



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:54 AM UTC

PDB ID : 4L5C / pdb_00004l5c
Title : Methylthioadenosine phosphorylase from *Schistosoma mansoni* in complex with adenine in space group P212121
Authors : Torini, J.R.; DeMarco, R.; Brandao-Neto, J.; Pereira, H.M.
Deposited on : 2013-06-10
Resolution : 2.08 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

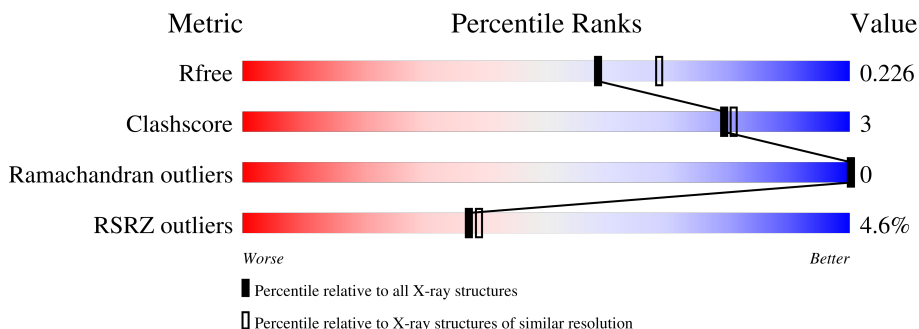
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.08 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	8172 (2.10-2.06)
Clashscore	190562	8714 (2.10-2.06)
Ramachandran outliers	187476	8641 (2.10-2.06)
RSRZ outliers	180081	8177 (2.10-2.06)

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	320	3% 85% 5% 10%
1	B	320	3% 84% 7% 10%
1	C	320	4% 85% 6% 9%
1	D	320	2% 86% 5% 10%
1	E	320	8% 82% 8% 10%
1	F	320	6% 84% 6% 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14646 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 S-methyl-5'-thioadenosine phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	0	0	0
			2209	1399	385	408	17			
1	B	289	Total	C	N	O	S	0	0	0
			2214	1404	387	406	17			
1	C	290	Total	C	N	O	S	0	0	0
			2215	1406	386	406	17			
1	D	289	Total	C	N	O	S	21	0	0
			2209	1399	385	408	17			
1	E	289	Total	C	N	O	S	0	0	0
			2207	1402	384	404	17			
1	F	289	Total	C	N	O	S	0	0	0
			2206	1398	384	407	17			

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP I0B503
A	-19	GLY	-	expression tag	UNP I0B503
A	-18	SER	-	expression tag	UNP I0B503
A	-17	SER	-	expression tag	UNP I0B503
A	-16	HIS	-	expression tag	UNP I0B503
A	-15	HIS	-	expression tag	UNP I0B503
A	-14	HIS	-	expression tag	UNP I0B503
A	-13	HIS	-	expression tag	UNP I0B503
A	-12	HIS	-	expression tag	UNP I0B503
A	-11	HIS	-	expression tag	UNP I0B503
A	-10	SER	-	expression tag	UNP I0B503
A	-9	SER	-	expression tag	UNP I0B503
A	-8	GLY	-	expression tag	UNP I0B503
A	-7	LEU	-	expression tag	UNP I0B503
A	-6	VAL	-	expression tag	UNP I0B503
A	-5	PRO	-	expression tag	UNP I0B503
A	-4	ARG	-	expression tag	UNP I0B503

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP I0B503
A	-2	SER	-	expression tag	UNP I0B503
A	-1	HIS	-	expression tag	UNP I0B503
A	0	MET	-	expression tag	UNP I0B503
B	-20	MET	-	expression tag	UNP I0B503
B	-19	GLY	-	expression tag	UNP I0B503
B	-18	SER	-	expression tag	UNP I0B503
B	-17	SER	-	expression tag	UNP I0B503
B	-16	HIS	-	expression tag	UNP I0B503
B	-15	HIS	-	expression tag	UNP I0B503
B	-14	HIS	-	expression tag	UNP I0B503
B	-13	HIS	-	expression tag	UNP I0B503
B	-12	HIS	-	expression tag	UNP I0B503
B	-11	HIS	-	expression tag	UNP I0B503
B	-10	SER	-	expression tag	UNP I0B503
B	-9	SER	-	expression tag	UNP I0B503
B	-8	GLY	-	expression tag	UNP I0B503
B	-7	LEU	-	expression tag	UNP I0B503
B	-6	VAL	-	expression tag	UNP I0B503
B	-5	PRO	-	expression tag	UNP I0B503
B	-4	ARG	-	expression tag	UNP I0B503
B	-3	GLY	-	expression tag	UNP I0B503
B	-2	SER	-	expression tag	UNP I0B503
B	-1	HIS	-	expression tag	UNP I0B503
B	0	MET	-	expression tag	UNP I0B503
C	-20	MET	-	expression tag	UNP I0B503
C	-19	GLY	-	expression tag	UNP I0B503
C	-18	SER	-	expression tag	UNP I0B503
C	-17	SER	-	expression tag	UNP I0B503
C	-16	HIS	-	expression tag	UNP I0B503
C	-15	HIS	-	expression tag	UNP I0B503
C	-14	HIS	-	expression tag	UNP I0B503
C	-13	HIS	-	expression tag	UNP I0B503
C	-12	HIS	-	expression tag	UNP I0B503
C	-11	HIS	-	expression tag	UNP I0B503
C	-10	SER	-	expression tag	UNP I0B503
C	-9	SER	-	expression tag	UNP I0B503
C	-8	GLY	-	expression tag	UNP I0B503
C	-7	LEU	-	expression tag	UNP I0B503
C	-6	VAL	-	expression tag	UNP I0B503
C	-5	PRO	-	expression tag	UNP I0B503
C	-4	ARG	-	expression tag	UNP I0B503

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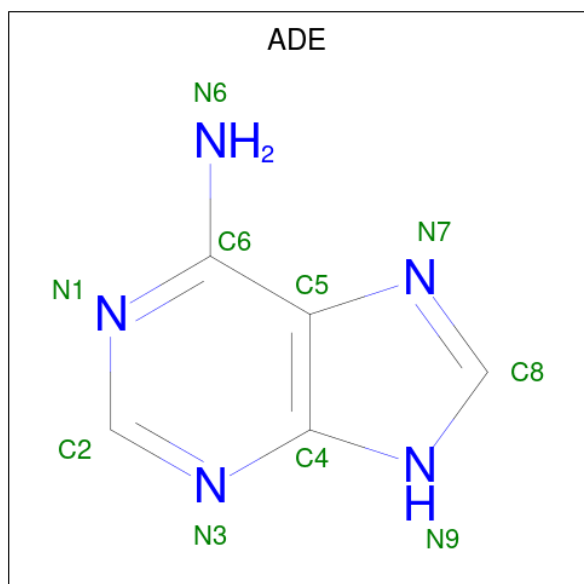
Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP I0B503
C	-2	SER	-	expression tag	UNP I0B503
C	-1	HIS	-	expression tag	UNP I0B503
C	0	MET	-	expression tag	UNP I0B503
D	-20	MET	-	expression tag	UNP I0B503
D	-19	GLY	-	expression tag	UNP I0B503
D	-18	SER	-	expression tag	UNP I0B503
D	-17	SER	-	expression tag	UNP I0B503
D	-16	HIS	-	expression tag	UNP I0B503
D	-15	HIS	-	expression tag	UNP I0B503
D	-14	HIS	-	expression tag	UNP I0B503
D	-13	HIS	-	expression tag	UNP I0B503
D	-12	HIS	-	expression tag	UNP I0B503
D	-11	HIS	-	expression tag	UNP I0B503
D	-10	SER	-	expression tag	UNP I0B503
D	-9	SER	-	expression tag	UNP I0B503
D	-8	GLY	-	expression tag	UNP I0B503
D	-7	LEU	-	expression tag	UNP I0B503
D	-6	VAL	-	expression tag	UNP I0B503
D	-5	PRO	-	expression tag	UNP I0B503
D	-4	ARG	-	expression tag	UNP I0B503
D	-3	GLY	-	expression tag	UNP I0B503
D	-2	SER	-	expression tag	UNP I0B503
D	-1	HIS	-	expression tag	UNP I0B503
D	0	MET	-	expression tag	UNP I0B503
E	-20	MET	-	expression tag	UNP I0B503
E	-19	GLY	-	expression tag	UNP I0B503
E	-18	SER	-	expression tag	UNP I0B503
E	-17	SER	-	expression tag	UNP I0B503
E	-16	HIS	-	expression tag	UNP I0B503
E	-15	HIS	-	expression tag	UNP I0B503
E	-14	HIS	-	expression tag	UNP I0B503
E	-13	HIS	-	expression tag	UNP I0B503
E	-12	HIS	-	expression tag	UNP I0B503
E	-11	HIS	-	expression tag	UNP I0B503
E	-10	SER	-	expression tag	UNP I0B503
E	-9	SER	-	expression tag	UNP I0B503
E	-8	GLY	-	expression tag	UNP I0B503
E	-7	LEU	-	expression tag	UNP I0B503
E	-6	VAL	-	expression tag	UNP I0B503
E	-5	PRO	-	expression tag	UNP I0B503
E	-4	ARG	-	expression tag	UNP I0B503

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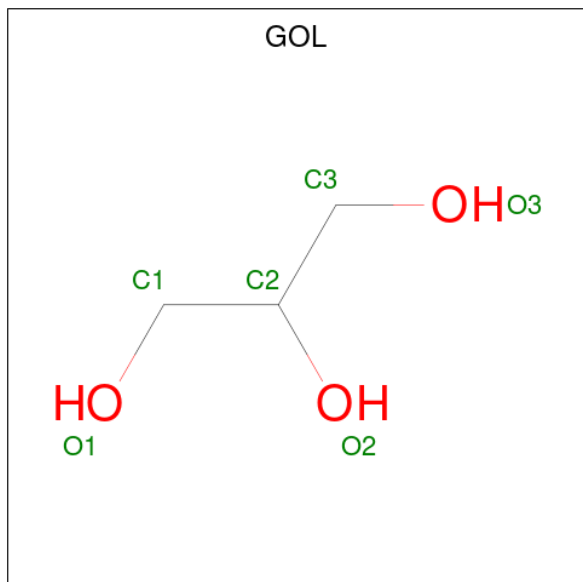
Chain	Residue	Modelled	Actual	Comment	Reference
E	-3	GLY	-	expression tag	UNP I0B503
E	-2	SER	-	expression tag	UNP I0B503
E	-1	HIS	-	expression tag	UNP I0B503
E	0	MET	-	expression tag	UNP I0B503
F	-20	MET	-	expression tag	UNP I0B503
F	-19	GLY	-	expression tag	UNP I0B503
F	-18	SER	-	expression tag	UNP I0B503
F	-17	SER	-	expression tag	UNP I0B503
F	-16	HIS	-	expression tag	UNP I0B503
F	-15	HIS	-	expression tag	UNP I0B503
F	-14	HIS	-	expression tag	UNP I0B503
F	-13	HIS	-	expression tag	UNP I0B503
F	-12	HIS	-	expression tag	UNP I0B503
F	-11	HIS	-	expression tag	UNP I0B503
F	-10	SER	-	expression tag	UNP I0B503
F	-9	SER	-	expression tag	UNP I0B503
F	-8	GLY	-	expression tag	UNP I0B503
F	-7	LEU	-	expression tag	UNP I0B503
F	-6	VAL	-	expression tag	UNP I0B503
F	-5	PRO	-	expression tag	UNP I0B503
F	-4	ARG	-	expression tag	UNP I0B503
F	-3	GLY	-	expression tag	UNP I0B503
F	-2	SER	-	expression tag	UNP I0B503
F	-1	HIS	-	expression tag	UNP I0B503
F	0	MET	-	expression tag	UNP I0B503

- Molecule 2 is ADENINE (CCD ID: ADE) (formula: $C_5H_5N_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			10	5	5		
2	B	1	Total	C	N	0	0
			10	5	5		
2	C	1	Total	C	N	0	0
			10	5	5		
2	D	1	Total	C	N	0	0
			10	5	5		
2	E	1	Total	C	N	0	0
			10	5	5		
2	F	1	Total	C	N	0	0
			10	5	5		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

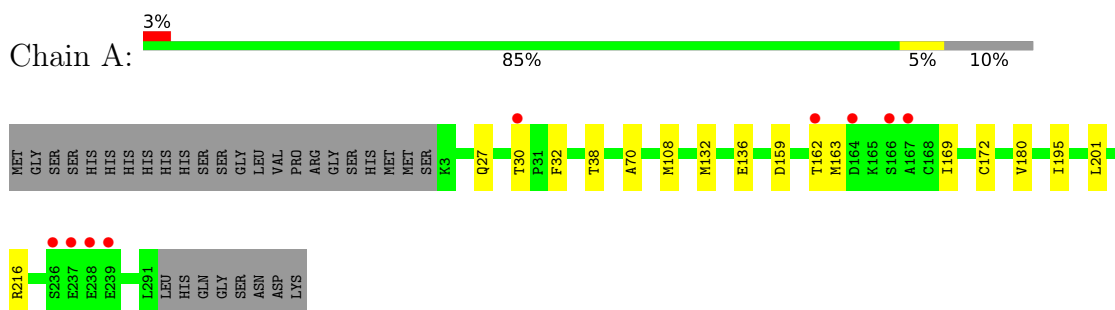
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	236	Total 236	O 236	0	0
4	B	216	Total 216	O 216	0	0
4	C	242	Total 242	O 242	0	0
4	D	220	Total 220	O 220	0	0
4	E	192	Total 192	O 192	0	0
4	F	184	Total 184	O 184	0	0

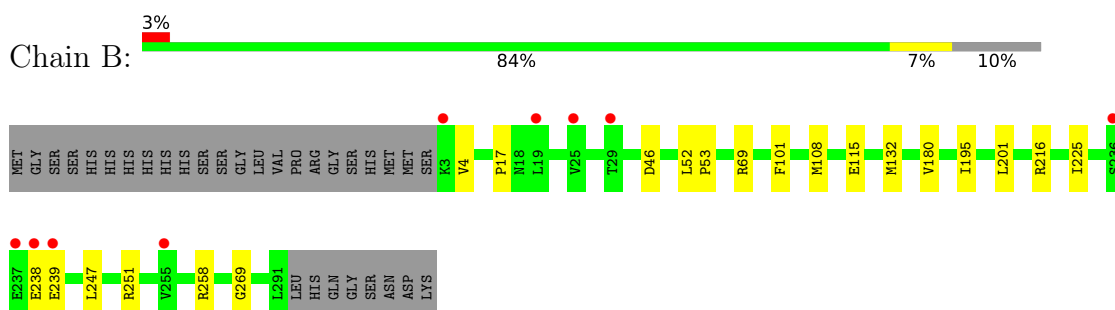
3 Residue-property plots [i](#)

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.

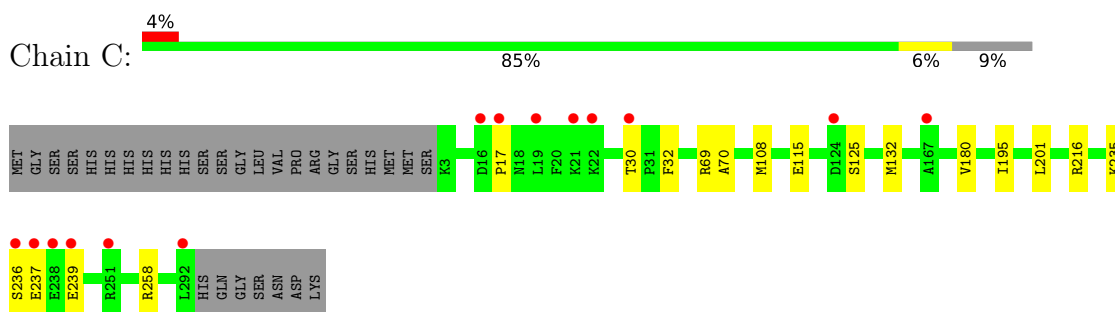
- Molecule 1: S-methyl-5'-thioadenosine phosphorylase



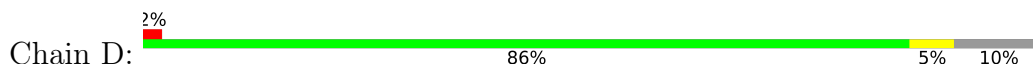
- Molecule 1: S-methyl-5'-thioadenosine phosphorylase

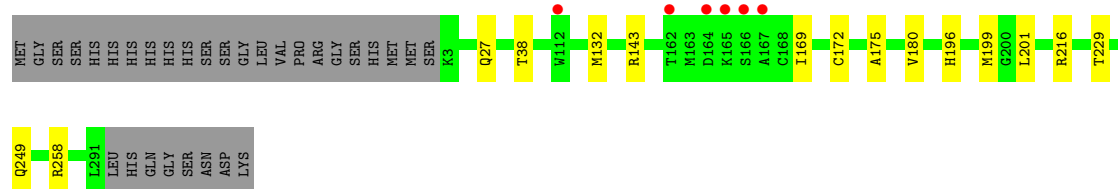


- Molecule 1: S-methyl-5'-thioadenosine phosphorylase

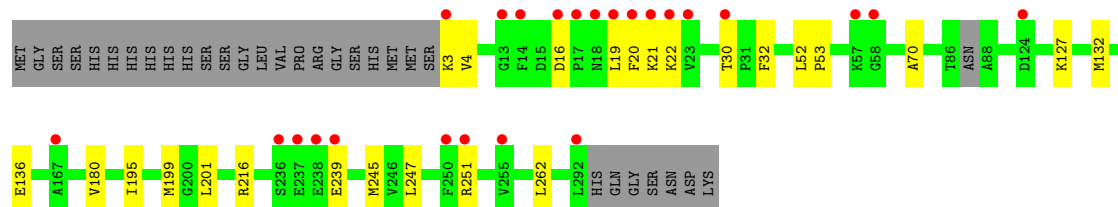
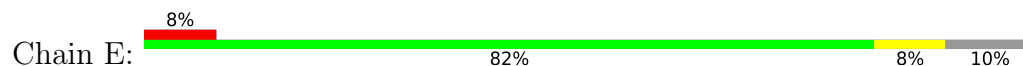


- Molecule 1: S-methyl-5'-thioadenosine phosphorylase

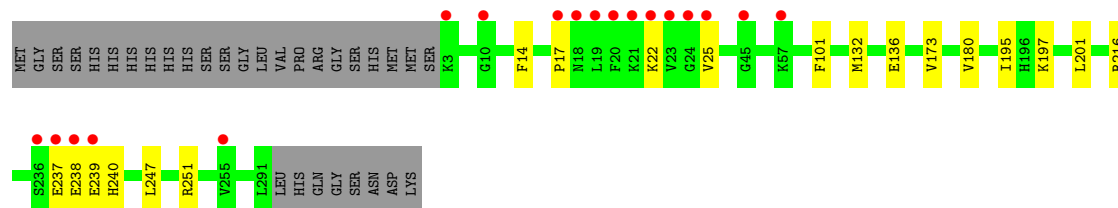
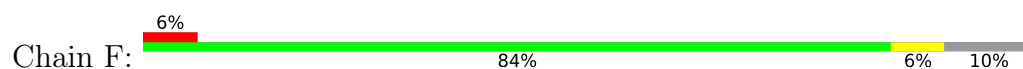




- Molecule 1: S-methyl-5'-thioadenosine phosphorylase



- Molecule 1: S-methyl-5'-thioadenosine phosphorylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	102.58Å 135.71Å 145.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.22 – 2.08 59.22 – 2.08	Depositor EDS
% Data completeness (in resolution range)	99.8 (59.22-2.08) 99.8 (59.22-2.08)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.10 (at 2.08Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.191 , 0.222 (Not available) , 0.226	Depositor DCC
R_{free} test set	6153 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	24.9	Xtriage
Anisotropy	0.401	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.1	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	14646	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.82 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4443e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ADE, 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	0.30	0/2254	0.69	2/3057 (0.1%)
1	B	0.29	0/2259	0.71	0/3061
1	C	0.29	0/2260	0.72	0/3064
1	D	0.29	0/2254	0.69	0/3057
1	E	0.29	0/2251	0.73	4/3050 (0.1%)
1	F	0.29	0/2251	0.71	2/3053 (0.1%)
All	All	0.29	0/13529	0.71	8/18342 (0.0%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	136	GLU	CA-C-N	6.48	126.10	119.56
1	F	136	GLU	C-N-CA	6.48	126.10	119.56
1	A	136	GLU	CA-C-N	5.09	125.17	119.87
1	A	136	GLU	C-N-CA	5.09	125.17	119.87
1	E	136	GLU	CA-C-N	5.02	125.09	119.87
1	E	136	GLU	C-N-CA	5.02	125.09	119.87
1	E	16	ASP	CA-C-N	5.01	124.18	118.97
1	E	16	ASP	C-N-CA	5.01	124.18	118.97

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	2209	0	2205	12	0
1	B	2214	0	2225	15	0
1	C	2215	0	2221	16	0
1	D	2209	0	2205	8	0
1	E	2207	0	2214	15	0
1	F	2206	0	2201	10	0
2	A	10	0	4	0	0
2	B	10	0	4	0	0
2	C	10	0	4	0	0
2	D	10	0	4	0	0
2	E	10	0	4	0	0
2	F	10	0	4	0	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
3	C	6	0	8	0	0
3	D	12	0	16	0	0
3	E	6	0	8	0	0
4	A	236	0	0	0	0
4	B	216	0	0	2	0
4	C	242	0	0	1	0
4	D	220	0	0	1	0
4	E	192	0	0	0	0
4	F	184	0	0	1	0
All	All	14646	0	13343	71	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 (71) 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:B:17:PRO:O	1:B:258:ARG:NH1	2.23	0.70
1:E:30:THR:HG21	1:E:70:ALA:HA	1.77	0.66
1:D:180:VAL:HB	1:D:201:LEU:HD13	1.78	0.65
1:A:180:VAL:HB	1:A:201:LEU:HD13	1.80	0.63
1:F:180:VAL:HB	1:F:201:LEU:HD13	1.78	0.63
1:C:30:THR:HG21	1:C:70:ALA:HA	1.81	0.63
1:B:108:MET:HE3	1:B:201:LEU:HD11	1.80	0.63
1:D:132:MET:HE2	1:D:216:ARG:HG2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:180:VAL:HB	1:E:201:LEU:HD13	1.82	0.61
1:E:3:LYS:HD3	1:E:4:VAL:H	1.66	0.60
1:E:239:GLU:HB2	1:E:245:MET:HE1	1.82	0.60
1:C:69:ARG:NH2	1:C:125:SER:OG	2.35	0.60
1:B:180:VAL:HB	1:B:201:LEU:HD13	1.85	0.59
1:A:30:THR:HG21	1:A:70:ALA:HA	1.84	0.59
1:E:20:PHE:HB3	1:E:21:LYS:C	2.27	0.59
1:A:132:MET:HE2	1:A:216:ARG:HG2	1.85	0.57
1:A:108:MET:HE3	1:C:195:ILE:HD13	1.86	0.57
1:D:27:GLN:HG2	1:D:38:THR:HG22	1.87	0.56
1:C:108:MET:HE3	1:C:201:LEU:HD11	1.86	0.55
1:C:30:THR:HG23	1:C:32:PHE:H	1.72	0.54
1:A:162:THR:HG23	1:A:163:MET:HG3	1.90	0.53
1:E:132:MET:HE2	1:E:216:ARG:HG2	1.91	0.52
1:B:132:MET:HE2	1:B:216:ARG:HG2	1.90	0.52
1:E:247:LEU:O	1:E:251:ARG:HG2	2.09	0.52
1:A:27:GLN:HG2	1:A:38:THR:HG22	1.92	0.52
1:D:258:ARG:NH2	4:D:582:HOH:O	2.43	0.52
1:A:30:THR:CG2	1:A:32:PHE:H	2.24	0.51
1:C:30:THR:CG2	1:C:32:PHE:H	2.24	0.51
1:C:132:MET:HE2	1:C:216:ARG:HG2	1.94	0.49
1:F:132:MET:HE2	1:F:216:ARG:HG2	1.93	0.49
1:A:195:ILE:HD13	1:B:108:MET:HE2	1.95	0.48
1:E:20:PHE:HB3	1:E:22:LYS:N	2.28	0.48
1:A:159:ASP:HB3	1:A:162:THR:HG22	1.95	0.48
1:E:30:THR:HG23	1:E:32:PHE:H	1.79	0.48
1:C:235:LYS:NZ	4:C:557:HOH:O	2.46	0.48
1:E:30:THR:CG2	1:E:32:PHE:H	2.27	0.47
1:B:69:ARG:HD2	1:B:115:GLU:CB	2.44	0.47
1:F:22:LYS:HE2	1:F:25:VAL:HG23	1.96	0.47
1:A:108:MET:HE3	1:C:195:ILE:HG21	1.96	0.47
1:D:196:HIS:HA	1:D:199:MET:HE3	1.96	0.47
1:E:19:LEU:HB3	1:E:262:LEU:HD21	1.98	0.46
1:A:30:THR:HG22	1:A:32:PHE:H	1.81	0.46
1:B:195:ILE:HD13	1:C:108:MET:HE2	1.98	0.45
1:B:4:VAL:HG21	1:B:269:GLY:HA2	1.99	0.45
1:D:143:ARG:NH2	1:D:175:ALA:O	2.48	0.45
1:B:69:ARG:HD2	1:B:115:GLU:HB3	1.99	0.44
4:B:489:HOH:O	1:C:108:MET:SD	2.60	0.44
1:C:235:LYS:HB3	1:C:236:SER:H	1.60	0.43
1:C:17:PRO:O	1:C:258:ARG:NH1	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:258:ARG:NE	4:B:609:HOH:O	2.37	0.43
1:E:199:MET:HE2	1:F:195:ILE:HD13	2.01	0.43
1:C:69:ARG:HD2	1:C:115:GLU:CB	2.49	0.42
1:C:180:VAL:HB	1:C:201:LEU:HD13	1.99	0.42
1:B:46:ASP:OD1	1:B:46:ASP:N	2.45	0.42
1:F:197:LYS:NZ	4:F:550:HOH:O	2.51	0.42
1:B:238:GLU:HA	1:B:239:GLU:HA	1.75	0.42
1:D:169:ILE:O	1:D:172:CYS:HB3	2.19	0.42
1:E:52:LEU:HD12	1:E:53:PRO:HD2	2.01	0.42
1:F:238:GLU:HA	1:F:239:GLU:HA	1.72	0.42
1:E:195:ILE:O	1:E:199:MET:HG3	2.20	0.42
1:A:169:ILE:O	1:A:172:CYS:HB3	2.20	0.42
1:F:101:PHE:HB2	1:F:173:VAL:HG22	2.02	0.42
1:F:247:LEU:O	1:F:251:ARG:HG3	2.19	0.42
1:B:247:LEU:O	1:B:251:ARG:HG3	2.21	0.41
1:D:229:THR:HA	1:D:249:GLN:HG2	2.03	0.41
1:E:127:LYS:HA	1:E:127:LYS:HD3	1.88	0.41
1:B:52:LEU:HD12	1:B:53:PRO:HD2	2.02	0.40
1:B:101:PHE:HB3	1:B:225:ILE:HD11	2.02	0.40
1:F:237:GLU:HA	1:F:240:HIS:CE1	2.56	0.40
1:C:237:GLU:O	1:C:239:GLU:HA	2.22	0.40
1:F:14:PHE:CE1	1:F:17:PRO:HA	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	287/320 (90%)	282 (98%)	5 (2%)	0	100	100
1	B	287/320 (90%)	283 (99%)	4 (1%)	0	100	100
1	C	288/320 (90%)	284 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	287/320 (90%)	283 (99%)	4 (1%)	0	100	100
1	E	285/320 (89%)	279 (98%)	6 (2%)	0	100	100
1	F	287/320 (90%)	283 (99%)	4 (1%)	0	100	100
All	All	1721/1920 (90%)	1694 (98%)	27 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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](#)

12 ligands are modelled in this entry.

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	$\# Z > 2$
2	ADE	E	301	-	11,11,11	0.40	0	15,15,15	0.44	0
3	GOL	E	302	-	5,5,5	0.35	0	5,5,5	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	A	302	-	5,5,5	0.37	0	5,5,5	0.32	0
2	ADE	C	301	-	11,11,11	0.44	0	15,15,15	0.43	0
3	GOL	D	302	-	5,5,5	0.37	0	5,5,5	0.29	0
3	GOL	D	303	-	5,5,5	0.36	0	5,5,5	0.27	0
2	ADE	A	301	-	11,11,11	0.41	0	15,15,15	0.43	0
2	ADE	D	301	-	11,11,11	0.42	0	15,15,15	0.43	0
3	GOL	C	302	-	5,5,5	0.36	0	5,5,5	0.28	0
2	ADE	F	301	-	11,11,11	0.40	0	15,15,15	0.42	0
2	ADE	B	301	-	11,11,11	0.42	0	15,15,15	0.44	0
3	GOL	B	302	-	5,5,5	0.33	0	5,5,5	0.34	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
2	ADE	E	301	-	-	-	0/2/2/2
3	GOL	E	302	-	-	0/4/4/4	-
3	GOL	A	302	-	-	0/4/4/4	-
2	ADE	C	301	-	-	-	0/2/2/2
3	GOL	D	302	-	-	0/4/4/4	-
3	GOL	D	303	-	-	1/4/4/4	-
3	GOL	C	302	-	-	0/4/4/4	-
2	ADE	A	301	-	-	-	0/2/2/2
2	ADE	D	301	-	-	-	0/2/2/2
2	ADE	F	301	-	-	-	0/2/2/2
2	ADE	B	301	-	-	-	0/2/2/2
3	GOL	B	302	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	303	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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	289/320 (90%)	-0.12	9 (3%)	51	53	10, 18, 42, 96	0
1	B	289/320 (90%)	0.03	9 (3%)	51	53	11, 23, 45, 116	0
1	C	290/320 (90%)	0.04	14 (4%)	35	37	11, 22, 50, 105	0
1	D	285/320 (89%)	-0.03	6 (2%)	63	66	13, 21, 42, 72	0
1	E	289/320 (90%)	0.29	24 (8%)	17	18	14, 26, 59, 128	0
1	F	289/320 (90%)	0.30	18 (6%)	26	28	14, 28, 62, 114	0
All	All	1731/1920 (90%)	0.09	80 (4%)	37	39	10, 22, 52, 128	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	238	GLU	6.3
1	C	238	GLU	5.5
1	F	25	VAL	5.5
1	A	236	SER	5.1
1	E	238	GLU	5.1
1	B	239	GLU	4.8
1	E	20	PHE	4.7
1	D	166	SER	4.6
1	B	237	GLU	4.4
1	F	238	GLU	4.4
1	A	239	GLU	4.3
1	E	19	LEU	4.2
1	F	237	GLU	4.2
1	A	238	GLU	4.2
1	A	237	GLU	4.2
1	F	239	GLU	4.1
1	F	236	SER	3.9
1	C	239	GLU	3.9
1	C	292	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
1	E	292	LEU	3.9
1	C	237	GLU	3.9
1	D	165	LYS	3.8
1	E	16	ASP	3.8
1	E	237	GLU	3.7
1	E	21	LYS	3.5
1	D	167	ALA	3.5
1	A	162	THR	3.5
1	C	236	SER	3.4
1	F	19	LEU	3.4
1	F	3	LYS	3.4
1	D	164	ASP	3.3
1	E	17	PRO	3.3
1	E	124	ASP	3.2
1	F	23	VAL	3.2
1	E	18	ASN	3.1
1	E	239	GLU	3.0
1	B	236	SER	3.0
1	E	13	GLY	2.9
1	F	24	GLY	2.9
1	F	17	PRO	2.8
1	E	57	LYS	2.8
1	E	14	PHE	2.8
1	F	45	GLY	2.8
1	F	255	VAL	2.8
1	E	3	LYS	2.7
1	E	251	ARG	2.7
1	C	251	ARG	2.7
1	C	22	LYS	2.7
1	E	58	GLY	2.7
1	E	167	ALA	2.7
1	F	20	PHE	2.7
1	F	10	GLY	2.7
1	E	23	VAL	2.6
1	B	255	VAL	2.6
1	C	19	LEU	2.6
1	D	112	TRP	2.6
1	C	124	ASP	2.5
1	F	21	LYS	2.5
1	B	3	LYS	2.5
1	E	22	LYS	2.5
1	E	236	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	16	ASP	2.4
1	C	30	THR	2.4
1	C	167	ALA	2.4
1	A	164	ASP	2.3
1	E	255	VAL	2.3
1	D	162	THR	2.3
1	A	167	ALA	2.3
1	B	29	THR	2.2
1	A	166	SER	2.2
1	E	250	PHE	2.2
1	A	30	THR	2.2
1	C	17	PRO	2.2
1	F	18	ASN	2.2
1	B	25	VAL	2.1
1	F	57	LYS	2.1
1	E	30	THR	2.1
1	C	21	LYS	2.1
1	B	19	LEU	2.0
1	F	22	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [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	GOL	D	303	6/6	0.92	0.11	32,33,35,36	0
3	GOL	B	302	6/6	0.94	0.07	15,18,20,22	0
3	GOL	E	302	6/6	0.94	0.08	18,21,24,28	0
2	ADE	D	301	10/10	0.95	0.06	18,20,23,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	A	302	6/6	0.96	0.06	14,14,18,20	0
2	ADE	E	301	10/10	0.96	0.06	16,20,24,24	0
2	ADE	C	301	10/10	0.97	0.06	11,14,17,18	0
2	ADE	A	301	10/10	0.97	0.07	10,16,18,18	0
3	GOL	C	302	6/6	0.97	0.05	17,21,25,26	0
2	ADE	B	301	10/10	0.97	0.05	10,13,15,16	0
2	ADE	F	301	10/10	0.97	0.05	12,15,19,19	0
3	GOL	D	302	6/6	0.98	0.05	16,18,19,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.