



wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 12:22 am BST

PDB ID : 3Q9E
Title : Crystal structure of H159A APAH complexed with acetylspermine
Authors : Lombardi, P.M.; Christianson, D.W.
Deposited on : 2011-01-07
Resolution : 2.50 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

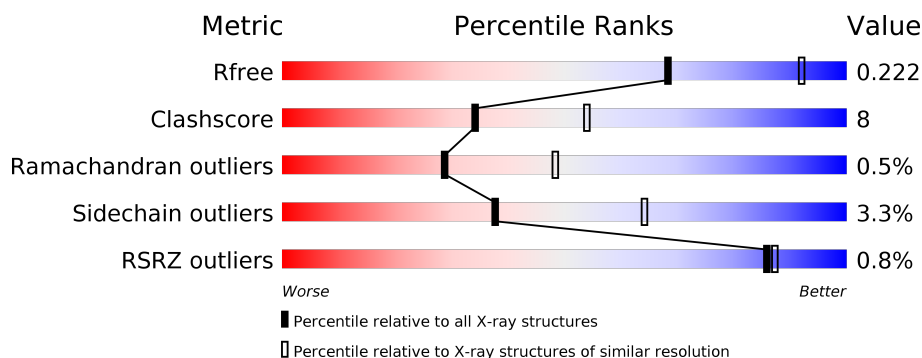
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 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	<div> <div>%</div> <div> <div></div> <div>74%</div> <div>24%</div> <div>.</div> </div> </div>
1	B	341	<div> <div>78%</div> <div>21%</div> <div>.</div> </div>
1	C	341	<div> <div>81%</div> <div>19%</div> </div>
1	D	341	<div> <div>%</div> <div> <div></div> <div>78%</div> <div>21%</div> <div>.</div> </div> </div>
1	E	341	<div> <div>77%</div> <div>22%</div> <div>.</div> </div>
1	F	341	<div> <div>%</div> <div> <div></div> <div>78%</div> <div>21%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	341	<div><div></div><div>83%16%</div><div></div></div>
1	H	341	<div><div>2%</div><div></div><div>81%18%</div><div></div></div>
1	I	341	<div><div>%</div><div></div><div>81%19%</div><div></div></div>
1	J	341	<div><div>%</div><div></div><div>70%29%</div><div></div></div>
1	K	341	<div><div></div><div>83%16%</div><div></div></div>
1	L	341	<div><div>3%</div><div></div><div>79%21%</div><div></div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 31939 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 Acetylpolyamine amidohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	0	0
			2563	1641	433	480	9			
1	B	341	Total	C	N	O	S	0	0	0
			2563	1641	433	480	9			
1	C	341	Total	C	N	O	S	0	0	0
			2563	1641	433	480	9			
1	D	341	Total	C	N	O	S	0	0	0
			2563	1641	433	480	9			
1	E	341	Total	C	N	O	S	0	0	0
			2563	1641	433	480	9			
1	F	341	Total	C	N	O	S	0	0	0
			2563	1641	433	480	9			
1	G	341	Total	C	N	O	S	0	0	0
			2563	1641	433	480	9			
1	H	341	Total	C	N	O	S	0	0	0
			2563	1641	433	480	9			
1	I	341	Total	C	N	O	S	0	0	0
			2563	1641	433	480	9			
1	J	341	Total	C	N	O	S	0	0	0
			2563	1641	433	480	9			
1	K	341	Total	C	N	O	S	0	0	0
			2563	1641	433	480	9			
1	L	341	Total	C	N	O	S	0	0	0
			2563	1641	433	480	9			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	159	ALA	HIS	ENGINEERED MUTATION	UNP Q48935
B	159	ALA	HIS	ENGINEERED MUTATION	UNP Q48935
C	159	ALA	HIS	ENGINEERED MUTATION	UNP Q48935
D	159	ALA	HIS	ENGINEERED MUTATION	UNP Q48935
E	159	ALA	HIS	ENGINEERED MUTATION	UNP Q48935

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Chain	Residue	Modelled	Actual	Comment	Reference
F	159	ALA	HIS	ENGINEERED MUTATION	UNP Q48935
G	159	ALA	HIS	ENGINEERED MUTATION	UNP Q48935
H	159	ALA	HIS	ENGINEERED MUTATION	UNP Q48935
I	159	ALA	HIS	ENGINEERED MUTATION	UNP Q48935
J	159	ALA	HIS	ENGINEERED MUTATION	UNP Q48935
K	159	ALA	HIS	ENGINEERED MUTATION	UNP Q48935
L	159	ALA	HIS	ENGINEERED MUTATION	UNP Q48935

- SP5
-
- Chemical structure of SP5, a peptide chain. The backbone is shown in grey, and the side chains are labeled with three-letter codes: CAA, CAC, CAF, CAG, CAH, CAI, CAJ, CAK, CAL, CAM, CAN, and CAQ. The N-terminus is labeled HAD and the C-terminus is labeled HAO.

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	H	1	Total	C	N	O	0	0
			17	12	4	1		
2	I	1	Total	C	N	O	0	0
			17	12	4	1		
2	J	1	Total	C	N	O	0	0
			17	12	4	1		
2	K	1	Total	C	N	O	0	0
			17	12	4	1		
2	L	1	Total	C	N	O	0	0
			17	12	4	1		

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

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

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	G	1	Total Zn 1 1	0	0
5	J	1	Total Zn 1 1	0	0
5	D	1	Total Zn 1 1	0	0
5	K	1	Total Zn 1 1	0	0
5	E	1	Total Zn 1 1	0	0
5	H	1	Total Zn 1 1	0	0
5	B	1	Total Zn 1 1	0	0
5	I	1	Total Zn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	1	Total 1	Zn 1	0	0
5	A	1	Total 1	Zn 1	0	0
5	L	1	Total 1	Zn 1	0	0
5	F	1	Total 1	Zn 1	0	0

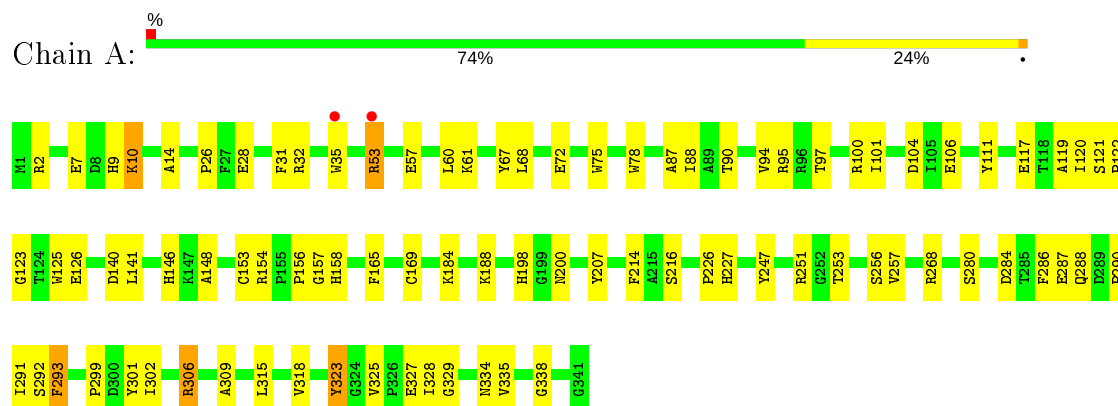
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	88	Total 88	O 88	0	0
6	B	69	Total 69	O 69	0	0
6	C	84	Total 84	O 84	0	0
6	D	85	Total 85	O 85	0	0
6	E	69	Total 69	O 69	0	0
6	F	90	Total 90	O 90	0	0
6	G	74	Total 74	O 74	0	0
6	H	65	Total 65	O 65	0	0
6	I	87	Total 87	O 87	0	0
6	J	78	Total 78	O 78	0	0
6	K	84	Total 84	O 84	0	0
6	L	70	Total 70	O 70	0	0

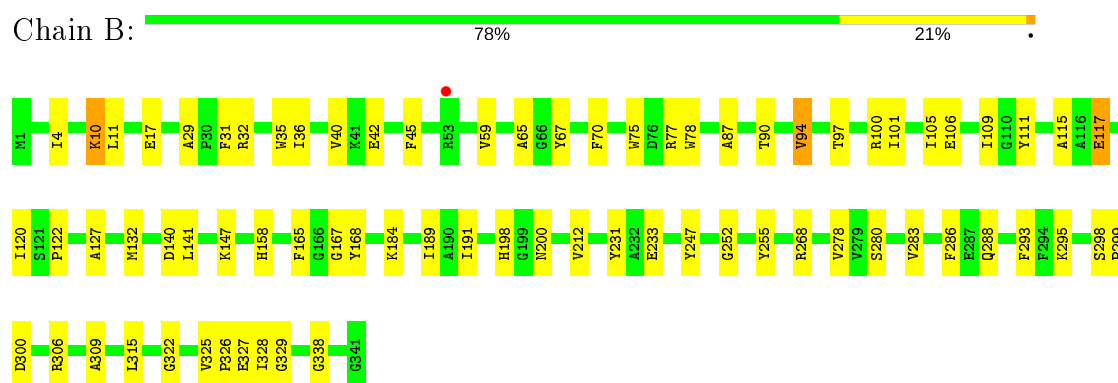
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ($\text{RSRZ} > 2$). 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.

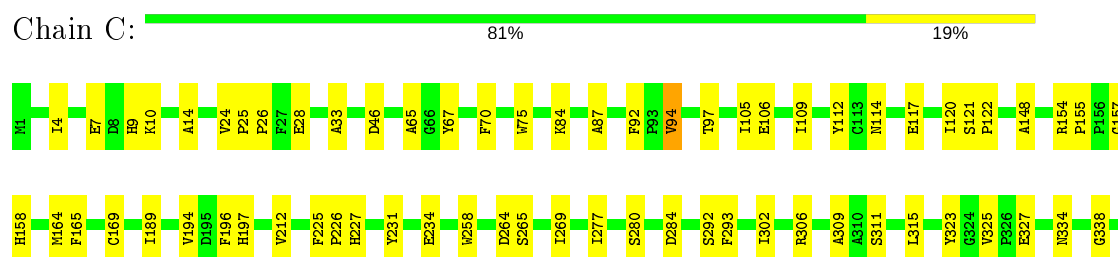
• Molecule 1: Acetylpolymine amidohydrolase



• Molecule 1: Acetylpolymine amidohydrolase

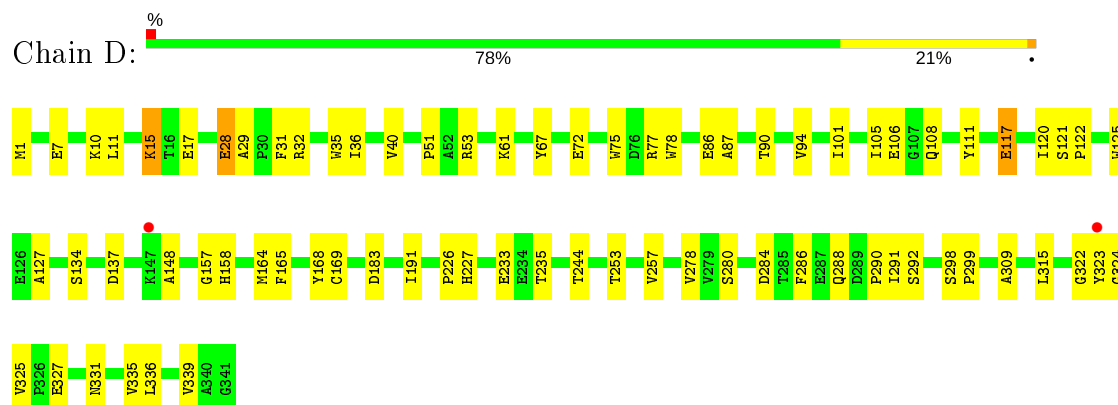


• Molecule 1: Acetylpolymine amidohydrolase

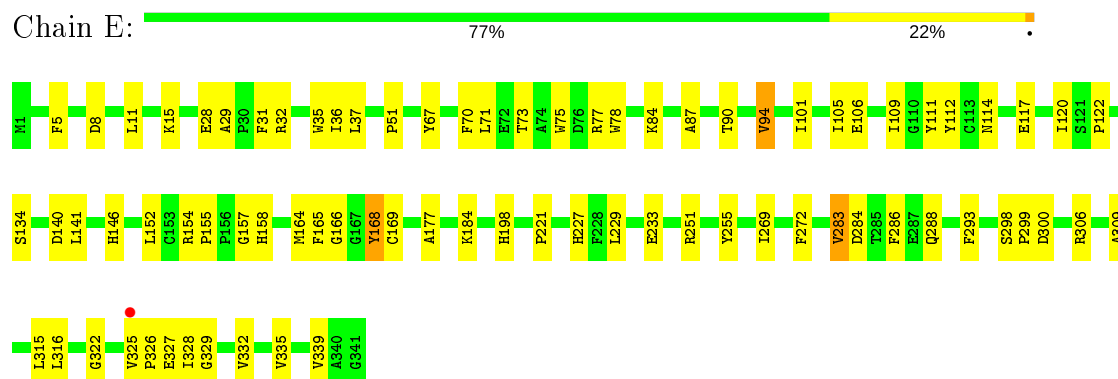


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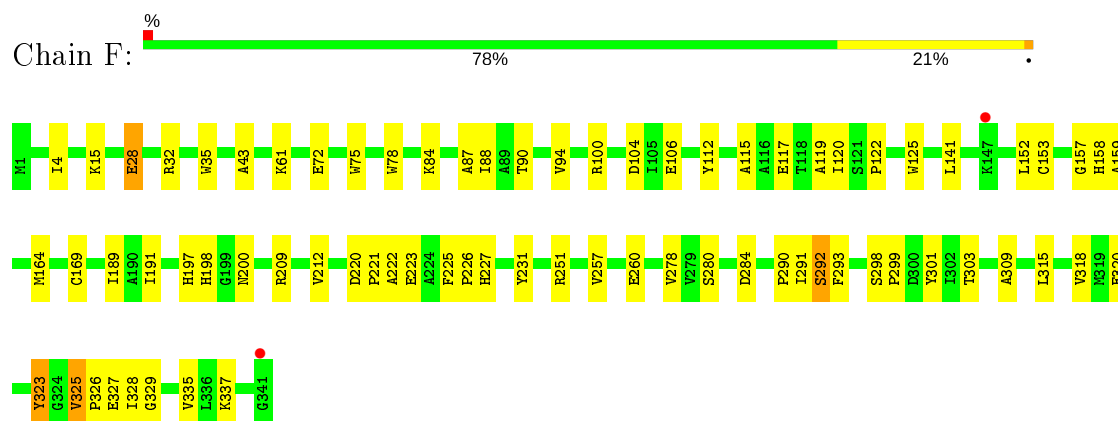
- Molecule 1: Acetylpolyamine amidohydrolase



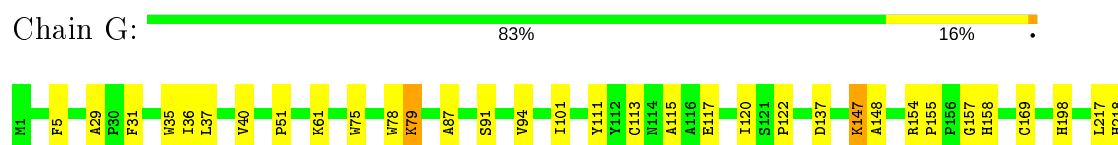
- Molecule 1: Acetylpolyamine amidohydrolase

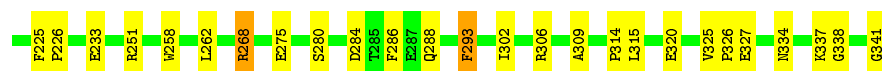


- Molecule 1: Acetylpolyamine amidohydrolase

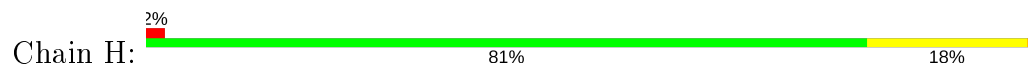


- Molecule 1: Acetylpolyamine amidohydrolase

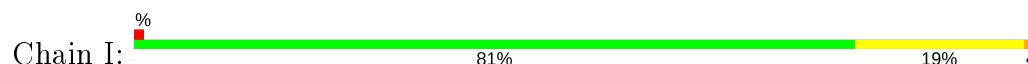




• Molecule 1: Acetylpolymine amidohydrolase



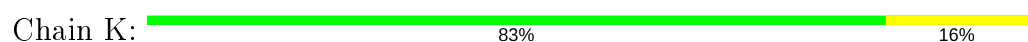
• Molecule 1: Acetylpolymine amidohydrolase

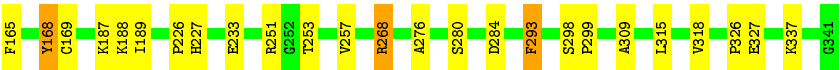


• Molecule 1: Acetylpolymine amidohydrolase

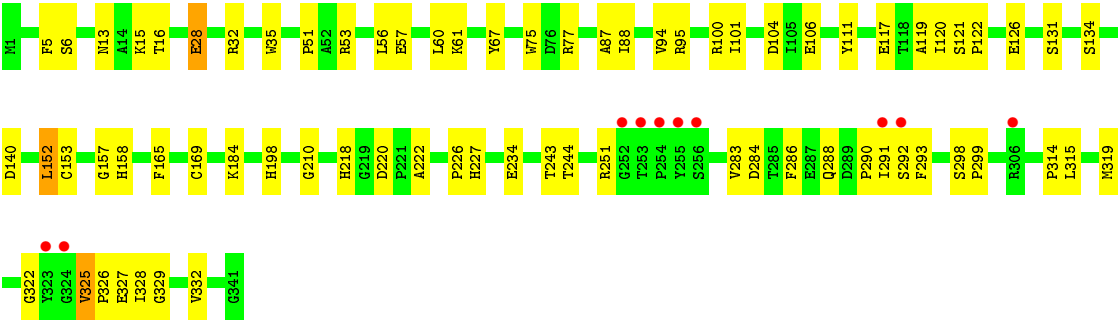
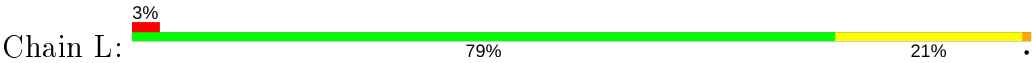


• Molecule 1: Acetylpolymine amidohydrolase





● Molecule 1: Acetylpolyamine amidohydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	117.64Å 119.50Å 118.44Å 98.23° 94.89° 115.73°	Depositor
Resolution (Å)	50.00 – 2.50 50.08 – 2.50	Depositor EDS
% Data completeness (in resolution range)	91.8 (50.00-2.50) 91.8 (50.08-2.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.190 , 0.230 0.184 , 0.222	Depositor DCC
R_{free} test set	19000 reflections (9.95%)	wwPDB-VP
Wilson B-factor (Å ²)	31.6	Xtriage
Anisotropy	0.323	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 49.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.005 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	31939	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.02% 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, ZN, K, SP5

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	0.42	0/2630	0.61	0/3574
1	B	0.40	0/2630	0.59	0/3574
1	C	0.41	0/2630	0.61	0/3574
1	D	0.39	0/2630	0.58	0/3574
1	E	0.38	0/2630	0.58	0/3574
1	F	0.39	0/2630	0.59	0/3574
1	G	0.39	0/2630	0.60	0/3574
1	H	0.38	0/2630	0.58	0/3574
1	I	0.40	0/2630	0.59	0/3574
1	J	0.39	0/2630	0.57	0/3574
1	K	0.42	0/2630	0.60	0/3574
1	L	0.39	0/2630	0.58	0/3574
All	All	0.40	0/31560	0.59	0/42888

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [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	2563	0	2489	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2563	0	2489	43	0
1	C	2563	0	2490	38	0
1	D	2563	0	2489	45	0
1	E	2563	0	2490	46	0
1	F	2563	0	2489	50	0
1	G	2563	0	2489	39	0
1	H	2563	0	2489	39	0
1	I	2563	0	2489	37	0
1	J	2563	0	2489	67	0
1	K	2563	0	2489	33	0
1	L	2563	0	2490	42	0
2	A	17	0	28	1	0
2	B	17	0	28	0	0
2	C	17	0	28	0	0
2	D	17	0	28	1	0
2	E	17	0	28	0	0
2	F	17	0	28	2	0
2	G	17	0	28	0	0
2	H	17	0	28	0	0
2	I	17	0	28	0	0
2	J	17	0	28	0	0
2	K	17	0	28	1	0
2	L	17	0	28	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	K	1	0	0	0	0
3	L	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	1	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	1	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	88	0	0	1	0
6	B	69	0	0	1	0
6	C	84	0	0	2	0
6	D	85	0	0	1	0
6	E	69	0	0	1	0
6	F	90	0	0	2	0
6	G	74	0	0	0	0
6	H	65	0	0	2	0
6	I	87	0	0	1	0
6	J	78	0	0	2	0
6	K	84	0	0	2	0
6	L	70	0	0	4	0
All	All	31939	0	30207	516	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 516 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:G:268:ARG:HH11	1:G:268:ARG:HB3	1.35	0.90
1:J:283:VAL:HG23	1:J:322:GLY:HA3	1.66	0.78
1:K:268:ARG:HH11	1:K:268:ARG:HB3	1.49	0.77
1:L:288:GLN:HB3	1:L:325:VAL:HG11	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:35:TRP:CZ3	1:L:326:PRO:HA	2.20	0.76

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%)	319 (94%)	18 (5%)	2 (1%)	25	43
1	B	339/341 (99%)	321 (95%)	17 (5%)	1 (0%)	41	61
1	C	339/341 (99%)	317 (94%)	21 (6%)	1 (0%)	41	61
1	D	339/341 (99%)	317 (94%)	19 (6%)	3 (1%)	17	31
1	E	339/341 (99%)	322 (95%)	16 (5%)	1 (0%)	41	61
1	F	339/341 (99%)	317 (94%)	18 (5%)	4 (1%)	13	24
1	G	339/341 (99%)	317 (94%)	21 (6%)	1 (0%)	41	61
1	H	339/341 (99%)	318 (94%)	20 (6%)	1 (0%)	41	61
1	I	339/341 (99%)	319 (94%)	19 (6%)	1 (0%)	41	61
1	J	339/341 (99%)	327 (96%)	11 (3%)	1 (0%)	41	61
1	K	339/341 (99%)	324 (96%)	14 (4%)	1 (0%)	41	61
1	L	339/341 (99%)	319 (94%)	17 (5%)	3 (1%)	17	31
All	All	4068/4092 (99%)	3837 (94%)	211 (5%)	20 (0%)	29	48

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	324	GLY
1	H	94	VAL
1	I	94	VAL
1	J	94	VAL

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Mol	Chain	Res	Type
1	D	94	VAL

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	252/252 (100%)	240 (95%)	12 (5%)	25	48
1	B	252/252 (100%)	245 (97%)	7 (3%)	43	70
1	C	252/252 (100%)	243 (96%)	9 (4%)	35	61
1	D	252/252 (100%)	244 (97%)	8 (3%)	39	65
1	E	252/252 (100%)	244 (97%)	8 (3%)	39	65
1	F	252/252 (100%)	244 (97%)	8 (3%)	39	65
1	G	252/252 (100%)	244 (97%)	8 (3%)	39	65
1	H	252/252 (100%)	247 (98%)	5 (2%)	55	79
1	I	252/252 (100%)	244 (97%)	8 (3%)	39	65
1	J	252/252 (100%)	242 (96%)	10 (4%)	31	56
1	K	252/252 (100%)	243 (96%)	9 (4%)	35	61
1	L	252/252 (100%)	245 (97%)	7 (3%)	43	70
All	All	3024/3024 (100%)	2925 (97%)	99 (3%)	38	64

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	28	GLU
1	G	147	LYS
1	K	293	PHE
1	F	117	GLU
1	F	303	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	197	HIS
1	H	108	GLN
1	J	146	HIS
1	F	13	ASN
1	H	197	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 48 ligands modelled in this entry, 36 are monoatomic - leaving 12 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$
2	SP5	G	407	5	16,16,16	1.08	1 (6%)	16,16,16	1.42	3 (18%)
2	SP5	J	410	5	16,16,16	1.04	1 (6%)	16,16,16	1.50	6 (37%)
2	SP5	C	403	5	16,16,16	1.08	1 (6%)	16,16,16	1.49	6 (37%)
2	SP5	D	404	5	16,16,16	0.97	1 (6%)	16,16,16	1.55	6 (37%)
2	SP5	K	411	5	16,16,16	1.04	1 (6%)	16,16,16	1.55	6 (37%)
2	SP5	A	401	5	16,16,16	1.08	1 (6%)	16,16,16	1.47	5 (31%)
2	SP5	I	409	5	16,16,16	1.03	1 (6%)	16,16,16	1.57	6 (37%)
2	SP5	H	408	5	16,16,16	0.99	1 (6%)	16,16,16	1.41	4 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SP5	F	406	5	16,16,16	1.01	1 (6%)	16,16,16	1.47	5 (31%)
2	SP5	L	412	5	16,16,16	0.99	1 (6%)	16,16,16	1.48	4 (25%)
2	SP5	B	402	5	16,16,16	1.07	1 (6%)	16,16,16	1.50	5 (31%)
2	SP5	E	405	5	16,16,16	1.08	1 (6%)	16,16,16	1.56	6 (37%)

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	SP5	G	407	5	-	7/14/14/14	-
2	SP5	J	410	5	-	6/14/14/14	-
2	SP5	C	403	5	-	8/14/14/14	-
2	SP5	D	404	5	-	8/14/14/14	-
2	SP5	K	411	5	-	6/14/14/14	-
2	SP5	A	401	5	-	7/14/14/14	-
2	SP5	I	409	5	-	6/14/14/14	-
2	SP5	H	408	5	-	4/14/14/14	-
2	SP5	F	406	5	-	8/14/14/14	-
2	SP5	L	412	5	-	6/14/14/14	-
2	SP5	B	402	5	-	8/14/14/14	-
2	SP5	E	405	5	-	6/14/14/14	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	405	SP5	CAC-NAD	3.76	1.45	1.34
2	C	403	SP5	CAC-NAD	3.74	1.45	1.34
2	A	401	SP5	CAC-NAD	3.69	1.44	1.34
2	I	409	SP5	CAC-NAD	3.60	1.44	1.34
2	B	402	SP5	CAC-NAD	3.53	1.44	1.34

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	409	SP5	CAB-CAC-NAD	2.62	120.73	116.09
2	E	405	SP5	CAF-CAG-NAH	2.42	118.66	112.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	402	SP5	CAB-CAC-NAD	2.33	120.21	116.09
2	K	411	SP5	CAB-CAC-NAD	2.32	120.20	116.09
2	D	404	SP5	CAF-CAG-NAH	2.32	118.39	112.14

There are no chirality outliers.

5 of 80 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	402	SP5	CAN-CAO-CAP-NAQ
2	B	402	SP5	NAM-CAN-CAO-CAP
2	L	412	SP5	CAJ-CAK-CAL-NAM
2	F	406	SP5	NAH-CAI-CAJ-CAK
2	E	405	SP5	CAJ-CAK-CAL-NAM

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	404	SP5	1	0
2	K	411	SP5	1	0
2	A	401	SP5	1	0
2	F	406	SP5	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	341/341 (100%)	-0.42	2 (0%) 89 90	22, 32, 47, 67	0
1	B	341/341 (100%)	-0.36	1 (0%) 94 94	23, 37, 50, 57	0
1	C	341/341 (100%)	-0.39	0 100 100	20, 34, 46, 54	0
1	D	341/341 (100%)	-0.35	2 (0%) 89 90	24, 35, 50, 67	0
1	E	341/341 (100%)	-0.40	1 (0%) 94 94	26, 38, 51, 63	0
1	F	341/341 (100%)	-0.31	2 (0%) 89 90	24, 36, 52, 68	0
1	G	341/341 (100%)	-0.54	0 100 100	25, 35, 47, 61	0
1	H	341/341 (100%)	-0.17	6 (1%) 68 71	25, 38, 53, 62	0
1	I	341/341 (100%)	-0.46	2 (0%) 89 90	22, 35, 47, 63	0
1	J	341/341 (100%)	-0.33	5 (1%) 73 75	26, 39, 56, 67	0
1	K	341/341 (100%)	-0.46	1 (0%) 94 94	22, 34, 46, 63	0
1	L	341/341 (100%)	-0.22	10 (2%) 51 55	26, 36, 53, 69	0
All	All	4092/4092 (100%)	-0.37	32 (0%) 86 87	20, 36, 51, 69	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	323	TYR	3.5
1	L	291	ILE	3.3
1	L	252	GLY	3.2
1	I	325	VAL	3.2
1	L	306	ARG	3.1

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. 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
5	ZN	B	344	1/1	0.78	0.08	116,116,116,116	0
2	SP5	H	408	17/17	0.81	0.25	60,64,79,79	0
5	ZN	I	344	1/1	0.81	0.18	105,105,105,105	0
2	SP5	J	410	17/17	0.82	0.24	51,57,78,78	0
2	SP5	L	412	17/17	0.83	0.32	59,62,86,87	0
2	SP5	D	404	17/17	0.83	0.31	72,76,88,88	0
2	SP5	G	407	17/17	0.83	0.24	59,65,72,72	0
5	ZN	K	344	1/1	0.85	0.04	115,115,115,115	0
2	SP5	A	401	17/17	0.86	0.26	74,76,87,87	0
5	ZN	G	344	1/1	0.86	0.06	94,94,94,94	0
5	ZN	J	344	1/1	0.86	0.06	102,102,102,102	0
2	SP5	F	406	17/17	0.87	0.25	77,79,86,86	0
2	SP5	C	403	17/17	0.88	0.26	62,63,80,80	0
2	SP5	E	405	17/17	0.88	0.17	58,61,68,68	0
4	NA	D	343	1/1	0.89	0.05	34,34,34,34	0
4	NA	G	343	1/1	0.89	0.12	32,32,32,32	0
2	SP5	B	402	17/17	0.89	0.19	50,52,70,71	0
2	SP5	K	411	17/17	0.90	0.18	48,54,61,62	0
2	SP5	I	409	17/17	0.92	0.20	40,43,57,57	0
4	NA	L	343	1/1	0.94	0.12	35,35,35,35	0
4	NA	B	343	1/1	0.94	0.09	36,36,36,36	0
5	ZN	E	344	1/1	0.95	0.10	88,88,88,88	0
5	ZN	C	344	1/1	0.96	0.08	80,80,80,80	0
5	ZN	H	344	1/1	0.96	0.05	75,75,75,75	0
5	ZN	F	344	1/1	0.96	0.06	79,79,79,79	0
4	NA	E	343	1/1	0.96	0.07	24,24,24,24	0
4	NA	H	343	1/1	0.97	0.05	41,41,41,41	0
4	NA	C	343	1/1	0.97	0.05	31,31,31,31	0
5	ZN	D	344	1/1	0.97	0.07	74,74,74,74	0
3	K	I	342	1/1	0.97	0.11	39,39,39,39	0
4	NA	F	343	1/1	0.97	0.07	32,32,32,32	0
4	NA	J	343	1/1	0.97	0.08	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	ZN	L	344	1/1	0.98	0.06	73,73,73,73	0
3	K	H	342	1/1	0.98	0.09	37,37,37,37	0
4	NA	I	343	1/1	0.98	0.06	33,33,33,33	0
3	K	J	342	1/1	0.98	0.10	36,36,36,36	0
5	ZN	A	344	1/1	0.98	0.08	76,76,76,76	0
4	NA	K	343	1/1	0.98	0.09	25,25,25,25	0
3	K	F	342	1/1	0.99	0.08	34,34,34,34	0
3	K	C	342	1/1	0.99	0.06	29,29,29,29	0
3	K	D	342	1/1	0.99	0.06	35,35,35,35	0
3	K	B	342	1/1	0.99	0.11	35,35,35,35	0
3	K	L	342	1/1	0.99	0.05	30,30,30,30	0
3	K	A	342	1/1	0.99	0.06	27,27,27,27	0
4	NA	A	343	1/1	0.99	0.04	30,30,30,30	0
3	K	K	342	1/1	1.00	0.13	34,34,34,34	0
3	K	G	342	1/1	1.00	0.11	32,32,32,32	0
3	K	E	342	1/1	1.00	0.09	36,36,36,36	0

6.5 Other polymers ⓘ

There are no such residues in this entry.