wwPDB X-ray Structure Validation Summary Report (i)

Sep 6, 2023 – 01:12 AM EDT

PDB ID	:	3VDD
Title	:	Structure of HRV2 capsid complexed with antiviral compound BTA798
Authors	:	Morton, C.J.; Feil, S.C.; Parker, M.W.
Deposited on	:	2012-01-05
Resolution	:	3.20 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 (i) 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 (i)) were used in the production of this report:

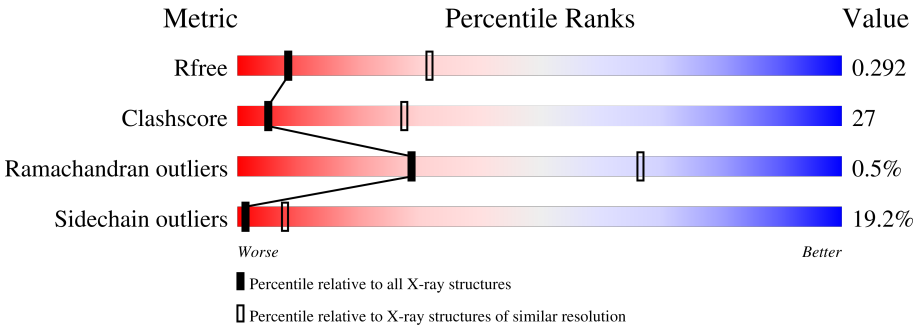
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	283	54% 36% 8% ··
2	B	261	52% 34% 9% ·
3	C	237	51% 37% 12%
4	D	69	28% 12% 13% 48%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	BT8	A	301	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6380 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 Protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	280	Total	C	N	O	S	0	0	0
			2248	1414	391	432	11			

- Molecule 2 is a protein called Protein VP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	251	Total	C	N	O	S	0	0	0
			1975	1252	343	372	8			

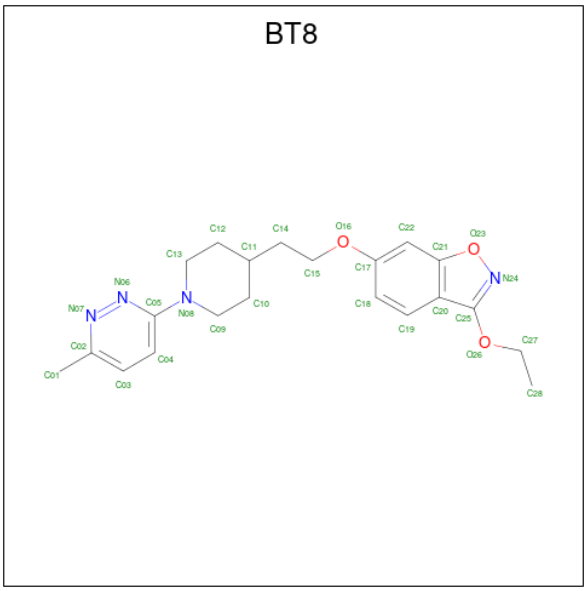
- Molecule 3 is a protein called Protein VP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	237	Total	C	N	O	S	0	0	0
			1834	1172	304	346	12			

- Molecule 4 is a protein called Protein VP4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	36	Total	C	N	O	0	0	0
			283	182	44	57			

- Molecule 5 is 3-ethoxy-6-{2-[1-(6-methylpyridazin-3-yl)piperidin-4-yl]ethoxy}-1,2-benzoxazole (three-letter code: BT8) (formula: $C_{21}H_{26}N_4O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O 28 21 4 3	0	0

- Molecule 6 is water.

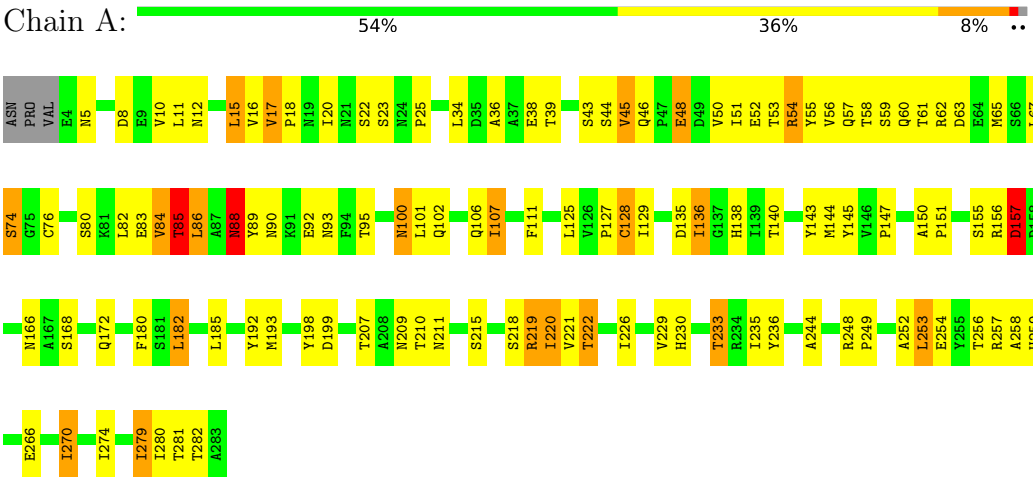
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	6	Total O 6 6	0	0
6	B	3	Total O 3 3	0	0
6	C	3	Total O 3 3	0	0

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. 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. 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.

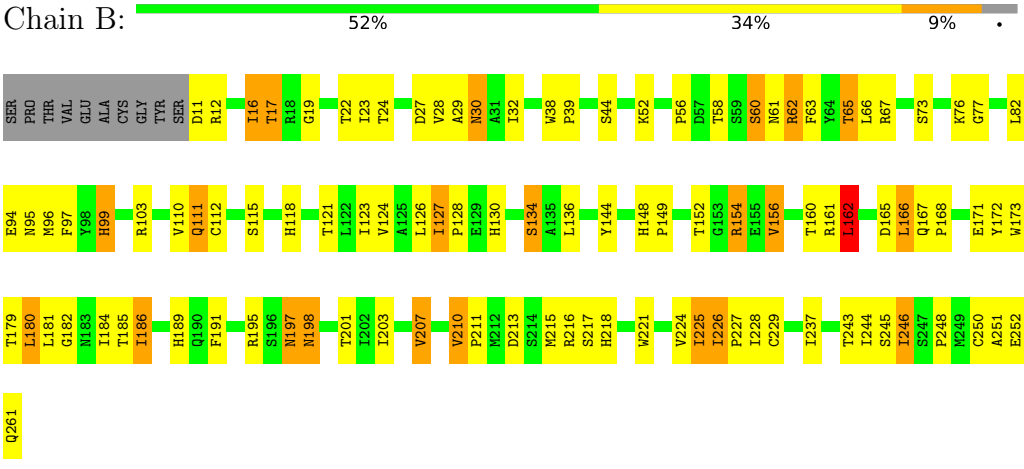
- Molecule 1: Protein VP1

Chain A:



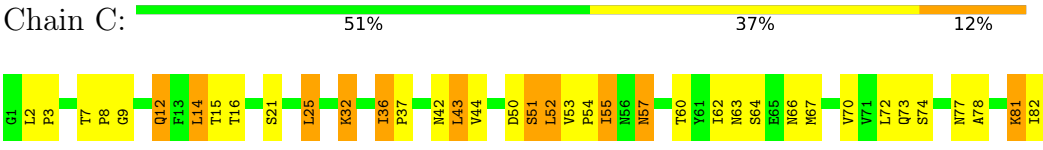
- Molecule 2: Protein VP2

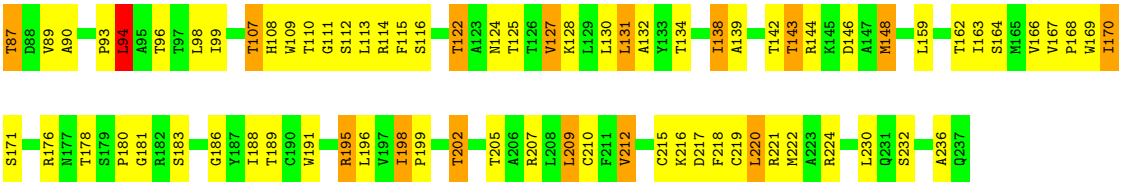
Chain B:



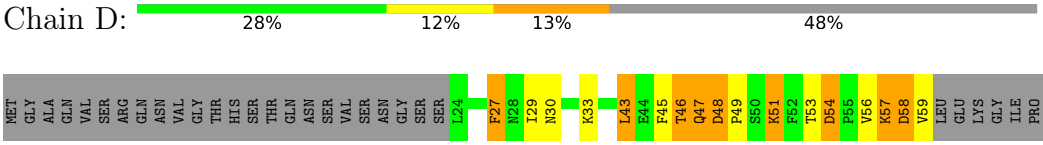
- Molecule 3: Protein VP3

Chain C:





• Molecule 4: Protein VP4



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, α, β, γ	310.49Å 345.68Å 378.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.94 – 3.20 24.94 – 2.74	Depositor EDS
% Data completeness (in resolution range)	99.9 (24.94-3.20) 93.4 (24.94-2.74)	Depositor EDS
R_{merge}	0.25	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.36 (at 2.76Å)	Xtriage
Refinement program	PHENIX 1.7_650	Depositor
R, R_{free}	0.230 , 0.273 0.287 , 0.292	Depositor DCC
R_{free} test set	49027 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	41.8	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 44.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.40$, $< L^2 > = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.81	EDS
Total number of atoms	6380	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.29% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BT8

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	1.01	2/2305 (0.1%)	0.96	3/3140 (0.1%)
2	B	0.98	2/2030 (0.1%)	0.98	2/2770 (0.1%)
3	C	0.99	0/1884	0.97	2/2579 (0.1%)
4	D	1.31	0/290	1.00	0/392
All	All	1.01	4/6509 (0.1%)	0.97	7/8881 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
2	B	0	2
4	D	0	2
All	All	0	6

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	112	CYS	CB-SG	-7.84	1.69	1.82
1	A	128	CYS	CB-SG	-6.15	1.71	1.82
2	B	250	CYS	CB-SG	-5.69	1.72	1.81
1	A	266	GLU	CG-CD	5.17	1.59	1.51

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	100	ASN	CB-CA-C	-6.11	98.18	110.40
2	B	62	ARG	NE-CZ-NH1	-5.88	117.36	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	86	ARG	NE-CZ-NH2	-5.77	117.41	120.30
2	B	162	LEU	CB-CG-CD1	5.44	120.25	111.00
1	A	10	VAL	CB-CA-C	5.40	121.65	111.40

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	157	ASP	Peptide
1	A	88	ASN	Peptide
2	B	182	GLY	Peptide
2	B	19	GLY	Peptide
4	D	47	GLN	Peptide

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	2248	0	2163	130	0
2	B	1975	0	1917	95	0
3	C	1834	0	1817	124	0
4	D	283	0	258	19	0
5	A	28	0	26	9	0
6	A	6	0	0	1	0
6	B	3	0	0	0	0
6	C	3	0	0	0	0
All	All	6380	0	6181	339	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 27.

The worst 5 of 339 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:B:177:ASP:OD1	2:B:179:THR:HG22	1.43	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:185:THR:HG23	2:B:189:HIS:CE1	1.86	1.09
1:A:257:ARG:HG3	3:C:236:ALA:HB3	1.40	1.02
3:C:107:THR:HG22	3:C:224:ARG:HG2	1.44	1.00
1:A:274:ILE:HD13	3:C:67:MET:HE1	1.44	1.00

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	278/283 (98%)	263 (95%)	13 (5%)	2 (1%)	22 61
2	B	249/261 (95%)	235 (94%)	13 (5%)	1 (0%)	34 69
3	C	235/237 (99%)	219 (93%)	16 (7%)	0	100 100
4	D	34/69 (49%)	28 (82%)	5 (15%)	1 (3%)	4 28
All	All	796/850 (94%)	745 (94%)	47 (6%)	4 (0%)	29 67

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	88	ASN
1	A	89	TYR
2	B	30	ASN
4	D	51	LYS

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	249/252 (99%)	209 (84%)	40 (16%)	2 11
2	B	218/226 (96%)	172 (79%)	46 (21%)	1 6
3	C	210/210 (100%)	169 (80%)	41 (20%)	1 7
4	D	30/60 (50%)	21 (70%)	9 (30%)	0 1
All	All	707/748 (94%)	571 (81%)	136 (19%)	1 8

5 of 136 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	159	LEU
3	C	195	ARG
4	D	46	THR
2	B	60	SER
2	B	58	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	139	ASN
3	C	66	ASN
2	B	148	HIS
4	D	30	ASN
2	B	197	ASN

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)

1 ligand 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	$\#\|Z\| > 2$
5	BT8	A	301	-	28,31,31	2.56	13 (46%)	34,42,42	4.13	11 (32%)

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
5	BT8	A	301	-	-	8/11/23/23	0/4/4/4

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	301	BT8	C05-N08	5.53	1.48	1.37
5	A	301	BT8	C20-C21	-4.30	1.34	1.43
5	A	301	BT8	N07-N06	4.03	1.44	1.34
5	A	301	BT8	C22-C17	3.91	1.44	1.37
5	A	301	BT8	C02-N07	3.82	1.37	1.33

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	301	BT8	C01-C02-N07	20.40	125.87	116.24
5	A	301	BT8	C13-N08-C05	5.73	133.69	120.39
5	A	301	BT8	C01-C02-C03	-4.59	112.23	121.63
5	A	301	BT8	C13-C12-C11	-4.29	101.12	111.99
5	A	301	BT8	C09-N08-C05	-3.73	111.72	120.39

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

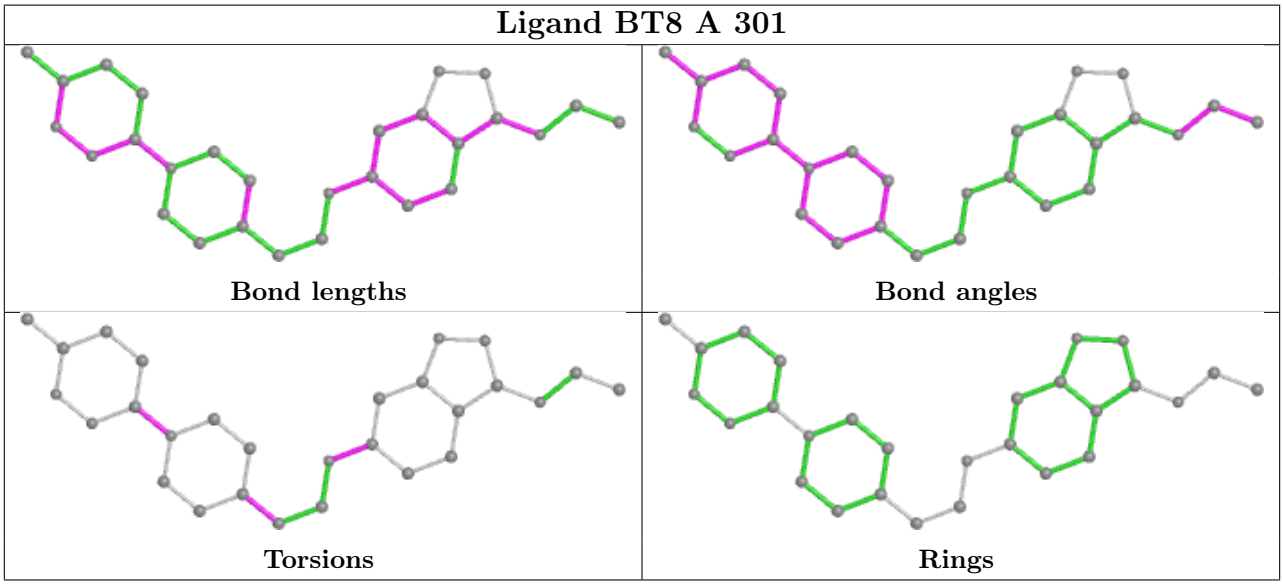
Mol	Chain	Res	Type	Atoms
5	A	301	BT8	C04-C05-N08-C13
5	A	301	BT8	C04-C05-N08-C09
5	A	301	BT8	N06-C05-N08-C13
5	A	301	BT8	N06-C05-N08-C09
5	A	301	BT8	C22-C17-O16-C15

There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	301	BT8	9	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 then 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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

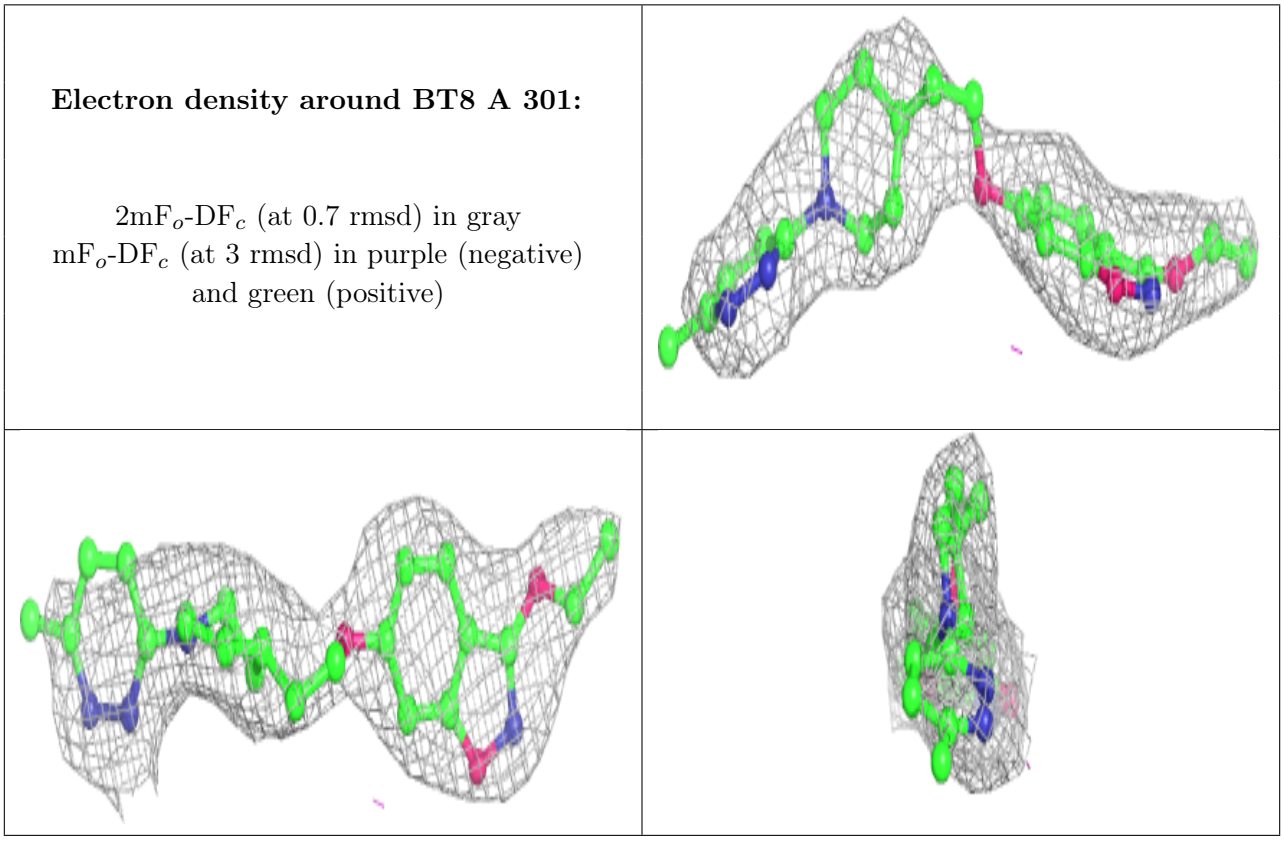
6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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 BT8 A 301:

$2mF_o$-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)

Unable to reproduce the depositors R factor - this section is therefore empty.