



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:24 PM UTC

PDB ID : 5F7Z / pdb_00005f7z
Title : Crystal structure of Double Mutant S12T and N87T of Adenosine/Methylthioadenosine Phosphorylase from *Schistosoma mansoni* in APO Form
Authors : Torini, J.R.; Brandao-Neto, J.; DeMarco, R.; Pereira, H.M.
Deposited on : 2015-12-08
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

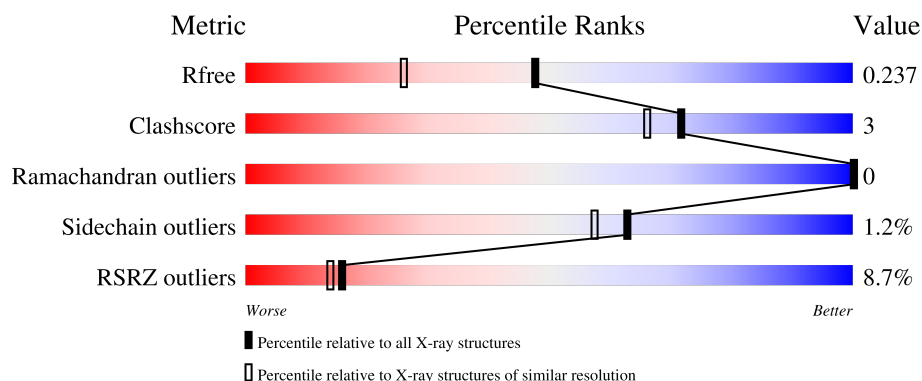
1 Overall quality at a glance

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	320	8% 80% 9% 11%
1	B	320	10% 84% 7% 10%
1	C	320	9% 83% 6% 10%
1	D	320	7% 83% 6% 12%
1	E	320	8% 79% 8% 13%

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Mol	Chain	Length	Quality of chain
1	F	320	5% 81% 6% 12%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14327 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 Methylthioadenosine phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	0	0	0
			2143	1356	372	399	16			
1	B	289	Total	C	N	O	S	0	0	0
			2176	1379	376	405	16			
1	C	287	Total	C	N	O	S	0	0	0
			2150	1365	370	399	16			
1	D	283	Total	C	N	O	S	0	0	0
			2113	1338	364	395	16			
1	E	279	Total	C	N	O	S	0	0	0
			2112	1341	365	390	16			
1	F	280	Total	C	N	O	S	0	0	0
			2110	1337	365	392	16			

There are 138 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	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
A	12	THR	SER	engineered mutation	UNP I0B503
A	87	THR	ASN	engineered mutation	UNP I0B503
B	-20	MET	-	initiating methionine	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
B	12	THR	SER	engineered mutation	UNP I0B503
B	87	THR	ASN	engineered mutation	UNP I0B503
C	-20	MET	-	initiating methionine	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

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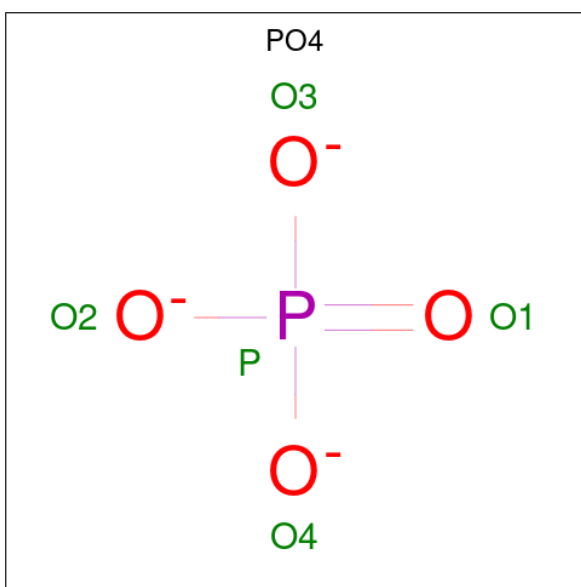
Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	LEU	-	expression tag	UNP I0B503
C	-6	VAL	-	expression tag	UNP I0B503
C	-5	PRO	-	expression tag	UNP I0B503
C	-4	ARG	-	expression tag	UNP I0B503
C	-3	GLY	-	expression tag	UNP I0B503
C	-2	SER	-	expression tag	UNP I0B503
C	-1	HIS	-	expression tag	UNP I0B503
C	0	MET	-	expression tag	UNP I0B503
C	12	THR	SER	engineered mutation	UNP I0B503
C	87	THR	ASN	engineered mutation	UNP I0B503
D	-20	MET	-	initiating methionine	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
D	12	THR	SER	engineered mutation	UNP I0B503
D	87	THR	ASN	engineered mutation	UNP I0B503
E	-20	MET	-	initiating methionine	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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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
E	12	THR	SER	engineered mutation	UNP I0B503
E	87	THR	ASN	engineered mutation	UNP I0B503
F	-20	MET	-	initiating methionine	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
F	12	THR	SER	engineered mutation	UNP I0B503
F	87	THR	ASN	engineered mutation	UNP I0B503

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

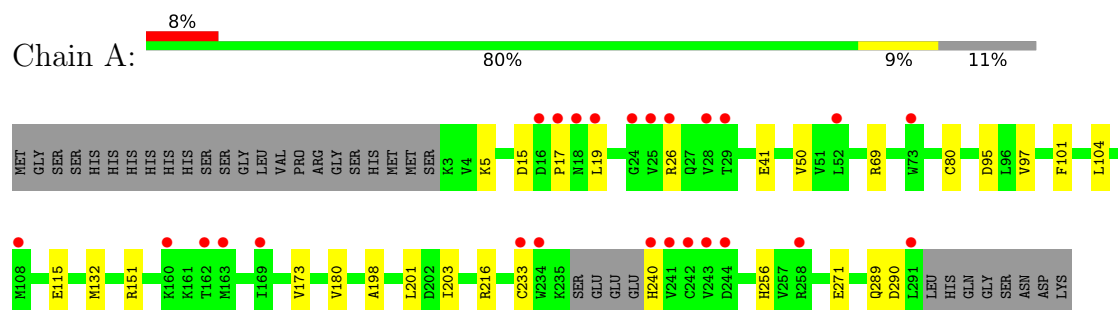
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	260	Total	O	0	0
			260	260		
3	B	215	Total	O	0	0
			215	215		
3	C	196	Total	O	0	0
			196	196		
3	D	299	Total	O	0	0
			299	299		
3	E	257	Total	O	0	0
			257	257		
3	F	266	Total	O	0	0
			266	266		

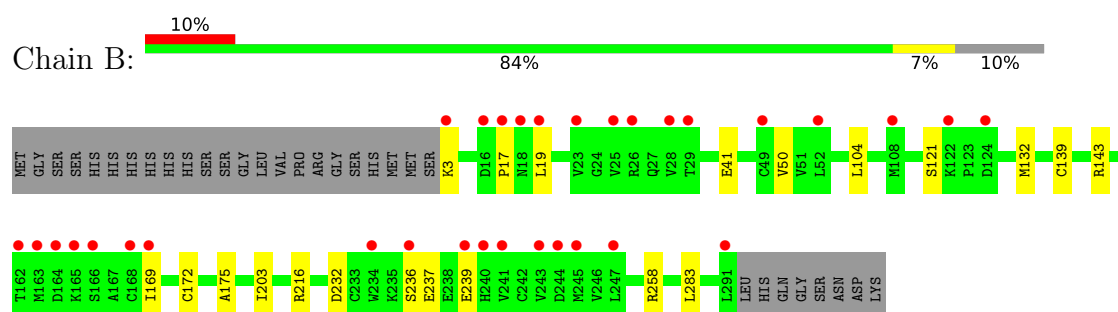
3 Residue-property plots [i](#)

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.

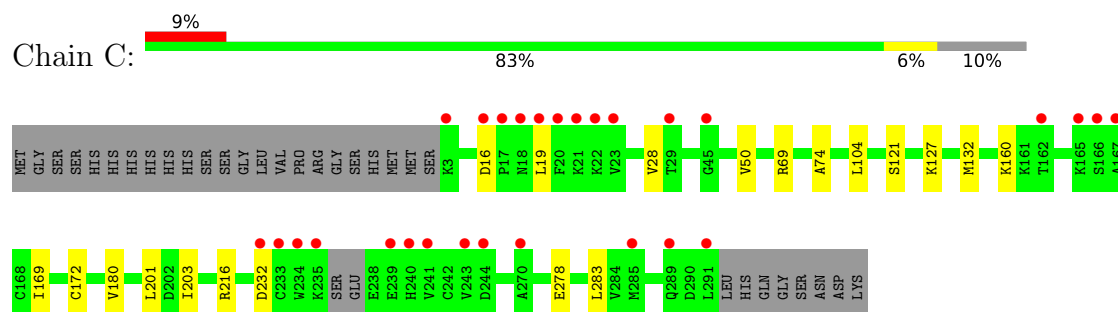
- Molecule 1: Methylthioadenosine phosphorylase



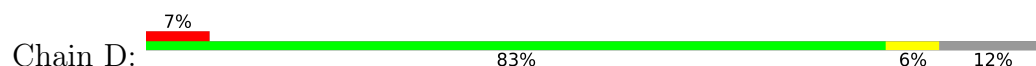
- Molecule 1: Methylthioadenosine phosphorylase

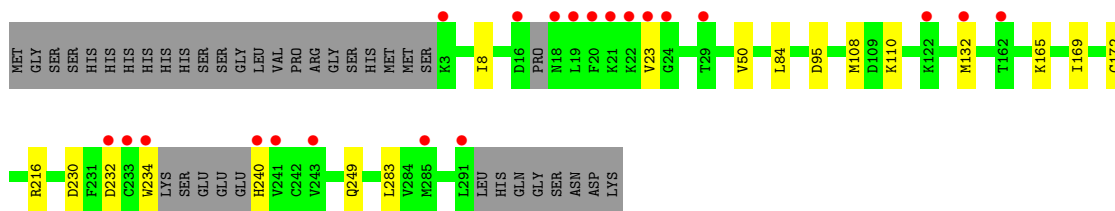


- Molecule 1: Methylthioadenosine phosphorylase

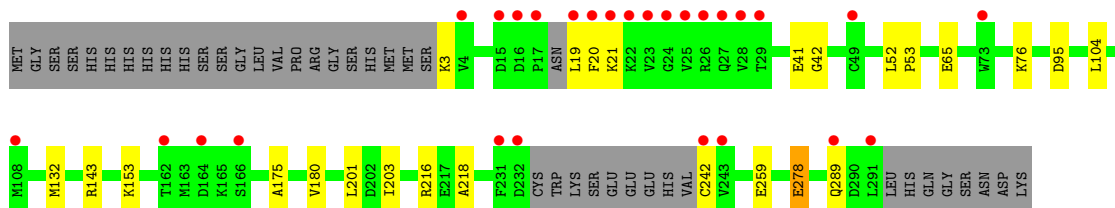
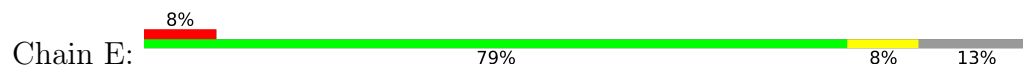


- Molecule 1: Methylthioadenosine phosphorylase

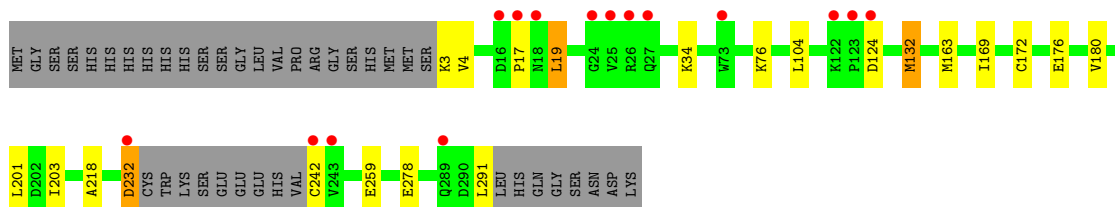
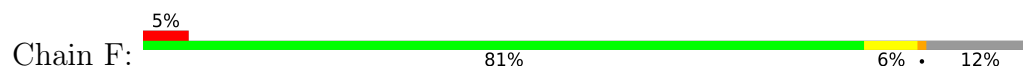




● Molecule 1: Methylthioadenosine phosphorylase



● Molecule 1: Methylthioadenosine phosphorylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	80.70Å 82.25Å 150.02Å 90.00° 101.42° 90.00°	Depositor
Resolution (Å)	79.10 – 1.80 79.10 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.4 (79.10-1.80) 99.8 (79.10-1.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 1.80Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.211 , 0.235 0.213 , 0.237	Depositor DCC
R_{free} test set	8789 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	19.0	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14327	wwPDB-VP
Average B, all atoms (Å ²)	32.0	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 39.60 % 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 3.0984e-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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.13	0/2185	0.33	0/2969
1	B	0.23	0/2220	0.39	1/3017 (0.0%)
1	C	0.24	0/2193	0.40	2/2982 (0.1%)
1	D	0.13	0/2152	0.31	0/2923
1	E	0.13	0/2152	0.31	0/2918
1	F	0.12	0/2151	0.32	0/2921
All	All	0.17	0/13053	0.35	3/17730 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	236	SER	N-CA-C	8.91	123.67	110.48
1	C	16	ASP	CA-C-N	-6.72	113.06	119.85
1	C	16	ASP	C-N-CA	-6.72	113.06	119.85

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2143	0	2104	22	0
1	B	2176	0	2130	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2150	0	2102	8	0
1	D	2113	0	2062	11	0
1	E	2112	0	2108	17	0
1	F	2110	0	2086	14	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	A	260	0	0	11	1
3	B	215	0	0	5	0
3	C	196	0	0	2	0
3	D	299	0	0	3	0
3	E	257	0	0	7	1
3	F	266	0	0	8	1
All	All	14327	0	12592	84	2

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 (84) 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:240:HIS:N	3:D:402:HOH:O	1.99	0.95
1:D:23:VAL:O	3:D:401:HOH:O	1.88	0.91
1:F:291:LEU:O	3:F:401:HOH:O	1.90	0.90
1:E:21:LYS:O	3:E:401:HOH:O	1.90	0.89
1:A:95:ASP:OD2	3:A:401:HOH:O	1.92	0.88
1:A:240:HIS:N	3:A:407:HOH:O	2.21	0.74
1:E:180:VAL:HB	1:E:201:LEU:HD13	1.72	0.72
1:B:139:CYS:SG	3:B:566:HOH:O	2.24	0.70
1:F:104:LEU:HD21	1:F:203:ILE:HD11	1.73	0.69
1:A:180:VAL:HB	1:A:201:LEU:HD13	1.75	0.68
1:C:132:MET:HE2	1:C:216:ARG:HG2	1.75	0.68
1:E:3:LYS:N	3:E:407:HOH:O	2.27	0.68
1:F:124:ASP:OD2	3:F:402:HOH:O	2.12	0.68
1:B:132:MET:HE2	1:B:216:ARG:HG2	1.75	0.67
1:F:232:ASP:N	1:F:232:ASP:OD1	2.26	0.67
1:E:242:CYS:SG	3:E:611:HOH:O	2.40	0.66
1:F:180:VAL:HB	1:F:201:LEU:HD13	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:132:MET:HE2	1:E:216:ARG:HG2	1.78	0.66
1:D:132:MET:HE2	1:D:216:ARG:HG2	1.76	0.65
1:A:132:MET:HE2	1:A:216:ARG:HG2	1.78	0.65
1:B:41:GLU:HG2	1:B:50:VAL:HG22	1.79	0.63
1:E:95:ASP:OD2	3:E:403:HOH:O	2.15	0.63
1:A:26:ARG:NH1	3:A:409:HOH:O	2.30	0.63
1:E:259:GLU:OE1	3:E:404:HOH:O	2.16	0.63
1:A:289:GLN:HG2	3:F:583:HOH:O	1.99	0.61
1:D:132:MET:HE1	1:D:283:LEU:HG	1.82	0.61
1:F:163:MET:HE1	3:F:509:HOH:O	1.99	0.61
1:E:153:LYS:HE2	1:E:259:GLU:HB3	1.83	0.60
1:D:95:ASP:OD2	1:D:165:LYS:NZ	2.32	0.59
1:B:258:ARG:NH1	3:B:408:HOH:O	2.36	0.57
1:A:290:ASP:O	3:A:403:HOH:O	2.18	0.57
1:A:15:ASP:OD2	3:A:404:HOH:O	2.18	0.55
1:A:256:HIS:HE1	3:A:600:HOH:O	1.90	0.54
1:A:69:ARG:HD2	1:A:115:GLU:HB3	1.89	0.53
1:B:17:PRO:HB2	1:B:19:LEU:HD13	1.91	0.53
1:D:249:GLN:NE2	3:D:410:HOH:O	2.43	0.52
1:A:69:ARG:HD2	1:A:115:GLU:CB	2.39	0.51
1:E:104:LEU:HD21	1:E:203:ILE:HD11	1.92	0.51
1:E:278:GLU:HG3	3:E:621:HOH:O	2.09	0.51
1:F:176:GLU:HG3	3:F:579:HOH:O	2.10	0.51
1:B:237:GLU:C	3:B:405:HOH:O	2.52	0.51
1:F:17:PRO:HB2	1:F:19:LEU:HD13	1.92	0.50
1:F:3:LYS:N	3:F:413:HOH:O	2.45	0.50
1:F:259:GLU:HG3	3:F:465:HOH:O	2.13	0.49
1:A:240:HIS:O	1:A:240:HIS:ND1	2.40	0.49
1:B:3:LYS:N	3:B:412:HOH:O	2.44	0.49
1:A:104:LEU:HD21	1:A:203:ILE:HD11	1.94	0.49
1:C:180:VAL:HB	1:C:201:LEU:HD13	1.93	0.49
1:A:271:GLU:O	3:A:406:HOH:O	2.20	0.48
1:D:8:ILE:HD13	1:D:84:LEU:HB2	1.94	0.48
1:C:160:LYS:O	3:C:402:HOH:O	2.20	0.47
1:D:232:ASP:O	1:D:234:TRP:N	2.47	0.47
1:E:143:ARG:NH2	1:E:175:ALA:O	2.48	0.47
1:C:132:MET:HE1	1:C:283:LEU:HG	1.98	0.46
1:B:104:LEU:HD21	1:B:203:ILE:HD11	1.97	0.46
1:E:41:GLU:OE2	3:E:405:HOH:O	2.21	0.46
1:A:233:CYS:SG	3:A:448:HOH:O	2.61	0.45
1:E:52:LEU:HD12	1:E:53:PRO:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:132:MET:HE2	1:F:132:MET:HB3	1.73	0.45
1:B:169:ILE:O	1:B:172:CYS:HB3	2.16	0.45
1:A:101:PHE:HD2	1:A:173:VAL:HG22	1.83	0.44
1:A:151:ARG:O	3:A:405:HOH:O	2.20	0.44
1:A:17:PRO:HB2	1:A:19:LEU:HD13	1.98	0.44
1:C:169:ILE:O	1:C:172:CYS:HB3	2.18	0.43
1:B:232:ASP:OD2	3:B:401:HOH:O	2.21	0.43
1:E:19:LEU:HD23	1:E:19:LEU:HA	1.85	0.43
1:B:143:ARG:NH2	1:B:175:ALA:O	2.52	0.42
1:A:26:ARG:CZ	3:A:409:HOH:O	2.66	0.42
1:C:121:SER:HB2	3:C:404:HOH:O	2.18	0.42
1:D:169:ILE:O	1:D:172:CYS:HB3	2.19	0.42
1:A:41:GLU:HG2	1:A:50:VAL:HG22	2.01	0.42
1:C:28:VAL:HG21	1:C:74:ALA:HB1	2.00	0.42
1:C:104:LEU:HD21	1:C:203:ILE:HD11	2.01	0.41
1:B:121:SER:OG	1:E:65:GLU:OE1	2.37	0.41
1:F:4:VAL:HG22	3:F:566:HOH:O	2.20	0.41
1:E:20:PHE:CE1	1:E:42:GLY:HA3	2.56	0.41
1:A:198:ALA:HA	3:A:576:HOH:O	2.20	0.41
1:D:108:MET:HE3	1:D:110:LYS:HD2	2.02	0.41
1:E:76:LYS:HD2	1:E:218:ALA:HB1	2.01	0.41
1:A:5:LYS:HB3	1:A:80:CYS:HA	2.03	0.41
1:D:230:ASP:OD1	1:D:232:ASP:HB2	2.20	0.41
1:F:169:ILE:O	1:F:172:CYS:HB3	2.21	0.41
1:B:132:MET:HE1	1:B:283:LEU:HG	2.02	0.40
1:F:76:LYS:HE2	1:F:218:ALA:O	2.21	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:513:HOH:O	3:F:632:HOH:O[2_846]	2.08	0.12
3:E:576:HOH:O	3:E:592:HOH:O[2_855]	2.18	0.02

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	281/320 (88%)	276 (98%)	5 (2%)	0	100	100
1	B	287/320 (90%)	282 (98%)	5 (2%)	0	100	100
1	C	283/320 (88%)	279 (99%)	4 (1%)	0	100	100
1	D	277/320 (87%)	273 (99%)	4 (1%)	0	100	100
1	E	273/320 (85%)	272 (100%)	1 (0%)	0	100	100
1	F	276/320 (86%)	274 (99%)	2 (1%)	0	100	100
All	All	1677/1920 (87%)	1656 (99%)	21 (1%)	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	230/274 (84%)	229 (100%)	1 (0%)	84	83
1	B	231/274 (84%)	230 (100%)	1 (0%)	84	83
1	C	228/274 (83%)	222 (97%)	6 (3%)	40	28
1	D	224/274 (82%)	223 (100%)	1 (0%)	84	83
1	E	229/274 (84%)	227 (99%)	2 (1%)	70	67
1	F	227/274 (83%)	221 (97%)	6 (3%)	40	28
All	All	1369/1644 (83%)	1352 (99%)	17 (1%)	63	57

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	VAL
1	B	239	GLU
1	C	19	LEU

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Mol	Chain	Res	Type
1	C	50	VAL
1	C	69	ARG
1	C	127	LYS
1	C	232	ASP
1	C	278	GLU
1	D	50	VAL
1	E	278	GLU
1	E	289	GLN
1	F	19	LEU
1	F	34	LYS
1	F	132	MET
1	F	232	ASP
1	F	242	CYS
1	F	278	GLU

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

Mol	Chain	Res	Type
1	A	148	GLN
1	A	249	GLN
1	B	148	GLN
1	B	249	GLN
1	D	249	GLN
1	F	148	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 [i](#)

6 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	PO4	A	301	-	4,4,4	0.97	0	6,6,6	0.45	0
2	PO4	F	301	-	4,4,4	0.96	0	6,6,6	0.56	0
2	PO4	B	301	-	4,4,4	0.90	0	6,6,6	0.52	0
2	PO4	D	301	-	4,4,4	0.94	0	6,6,6	0.55	0
2	PO4	E	301	-	4,4,4	0.98	0	6,6,6	0.51	0
2	PO4	C	301	-	4,4,4	0.94	0	6,6,6	0.44	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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	285/320 (89%)	0.43	25 (8%) 15 13	18, 28, 58, 76	0
1	B	289/320 (90%)	0.61	32 (11%) 10 8	17, 33, 60, 74	0
1	C	287/320 (89%)	0.56	28 (9%) 13 11	18, 32, 59, 71	0
1	D	283/320 (88%)	0.28	21 (7%) 20 19	15, 26, 52, 85	0
1	E	279/320 (87%)	0.43	27 (9%) 13 11	16, 27, 57, 85	0
1	F	280/320 (87%)	0.26	15 (5%) 31 30	16, 25, 50, 66	0
All	All	1703/1920 (88%)	0.43	148 (8%) 16 14	15, 28, 57, 85	0

All (148) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	25	VAL	7.6
1	D	234	TRP	6.3
1	F	25	VAL	6.2
1	A	234	TRP	5.8
1	D	23	VAL	5.7
1	E	16	ASP	5.6
1	E	28	VAL	5.5
1	E	17	PRO	5.4
1	E	20	PHE	5.3
1	E	24	GLY	5.2
1	F	124	ASP	5.1
1	B	291	LEU	5.1
1	D	19	LEU	5.0
1	D	241	VAL	4.8
1	F	17	PRO	4.6
1	E	23	VAL	4.6
1	A	18	ASN	4.5
1	C	162	THR	4.5
1	E	19	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
1	C	234	TRP	4.3
1	F	26	ARG	4.3
1	A	240	HIS	4.2
1	E	29	THR	4.2
1	C	17	PRO	4.2
1	B	241	VAL	4.2
1	A	241	VAL	4.1
1	C	232	ASP	4.0
1	C	291	LEU	3.8
1	E	26	ARG	3.8
1	A	291	LEU	3.7
1	C	18	ASN	3.7
1	A	162	THR	3.6
1	F	18	ASN	3.5
1	F	232	ASP	3.5
1	B	26	ARG	3.5
1	A	16	ASP	3.5
1	B	244	ASP	3.5
1	F	242	CYS	3.4
1	C	241	VAL	3.4
1	C	240	HIS	3.4
1	D	22	LYS	3.4
1	D	24	GLY	3.4
1	E	27	GLN	3.4
1	B	18	ASN	3.3
1	E	21	LYS	3.3
1	C	239	GLU	3.3
1	C	19	LEU	3.3
1	A	243	VAL	3.3
1	D	291	LEU	3.3
1	B	162	THR	3.2
1	D	20	PHE	3.2
1	C	244	ASP	3.2
1	A	17	PRO	3.1
1	E	243	VAL	3.1
1	F	243	VAL	3.1
1	B	3	LYS	3.1
1	B	17	PRO	3.1
1	D	240	HIS	3.1
1	D	21	LYS	3.1
1	F	27	GLN	3.1
1	E	49	CYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	236	SER	3.1
1	C	166	SER	3.0
1	A	25	VAL	3.0
1	F	122	LYS	3.0
1	D	285	MET	3.0
1	C	235	LYS	2.9
1	A	52	LEU	2.9
1	B	52	LEU	2.9
1	E	289	GLN	2.8
1	E	242	CYS	2.8
1	E	73	TRP	2.8
1	D	243	VAL	2.8
1	D	232	ASP	2.8
1	A	24	GLY	2.8
1	D	29	THR	2.8
1	D	18	ASN	2.7
1	E	22	LYS	2.7
1	A	19	LEU	2.7
1	B	28	VAL	2.7
1	B	122	LYS	2.7
1	B	29	THR	2.7
1	B	245	MET	2.7
1	E	15	ASP	2.7
1	B	19	LEU	2.7
1	C	289	GLN	2.7
1	B	234	TRP	2.7
1	A	242	CYS	2.7
1	F	24	GLY	2.6
1	A	26	ARG	2.6
1	B	168	CYS	2.6
1	D	122	LYS	2.6
1	A	73	TRP	2.6
1	A	258	ARG	2.6
1	B	25	VAL	2.6
1	B	243	VAL	2.6
1	C	243	VAL	2.6
1	E	4	VAL	2.6
1	E	162	THR	2.6
1	A	108	MET	2.5
1	A	244	ASP	2.5
1	F	73	TRP	2.5
1	C	23	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	165	LYS	2.5
1	D	162	THR	2.5
1	F	123	PRO	2.5
1	D	233	CYS	2.4
1	C	167	ALA	2.4
1	C	233	CYS	2.4
1	D	16	ASP	2.4
1	B	165	LYS	2.4
1	F	16	ASP	2.4
1	E	166	SER	2.4
1	A	233	CYS	2.4
1	B	16	ASP	2.3
1	A	169	ILE	2.3
1	D	132	MET	2.3
1	C	22	LYS	2.3
1	E	291	LEU	2.3
1	A	29	THR	2.3
1	C	3	LYS	2.3
1	B	124	ASP	2.3
1	B	240	HIS	2.3
1	C	285	MET	2.3
1	C	21	LYS	2.3
1	B	169	ILE	2.2
1	E	164	ASP	2.2
1	E	232	ASP	2.2
1	B	239	GLU	2.2
1	E	231	PHE	2.2
1	D	3	LYS	2.2
1	C	20	PHE	2.2
1	B	23	VAL	2.2
1	C	16	ASP	2.2
1	B	49	CYS	2.2
1	B	166	SER	2.2
1	B	247	LEU	2.2
1	C	45	GLY	2.2
1	E	108	MET	2.1
1	B	164	ASP	2.1
1	C	29	THR	2.1
1	C	270	ALA	2.1
1	A	160	LYS	2.1
1	A	28	VAL	2.1
1	A	163	MET	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	108	MET	2.0
1	B	163	MET	2.0
1	F	289	GLN	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(Å ²)	Q<0.9
2	PO4	A	301	5/5	0.98	0.05	20,20,24,27	0
2	PO4	E	301	5/5	0.98	0.04	17,18,21,22	0
2	PO4	C	301	5/5	0.99	0.04	17,20,21,21	0
2	PO4	D	301	5/5	0.99	0.03	15,16,17,18	0
2	PO4	B	301	5/5	0.99	0.04	20,21,22,23	0
2	PO4	F	301	5/5	0.99	0.04	16,17,17,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.