



# wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 03:45 PM GMT

PDB ID : 2DKF  
Title : Crystal Structure of TTHA0252 from *Thermus thermophilus* HB8, a RNA Degradation Protein of the Metallo-beta-lactamase Superfamily  
Authors : Ishikawa, I.; Nakagawa, N.; Kuramitsu, S.; Yokoyama, S.; Masui, R.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2006-04-10  
Resolution : 2.80 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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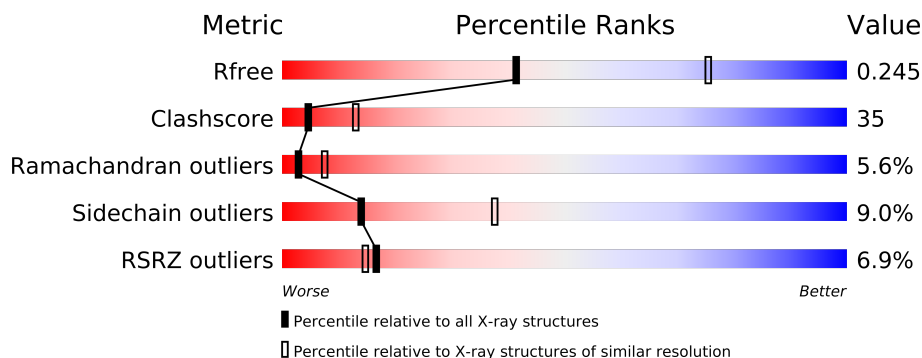
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.80 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))
$R_{free}$	66092	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	431	
1	B	431	
1	C	431	
1	D	431	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	ZN	B	432	-	X
2	ZN	B	433	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13404 atoms, of which 0 are hydrogen and 0 are deuterium.

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 metallo-beta-lactamasesuperfamily protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	Se	0	0	0
			3326	2127	597	594	1	7			
1	B	431	Total	C	N	O	S	Se	0	0	0
			3326	2127	597	594	1	7			
1	C	431	Total	C	N	O	S	Se	0	0	0
			3326	2127	597	594	1	7			
1	D	431	Total	C	N	O	S	Se	0	0	0
			3326	2127	597	594	1	7			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	GB 55771634
A	32	MSE	MET	MODIFIED RESIDUE	GB 55771634
A	90	MSE	MET	MODIFIED RESIDUE	GB 55771634
A	101	MSE	MET	MODIFIED RESIDUE	GB 55771634
A	253	MSE	MET	MODIFIED RESIDUE	GB 55771634
A	307	MSE	MET	MODIFIED RESIDUE	GB 55771634
A	315	MSE	MET	MODIFIED RESIDUE	GB 55771634
B	1	MSE	MET	MODIFIED RESIDUE	GB 55771634
B	32	MSE	MET	MODIFIED RESIDUE	GB 55771634
B	90	MSE	MET	MODIFIED RESIDUE	GB 55771634
B	101	MSE	MET	MODIFIED RESIDUE	GB 55771634
B	253	MSE	MET	MODIFIED RESIDUE	GB 55771634
B	307	MSE	MET	MODIFIED RESIDUE	GB 55771634
B	315	MSE	MET	MODIFIED RESIDUE	GB 55771634
C	1	MSE	MET	MODIFIED RESIDUE	GB 55771634
C	32	MSE	MET	MODIFIED RESIDUE	GB 55771634
C	90	MSE	MET	MODIFIED RESIDUE	GB 55771634
C	101	MSE	MET	MODIFIED RESIDUE	GB 55771634
C	253	MSE	MET	MODIFIED RESIDUE	GB 55771634
C	307	MSE	MET	MODIFIED RESIDUE	GB 55771634
C	315	MSE	MET	MODIFIED RESIDUE	GB 55771634

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MSE	MET	MODIFIED RESIDUE	GB 55771634
D	32	MSE	MET	MODIFIED RESIDUE	GB 55771634
D	90	MSE	MET	MODIFIED RESIDUE	GB 55771634
D	101	MSE	MET	MODIFIED RESIDUE	GB 55771634
D	253	MSE	MET	MODIFIED RESIDUE	GB 55771634
D	307	MSE	MET	MODIFIED RESIDUE	GB 55771634
D	315	MSE	MET	MODIFIED RESIDUE	GB 55771634

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is water.

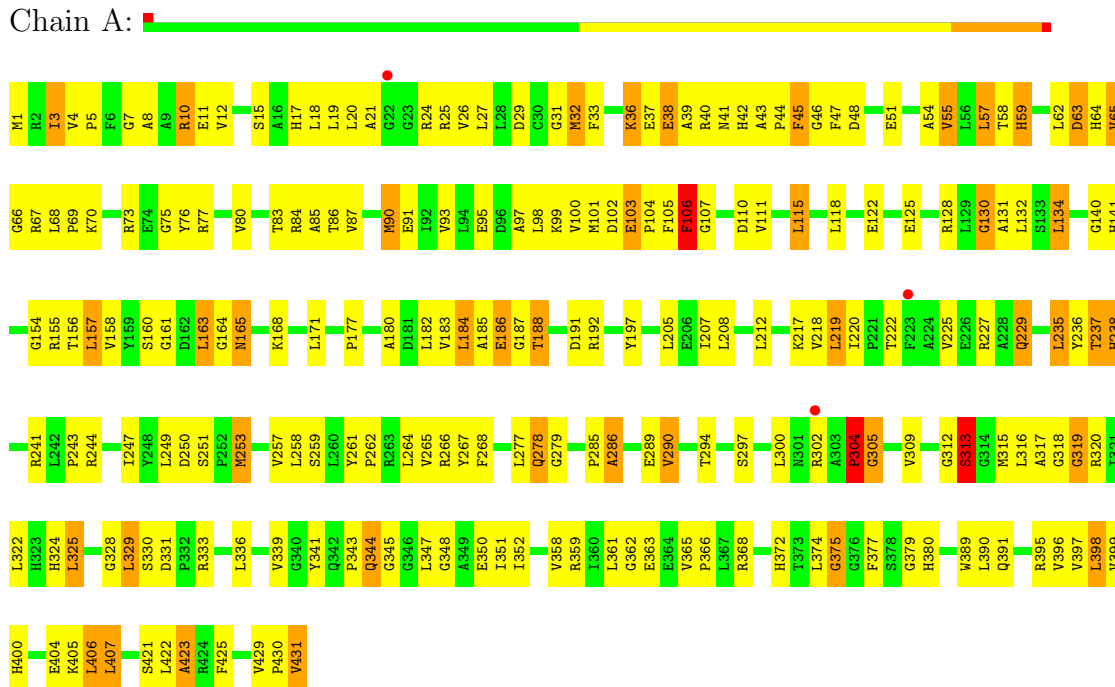
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	32	Total 32	O 32	0	0
3	B	28	Total 28	O 28	0	0
3	C	16	Total 16	O 16	0	0
3	D	16	Total 16	O 16	0	0

### 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 errors 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.

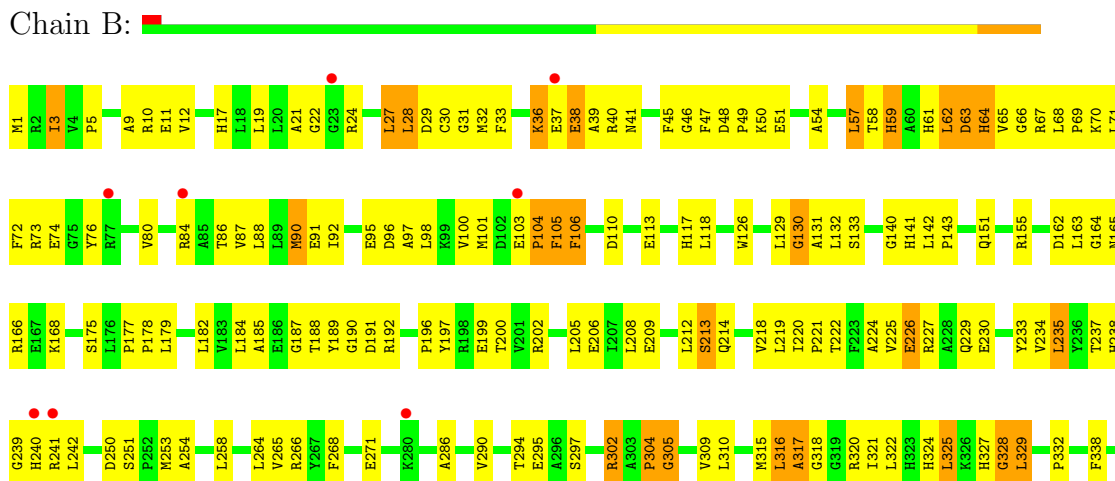
- Molecule 1: metallo-beta-lactamasesuperfamily protein

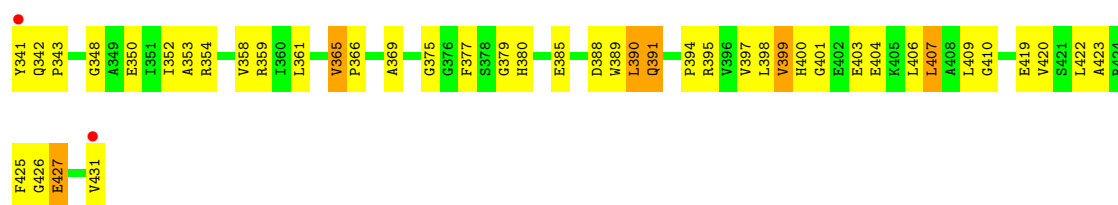
Chain A:



- Molecule 1: metallo-beta-lactamasesuperfamily protein

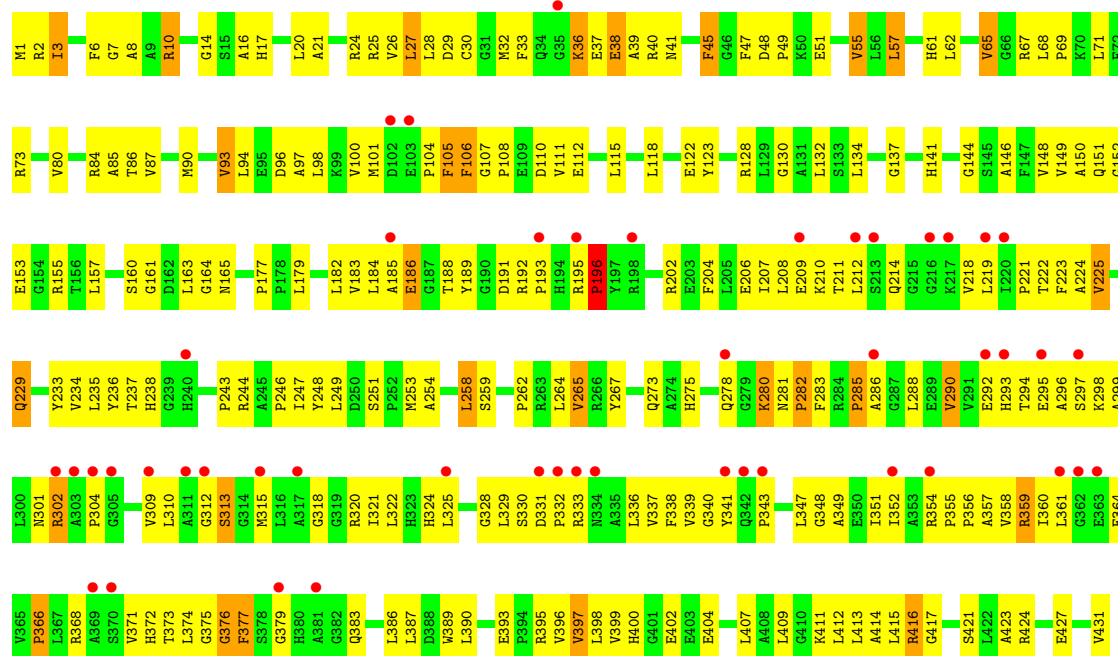
Chain B:





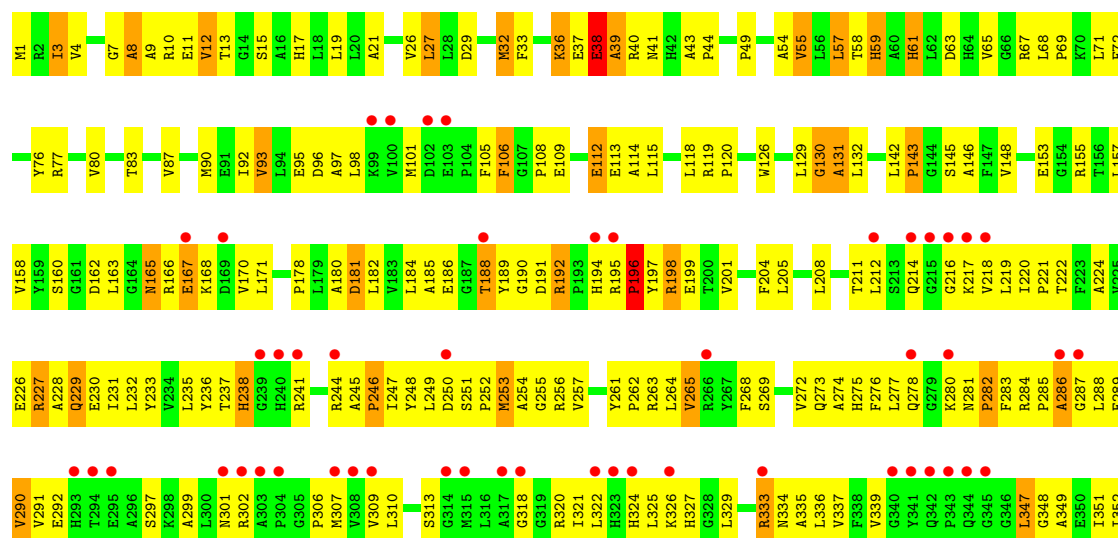
● Molecule 1: metallo-beta-lactamasesuperfamily protein

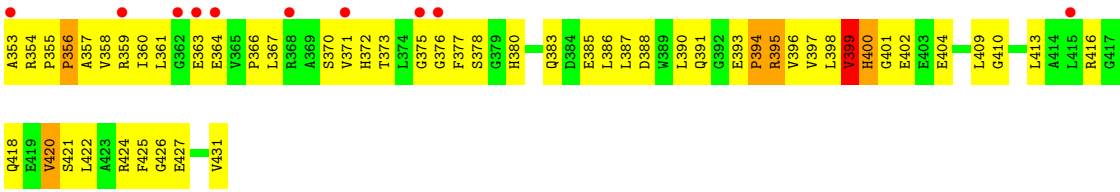
Chain C:



● Molecule 1: metallo-beta-lactamasesuperfamily protein

Chain D:





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	143.22Å 147.10Å 121.23Å 90.00° 109.25° 90.00°	Depositor
Resolution (Å)	19.99 – 2.80 19.99 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.0 (19.99-2.80) 96.1 (19.99-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	28.81 (at 2.79Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.242 , 0.285 0.246 , 0.245	Depositor DCC
$R_{free}$ test set	2847 reflections (5.09%)	DCC
Wilson B-factor (Å <sup>2</sup> )	59.7	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 28.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 55906 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	13404	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.



## 5 Model quality

### 5.1 Standard geometry

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

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	0.59	4/3401 (0.1%)	0.84	5/4603 (0.1%)
1	B	0.59	1/3401 (0.0%)	0.80	2/4603 (0.0%)
1	C	0.47	0/3401	0.67	2/4603 (0.0%)
1	D	0.45	1/3401 (0.0%)	0.65	0/4603
All	All	0.53	6/13604 (0.0%)	0.75	9/18412 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	253	MSE	CG-SE	-6.77	1.72	1.95
1	A	90	MSE	SE-CE	-6.12	1.59	1.95
1	B	90	MSE	CG-SE	-6.07	1.74	1.95
1	A	90	MSE	CG-SE	-5.91	1.75	1.95
1	A	32	MSE	SE-CE	-5.21	1.64	1.95

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	375	GLY	N-CA-C	-8.06	92.94	113.10
1	B	375	GLY	N-CA-C	-6.94	95.75	113.10
1	C	161	GLY	N-CA-C	-5.78	98.66	113.10
1	A	161	GLY	N-CA-C	-5.76	98.69	113.10
1	C	105	PHE	N-CA-C	-5.18	97.00	111.00

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3326	0	3351	206	0
1	B	3326	0	3351	224	0
1	C	3326	0	3351	242	0
1	D	3326	0	3351	272	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	32	0	0	3	0
3	B	28	0	0	0	0
3	C	16	0	0	1	0
3	D	16	0	0	0	0
All	All	13404	0	13404	933	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 35.

The worst 5 of 933 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:37:GLU:HB3	1:C:40:ARG:HH11	0.97	1.13
1:C:37:GLU:HB3	1:C:40:ARG:NH1	1.76	1.00
1:D:227:ARG:HB2	1:D:227:ARG:HH21	1.25	0.99
1:C:73:ARG:HE	1:C:106:PHE:HA	1.24	0.98
1:C:235:LEU:HD23	1:C:247:ILE:HD13	1.45	0.97

There are no symmetry-related clashes.

## 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	429/431 (100%)	361 (84%)	45 (10%)	23 (5%)	3	8
1	B	429/431 (100%)	364 (85%)	45 (10%)	20 (5%)	4	11
1	C	429/431 (100%)	340 (79%)	64 (15%)	25 (6%)	3	7
1	D	429/431 (100%)	333 (78%)	68 (16%)	28 (6%)	2	5
All	All	1716/1724 (100%)	1398 (82%)	222 (13%)	96 (6%)	3	7

5 of 96 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	38	GLU
1	A	59	HIS
1	A	106	PHE
1	A	286	ALA
1	A	304	PRO

### 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	342/335 (102%)	299 (87%)	43 (13%)	7	19
1	B	342/335 (102%)	313 (92%)	29 (8%)	15	41
1	C	342/335 (102%)	317 (93%)	25 (7%)	20	49
1	D	342/335 (102%)	316 (92%)	26 (8%)	19	46
All	All	1368/1340 (102%)	1245 (91%)	123 (9%)	14	37

5 of 123 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	165	ASN
1	B	390	LEU
1	D	188	THR
1	B	184	LEU
1	B	258	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	324	HIS
1	C	117	HIS
1	D	278	GLN
1	B	383	GLN
1	C	41	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

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.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	431/431 (100%)	-0.23	3 (0%) 84 85	21, 44, 67, 82	0
1	B	431/431 (100%)	-0.11	10 (2%) 57 58	22, 45, 77, 93	0
1	C	431/431 (100%)	0.53	47 (10%) 6 5	33, 78, 134, 141	0
1	D	431/431 (100%)	0.69	60 (13%) 4 3	36, 90, 146, 160	0
All	All	1724/1724 (100%)	0.22	120 (6%) 17 14	21, 57, 136, 160	0

The worst 5 of 120 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	333	ARG	8.5
1	D	216	GLY	7.4
1	D	215	GLY	6.6
1	C	341	TYR	5.3
1	D	341	TYR	5.1

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	B	432	1/1	0.21	3.65	28,28,28,28	1
2	ZN	B	433	1/1	0.20	2.04	42,42,42,42	1
2	ZN	A	433	1/1	0.20	1.78	37,37,37,37	1
2	ZN	D	432	1/1	0.22	0.68	59,59,59,59	1
2	ZN	C	432	1/1	0.20	0.42	48,48,48,48	1
2	ZN	D	433	1/1	0.19	0.03	73,73,73,73	1
2	ZN	C	433	1/1	0.18	-0.07	44,44,44,44	1
2	ZN	A	432	1/1	0.11	-1.53	19,19,19,19	1

## 6.5 Other polymers ⓘ

There are no such residues in this entry.