



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2021 – 05:09 PM JST

PDB ID : 7CV1  
Title : Structure of human tRNA<sup>His</sup> guanylyltransferase (Thg1) in the presence of human mitochondrial tRNA<sup>His</sup>  
Authors : Nakamura, A.; Wang, D.; Komatsu, Y.  
Deposited on : 2020-08-25  
Resolution : 4.00 Å(reported)

This is a Full wwPDB X-ray Structure 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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  
Xtriage (Phenix) : 1.13  
EDS : 2.18  
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) : 2.18

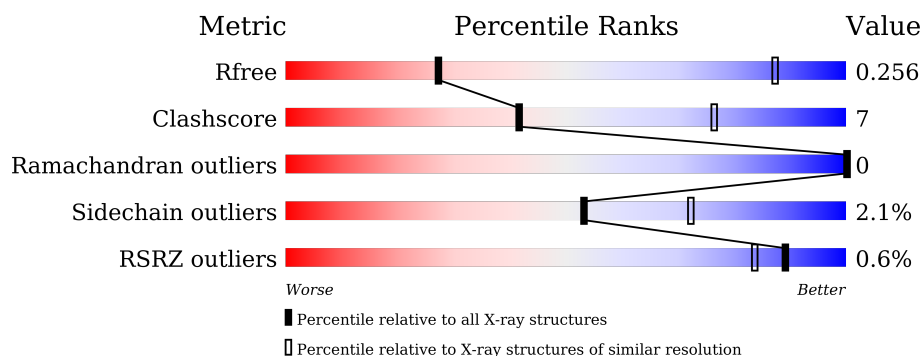
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



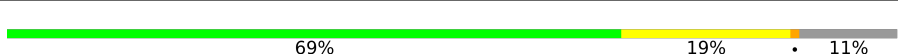

The reported resolution of this entry is 4.00 Å.

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	1087 (4.30-3.70)
Clashscore	141614	1148 (4.30-3.70)
Ramachandran outliers	138981	1108 (4.30-3.70)
Sidechain outliers	138945	1099 (4.30-3.70)
RSRZ outliers	127900	1028 (4.34-3.66)

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  $\geq 3$ , 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	277	
1	B	277	
1	C	277	
1	D	277	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8211 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 Probable tRNA(His) guanylyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	0	0
			2087	1340	358	379	10			
1	B	241	Total	C	N	O	S	0	0	0
			2009	1293	344	363	9			
1	C	246	Total	C	N	O	S	0	0	0
			2051	1317	352	373	9			
1	D	248	Total	C	N	O	S	0	0	0
			2064	1325	354	375	10			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	expression tag	UNP Q9NWX6
A	-6	GLY	-	expression tag	UNP Q9NWX6
A	-5	HIS	-	expression tag	UNP Q9NWX6
A	-4	HIS	-	expression tag	UNP Q9NWX6
A	-3	HIS	-	expression tag	UNP Q9NWX6
A	-2	HIS	-	expression tag	UNP Q9NWX6
A	-1	HIS	-	expression tag	UNP Q9NWX6
A	0	HIS	-	expression tag	UNP Q9NWX6
B	-7	MET	-	expression tag	UNP Q9NWX6
B	-6	GLY	-	expression tag	UNP Q9NWX6
B	-5	HIS	-	expression tag	UNP Q9NWX6
B	-4	HIS	-	expression tag	UNP Q9NWX6
B	-3	HIS	-	expression tag	UNP Q9NWX6
B	-2	HIS	-	expression tag	UNP Q9NWX6
B	-1	HIS	-	expression tag	UNP Q9NWX6
B	0	HIS	-	expression tag	UNP Q9NWX6
C	-7	MET	-	expression tag	UNP Q9NWX6
C	-6	GLY	-	expression tag	UNP Q9NWX6
C	-5	HIS	-	expression tag	UNP Q9NWX6
C	-4	HIS	-	expression tag	UNP Q9NWX6
C	-3	HIS	-	expression tag	UNP Q9NWX6

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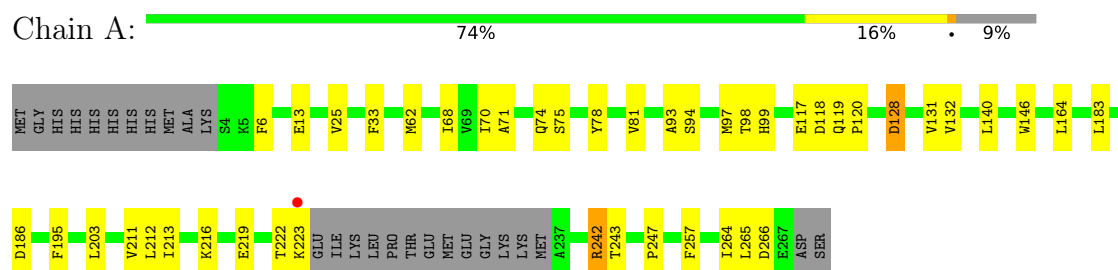
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	HIS	-	expression tag	UNP Q9NWX6
C	-1	HIS	-	expression tag	UNP Q9NWX6
C	0	HIS	-	expression tag	UNP Q9NWX6
D	-7	MET	-	expression tag	UNP Q9NWX6
D	-6	GLY	-	expression tag	UNP Q9NWX6
D	-5	HIS	-	expression tag	UNP Q9NWX6
D	-4	HIS	-	expression tag	UNP Q9NWX6
D	-3	HIS	-	expression tag	UNP Q9NWX6
D	-2	HIS	-	expression tag	UNP Q9NWX6
D	-1	HIS	-	expression tag	UNP Q9NWX6
D	0	HIS	-	expression tag	UNP Q9NWX6

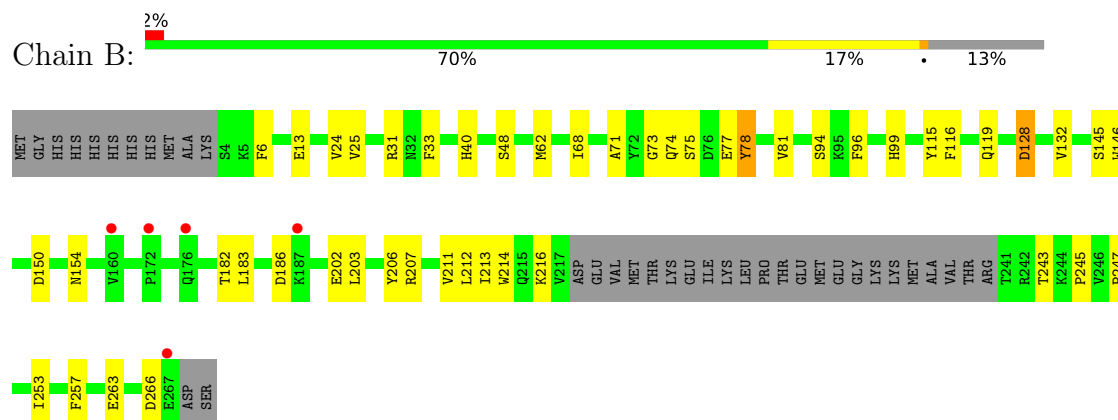
### 3 Residue-property plots

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.

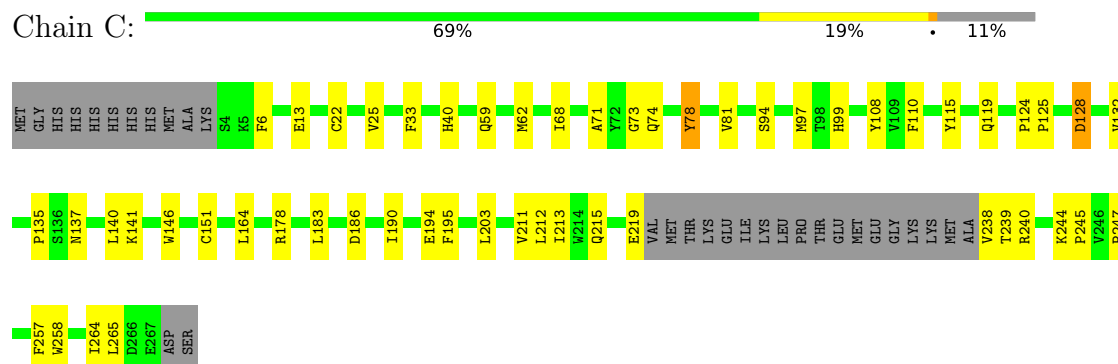
- Molecule 1: Probable tRNA(His) guanylyltransferase



- Molecule 1: Probable tRNA(His) guanylyltransferase



- Molecule 1: Probable tRNA(His) guanylyltransferase



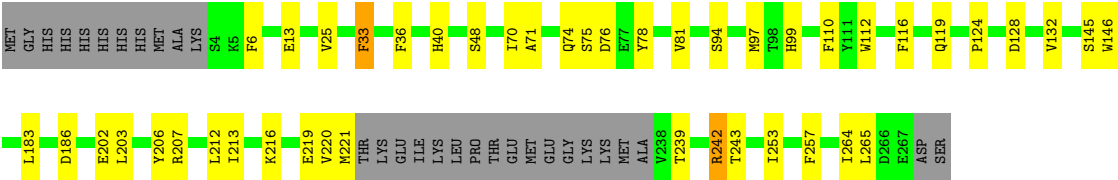
● Molecule 1: Probable tRNA(His) guanylyltransferase

Chain D: 

73%

16%

10%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	155.88Å 155.88Å 201.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.46 – 4.00 49.46 – 4.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.46-4.00) 90.9 (49.46-4.00)	Depositor EDS
$R_{merge}$	1.01	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.97 (at 4.00Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, $R_{free}$	0.242 , 0.255 0.243 , 0.256	Depositor DCC
$R_{free}$ test set	2436 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	108.9	Xtriage
Anisotropy	0.311	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 75.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.036 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	8211	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	138.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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](#)

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	0.26	0/2145	0.42	0/2908
1	B	0.26	0/2067	0.42	0/2803
1	C	0.26	0/2109	0.42	0/2860
1	D	0.26	0/2122	0.43	0/2877
All	All	0.26	0/8443	0.42	0/11448

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	2087	0	2008	28	0
1	B	2009	0	1926	28	0
1	C	2051	0	1965	40	0
1	D	2064	0	1976	34	0
All	All	8211	0	7875	112	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 7.

All (112) 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:B:74:GLN:HG2	1:B:77:GLU:HG2	1.61	0.83
1:B:216:LYS:HG2	1:B:243:THR:HG22	1.72	0.71
1:D:33:PHE:CE1	1:D:36:PHE:CD2	2.78	0.71
1:D:33:PHE:CE1	1:D:36:PHE:HD2	2.10	0.70
1:C:94:SER:HB2	1:D:97:MET:HE1	1.74	0.69
1:C:238:VAL:HG12	1:C:239:THR:HG23	1.77	0.66
1:D:74:GLN:HG2	1:D:75:SER:H	1.62	0.65
1:C:6:PHE:HB3	1:D:146:TRP:HB2	1.79	0.65
1:D:25:VAL:HG22	1:D:81:VAL:HG22	1.79	0.65
1:A:6:PHE:HB3	1:B:146:TRP:HB2	1.79	0.64
1:B:40:HIS:O	1:B:119:GLN:NE2	2.32	0.63
1:C:40:HIS:O	1:C:119:GLN:NE2	2.31	0.62
1:C:146:TRP:HB2	1:D:6:PHE:HB3	1.81	0.62
1:D:70:ILE:HB	1:D:264:ILE:HD11	1.82	0.62
1:C:219:GLU:HB3	1:C:240:ARG:HD3	1.82	0.61
1:D:216:LYS:HD3	1:D:243:THR:HG22	1.82	0.61
1:A:222:THR:HG22	1:A:223:LYS:H	1.65	0.60
1:A:74:GLN:HG2	1:A:75:SER:H	1.67	0.59
1:C:124:PRO:HD3	1:D:110:PHE:HD2	1.67	0.59
1:C:97:MET:HE1	1:D:94:SER:HB2	1.85	0.58
1:C:124:PRO:HD3	1:D:110:PHE:CD2	2.39	0.58
1:C:178:ARG:NH1	1:C:178:ARG:O	2.37	0.57
1:D:219:GLU:OE2	1:D:242:ARG:NH1	2.37	0.57
1:A:97:MET:HE1	1:B:94:SER:HB2	1.86	0.56
1:C:99:HIS:CE1	1:D:128:ASP:HB3	2.40	0.56
1:C:183:LEU:H	1:C:186:ASP:HB2	1.70	0.56
1:C:190:ILE:O	1:C:194:GLU:HB2	2.05	0.56
1:A:219:GLU:OE2	1:A:242:ARG:NH1	2.40	0.55
1:B:25:VAL:HG22	1:B:81:VAL:HG22	1.87	0.55
1:C:211:VAL:O	1:C:247:PRO:HA	2.07	0.55
1:D:220:VAL:HG22	1:D:239:THR:HA	1.89	0.55
1:C:71:ALA:HB3	1:C:212:LEU:HB2	1.89	0.54
1:D:220:VAL:HG12	1:D:221:MET:H	1.72	0.54
1:C:213:ILE:HD11	1:C:257:PHE:HZ	1.72	0.54
1:A:99:HIS:CE1	1:B:128:ASP:HB3	2.43	0.53
1:A:70:ILE:HB	1:A:264:ILE:HD11	1.90	0.53
1:A:81:VAL:HG11	1:A:140:LEU:HD21	1.90	0.53
1:C:73:GLY:HA3	1:C:78:TYR:CZ	2.44	0.53
1:D:213:ILE:HD11	1:D:257:PHE:HZ	1.74	0.52
1:D:220:VAL:HG13	1:D:239:THR:H	1.74	0.52
1:A:183:LEU:H	1:A:186:ASP:HB2	1.76	0.51
1:D:183:LEU:H	1:D:186:ASP:HB2	1.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:25:VAL:HG22	1:C:81:VAL:HG22	1.92	0.51
1:A:119:GLN:OE1	1:A:120:PRO:HD2	2.11	0.51
1:D:202:GLU:O	1:D:207:ARG:NH1	2.44	0.51
1:D:116:PHE:HB3	1:D:119:GLN:HB2	1.93	0.51
1:C:81:VAL:HG11	1:C:140:LEU:HD21	1.93	0.50
1:A:25:VAL:HG22	1:A:81:VAL:HG22	1.92	0.50
1:C:13:GLU:HG2	1:D:132:VAL:HG22	1.94	0.50
1:A:132:VAL:HG22	1:B:13:GLU:HG2	1.93	0.49
1:A:213:ILE:HD11	1:A:257:PHE:HZ	1.77	0.49
1:C:128:ASP:HB3	1:D:99:HIS:CE1	2.47	0.49
1:A:128:ASP:HB3	1:B:99:HIS:NE2	2.28	0.48
1:D:74:GLN:HG2	1:D:75:SER:N	2.28	0.48
1:A:164:LEU:HD23	1:A:195:PHE:HZ	1.79	0.48
1:D:33:PHE:CD2	1:D:76:ASP:HB2	2.48	0.48
1:C:108:TYR:HD2	1:C:125:PRO:HG3	1.79	0.47
1:B:48:SER:HG	1:B:206:TYR:HH	1.61	0.47
1:B:73:GLY:HA3	1:B:78:TYR:CZ	2.49	0.47
1:C:108:TYR:CD2	1:C:125:PRO:HG3	2.50	0.47
1:C:132:VAL:HG22	1:D:13:GLU:HG2	1.97	0.47
1:A:146:TRP:HB2	1:B:6:PHE:HB3	1.95	0.47
1:B:71:ALA:HB3	1:B:212:LEU:HB2	1.97	0.46
1:A:264:ILE:HG23	1:A:265:LEU:HD13	1.96	0.46
1:B:24:VAL:HG11	1:B:96:PHE:CD1	2.49	0.46
1:C:164:LEU:HD23	1:C:195:PHE:HZ	1.79	0.46
1:B:145:SER:HA	1:B:253:ILE:HG12	1.97	0.46
1:C:141:LYS:HD2	1:C:258:TRP:CD1	2.50	0.45
1:B:62:MET:HG2	1:B:68:ILE:HG21	1.98	0.45
1:B:203:LEU:H	1:B:203:LEU:HD12	1.81	0.45
1:D:71:ALA:HB3	1:D:212:LEU:HB2	1.98	0.45
1:D:40:HIS:HD2	1:D:112:TRP:CZ2	2.35	0.45
1:D:203:LEU:HD12	1:D:203:LEU:H	1.82	0.45
1:D:145:SER:HA	1:D:253:ILE:HG12	2.00	0.44
1:B:183:LEU:H	1:B:186:ASP:HB2	1.81	0.44
1:C:59:GLN:NE2	1:C:245:PRO:O	2.43	0.44
1:C:110:PHE:CD2	1:D:124:PRO:HD3	2.52	0.44
1:A:203:LEU:HD12	1:A:203:LEU:H	1.82	0.44
1:C:213:ILE:HG23	1:C:264:ILE:HD11	2.00	0.44
1:D:264:ILE:HG23	1:D:265:LEU:HD13	1.98	0.44
1:C:62:MET:HG2	1:C:68:ILE:HG21	2.00	0.44
1:B:74:GLN:HG3	1:B:75:SER:N	2.32	0.43
1:D:48:SER:OG	1:D:206:TYR:OH	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:VAL:O	1:B:247:PRO:HA	2.19	0.43
1:C:62:MET:HA	1:C:68:ILE:HD12	2.00	0.43
1:A:211:VAL:O	1:A:247:PRO:HA	2.18	0.43
1:A:71:ALA:HB3	1:A:212:LEU:HB2	2.01	0.43
1:C:137:ASN:HB3	1:C:265:LEU:HD21	2.01	0.43
1:A:216:LYS:HD3	1:A:243:THR:HG22	2.00	0.43
1:D:33:PHE:CD2	1:D:76:ASP:CB	3.01	0.43
1:A:93:ALA:HB1	1:A:131:VAL:HG21	2.01	0.42
1:A:74:GLN:HG2	1:A:75:SER:N	2.31	0.42
1:C:244:LYS:HE2	1:C:244:LYS:HB3	1.92	0.42
1:C:183:LEU:N	1:C:186:ASP:HB2	2.35	0.42
1:C:115:TYR:CD2	1:C:115:TYR:N	2.88	0.42
1:B:116:PHE:HB3	1:B:119:GLN:HB3	2.02	0.42
1:C:203:LEU:H	1:C:203:LEU:HD12	1.85	0.42
1:B:202:GLU:O	1:B:207:ARG:NH1	2.53	0.42
1:B:213:ILE:HD11	1:B:257:PHE:HZ	1.85	0.41
1:B:115:TYR:N	1:B:115:TYR:CD2	2.88	0.41
1:A:117:GLU:H	1:A:117:GLU:HG2	1.65	0.41
1:C:115:TYR:N	1:C:115:TYR:HD2	2.18	0.41
1:A:94:SER:O	1:A:98:THR:OG1	2.34	0.41
1:B:150:ASP:OD1	1:B:154:ASN:ND2	2.52	0.41
1:B:214:TRP:CZ3	1:B:245:PRO:HD3	2.56	0.41
1:C:213:ILE:CG2	1:C:264:ILE:HD11	2.50	0.41
1:A:13:GLU:HG2	1:B:132:VAL:HG22	2.02	0.40
1:C:22:CYS:SG	1:C:135:PRO:HA	2.61	0.40
1:C:74:GLN:OE1	1:C:151:CYS:HB2	2.21	0.40
1:A:222:THR:O	1:A:223:LYS:HB2	2.20	0.40
1:B:182:THR:HB	1:B:186:ASP:HB3	2.03	0.40
1:A:62:MET:HG2	1:A:68:ILE:HG21	2.03	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	247/277 (89%)	243 (98%)	4 (2%)	0	100	100
1	B	237/277 (86%)	234 (99%)	3 (1%)	0	100	100
1	C	242/277 (87%)	238 (98%)	4 (2%)	0	100	100
1	D	244/277 (88%)	240 (98%)	4 (2%)	0	100	100
All	All	970/1108 (88%)	955 (98%)	15 (2%)	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	225/248 (91%)	219 (97%)	6 (3%)	44	66
1	B	216/248 (87%)	210 (97%)	6 (3%)	43	65
1	C	221/248 (89%)	217 (98%)	4 (2%)	59	77
1	D	222/248 (90%)	219 (99%)	3 (1%)	67	81
All	All	884/992 (89%)	865 (98%)	19 (2%)	53	72

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	PHE
1	A	78	TYR
1	A	118	ASP
1	A	128	ASP
1	A	242	ARG
1	A	266	ASP
1	B	31	ARG
1	B	33	PHE
1	B	78	TYR
1	B	128	ASP
1	B	263	GLU
1	B	266	ASP
1	C	33	PHE

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Mol	Chain	Res	Type
1	C	78	TYR
1	C	128	ASP
1	C	215	GLN
1	D	33	PHE
1	D	78	TYR
1	D	242	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	99	HIS
1	C	249	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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, 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	251/277 (90%)	-0.25	1 (0%) 92 87	104, 133, 169, 200	0
1	B	241/277 (87%)	0.06	5 (2%) 63 54	107, 166, 230, 238	0
1	C	246/277 (88%)	-0.26	0 100 100	99, 122, 154, 214	0
1	D	248/277 (89%)	-0.28	0 100 100	96, 122, 166, 196	0
All	All	986/1108 (88%)	-0.18	6 (0%) 89 84	96, 132, 202, 238	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	187	LYS	3.4
1	B	267	GLU	3.1
1	B	172	PRO	2.8
1	B	176	GLN	2.8
1	A	223	LYS	2.2
1	B	160	VAL	2.1

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.