



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 10:18 AM UTC

PDB ID : 3Q9F / pdb_00003q9f
Title : Crystal Structure of APAH complexed with CAPS
Authors : Lombardi, P.M.; Christianson, D.W.
Deposited on : 2011-01-07
Resolution : 2.35 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

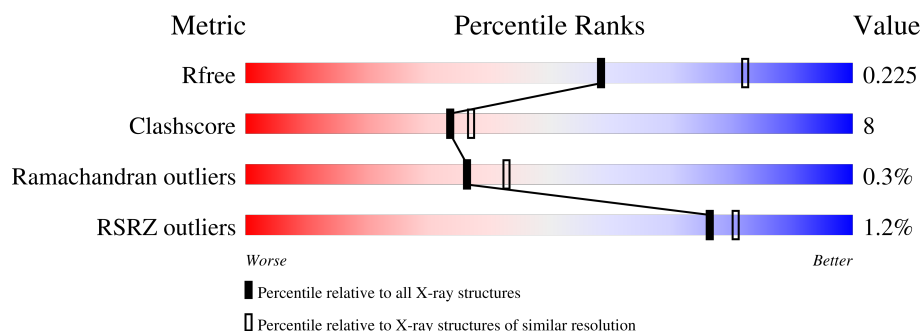
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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.



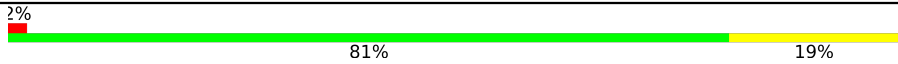
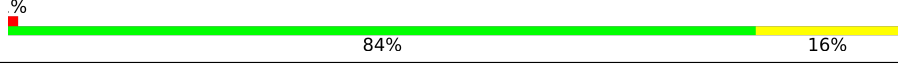
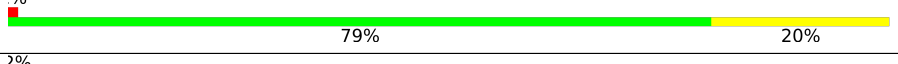
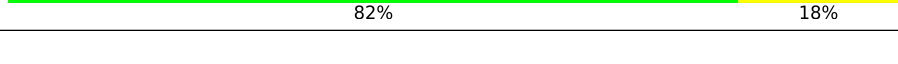
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	341	81%19%
1	B	341	84%16%
1	C	341	83%17%
1	D	341	83%17%
1	E	341	79%21%
1	F	341	83%16%

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Mol	Chain	Length	Quality of chain
1	G	341	 2% 81% 19%
1	H	341	 % 84% 16%
1	I	341	 % 79% 20%
1	J	341	 2% 82% 18%
1	K	341	 0% 81% 19%
1	L	341	 % 82% 18%

2 Entry composition

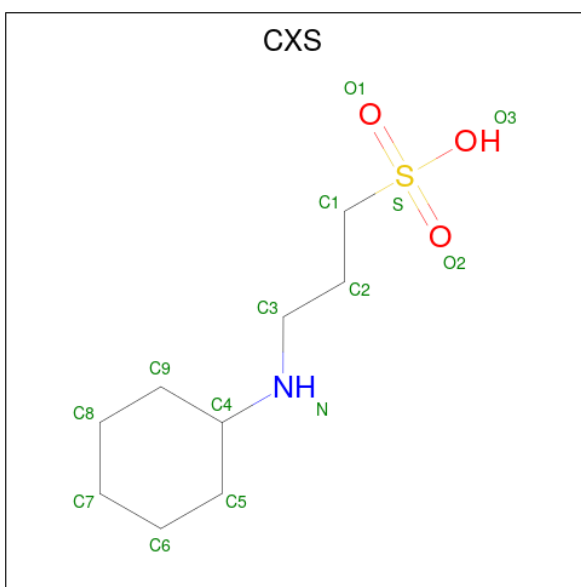
There are 7 unique types of molecules in this entry. The entry contains 32471 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Acetylpolysamine amidohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	0	0
			2568	1644	435	480	9			
1	B	341	Total	C	N	O	S	0	0	0
			2568	1644	435	480	9			
1	C	341	Total	C	N	O	S	0	0	0
			2568	1644	435	480	9			
1	D	341	Total	C	N	O	S	0	0	0
			2568	1644	435	480	9			
1	E	341	Total	C	N	O	S	0	0	0
			2568	1644	435	480	9			
1	F	341	Total	C	N	O	S	0	0	0
			2568	1644	435	480	9			
1	G	341	Total	C	N	O	S	0	0	0
			2568	1644	435	480	9			
1	H	341	Total	C	N	O	S	0	0	0
			2568	1644	435	480	9			
1	I	340	Total	C	N	O	S	0	0	0
			2563	1642	434	478	9			
1	J	340	Total	C	N	O	S	0	0	0
			2563	1642	434	478	9			
1	K	341	Total	C	N	O	S	0	0	0
			2568	1644	435	480	9			
1	L	341	Total	C	N	O	S	0	0	0
			2568	1644	435	480	9			

- Molecule 2 is 3-CYCLOHEXYL-1-PROPYLSULFONIC ACID (CCD ID: CXS) (formula: $C_9H_{19}NO_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
2	B	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
2	C	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
2	D	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
2	E	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
2	F	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
2	G	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
2	H	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
2	I	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
2	J	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
2	K	1	Total	C	N	O	S	0	0
			14	9	1	3	1		
2	L	1	Total	C	N	O	S	0	0
			14	9	1	3	1		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	E	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		
3	G	1	Total	O	P	0	0
			5	4	1		
3	H	1	Total	O	P	0	0
			5	4	1		
3	I	1	Total	O	P	0	0
			5	4	1		
3	J	1	Total	O	P	0	0
			5	4	1		
3	K	1	Total	O	P	0	0
			5	4	1		
3	L	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total K 2 2	0	0
4	B	1	Total K 1 1	0	0
4	C	2	Total K 2 2	0	0
4	D	2	Total K 2 2	0	0
4	E	2	Total K 2 2	0	0
4	F	2	Total K 2 2	0	0
4	G	2	Total K 2 2	0	0
4	H	2	Total K 2 2	0	0
4	I	1	Total K 1 1	0	0
4	J	1	Total K 1 1	0	0
4	K	1	Total K 1 1	0	0
4	L	2	Total K 2 2	0	0

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

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

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	I	1	Total 1	Na 1	0	0
5	J	1	Total 1	Na 1	0	0
5	K	1	Total 1	Na 1	0	0
5	L	1	Total 1	Na 1	0	0

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total 1	Zn 1	0	0
6	B	1	Total 1	Zn 1	0	0
6	C	1	Total 1	Zn 1	0	0
6	D	1	Total 1	Zn 1	0	0
6	E	1	Total 1	Zn 1	0	0
6	F	1	Total 1	Zn 1	0	0
6	G	1	Total 1	Zn 1	0	0
6	H	1	Total 1	Zn 1	0	0
6	I	1	Total 1	Zn 1	0	0
6	J	1	Total 1	Zn 1	0	0
6	K	1	Total 1	Zn 1	0	0
6	L	1	Total 1	Zn 1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	129	Total 129	O 129	0	0

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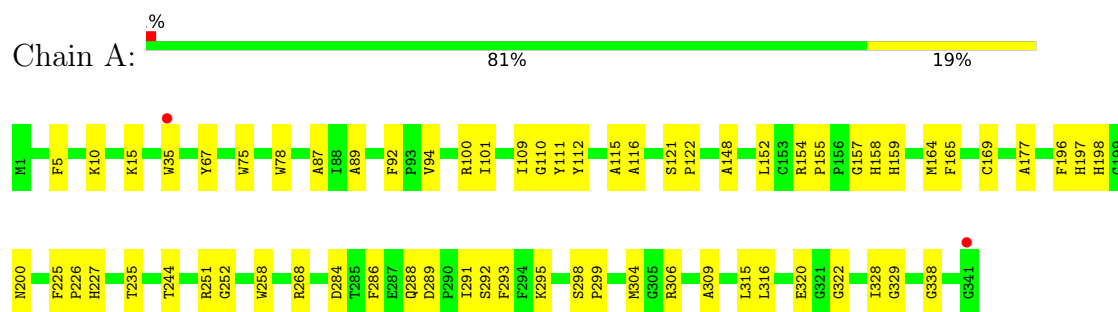
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	117	Total 117	O 117	0	0
7	C	124	Total 124	O 124	0	0
7	D	125	Total 125	O 125	0	0
7	E	115	Total 115	O 115	0	0
7	F	107	Total 107	O 107	0	0
7	G	106	Total 106	O 106	0	0
7	H	112	Total 112	O 112	0	0
7	I	132	Total 132	O 132	0	0
7	J	98	Total 98	O 98	0	0
7	K	113	Total 113	O 113	0	0
7	L	115	Total 115	O 115	0	0

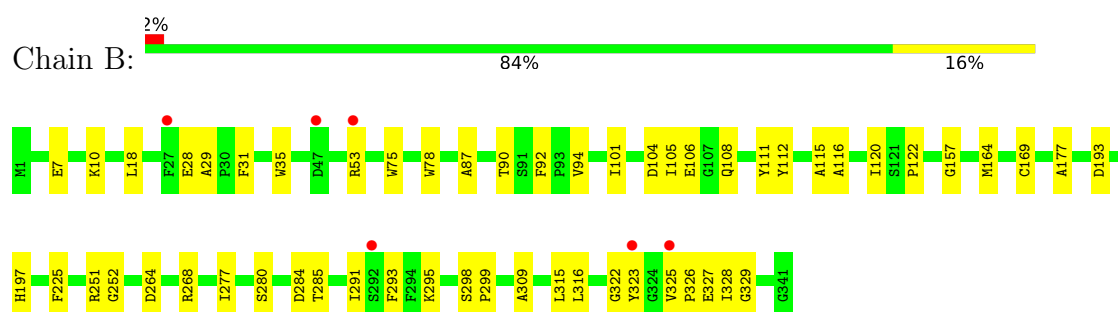
3 Residue-property plots

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.

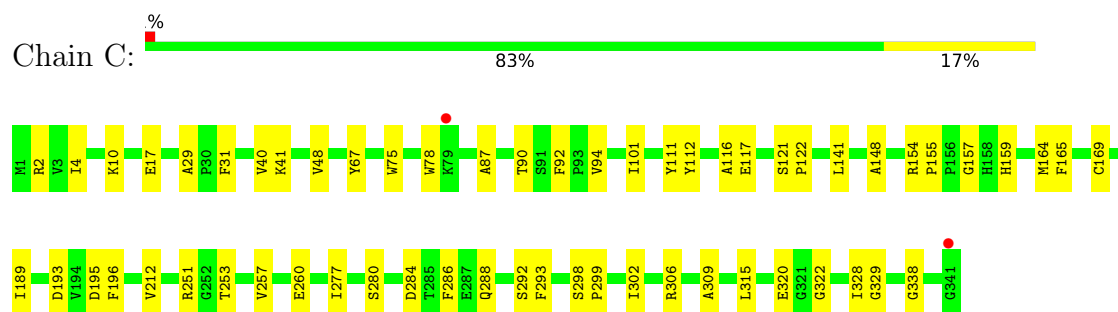
• Molecule 1: Acetypolyamine amidohydrolase



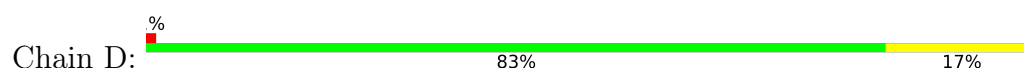
• Molecule 1: Acetypolyamine amidohydrolase

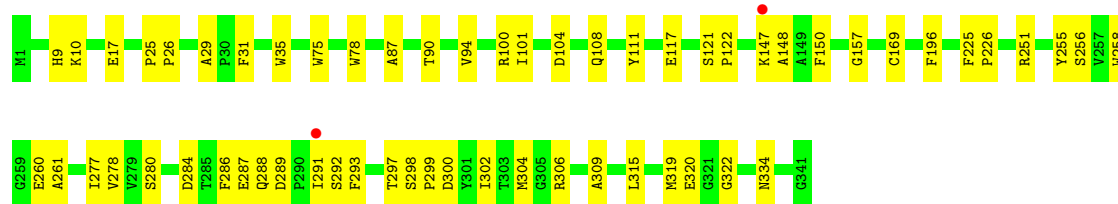


• Molecule 1: Acetypolyamine amidohydrolase

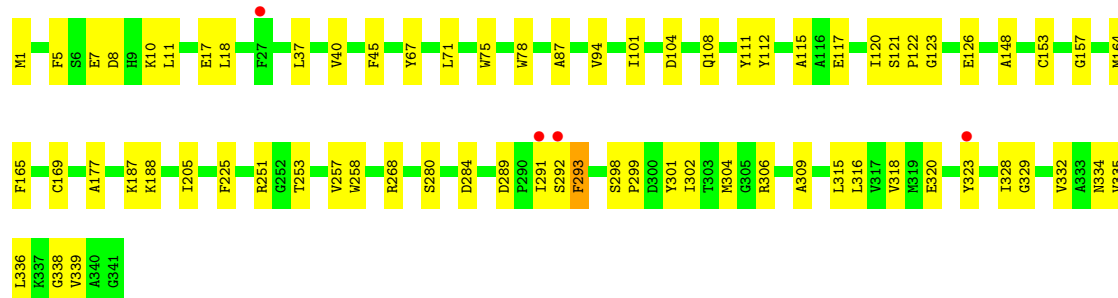
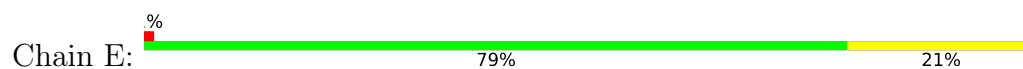


• Molecule 1: Acetypolyamine amidohydrolase

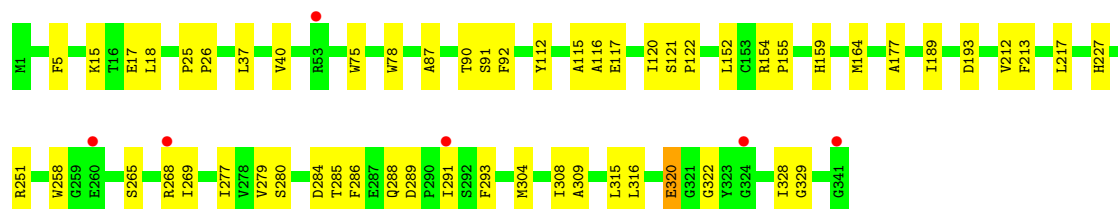
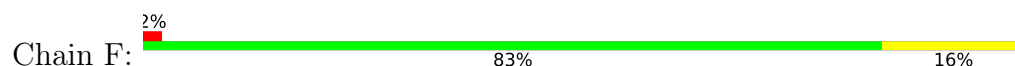




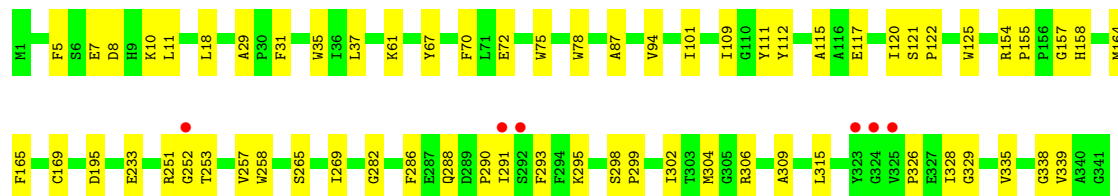
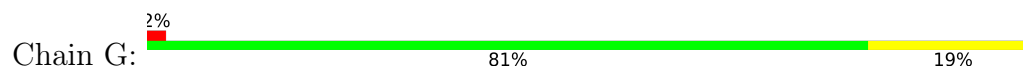
● Molecule 1: Acetypolyamine amidohydrolase



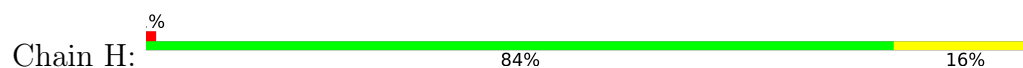
● Molecule 1: Acetypolyamine amidohydrolase



● Molecule 1: Acetypolyamine amidohydrolase

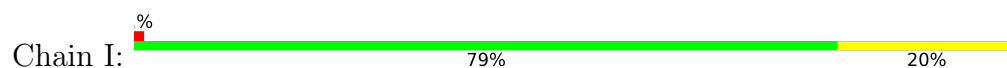


● Molecule 1: Acetypolyamine amidohydrolase

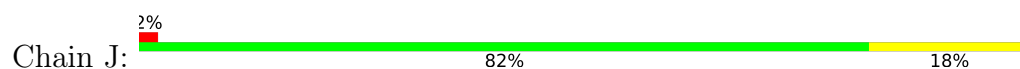




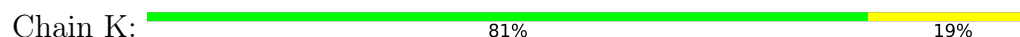
- Molecule 1: Acetylpolymine amidohydrolase



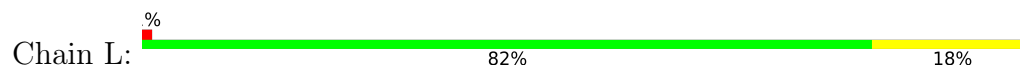
- Molecule 1: Acetylpolymine amidohydrolase



- Molecule 1: Acetylpolymine amidohydrolase



- Molecule 1: Acetylpolymine amidohydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	118.25Å 119.65Å 119.57Å 98.34° 94.94° 114.95°	Depositor
Resolution (Å)	50.00 – 2.35 50.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	91.1 (50.00-2.35) 91.1 (50.00-2.35)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 2.34Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.189 , 0.225 0.189 , 0.225	Depositor DCC
R_{free} test set	11750 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.001 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	32471	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, K, ZN, CXS, 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	0.48	0/2636	0.90	2/3582 (0.1%)
1	B	0.45	0/2636	0.87	1/3582 (0.0%)
1	C	0.48	0/2636	0.92	1/3582 (0.0%)
1	D	0.47	0/2636	0.88	2/3582 (0.1%)
1	E	0.44	0/2636	0.89	2/3582 (0.1%)
1	F	0.44	0/2636	0.87	5/3582 (0.1%)
1	G	0.45	0/2636	0.87	1/3582 (0.0%)
1	H	0.43	0/2636	0.87	3/3582 (0.1%)
1	I	0.45	0/2631	0.88	3/3577 (0.1%)
1	J	0.42	0/2631	0.89	1/3577 (0.0%)
1	K	0.45	0/2636	0.89	2/3582 (0.1%)
1	L	0.44	0/2636	0.88	0/3582
All	All	0.45	0/31622	0.88	23/42974 (0.1%)

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	285	THR	N-CA-C	-7.36	104.31	113.28
1	I	285	THR	N-CA-C	-7.16	104.28	113.16
1	K	205	ILE	N-CA-C	6.71	117.46	110.62
1	J	285	THR	N-CA-C	-6.39	105.48	113.28
1	H	205	ILE	N-CA-C	5.95	116.69	110.62

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	2568	0	2490	41	0
1	B	2568	0	2492	37	0
1	C	2568	0	2491	37	0
1	D	2568	0	2491	44	0
1	E	2568	0	2491	46	0
1	F	2568	0	2490	39	0
1	G	2568	0	2492	39	0
1	H	2568	0	2492	37	0
1	I	2563	0	2488	44	0
1	J	2563	0	2488	39	0
1	K	2568	0	2491	39	0
1	L	2568	0	2492	43	0
2	A	14	0	19	1	0
2	B	14	0	18	4	0
2	C	14	0	18	1	0
2	D	14	0	18	6	0
2	E	14	0	18	3	0
2	F	14	0	19	1	0
2	G	14	0	18	1	0
2	H	14	0	19	0	0
2	I	14	0	18	4	0
2	J	14	0	18	1	0
2	K	14	0	18	3	0
2	L	14	0	18	1	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
3	G	5	0	0	0	0
3	H	5	0	0	0	0
3	I	5	0	0	0	0
3	J	5	0	0	0	0
3	K	5	0	0	0	0
3	L	5	0	0	0	0
4	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
4	G	2	0	0	0	0
4	H	2	0	0	0	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
4	K	1	0	0	0	0
4	L	2	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
5	I	1	0	0	0	0
5	J	1	0	0	0	0
5	K	1	0	0	0	0
5	L	1	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
6	G	1	0	0	0	0
6	H	1	0	0	0	0
6	I	1	0	0	0	0
6	J	1	0	0	0	0
6	K	1	0	0	0	0
6	L	1	0	0	0	0
7	A	129	0	0	1	0
7	B	117	0	0	1	0
7	C	124	0	0	0	0
7	D	125	0	0	0	0
7	E	115	0	0	3	0
7	F	107	0	0	1	0
7	G	106	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	H	112	0	0	1	0
7	I	132	0	0	2	0
7	J	98	0	0	1	0
7	K	113	0	0	0	0
7	L	115	0	0	2	0
All	All	32471	0	30107	469	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 8.

The worst 5 of 469 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:L:157:GLY:HA2	1:L:169:CYS:HB3	1.63	0.79
1:E:306:ARG:HD2	1:E:338:GLY:O	1.87	0.75
1:D:289:ASP:OD1	1:D:291:ILE:HG12	1.88	0.74
1:I:291:ILE:HD12	2:I:409:CXS:H51	1.71	0.73
1:H:157:GLY:HA2	1:H:169:CYS:HB3	1.70	0.72

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	339/341 (99%)	322 (95%)	16 (5%)	1 (0%)	36	43
1	B	339/341 (99%)	321 (95%)	17 (5%)	1 (0%)	36	43
1	C	339/341 (99%)	322 (95%)	16 (5%)	1 (0%)	36	43
1	D	339/341 (99%)	323 (95%)	15 (4%)	1 (0%)	36	43
1	E	309/341 (91%)	297 (96%)	11 (4%)	1 (0%)	36	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	176/341 (52%)	166 (94%)	10 (6%)	0	100	100
1	G	339/341 (99%)	319 (94%)	17 (5%)	3 (1%)	14	14
1	H	339/341 (99%)	322 (95%)	16 (5%)	1 (0%)	36	43
1	I	338/341 (99%)	324 (96%)	13 (4%)	1 (0%)	36	43
1	J	338/341 (99%)	319 (94%)	18 (5%)	1 (0%)	36	43
1	K	339/341 (99%)	326 (96%)	12 (4%)	1 (0%)	36	43
1	L	339/341 (99%)	319 (94%)	19 (6%)	1 (0%)	36	43
All	All	3873/4092 (95%)	3680 (95%)	180 (5%)	13 (0%)	36	43

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	290	PRO
1	G	291	ILE
1	D	94	VAL
1	A	94	VAL
1	H	94	VAL

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](#)

Of 68 ligands modelled in this entry, 44 are monoatomic - leaving 24 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	PO4	I	353	-	4,4,4	1.74	0	6,6,6	0.48	0
2	CXS	E	405	6	14,14,14	1.48	2 (14%)	18,18,18	2.20	4 (22%)
2	CXS	I	409	6	14,14,14	1.50	2 (14%)	18,18,18	2.19	3 (16%)
2	CXS	H	408	6	14,14,14	1.85	2 (14%)	18,18,18	1.89	4 (22%)
3	PO4	L	352	-	4,4,4	1.72	0	6,6,6	0.48	0
2	CXS	G	407	6	14,14,14	1.65	2 (14%)	18,18,18	2.25	4 (22%)
2	CXS	K	411	6	14,14,14	1.56	1 (7%)	18,18,18	2.01	4 (22%)
2	CXS	D	404	6	14,14,14	1.77	2 (14%)	18,18,18	1.99	5 (27%)
3	PO4	K	353	-	4,4,4	1.70	0	6,6,6	0.48	0
3	PO4	E	353	-	4,4,4	1.84	2 (50%)	6,6,6	0.45	0
3	PO4	H	352	-	4,4,4	1.66	0	6,6,6	0.48	0
3	PO4	F	352	-	4,4,4	1.70	1 (25%)	6,6,6	0.47	0
3	PO4	J	352	-	4,4,4	1.64	0	6,6,6	0.46	0
3	PO4	G	353	-	4,4,4	1.69	0	6,6,6	0.45	0
2	CXS	A	401	6	14,14,14	1.64	2 (14%)	18,18,18	2.16	4 (22%)
2	CXS	F	406	6	14,14,14	1.64	1 (7%)	18,18,18	1.92	4 (22%)
3	PO4	C	353	-	4,4,4	1.70	0	6,6,6	0.46	0
3	PO4	D	352	-	4,4,4	1.73	1 (25%)	6,6,6	0.48	0
2	CXS	C	403	6	14,14,14	1.64	2 (14%)	18,18,18	2.07	4 (22%)
2	CXS	L	412	6	14,14,14	1.64	1 (7%)	18,18,18	2.13	3 (16%)
2	CXS	B	402	6	14,14,14	1.53	2 (14%)	18,18,18	2.21	5 (27%)
3	PO4	B	352	-	4,4,4	1.74	1 (25%)	6,6,6	0.49	0
2	CXS	J	410	6	14,14,14	1.58	2 (14%)	18,18,18	2.14	5 (27%)
3	PO4	A	353	-	4,4,4	1.68	1 (25%)	6,6,6	0.47	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	CXS	A	401	6	-	3/8/16/16	0/1/1/1
2	CXS	F	406	6	-	3/8/16/16	0/1/1/1
2	CXS	J	410	6	-	2/8/16/16	0/1/1/1
2	CXS	G	407	6	-	2/8/16/16	0/1/1/1
2	CXS	K	411	6	-	3/8/16/16	0/1/1/1
2	CXS	I	409	6	-	2/8/16/16	0/1/1/1
2	CXS	D	404	6	-	4/8/16/16	0/1/1/1
2	CXS	C	403	6	-	3/8/16/16	0/1/1/1
2	CXS	E	405	6	-	1/8/16/16	0/1/1/1
2	CXS	L	412	6	-	3/8/16/16	0/1/1/1
2	CXS	B	402	6	-	2/8/16/16	0/1/1/1
2	CXS	H	408	6	-	3/8/16/16	0/1/1/1

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	408	CXS	C1-S	-5.46	1.69	1.77
2	D	404	CXS	C1-S	-5.37	1.70	1.77
2	F	406	CXS	C1-S	-4.81	1.70	1.77
2	L	412	CXS	C1-S	-4.81	1.70	1.77
2	K	411	CXS	C1-S	-4.59	1.71	1.77

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	402	CXS	C3-N-C4	6.12	125.96	114.18
2	I	409	CXS	C3-N-C4	6.05	125.83	114.18
2	G	407	CXS	C3-N-C4	5.90	125.54	114.18
2	J	410	CXS	O3-S-C1	5.85	117.44	106.00
2	A	401	CXS	C3-N-C4	5.68	125.11	114.18

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	CXS	C1-C2-C3-N
2	A	401	CXS	C9-C4-N-C3
2	B	402	CXS	C1-C2-C3-N
2	C	403	CXS	C1-C2-C3-N
2	C	403	CXS	C9-C4-N-C3

There are no ring outliers.

11 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	405	CXS	3	0
2	I	409	CXS	4	0
2	G	407	CXS	1	0
2	K	411	CXS	3	0
2	D	404	CXS	6	0
2	A	401	CXS	1	0
2	F	406	CXS	1	0
2	C	403	CXS	1	0
2	L	412	CXS	1	0
2	B	402	CXS	4	0
2	J	410	CXS	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	341/341 (100%)	-0.20	2 (0%) 85 89	22, 33, 46, 63	0
1	B	341/341 (100%)	-0.01	6 (1%) 67 72	24, 36, 52, 60	0
1	C	341/341 (100%)	-0.06	2 (0%) 85 89	21, 34, 47, 66	0
1	D	341/341 (100%)	-0.13	2 (0%) 85 89	23, 34, 46, 60	0
1	E	341/341 (100%)	-0.05	4 (1%) 76 81	25, 36, 52, 61	0
1	F	341/341 (100%)	0.11	6 (1%) 67 72	23, 38, 57, 65	0
1	G	341/341 (100%)	0.00	6 (1%) 67 72	24, 36, 52, 65	0
1	H	341/341 (100%)	0.03	4 (1%) 76 81	23, 38, 53, 66	0
1	I	340/341 (99%)	-0.08	3 (0%) 81 84	24, 36, 48, 66	0
1	J	340/341 (99%)	0.24	8 (2%) 59 66	26, 41, 64, 76	0
1	K	341/341 (100%)	-0.03	1 (0%) 90 92	26, 36, 49, 66	0
1	L	341/341 (100%)	0.05	5 (1%) 72 77	26, 38, 52, 67	0
All	All	4090/4092 (99%)	-0.01	49 (1%) 76 81	21, 36, 52, 76	0

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	291	ILE	5.2
1	L	291	ILE	3.9
1	J	43	ALA	3.7
1	G	324	GLY	3.6
1	L	35	TRP	3.5

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
3	PO4	L	352	5/5	0.72	0.17	102,102,103,103	0
4	K	F	344	1/1	0.73	0.15	100,100,100,100	0
3	PO4	H	352	5/5	0.75	0.15	97,97,98,98	0
3	PO4	F	352	5/5	0.78	0.14	90,91,92,92	0
3	PO4	A	353	5/5	0.81	0.14	71,73,73,74	0
2	CXS	J	410	14/14	0.83	0.31	88,93,99,99	0
2	CXS	H	408	14/14	0.83	0.33	94,98,103,103	0
3	PO4	K	353	5/5	0.84	0.13	87,87,88,89	0
3	PO4	B	352	5/5	0.84	0.12	65,66,67,68	0
4	K	E	344	1/1	0.84	0.13	96,96,96,96	0
3	PO4	D	352	5/5	0.84	0.14	78,79,79,79	0
2	CXS	D	404	14/14	0.85	0.27	78,84,88,88	0
2	CXS	F	406	14/14	0.85	0.32	97,102,106,106	0
2	CXS	B	402	14/14	0.85	0.26	85,92,96,96	0
3	PO4	J	352	5/5	0.85	0.12	84,84,85,85	0
2	CXS	E	405	14/14	0.86	0.27	78,85,90,90	0
2	CXS	L	412	14/14	0.86	0.26	85,90,96,96	0
2	CXS	G	407	14/14	0.87	0.24	76,80,86,86	0
2	CXS	A	401	14/14	0.87	0.28	89,95,98,98	0
2	CXS	C	403	14/14	0.88	0.26	85,92,97,97	0
3	PO4	C	353	5/5	0.88	0.11	75,76,77,77	0
3	PO4	G	353	5/5	0.88	0.12	77,77,79,79	0
2	CXS	K	411	14/14	0.89	0.26	92,96,100,101	0
2	CXS	I	409	14/14	0.89	0.24	80,87,91,91	0
3	PO4	I	353	5/5	0.90	0.12	87,87,88,88	0
3	PO4	E	353	5/5	0.90	0.11	74,74,75,76	0
4	K	C	344	1/1	0.91	0.10	77,77,77,77	0
4	K	G	344	1/1	0.91	0.09	120,120,120,120	0
4	K	H	344	1/1	0.93	0.09	72,72,72,72	0
4	K	D	344	1/1	0.94	0.08	69,69,69,69	0
4	K	A	344	1/1	0.95	0.08	73,73,73,73	0
4	K	L	344	1/1	0.95	0.06	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	NA	L	343	1/1	0.95	0.07	25,25,25,25	0
5	NA	F	343	1/1	0.96	0.09	27,27,27,27	0
5	NA	H	343	1/1	0.97	0.06	24,24,24,24	0
5	NA	J	343	1/1	0.97	0.07	22,22,22,22	0
5	NA	G	343	1/1	0.97	0.11	16,16,16,16	0
6	ZN	I	344	1/1	0.97	0.04	51,51,51,51	0
5	NA	E	343	1/1	0.98	0.07	16,16,16,16	0
5	NA	K	343	1/1	0.98	0.08	19,19,19,19	0
4	K	C	342	1/1	0.98	0.03	29,29,29,29	0
5	NA	I	343	1/1	0.98	0.10	20,20,20,20	0
6	ZN	K	344	1/1	0.98	0.04	53,53,53,53	0
5	NA	A	343	1/1	0.99	0.12	14,14,14,14	0
5	NA	B	343	1/1	0.99	0.08	13,13,13,13	0
4	K	F	342	1/1	0.99	0.05	31,31,31,31	0
4	K	D	342	1/1	0.99	0.04	29,29,29,29	0
4	K	G	342	1/1	0.99	0.02	30,30,30,30	0
4	K	A	342	1/1	0.99	0.02	29,29,29,29	0
4	K	H	342	1/1	0.99	0.02	34,34,34,34	0
4	K	E	342	1/1	0.99	0.02	33,33,33,33	0
4	K	I	342	1/1	0.99	0.03	32,32,32,32	0
4	K	K	342	1/1	0.99	0.03	33,33,33,33	0
6	ZN	A	345	1/1	0.99	0.07	52,52,52,52	0
6	ZN	B	344	1/1	0.99	0.05	53,53,53,53	0
6	ZN	C	345	1/1	0.99	0.03	51,51,51,51	0
6	ZN	D	345	1/1	0.99	0.05	46,46,46,46	0
6	ZN	E	345	1/1	0.99	0.03	50,50,50,50	0
6	ZN	F	345	1/1	0.99	0.06	58,58,58,58	0
6	ZN	H	345	1/1	0.99	0.04	51,51,51,51	0
4	K	L	342	1/1	0.99	0.03	31,31,31,31	0
6	ZN	J	344	1/1	0.99	0.03	58,58,58,58	0
4	K	B	342	1/1	0.99	0.03	32,32,32,32	0
6	ZN	L	345	1/1	0.99	0.05	49,49,49,49	0
4	K	J	342	1/1	1.00	0.02	39,39,39,39	0
5	NA	C	343	1/1	1.00	0.11	14,14,14,14	0
6	ZN	G	345	1/1	1.00	0.03	48,48,48,48	0
5	NA	D	343	1/1	1.00	0.11	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.