



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 02:18 PM UTC

PDB ID : 4KN4 / pdb_00004kn4
Title : X-ray crystal structure of the Escherichia coli RNA polymerase in complex with Benzoxazinorifamycin-2b
Authors : Murakami, K.S.
Deposited on : 2013-05-08
Resolution : 3.96 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

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>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

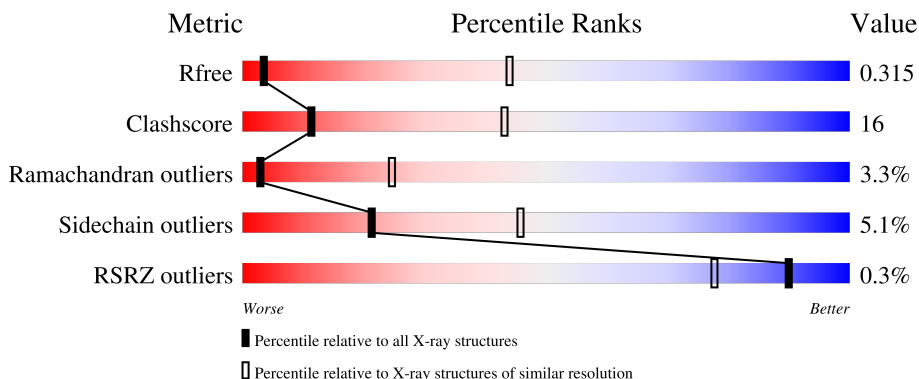
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.96 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}	180053	1046 (4.16-3.76)
Clashscore	190562	1019 (4.14-3.78)
Ramachandran outliers	187476	1031 (4.16-3.76)
Sidechain outliers	187428	1024 (4.16-3.76)
RSRZ outliers	180081	1046 (4.16-3.76)

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 ≥ 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	
1	B	329	
1	F	329	
1	G	329	
2	C	1342	

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Mol	Chain	Length	Quality of chain
2	H	1342	 67% 28% . .
3	D	1407	 48% 31% . 18%
3	I	1407	 50% 29% . 18%
4	E	91	 73% 22% . . .
4	J	91	 59% 21% . . 16%
5	X	613	 % 59% 23% . 16%
5	Y	613	 55% 18% . 25%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 56333 atoms, of which 122 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			

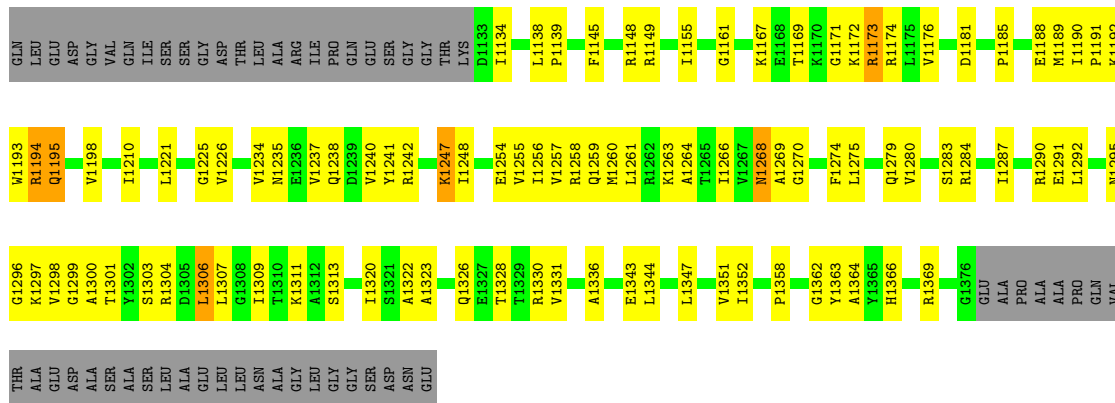
- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

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			

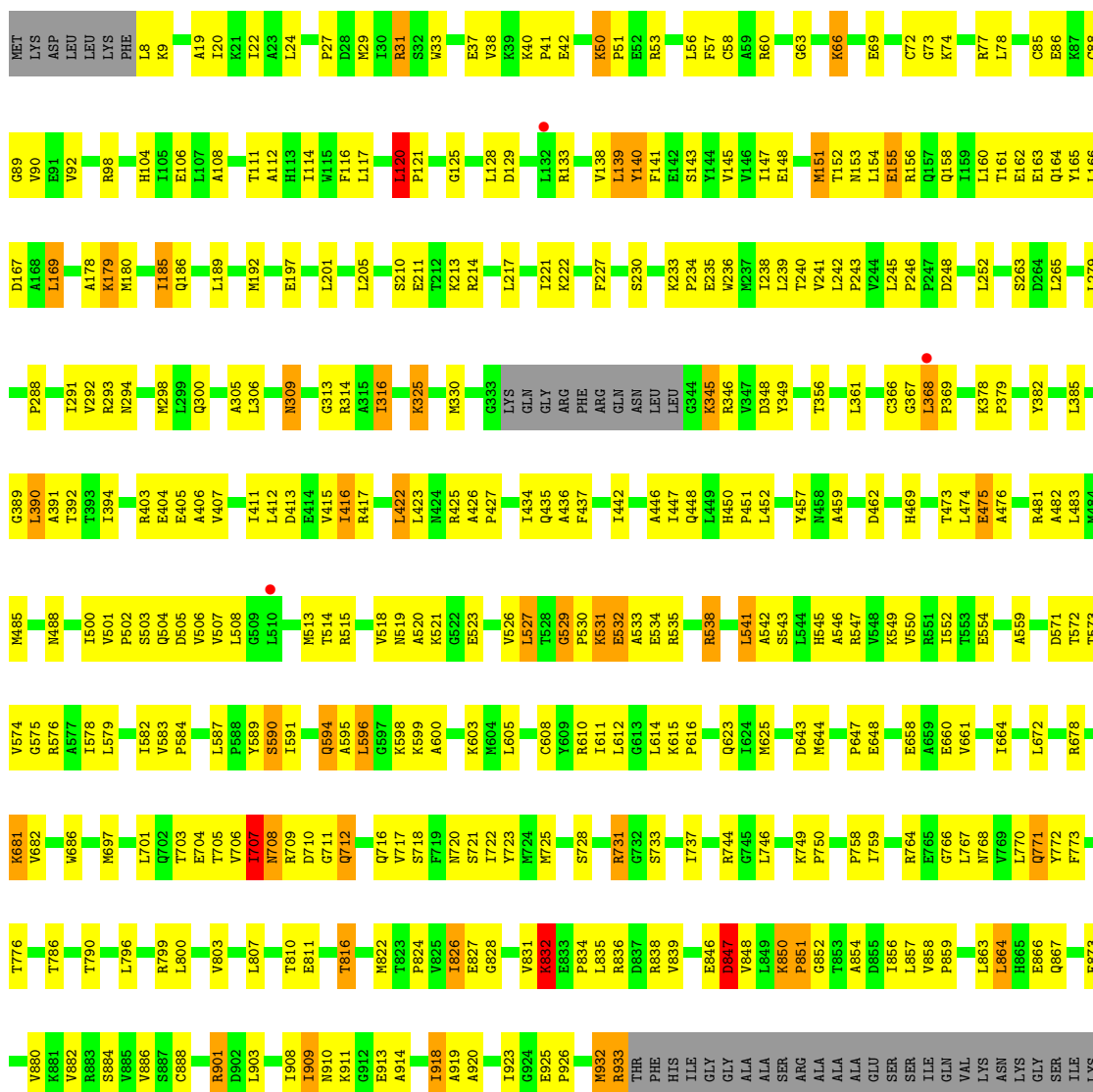
- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

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			

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	D	1	Total	Mg	0	0
			1	1		
8	I	1	Total	Mg	0	0
			1	1		



• 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, α , β , γ	184.68Å 203.97Å 307.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.77 – 3.96 29.77 – 3.96	Depositor EDS
% Data completeness (in resolution range)	94.5 (29.77-3.96) 89.6 (29.77-3.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 3.98Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.251 , 0.315 0.252 , 0.315	Depositor DCC
R_{free} test set	4761 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	151.9	Xtrriage
Anisotropy	0.117	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 74.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	56333	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.43% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: 1RL, ZN, MG

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	0.25	0/2548	0.72	1/3454 (0.0%)
1	B	0.25	0/1725	0.69	0/2337
1	F	0.26	0/1797	0.74	3/2436 (0.1%)
1	G	0.25	0/1690	0.68	0/2290
2	C	0.25	0/10690	0.72	7/14423 (0.0%)
2	H	0.25	0/10690	0.72	5/14423 (0.0%)
3	D	0.26	0/9198	0.74	7/12413 (0.1%)
3	I	0.26	0/9198	0.74	7/12413 (0.1%)
4	E	0.25	0/710	0.69	0/956
4	J	0.25	0/607	0.68	0/817
5	X	0.25	0/4253	0.70	0/5719
5	Y	0.25	0/3783	0.68	0/5083
All	All	0.25	0/56889	0.72	30/76764 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	120	LEU	CA-C-N	-7.20	112.00	120.13
3	I	120	LEU	C-N-CA	-7.20	112.00	120.13
3	D	120	LEU	CA-C-N	-7.01	112.21	120.13
3	D	120	LEU	C-N-CA	-7.01	112.21	120.13
2	C	42	ASP	CA-C-N	6.78	128.31	119.84

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	68	0
1	B	1706	0	1738	62	0
1	F	1775	0	1800	40	0
1	G	1671	0	1706	46	0
2	C	10523	0	10546	385	0
2	H	10523	0	10546	357	0
3	D	9060	0	9256	404	0
3	I	9060	0	9255	364	0
4	E	708	0	719	21	0
4	J	605	0	612	18	0
5	X	4198	0	4250	115	0
5	Y	3732	0	3809	81	0
6	C	65	61	61	5	0
6	H	65	61	61	10	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	56211	122	56925	1828	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 16.

The worst 5 of 1828 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)
3:I:1173:ARG:HA	3:I:1174:ARG:HB2	1.32	1.10
2:H:1119:MET:HG2	2:H:1228:GLY:HA2	1.34	1.09
3:D:1173:ARG:HA	3:D:1174:ARG:HB2	1.30	1.06
3:D:310:GLY:HA3	3:D:311:ARG:HB2	1.34	1.04
2:C:42:ASP:HB3	2:C:43:PRO:HD2	1.35	1.03

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%)	263 (82%)	42 (13%)	16 (5%)	1	18
1	B	217/329 (66%)	187 (86%)	25 (12%)	5 (2%)	5	31
1	F	227/329 (69%)	195 (86%)	27 (12%)	5 (2%)	5	31
1	G	213/329 (65%)	188 (88%)	22 (10%)	3 (1%)	9	39
2	C	1333/1342 (99%)	1087 (82%)	204 (15%)	42 (3%)	3	25
2	H	1333/1342 (99%)	1091 (82%)	197 (15%)	45 (3%)	3	24
3	D	1154/1407 (82%)	933 (81%)	180 (16%)	41 (4%)	2	23
3	I	1154/1407 (82%)	934 (81%)	180 (16%)	40 (4%)	3	23
4	E	88/91 (97%)	77 (88%)	6 (7%)	5 (6%)	1	17
4	J	74/91 (81%)	64 (86%)	5 (7%)	5 (7%)	1	14
5	X	511/613 (83%)	453 (89%)	44 (9%)	14 (3%)	4	28
5	Y	454/613 (74%)	414 (91%)	30 (7%)	10 (2%)	5	31
All	All	7079/8222 (86%)	5886 (83%)	962 (14%)	231 (3%)	3	24

5 of 231 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	PRO
1	A	319	GLU
1	B	20	SER
2	C	21	VAL
2	C	39	ILE

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%)	272 (97%)	9 (3%)	34	56
1	B	189/286 (66%)	183 (97%)	6 (3%)	34	56
1	F	197/286 (69%)	194 (98%)	3 (2%)	57	70
1	G	185/286 (65%)	184 (100%)	1 (0%)	81	82
2	C	1150/1157 (99%)	1084 (94%)	66 (6%)	18	44
2	H	1150/1157 (99%)	1084 (94%)	66 (6%)	18	44
3	D	971/1168 (83%)	909 (94%)	62 (6%)	16	41
3	I	971/1168 (83%)	908 (94%)	63 (6%)	15	41
4	E	74/75 (99%)	71 (96%)	3 (4%)	27	50
4	J	65/75 (87%)	61 (94%)	4 (6%)	16	42
5	X	460/540 (85%)	444 (96%)	16 (4%)	32	54
5	Y	407/540 (75%)	392 (96%)	15 (4%)	30	53
All	All	6100/7024 (87%)	5786 (95%)	314 (5%)	21	46

5 of 314 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	1339	LEU
3	I	932	MET
3	I	114	ILE
3	I	500	ILE
5	Y	266	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 74 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	1134	GLN
4	J	15	ASN
2	H	1264	GLN
3	I	465	GLN
3	D	164	GLN

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 oligosaccharides 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	1RL	H	1401	-	68,70,70	3.29	21 (30%)	89,104,104	2.31	32 (35%)
6	1RL	C	1401	-	68,70,70	3.30	20 (29%)	89,104,104	2.18	23 (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	1RL	H	1401	-	-	31/65/84/84	0/5/6/6
6	1RL	C	1401	-	-	32/65/84/84	0/5/6/6

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1401	1RL	O3-C6	12.53	1.60	1.37
6	H	1401	1RL	O3-C6	12.52	1.60	1.37
6	C	1401	1RL	C6-C7	10.81	1.58	1.39
6	H	1401	1RL	C6-C7	10.71	1.58	1.39
6	C	1401	1RL	C5-C6	-8.19	1.29	1.39

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	1401	1RL	C20-C19-C18	-8.33	108.88	126.11
6	H	1401	1RL	C12-O3-C6	-7.70	94.83	107.69
6	H	1401	1RL	C8-C7-C6	-7.56	106.66	116.86
6	C	1401	1RL	C12-O3-C6	-7.50	95.17	107.69
6	C	1401	1RL	C8-C7-C6	-7.16	107.20	116.86

There are no chirality outliers.

5 of 63 torsion outliers are listed below:

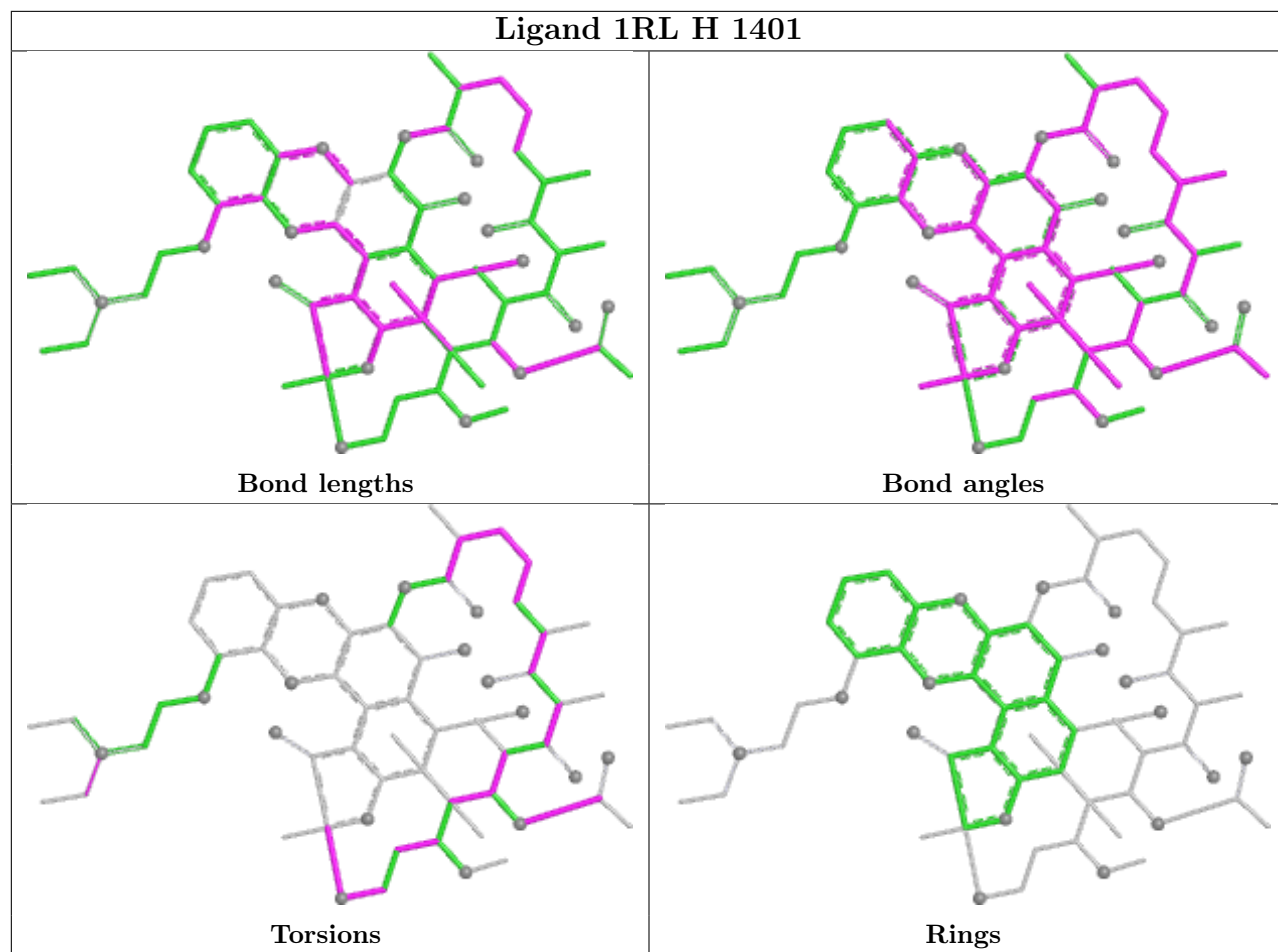
Mol	Chain	Res	Type	Atoms
6	C	1401	1RL	C11-C12-O5-C29
6	C	1401	1RL	C13-C12-O5-C29
6	C	1401	1RL	C16-C17-C18-C19
6	C	1401	1RL	C19-C20-C21-O10
6	C	1401	1RL	C31-C20-C21-C22

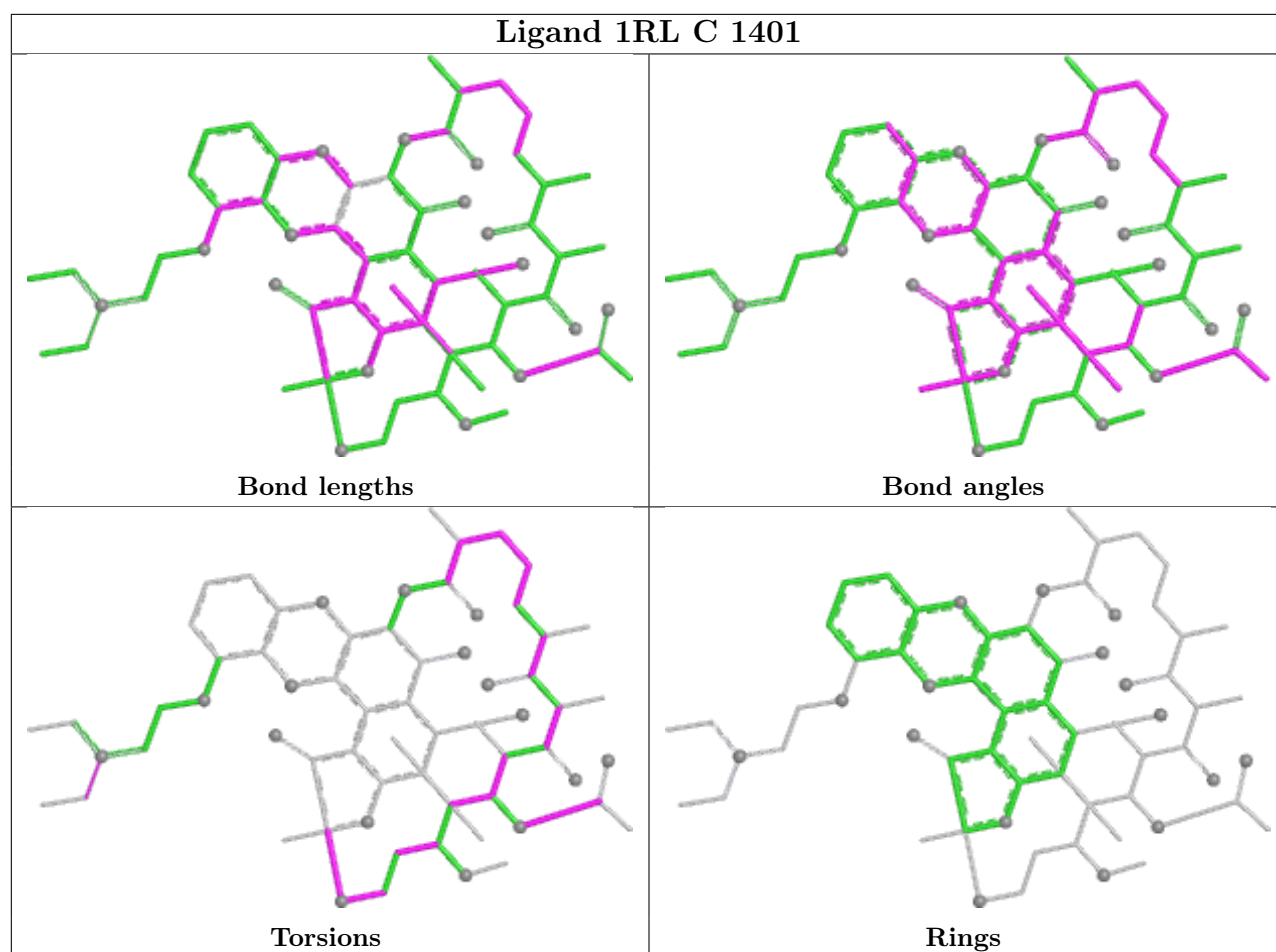
There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	H	1401	1RL	10	0
6	C	1401	1RL	5	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, 95th 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 ²)	Q<0.9
1	A	323/329 (98%)	-0.68	0 100 100	0, 68, 172, 270	0
1	B	221/329 (67%)	-0.50	1 (0%) 87 72	6, 90, 201, 277	0
1	F	229/329 (69%)	-0.43	1 (0%) 88 75	9, 123, 209, 249	0
1	G	217/329 (65%)	-0.49	2 (0%) 81 62	34, 112, 176, 230	0
2	C	1335/1342 (99%)	-0.56	5 (0%) 88 75	0, 43, 165, 367	0
2	H	1335/1342 (99%)	-0.63	0 100 100	0, 81, 205, 388	0
3	D	1160/1407 (82%)	-0.59	1 (0%) 92 87	0, 34, 158, 313	0
3	I	1160/1407 (82%)	-0.58	4 (0%) 90 78	0, 50, 190, 338	0
4	E	90/91 (98%)	-0.74	0 100 100	0, 34, 108, 170	0
4	J	76/91 (83%)	-0.75	0 100 100	3, 75, 160, 201	0
5	X	517/613 (84%)	-0.60	4 (0%) 82 64	1, 99, 236, 425	0
5	Y	458/613 (74%)	-0.61	2 (0%) 88 75	1, 102, 234, 374	0
All	All	7121/8222 (86%)	-0.59	20 (0%) 90 78	0, 66, 199, 425	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	I	1215	GLU	4.2
2	C	194	LEU	3.6
5	X	56	MET	3.5
1	G	39	LEU	3.5
5	X	497	VAL	3.0

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

There are no oligosaccharides in this entry.

6.4 Ligands

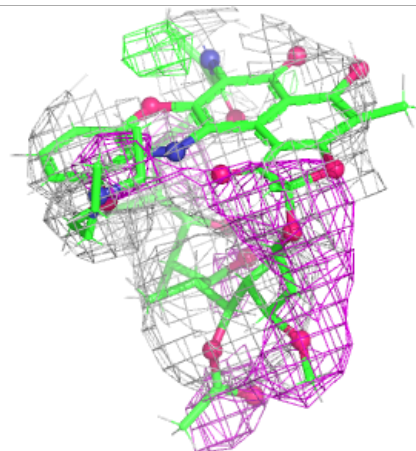
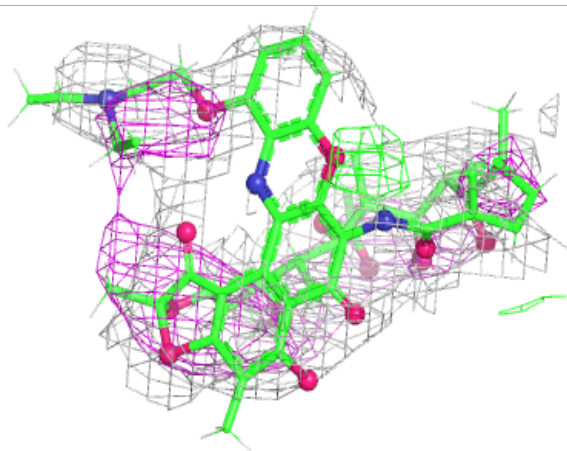
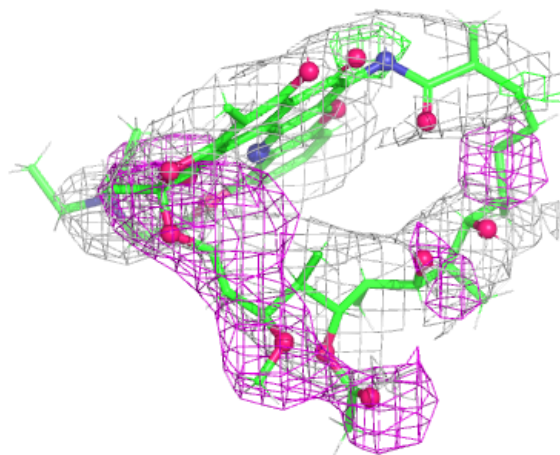
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

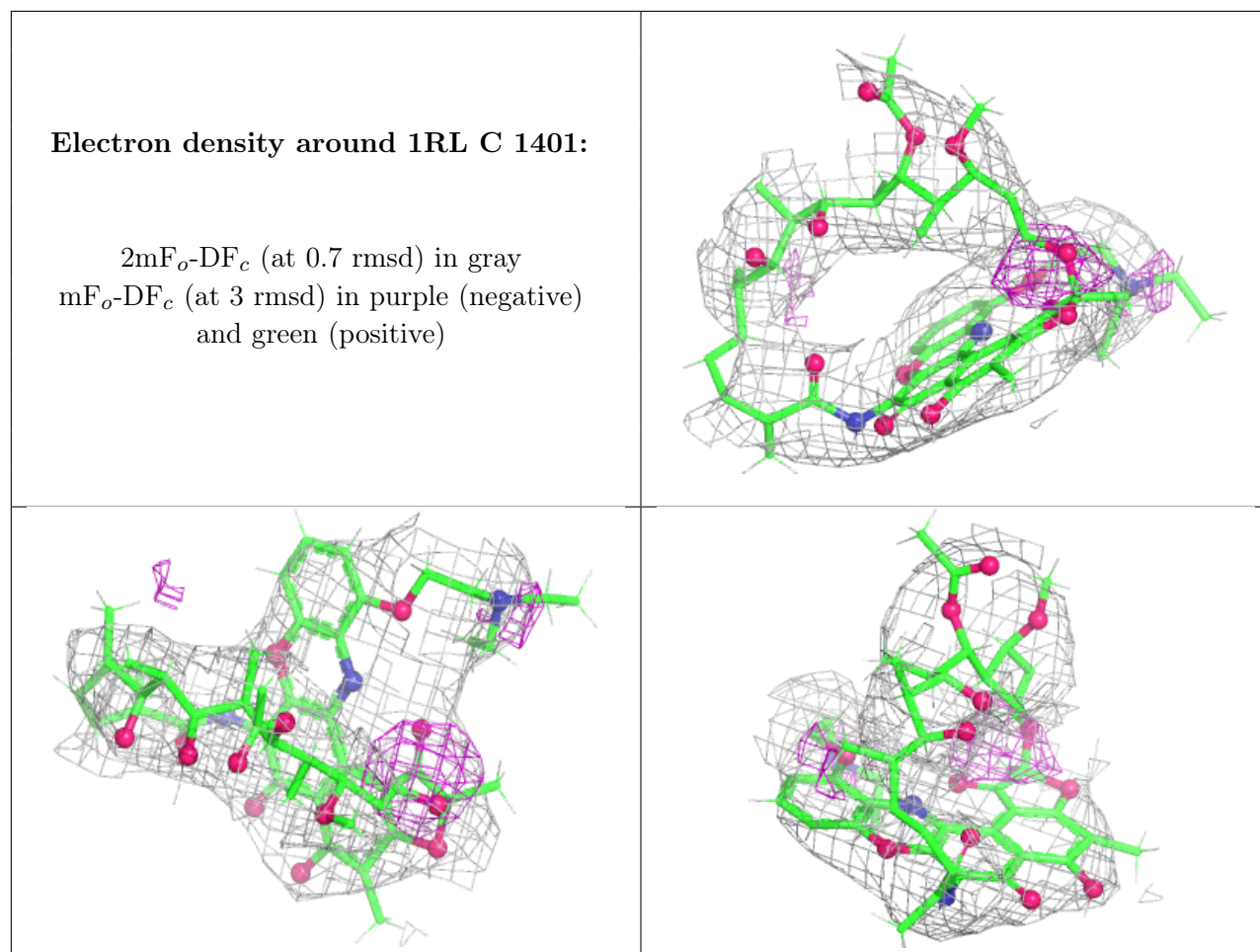
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	1RL	H	1401	65/65	0.82	0.09	20,20,20,20	0
6	1RL	C	1401	65/65	0.89	0.07	20,20,20,20	0
8	MG	I	1503	1/1	0.92	0.19	20,20,20,20	0
8	MG	D	1503	1/1	0.96	0.08	24,24,24,24	0
7	ZN	D	1501	1/1	0.98	0.03	54,54,54,54	0
7	ZN	I	1502	1/1	0.99	0.06	49,49,49,49	0
7	ZN	I	1501	1/1	1.00	0.01	60,60,60,60	0
7	ZN	D	1502	1/1	1.00	0.04	8,8,8,8	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 1RL H 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.