wwPDB X-ray Structure Validation Summary Report (i)

Jan 13, 2024 – 04:54 pm GMT

PDB ID	:	6T8U
Title	:	Complement factor B in complex with 5-Bromo-3-chloro-N-(4,5-dihydro-1H-imidazol-2-yl)-7-methyl-1H-indol-4-amine
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Deposited on	:	2019-10-25
Resolution	:	2.84 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:

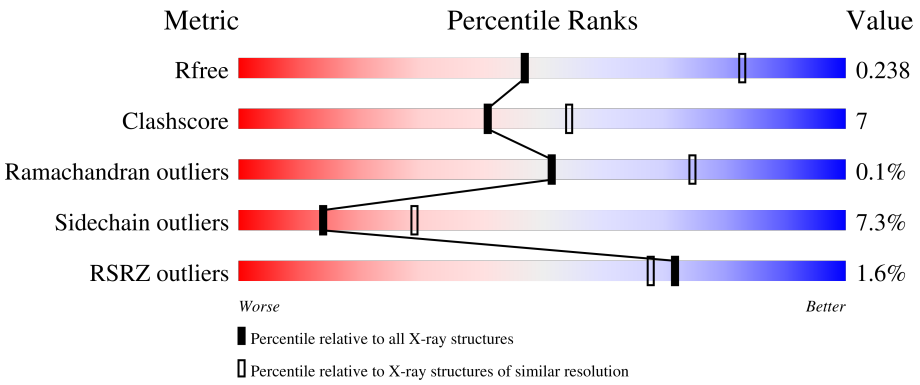
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13

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 2.84 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	1031 (2.86-2.82)
Clashscore	141614	1078 (2.86-2.82)
Ramachandran outliers	138981	1050 (2.86-2.82)
Sidechain outliers	138945	1051 (2.86-2.82)
RSRZ outliers	127900	1019 (2.86-2.82)

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% 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.

EDS	:	2.36
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)	:	2.36

Mol	Chain	Length	Quality of chain
1	AAA	291	2% 76% 15% • 7%
1	BBB	291	% 73% 16% • 9%
1	CCC	291	% 73% 17% • 9%

2 Entry composition (i)

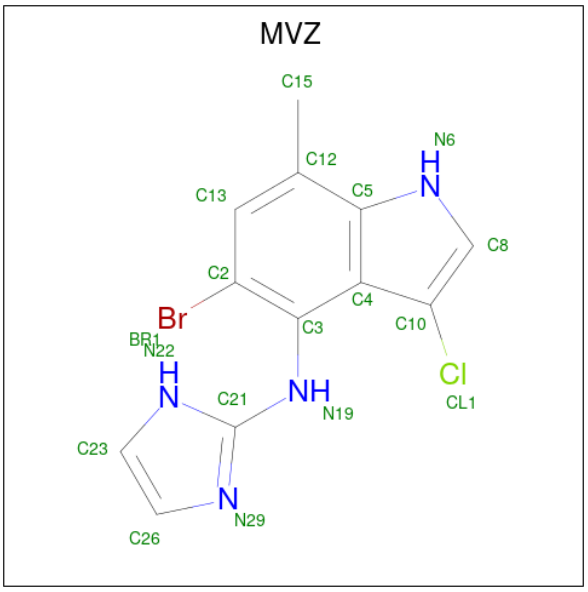
There are 4 unique types of molecules in this entry. The entry contains 6423 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Complement factor B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	270	2108	1345	360	391	12	0	0	0
1	BBB	265	2085	1331	357	385	12	0	0	0
1	CCC	266	2091	1335	355	389	12	0	0	0

- Molecule 2 is 5-bromanyl-3-chloranyl- {N}-(1 {H}-imidazol-2-yl)-7-methyl-1 {H}-indol-4-amine (three-letter code: MVZ) (formula: $C_{12}H_{10}BrClN_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	Br	C	Cl	N		
2	AAA	1	18	1	12	1	4	0	0
2	BBB	1	18	1	12	1	4	0	0

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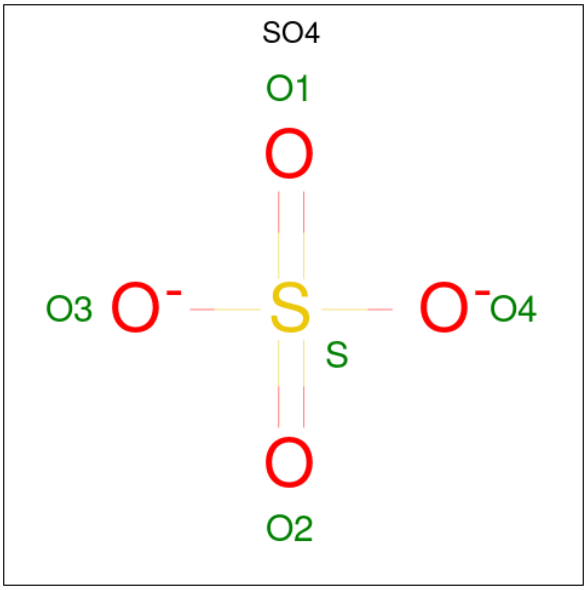
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	Br	C	Cl	N		
2	CCC	1	18	1	12	1	4	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	AAA	1	5	4	1	0	0
			Total	O	S		
3	AAA	1	5	4	1	0	0
			Total	O	S		
3	AAA	1	5	4	1	0	0
			Total	O	S		
3	BBB	1	5	4	1	0	0
			Total	O	S		
3	BBB	1	5	4	1	0	0
			Total	O	S		
3	BBB	1	5	4	1	0	0
			Total	O	S		
3	CCC	1	5	4	1	0	0
			Total	O	S		
3	CCC	1	5	4	1	0	0

- Molecule 4 is water.

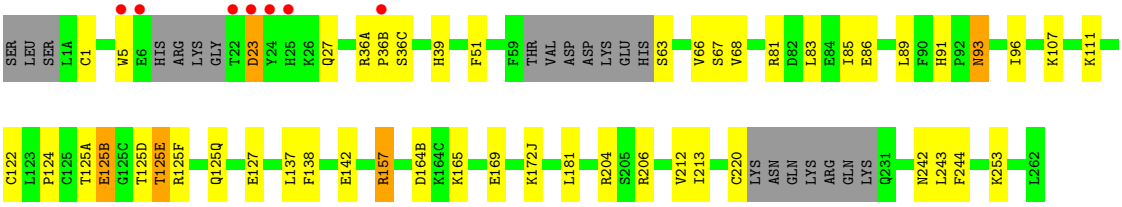
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	AAA	17	17	17	0	0
			Total	O		
4	BBB	17	17	17	0	0
			Total	O		
4	CCC	11	11	11	0	0

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 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.

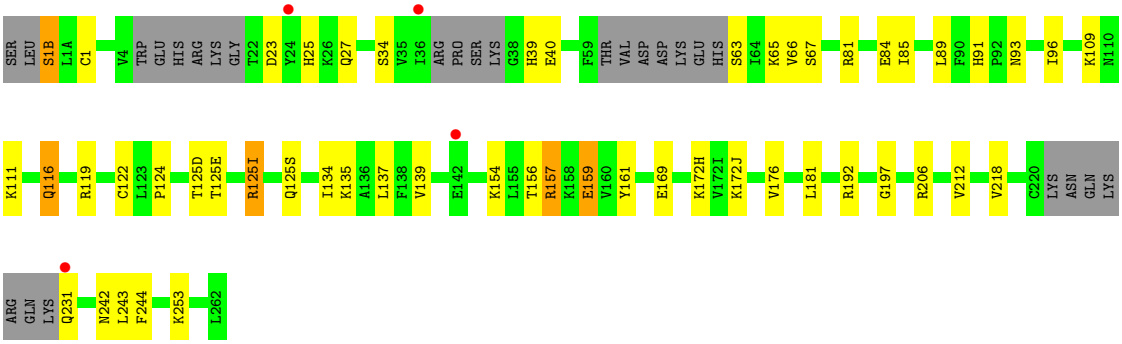
• Molecule 1: Complement factor B

Chain AAA:



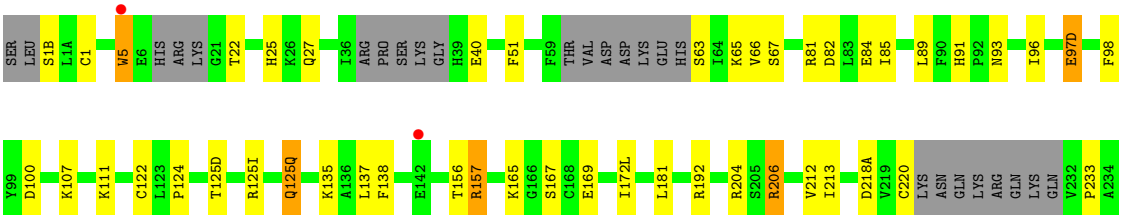
• Molecule 1: Complement factor B

Chain BBB:



• Molecule 1: Complement factor B

Chain CCC:



H235
N242
L243
F244
K253
D258
L259
L262

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	91.93Å 91.93Å 260.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	86.68 – 2.84 86.68 – 2.84	Depositor EDS
% Data completeness (in resolution range)	100.0 (86.68-2.84) 100.0 (86.68-2.84)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.73 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.198 , 0.239 0.198 , 0.238	Depositor DCC
R_{free} test set	1366 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	29.8	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 39.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	6423	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MVZ, SO4

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	AAA	0.48	1/2154 (0.0%)	0.88	2/2915 (0.1%)
1	BBB	0.52	2/2128 (0.1%)	0.83	0/2873
1	CCC	0.47	0/2135	0.83	1/2885 (0.0%)
All	All	0.49	3/6417 (0.0%)	0.85	3/8673 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	125(B)	GLU	CD-OE2	5.64	1.31	1.25
1	BBB	84	GLU	CD-OE2	5.34	1.31	1.25
1	BBB	1(B)	SER	N-CA	5.09	1.56	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AAA	125(F)	ARG	CB-CA-C	7.32	125.03	110.40
1	AAA	23	ASP	CB-CA-C	6.63	123.66	110.40
1	CCC	206	ARG	NE-CZ-NH1	5.08	122.84	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	AAA	2108	0	2076	24	0
1	BBB	2085	0	2084	30	0
1	CCC	2091	0	2071	33	0
2	AAA	18	0	0	1	0
2	BBB	18	0	0	1	0
2	CCC	18	0	0	1	0
3	AAA	15	0	0	0	0
3	BBB	15	0	0	1	0
3	CCC	10	0	0	0	0
4	AAA	17	0	0	0	0
4	BBB	17	0	0	1	0
4	CCC	11	0	0	2	0
All	All	6423	0	6231	90	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 7.

The worst 5 of 90 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:BBB:169:GLU:HG2	1:BBB:176:VAL:HG11	1.42	1.00
1:CCC:65:LYS:HB3	1:CCC:82:ASP:OD2	1.74	0.88
1:CCC:91:HIS:HD2	1:CCC:93:ASN:H	1.20	0.87
1:AAA:91:HIS:HD2	1:AAA:93:ASN:H	1.19	0.87
1:BBB:91:HIS:HD2	1:BBB:93:ASN:H	1.19	0.84

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	AAA	262/291 (90%)	256 (98%)	5 (2%)	1 (0%)	34 56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BBB	255/291 (88%)	249 (98%)	6 (2%)	0	100	100
1	CCC	256/291 (88%)	250 (98%)	6 (2%)	0	100	100
All	All	773/873 (88%)	755 (98%)	17 (2%)	1 (0%)	51	75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	36(B)	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	AAA	229/256 (90%)	213 (93%)	16 (7%)	15	30
1	BBB	230/256 (90%)	213 (93%)	17 (7%)	13	29
1	CCC	229/256 (90%)	212 (93%)	17 (7%)	13	29
All	All	688/768 (90%)	638 (93%)	50 (7%)	14	29

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	BBB	157	ARG
1	CCC	40	GLU
1	CCC	258	ASP
1	BBB	159	GLU
1	BBB	218	VAL

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

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)

11 ligands are 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	$\#\|Z\| > 2$
3	SO4	BBB	303	-	4,4,4	0.32	0	6,6,6	0.22	0
3	SO4	AAA	303	-	4,4,4	0.40	0	6,6,6	0.29	0
2	MVZ	BBB	301	-	18,20,20	2.37	6 (33%)	9,29,29	3.40	4 (44%)
3	SO4	CCC	302	-	4,4,4	0.28	0	6,6,6	0.17	0
3	SO4	BBB	304	-	4,4,4	0.37	0	6,6,6	0.20	0
3	SO4	AAA	302	-	4,4,4	0.29	0	6,6,6	0.25	0
2	MVZ	AAA	301	-	18,20,20	2.03	7 (38%)	9,29,29	3.83	4 (44%)
2	MVZ	CCC	301	-	18,20,20	2.36	6 (33%)	9,29,29	4.03	5 (55%)
3	SO4	AAA	304	-	4,4,4	0.36	0	6,6,6	0.21	0
3	SO4	BBB	302	-	4,4,4	0.32	0	6,6,6	0.18	0
3	SO4	CCC	303	-	4,4,4	0.35	0	6,6,6	0.17	0

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	MVZ	AAA	301	-	-	1/2/4/4	0/3/3/3
2	MVZ	BBB	301	-	-	1/2/4/4	0/3/3/3
2	MVZ	CCC	301	-	-	1/2/4/4	0/3/3/3

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	CCC	301	MVZ	C3-C4	-5.85	1.34	1.43
2	BBB	301	MVZ	C3-C4	-5.70	1.34	1.43
2	BBB	301	MVZ	C26-C23	4.22	1.57	1.37
2	CCC	301	MVZ	C26-C23	4.09	1.56	1.37
2	AAA	301	MVZ	C3-C4	-4.03	1.37	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	AAA	301	MVZ	C8-C10-CL1	7.04	134.55	126.90
2	CCC	301	MVZ	C8-C10-CL1	6.91	134.40	126.90
2	AAA	301	MVZ	C15-C12-C5	6.69	126.52	120.03
2	BBB	301	MVZ	C8-C10-CL1	6.55	134.01	126.90
2	CCC	301	MVZ	C15-C12-C5	6.31	126.15	120.03

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AAA	301	MVZ	C4-C3-N19-C21
2	BBB	301	MVZ	C4-C3-N19-C21
2	CCC	301	MVZ	C4-C3-N19-C21

There are no ring outliers.

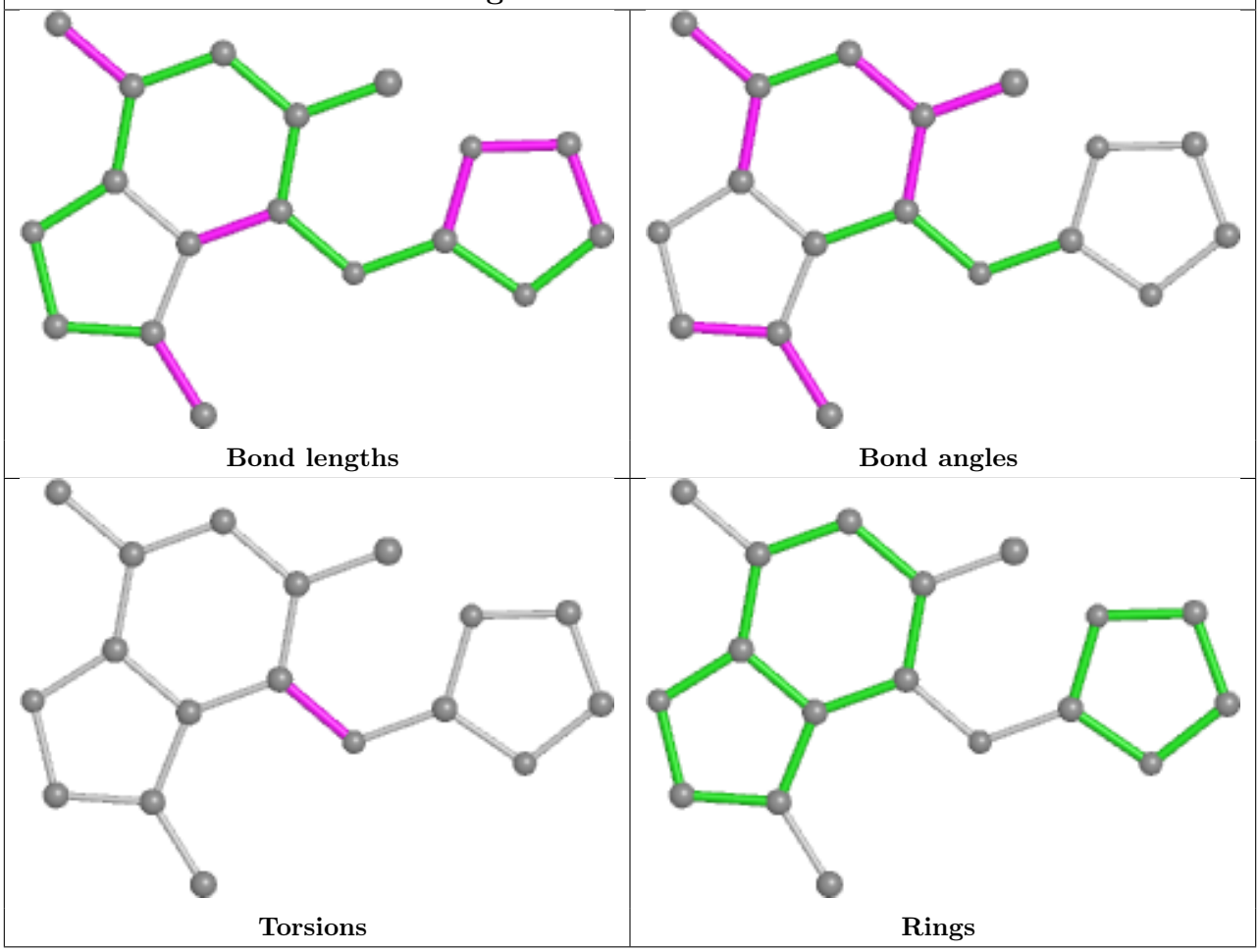
4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	BBB	301	MVZ	1	0
3	BBB	304	SO4	1	0
2	AAA	301	MVZ	1	0
2	CCC	301	MVZ	1	0

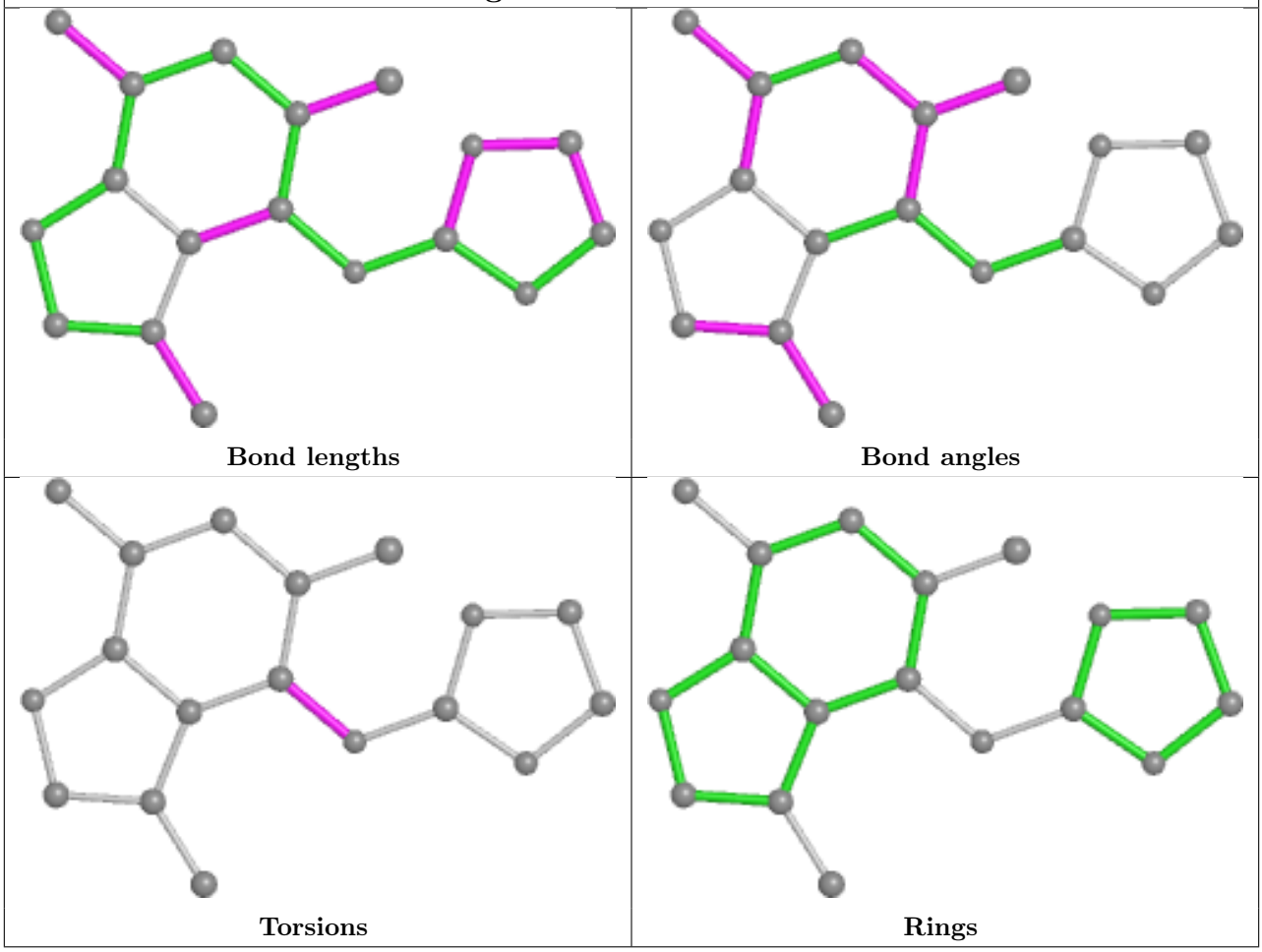
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

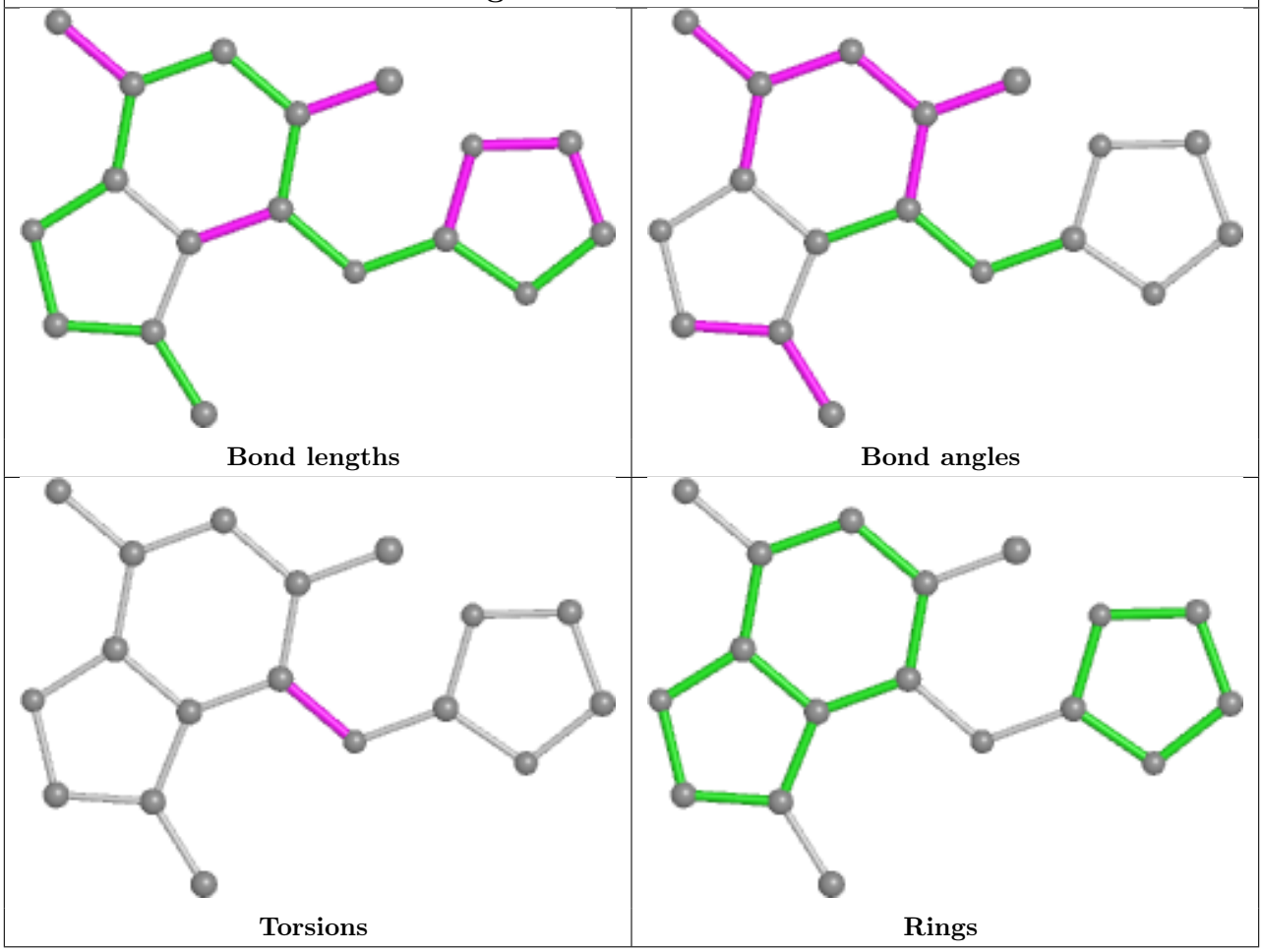
Ligand MVZ BBB 301



Ligand MVZ AAA 301



Ligand MVZ CCC 301



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	AAA	270/291 (92%)	-0.05	7 (2%)	56	51	10, 20, 70, 121	0
1	BBB	265/291 (91%)	-0.13	4 (1%)	73	70	8, 18, 51, 104	0
1	CCC	266/291 (91%)	-0.12	2 (0%)	86	85	10, 21, 61, 110	0
All	All	801/873 (91%)	-0.10	13 (1%)	72	68	8, 20, 63, 121	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	36(B)	PRO	5.3
1	BBB	231	GLN	4.6
1	AAA	6	GLU	4.0
1	AAA	24	TYR	3.8
1	AAA	5	TRP	3.4

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)

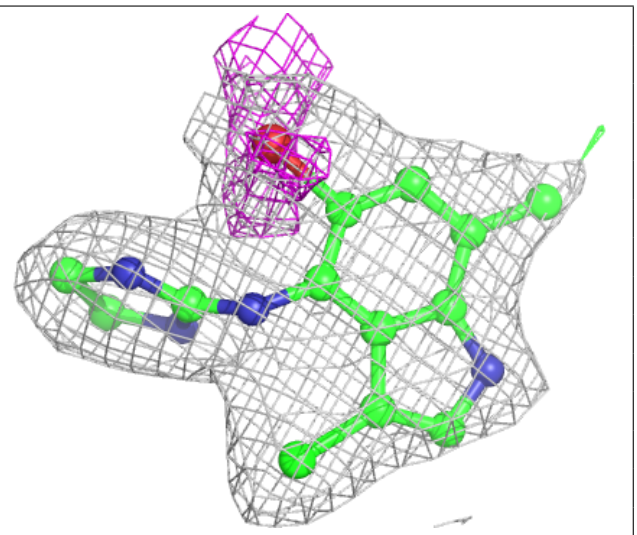
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

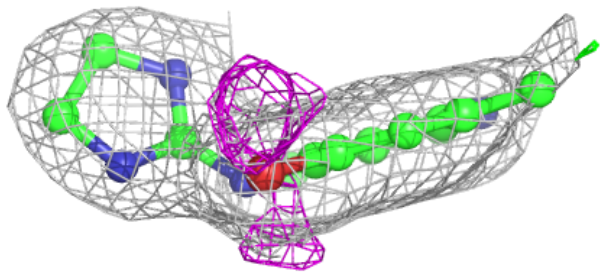
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	MVZ	AAA	301	18/18	0.91	0.19	30,41,52,74	0
2	MVZ	BBB	301	18/18	0.92	0.22	27,32,41,61	0
2	MVZ	CCC	301	18/18	0.93	0.19	24,42,52,64	0
3	SO4	CCC	303	5/5	0.95	0.12	45,46,53,57	0
3	SO4	AAA	304	5/5	0.96	0.17	63,66,69,71	0
3	SO4	BBB	302	5/5	0.96	0.18	48,48,50,51	0
3	SO4	BBB	303	5/5	0.96	0.16	40,47,50,53	0
3	SO4	BBB	304	5/5	0.96	0.17	50,51,53,54	0
3	SO4	AAA	302	5/5	0.96	0.13	46,47,50,50	0
3	SO4	CCC	302	5/5	0.97	0.12	48,49,54,54	0
3	SO4	AAA	303	5/5	0.97	0.13	36,38,40,40	0

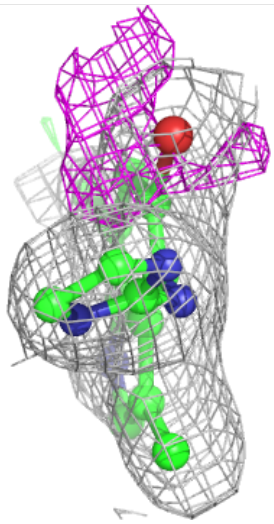
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around MVZ AAA 301:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

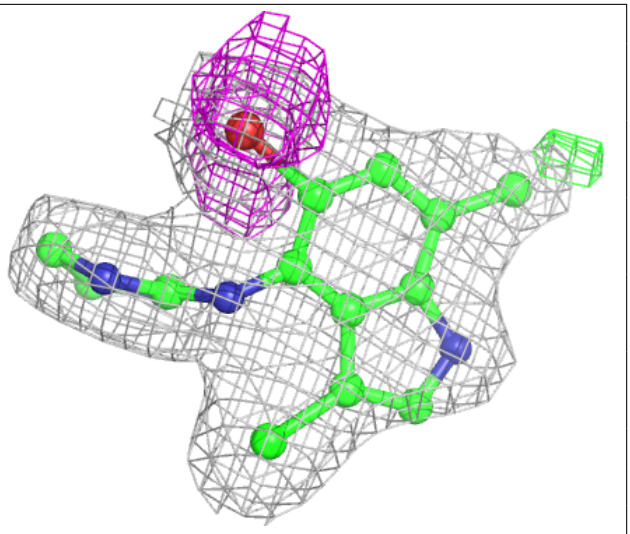


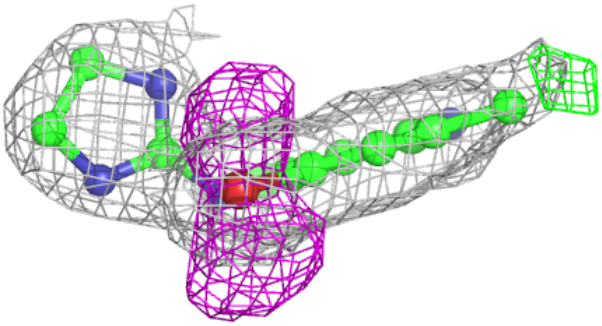


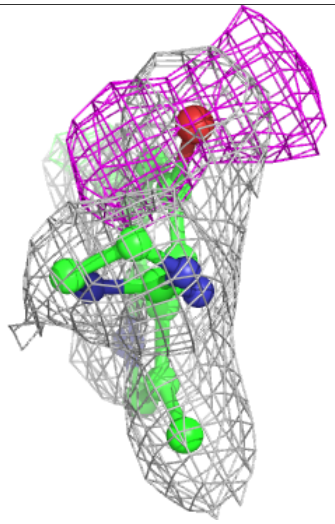


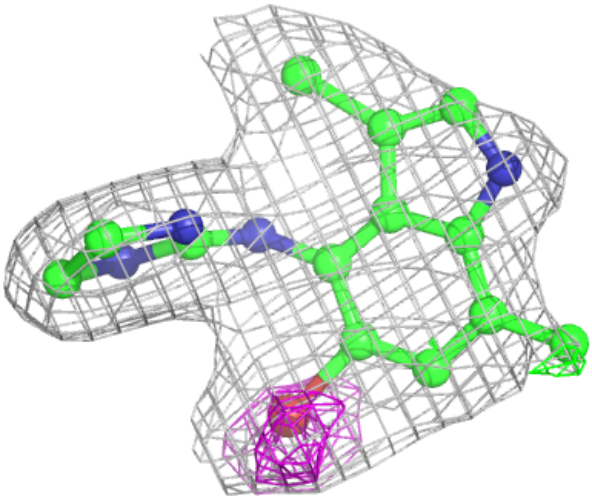
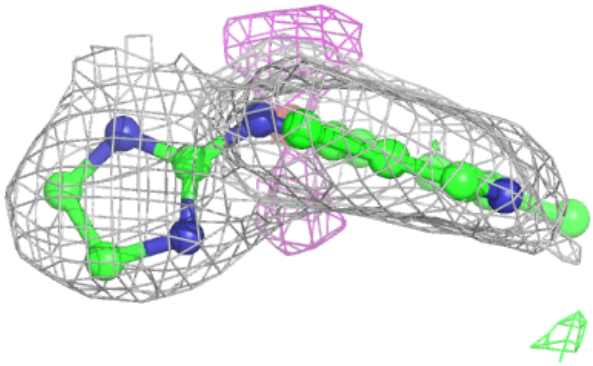
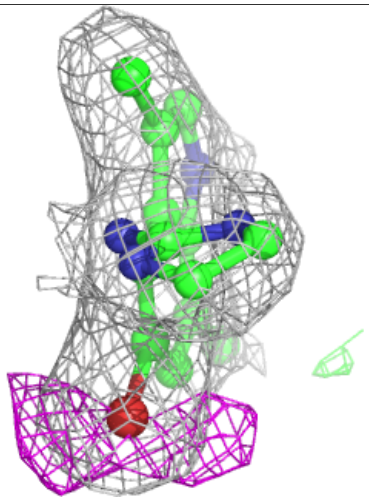
Electron density around MVZ BBB 301:

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







Electron density around MVZ CCC 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)

There are no such residues in this entry.