



Full wwPDB X-ray Structure Validation Report

Apr 7, 2014 – 04:13 PM EDT

PDB ID : 4HGZ
Title : Structure of the CcbJ Methyltransferase from *Streptomyces caelestis*
Authors : Bauer, J.A.; Ondrovicova, G.; Kutejova, E.; Janata, J.
Deposited on : 2012-10-09
Resolution : 2.70 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

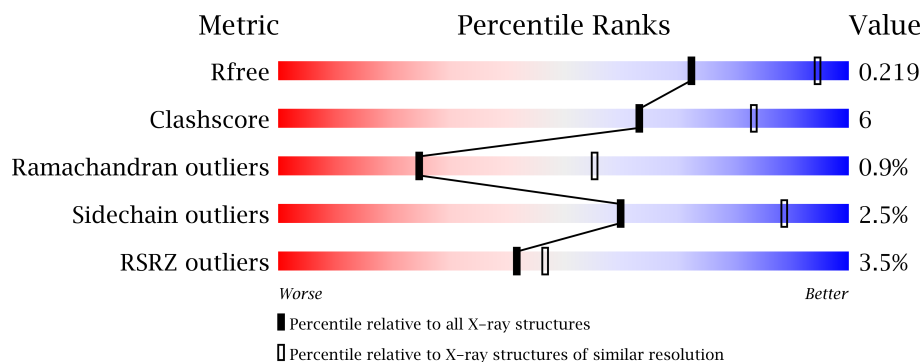
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : **FAILED**
Xtriage (Phenix) : dev-1439
EDS : stable22978
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22978

1 Overall quality at a glance

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	276	
1	B	276	
1	C	276	
1	D	276	
1	E	276	
1	F	276	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	SO4	A	302	-	X
2	SO4	A	303	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
2	SO4	E	302	-	X
3	EDO	B	302	-	X
3	EDO	C	302	-	X
3	EDO	E	303	-	X
4	LI	C	301	-	X
4	LI	D	301	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10930 atoms, of which 0 are hydrogen and 0 are deuterium.

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 CcbJ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	236	Total	C	N	O	S	0	0	0
			1801	1138	322	335	6			
1	B	228	Total	C	N	O	S	0	0	0
			1742	1099	313	324	6			
1	C	237	Total	C	N	O	S	0	0	0
			1809	1142	323	338	6			
1	D	235	Total	C	N	O	S	0	0	0
			1796	1135	321	334	6			
1	E	236	Total	C	N	O	S	0	0	0
			1801	1138	322	335	6			
1	F	234	Total	C	N	O	S	0	0	0
			1787	1130	320	331	6			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP E9JES0
A	-18	GLY	-	EXPRESSION TAG	UNP E9JES0
A	-17	SER	-	EXPRESSION TAG	UNP E9JES0
A	-16	SER	-	EXPRESSION TAG	UNP E9JES0
A	-15	HIS	-	EXPRESSION TAG	UNP E9JES0
A	-14	HIS	-	EXPRESSION TAG	UNP E9JES0
A	-13	HIS	-	EXPRESSION TAG	UNP E9JES0
A	-12	HIS	-	EXPRESSION TAG	UNP E9JES0
A	-11	HIS	-	EXPRESSION TAG	UNP E9JES0
A	-10	HIS	-	EXPRESSION TAG	UNP E9JES0
A	-9	SER	-	EXPRESSION TAG	UNP E9JES0
A	-8	SER	-	EXPRESSION TAG	UNP E9JES0
A	-7	GLY	-	EXPRESSION TAG	UNP E9JES0
A	-6	LEU	-	EXPRESSION TAG	UNP E9JES0
A	-5	VAL	-	EXPRESSION TAG	UNP E9JES0
A	-4	PRO	-	EXPRESSION TAG	UNP E9JES0
A	-3	ARG	-	EXPRESSION TAG	UNP E9JES0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP E9JES0
A	-1	SER	-	EXPRESSION TAG	UNP E9JES0
A	0	HIS	-	EXPRESSION TAG	UNP E9JES0
B	-19	MET	-	EXPRESSION TAG	UNP E9JES0
B	-18	GLY	-	EXPRESSION TAG	UNP E9JES0
B	-17	SER	-	EXPRESSION TAG	UNP E9JES0
B	-16	SER	-	EXPRESSION TAG	UNP E9JES0
B	-15	HIS	-	EXPRESSION TAG	UNP E9JES0
B	-14	HIS	-	EXPRESSION TAG	UNP E9JES0
B	-13	HIS	-	EXPRESSION TAG	UNP E9JES0
B	-12	HIS	-	EXPRESSION TAG	UNP E9JES0
B	-11	HIS	-	EXPRESSION TAG	UNP E9JES0
B	-10	HIS	-	EXPRESSION TAG	UNP E9JES0
B	-9	SER	-	EXPRESSION TAG	UNP E9JES0
B	-8	SER	-	EXPRESSION TAG	UNP E9JES0
B	-7	GLY	-	EXPRESSION TAG	UNP E9JES0
B	-6	LEU	-	EXPRESSION TAG	UNP E9JES0
B	-5	VAL	-	EXPRESSION TAG	UNP E9JES0
B	-4	PRO	-	EXPRESSION TAG	UNP E9JES0
B	-3	ARG	-	EXPRESSION TAG	UNP E9JES0
B	-2	GLY	-	EXPRESSION TAG	UNP E9JES0
B	-1	SER	-	EXPRESSION TAG	UNP E9JES0
B	0	HIS	-	EXPRESSION TAG	UNP E9JES0
C	-19	MET	-	EXPRESSION TAG	UNP E9JES0
C	-18	GLY	-	EXPRESSION TAG	UNP E9JES0
C	-17	SER	-	EXPRESSION TAG	UNP E9JES0
C	-16	SER	-	EXPRESSION TAG	UNP E9JES0
C	-15	HIS	-	EXPRESSION TAG	UNP E9JES0
C	-14	HIS	-	EXPRESSION TAG	UNP E9JES0
C	-13	HIS	-	EXPRESSION TAG	UNP E9JES0
C	-12	HIS	-	EXPRESSION TAG	UNP E9JES0
C	-11	HIS	-	EXPRESSION TAG	UNP E9JES0
C	-10	HIS	-	EXPRESSION TAG	UNP E9JES0
C	-9	SER	-	EXPRESSION TAG	UNP E9JES0
C	-8	SER	-	EXPRESSION TAG	UNP E9JES0
C	-7	GLY	-	EXPRESSION TAG	UNP E9JES0
C	-6	LEU	-	EXPRESSION TAG	UNP E9JES0
C	-5	VAL	-	EXPRESSION TAG	UNP E9JES0
C	-4	PRO	-	EXPRESSION TAG	UNP E9JES0
C	-3	ARG	-	EXPRESSION TAG	UNP E9JES0
C	-2	GLY	-	EXPRESSION TAG	UNP E9JES0
C	-1	SER	-	EXPRESSION TAG	UNP E9JES0

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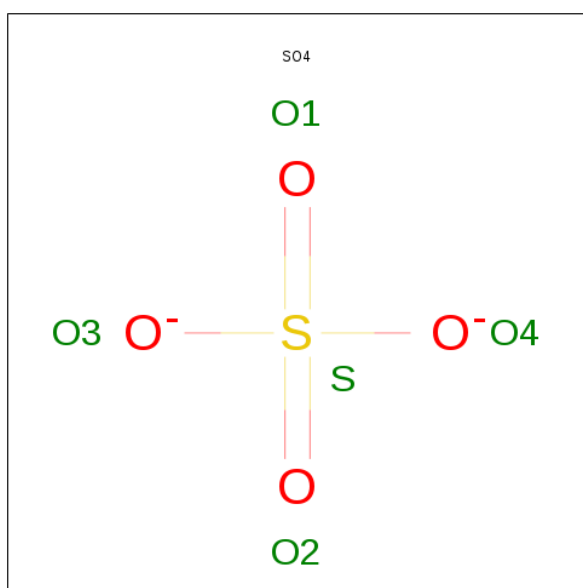
Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	EXPRESSION TAG	UNP E9JES0
D	-19	MET	-	EXPRESSION TAG	UNP E9JES0
D	-18	GLY	-	EXPRESSION TAG	UNP E9JES0
D	-17	SER	-	EXPRESSION TAG	UNP E9JES0
D	-16	SER	-	EXPRESSION TAG	UNP E9JES0
D	-15	HIS	-	EXPRESSION TAG	UNP E9JES0
D	-14	HIS	-	EXPRESSION TAG	UNP E9JES0
D	-13	HIS	-	EXPRESSION TAG	UNP E9JES0
D	-12	HIS	-	EXPRESSION TAG	UNP E9JES0
D	-11	HIS	-	EXPRESSION TAG	UNP E9JES0
D	-10	HIS	-	EXPRESSION TAG	UNP E9JES0
D	-9	SER	-	EXPRESSION TAG	UNP E9JES0
D	-8	SER	-	EXPRESSION TAG	UNP E9JES0
D	-7	GLY	-	EXPRESSION TAG	UNP E9JES0
D	-6	LEU	-	EXPRESSION TAG	UNP E9JES0
D	-5	VAL	-	EXPRESSION TAG	UNP E9JES0
D	-4	PRO	-	EXPRESSION TAG	UNP E9JES0
D	-3	ARG	-	EXPRESSION TAG	UNP E9JES0
D	-2	GLY	-	EXPRESSION TAG	UNP E9JES0
D	-1	SER	-	EXPRESSION TAG	UNP E9JES0
D	0	HIS	-	EXPRESSION TAG	UNP E9JES0
E	-19	MET	-	EXPRESSION TAG	UNP E9JES0
E	-18	GLY	-	EXPRESSION TAG	UNP E9JES0
E	-17	SER	-	EXPRESSION TAG	UNP E9JES0
E	-16	SER	-	EXPRESSION TAG	UNP E9JES0
E	-15	HIS	-	EXPRESSION TAG	UNP E9JES0
E	-14	HIS	-	EXPRESSION TAG	UNP E9JES0
E	-13	HIS	-	EXPRESSION TAG	UNP E9JES0
E	-12	HIS	-	EXPRESSION TAG	UNP E9JES0
E	-11	HIS	-	EXPRESSION TAG	UNP E9JES0
E	-10	HIS	-	EXPRESSION TAG	UNP E9JES0
E	-9	SER	-	EXPRESSION TAG	UNP E9JES0
E	-8	SER	-	EXPRESSION TAG	UNP E9JES0
E	-7	GLY	-	EXPRESSION TAG	UNP E9JES0
E	-6	LEU	-	EXPRESSION TAG	UNP E9JES0
E	-5	VAL	-	EXPRESSION TAG	UNP E9JES0
E	-4	PRO	-	EXPRESSION TAG	UNP E9JES0
E	-3	ARG	-	EXPRESSION TAG	UNP E9JES0
E	-2	GLY	-	EXPRESSION TAG	UNP E9JES0
E	-1	SER	-	EXPRESSION TAG	UNP E9JES0
E	0	HIS	-	EXPRESSION TAG	UNP E9JES0
F	-19	MET	-	EXPRESSION TAG	UNP E9JES0

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-18	GLY	-	EXPRESSION TAG	UNP E9JES0
F	-17	SER	-	EXPRESSION TAG	UNP E9JES0
F	-16	SER	-	EXPRESSION TAG	UNP E9JES0
F	-15	HIS	-	EXPRESSION TAG	UNP E9JES0
F	-14	HIS	-	EXPRESSION TAG	UNP E9JES0
F	-13	HIS	-	EXPRESSION TAG	UNP E9JES0
F	-12	HIS	-	EXPRESSION TAG	UNP E9JES0
F	-11	HIS	-	EXPRESSION TAG	UNP E9JES0
F	-10	HIS	-	EXPRESSION TAG	UNP E9JES0
F	-9	SER	-	EXPRESSION TAG	UNP E9JES0
F	-8	SER	-	EXPRESSION TAG	UNP E9JES0
F	-7	GLY	-	EXPRESSION TAG	UNP E9JES0
F	-6	LEU	-	EXPRESSION TAG	UNP E9JES0
F	-5	VAL	-	EXPRESSION TAG	UNP E9JES0
F	-4	PRO	-	EXPRESSION TAG	UNP E9JES0
F	-3	ARG	-	EXPRESSION TAG	UNP E9JES0
F	-2	GLY	-	EXPRESSION TAG	UNP E9JES0
F	-1	SER	-	EXPRESSION TAG	UNP E9JES0
F	0	HIS	-	EXPRESSION TAG	UNP E9JES0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



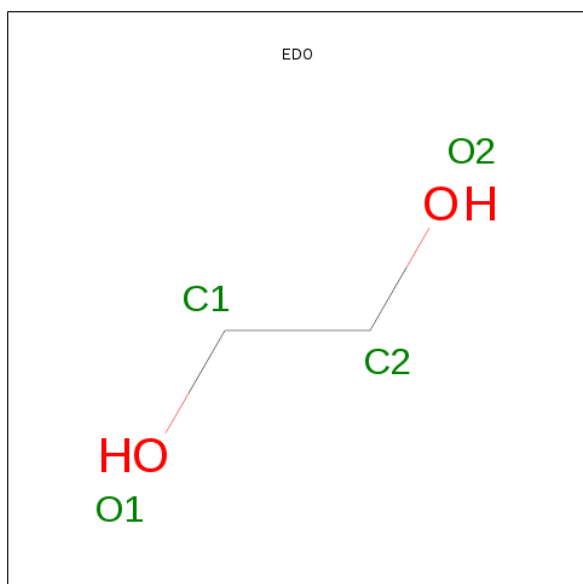
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 4 is LITHIUM ION (three-letter code: LI) (formula: Li).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total 1	Li 1	0	0
4	C	1	Total 1	Li 1	0	0

- Molecule 5 is water.

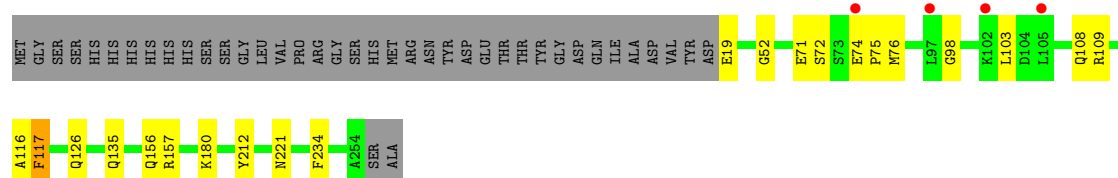
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	25	Total 25	O 25	0	0
5	B	20	Total 20	O 20	0	0
5	C	27	Total 27	O 27	0	0
5	D	18	Total 18	O 18	0	0
5	E	25	Total 25	O 25	0	0
5	F	21	Total 21	O 21	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

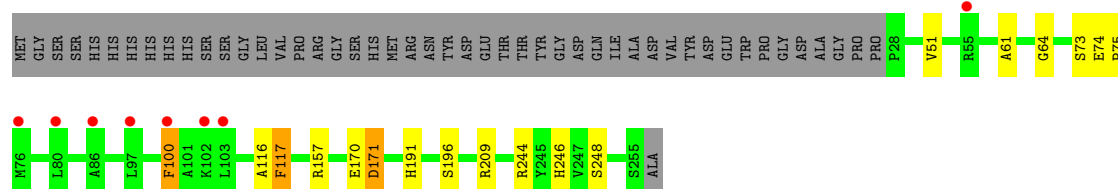
• Molecule 1: CcbJ

Chain A: 



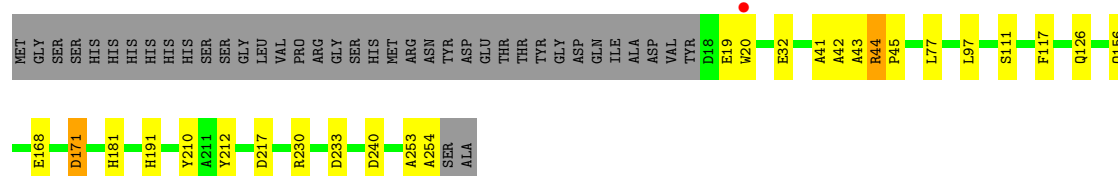
• Molecule 1: CcbJ

Chain B: 



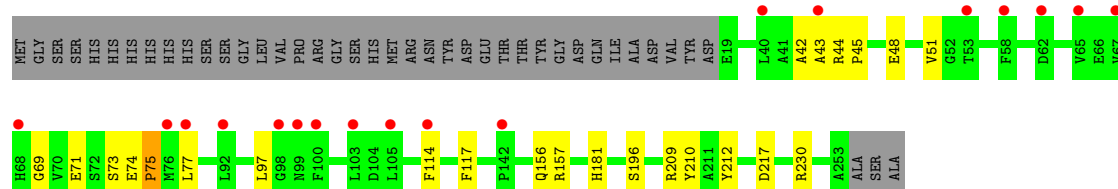
• Molecule 1: CcbJ

Chain C: 

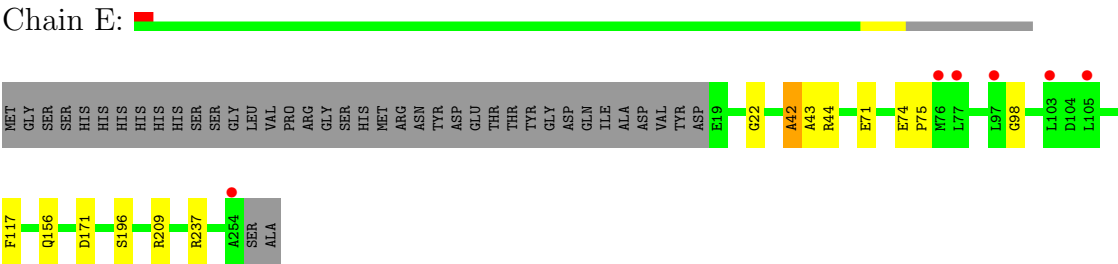


• Molecule 1: CcbJ

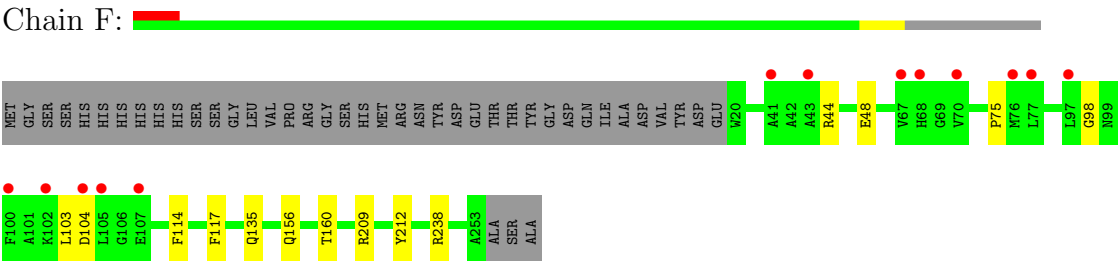
Chain D: 



● Molecule 1: CcbJ



● Molecule 1: CcbJ



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	168.02Å 244.55Å 117.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.27 – 2.70 54.27 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (54.27-2.70) 99.8 (54.27-2.70)	Depositor EDS
R_{merge}	7.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.34 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.181 , 0.224 0.176 , 0.219	Depositor DCC
R_{free} test set	3353 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	59.9	Xtriage
Anisotropy	0.227	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 34.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 66692 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10930	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.34% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, SO4, LI

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	0.38	0/1841	0.55	0/2503
1	B	0.39	0/1777	0.55	0/2411
1	C	0.39	0/1849	0.54	0/2514
1	D	0.34	0/1836	0.53	0/2496
1	E	0.38	0/1841	0.55	0/2503
1	F	0.36	0/1827	0.52	0/2484
All	All	0.37	0/10971	0.54	0/14911

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1801	0	0	12	0
1	B	1742	0	11	9	0
1	C	1809	0	9	18	0
1	D	1796	0	0	16	0
1	E	1801	0	0	4	0
1	F	1787	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	15	0	0	1	0
2	B	5	0	0	0	0
2	E	10	0	0	1	0
2	F	10	0	0	0	0
3	B	4	0	6	0	0
3	C	4	0	6	1	0
3	D	4	0	6	0	0
3	E	4	0	6	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	25	0	0	3	0
5	B	20	0	0	1	0
5	C	27	0	0	0	0
5	D	18	0	0	0	0
5	E	25	0	0	0	0
5	F	21	0	0	0	0
All	All	10930	0	44	60	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

All (60) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:51:VAL:CG2	1:D:69:GLY:CA	2.36	1.04
1:C:42:ALA:O	1:C:44:ARG:N	2.09	0.85
1:C:44:ARG:CG	1:C:45:PRO:CD	2.63	0.77
1:D:74:GLU:CG	1:D:97:LEU:CD2	2.63	0.76
1:A:126:GLN:N	2:A:302:SO4:O3	2.21	0.73
1:B:74:GLU:N	1:B:75:PRO:CD	2.53	0.70
1:B:171:ASP:N	1:B:171:ASP:OD1	2.25	0.68
1:C:77:LEU:CD2	1:C:97:LEU:CB	2.75	0.65
1:C:44:ARG:CD	1:C:45:PRO:CD	2.76	0.64
1:D:51:VAL:CG2	1:D:69:GLY:C	2.66	0.64
1:E:74:GLU:N	1:E:75:PRO:CD	2.66	0.58
1:D:44:ARG:CG	1:D:45:PRO:CD	2.82	0.57
1:C:217:ASP:OD2	1:C:230:ARG:NH2	2.39	0.55
1:A:98:GLY:CA	1:A:103:LEU:CD2	2.85	0.55
1:D:74:GLU:N	1:D:75:PRO:CD	2.69	0.55
1:D:77:LEU:CD2	1:D:97:LEU:CB	2.87	0.53
1:E:237:ARG:NE	2:E:301:SO4:O2	2.42	0.53
1:A:108:GLN:O	1:A:109:ARG:NH1	2.42	0.53
1:B:100:PHE:CD2	1:B:100:PHE:N	2.75	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:51:VAL:O	1:D:71:GLU:OE2	2.25	0.53
1:A:19:GLU:CB	5:A:410:HOH:O	2.57	0.52
1:C:32:GLU:N	1:C:32:GLU:OE1	2.42	0.52
1:F:98:GLY:CA	1:F:103:LEU:CD2	2.88	0.52
1:A:221:ASN:ND2	5:A:418:HOH:O	2.43	0.51
1:C:171:ASP:OD1	1:C:171:ASP:N	2.44	0.51
1:C:181:HIS:NE2	1:C:210:TYR:OH	2.44	0.51
1:C:42:ALA:C	1:C:44:ARG:N	2.62	0.51
1:C:44:ARG:CB	1:C:45:PRO:CD	2.88	0.50
1:E:42:ALA:O	1:E:43:ALA:C	2.50	0.50
1:A:234:PHE:N	5:A:404:HOH:O	2.44	0.50
1:C:253:ALA:O	1:C:254:ALA:C	2.50	0.49
1:A:116:ALA:O	1:A:117:PHE:C	2.51	0.49
1:C:212:TYR:CZ	1:D:212:TYR:CZ	3.01	0.47
1:B:61:ALA:O	1:B:64:GLY:N	2.48	0.47
1:B:244:ARG:NH2	5:B:412:HOH:O	2.48	0.46
1:D:73:SER:C	1:D:75:PRO:CD	2.84	0.46
1:C:126:GLN:N	3:C:302:EDO:H22	2.31	0.45
1:C:233:ASP:OD1	1:C:233:ASP:C	2.55	0.45
1:A:212:TYR:CZ	1:F:212:TYR:CZ	3.06	0.44
1:A:52:GLY:N	1:A:71:GLU:OE2	2.51	0.44
1:A:74:GLU:N	1:A:75:PRO:CD	2.82	0.43
1:D:217:ASP:OD2	1:D:230:ARG:NH2	2.52	0.42
1:D:42:ALA:C	1:D:44:ARG:N	2.71	0.42
1:F:48:GLU:CB	1:F:114:PHE:CZ	3.03	0.42
1:B:73:SER:C	1:B:75:PRO:CD	2.88	0.42
1:D:42:ALA:O	1:D:43:ALA:C	2.58	0.42
1:A:157:ARG:NH1	1:F:160:THR:OG1	2.53	0.42
1:F:103:LEU:O	1:F:135:GLN:NE2	2.53	0.42
1:A:180:LYS:NZ	1:C:168:GLU:OE2	2.52	0.42
1:B:170:GLU:O	1:C:191:HIS:CE1	2.73	0.42
1:C:41:ALA:O	1:C:111:SER:CB	2.67	0.42
1:B:116:ALA:O	1:B:117:PHE:C	2.57	0.41
1:B:246:HIS:ND1	1:B:248:SER:OG	2.53	0.41
1:D:181:HIS:NE2	1:D:210:TYR:OH	2.54	0.41
1:F:104:ASP:C	1:F:104:ASP:OD1	2.59	0.41
1:E:71:GLU:O	1:E:98:GLY:N	2.53	0.41
1:C:240:ASP:OD1	1:C:240:ASP:C	2.59	0.41
1:D:73:SER:O	1:D:74:GLU:C	2.60	0.41
1:D:42:ALA:O	1:D:44:ARG:N	2.54	0.41
1:D:48:GLU:CG	1:D:114:PHE:CE1	3.04	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	234/276 (85%)	228 (97%)	5 (2%)	1 (0%)	43	76
1	B	226/276 (82%)	217 (96%)	8 (4%)	1 (0%)	43	76
1	C	235/276 (85%)	226 (96%)	7 (3%)	2 (1%)	25	55
1	D	233/276 (84%)	221 (95%)	9 (4%)	3 (1%)	18	43
1	E	234/276 (85%)	223 (95%)	7 (3%)	4 (2%)	14	33
1	F	232/276 (84%)	223 (96%)	7 (3%)	2 (1%)	25	55
All	All	1394/1656 (84%)	1338 (96%)	43 (3%)	13 (1%)	25	55

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	43	ALA
1	A	117	PHE
1	B	117	PHE
1	E	42	ALA
1	D	117	PHE
1	D	157	ARG
1	C	117	PHE
1	D	75	PRO
1	E	44	ARG
1	F	117	PHE
1	E	117	PHE
1	E	22	GLY
1	F	75	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	A	183/217 (84%)	179 (98%)	4 (2%)	64	90
1	B	178/217 (82%)	171 (96%)	7 (4%)	43	76
1	C	184/217 (85%)	179 (97%)	5 (3%)	57	87
1	D	183/217 (84%)	180 (98%)	3 (2%)	75	94
1	E	183/217 (84%)	179 (98%)	4 (2%)	64	90
1	F	182/217 (84%)	178 (98%)	4 (2%)	64	90
All	All	1093/1302 (84%)	1066 (98%)	27 (2%)	60	89

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	SER
1	A	76	MET
1	A	135	GLN
1	A	156	GLN
1	B	51	VAL
1	B	100	PHE
1	B	157	ARG
1	B	171	ASP
1	B	191	HIS
1	B	196	SER
1	B	209	ARG
1	C	19	GLU
1	C	20	TRP
1	C	44	ARG
1	C	156	GLN
1	C	171	ASP
1	D	156	GLN
1	D	196	SER
1	D	209	ARG
1	E	156	GLN
1	E	171	ASP
1	E	196	SER
1	E	209	ARG
1	F	44	ARG
1	F	156	GLN
1	F	209	ARG
1	F	238	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.5 Carbohydrates ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.6 Ligand geometry ⓘ

Mogul failed to run properly - this section will therefore be empty.

5.7 Other polymers ⓘ

Mogul failed to run properly - this section will therefore be empty.

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	A	236/276 (85%)	0.05	4 (1%) 67 73	30, 49, 96, 125	0
1	B	228/276 (82%)	0.27	8 (3%) 42 47	28, 53, 123, 167	0
1	C	237/276 (85%)	0.01	1 (0%) 90 93	34, 51, 89, 140	0
1	D	235/276 (85%)	0.56	18 (7%) 13 14	27, 70, 137, 151	0
1	E	236/276 (85%)	0.16	6 (2%) 54 61	25, 51, 108, 132	0
1	F	234/276 (84%)	0.39	13 (5%) 24 25	29, 64, 130, 151	0
All	All	1406/1656 (84%)	0.24	50 (3%) 42 46	25, 55, 118, 167	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	103	LEU	5.9
1	B	102	LYS	5.0
1	D	103	LEU	3.9
1	F	105	LEU	3.8
1	D	76	MET	3.8
1	E	254	ALA	3.5
1	D	92	LEU	3.5
1	A	97	LEU	3.5
1	F	100	PHE	3.5
1	F	102	LYS	3.4
1	D	43	ALA	3.4
1	D	100	PHE	3.2
1	B	97	LEU	3.2
1	D	68	HIS	3.1
1	F	97	LEU	3.0
1	D	99	ASN	2.9
1	D	65	VAL	2.9
1	F	70	VAL	2.8
1	C	20	TRP	2.8

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Mol	Chain	Res	Type	RSRZ
1	E	103	LEU	2.8
1	B	80	LEU	2.8
1	F	77	LEU	2.8
1	D	40	LEU	2.7
1	D	77	LEU	2.7
1	E	97	LEU	2.7
1	B	55	ARG	2.7
1	F	76	MET	2.6
1	E	77	LEU	2.6
1	F	104	ASP	2.6
1	A	74	GLU	2.5
1	B	100	PHE	2.5
1	B	86	ALA	2.4
1	E	76	MET	2.4
1	D	105	LEU	2.4
1	E	105	LEU	2.4
1	F	43	ALA	2.4
1	F	67	VAL	2.4
1	F	68	HIS	2.3
1	D	62	ASP	2.3
1	B	76	MET	2.3
1	F	107	GLU	2.3
1	D	114	PHE	2.2
1	D	67	VAL	2.2
1	D	53	THR	2.2
1	D	98	GLY	2.1
1	F	41	ALA	2.1
1	D	58	PHE	2.1
1	A	102	LYS	2.1
1	A	105	LEU	2.1
1	D	142	PRO	2.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	LI	D	301	1/1	0.55	15.70	2,2,2,2	1
4	LI	C	301	1/1	0.46	7.93	12,12,12,12	1
2	SO4	E	302	5/5	0.22	6.30	84,107,125,137	0
2	SO4	A	303	5/5	0.27	3.82	105,107,118,125	0
3	EDO	B	302	4/4	0.22	3.41	34,72,88,93	0
3	EDO	C	302	4/4	0.20	2.86	48,60,67,81	0
2	SO4	A	302	5/5	0.24	2.71	71,80,89,98	0
3	EDO	E	303	4/4	0.22	2.10	39,57,72,84	0
2	SO4	A	301	5/5	0.17	-0.31	54,65,98,109	0
3	EDO	D	302	4/4	0.14	-0.61	53,55,82,85	0
2	SO4	F	302	5/5	0.16	-0.76	69,78,82,94	0
2	SO4	F	301	5/5	0.15	-1.20	61,73,94,106	0
2	SO4	B	301	5/5	0.12	-1.57	89,93,102,112	0
2	SO4	E	301	5/5	0.14	-4.02	46,79,108,109	0

6.5 Other polymers ⓘ

There are no such residues in this entry.