



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 27, 2022 – 02:14 PM JST

PDB ID : 7CJL
Title : Metallo-Beta-Lactamase VIM-2 in complex with (S)-N-(3-(2H-tetrazol-5-yl)phenyl)-3-mercapto-2-methylpropanamide
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Deposited on : 2020-07-11
Resolution : 1.79 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

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 : 4.02b-467
Mogul : ?? (???), CSD ??CSD?? (????)
Xtriage (Phenix) : 1.13
EDS : 2.29
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) : 2.29

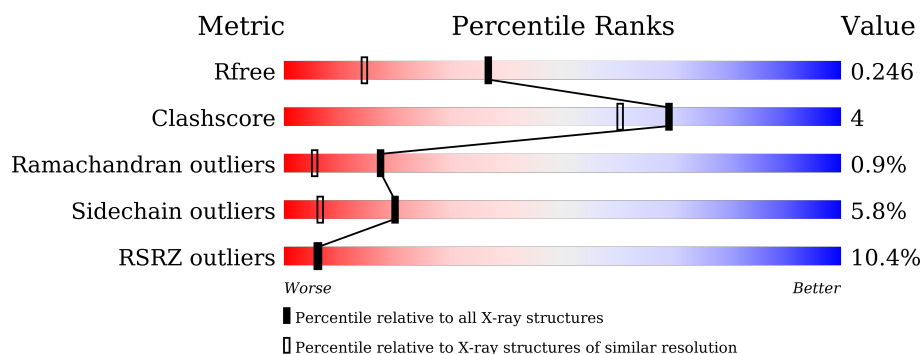
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.79 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	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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	231	<div> <div>15%</div> <div>85%</div> <div>15%</div> </div>
1	B	231	<div> <div>6%</div> <div>88%</div> <div>11%</div> <div>.</div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3749 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.

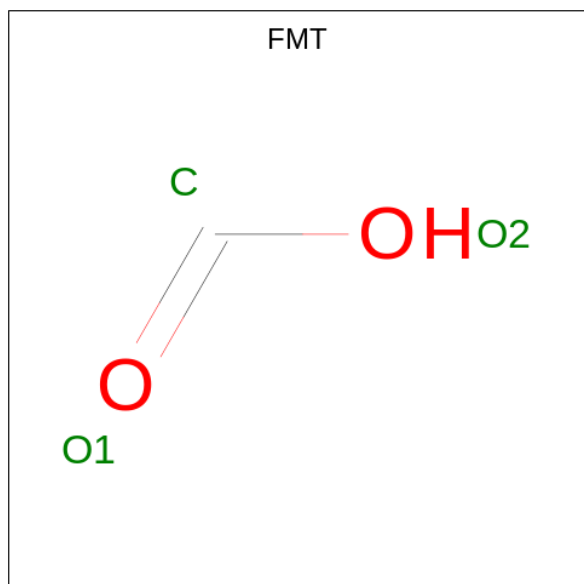
- Molecule 1 is a protein called Beta-lactamase class B VIM-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	231	Total	C	N	O	S	0	0	0
			1730	1093	299	337	1			
1	A	231	Total	C	N	O	S	0	0	0
			1726	1090	298	337	1			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

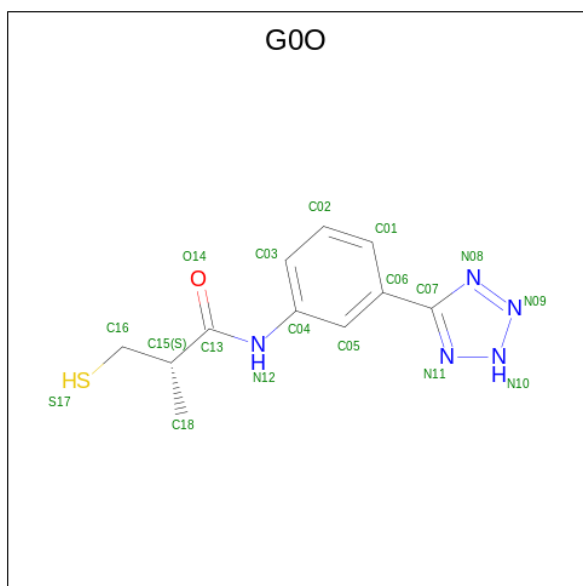
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			3	1	2		

- Molecule 4 is (S)-N-(3-(2H-tetrazol-5-yl)phenyl)-3-mercapto-2-methylpropanamide (three-letter code: G0O) (formula: C₁₁H₁₃N₅OS) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			18	11	5	1	1		
4	A	1	Total	C	N	O	S	0	0
			18	11	5	1	1		

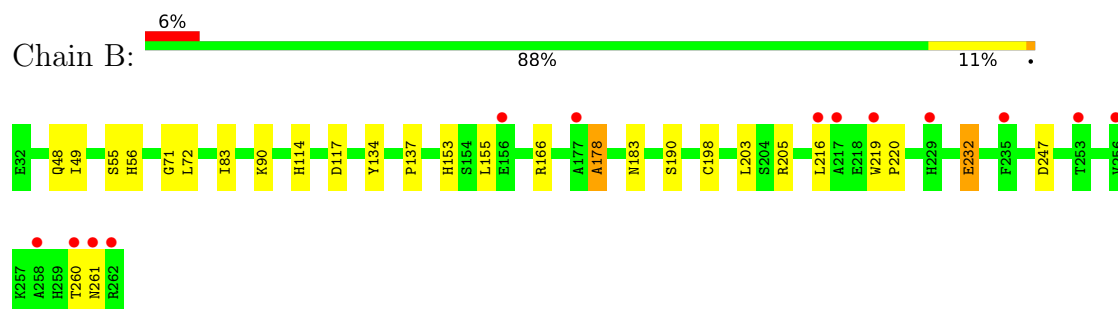
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	128	Total	O	0	0
			128	128		
5	A	122	Total	O	0	0
			122	122		

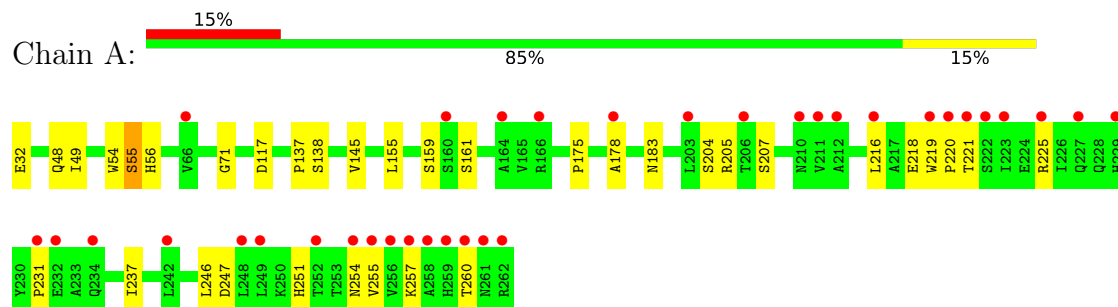
3 Residue-property plots

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: Beta-lactamase class B VIM-2



- Molecule 1: Beta-lactamase class B VIM-2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	45.36Å 90.13Å 125.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.07 – 1.79 45.07 – 1.79	Depositor EDS
% Data completeness (in resolution range)	85.5 (45.07-1.79) 85.5 (45.07-1.79)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 1.79Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.205 , 0.246 0.214 , 0.246	Depositor DCC
R_{free} test set	1999 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 49.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3749	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.56 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.6858e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: G0O, ZN, FMT

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	0.69	2/1767 (0.1%)	0.74	0/2421
1	B	0.67	0/1771	0.72	0/2425
All	All	0.68	2/3538 (0.1%)	0.73	0/4846

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	55	SER	CB-OG	-6.85	1.33	1.42
1	A	54	TRP	CB-CG	-5.04	1.41	1.50

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	1726	0	1663	13	0
1	B	1730	0	1674	12	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	B	3	0	1	0	0
4	A	18	0	0	0	0
4	B	18	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	122	0	0	2	1
5	B	128	0	0	2	0
All	All	3749	0	3338	25	1

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 4.

All (25) 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:32:GLU:N	5:A:401:HOH:O	2.03	0.91
1:A:251:HIS:O	1:A:255:VAL:HG23	1.99	0.62
1:A:216:LEU:H	1:A:216:LEU:HD12	1.68	0.58
1:B:216:LEU:O	5:B:401:HOH:O	2.18	0.56
1:B:247:ASP:OD1	1:B:247:ASP:N	2.39	0.53
1:A:56:HIS:CE1	1:A:71:GLY:HA3	2.44	0.53
1:A:49:ILE:HD13	1:A:237:ILE:HD11	1.93	0.51
1:A:221:THR:O	1:A:225:ARG:HG3	2.10	0.50
1:A:49:ILE:HD11	1:A:55:SER:HB3	1.96	0.48
1:B:178:ALA:HB1	1:B:219:TRP:CD1	2.48	0.48
1:B:56:HIS:CE1	1:B:71:GLY:HA3	2.49	0.48
1:A:257:LYS:O	1:A:260:THR:N	2.47	0.47
1:A:145:VAL:O	5:A:402:HOH:O	2.20	0.46
1:B:219:TRP:HB3	1:B:220:PRO:HD3	1.99	0.44
1:A:219:TRP:HB3	1:A:220:PRO:HD3	1.99	0.43
1:A:231:PRO:O	1:A:246:LEU:HD11	2.19	0.43
1:B:134:TYR:CD2	1:B:153:HIS:HB2	2.55	0.42
1:A:137:PRO:HD3	1:A:155:LEU:O	2.20	0.42
1:B:90:LYS:HE2	5:B:514:HOH:O	2.18	0.42
1:B:232:GLU:CD	1:B:232:GLU:H	2.23	0.42
1:B:114:HIS:HE1	1:B:198:CYS:SG	2.43	0.41
1:B:49:ILE:HD11	1:B:55:SER:HB3	2.02	0.41
1:B:72:LEU:HB3	1:B:83:ILE:HB	2.03	0.41
1:B:137:PRO:HD3	1:B:155:LEU:O	2.21	0.40
1:A:231:PRO:O	1:A:246:LEU:CD1	2.69	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:486:HOH:O	5:A:500:HOH:O[4_476]	2.03	0.17

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	229/231 (99%)	215 (94%)	11 (5%)	3 (1%)	12	3
1	B	229/231 (99%)	223 (97%)	5 (2%)	1 (0%)	34	19
All	All	458/462 (99%)	438 (96%)	16 (4%)	4 (1%)	17	5

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	178	ALA
1	B	178	ALA
1	A	161	SER
1	A	175	PRO

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	180/184 (98%)	169 (94%)	11 (6%)	18	6
1	B	181/184 (98%)	171 (94%)	10 (6%)	21	7
All	All	361/368 (98%)	340 (94%)	21 (6%)	20	6

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	48	GLN
1	B	117	ASP
1	B	166	ARG
1	B	183	ASN
1	B	190	SER
1	B	203	LEU
1	B	205	ARG
1	B	232	GLU
1	B	260	THR
1	B	261	ASN
1	A	48	GLN
1	A	117	ASP
1	A	138	SER
1	A	159	SER
1	A	183	ASN
1	A	204	SER
1	A	205	ARG
1	A	207	SER
1	A	218	GLU
1	A	247	ASP
1	A	254	ASN

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

Mol	Chain	Res	Type
1	A	48	GLN

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 ⓘ

Of 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

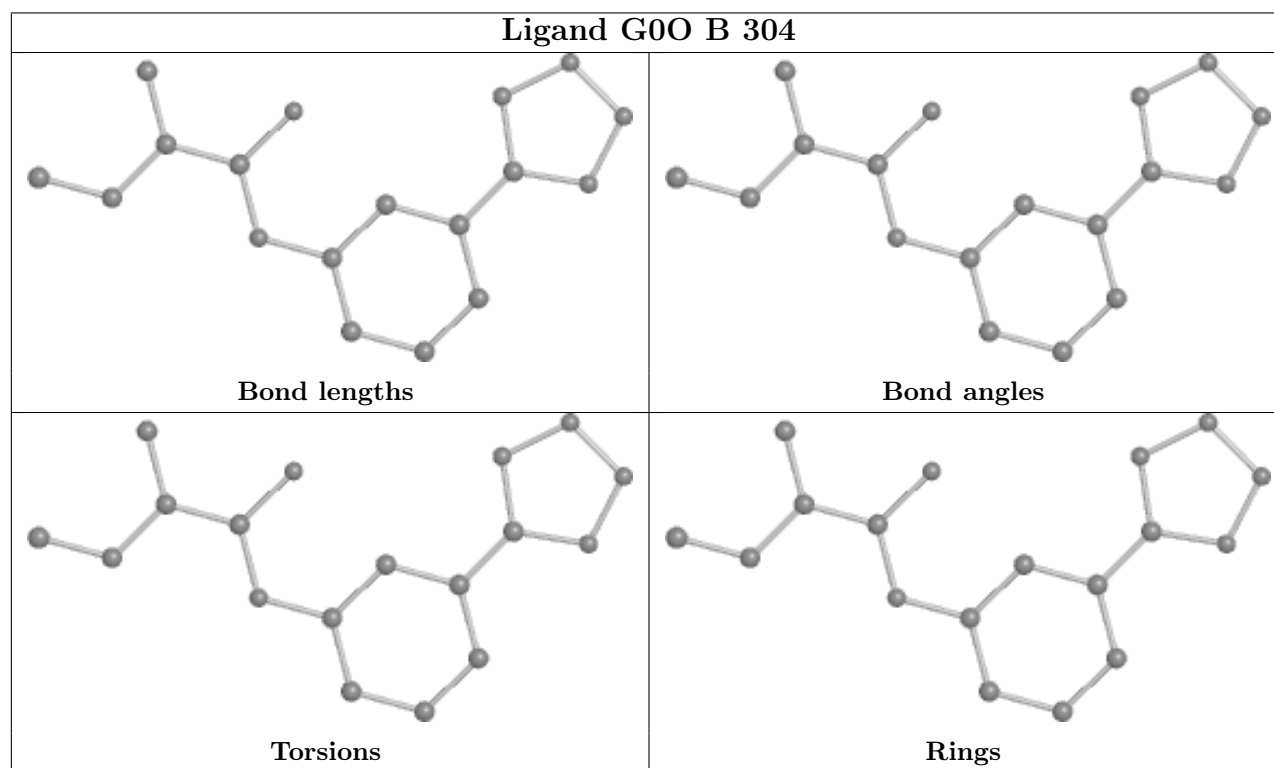
There are no chirality outliers.

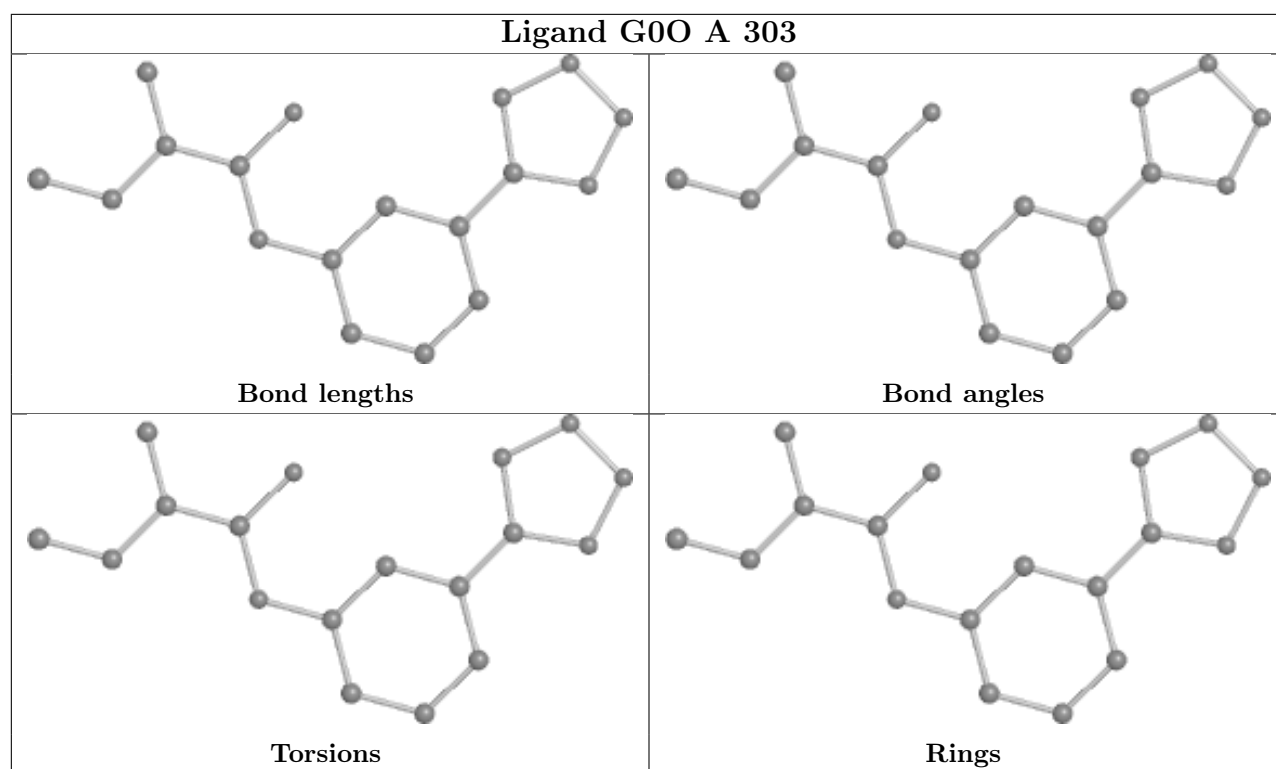
There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

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, 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	231/231 (100%)	0.93	35 (15%) 2 2	10, 25, 56, 84	0
1	B	231/231 (100%)	0.75	13 (5%) 24 23	11, 26, 47, 83	0
All	All	462/462 (100%)	0.84	48 (10%) 6 6	10, 26, 51, 84	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	261	ASN	6.5
1	A	260	THR	6.5
1	B	261	ASN	6.4
1	B	260	THR	5.3
1	B	262	ARG	5.2
1	A	206	THR	3.9
1	A	254	ASN	3.9
1	B	258	ALA	3.9
1	A	258	ALA	3.9
1	A	256	VAL	3.8
1	B	256	VAL	3.7
1	A	221	THR	3.7
1	B	229	HIS	3.6
1	A	231	PRO	3.6
1	A	262	ARG	3.5
1	B	177	ALA	3.2
1	A	223	ILE	3.1
1	A	203	LEU	3.1
1	A	255	VAL	3.0
1	A	259	HIS	2.9
1	A	210	ASN	2.9
1	A	252	THR	2.9
1	A	227	GLN	2.9
1	A	216	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	242	LEU	2.8
1	A	220	PRO	2.7
1	A	212	ALA	2.6
1	A	178	ALA	2.6
1	A	219	TRP	2.6
1	A	225	ARG	2.6
1	B	156	GLU	2.5
1	A	166	ARG	2.4
1	B	216	LEU	2.4
1	A	211	VAL	2.4
1	B	235	PHE	2.3
1	A	232	GLU	2.3
1	A	229	HIS	2.2
1	A	164	ALA	2.2
1	A	248	LEU	2.2
1	A	160	SER	2.2
1	A	222	SER	2.2
1	A	66	VAL	2.2
1	B	219	TRP	2.1
1	B	217	ALA	2.1
1	A	249	LEU	2.0
1	B	253	THR	2.0
1	A	234	GLN	2.0
1	A	257	LYS	2.0

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 [i](#)

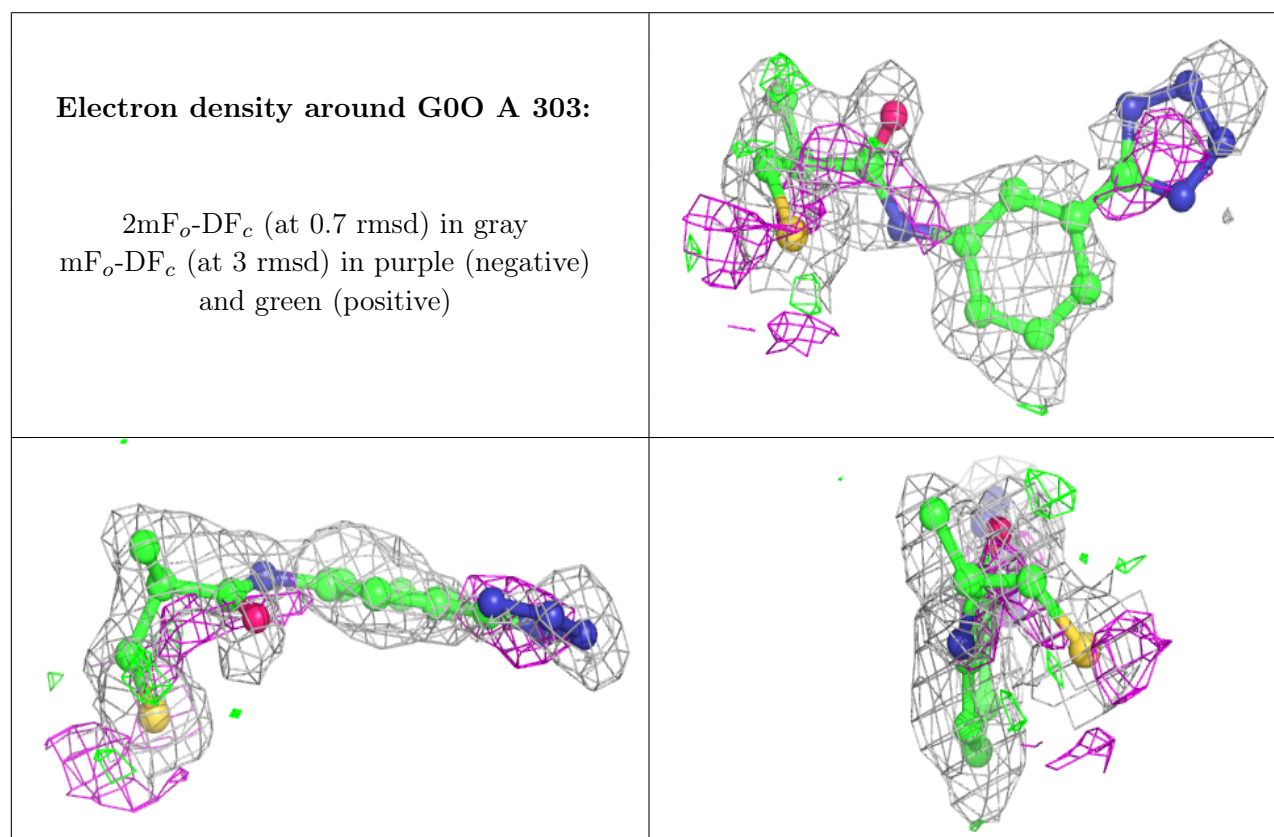
There are no monosaccharides in this entry.

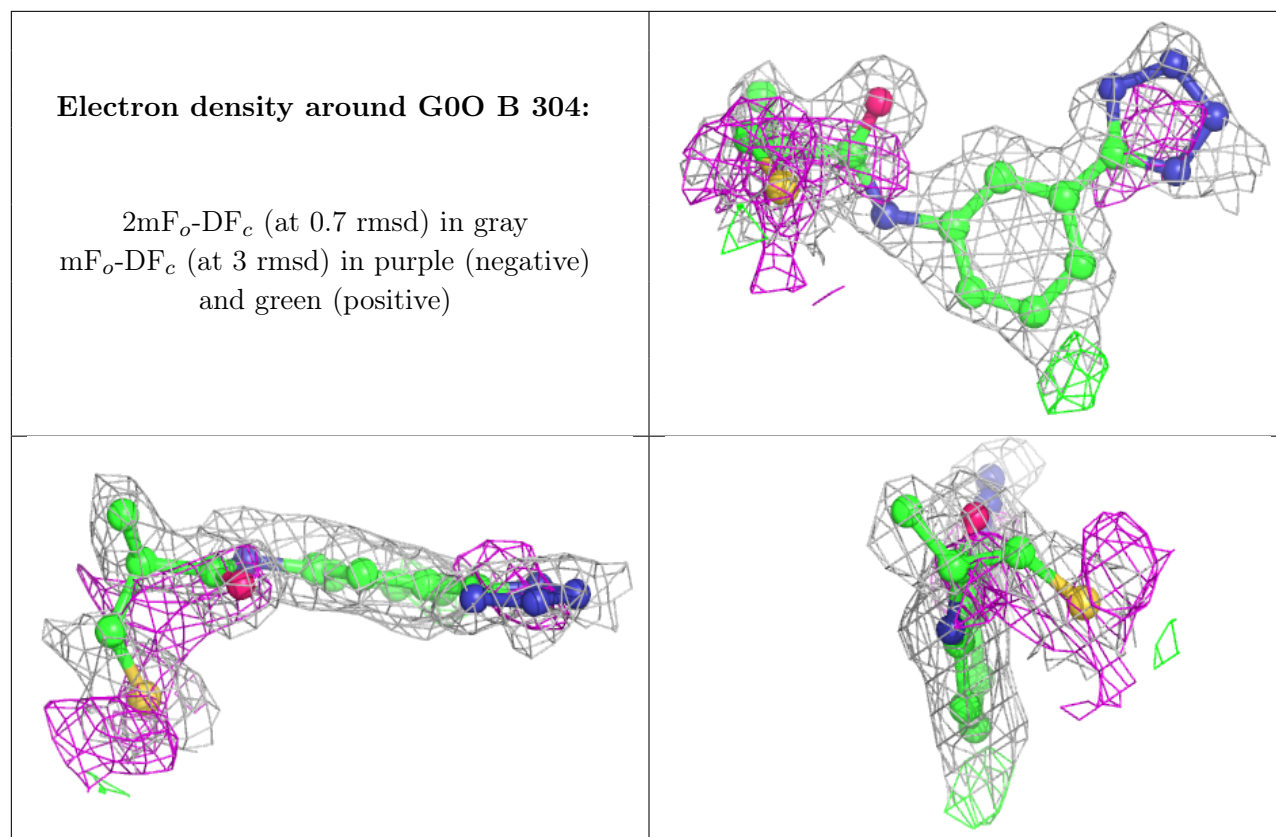
6.4 Ligands [i](#)

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, 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
4	G0O	A	303	18/18	0.76	0.23	28,44,61,62	0
3	FMT	B	303	3/3	0.81	0.20	26,26,39,49	0
4	G0O	B	304	18/18	0.84	0.21	27,32,55,55	0
2	ZN	A	302	1/1	0.98	0.09	28,28,28,28	0
2	ZN	A	301	1/1	0.98	0.09	27,27,27,27	0
2	ZN	B	301	1/1	0.99	0.09	21,21,21,21	0
2	ZN	B	302	1/1	1.00	0.09	23,23,23,23	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.