



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 04:17 AM GMT

PDB ID : 2C46  
Title : CRYSTAL STRUCTURE OF THE HUMAN RNA guanylyltransferase and 5'-phosphatase  
Authors : Debreczeni, J.; Johansson, C.; Longman, E.; Gileadi, O.; Savitskysmee, P.; Smee, C.; Bunkoczi, G.; Ugochukwu, E.; Von Delft, F.; Sundstrom, M.; Weigelt, J.; Arrowsmith, C.; Edwards, A.; Knapp, S.  
Deposited on : 2005-10-15  
Resolution : 1.60 Å(reported)

This is a full wwPDB validation 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>

---

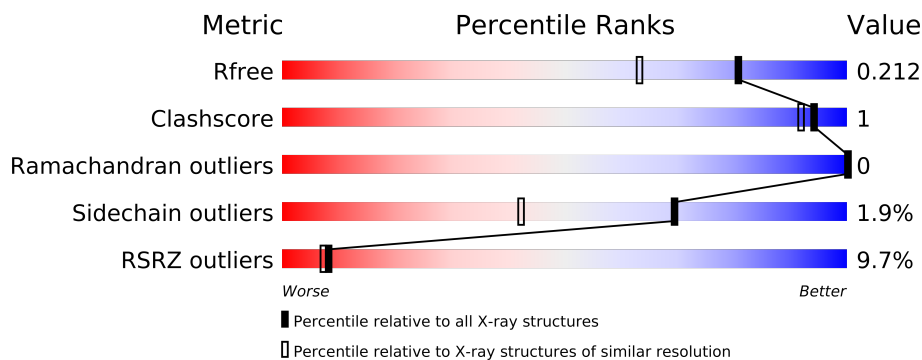
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.60 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	1872 (1.60-1.60)
Clashscore	79885	2199 (1.60-1.60)
Ramachandran outliers	78287	2126 (1.60-1.60)
Sidechain outliers	78261	2125 (1.60-1.60)
RSRZ outliers	66119	1872 (1.60-1.60)

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 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	241	
1	B	241	
1	C	241	
1	D	241	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6719 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 MRNA CAPPING ENZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	200	Total	C	N	O	S	0	2	0
			1603	1030	274	287	12			
1	B	201	Total	C	N	O	S	0	5	0
			1628	1041	274	301	12			
1	C	197	Total	C	N	O	S	0	0	0
			1553	995	262	285	11			
1	D	189	Total	C	N	O	S	0	0	0
			1475	946	244	274	11			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	EXPRESSION TAG	UNP O60942
A	-20	HIS	-	EXPRESSION TAG	UNP O60942
A	-19	HIS	-	EXPRESSION TAG	UNP O60942
A	-18	HIS	-	EXPRESSION TAG	UNP O60942
A	-17	HIS	-	EXPRESSION TAG	UNP O60942
A	-16	HIS	-	EXPRESSION TAG	UNP O60942
A	-15	HIS	-	EXPRESSION TAG	UNP O60942
A	-14	SER	-	EXPRESSION TAG	UNP O60942
A	-13	SER	-	EXPRESSION TAG	UNP O60942
A	-12	GLY	-	EXPRESSION TAG	UNP O60942
A	-11	VAL	-	EXPRESSION TAG	UNP O60942
A	-10	ASP	-	EXPRESSION TAG	UNP O60942
A	-9	LEU	-	EXPRESSION TAG	UNP O60942
A	-8	GLY	-	EXPRESSION TAG	UNP O60942
A	-7	THR	-	EXPRESSION TAG	UNP O60942
A	-6	GLU	-	EXPRESSION TAG	UNP O60942
A	-5	ASN	-	EXPRESSION TAG	UNP O60942
A	-4	LEU	-	EXPRESSION TAG	UNP O60942
A	-3	TYR	-	EXPRESSION TAG	UNP O60942
A	-2	PHE	-	EXPRESSION TAG	UNP O60942
A	-1	GLN	-	EXPRESSION TAG	UNP O60942

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP O60942
A	212	THR	PRO	CONFLICT	UNP O60942
B	-21	MET	-	EXPRESSION TAG	UNP O60942
B	-20	HIS	-	EXPRESSION TAG	UNP O60942
B	-19	HIS	-	EXPRESSION TAG	UNP O60942
B	-18	HIS	-	EXPRESSION TAG	UNP O60942
B	-17	HIS	-	EXPRESSION TAG	UNP O60942
B	-16	HIS	-	EXPRESSION TAG	UNP O60942
B	-15	HIS	-	EXPRESSION TAG	UNP O60942
B	-14	SER	-	EXPRESSION TAG	UNP O60942
B	-13	SER	-	EXPRESSION TAG	UNP O60942
B	-12	GLY	-	EXPRESSION TAG	UNP O60942
B	-11	VAL	-	EXPRESSION TAG	UNP O60942
B	-10	ASP	-	EXPRESSION TAG	UNP O60942
B	-9	LEU	-	EXPRESSION TAG	UNP O60942
B	-8	GLY	-	EXPRESSION TAG	UNP O60942
B	-7	THR	-	EXPRESSION TAG	UNP O60942
B	-6	GLU	-	EXPRESSION TAG	UNP O60942
B	-5	ASN	-	EXPRESSION TAG	UNP O60942
B	-4	LEU	-	EXPRESSION TAG	UNP O60942
B	-3	TYR	-	EXPRESSION TAG	UNP O60942
B	-2	PHE	-	EXPRESSION TAG	UNP O60942
B	-1	GLN	-	EXPRESSION TAG	UNP O60942
B	0	SER	-	EXPRESSION TAG	UNP O60942
B	212	THR	PRO	CONFLICT	UNP O60942
C	-21	MET	-	EXPRESSION TAG	UNP O60942
C	-20	HIS	-	EXPRESSION TAG	UNP O60942
C	-19	HIS	-	EXPRESSION TAG	UNP O60942
C	-18	HIS	-	EXPRESSION TAG	UNP O60942
C	-17	HIS	-	EXPRESSION TAG	UNP O60942
C	-16	HIS	-	EXPRESSION TAG	UNP O60942
C	-15	HIS	-	EXPRESSION TAG	UNP O60942
C	-14	SER	-	EXPRESSION TAG	UNP O60942
C	-13	SER	-	EXPRESSION TAG	UNP O60942
C	-12	GLY	-	EXPRESSION TAG	UNP O60942
C	-11	VAL	-	EXPRESSION TAG	UNP O60942
C	-10	ASP	-	EXPRESSION TAG	UNP O60942
C	-9	LEU	-	EXPRESSION TAG	UNP O60942
C	-8	GLY	-	EXPRESSION TAG	UNP O60942
C	-7	THR	-	EXPRESSION TAG	UNP O60942
C	-6	GLU	-	EXPRESSION TAG	UNP O60942
C	-5	ASN	-	EXPRESSION TAG	UNP O60942

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	LEU	-	EXPRESSION TAG	UNP O60942
C	-3	TYR	-	EXPRESSION TAG	UNP O60942
C	-2	PHE	-	EXPRESSION TAG	UNP O60942
C	-1	GLN	-	EXPRESSION TAG	UNP O60942
C	0	SER	-	EXPRESSION TAG	UNP O60942
C	212	THR	PRO	CONFLICT	UNP O60942
D	-21	MET	-	EXPRESSION TAG	UNP O60942
D	-20	HIS	-	EXPRESSION TAG	UNP O60942
D	-19	HIS	-	EXPRESSION TAG	UNP O60942
D	-18	HIS	-	EXPRESSION TAG	UNP O60942
D	-17	HIS	-	EXPRESSION TAG	UNP O60942
D	-16	HIS	-	EXPRESSION TAG	UNP O60942
D	-15	HIS	-	EXPRESSION TAG	UNP O60942
D	-14	SER	-	EXPRESSION TAG	UNP O60942
D	-13	SER	-	EXPRESSION TAG	UNP O60942
D	-12	GLY	-	EXPRESSION TAG	UNP O60942
D	-11	VAL	-	EXPRESSION TAG	UNP O60942
D	-10	ASP	-	EXPRESSION TAG	UNP O60942
D	-9	LEU	-	EXPRESSION TAG	UNP O60942
D	-8	GLY	-	EXPRESSION TAG	UNP O60942
D	-7	THR	-	EXPRESSION TAG	UNP O60942
D	-6	GLU	-	EXPRESSION TAG	UNP O60942
D	-5	ASN	-	EXPRESSION TAG	UNP O60942
D	-4	LEU	-	EXPRESSION TAG	UNP O60942
D	-3	TYR	-	EXPRESSION TAG	UNP O60942
D	-2	PHE	-	EXPRESSION TAG	UNP O60942
D	-1	GLN	-	EXPRESSION TAG	UNP O60942
D	0	SER	-	EXPRESSION TAG	UNP O60942
D	212	THR	PRO	CONFLICT	UNP O60942

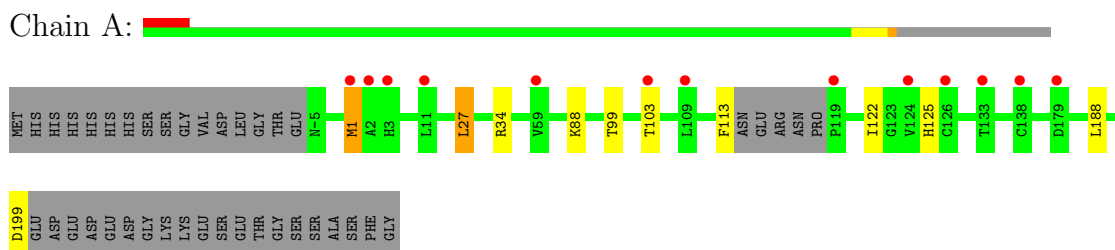
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	146	Total O 146 146	0	0
2	B	147	Total O 147 147	0	0
2	C	83	Total O 83 83	0	0
2	D	84	Total O 84 84	0	0

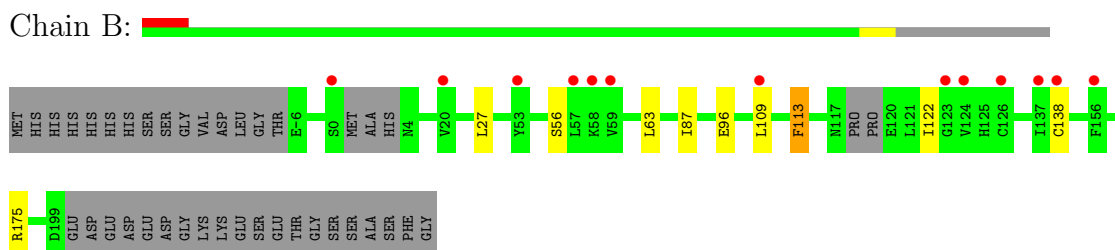
### 3 Residue-property plots

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.

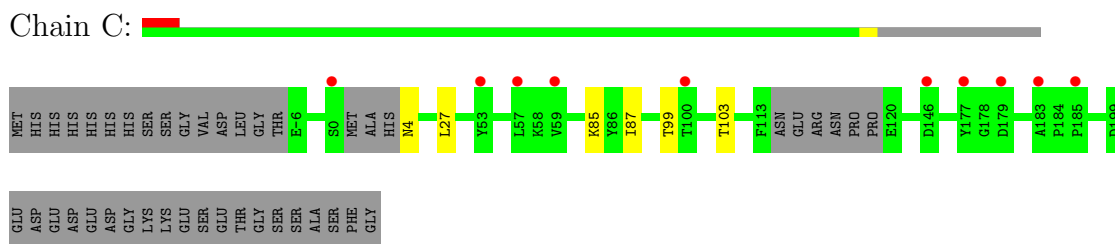
- Molecule 1: MRNA CAPPING ENZYME



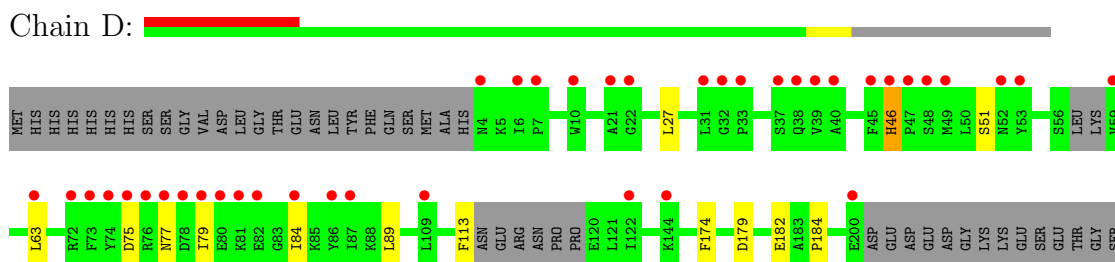
- Molecule 1: MRNA CAPPING ENZYME



- Molecule 1: MRNA CAPPING ENZYME



- Molecule 1: MRNA CAPPING ENZYME



SER  
ALA  
SER  
PHE  
GLY

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.40Å 161.60Å 60.70Å 90.00° 104.70° 90.00°	Depositor
Resolution (Å)	80.85 – 1.60 47.94 – 1.60	Depositor EDS
% Data completeness (in resolution range)	90.4 (80.85-1.60) 89.1 (47.94-1.60)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.07 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.204 , 0.234 0.202 , 0.212	Depositor DCC
$R_{free}$ test set	6714 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	19.9	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 43.8	EDS
Estimated twinning fraction	0.116 for l,-k,h	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 133439 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6719	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.77% 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

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	0.58	0/1654	0.70	1/2242 (0.0%)
1	B	0.63	1/1683 (0.1%)	0.71	2/2281 (0.1%)
1	C	0.47	0/1594	0.61	0/2163
1	D	0.43	0/1515	0.59	0/2060
All	All	0.54	1/6446 (0.0%)	0.66	3/8746 (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
1	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	138	CYS	CB-SG	-5.03	1.73	1.81

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	175	ARG	NE-CZ-NH2	-5.83	117.38	120.30
1	B	175	ARG	NE-CZ-NH1	5.73	123.16	120.30
1	A	199	ASP	CB-CG-OD2	5.13	122.92	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	113	PHE	Peptide

## 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	1603	0	1542	5	0
1	B	1628	0	1563	4	0
1	C	1553	0	1464	2	0
1	D	1475	0	1373	7	0
2	A	146	0	0	0	0
2	B	147	0	0	1	0
2	C	83	0	0	0	0
2	D	84	0	0	0	0
All	All	6719	0	5942	18	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 1.

All (18) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:99:THR:O	1:A:103:THR:HG23	1.85	0.76
1:D:75:ASP:OD1	1:D:77:ASN:ND2	2.39	0.54
1:D:46:HIS:ND1	1:D:46:HIS:N	2.44	0.54
1:B:113:PHE:HB2	1:B:122:ILE:HD11	1.91	0.53
1:D:174:PHE:CE1	1:D:184:PRO:HD3	2.46	0.51
1:A:1:MET:HE2	1:A:34:ARG:CB	2.42	0.50
1:A:27:LEU:HG	1:A:125:HIS:HB3	1.93	0.50
1:B:96:GLU:OE1	2:B:2074:HOH:O	2.19	0.49
1:D:63:LEU:HB2	1:D:113:PHE:CZ	2.49	0.48
1:A:1:MET:CE	1:A:34:ARG:CB	2.92	0.47
1:C:99:THR:O	1:C:103:THR:HG23	2.17	0.45
1:B:87[B]:ILE:HG21	1:B:109:LEU:HD21	1.99	0.44
1:D:79:ILE:HG22	1:D:84:ILE:HB	2.00	0.43
1:C:85:LYS:HZ3	1:C:87:ILE:CG1	2.32	0.42
1:A:113:PHE:HB2	1:A:122:ILE:HD11	2.03	0.41
1:D:179:ASP:HB3	1:D:182:GLU:HG3	2.02	0.41
1:B:63:LEU:HD11	1:B:87[B]:ILE:HG22	2.03	0.40
1:D:179:ASP:HB3	1:D:182:GLU:CG	2.51	0.40

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	198/241 (82%)	189 (96%)	9 (4%)	0	100	100
1	B	200/241 (83%)	194 (97%)	6 (3%)	0	100	100
1	C	191/241 (79%)	185 (97%)	6 (3%)	0	100	100
1	D	183/241 (76%)	177 (97%)	6 (3%)	0	100	100
All	All	772/964 (80%)	745 (96%)	27 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	168/212 (79%)	164 (98%)	4 (2%)	61	31
1	B	173/212 (82%)	171 (99%)	2 (1%)	82	63
1	C	160/212 (76%)	158 (99%)	2 (1%)	80	60
1	D	152/212 (72%)	148 (97%)	4 (3%)	59	28
All	All	653/848 (77%)	641 (98%)	12 (2%)	69	44

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	27	LEU
1	A	88	LYS
1	A	188	LEU
1	B	27	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	56	SER
1	C	4	ASN
1	C	27	LEU
1	D	27	LEU
1	D	46	HIS
1	D	51	SER
1	D	89	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	77	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 ⓘ

There are no ligands in this entry.

## 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	200/241 (82%)	0.68	13 (6%) 18 18	21, 30, 42, 47	0
1	B	201/241 (83%)	0.73	13 (6%) 18 18	21, 30, 42, 52	0
1	C	197/241 (81%)	0.39	10 (5%) 27 25	21, 31, 39, 45	0
1	D	189/241 (78%)	1.02	40 (21%) 1 1	22, 32, 39, 46	0
All	All	787/964 (81%)	0.70	76 (9%) 8 7	21, 31, 41, 52	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	32	GLY	6.6
1	D	33	PRO	6.0
1	D	31	LEU	6.0
1	D	53	TYR	5.7
1	D	6	ILE	4.9
1	D	46	HIS	4.7
1	D	79	ILE	4.7
1	D	59	VAL	4.2
1	D	63	LEU	4.2
1	D	81	LYS	4.1
1	A	1	MET	3.7
1	B	0	SER	3.5
1	D	86	TYR	3.4
1	C	0	SER	3.4
1	D	78	ASP	3.4
1	D	77	ASN	3.3
1	D	200	GLU	3.3
1	A	59	VAL	3.3
1	D	73	PHE	3.2
1	A	3	HIS	3.1
1	D	7	PRO	3.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	2	ALA	3.1
1	D	49	MET	3.0
1	A	109	LEU	3.0
1	B	59	VAL	3.0
1	D	4	ASN	3.0
1	C	59	VAL	3.0
1	D	87	ILE	2.9
1	D	47	PRO	2.9
1	B	53	TYR	2.9
1	D	74	TYR	2.9
1	B	126	CYS	2.8
1	D	84	ILE	2.7
1	A	138	CYS	2.7
1	C	146	ASP	2.6
1	C	179	ASP	2.6
1	D	75	ASP	2.6
1	D	37	SER	2.5
1	B	109	LEU	2.5
1	C	57	LEU	2.5
1	D	109	LEU	2.5
1	D	48	SER	2.5
1	B	137	ILE	2.5
1	D	144	LYS	2.5
1	D	72	ARG	2.4
1	C	185	PRO	2.4
1	D	45	PHE	2.4
1	A	11	LEU	2.4
1	D	22	GLY	2.4
1	D	38	GLN	2.4
1	B	156	PHE	2.4
1	D	76	ARG	2.3
1	B	124	VAL	2.3
1	A	124	VAL	2.3
1	D	21	ALA	2.3
1	C	53	TYR	2.3
1	B	20	VAL	2.3
1	D	82	GLU	2.2
1	D	52	ASN	2.2
1	D	10	TRP	2.2
1	C	183	ALA	2.2
1	C	100	THR	2.2
1	D	39	VAL	2.2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	D	122	ILE	2.2
1	B	138	CYS	2.2
1	D	40	ALA	2.2
1	A	179	ASP	2.1
1	A	119	PRO	2.1
1	B	57	LEU	2.1
1	C	177	TYR	2.1
1	A	103	THR	2.1
1	D	80	GLU	2.1
1	A	126	CYS	2.0
1	A	133	THR	2.0
1	B	123	GLY	2.0
1	B	58	LYS	2.0

## 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 ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.