



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 17, 2021 – 10:20 PM JST

PDB ID : 7DID  
Title : Mycoplasma genitalium RNase R in complex with ribose methylated single-stranded RNA  
Authors : Abula, A.; Quan, X.; Li, X.; Yang, T.; Li, T.; Chen, Q.; Ji, X.  
Deposited on : 2020-11-18  
Resolution : 1.90 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  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.18  
buster-report : 1.1.7 (2018)  
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

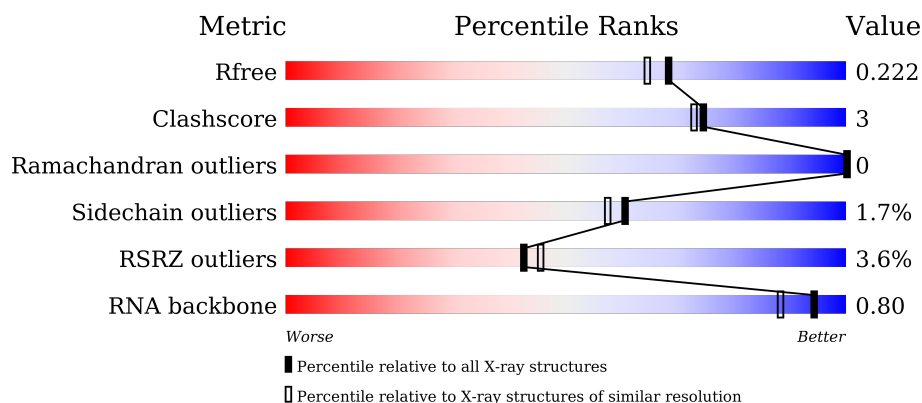
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)
RNA backbone	3102	1013 (2.42-1.38)

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	747	
2	C	4	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5782 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 R.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	644	Total	C	N	O	S	0	1	0
			5202	3325	871	990	16			

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	expression tag	UNP P47350
A	-20	GLY	-	expression tag	UNP P47350
A	-19	HIS	-	expression tag	UNP P47350
A	-18	HIS	-	expression tag	UNP P47350
A	-17	HIS	-	expression tag	UNP P47350
A	-16	HIS	-	expression tag	UNP P47350
A	-15	HIS	-	expression tag	UNP P47350
A	-14	HIS	-	expression tag	UNP P47350
A	-13	HIS	-	expression tag	UNP P47350
A	-12	HIS	-	expression tag	UNP P47350
A	-11	HIS	-	expression tag	UNP P47350
A	-10	HIS	-	expression tag	UNP P47350
A	-9	SER	-	expression tag	UNP P47350
A	-8	SER	-	expression tag	UNP P47350
A	-7	GLY	-	expression tag	UNP P47350
A	-6	HIS	-	expression tag	UNP P47350
A	-5	ILE	-	expression tag	UNP P47350
A	-4	ASP	-	expression tag	UNP P47350
A	-3	ASP	-	expression tag	UNP P47350
A	-2	ASP	-	expression tag	UNP P47350
A	-1	ASP	-	expression tag	UNP P47350
A	0	LYS	-	expression tag	UNP P47350
A	284	ALA	ASP	engineered mutation	UNP P47350

- Molecule 2 is a RNA chain called RNA (5'-R(\*AP\*AP\*AP\*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	4	Total	C	N	O	P	0	0	0
			86	41	20	22	3			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

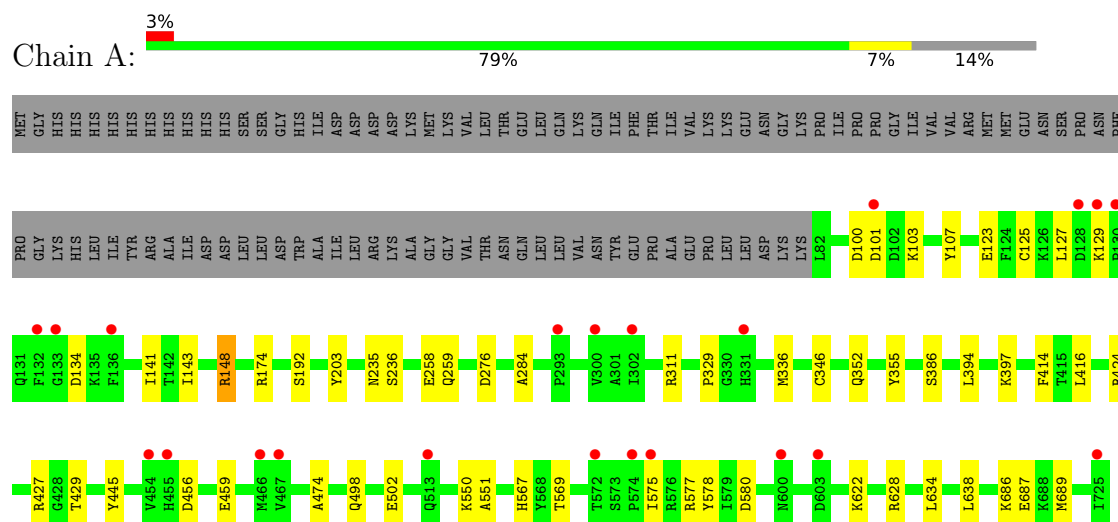
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	485	Total	O	0	0
			485	485		
4	C	8	Total	O	0	0
			8	8		

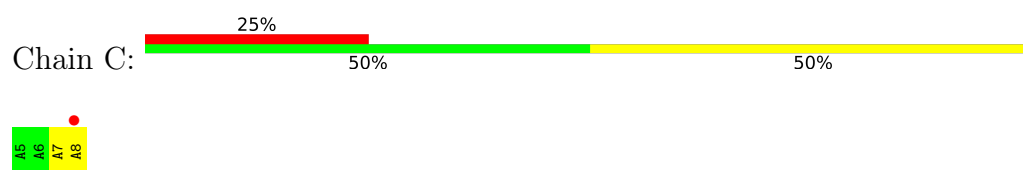
### 3 Residue-property plots [i](#)

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 R



#### • Molecule 2: RNA (5'-R(\*AP\*AP\*AP\*A)-3')



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.29Å 80.78Å 175.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.98 – 1.90 29.98 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.98-1.90) 88.2 (29.98-1.90)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.67 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.10_2148	Depositor
R, $R_{free}$	0.188 , 0.222 0.188 , 0.222	Depositor DCC
$R_{free}$ test set	2000 reflections (2.55%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.2	Xtriage
Anisotropy	0.407	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 42.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5782	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, A2M

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	0.53	0/5304	0.63	1/7193 (0.0%)
2	C	0.57	0/71	0.73	0/109
All	All	0.53	0/5375	0.64	1/7302 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	577	ARG	NE-CZ-NH1	5.03	122.81	120.30

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	5202	0	5218	33	0
2	C	86	0	48	1	0
3	A	1	0	0	0	0
4	A	485	0	0	10	0
4	C	8	0	0	1	0
All	All	5782	0	5266	34	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 3.

All (34) 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:A:148:ARG:NH2	1:A:236:SER:OG	2.10	0.84
1:A:336:MET:HE1	1:A:578:TYR:HB2	1.66	0.78
2:C:8:A:O2'	4:C:101:HOH:O	2.03	0.75
1:A:174:ARG:NH2	4:A:901:HOH:O	2.18	0.75
1:A:456:ASP:HB3	1:A:459:GLU:HB3	1.75	0.68
1:A:127:LEU:HB3	1:A:129:LYS:HG2	1.75	0.68
1:A:148:ARG:HH21	1:A:236:SER:HG	1.42	0.65
1:A:336:MET:CE	1:A:578:TYR:HB2	2.26	0.64
1:A:689:MET:CE	4:A:1111:HOH:O	2.47	0.62
1:A:567:HIS:HE1	4:A:1326:HOH:O	1.87	0.57
1:A:628:ARG:NH2	4:A:909:HOH:O	2.36	0.57
1:A:689:MET:HE3	4:A:1111:HOH:O	2.03	0.57
1:A:174:ARG:NH2	4:A:909:HOH:O	2.37	0.56
1:A:107:TYR:OH	1:A:134:ASP:OD1	2.17	0.55
1:A:498:GLN:O	1:A:502:GLU:HG3	2.08	0.54
1:A:235:ASN:O	1:A:622:LYS:HD2	2.09	0.52
1:A:352:GLN:NE2	4:A:910:HOH:O	2.39	0.52
1:A:567:HIS:HD2	4:A:1027:HOH:O	1.94	0.50
1:A:346:CYS:O	1:A:575:ILE:HD11	2.11	0.50
1:A:550:LYS:HG2	1:A:551:ALA:O	2.12	0.50
1:A:259:GLN:OE1	4:A:902:HOH:O	2.20	0.50
1:A:258:GLU:HB3	1:A:355:TYR:CZ	2.48	0.48
1:A:100:ASP:O	1:A:103:LYS:HE2	2.14	0.47
1:A:329:PRO:HG2	1:A:634:LEU:HD12	1.97	0.46
1:A:284:ALA:HB2	1:A:575:ILE:HD12	1.97	0.46
1:A:276:ASP:O	1:A:386:SER:HA	2.16	0.45
1:A:474:ALA:HB2	1:A:569:THR:HG22	1.99	0.43
1:A:125:CYS:HB3	1:A:141:ILE:HD11	2.00	0.43
1:A:424:ARG:HG2	1:A:429:THR:HB	1.99	0.43
1:A:686:LYS:HG2	1:A:687:GLU:N	2.34	0.42
1:A:689:MET:HE1	4:A:1111:HOH:O	2.13	0.42
1:A:143:ILE:HD12	1:A:203:TYR:OH	2.20	0.41
1:A:123:GLU:HG2	1:A:141:ILE:HB	2.02	0.41
1:A:394:LEU:HD11	1:A:414:PHE:CE1	2.56	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	643/747 (86%)	629 (98%)	14 (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	589/680 (87%)	579 (98%)	10 (2%)	60	57

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	ASP
1	A	148	ARG
1	A	192	SER
1	A	311	ARG
1	A	397	LYS
1	A	416	LEU
1	A	427	ARG
1	A	445	TYR
1	A	580	ASP
1	A	638	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	3/4 (75%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	A2M	C	7	2	18,25,26	4.29	7 (38%)	18,36,39	2.98	4 (22%)

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	A2M	C	7	2	-	0/5/27/28	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	7	A2M	O4'-C1'	15.55	1.62	1.41
2	C	7	A2M	O4'-C4'	-6.16	1.31	1.45
2	C	7	A2M	C6-N6	3.13	1.45	1.34
2	C	7	A2M	O2'-C2'	3.06	1.50	1.42
2	C	7	A2M	O3'-C3'	-2.80	1.36	1.43
2	C	7	A2M	C2-N3	2.57	1.36	1.32
2	C	7	A2M	C5-C4	-2.43	1.34	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	C	7	A2M	C1'-N9-C4	7.23	139.34	126.64
2	C	7	A2M	C5-C6-N6	6.85	130.76	120.35
2	C	7	A2M	N3-C2-N1	-5.54	120.02	128.68
2	C	7	A2M	N6-C6-N1	-4.67	108.87	118.57

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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.

No monomer is involved in short contacts.

## 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, 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	644/747 (86%)	-0.02	22 (3%) 45 48	26, 42, 67, 107	0
2	C	3/4 (75%)	0.70	1 (33%) 0 0	73, 73, 77, 92	0
All	All	647/751 (86%)	-0.01	23 (3%) 42 45	26, 42, 68, 107	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	132	PHE	4.4
1	A	101	ASP	4.4
1	A	454	VAL	4.2
1	A	128	ASP	4.0
1	A	455	HIS	3.9
1	A	133	GLY	3.6
1	A	130	PRO	3.3
1	A	300	VAL	3.1
1	A	572	THR	3.0
1	A	129	LYS	2.9
1	A	293	PRO	2.7
1	A	600	ASN	2.6
1	A	513	GLN	2.5
1	A	574	PRO	2.4
1	A	603	ASP	2.4
1	A	575	ILE	2.3
1	A	467	VAL	2.2
1	A	302	ILE	2.2
2	C	8	A	2.2
1	A	136	PHE	2.2
1	A	466	MET	2.2
1	A	725	ILE	2.1
1	A	331	HIS	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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, 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	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	A2M	C	7	23/24	0.81	0.22	74,83,90,92	0

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

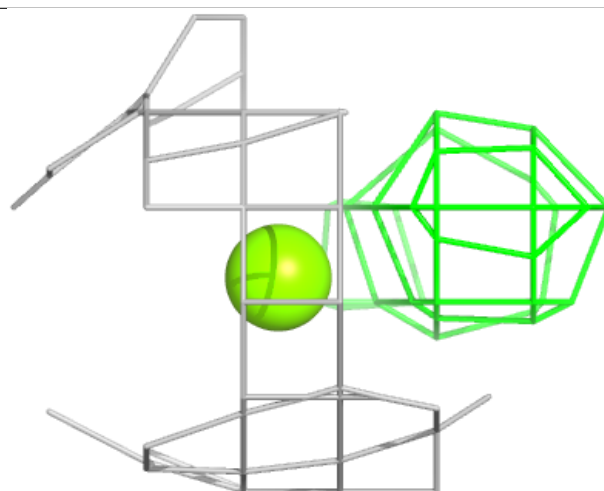
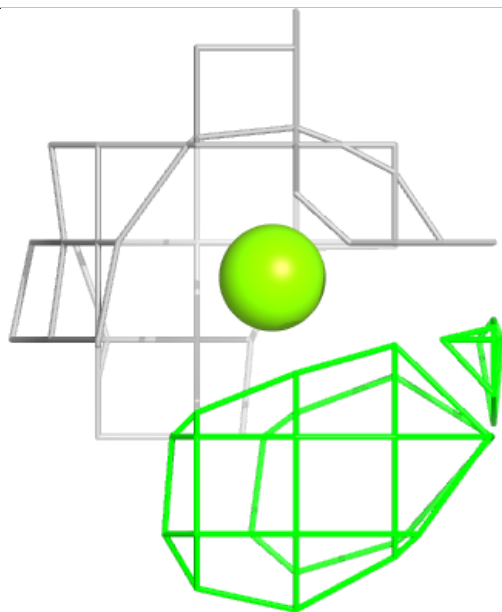
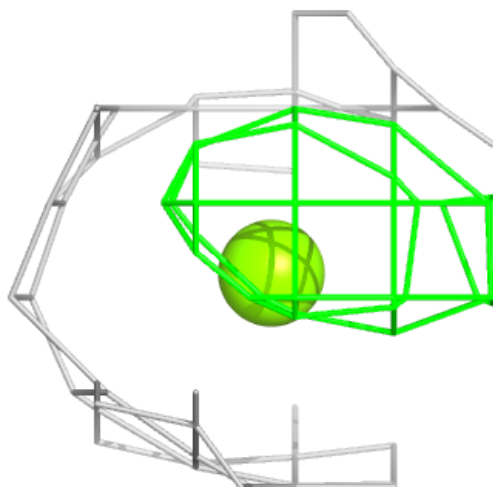
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	MG	A	801	1/1	0.95	0.16	39,39,39,39	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around MG A 801:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers ⓘ

There are no such residues in this entry.