



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 2, 2023 – 12:01 AM EDT

PDB ID : 3IE1
Title : Crystal structure of H380A mutant TTHA0252 from *Thermus thermophilus* HB8 complexed with RNA
Authors : Ishikawa, H.; Nakagawa, N.; Kuramitsu, S.; Yokoyama, S.; Masui, R.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2009-07-22
Resolution : 2.85 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

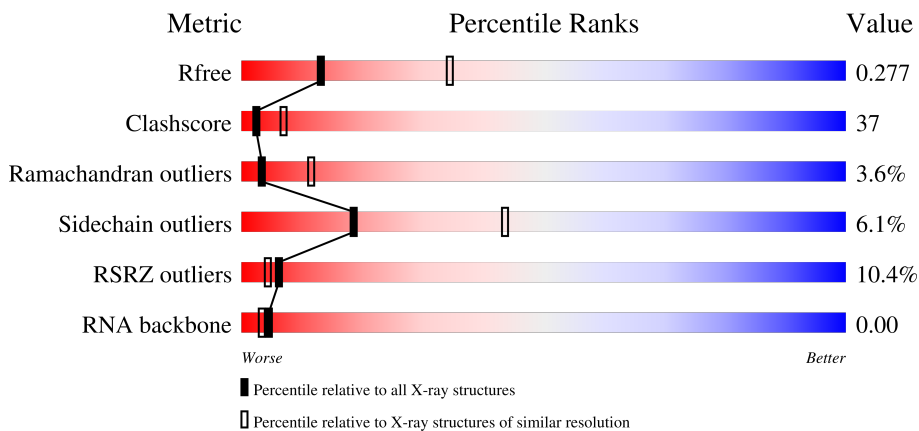
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)
RNA backbone	3102	1088 (3.12-2.60)

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	431	
1	B	431	
1	C	431	
1	D	431	

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Mol	Chain	Length	Quality of chain
2	E	4	
2	F	4	
2	G	4	
2	H	4	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	A	444	-	-	-	X
3	SO4	D	437	-	-	X	-
4	FLC	A	451	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13910 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 Ribonuclease TTHA0252.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	431	3321	2124	595	594	8	0	0	0
1	B	431	3321	2124	595	594	8	0	0	0
1	C	431	3321	2124	595	594	8	0	0	0
1	D	431	3321	2124	595	594	8	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	380	ALA	HIS	engineered mutation	UNP Q5SLP1
B	380	ALA	HIS	engineered mutation	UNP Q5SLP1
C	380	ALA	HIS	engineered mutation	UNP Q5SLP1
D	380	ALA	HIS	engineered mutation	UNP Q5SLP1

- Molecule 2 is a RNA chain called RNA (5'-R(P*UP*UP*UP*U)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	E	4	81	36	8	33	4	0	0	0
2	F	4	81	36	8	33	4	0	0	0
2	G	2	41	18	4	17	2	0	0	0
2	H	4	81	36	8	33	4	0	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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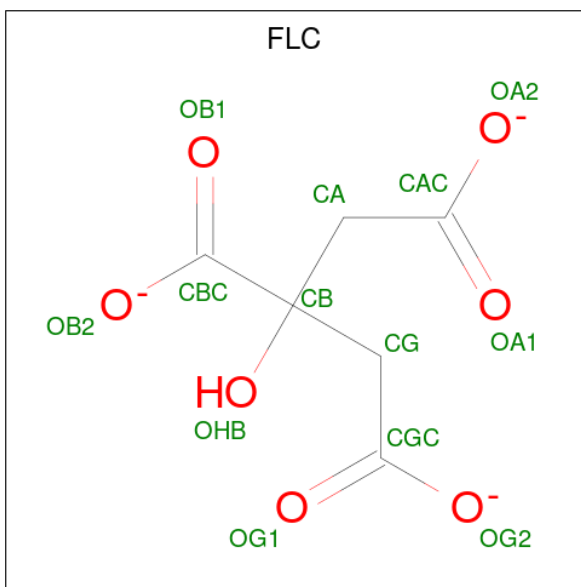
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is CITRATE ANION (three-letter code: FLC) (formula: C₆H₅O₇).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 13 6 7	0	0
4	A	1	Total C O 13 6 7	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Zn 2 2	0	0
5	B	2	Total Zn 2 2	0	0
5	C	2	Total Zn 2 2	0	0
5	D	2	Total Zn 2 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	14	Total O 14 14	0	0
6	B	11	Total O 11 11	0	0
6	C	4	Total O 4 4	0	0

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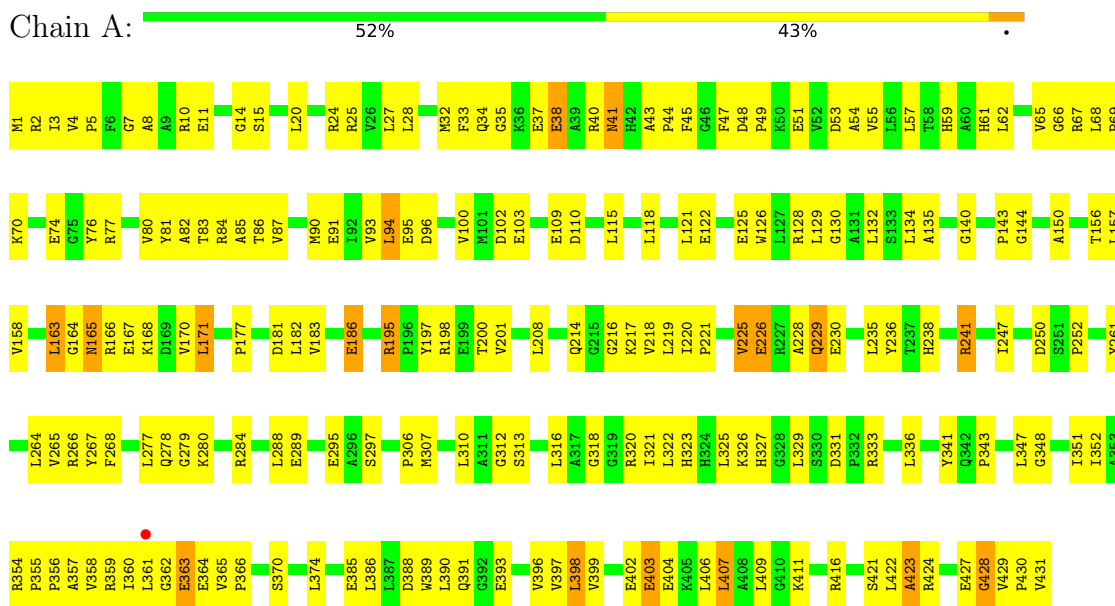
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	D	7	Total O 7 7	0	0
6	E	1	Total O 1 1	0	0
6	G	1	Total O 1 1	0	0

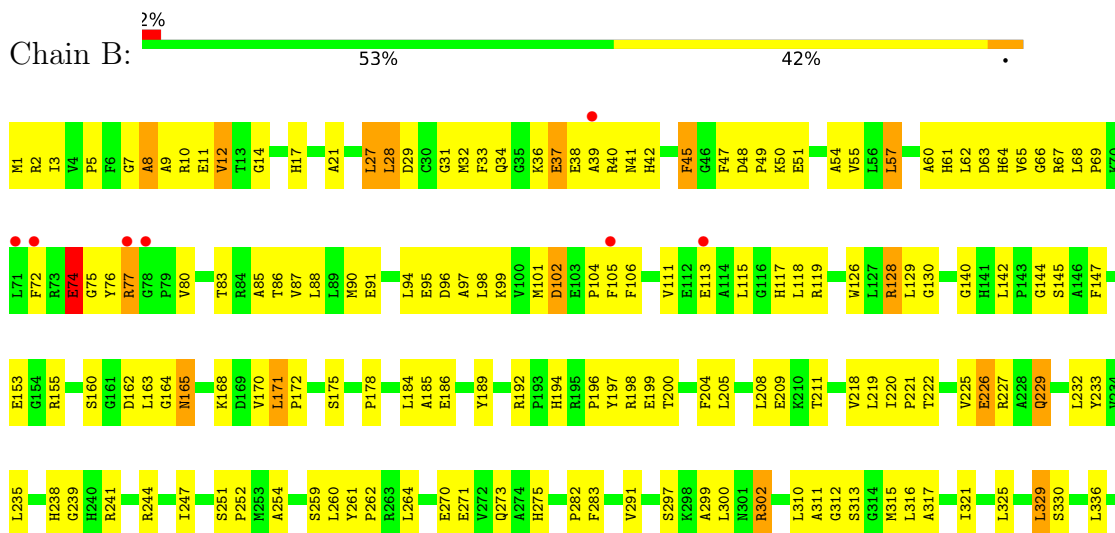
3 Residue-property plots

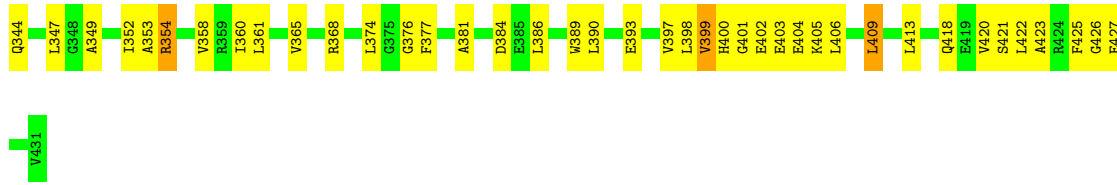
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Ribonuclease TTHA0252

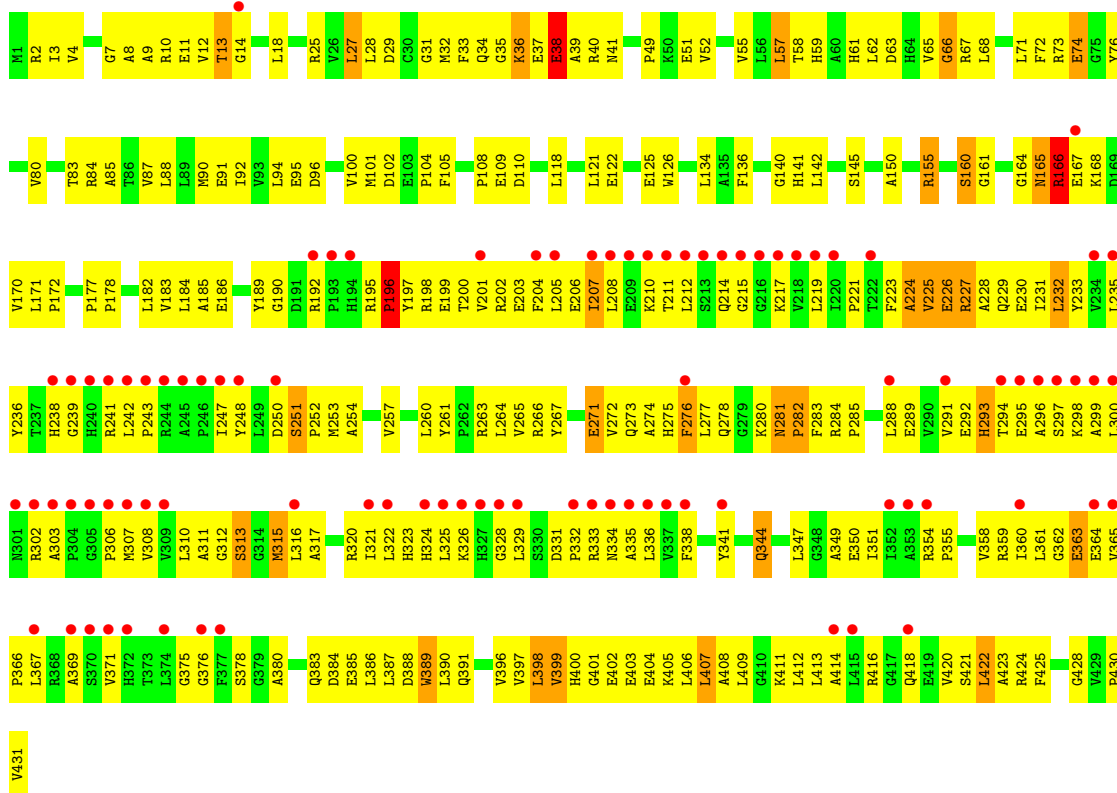


• Molecule 1: Ribonuclease TTHA0252

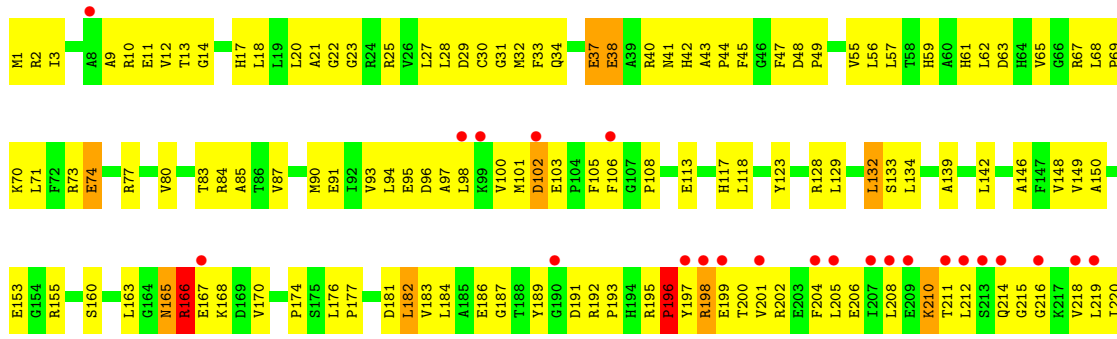
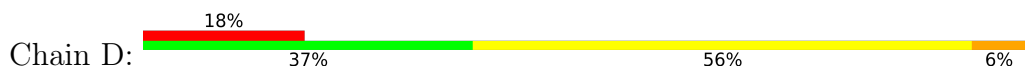


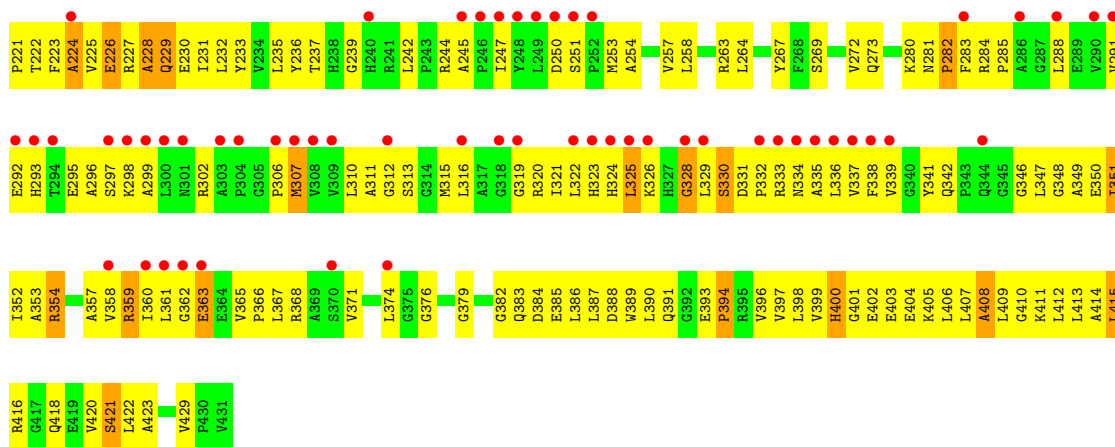


• Molecule 1: Ribonuclease TTHA0252

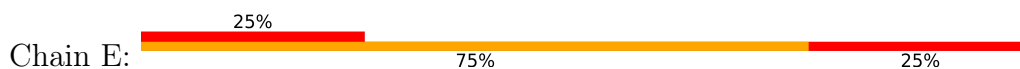


• Molecule 1: Ribonuclease TTHA0252





- Molecule 2: RNA (5'-R(P*UP*UP*UP*U)-3')



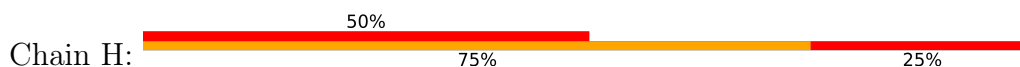
- Molecule 2: RNA (5'-R(P*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*U)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	143.42Å 148.16Å 120.84Å 90.00° 109.61° 90.00°	Depositor
Resolution (Å)	50.00 – 2.85 49.92 – 2.85	Depositor EDS
% Data completeness (in resolution range)	97.2 (50.00-2.85) 97.5 (49.92-2.85)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.11 (at 2.86Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.231 , 0.291 0.220 , 0.277	Depositor DCC
R_{free} test set	5592 reflections (10.14%)	wwPDB-VP
Wilson B-factor (Å ²)	65.4	Xtrriage
Anisotropy	0.147	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 59.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13910	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% 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: ZN, FLC, SO4

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	0.44	0/3401	0.70	0/4613
1	B	0.44	0/3401	0.71	0/4613
1	C	0.33	0/3401	0.59	1/4613 (0.0%)
1	D	0.33	0/3401	0.58	0/4613
2	E	0.94	1/88 (1.1%)	0.85	0/132
2	F	1.03	1/88 (1.1%)	0.87	0/132
2	G	1.32	1/44 (2.3%)	0.82	0/64
2	H	0.97	1/88 (1.1%)	0.84	0/132
All	All	0.41	4/13912 (0.0%)	0.65	1/18912 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	E	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	1	U	OP3-P	-7.19	1.52	1.61
2	F	1	U	OP3-P	-7.16	1.52	1.61
2	G	1	U	OP3-P	-7.11	1.52	1.61
2	E	1	U	OP3-P	-6.32	1.53	1.61

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	161	GLY	N-CA-C	-5.33	99.79	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	E	1	U	Sidechain

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	3321	0	3349	192	0
1	B	3321	0	3349	196	0
1	C	3321	0	3349	322	0
1	D	3321	0	3349	313	0
2	E	81	0	41	6	0
2	F	81	0	41	8	0
2	G	41	0	21	5	0
2	H	81	0	41	16	0
3	A	90	0	0	2	0
3	B	85	0	0	3	0
3	C	50	0	0	1	0
3	D	45	0	0	5	0
4	A	26	0	10	6	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
6	A	14	0	0	0	0
6	B	11	0	0	0	0
6	C	4	0	0	0	0
6	D	7	0	0	0	0
6	E	1	0	0	0	0
6	G	1	0	0	0	0
All	All	13910	0	13550	1026	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 37.

The worst 5 of 1026 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:C:363:GLU:HG2	1:C:364:GLU:H	1.26	0.99
1:D:37:GLU:HG3	1:D:40:ARG:HH11	1.26	0.99
1:C:359:ARG:HH12	1:C:362:GLY:HA2	1.25	0.99
1:D:1:MET:HG3	1:D:21:ALA:HB2	1.40	0.98
1:C:250:ASP:HB3	1:C:311:ALA:HB2	1.45	0.98

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	429/431 (100%)	393 (92%)	31 (7%)	5 (1%)	13	35
1	B	429/431 (100%)	374 (87%)	46 (11%)	9 (2%)	7	22
1	C	429/431 (100%)	334 (78%)	73 (17%)	22 (5%)	2	5
1	D	429/431 (100%)	345 (80%)	58 (14%)	26 (6%)	1	3
All	All	1716/1724 (100%)	1446 (84%)	208 (12%)	62 (4%)	3	11

5 of 62 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	8	ALA
1	B	38	GLU
1	B	316	LEU
1	B	354	ARG
1	C	166	ARG

5.3.2 Protein sidechains [i](#)

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	341/341 (100%)	315 (92%)	26 (8%)	13	33
1	B	341/341 (100%)	316 (93%)	25 (7%)	14	35
1	C	341/341 (100%)	324 (95%)	17 (5%)	24	53
1	D	341/341 (100%)	326 (96%)	15 (4%)	28	58
All	All	1364/1364 (100%)	1281 (94%)	83 (6%)	18	43

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	155	ARG
1	D	96	ASP
1	C	166	ARG
1	C	389	TRP
1	D	196	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	214	GLN
1	D	229	GLN
1	B	344	GLN
1	B	275	HIS
1	D	273	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	3/4 (75%)	3 (100%)	0
2	F	4/4 (100%)	3 (75%)	1 (25%)
2	G	1/4 (25%)	1 (100%)	0
2	H	4/4 (100%)	2 (50%)	2 (50%)
All	All	12/16 (75%)	9 (75%)	3 (25%)

5 of 9 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	E	2	U

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Mol	Chain	Res	Type
2	E	3	U
2	E	4	U
2	F	2	U
2	F	3	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	F	1	U
2	H	1	U
2	H	3	U

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 64 ligands modelled in this entry, 8 are monoatomic - leaving 56 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	SO4	A	439	-	4,4,4	1.01	0	6,6,6	0.66	0
3	SO4	A	445	-	4,4,4	1.01	0	6,6,6	0.66	0
3	SO4	A	448	-	4,4,4	1.00	0	6,6,6	0.68	0
3	SO4	B	435	-	4,4,4	1.03	0	6,6,6	0.65	0
3	SO4	D	435	-	4,4,4	1.02	0	6,6,6	0.66	0
3	SO4	A	438	-	4,4,4	0.91	0	6,6,6	0.68	0
3	SO4	C	436	-	4,4,4	1.02	0	6,6,6	0.64	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	FLC	A	450	-	12,12,12	1.60	4 (33%)	17,17,17	1.44	1 (5%)
3	SO4	D	432	-	4,4,4	1.03	0	6,6,6	0.65	0
3	SO4	B	432	-	4,4,4	1.00	0	6,6,6	0.65	0
3	SO4	B	443	-	4,4,4	1.04	0	6,6,6	0.65	0
3	SO4	A	441	-	4,4,4	0.98	0	6,6,6	0.68	0
3	SO4	A	433	-	4,4,4	1.00	0	6,6,6	0.68	0
3	SO4	D	440	-	4,4,4	1.00	0	6,6,6	0.67	0
3	SO4	D	434	-	4,4,4	0.99	0	6,6,6	0.66	0
3	SO4	B	434	-	4,4,4	0.99	0	6,6,6	0.68	0
3	SO4	B	437	-	4,4,4	1.02	0	6,6,6	0.66	0
3	SO4	A	435	-	4,4,4	1.01	0	6,6,6	0.65	0
3	SO4	B	446	-	4,4,4	1.03	0	6,6,6	0.67	0
3	SO4	B	436	-	4,4,4	1.04	0	6,6,6	0.64	0
3	SO4	B	444	-	4,4,4	1.07	0	6,6,6	0.63	0
4	FLC	A	451	-	12,12,12	1.73	3 (25%)	17,17,17	1.53	2 (11%)
3	SO4	A	432	-	4,4,4	1.07	0	6,6,6	0.62	0
3	SO4	B	448	-	4,4,4	1.08	0	6,6,6	0.63	0
3	SO4	D	436	-	4,4,4	1.00	0	6,6,6	0.67	0
3	SO4	C	438	-	4,4,4	1.01	0	6,6,6	0.67	0
3	SO4	A	442	-	4,4,4	1.02	0	6,6,6	0.65	0
3	SO4	B	433	-	4,4,4	1.01	0	6,6,6	0.65	0
3	SO4	C	435	-	4,4,4	1.00	0	6,6,6	0.66	0
3	SO4	C	437	-	4,4,4	0.99	0	6,6,6	0.67	0
3	SO4	A	437	-	4,4,4	1.02	0	6,6,6	0.66	0
3	SO4	A	440	-	4,4,4	1.03	0	6,6,6	0.67	0
3	SO4	A	443	-	4,4,4	0.97	0	6,6,6	0.66	0
3	SO4	A	434	-	4,4,4	1.02	0	6,6,6	0.66	0
3	SO4	A	446	-	4,4,4	1.01	0	6,6,6	0.69	0
3	SO4	A	436	-	4,4,4	1.01	0	6,6,6	0.65	0
3	SO4	A	447	-	4,4,4	0.97	0	6,6,6	0.67	0
3	SO4	C	440	-	4,4,4	1.00	0	6,6,6	0.66	0
3	SO4	B	438	-	4,4,4	1.02	0	6,6,6	0.62	0
3	SO4	C	439	-	4,4,4	1.00	0	6,6,6	0.69	0
3	SO4	C	434	-	4,4,4	1.01	0	6,6,6	0.67	0
3	SO4	D	438	-	4,4,4	1.01	0	6,6,6	0.62	0
3	SO4	B	442	-	4,4,4	0.98	0	6,6,6	0.68	0
3	SO4	A	444	-	4,4,4	1.02	0	6,6,6	0.66	0
3	SO4	C	433	-	4,4,4	0.99	0	6,6,6	0.65	0
3	SO4	C	432	-	4,4,4	1.00	0	6,6,6	0.68	0
3	SO4	D	437	-	4,4,4	1.01	0	6,6,6	0.62	0
3	SO4	B	447	-	4,4,4	0.99	0	6,6,6	0.65	0
3	SO4	A	449	-	4,4,4	1.01	0	6,6,6	0.65	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	B	440	-	4,4,4	0.97	0	6,6,6	0.75	0
3	SO4	B	441	-	4,4,4	1.01	0	6,6,6	0.63	0
3	SO4	D	439	-	4,4,4	1.01	0	6,6,6	0.64	0
3	SO4	B	439	-	4,4,4	0.99	0	6,6,6	0.66	0
3	SO4	C	441	-	4,4,4	1.03	0	6,6,6	0.65	0
3	SO4	D	433	-	4,4,4	1.02	0	6,6,6	0.67	0
3	SO4	B	445	-	4,4,4	1.01	0	6,6,6	0.67	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
4	FLC	A	451	-	-	0/16/16/16	-
4	FLC	A	450	-	-	0/16/16/16	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	451	FLC	OA2-CAC	-2.73	1.21	1.30
4	A	451	FLC	CG-CB	2.53	1.57	1.53
4	A	450	FLC	OG2-CGC	-2.48	1.22	1.30
4	A	451	FLC	OG2-CGC	-2.45	1.22	1.30
4	A	450	FLC	OA2-CAC	-2.43	1.22	1.30

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	451	FLC	OB2-CBC-CB	4.49	120.85	113.05
4	A	450	FLC	OB2-CBC-CB	4.27	120.47	113.05
4	A	451	FLC	OBI-CBC-CB	-2.03	119.38	122.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	436	SO4	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	450	FLC	1	0
4	A	451	FLC	5	0
3	A	432	SO4	1	0
3	D	436	SO4	1	0
3	A	446	SO4	1	0
3	D	437	SO4	4	0
3	B	447	SO4	1	0
3	B	440	SO4	1	0
3	B	441	SO4	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	431/431 (100%)	-0.13	1 (0%) 95 95	25, 46, 69, 83	0
1	B	431/431 (100%)	-0.10	7 (1%) 72 70	24, 46, 84, 103	0
1	C	431/431 (100%)	0.99	90 (20%) 1 0	34, 94, 165, 167	0
1	D	431/431 (100%)	0.88	79 (18%) 1 1	40, 88, 152, 163	0
2	E	4/4 (100%)	1.30	1 (25%) 0 0	70, 76, 81, 95	0
2	F	4/4 (100%)	1.15	0 100 100	83, 90, 98, 100	0
2	G	2/4 (50%)	1.46	0 100 100	145, 145, 145, 151	0
2	H	4/4 (100%)	1.74	2 (50%) 0 0	118, 125, 139, 151	0
All	All	1738/1740 (99%)	0.42	180 (10%) 6 4	24, 62, 155, 167	0

The worst 5 of 180 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	335	ALA	12.3
1	C	322	LEU	8.6
1	C	337	VAL	8.4
1	C	219	LEU	7.8
1	C	329	LEU	7.5

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 monosaccharides 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	SO4	D	435	5/5	0.43	0.33	152,152,153,153	0
3	SO4	A	432	5/5	0.67	0.32	140,140,141,141	0
3	SO4	D	434	5/5	0.68	0.25	139,139,139,140	0
4	FLC	A	450	13/13	0.73	0.38	122,124,126,128	0
3	SO4	A	436	5/5	0.75	0.30	171,171,171,171	0
3	SO4	A	444	5/5	0.78	0.49	134,134,134,135	0
3	SO4	C	441	5/5	0.78	0.19	125,125,126,126	0
3	SO4	D	433	5/5	0.78	0.17	135,136,136,136	0
3	SO4	B	445	5/5	0.80	0.21	130,131,131,131	0
3	SO4	A	442	5/5	0.80	0.23	139,140,140,140	0
3	SO4	A	437	5/5	0.80	0.20	152,152,152,152	0
3	SO4	B	436	5/5	0.82	0.33	143,143,144,144	0
3	SO4	A	446	5/5	0.82	0.26	117,118,118,118	0
3	SO4	C	434	5/5	0.82	0.34	137,137,137,137	0
3	SO4	A	449	5/5	0.82	0.23	124,124,125,125	0
3	SO4	B	438	5/5	0.83	0.24	96,97,97,98	0
3	SO4	A	435	5/5	0.83	0.22	148,148,149,149	0
4	FLC	A	451	13/13	0.83	0.31	71,76,85,86	0
3	SO4	D	440	5/5	0.84	0.17	148,148,148,149	0
3	SO4	A	440	5/5	0.84	0.16	132,132,133,133	0
3	SO4	B	434	5/5	0.84	0.21	129,129,130,130	0
3	SO4	A	445	5/5	0.85	0.24	109,110,110,111	0
3	SO4	B	432	5/5	0.85	0.44	137,138,138,139	0
3	SO4	D	432	5/5	0.85	0.19	130,130,130,130	0
3	SO4	B	442	5/5	0.86	0.26	116,116,117,117	0
3	SO4	A	448	5/5	0.86	0.29	126,126,126,127	0
3	SO4	B	447	5/5	0.86	0.37	153,153,153,153	0
3	SO4	A	439	5/5	0.87	0.17	135,135,136,136	0
3	SO4	D	437	5/5	0.88	0.18	114,114,115,115	0
3	SO4	C	432	5/5	0.88	0.18	131,132,132,132	0
3	SO4	C	435	5/5	0.89	0.19	110,110,110,111	0
3	SO4	A	441	5/5	0.89	0.16	118,118,119,119	0
3	SO4	B	435	5/5	0.90	0.22	116,116,116,117	0
3	SO4	B	437	5/5	0.90	0.12	132,132,132,132	0
3	SO4	C	437	5/5	0.91	0.16	119,119,120,120	0
3	SO4	C	433	5/5	0.91	0.25	95,95,96,96	0
3	SO4	C	440	5/5	0.92	0.11	116,116,117,117	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SO4	B	444	5/5	0.92	0.26	78,79,80,80	0
3	SO4	B	433	5/5	0.93	0.18	105,105,105,106	0
3	SO4	C	438	5/5	0.93	0.14	116,117,118,118	0
5	ZN	C	443	1/1	0.93	0.12	104,104,104,104	0
3	SO4	A	434	5/5	0.94	0.18	94,95,95,95	0
3	SO4	D	438	5/5	0.94	0.17	80,81,83,83	0
3	SO4	D	439	5/5	0.94	0.17	99,99,100,101	0
3	SO4	C	436	5/5	0.94	0.12	128,128,128,128	0
3	SO4	B	439	5/5	0.94	0.16	104,104,104,104	0
3	SO4	B	441	5/5	0.94	0.12	98,98,98,99	0
3	SO4	B	446	5/5	0.94	0.12	104,104,105,105	0
3	SO4	D	436	5/5	0.96	0.19	86,86,87,87	0
3	SO4	B	440	5/5	0.96	0.19	66,67,69,72	0
3	SO4	A	438	5/5	0.96	0.19	61,62,63,65	0
3	SO4	C	439	5/5	0.96	0.14	74,75,76,77	0
5	ZN	D	441	1/1	0.96	0.12	88,88,88,88	0
3	SO4	A	433	5/5	0.97	0.18	53,54,55,58	0
5	ZN	B	449	1/1	0.97	0.05	61,61,61,61	0
5	ZN	B	450	1/1	0.97	0.10	65,65,65,65	0
3	SO4	A	443	5/5	0.97	0.14	88,88,89,89	0
3	SO4	B	443	5/5	0.97	0.15	94,95,95,96	0
3	SO4	B	448	5/5	0.98	0.13	54,59,60,60	0
5	ZN	C	442	1/1	0.98	0.12	109,109,109,109	0
5	ZN	D	442	1/1	0.98	0.11	86,86,86,86	0
3	SO4	A	447	5/5	0.99	0.13	41,41,43,47	0
5	ZN	A	452	1/1	0.99	0.07	58,58,58,58	0
5	ZN	A	453	1/1	0.99	0.09	59,59,59,59	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.