



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 10, 2023 – 10:56 AM EDT

PDB ID : 4KN7  
Title : X-ray crystal structure of the Escherichia coli RNA polymerase in complex with Benzoxazinorifamycin-2c  
Authors : Murakami, K.S.  
Deposited on : 2013-05-08  
Resolution : 3.69 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](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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 2.35.1  
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) : 2.35.1

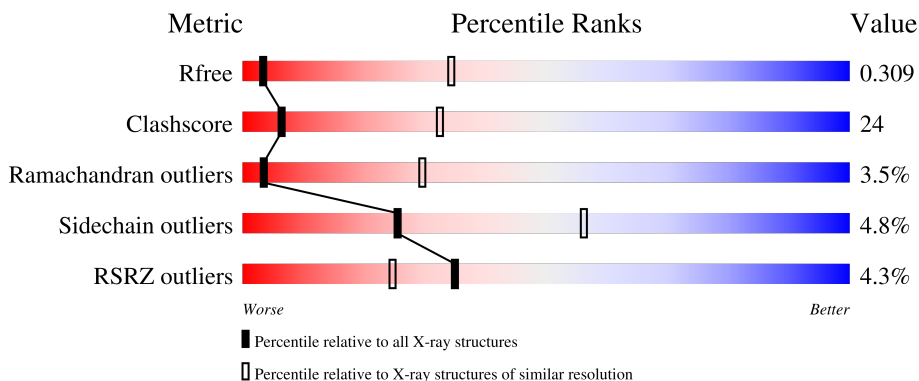
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.69 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	1013 (3.84-3.52)
Clashscore	141614	1070 (3.84-3.52)
Ramachandran outliers	138981	1036 (3.84-3.52)
Sidechain outliers	138945	1033 (3.84-3.52)
RSRZ outliers	127900	1471 (3.86-3.50)

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	329	 2% 62% 33%
1	B	329	 3% 40% 24% 33%
1	F	329	 4% 48% 20% 30%
1	G	329	 5% 41% 23% 34%
2	C	1342	 3% 53% 41% 5%

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Mol	Chain	Length	Quality of chain
2	H	1342	<p>5% 55% 39% 5%</p>
3	D	1407	<p>2% 40% 38% 5% 18%</p>
3	I	1407	<p>4% 41% 37% • 18%</p>
4	E	91	<p>% 68% 27% ...</p>
4	J	91	<p>3% 52% 29% •• 16%</p>
5	X	613	<p>6% 49% 32% • 16%</p>
5	Y	613	<p>5% 44% 29% • 25%</p>

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 56331 atoms, of which 117 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 DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	323	Total	C	N	O	S	0	0	0
			2514	1571	443	492	8			
1	B	221	Total	C	N	O	S	0	0	0
			1706	1065	300	335	6			
1	F	229	Total	C	N	O	S	0	0	0
			1775	1106	313	350	6			
1	G	217	Total	C	N	O	S	0	0	0
			1671	1045	293	327	6			

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	1335	Total	C	N	O	S	0	0	0
			10523	6601	1836	2043	43			
2	H	1335	Total	C	N	O	S	0	0	0
			10523	6601	1836	2043	43			

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	D	1160	Total	C	N	O	S	0	0	0
			9060	5695	1621	1697	47			
3	I	1160	Total	C	N	O	S	0	0	0
			9060	5695	1621	1697	47			

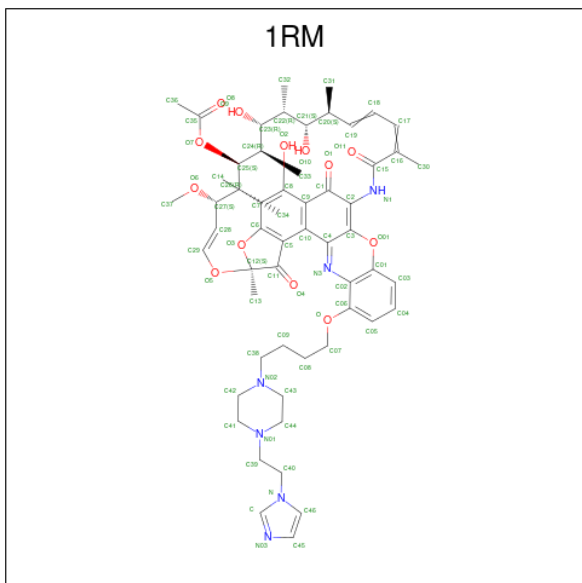
- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	E	90	Total	C	N	O	S	0	0	0
			708	430	136	141	1			
4	J	76	Total	C	N	O	S	0	0	0
			605	368	115	121	1			

- Molecule 5 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	X	517	Total	C	N	O	S	0	0	0
			4198	2621	745	806	26			
5	Y	458	Total	C	N	O	S	0	0	0
			3732	2335	671	703	23			

- Molecule 6 is Benzoxazinorifamycin-2c (three-letter code: 1RM) (formula: C<sub>56</sub>H<sub>70</sub>N<sub>6</sub>O<sub>13</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
6	C	1	Total	C	H	N	O	0	0
			145	56	70	6	13		
6	H	1	Total	C	H	N	O	0	0
			105	43	47	2	13		

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
7	D	2	Total	Zn	0	0
			2	2		
7	I	2	Total	Zn	0	0
			2	2		

- Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
8	D	1	Total 1	Mg 1	0	0
8	I	1	Total 1	Mg 1	0	0

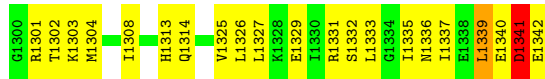
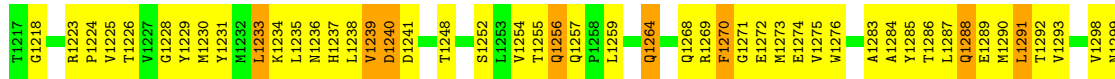




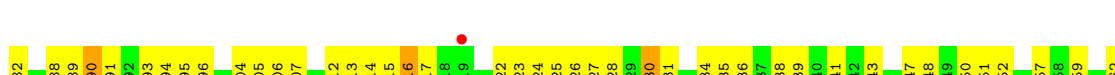
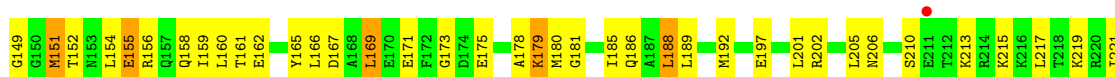
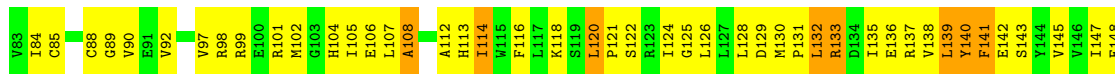
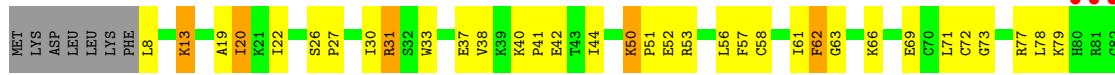








● Molecule 3: DNA-directed RNA polymerase subunit beta'











## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	185.83Å 204.58Å 308.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.88 – 3.69 29.88 – 3.69	Depositor EDS
% Data completeness (in resolution range)	93.1 (29.88-3.69) 87.0 (29.88-3.69)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.28 (at 3.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.252 , 0.309 0.252 , 0.309	Depositor DCC
$R_{free}$ test set	5907 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	120.4	Xtriage
Anisotropy	0.283	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 28.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	56331	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.72% 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, ZN, 1RM

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	0.19	0/2548	0.37	0/3454
1	B	0.19	0/1725	0.41	0/2337
1	F	0.19	0/1797	0.40	0/2436
1	G	0.20	0/1690	0.40	0/2290
2	C	0.20	0/10690	0.39	0/14423
2	H	0.20	0/10690	0.39	0/14423
3	D	0.20	0/9198	0.40	0/12413
3	I	0.20	0/9198	0.40	0/12413
4	E	0.19	0/710	0.36	0/956
4	J	0.19	0/607	0.37	0/817
5	X	0.20	0/4253	0.37	0/5719
5	Y	0.20	0/3783	0.37	0/5083
All	All	0.20	0/56889	0.39	0/76764

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	2514	0	2566	102	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1706	0	1738	86	0
1	F	1775	0	1800	65	0
1	G	1671	0	1706	80	0
2	C	10523	0	10546	566	0
2	H	10523	0	10546	538	0
3	D	9060	0	9257	589	0
3	I	9060	0	9256	532	0
4	E	708	0	719	31	0
4	J	605	0	612	28	0
5	X	4198	0	4250	180	0
5	Y	3732	0	3809	139	0
6	C	75	70	70	9	0
6	H	58	47	46	8	0
7	D	2	0	0	0	0
7	I	2	0	0	0	0
8	D	1	0	0	0	0
8	I	1	0	0	0	0
All	All	56214	117	56921	2717	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 24.

The worst 5 of 2717 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)
2:H:1119:MET:HG2	2:H:1228:GLY:HA2	1.26	1.17
3:D:1173:ARG:HA	3:D:1174:ARG:HB2	1.28	1.14
3:D:310:GLY:HA3	3:D:311:ARG:HB2	1.22	1.13
2:C:1119:MET:HG2	2:C:1228:GLY:HA2	1.31	1.10
3:I:1173:ARG:HA	3:I:1174:ARG:HB2	1.29	1.09

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	321/329 (98%)	266 (83%)	40 (12%)	15 (5%)	2	22
1	B	217/329 (66%)	187 (86%)	22 (10%)	8 (4%)	3	28
1	F	227/329 (69%)	196 (86%)	25 (11%)	6 (3%)	5	33
1	G	213/329 (65%)	187 (88%)	22 (10%)	4 (2%)	8	40
2	C	1333/1342 (99%)	1069 (80%)	216 (16%)	48 (4%)	3	29
2	H	1333/1342 (99%)	1069 (80%)	215 (16%)	49 (4%)	3	28
3	D	1154/1407 (82%)	918 (80%)	194 (17%)	42 (4%)	3	29
3	I	1154/1407 (82%)	920 (80%)	192 (17%)	42 (4%)	3	29
4	E	88/91 (97%)	78 (89%)	5 (6%)	5 (6%)	1	19
4	J	74/91 (81%)	65 (88%)	4 (5%)	5 (7%)	1	16
5	X	511/613 (83%)	449 (88%)	49 (10%)	13 (2%)	5	34
5	Y	454/613 (74%)	410 (90%)	34 (8%)	10 (2%)	6	37
All	All	7079/8222 (86%)	5814 (82%)	1018 (14%)	247 (4%)	3	29

5 of 247 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	PRO
1	A	319	GLU
1	B	20	SER
1	B	52	PRO
2	C	21	VAL

### 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	281/286 (98%)	273 (97%)	8 (3%)	43	67
1	B	189/286 (66%)	186 (98%)	3 (2%)	62	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	197/286 (69%)	193 (98%)	4 (2%)	55	74
1	G	185/286 (65%)	179 (97%)	6 (3%)	39	64
2	C	1150/1157 (99%)	1083 (94%)	67 (6%)	20	52
2	H	1150/1157 (99%)	1085 (94%)	65 (6%)	20	52
3	D	971/1168 (83%)	920 (95%)	51 (5%)	22	54
3	I	971/1168 (83%)	920 (95%)	51 (5%)	22	54
4	E	74/75 (99%)	72 (97%)	2 (3%)	44	68
4	J	65/75 (87%)	63 (97%)	2 (3%)	40	65
5	X	460/540 (85%)	443 (96%)	17 (4%)	34	61
5	Y	407/540 (75%)	391 (96%)	16 (4%)	32	60
All	All	6100/7024 (87%)	5808 (95%)	292 (5%)	25	56

5 of 292 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	I	151	MET
5	Y	477	GLU
3	I	325	LYS
3	I	867	GLN
3	D	505	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 90 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	517	GLN
2	H	1288	GLN
2	H	684	ASN
2	H	952	GLN
3	I	309	ASN

### 5.3.3 RNA ⓘ

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](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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
6	1RM	C	1401	-	79,82,82	1.71	14 (17%)	105,120,120	1.91	26 (24%)
6	1RM	H	1401	-	61,63,82	1.90	16 (26%)	84,96,120	1.84	21 (25%)

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
6	1RM	C	1401	-	-	38/68/97/97	0/7/8/8
6	1RM	H	1401	-	-	31/55/74/97	0/5/6/8

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	H	1401	1RM	O3-C6	7.86	1.52	1.37
6	C	1401	1RM	O3-C6	7.84	1.52	1.37
6	C	1401	1RM	O7-C25	-4.55	1.37	1.44
6	C	1401	1RM	C15-N1	4.45	1.45	1.37
6	H	1401	1RM	O7-C25	-4.45	1.38	1.44

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	1401	1RM	C6-C5-C11	-6.26	100.59	107.05
6	H	1401	1RM	C6-C5-C11	-5.72	101.15	107.05
6	C	1401	1RM	C38-N02-C42	5.35	124.91	111.23
6	C	1401	1RM	C9-C10-C5	-5.06	113.08	119.90
6	C	1401	1RM	C12-O3-C6	-4.90	99.42	107.68

There are no chirality outliers.

5 of 69 torsion outliers are listed below:

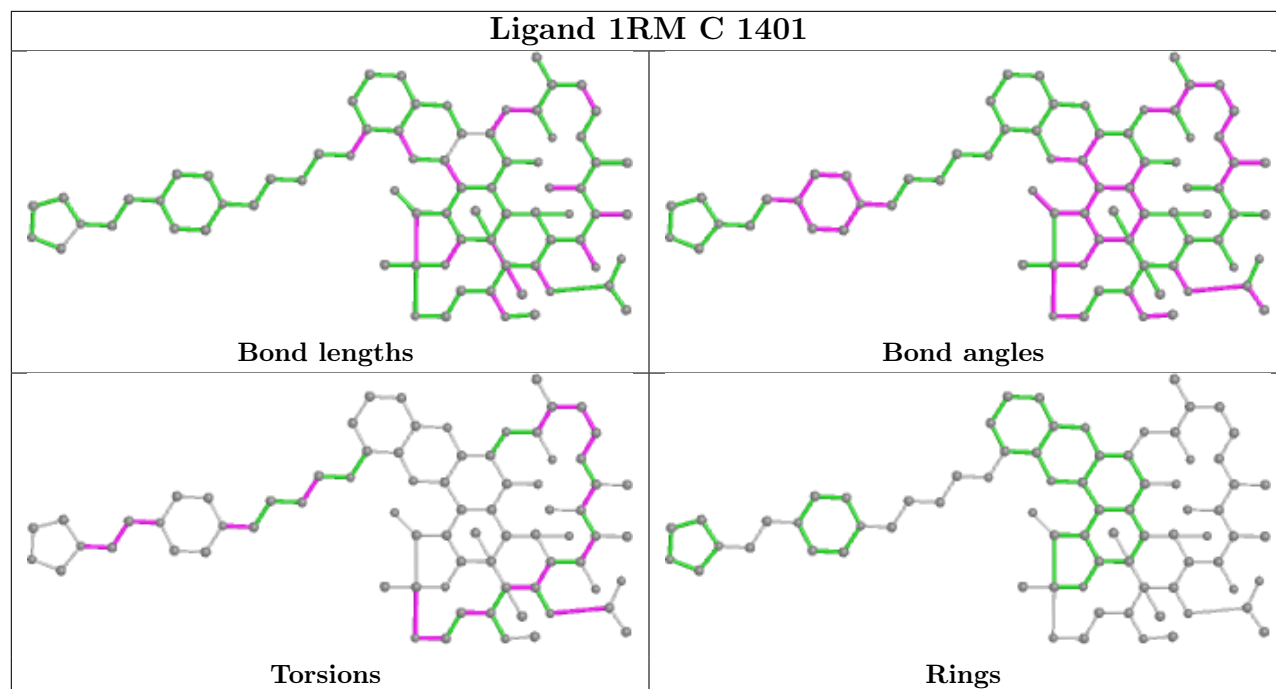
Mol	Chain	Res	Type	Atoms
6	C	1401	1RM	C11-C12-O5-C29
6	C	1401	1RM	C13-C12-O5-C29
6	C	1401	1RM	O3-C12-O5-C29
6	C	1401	1RM	C30-C16-C17-C18
6	C	1401	1RM	C31-C20-C21-C22

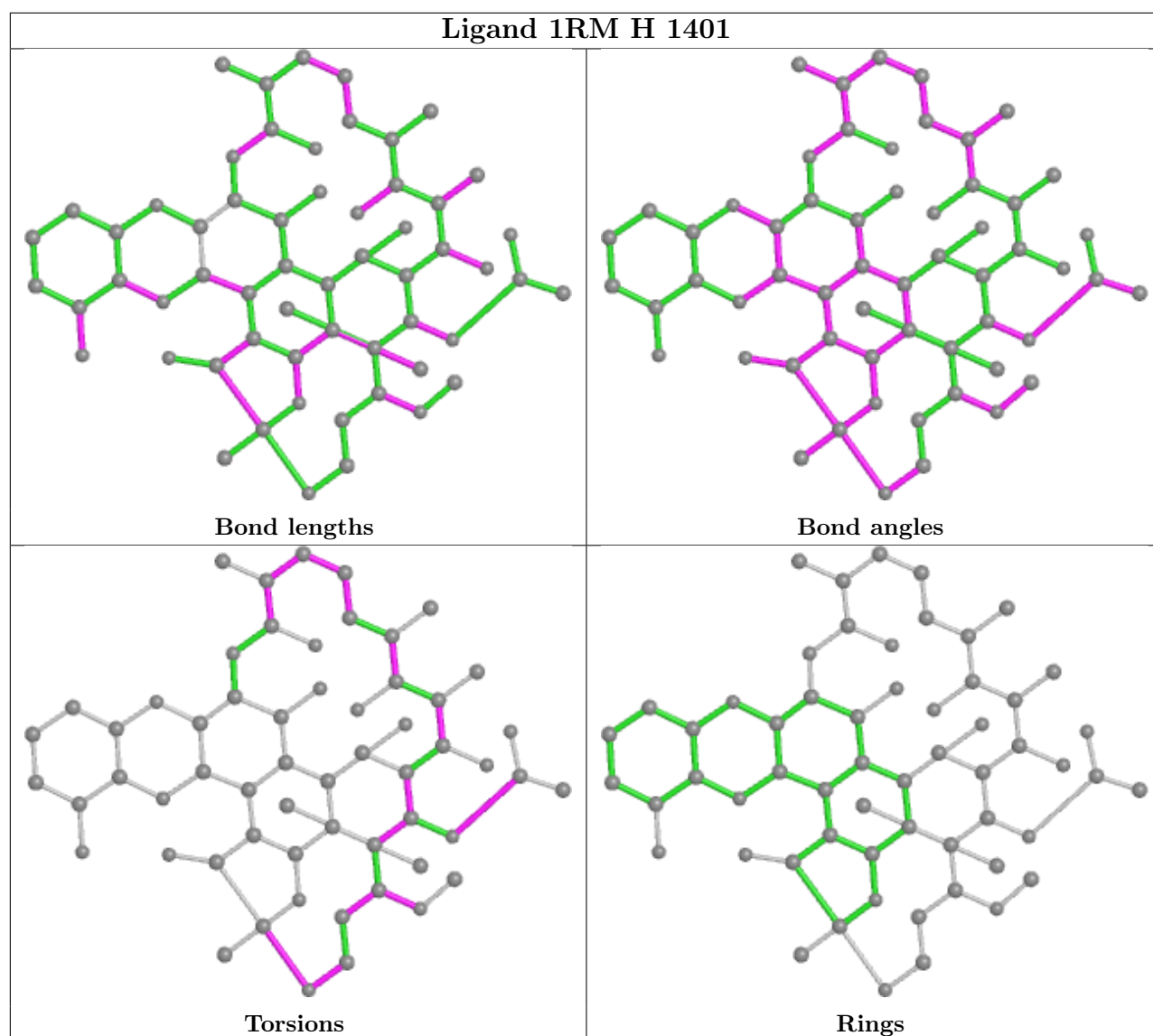
There are no ring outliers.

2 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	1401	1RM	9	0
6	H	1401	1RM	8	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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	323/329 (98%)	-0.12	8 (2%) 57 43	0, 59, 154, 247	0
1	B	221/329 (67%)	0.14	11 (4%) 28 20	5, 86, 172, 210	0
1	F	229/329 (69%)	0.19	13 (5%) 23 16	20, 107, 186, 257	0
1	G	217/329 (65%)	0.26	15 (6%) 16 11	23, 106, 166, 211	0
2	C	1335/1342 (99%)	-0.22	38 (2%) 53 39	0, 35, 155, 279	0
2	H	1335/1342 (99%)	0.03	73 (5%) 25 17	1, 78, 192, 314	0
3	D	1160/1407 (82%)	-0.16	27 (2%) 60 47	0, 30, 149, 264	0
3	I	1160/1407 (82%)	-0.01	52 (4%) 33 23	1, 49, 170, 288	0
4	E	90/91 (98%)	-0.40	1 (1%) 80 70	0, 32, 101, 141	0
4	J	76/91 (83%)	-0.06	3 (3%) 39 27	7, 72, 156, 198	0
5	X	517/613 (84%)	0.11	36 (6%) 16 10	1, 95, 219, 329	0
5	Y	458/613 (74%)	0.11	28 (6%) 21 14	2, 98, 217, 320	0
All	All	7121/8222 (86%)	-0.04	305 (4%) 35 25	0, 62, 183, 329	0

The worst 5 of 305 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	I	10	ALA	11.8
2	H	1002	LEU	9.5
2	H	1003	THR	7.8
5	Y	239	GLY	7.6
5	X	24	TYR	7.2

### 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](#)

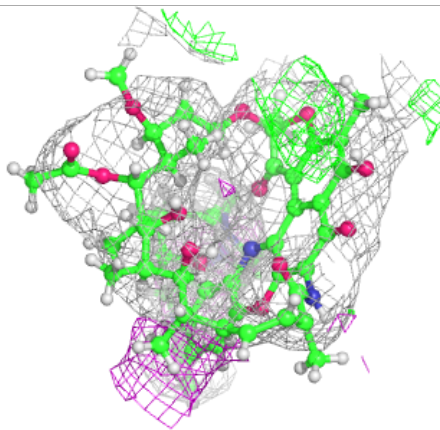
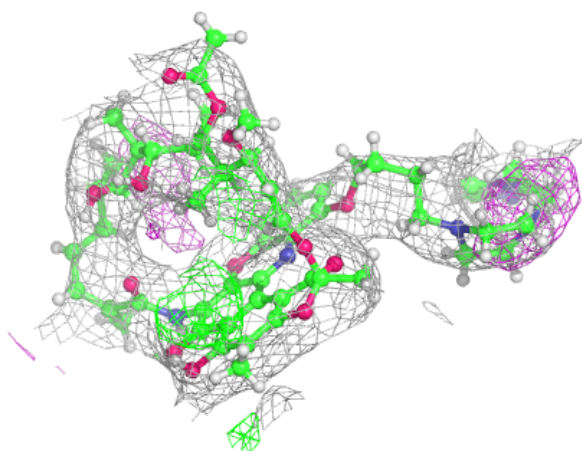
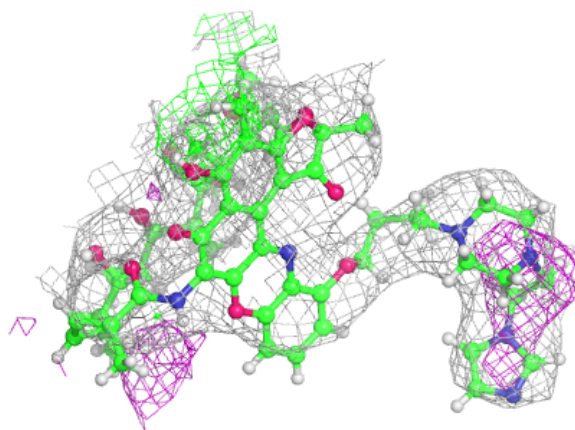
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

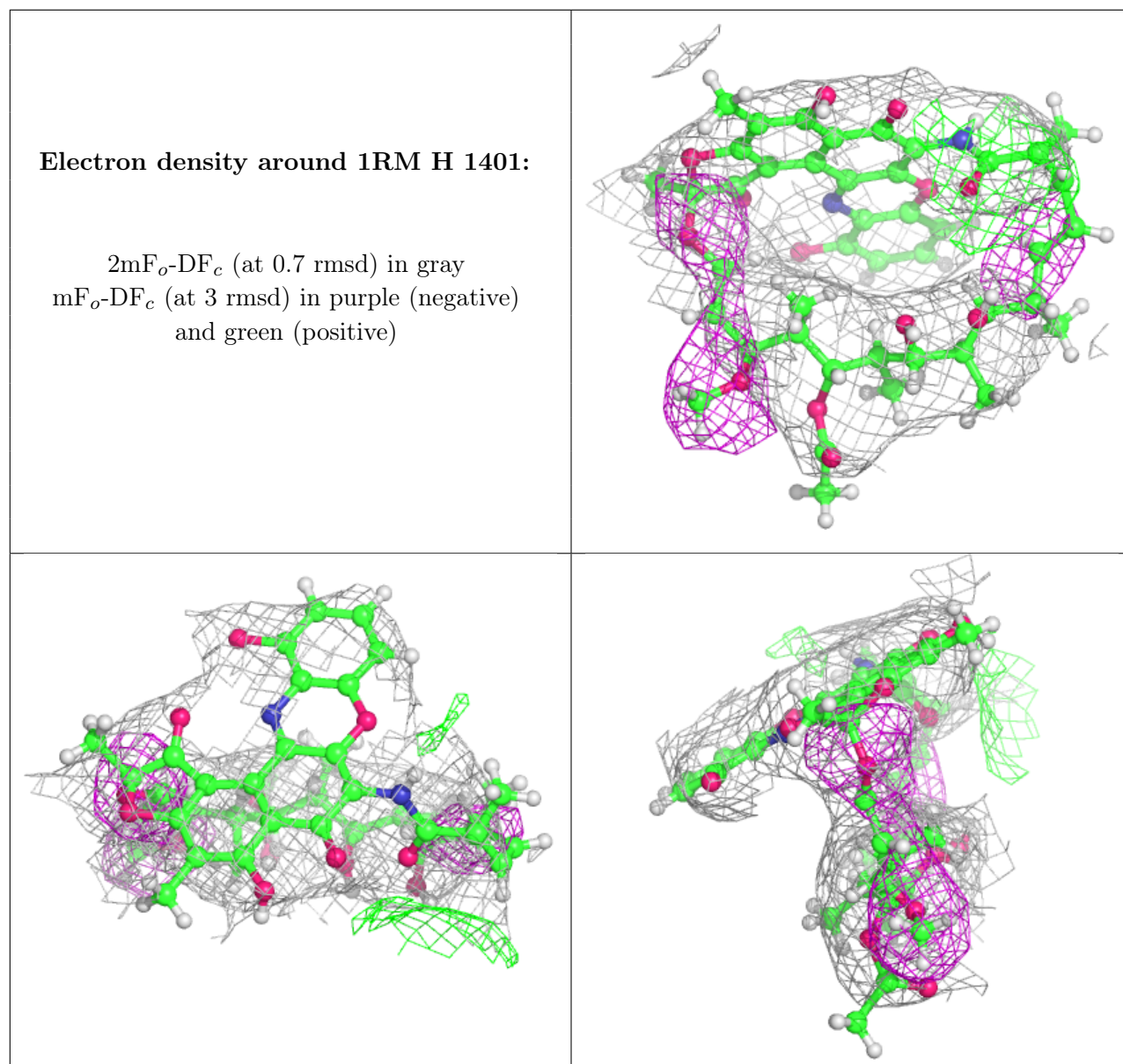
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	1RM	C	1401	75/75	0.76	0.37	20,20,20,20	0
6	1RM	H	1401	58/75	0.83	0.32	20,20,20,20	0
8	MG	D	1503	1/1	0.86	0.49	24,24,24,24	0
8	MG	I	1503	1/1	0.93	0.74	20,20,20,20	0
7	ZN	I	1501	1/1	0.96	0.10	60,60,60,60	0
7	ZN	D	1502	1/1	0.97	0.20	8,8,8,8	0
7	ZN	I	1502	1/1	0.97	0.15	49,49,49,49	0
7	ZN	D	1501	1/1	0.98	0.10	54,54,54,54	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 1RM C 1401:**

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





## 6.5 Other polymers [i](#)

There are no such residues in this entry.