



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:01 PM UTC

PDB ID : 4KT2 / pdb_00004kt2
Title : Crystal structure of d-mannonate dehydratase from chromohalobacter salexigens complexed with mg and glycerol
Authors : Fedorov, A.A.; Fedorov, E.V.; Wichelecki, D.; Gerlt, J.A.; Almo, S.C.
Deposited on : 2013-05-19
Resolution : 1.80 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:

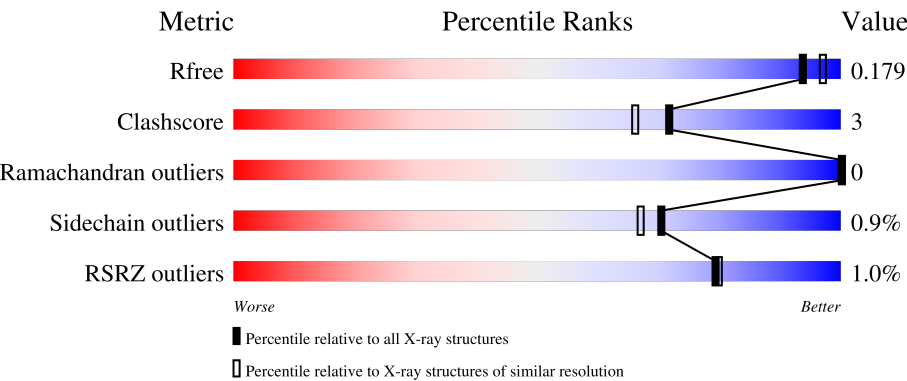
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (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 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	405	88%6%5%
1	B	405	90%7%.5%
1	C	405	% 88%6%5%
1	D	405	% 87%7%.5%
1	E	405	% 89%8%.5%

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Mol	Chain	Length	Quality of chain
1	F	405	% 88% 8%
1	G	405	% 88% 6% 5%
1	H	405	% 86% 9%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 26989 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 D-mannonate dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	384	Total	C	N	O	S	0	3	0
			3062	1943	548	557	14			
1	B	391	Total	C	N	O	S	0	3	0
			3112	1972	552	573	15			
1	C	385	Total	C	N	O	S	0	2	0
			3065	1944	549	558	14			
1	D	385	Total	C	N	O	S	0	0	0
			3049	1932	546	557	14			
1	E	395	Total	C	N	O	S	0	3	0
			3154	1999	560	580	15			
1	F	387	Total	C	N	O	S	0	0	0
			3065	1942	548	561	14			
1	G	385	Total	C	N	O	S	0	2	0
			3064	1941	547	562	14			
1	H	388	Total	C	N	O	S	0	0	0
			3069	1944	549	562	14			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	SER	-	expression tag	UNP Q1QT89
A	3	LEU	-	expression tag	UNP Q1QT89
B	2	SER	-	expression tag	UNP Q1QT89
B	3	LEU	-	expression tag	UNP Q1QT89
C	2	SER	-	expression tag	UNP Q1QT89
C	3	LEU	-	expression tag	UNP Q1QT89
D	2	SER	-	expression tag	UNP Q1QT89
D	3	LEU	-	expression tag	UNP Q1QT89
E	2	SER	-	expression tag	UNP Q1QT89
E	3	LEU	-	expression tag	UNP Q1QT89
F	2	SER	-	expression tag	UNP Q1QT89
F	3	LEU	-	expression tag	UNP Q1QT89
G	2	SER	-	expression tag	UNP Q1QT89

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Chain	Residue	Modelled	Actual	Comment	Reference
G	3	LEU	-	expression tag	UNP Q1QT89
H	2	SER	-	expression tag	UNP Q1QT89
H	3	LEU	-	expression tag	UNP Q1QT89

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

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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

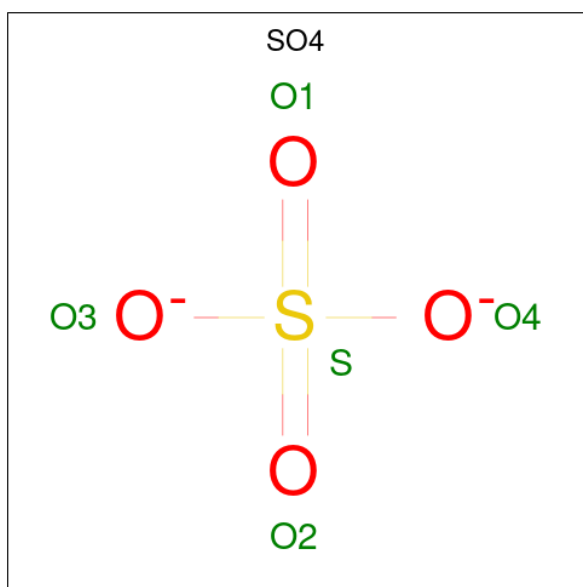
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0
3	E	1	Total Mg 1 1	0	0
3	F	1	Total Mg 1 1	0	0
3	G	1	Total Mg 1 1	0	0
3	H	1	Total Mg 1 1	0	0

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



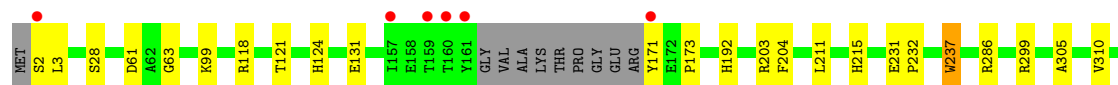
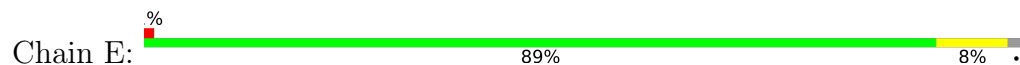
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	F	1	Total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

- Molecule 6 is water.

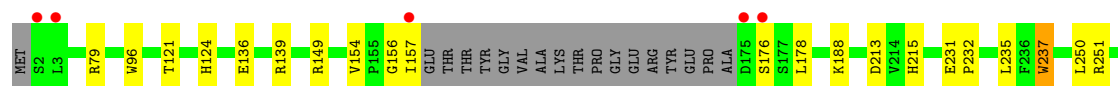
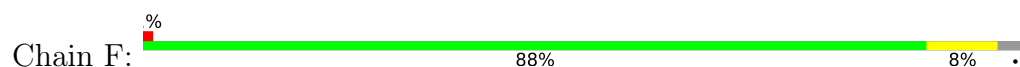
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	275	Total 275	O 275	0	0
6	B	273	Total 275	O 275	0	2
6	C	264	Total 264	O 264	0	0
6	D	263	Total 264	O 264	0	1
6	E	281	Total 281	O 281	0	0
6	F	282	Total 282	O 282	0	0
6	G	293	Total 294	O 294	0	1
6	H	278	Total 278	O 278	0	0



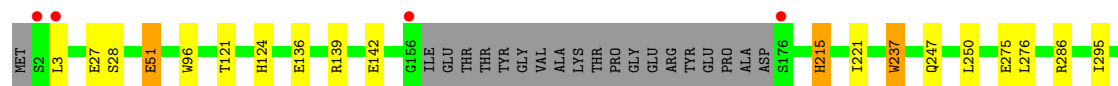
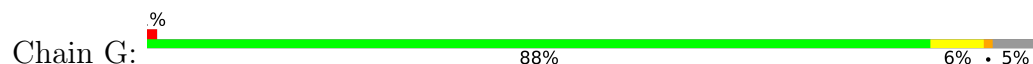
• Molecule 1: D-mannonate dehydratase



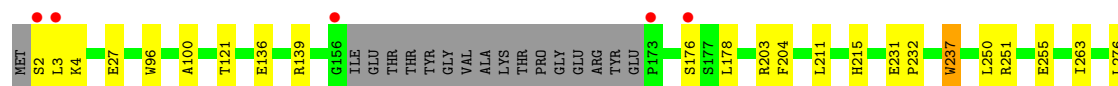
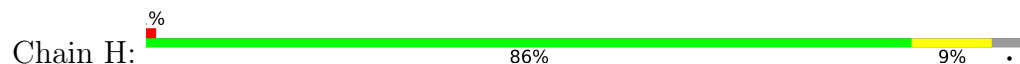
• Molecule 1: D-mannonate dehydratase



• Molecule 1: D-mannonate dehydratase



• Molecule 1: D-mannonate dehydratase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	86.58Å 177.79Å 109.99Å 90.00° 102.62° 90.00°	Depositor
Resolution (Å)	35.17 – 1.80 35.17 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.5 (35.17-1.80) 98.4 (35.17-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 1.79Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.149 , 0.182 0.147 , 0.179	Depositor DCC
R_{free} test set	14933 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	19.4	Xtriage
Anisotropy	0.258	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 46.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	26989	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, CL, MG, GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.43	0/3156	0.73	0/4296
1	B	0.43	0/3207	0.72	0/4367
1	C	0.41	0/3156	0.72	0/4296
1	D	0.41	0/3134	0.72	0/4267
1	E	0.43	0/3248	0.72	0/4424
1	F	0.43	0/3150	0.71	0/4289
1	G	0.45	0/3152	0.73	0/4291
1	H	0.42	0/3155	0.72	0/4296
All	All	0.43	0/25358	0.72	0/34526

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3062	0	2966	17	0
1	B	3112	0	3001	21	0
1	C	3065	0	2966	20	0
1	D	3049	0	2941	24	0
1	E	3154	0	3038	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3065	0	2956	18	0
1	G	3064	0	2952	19	0
1	H	3069	0	2958	26	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	F	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	6	0	8	0	0
4	B	6	0	8	0	0
4	C	6	0	8	0	0
4	D	6	0	8	0	0
4	E	6	0	8	0	0
4	F	12	0	16	0	0
4	G	6	0	8	0	0
4	H	6	0	8	0	0
5	A	10	0	0	0	0
5	B	5	0	0	0	0
5	C	10	0	0	0	0
5	D	10	0	0	1	0
5	E	5	0	0	0	0
5	F	10	0	0	0	0
5	G	10	0	0	0	0
5	H	10	0	0	0	0
6	A	275	0	0	2	0
6	B	275	0	0	2	0
6	C	264	0	0	4	0
6	D	264	0	0	2	0
6	E	281	0	0	3	0
6	F	282	0	0	3	0
6	G	294	0	0	0	0
6	H	278	0	0	2	0
All	All	26989	0	23850	161	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (161) 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:D:250:LEU:HD22	1:D:276:LEU:HD22	1.50	0.94
1:G:250:LEU:HD22	1:G:276:LEU:HD22	1.50	0.93
1:B:157:ILE:HG22	1:B:158:GLU:HG2	1.51	0.90
1:D:318:THR:HG23	1:D:344:MET:HE2	1.60	0.82
1:A:250[A]:LEU:HD22	1:A:276:LEU:HD22	1.65	0.78
1:E:2:SER:HB3	1:E:61:ASP:OD2	1.86	0.75
1:H:3:LEU:HD23	1:H:4:LYS:H	1.52	0.75
1:H:250:LEU:HD22	1:H:276:LEU:HD22	1.69	0.74
1:A:3:LEU:HD13	1:A:28:SER:HB3	1.71	0.73
1:G:136:GLU:OE2	1:G:139:ARG:HD3	1.87	0.73
1:D:359:ARG:NH2	6:D:856:HOH:O	2.27	0.68
1:D:2:SER:O	1:D:3:LEU:HD23	1.94	0.67
1:G:3:LEU:CD1	1:G:28:SER:HB3	2.25	0.66
1:H:287:MET:HE3	1:H:298:MET:SD	2.35	0.66
1:A:99:LYS:HG2	1:A:110:LEU:HD21	1.78	0.65
1:B:124:HIS:CE1	1:B:344[A]:MET:SD	2.90	0.64
1:F:384:LYS:NZ	6:F:882:HOH:O	2.31	0.64
1:B:3:LEU:HD13	1:B:28:SER:HB3	1.78	0.64
1:C:359:ARG:NH2	6:C:858:HOH:O	2.31	0.62
1:G:124:HIS:CE1	1:G:344:MET:SD	2.93	0.61
1:H:3:LEU:HD23	1:H:4:LYS:N	2.16	0.61
1:G:317:PRO:HA	1:G:344:MET:SD	2.41	0.61
1:E:203[B]:ARG:HG2	1:E:204:PHE:CE2	2.36	0.60
1:F:156:GLY:O	1:F:188:LYS:HE2	2.03	0.59
1:C:250:LEU:HD22	1:C:276:LEU:HD22	1.86	0.58
1:G:136:GLU:HA	1:G:139:ARG:HG2	1.86	0.58
1:C:215:HIS:ND1	1:C:405:TRP:OXT	2.31	0.57
1:C:43:MET:HG3	1:G:51:GLU:HG3	1.87	0.56
1:H:4:LYS:HB3	1:H:27:GLU:HG3	1.88	0.56
1:A:126:THR:OG1	1:A:149:ARG:NH1	2.38	0.56
1:C:136:GLU:OE1	1:C:139:ARG:NH1	2.37	0.56
1:B:43:MET:HE3	6:B:832[A]:HOH:O	2.06	0.55
1:H:136:GLU:OE2	1:H:139:ARG:HD3	2.07	0.54
1:F:359:ARG:NH2	6:F:860:HOH:O	2.41	0.54
1:F:176:SER:HB2	1:F:178:LEU:O	2.07	0.54
1:D:2:SER:HB3	1:D:27:GLU:OE2	2.07	0.53
1:E:192:HIS:HE1	6:E:751:HOH:O	1.91	0.53
1:D:2:SER:OG	1:D:3:LEU:N	2.36	0.53
1:D:6:ARG:NH2	6:D:860:HOH:O	2.42	0.53
1:D:215:HIS:ND1	1:D:405:TRP:OXT	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:250:LEU:HD22	1:F:276:LEU:HD22	1.90	0.52
1:C:111:LEU:HD22	1:C:299:ARG:HH11	1.75	0.52
1:G:295:ILE:O	1:G:299:ARG:HG3	2.10	0.52
1:E:3:LEU:HD13	1:E:28:SER:HB3	1.91	0.52
1:E:131:GLU:OE2	1:E:203[A]:ARG:NH2	2.29	0.52
1:C:255:GLU:OE2	6:C:856:HOH:O	2.19	0.51
1:B:299:ARG:HD3	1:C:299:ARG:HH21	1.76	0.51
1:B:3:LEU:CD1	1:B:28:SER:HB3	2.41	0.50
1:E:2:SER:OG	1:E:63:GLY:HA3	2.11	0.50
1:F:286:ARG:HD2	1:F:313:GLY:O	2.12	0.50
1:D:403:TRP:CG	1:D:404:HIS:H	2.30	0.50
1:A:286:ARG:HD2	1:A:313:GLY:O	2.11	0.49
1:E:118:ARG:NH1	6:E:742:HOH:O	2.45	0.49
1:F:136:GLU:OE2	1:F:139:ARG:HD3	2.12	0.49
1:H:403:TRP:CG	1:H:404:HIS:H	2.31	0.49
1:F:136:GLU:HA	1:F:139:ARG:HG2	1.95	0.49
1:E:118:ARG:HD2	1:E:364:HIS:CD2	2.49	0.48
1:E:403:TRP:CG	1:E:404:HIS:H	2.31	0.48
1:D:14:CYS:HA	1:D:17:ARG:O	2.14	0.48
1:E:3:LEU:CD1	1:E:28:SER:HB3	2.43	0.48
1:F:121:THR:HA	1:F:341:GLN:O	2.14	0.48
1:A:403:TRP:CG	1:A:404:HIS:H	2.32	0.48
1:C:118:ARG:HD2	1:C:364:HIS:CG	2.49	0.48
1:C:403:TRP:CG	1:C:404:HIS:H	2.32	0.48
1:E:286:ARG:HD2	1:E:313:GLY:O	2.14	0.47
1:H:286:ARG:HD2	1:H:313:GLY:O	2.13	0.47
1:E:380:GLU:O	1:E:384:LYS:NZ	2.43	0.47
1:G:121:THR:HA	1:G:341:GLN:O	2.14	0.47
1:C:118:ARG:NH1	6:C:838:HOH:O	2.46	0.47
1:G:286:ARG:HD2	1:G:313:GLY:O	2.14	0.47
1:H:2:SER:HB2	6:H:697:HOH:O	2.15	0.47
1:B:315:HIS:CE1	1:B:317:PRO:HG3	2.50	0.47
1:B:317:PRO:HA	1:B:344[A]:MET:SD	2.55	0.47
1:D:149:ARG:HD2	1:D:213:ASP:HB2	1.95	0.47
1:F:154:VAL:HB	1:F:157:ILE:HD11	1.98	0.46
1:E:211:LEU:HD23	1:E:237:TRP:CE2	2.50	0.46
1:E:305:ALA:HB1	1:E:310:VAL:HB	1.98	0.46
1:B:51[B]:GLU:HG2	1:D:43:MET:HG3	1.98	0.46
1:H:359:ARG:NH2	6:H:810:HOH:O	2.48	0.46
1:H:3:LEU:CD2	1:H:27:GLU:HB2	2.46	0.45
1:A:332:ASP:OD2	1:A:341:GLN:NE2	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:171:TYR:CE2	1:E:173:PRO:HG3	2.51	0.45
1:B:255:GLU:OE2	6:B:871:HOH:O	2.21	0.45
1:D:231:GLU:N	1:D:232:PRO:CD	2.80	0.45
1:H:121:THR:HA	1:H:341:GLN:O	2.16	0.45
1:G:3:LEU:HD22	1:G:27:GLU:OE1	2.16	0.45
1:H:211:LEU:HD23	1:H:237:TRP:CE2	2.52	0.45
1:H:176:SER:HB2	1:H:178:LEU:O	2.17	0.45
1:D:192:HIS:HE1	5:D:503:SO4:O4	2.00	0.45
1:H:3:LEU:HD22	1:H:27:GLU:HB2	1.98	0.45
1:E:393:PRO:HG2	1:E:405:TRP:CE2	2.52	0.44
1:B:403:TRP:CG	1:B:404:HIS:H	2.34	0.44
1:D:3:LEU:HD22	1:D:26:THR:HG21	2.00	0.44
1:C:237:TRP:C	1:C:237:TRP:CD1	2.96	0.44
1:D:237:TRP:C	1:D:237:TRP:CD1	2.96	0.44
1:G:96:TRP:CD1	1:G:295:ILE:HB	2.53	0.44
1:E:121:THR:HA	1:E:341:GLN:O	2.17	0.44
1:B:120:MET:HA	1:B:364:HIS:CD2	2.53	0.44
1:D:250:LEU:CD2	1:D:282:ILE:CG2	2.96	0.44
1:H:315:HIS:CE1	1:H:317:PRO:HG3	2.52	0.44
1:H:332:ASP:OD2	1:H:341:GLN:NE2	2.42	0.44
1:F:251:ARG:NH1	1:F:255:GLU:OE2	2.51	0.44
1:G:305:ALA:HB1	1:G:310:VAL:HB	2.00	0.44
1:H:3:LEU:CD2	1:H:4:LYS:H	2.27	0.43
1:H:100:ALA:HB3	1:H:372:GLY:HA2	2.00	0.43
1:C:118:ARG:HD2	1:C:364:HIS:CD2	2.53	0.43
1:A:118:ARG:NH1	1:A:364:HIS:NE2	2.66	0.43
1:C:120:MET:HA	1:C:364:HIS:CD2	2.53	0.43
1:E:192:HIS:CE1	6:E:751:HOH:O	2.70	0.43
1:D:121:THR:HA	1:D:341:GLN:O	2.19	0.43
1:G:403:TRP:CG	1:G:404:HIS:H	2.36	0.43
1:H:96:TRP:CD1	1:H:295:ILE:HB	2.53	0.43
1:H:231:GLU:N	1:H:232:PRO:CD	2.82	0.43
1:A:118:ARG:NH1	6:A:868:HOH:O	2.48	0.42
1:C:211:LEU:HD23	1:C:237:TRP:CE2	2.53	0.42
1:F:403:TRP:CG	1:F:404:HIS:H	2.36	0.42
1:C:315:HIS:CE1	1:C:317:PRO:HG3	2.54	0.42
1:F:124:HIS:CE1	1:F:344:MET:SD	3.12	0.42
1:B:124:HIS:NE2	1:B:342:GLU:OE2	2.46	0.42
1:C:290:THR:HB	1:C:320:LEU:HD22	2.01	0.42
1:D:124:HIS:CE1	1:D:344:MET:SD	3.12	0.42
1:F:96:TRP:CD1	1:F:295:ILE:HB	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:286:ARG:HD2	1:B:313:GLY:O	2.20	0.42
1:D:211:LEU:HD23	1:D:237:TRP:CE2	2.54	0.42
1:F:231:GLU:N	1:F:232:PRO:CD	2.82	0.42
1:B:318:THR:HG23	1:B:344[A]:MET:HE2	2.02	0.42
1:B:51[B]:GLU:HG2	1:D:43:MET:CG	2.50	0.42
1:B:231:GLU:N	1:B:232:PRO:CD	2.82	0.42
1:A:54:VAL:HB	1:A:55:PRO:HD3	2.02	0.42
1:A:215:HIS:ND1	1:A:405:TRP:OXT	2.35	0.42
1:C:142:GLU:HG2	6:C:724:HOH:O	2.19	0.41
1:G:247:GLN:CD	1:G:275[B]:GLU:HG2	2.45	0.41
1:A:100:ALA:HB3	1:A:372:GLY:HA2	2.02	0.41
1:G:237:TRP:CD1	1:G:237:TRP:C	2.98	0.41
1:D:250:LEU:HD23	1:D:282:ILE:CG2	2.50	0.41
1:E:124:HIS:CG	1:E:344[B]:MET:SD	3.13	0.41
1:H:291:HIS:CE1	1:H:320:LEU:HD21	2.56	0.41
1:B:315:HIS:CD2	1:B:317:PRO:HD3	2.55	0.41
1:E:299:ARG:HH11	1:H:299:ARG:NH2	2.18	0.41
1:F:149:ARG:HD2	1:F:213:ASP:HB2	2.02	0.41
1:A:6:ARG:NH2	6:A:831:HOH:O	2.54	0.41
1:A:127:GLY:O	1:A:152:SER:HA	2.20	0.41
1:E:231:GLU:N	1:E:232:PRO:CD	2.84	0.41
1:H:211:LEU:N	1:H:211:LEU:HD12	2.35	0.41
1:F:237:TRP:CD1	1:F:237:TRP:C	2.99	0.41
1:G:247:GLN:OE1	1:G:275[B]:GLU:HG2	2.20	0.41
1:C:124:HIS:NE2	1:C:342:GLU:OE2	2.51	0.41
1:B:149:ARG:HD2	1:B:213:ASP:HB2	2.03	0.41
1:C:154:VAL:HA	1:C:155:PRO:HD3	1.84	0.41
1:G:221:ILE:HD12	1:G:221:ILE:HA	1.96	0.41
1:A:218:LEU:O	1:A:242:VAL:HG12	2.21	0.40
1:B:156:GLY:O	1:B:157:ILE:HD13	2.20	0.40
1:D:93:MET:HE3	1:D:93:MET:HB2	1.94	0.40
1:F:79:ARG:HA	6:F:754:HOH:O	2.22	0.40
1:G:215:HIS:ND1	1:G:405:TRP:OXT	2.34	0.40
1:H:251:ARG:NH1	1:H:255:GLU:OE2	2.54	0.40
1:A:126:THR:HG1	1:A:149:ARG:HH12	1.68	0.40
1:H:203:ARG:HG2	1:H:204:PHE:CE2	2.57	0.40
1:A:237:TRP:CD1	1:A:237:TRP:C	2.99	0.40
1:B:3:LEU:HB3	1:B:27:GLU:HG2	2.04	0.40
1:D:120:MET:HA	1:D:364:HIS:CD2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	383/405 (95%)	374 (98%)	9 (2%)	0	100	100
1	B	390/405 (96%)	381 (98%)	9 (2%)	0	100	100
1	C	383/405 (95%)	372 (97%)	11 (3%)	0	100	100
1	D	381/405 (94%)	370 (97%)	11 (3%)	0	100	100
1	E	394/405 (97%)	385 (98%)	9 (2%)	0	100	100
1	F	383/405 (95%)	369 (96%)	14 (4%)	0	100	100
1	G	383/405 (95%)	374 (98%)	9 (2%)	0	100	100
1	H	384/405 (95%)	372 (97%)	12 (3%)	0	100	100
All	All	3081/3240 (95%)	2997 (97%)	84 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	318/332 (96%)	316 (99%)	2 (1%)	78	77
1	B	324/332 (98%)	322 (99%)	2 (1%)	78	77
1	C	318/332 (96%)	315 (99%)	3 (1%)	70	67
1	D	316/332 (95%)	313 (99%)	3 (1%)	70	67
1	E	328/332 (99%)	325 (99%)	3 (1%)	70	67
1	F	318/332 (96%)	315 (99%)	3 (1%)	70	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	318/332 (96%)	314 (99%)	4 (1%)	61	54
1	H	318/332 (96%)	315 (99%)	3 (1%)	70	67
All	All	2558/2656 (96%)	2535 (99%)	23 (1%)	70	67

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	215	HIS
1	A	237	TRP
1	B	99	LYS
1	B	237	TRP
1	C	215	HIS
1	C	235	LEU
1	C	237	TRP
1	D	3	LEU
1	D	215	HIS
1	D	237	TRP
1	E	99	LYS
1	E	215	HIS
1	E	237	TRP
1	F	215	HIS
1	F	235	LEU
1	F	237	TRP
1	G	51	GLU
1	G	142	GLU
1	G	215	HIS
1	G	237	TRP
1	H	215	HIS
1	H	237	TRP
1	H	263	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	280	GLN
1	B	278	GLN
1	C	234	HIS
1	C	280	GLN
1	D	278	GLN
1	D	280	GLN

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Mol	Chain	Res	Type
1	H	278	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 35 ligands modelled in this entry, 12 are monoatomic - leaving 23 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	SO4	H	503	-	4,4,4	0.25	0	6,6,6	0.12	0
4	GOL	B	503	-	5,5,5	0.42	0	5,5,5	0.26	0
4	GOL	F	503	-	5,5,5	0.41	0	5,5,5	0.33	0
5	SO4	B	504	-	4,4,4	0.22	0	6,6,6	0.08	0
4	GOL	G	502	-	5,5,5	0.43	0	5,5,5	0.58	0
5	SO4	C	505	-	4,4,4	0.30	0	6,6,6	0.08	0
5	SO4	D	503	-	4,4,4	0.25	0	6,6,6	0.12	0
4	GOL	C	503	-	5,5,5	0.31	0	5,5,5	0.49	0
5	SO4	F	506	-	4,4,4	0.27	0	6,6,6	0.17	0
4	GOL	D	502	-	5,5,5	0.38	0	5,5,5	0.44	0
5	SO4	D	504	-	4,4,4	0.27	0	6,6,6	0.12	0
4	GOL	F	504	-	5,5,5	0.34	0	5,5,5	0.23	0
5	SO4	E	503	-	4,4,4	0.26	0	6,6,6	0.05	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	F	505	-	4,4,4	0.22	0	6,6,6	0.09	0
5	SO4	G	504	-	4,4,4	0.25	0	6,6,6	0.14	0
5	SO4	C	504	-	4,4,4	0.25	0	6,6,6	0.10	0
5	SO4	A	504	-	4,4,4	0.26	0	6,6,6	0.11	0
4	GOL	A	503	-	5,5,5	0.44	0	5,5,5	0.41	0
4	GOL	E	502	-	5,5,5	0.35	0	5,5,5	0.55	0
5	SO4	H	504	-	4,4,4	0.25	0	6,6,6	0.13	0
5	SO4	A	505	-	4,4,4	0.25	0	6,6,6	0.19	0
5	SO4	G	503	-	4,4,4	0.27	0	6,6,6	0.16	0
4	GOL	H	502	-	5,5,5	0.42	0	5,5,5	0.40	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
4	GOL	C	503	-	-	2/4/4/4	-
4	GOL	F	504	-	-	2/4/4/4	-
4	GOL	B	503	-	-	4/4/4/4	-
4	GOL	A	503	-	-	2/4/4/4	-
4	GOL	E	502	-	-	2/4/4/4	-
4	GOL	F	503	-	-	2/4/4/4	-
4	GOL	G	502	-	-	2/4/4/4	-
4	GOL	D	502	-	-	4/4/4/4	-
4	GOL	H	502	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	503	GOL	C1-C2-C3-O3
4	C	503	GOL	O1-C1-C2-O2
4	C	503	GOL	O1-C1-C2-C3
4	D	502	GOL	O1-C1-C2-C3
4	D	502	GOL	C1-C2-C3-O3
4	E	502	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
4	E	502	GOL	O2-C2-C3-O3
4	F	503	GOL	C1-C2-C3-O3
4	G	502	GOL	C1-C2-C3-O3
4	G	502	GOL	O2-C2-C3-O3
4	A	503	GOL	O2-C2-C3-O3
4	F	503	GOL	O2-C2-C3-O3
4	A	503	GOL	C1-C2-C3-O3
4	B	503	GOL	O1-C1-C2-C3
4	F	504	GOL	O1-C1-C2-C3
4	H	502	GOL	C1-C2-C3-O3
4	B	503	GOL	O2-C2-C3-O3
4	D	502	GOL	O2-C2-C3-O3
4	H	502	GOL	O2-C2-C3-O3
4	B	503	GOL	O1-C1-C2-O2
4	D	502	GOL	O1-C1-C2-O2
4	F	504	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	503	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	384/405 (94%)	-0.51	2 (0%) 87 88	10, 18, 33, 46	3 (0%)
1	B	391/405 (96%)	-0.45	2 (0%) 87 88	12, 20, 36, 69	3 (0%)
1	C	385/405 (95%)	-0.44	3 (0%) 82 83	12, 20, 36, 54	2 (0%)
1	D	385/405 (95%)	-0.42	4 (1%) 79 80	14, 20, 38, 67	0
1	E	395/405 (97%)	-0.47	6 (1%) 72 72	13, 19, 36, 62	3 (0%)
1	F	387/405 (95%)	-0.49	5 (1%) 75 75	12, 18, 36, 61	0
1	G	385/405 (95%)	-0.54	4 (1%) 79 80	10, 17, 33, 63	2 (0%)
1	H	388/405 (95%)	-0.45	5 (1%) 75 75	13, 19, 36, 60	0
All	All	3100/3240 (95%)	-0.47	31 (1%) 79 80	10, 19, 36, 69	13 (0%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	2	SER	7.5
1	H	3	LEU	5.1
1	C	157	ILE	4.5
1	F	176	SER	4.5
1	H	173	PRO	3.8
1	D	2	SER	3.6
1	G	2	SER	3.5
1	B	157	ILE	3.5
1	F	3	LEU	3.4
1	E	171	TYR	3.2
1	D	3	LEU	3.0
1	B	158	GLU	3.0
1	G	176	SER	3.0
1	G	156	GLY	2.9
1	E	159	THR	2.7
1	H	156	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	156	GLY	2.5
1	E	2	SER	2.5
1	F	2	SER	2.5
1	F	157	ILE	2.5
1	C	3	LEU	2.5
1	E	161	TYR	2.5
1	F	175	ASP	2.5
1	G	3	LEU	2.4
1	D	176	SER	2.4
1	H	176	SER	2.4
1	A	3	LEU	2.3
1	E	157	ILE	2.3
1	D	156	GLY	2.3
1	E	160	THR	2.3
1	C	176	SER	2.2

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
5	SO4	E	503	5/5	0.87	0.10	56,62,69,69	0
5	SO4	G	503	5/5	0.87	0.10	46,61,65,66	0
4	GOL	F	504	6/6	0.89	0.12	35,37,42,45	0
5	SO4	D	504	5/5	0.90	0.09	41,41,52,58	0
5	SO4	H	504	5/5	0.90	0.09	39,43,54,58	0
5	SO4	C	504	5/5	0.91	0.08	49,55,62,62	0
5	SO4	B	504	5/5	0.92	0.10	58,61,65,68	0
5	SO4	G	504	5/5	0.92	0.09	28,33,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GOL	D	502	6/6	0.92	0.11	20,33,39,40	0
5	SO4	F	506	5/5	0.93	0.08	28,39,52,52	0
2	CL	F	501	1/1	0.94	0.09	22,22,22,22	0
5	SO4	F	505	5/5	0.94	0.07	38,46,51,53	0
5	SO4	A	504	5/5	0.94	0.07	50,52,60,60	0
5	SO4	C	505	5/5	0.94	0.07	34,40,51,51	0
5	SO4	D	503	5/5	0.94	0.07	49,54,58,60	0
5	SO4	H	503	5/5	0.94	0.07	42,53,59,61	0
5	SO4	A	505	5/5	0.94	0.08	35,37,50,57	0
2	CL	C	501	1/1	0.95	0.07	24,24,24,24	0
2	CL	A	501	1/1	0.95	0.08	24,24,24,24	0
2	CL	B	501	1/1	0.95	0.08	23,23,23,23	0
4	GOL	H	502	6/6	0.96	0.08	22,30,36,40	0
4	GOL	A	503	6/6	0.96	0.08	20,27,34,39	0
4	GOL	E	502	6/6	0.96	0.07	22,27,37,37	0
4	GOL	B	503	6/6	0.96	0.08	22,32,33,37	0
4	GOL	G	502	6/6	0.96	0.08	21,22,30,35	0
4	GOL	F	503	6/6	0.97	0.06	22,27,34,36	0
4	GOL	C	503	6/6	0.97	0.06	20,25,32,39	0
3	MG	H	501	1/1	0.98	0.03	25,25,25,25	0
3	MG	B	502	1/1	0.98	0.04	27,27,27,27	0
3	MG	C	502	1/1	0.98	0.04	25,25,25,25	0
3	MG	D	501	1/1	0.98	0.03	24,24,24,24	0
3	MG	E	501	1/1	0.98	0.04	30,30,30,30	0
3	MG	G	501	1/1	0.98	0.03	18,18,18,18	0
3	MG	A	502	1/1	0.99	0.03	24,24,24,24	0
3	MG	F	502	1/1	1.00	0.01	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.