE:HD11	2.47	0.45
1:2:12:PRO:HB2	1:2:15:LEU:HD13	1.98	0.44
1:2:84:LEU:CD2	1:3:53:ILE:HG21	2.48	0.44
1:U:16:ASP:HB3	1:U:19:GLU:CG	2.47	0.44
1:f:90:ARG:NE	1:f:93:LYS:O	2.50	0.44
1:4:61:HIS:CD2	1:W:1:MET:HG2	2.53	0.44
1:a:45:ARG:HD2	1:a:49:LYS:O	2.18	0.44
1:W:10:ASN:ND2	4:W:2005:HOH:O	2.48	0.44
1:Z:19:GLU:O	1:Z:23:LEU:N	2.45	0.44
1:a:9:VAL:HG23	1:a:51:GLY:HA2	2.00	0.44
1:e:45:ARG:NH1	1:e:45:ARG:HG3	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:6:ARG:CZ	1:6:53:ILE:HD11	2.48	0.44
1:d:74:PHE:N	1:d:75:PRO:HD2	2.32	0.44
1:W:45:ARG:HG2	1:Y:65:HIS:CE1	2.52	0.44
1:e:53:ILE:HG21	1:f:84:LEU:CD2	2.48	0.44
1:P:12:PRO:HD3	1:P:76:TYR:CD1	2.53	0.43
1:c:14:ASN:OD1	1:c:14:ASN:C	2.61	0.43
1:4:45:ARG:NH1	1:4:51:GLY:O	2.51	0.43
1:e:53:ILE:HG21	1:f:84:LEU:HD22	2.00	0.43
1:1:9:VAL:HG23	1:1:51:GLY:HA2	2.00	0.43
1:V:84:LEU:CD2	1:W:53:ILE:HG21	2.49	0.43
1:2:1:MET:SD	1:5:1:MET:HE1	2.57	0.43
1:W:12:PRO:HG2	1:W:15:LEU:HG	2.00	0.43
1:c:65:HIS:CE1	1:e:45:ARG:CD	3.00	0.43
1:e:82:GLU:HA	1:e:83:PRO:HD3	1.86	0.43
4:D:2143:HOH:O	1:d:91:VAL:O	2.21	0.43
1:V:90:ARG:HD2	1:V:91:VAL:N	2.34	0.43
1:M:53:ILE:HD13	1:N:84:LEU:HD21	2.01	0.43
1:5:45:ARG:HD2	1:W:65:HIS:NE2	2.34	0.43
1:H:18:ARG:HA	1:H:18:ARG:HE	1.83	0.43
1:B:1:MET:CE	1:I:1:MET:SD	3.04	0.43
1:J:6:ARG:CZ	1:J:53:ILE:HD11	2.49	0.43
1:e:47:THR:HG23	1:f:83:PRO:O	2.19	0.43
1:W:16:ASP:HB3	1:W:19:GLU:HG2	2.01	0.43
1:5:74:PHE:HB3	1:5:75:PRO:HD3	2.01	0.42
1:I:1:MET:CE	1:I:59:ASN:O	2.67	0.42
1:P:4:LEU:HD23	3:P:1097:EDO:H11	2.01	0.42
1:U:16:ASP:HB3	1:U:19:GLU:HG2	2.01	0.42
1:X:45:ARG:NH2	2:X:1095:CL:CL	2.89	0.42
1:a:9:VAL:HG22	1:a:77:LEU:CD2	2.49	0.42
1:9:15:LEU:HD13	1:9:20:GLU:HB2	2.02	0.42
1:e:4:LEU:HD23	3:e:1094:EDO:H11	2.01	0.42
1:9:74:PHE:N	1:9:75:PRO:CD	2.82	0.42
1:M:53:ILE:HD13	1:N:84:LEU:CD2	2.49	0.42
1:Y:45:ARG:HD3	1:Y:51:GLY:O	2.19	0.42
1:1:17:PRO:O	1:1:18:ARG:C	2.62	0.42
1:4:41:ARG:HD3	1:4:42:TYR:CZ	2.55	0.42
1:c:83:PRO:HG3	1:f:83:PRO:HG3	2.00	0.42
1:W:41:ARG:CZ	1:W:94:ASP:O	2.67	0.42
1:6:45:ARG:HG3	1:6:51:GLY:O	2.19	0.42
1:M:14:ASN:OD1	1:M:14:ASN:C	2.62	0.42
1:U:15:LEU:H	1:U:15:LEU:HD22	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:8:9:VAL:HG22	1:8:77:LEU:CD2	2.50	0.42
1:9:15:LEU:HD23	1:9:15:LEU:HA	1.95	0.42
1:P:45:ARG:HG3	1:P:45:ARG:HH11	1.84	0.42
1:U:22:ARG:HG2	1:U:23:LEU:N	2.33	0.42
1:d:8:THR:OG1	1:d:78:THR:HB	2.20	0.42
1:C:9:VAL:HG23	1:C:51:GLY:HA2	2.02	0.42
1:O:16:ASP:OD1	1:O:16:ASP:C	2.63	0.42
1:T:9:VAL:CG1	1:T:11:LEU:HD13	2.50	0.42
1:V:47:THR:HG23	1:W:83:PRO:O	2.20	0.42
1:K:9:VAL:HG22	1:K:77:LEU:CD2	2.50	0.41
1:V:27:GLU:HA	1:V:72:PRO:HG2	2.01	0.41
1:Z:37:GLN:NE2	4:Z:2020:HOH:O	2.53	0.41
1:F:9:VAL:CG1	1:F:11:LEU:HD13	2.51	0.41
1:U:18:ARG:HB2	1:U:18:ARG:NH1	2.35	0.41
1:f:41:ARG:HD3	1:f:42:TYR:CE2	2.55	0.41
1:1:1:MET:HE1	1:X:1:MET:SD	2.61	0.41
1:4:1:MET:HE1	1:W:1:MET:SD	2.59	0.41
1:6:74:PHE:HB3	1:6:75:PRO:HD3	2.01	0.41
1:7:41:ARG:HD3	1:7:42:TYR:CZ	2.55	0.41
1:N:46:THR:CG2	1:N:53:ILE:HG12	2.50	0.41
1:I:16:ASP:HB3	1:I:19:GLU:HB2	2.03	0.41
1:O:58:VAL:HG21	1:O:64:LEU:HB2	2.03	0.41
1:P:13:ARG:CZ	1:S:12:PRO:HB3	2.49	0.41
1:E:16:ASP:O	1:E:17:PRO:C	2.64	0.41
1:O:41:ARG:HD3	1:O:42:TYR:CZ	2.55	0.41
1:Y:20:GLU:O	1:Y:24:LYS:HB2	2.21	0.41
1:6:45:ARG:HD2	1:e:65:HIS:CE1	2.56	0.41
1:I:93:LYS:HG2	1:I:94:ASP:N	2.35	0.41
1:Y:31:SER:O	1:Y:35:GLN:HG3	2.21	0.41
1:b:16:ASP:HB3	1:b:19:GLU:HG2	2.02	0.41
1:d:29:ALA:O	1:d:33:THR:HG22	2.20	0.41
1:F:9:VAL:HG12	1:F:11:LEU:HD13	2.01	0.41
1:e:45:ARG:HG3	1:e:45:ARG:HH11	1.86	0.41
1:P:41:ARG:HD3	1:P:42:TYR:CZ	2.56	0.41
1:V:32:ARG:NH1	1:V:36:GLU:OE2	2.50	0.41
1:3:31:SER:CB	3:3:1096:EDO:H12	2.50	0.41
1:7:40:TRP:CZ2	1:7:43:LEU:HD13	2.56	0.41
1:H:18:ARG:NH2	1:H:21:GLU:OE1	2.53	0.41
1:K:1:MET:SD	1:N:60:SER:HA	2.61	0.41
1:X:1:MET:HE3	1:X:1:MET:HB2	1.94	0.41
1:a:18:ARG:O	1:a:22:ARG:CD	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:19:GLU:CB	1:b:22:ARG:NH2	2.83	0.41
1:b:19:GLU:HB2	1:b:22:ARG:NH2	2.36	0.41
1:1:1:MET:SD	1:X:60:SER:HA	2.61	0.41
1:2:82:GLU:OE2	1:3:46:THR:HG23	2.21	0.41
1:a:16:ASP:O	1:a:19:GLU:HB3	2.20	0.41
1:A:74:PHE:HB3	1:A:75:PRO:HD3	2.03	0.40
1:L:23:LEU:HD23	1:L:23:LEU:HA	1.96	0.40
1:3:74:PHE:N	1:3:75:PRO:CD	2.85	0.40
1:4:19:GLU:OE1	1:4:22:ARG:NE	2.54	0.40
1:8:74:PHE:HB3	1:8:75:PRO:HD3	2.03	0.40
1:E:16:ASP:O	1:E:19:GLU:N	2.54	0.40
1:Y:40:TRP:CH2	3:Y:1094:EDO:H21	2.57	0.40
1:4:61:HIS:HB3	1:V:47:THR:HG21	2.03	0.40
1:U:93:LYS:N	1:U:93:LYS:CD	2.84	0.40
1:V:60:SER:HA	1:Y:1:MET:SD	2.60	0.40
1:d:6:ARG:CZ	1:d:53:ILE:HD11	2.52	0.40
1:1:45:ARG:NH1	1:1:51:GLY:O	2.55	0.40
1:7:74:PHE:HB3	1:7:75:PRO:HD3	2.03	0.40
1:P:45:ARG:HG3	1:P:45:ARG:NH1	2.37	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	1	92/94 (98%)	89 (97%)	2 (2%)	1 (1%)	12	8
1	2	91/94 (97%)	89 (98%)	2 (2%)	0	100	100
1	3	88/94 (94%)	86 (98%)	2 (2%)	0	100	100
1	4	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
1	5	90/94 (96%)	88 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	6	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	7	90/94 (96%)	86 (96%)	4 (4%)	0	100	100
1	8	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	9	87/94 (93%)	85 (98%)	2 (2%)	0	100	100
1	A	92/94 (98%)	90 (98%)	1 (1%)	1 (1%)	12	8
1	B	92/94 (98%)	92 (100%)	0	0	100	100
1	C	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
1	D	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	E	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
1	F	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
1	G	92/94 (98%)	92 (100%)	0	0	100	100
1	H	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
1	I	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	J	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	K	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
1	L	93/94 (99%)	93 (100%)	0	0	100	100
1	M	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	N	92/94 (98%)	92 (100%)	0	0	100	100
1	O	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	P	92/94 (98%)	92 (100%)	0	0	100	100
1	R	93/94 (99%)	93 (100%)	0	0	100	100
1	S	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
1	T	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	U	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
1	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
1	W	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
1	X	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	Y	90/94 (96%)	89 (99%)	1 (1%)	0	100	100
1	Z	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	a	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	b	92/94 (98%)	92 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	c	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	d	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
1	e	90/94 (96%)	89 (99%)	1 (1%)	0	100	100
1	f	92/94 (98%)	92 (100%)	0	0	100	100
All	All	3664/3760 (97%)	3609 (98%)	53 (1%)	2 (0%)	48	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	17	PRO
1	A	17	PRO

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	1	87/87 (100%)	84 (97%)	3 (3%)	32	35
1	2	86/87 (99%)	80 (93%)	6 (7%)	12	10
1	3	85/87 (98%)	80 (94%)	5 (6%)	16	14
1	4	87/87 (100%)	85 (98%)	2 (2%)	45	51
1	5	85/87 (98%)	80 (94%)	5 (6%)	16	14
1	6	87/87 (100%)	84 (97%)	3 (3%)	32	35
1	7	85/87 (98%)	84 (99%)	1 (1%)	67	74
1	8	87/87 (100%)	81 (93%)	6 (7%)	13	10
1	9	84/87 (97%)	80 (95%)	4 (5%)	21	21
1	A	87/87 (100%)	86 (99%)	1 (1%)	70	77
1	B	87/87 (100%)	82 (94%)	5 (6%)	17	15
1	C	87/87 (100%)	86 (99%)	1 (1%)	70	77
1	D	87/87 (100%)	86 (99%)	1 (1%)	70	77
1	E	87/87 (100%)	84 (97%)	3 (3%)	32	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	87/87 (100%)	80 (92%)	7 (8%)	10	7
1	G	87/87 (100%)	87 (100%)	0	100	100
1	H	87/87 (100%)	85 (98%)	2 (2%)	45	51
1	I	87/87 (100%)	87 (100%)	0	100	100
1	J	87/87 (100%)	85 (98%)	2 (2%)	45	51
1	K	87/87 (100%)	85 (98%)	2 (2%)	45	51
1	L	88/87 (101%)	84 (96%)	4 (4%)	23	24
1	M	87/87 (100%)	85 (98%)	2 (2%)	45	51
1	N	87/87 (100%)	86 (99%)	1 (1%)	70	77
1	O	87/87 (100%)	85 (98%)	2 (2%)	45	51
1	P	87/87 (100%)	84 (97%)	3 (3%)	32	35
1	R	88/87 (101%)	86 (98%)	2 (2%)	45	51
1	S	87/87 (100%)	87 (100%)	0	100	100
1	T	87/87 (100%)	84 (97%)	3 (3%)	32	35
1	U	87/87 (100%)	82 (94%)	5 (6%)	17	15
1	V	87/87 (100%)	83 (95%)	4 (5%)	23	23
1	W	87/87 (100%)	81 (93%)	6 (7%)	13	10
1	X	87/87 (100%)	84 (97%)	3 (3%)	32	35
1	Y	86/87 (99%)	80 (93%)	6 (7%)	12	10
1	Z	87/87 (100%)	84 (97%)	3 (3%)	32	35
1	a	87/87 (100%)	82 (94%)	5 (6%)	17	15
1	b	87/87 (100%)	82 (94%)	5 (6%)	17	15
1	c	87/87 (100%)	85 (98%)	2 (2%)	45	51
1	d	87/87 (100%)	81 (93%)	6 (7%)	13	10
1	e	85/87 (98%)	82 (96%)	3 (4%)	31	34
1	f	87/87 (100%)	86 (99%)	1 (1%)	70	77
All	All	3469/3480 (100%)	3344 (96%)	125 (4%)	30	32

All (125) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	11	LEU
1	1	15	LEU

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Mol	Chain	Res	Type
1	1	21	GLU
1	2	14	ASN
1	2	15	LEU
1	2	16	ASP
1	2	20	GLU
1	2	45	ARG
1	2	69	TRP
1	3	14	ASN
1	3	19	GLU
1	3	20	GLU
1	3	46	THR
1	3	53	ILE
1	4	21	GLU
1	4	23	LEU
1	5	15	LEU
1	5	32	ARG
1	5	41	ARG
1	5	46	THR
1	5	53	ILE
1	6	1	MET
1	6	13	ARG
1	6	94	ASP
1	7	21	GLU
1	8	11	LEU
1	8	13	ARG
1	8	18	ARG
1	8	19	GLU
1	8	20	GLU
1	8	47	THR
1	9	15	LEU
1	9	32	ARG
1	9	66	GLU
1	9	93	LYS
1	A	19	GLU
1	B	13	ARG
1	B	19	GLU
1	B	22	ARG
1	B	39	GLN
1	B	45	ARG
1	C	15	LEU
1	D	11	LEU
1	E	13	ARG

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Mol	Chain	Res	Type
1	E	14	ASN
1	E	93	LYS
1	F	11	LEU
1	F	13	ARG
1	F	15	LEU
1	F	30	ARG
1	F	41	ARG
1	F	91	VAL
1	F	93	LYS
1	H	18	ARG
1	H	23	LEU
1	J	8	THR
1	J	23	LEU
1	K	1	MET
1	K	15	LEU
1	L	13	ARG
1	L	15	LEU
1	L	23	LEU
1	L	47	THR
1	M	18	ARG
1	M	21	GLU
1	N	13	ARG
1	O	24	LYS
1	O	47	THR
1	P	26	SER
1	P	30	ARG
1	P	47	THR
1	R	53[A]	ILE
1	R	53[B]	ILE
1	T	11	LEU
1	T	41	ARG
1	T	53	ILE
1	U	1	MET
1	U	11	LEU
1	U	15	LEU
1	U	78	THR
1	U	93	LYS
1	V	21	GLU
1	V	47	THR
1	V	58	VAL
1	V	93	LYS
1	W	18	ARG

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Mol	Chain	Res	Type
1	W	21	GLU
1	W	32	ARG
1	W	39	GLN
1	W	66	GLU
1	W	93	LYS
1	X	15	LEU
1	X	47	THR
1	X	93	LYS
1	Y	1	MET
1	Y	9	VAL
1	Y	15	LEU
1	Y	22	ARG
1	Y	23	LEU
1	Y	84	LEU
1	Z	15	LEU
1	Z	37	GLN
1	Z	47	THR
1	a	10	ASN
1	a	14	ASN
1	a	18	ARG
1	a	23	LEU
1	a	91	VAL
1	b	10	ASN
1	b	11	LEU
1	b	13	ARG
1	b	30	ARG
1	b	37	GLN
1	c	15	LEU
1	c	23	LEU
1	d	18	ARG
1	d	22	ARG
1	d	32	ARG
1	d	33	THR
1	d	66	GLU
1	d	93	LYS
1	e	1	MET
1	e	15	LEU
1	e	47	THR
1	f	47	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	14	ASN
1	3	59	ASN
1	4	65	HIS
1	5	10	ASN
1	7	14	ASN
1	7	37	GLN
1	8	61	HIS
1	B	37	GLN
1	C	61	HIS
1	D	61	HIS
1	E	86	HIS
1	F	37	GLN
1	H	37	GLN
1	I	61	HIS
1	J	61	HIS
1	K	37	GLN
1	M	61	HIS
1	P	14	ASN
1	R	37	GLN
1	R	59	ASN
1	S	37	GLN
1	T	37	GLN
1	U	37	GLN
1	V	14	ASN
1	V	61	HIS
1	V	86	HIS
1	Y	14	ASN
1	b	10	ASN
1	d	10	ASN
1	f	37	GLN

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 118 ligands modelled in this entry, 40 are monoatomic - leaving 78 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	$\# Z > 2$
3	EDO	J	1096	-	3,3,3	0.40	0	2,2,2	0.35	0
3	EDO	b	1096	-	3,3,3	0.38	0	2,2,2	0.56	0
3	EDO	8	1096	-	3,3,3	0.40	0	2,2,2	0.61	0
3	EDO	f	1096	-	3,3,3	0.44	0	2,2,2	0.40	0
3	EDO	X	1096	-	3,3,3	0.48	0	2,2,2	0.28	0
3	EDO	T	1096	-	3,3,3	0.42	0	2,2,2	0.36	0
3	EDO	9	1095	-	3,3,3	0.40	0	2,2,2	0.65	0
3	EDO	O	1096	-	3,3,3	0.46	0	2,2,2	0.29	0
3	EDO	A	1097	-	3,3,3	0.43	0	2,2,2	0.29	0
3	EDO	d	1097	-	3,3,3	0.42	0	2,2,2	0.36	0
3	EDO	H	1096	-	3,3,3	0.54	0	2,2,2	0.42	0
3	EDO	e	1094	-	3,3,3	0.45	0	2,2,2	0.50	0
3	EDO	M	1097	-	3,3,3	0.44	0	2,2,2	0.34	0
3	EDO	5	1095	-	3,3,3	0.40	0	2,2,2	0.37	0
3	EDO	A	1096	-	3,3,3	0.40	0	2,2,2	0.39	0
3	EDO	B	1097	-	3,3,3	0.41	0	2,2,2	0.38	0
3	EDO	J	1097	-	3,3,3	0.44	0	2,2,2	0.32	0
3	EDO	b	1097	-	3,3,3	0.44	0	2,2,2	0.31	0
3	EDO	a	1097	-	3,3,3	0.42	0	2,2,2	0.35	0
3	EDO	7	1095	-	3,3,3	0.43	0	2,2,2	0.35	0
3	EDO	1	1097	-	3,3,3	0.44	0	2,2,2	0.35	0
3	EDO	4	1096	-	3,3,3	0.46	0	2,2,2	0.29	0
3	EDO	3	1097	-	3,3,3	0.43	0	2,2,2	0.41	0
3	EDO	F	1096	-	3,3,3	0.46	0	2,2,2	0.38	0
3	EDO	c	1097	-	3,3,3	0.44	0	2,2,2	0.32	0
3	EDO	B	1096	-	3,3,3	0.48	0	2,2,2	0.38	0
3	EDO	Z	1096	-	3,3,3	0.41	0	2,2,2	0.37	0
3	EDO	R	1096	-	3,3,3	0.49	0	2,2,2	0.32	0
3	EDO	C	1097	-	3,3,3	0.42	0	2,2,2	0.36	0
3	EDO	M	1096	-	3,3,3	0.45	0	2,2,2	0.31	0
3	EDO	P	1097	-	3,3,3	0.41	0	2,2,2	0.31	0
3	EDO	D	1096	-	3,3,3	0.40	0	2,2,2	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	Y	1094	-	3,3,3	0.44	0	2,2,2	0.31	0
3	EDO	R	1097	-	3,3,3	0.43	0	2,2,2	0.39	0
3	EDO	2	1096	-	3,3,3	0.43	0	2,2,2	0.36	0
3	EDO	e	1095	-	3,3,3	0.43	0	2,2,2	0.31	0
3	EDO	9	1096	-	3,3,3	0.44	0	2,2,2	0.33	0
3	EDO	O	1097	-	3,3,3	0.43	0	2,2,2	0.34	0
3	EDO	E	1096	-	3,3,3	0.50	0	2,2,2	0.25	0
3	EDO	T	1097	-	3,3,3	0.44	0	2,2,2	0.41	0
3	EDO	U	1096	-	3,3,3	0.43	0	2,2,2	0.40	0
3	EDO	G	1097	-	3,3,3	0.38	0	2,2,2	0.50	0
3	EDO	C	1096	-	3,3,3	0.50	0	2,2,2	0.41	0
3	EDO	f	1097	-	3,3,3	0.44	0	2,2,2	0.30	0
3	EDO	S	1096	-	3,3,3	0.41	0	2,2,2	0.37	0
3	EDO	L	1097	-	3,3,3	0.43	0	2,2,2	0.32	0
3	EDO	d	1096	-	3,3,3	0.41	0	2,2,2	0.34	0
3	EDO	W	1097	-	3,3,3	0.40	0	2,2,2	0.34	0
3	EDO	L	1096	-	3,3,3	0.44	0	2,2,2	0.39	0
3	EDO	2	1095	-	3,3,3	0.44	0	2,2,2	0.28	0
3	EDO	V	1096	-	3,3,3	0.38	0	2,2,2	0.39	0
3	EDO	X	1097	-	3,3,3	0.43	0	2,2,2	0.33	0
3	EDO	E	1097	-	3,3,3	0.42	0	2,2,2	0.37	0
3	EDO	H	1097	-	3,3,3	0.44	0	2,2,2	0.34	0
3	EDO	8	1097	-	3,3,3	0.42	0	2,2,2	0.37	0
3	EDO	3	1096	-	3,3,3	0.41	0	2,2,2	0.29	0
3	EDO	D	1097	-	3,3,3	0.43	0	2,2,2	0.31	0
3	EDO	F	1097	-	3,3,3	0.40	0	2,2,2	0.37	0
3	EDO	G	1096	-	3,3,3	0.41	0	2,2,2	0.36	0
3	EDO	7	1094	-	3,3,3	0.41	0	2,2,2	0.43	0
3	EDO	P	1096	-	3,3,3	0.43	0	2,2,2	0.35	0
3	EDO	1	1096	-	3,3,3	0.39	0	2,2,2	0.31	0
3	EDO	4	1097	-	3,3,3	0.39	0	2,2,2	0.35	0
3	EDO	W	1096	-	3,3,3	0.40	0	2,2,2	0.39	0
3	EDO	6	1097	-	3,3,3	0.39	0	2,2,2	0.25	0
3	EDO	a	1096	-	3,3,3	0.47	0	2,2,2	0.45	0
3	EDO	S	1097	-	3,3,3	0.42	0	2,2,2	0.37	0
3	EDO	5	1094	-	3,3,3	0.43	0	2,2,2	0.38	0
3	EDO	I	1096	-	3,3,3	0.34	0	2,2,2	0.83	0
3	EDO	V	1097	-	3,3,3	0.43	0	2,2,2	0.35	0
3	EDO	K	1097	-	3,3,3	0.44	0	2,2,2	0.31	0
3	EDO	c	1096	-	3,3,3	0.40	0	2,2,2	0.37	0
3	EDO	Y	1093	-	3,3,3	0.39	0	2,2,2	0.48	0
3	EDO	K	1096	-	3,3,3	0.40	0	2,2,2	0.81	0
3	EDO	N	1097	-	3,3,3	0.42	0	2,2,2	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	I	1097	-	3,3,3	0.42	0	2,2,2	0.40	0
3	EDO	N	1096	-	3,3,3	0.46	0	2,2,2	0.32	0
3	EDO	6	1096	-	3,3,3	0.45	0	2,2,2	0.28	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
3	EDO	J	1096	-	-	0/1/1/1	-
3	EDO	b	1096	-	-	0/1/1/1	-
3	EDO	8	1096	-	-	0/1/1/1	-
3	EDO	f	1096	-	-	0/1/1/1	-
3	EDO	X	1096	-	-	0/1/1/1	-
3	EDO	T	1096	-	-	0/1/1/1	-
3	EDO	9	1095	-	-	1/1/1/1	-
3	EDO	O	1096	-	-	0/1/1/1	-
3	EDO	A	1097	-	-	0/1/1/1	-
3	EDO	d	1097	-	-	0/1/1/1	-
3	EDO	H	1096	-	-	0/1/1/1	-
3	EDO	e	1094	-	-	1/1/1/1	-
3	EDO	M	1097	-	-	0/1/1/1	-
3	EDO	5	1095	-	-	0/1/1/1	-
3	EDO	A	1096	-	-	0/1/1/1	-
3	EDO	B	1097	-	-	0/1/1/1	-
3	EDO	J	1097	-	-	0/1/1/1	-
3	EDO	b	1097	-	-	0/1/1/1	-
3	EDO	a	1097	-	-	0/1/1/1	-
3	EDO	7	1095	-	-	0/1/1/1	-
3	EDO	1	1097	-	-	0/1/1/1	-
3	EDO	4	1096	-	-	0/1/1/1	-
3	EDO	3	1097	-	-	0/1/1/1	-
3	EDO	F	1096	-	-	1/1/1/1	-
3	EDO	c	1097	-	-	0/1/1/1	-
3	EDO	B	1096	-	-	0/1/1/1	-
3	EDO	Z	1096	-	-	0/1/1/1	-
3	EDO	R	1096	-	-	0/1/1/1	-
3	EDO	C	1097	-	-	0/1/1/1	-
3	EDO	M	1096	-	-	0/1/1/1	-
3	EDO	P	1097	-	-	0/1/1/1	-
3	EDO	D	1096	-	-	1/1/1/1	-
3	EDO	Y	1094	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	R	1097	-	-	0/1/1/1	-
3	EDO	2	1096	-	-	0/1/1/1	-
3	EDO	e	1095	-	-	0/1/1/1	-
3	EDO	9	1096	-	-	0/1/1/1	-
3	EDO	O	1097	-	-	1/1/1/1	-
3	EDO	E	1096	-	-	0/1/1/1	-
3	EDO	T	1097	-	-	0/1/1/1	-
3	EDO	U	1096	-	-	0/1/1/1	-
3	EDO	G	1097	-	-	0/1/1/1	-
3	EDO	C	1096	-	-	0/1/1/1	-
3	EDO	f	1097	-	-	0/1/1/1	-
3	EDO	S	1096	-	-	0/1/1/1	-
3	EDO	L	1097	-	-	0/1/1/1	-
3	EDO	d	1096	-	-	0/1/1/1	-
3	EDO	W	1097	-	-	1/1/1/1	-
3	EDO	L	1096	-	-	0/1/1/1	-
3	EDO	2	1095	-	-	0/1/1/1	-
3	EDO	V	1096	-	-	1/1/1/1	-
3	EDO	X	1097	-	-	0/1/1/1	-
3	EDO	E	1097	-	-	0/1/1/1	-
3	EDO	H	1097	-	-	0/1/1/1	-
3	EDO	8	1097	-	-	0/1/1/1	-
3	EDO	3	1096	-	-	0/1/1/1	-
3	EDO	D	1097	-	-	0/1/1/1	-
3	EDO	F	1097	-	-	0/1/1/1	-
3	EDO	G	1096	-	-	0/1/1/1	-
3	EDO	7	1094	-	-	0/1/1/1	-
3	EDO	P	1096	-	-	0/1/1/1	-
3	EDO	1	1096	-	-	0/1/1/1	-
3	EDO	4	1097	-	-	1/1/1/1	-
3	EDO	W	1096	-	-	0/1/1/1	-
3	EDO	6	1097	-	-	0/1/1/1	-
3	EDO	a	1096	-	-	0/1/1/1	-
3	EDO	S	1097	-	-	0/1/1/1	-
3	EDO	5	1094	-	-	0/1/1/1	-
3	EDO	I	1096	-	-	0/1/1/1	-
3	EDO	V	1097	-	-	1/1/1/1	-
3	EDO	K	1097	-	-	0/1/1/1	-
3	EDO	c	1096	-	-	0/1/1/1	-
3	EDO	Y	1093	-	-	1/1/1/1	-
3	EDO	K	1096	-	-	1/1/1/1	-
3	EDO	N	1097	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	I	1097	-	-	0/1/1/1	-
3	EDO	N	1096	-	-	0/1/1/1	-
3	EDO	6	1096	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	4	1097	EDO	O1-C1-C2-O2
3	K	1096	EDO	O1-C1-C2-O2
3	Y	1093	EDO	O1-C1-C2-O2
3	W	1097	EDO	O1-C1-C2-O2
3	V	1096	EDO	O1-C1-C2-O2
3	V	1097	EDO	O1-C1-C2-O2
3	e	1094	EDO	O1-C1-C2-O2
3	O	1097	EDO	O1-C1-C2-O2
3	D	1096	EDO	O1-C1-C2-O2
3	F	1096	EDO	O1-C1-C2-O2
3	9	1095	EDO	O1-C1-C2-O2

There are no ring outliers.

8 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	e	1094	EDO	1	0
3	A	1096	EDO	1	0
3	P	1097	EDO	1	0
3	Y	1094	EDO	1	0
3	L	1097	EDO	1	0
3	3	1096	EDO	1	0
3	F	1097	EDO	1	0
3	6	1097	EDO	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	1	94/94 (100%)	-0.19	1 (1%) 77 78	26, 41, 88, 121	0
1	2	93/94 (98%)	-0.26	1 (1%) 77 78	25, 39, 89, 113	0
1	3	92/94 (97%)	-0.38	2 (2%) 62 64	26, 37, 74, 106	0
1	4	94/94 (100%)	-0.13	0 100 100	29, 45, 91, 104	0
1	5	92/94 (97%)	-0.31	1 (1%) 77 78	23, 39, 59, 93	0
1	6	94/94 (100%)	-0.27	1 (1%) 77 78	25, 42, 82, 115	0
1	7	92/94 (97%)	-0.35	1 (1%) 77 78	25, 41, 73, 83	0
1	8	94/94 (100%)	-0.31	0 100 100	25, 41, 87, 105	0
1	9	91/94 (96%)	-0.36	1 (1%) 77 78	26, 40, 89, 105	0
1	A	94/94 (100%)	-0.56	0 100 100	18, 31, 71, 89	0
1	B	94/94 (100%)	-0.49	1 (1%) 77 78	16, 29, 82, 100	0
1	C	94/94 (100%)	-0.76	0 100 100	14, 24, 57, 86	0
1	D	94/94 (100%)	-0.81	0 100 100	15, 24, 68, 102	0
1	E	94/94 (100%)	-0.45	1 (1%) 77 78	15, 31, 82, 113	0
1	F	94/94 (100%)	-0.49	1 (1%) 77 78	16, 30, 70, 101	0
1	G	94/94 (100%)	-0.84	0 100 100	15, 24, 41, 67	0
1	H	94/94 (100%)	-0.60	2 (2%) 63 65	17, 28, 75, 133	0
1	I	94/94 (100%)	-0.56	1 (1%) 77 78	18, 28, 67, 92	0
1	J	94/94 (100%)	-0.64	0 100 100	15, 28, 77, 108	0
1	K	94/94 (100%)	-0.64	0 100 100	17, 31, 67, 88	0
1	L	94/94 (100%)	-0.60	1 (1%) 77 78	18, 29, 67, 102	1 (1%)
1	M	94/94 (100%)	-0.51	0 100 100	21, 34, 73, 103	0
1	N	94/94 (100%)	-0.69	0 100 100	18, 31, 51, 69	0
1	O	94/94 (100%)	-0.42	0 100 100	19, 34, 68, 104	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	P	94/94 (100%)	-0.44	0 100 100	21, 34, 84, 127	0
1	R	94/94 (100%)	-0.66	0 100 100	18, 29, 59, 76	1 (1%)
1	S	94/94 (100%)	-0.68	0 100 100	19, 29, 49, 77	0
1	T	94/94 (100%)	-0.65	0 100 100	17, 28, 67, 98	0
1	U	94/94 (100%)	-0.34	3 (3%) 50 52	21, 34, 87, 122	0
1	V	94/94 (100%)	0.05	1 (1%) 77 78	26, 47, 104, 166	0
1	W	94/94 (100%)	0.13	4 (4%) 40 42	25, 47, 84, 115	0
1	X	94/94 (100%)	-0.23	0 100 100	29, 40, 73, 105	0
1	Y	91/94 (96%)	-0.05	5 (5%) 32 34	25, 40, 80, 111	1 (1%)
1	Z	94/94 (100%)	-0.30	1 (1%) 77 78	25, 38, 75, 124	0
1	a	94/94 (100%)	-0.37	0 100 100	25, 39, 84, 104	0
1	b	94/94 (100%)	-0.57	0 100 100	23, 34, 53, 84	0
1	c	94/94 (100%)	-0.56	0 100 100	21, 32, 55, 81	0
1	d	94/94 (100%)	-0.36	0 100 100	24, 38, 80, 105	0
1	e	92/94 (97%)	-0.47	0 100 100	21, 33, 65, 82	0
1	f	94/94 (100%)	-0.52	0 100 100	19, 31, 65, 100	0
All	All	3745/3760 (99%)	-0.44	29 (0%) 82 83	14, 35, 77, 166	3 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	15	LEU	4.7
1	Y	17	PRO	4.0
1	W	94	ASP	3.8
1	W	93	LYS	3.4
1	I	14	ASN	2.9
1	V	18	ARG	2.7
1	7	92	GLY	2.7
1	Y	18	ARG	2.7
1	B	18	ARG	2.6
1	Y	51	GLY	2.6
1	1	14	ASN	2.6
1	H	17	PRO	2.5
1	F	18	ARG	2.4
1	W	60	SER	2.3
1	Y	16	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	Z	17	PRO	2.3
1	H	18	ARG	2.3
1	U	15	LEU	2.3
1	3	17	PRO	2.2
1	5	13	ARG	2.1
1	9	93	LYS	2.1
1	W	89	ALA	2.1
1	L	13	ARG	2.1
1	U	17	PRO	2.1
1	3	13	ARG	2.1
1	Y	15	LEU	2.1
1	6	93	LYS	2.0
1	U	18	ARG	2.0
1	2	69	TRP	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
3	EDO	O	1097	4/4	0.82	0.12	43,52,53,53	0
3	EDO	Y	1093	4/4	0.82	0.13	44,53,54,54	0
3	EDO	A	1096	4/4	0.84	0.12	35,42,49,49	0
3	EDO	X	1096	4/4	0.84	0.09	41,49,51,52	0
3	EDO	I	1096	4/4	0.84	0.13	44,53,55,57	0
3	EDO	V	1096	4/4	0.85	0.11	42,51,52,52	0
3	EDO	6	1097	4/4	0.87	0.13	39,47,50,50	0
3	EDO	3	1097	4/4	0.87	0.12	40,48,50,51	0
3	EDO	4	1096	4/4	0.87	0.10	40,48,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	K	1096	4/4	0.87	0.09	37,44,47,49	0
3	EDO	D	1096	4/4	0.88	0.10	27,33,36,36	0
3	EDO	9	1095	4/4	0.88	0.08	42,51,54,55	0
3	EDO	J	1096	4/4	0.88	0.11	37,45,47,53	0
3	EDO	7	1094	4/4	0.88	0.10	39,46,50,52	0
3	EDO	c	1096	4/4	0.88	0.08	35,42,44,47	0
3	EDO	1	1096	4/4	0.89	0.08	43,52,53,55	0
3	EDO	P	1097	4/4	0.89	0.11	41,49,51,54	0
3	EDO	B	1096	4/4	0.89	0.10	30,36,39,40	0
3	EDO	e	1094	4/4	0.89	0.09	32,38,41,45	0
3	EDO	G	1097	4/4	0.90	0.10	29,35,42,42	0
3	EDO	H	1096	4/4	0.90	0.08	34,41,43,45	0
3	EDO	2	1095	4/4	0.90	0.09	41,50,52,53	0
3	EDO	8	1096	4/4	0.90	0.09	40,48,51,51	0
2	CL	V	1095	1/1	0.90	0.09	43,43,43,43	0
3	EDO	Y	1094	4/4	0.90	0.13	38,46,47,48	0
3	EDO	L	1096	4/4	0.90	0.09	36,43,46,48	0
3	EDO	L	1097	4/4	0.90	0.12	25,33,39,39	0
2	CL	e	1093	1/1	0.91	0.09	38,38,38,38	0
3	EDO	4	1097	4/4	0.91	0.11	37,44,49,50	0
3	EDO	a	1096	4/4	0.91	0.09	37,44,47,50	0
3	EDO	V	1097	4/4	0.91	0.11	39,47,49,49	0
3	EDO	5	1095	4/4	0.91	0.11	40,48,51,52	0
3	EDO	5	1094	4/4	0.92	0.14	37,45,47,48	0
3	EDO	T	1097	4/4	0.92	0.09	34,41,45,45	0
3	EDO	3	1096	4/4	0.92	0.09	35,42,47,47	0
3	EDO	b	1096	4/4	0.92	0.12	40,48,53,53	0
3	EDO	C	1096	4/4	0.92	0.07	29,35,37,37	0
3	EDO	9	1096	4/4	0.92	0.10	29,35,39,41	0
3	EDO	f	1096	4/4	0.92	0.07	37,45,46,47	0
3	EDO	O	1096	4/4	0.93	0.09	27,33,35,37	0
2	CL	Y	1092	1/1	0.93	0.09	42,42,42,42	0
3	EDO	W	1096	4/4	0.93	0.09	37,44,46,48	0
3	EDO	W	1097	4/4	0.93	0.10	34,40,47,47	0
3	EDO	S	1097	4/4	0.94	0.08	27,33,35,37	0
3	EDO	6	1096	4/4	0.94	0.07	25,30,32,35	0
2	CL	N	1095	1/1	0.94	0.08	32,32,32,32	0
3	EDO	N	1097	4/4	0.94	0.08	23,28,31,34	0
3	EDO	8	1097	4/4	0.94	0.08	31,37,39,40	0
3	EDO	E	1096	4/4	0.94	0.07	28,34,37,37	0
3	EDO	F	1097	4/4	0.94	0.09	25,31,36,36	0
2	CL	8	1095	1/1	0.95	0.08	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	F	1096	4/4	0.95	0.06	31,37,37,40	0
2	CL	5	1093	1/1	0.95	0.07	34,34,34,34	0
3	EDO	b	1097	4/4	0.95	0.07	30,36,37,40	0
3	EDO	2	1096	4/4	0.95	0.09	28,34,36,36	0
3	EDO	d	1096	4/4	0.95	0.05	30,36,38,38	0
3	EDO	d	1097	4/4	0.95	0.08	27,33,36,41	0
2	CL	S	1095	1/1	0.95	0.06	34,34,34,34	0
3	EDO	e	1095	4/4	0.95	0.08	33,39,41,41	0
3	EDO	M	1097	4/4	0.95	0.07	32,39,41,41	0
3	EDO	Z	1096	4/4	0.96	0.08	30,37,38,41	0
3	EDO	N	1096	4/4	0.96	0.06	20,28,32,34	0
3	EDO	7	1095	4/4	0.96	0.08	31,37,39,41	0
3	EDO	E	1097	4/4	0.96	0.05	21,27,28,33	0
2	CL	d	1095	1/1	0.96	0.07	42,42,42,42	0
3	EDO	M	1096	4/4	0.96	0.05	30,36,40,42	0
3	EDO	R	1096	4/4	0.96	0.05	25,30,32,34	0
3	EDO	X	1097	4/4	0.96	0.12	33,39,42,42	0
3	EDO	S	1096	4/4	0.96	0.07	26,32,37,38	0
3	EDO	A	1097	4/4	0.96	0.07	20,28,30,33	0
3	EDO	H	1097	4/4	0.97	0.05	22,27,31,32	0
2	CL	6	1095	1/1	0.97	0.05	36,36,36,36	0
3	EDO	1	1097	4/4	0.97	0.06	27,32,34,34	0
3	EDO	P	1096	4/4	0.97	0.06	27,32,35,35	0
3	EDO	J	1097	4/4	0.97	0.05	24,29,32,35	0
2	CL	7	1093	1/1	0.97	0.04	34,34,34,34	0
3	EDO	R	1097	4/4	0.97	0.06	22,27,32,33	0
3	EDO	a	1097	4/4	0.97	0.07	29,35,37,38	0
3	EDO	K	1097	4/4	0.97	0.09	19,25,30,30	0
2	CL	4	1095	1/1	0.97	0.07	34,34,34,34	0
3	EDO	T	1096	4/4	0.97	0.07	24,29,32,32	0
2	CL	3	1095	1/1	0.97	0.05	37,37,37,37	0
3	EDO	U	1096	4/4	0.97	0.09	29,35,38,41	0
2	CL	O	1095	1/1	0.97	0.05	32,32,32,32	0
2	CL	f	1095	1/1	0.97	0.05	30,30,30,30	0
3	EDO	B	1097	4/4	0.97	0.06	19,23,26,28	0
3	EDO	f	1097	4/4	0.97	0.10	27,33,35,35	0
2	CL	B	1095	1/1	0.98	0.04	23,23,23,23	0
2	CL	P	1095	1/1	0.98	0.06	35,35,35,35	0
2	CL	D	1095	1/1	0.98	0.03	21,21,21,21	0
3	EDO	C	1097	4/4	0.98	0.05	17,21,21,23	0
2	CL	T	1095	1/1	0.98	0.04	31,31,31,31	0
3	EDO	D	1097	4/4	0.98	0.08	18,22,25,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CL	J	1095	1/1	0.98	0.04	26,26,26,26	0
2	CL	W	1095	1/1	0.98	0.04	30,30,30,30	0
3	EDO	c	1097	4/4	0.98	0.05	24,29,32,34	0
2	CL	X	1095	1/1	0.98	0.05	33,33,33,33	0
2	CL	L	1095	1/1	0.98	0.05	26,26,26,26	0
3	EDO	G	1096	4/4	0.98	0.04	17,23,24,28	0
2	CL	a	1095	1/1	0.98	0.04	31,31,31,31	0
2	CL	b	1095	1/1	0.98	0.04	33,33,33,33	0
2	CL	1	1095	1/1	0.98	0.04	29,29,29,29	0
2	CL	2	1094	1/1	0.99	0.03	29,29,29,29	0
2	CL	M	1095	1/1	0.99	0.03	29,29,29,29	0
2	CL	C	1095	1/1	0.99	0.02	20,20,20,20	0
2	CL	Z	1095	1/1	0.99	0.05	36,36,36,36	0
2	CL	9	1094	1/1	0.99	0.04	32,32,32,32	0
2	CL	E	1095	1/1	0.99	0.03	27,27,27,27	0
2	CL	c	1095	1/1	0.99	0.04	31,31,31,31	0
2	CL	R	1095	1/1	0.99	0.03	22,22,22,22	0
2	CL	F	1095	1/1	0.99	0.04	29,29,29,29	0
3	EDO	I	1097	4/4	0.99	0.03	18,21,24,28	0
2	CL	G	1095	1/1	0.99	0.02	22,22,22,22	0
2	CL	U	1095	1/1	0.99	0.02	24,24,24,24	0
2	CL	A	1095	1/1	0.99	0.03	23,23,23,23	0
2	CL	K	1095	1/1	1.00	0.02	22,22,22,22	0
2	CL	I	1095	1/1	1.00	0.04	21,21,21,21	0
2	CL	H	1095	1/1	1.00	0.02	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.