



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 05:14 PM BST

PDB ID : 2YME  
Title : Crystal structure of a mutant binding protein (5HTBP-AChBP) in complex with granisetron  
Authors : Kesters, D.; Thompson, A.J.; Brams, M.; Elk, R.v.; Spurny, R.; Geitmann, M.; Villalgordo, J.M.; Guskov, A.; Danielson, U.H.; Lummis, S.C.R.; Smit, A.B.; Ulens, C.  
Deposited on : 2012-10-09  
Resolution : 2.40 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 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	:	2.13.1
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)	:	2.13.1

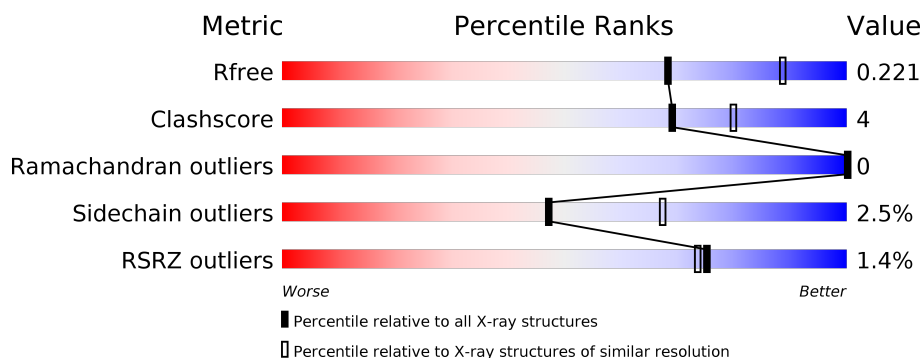
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 on 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	205	<div> <div>94%</div> <div>5%</div> </div>
1	B	205	<div> <div>91%</div> <div>9%</div> </div>
1	C	205	<div> <div>87%</div> <div>12%</div> </div>
1	D	205	<div> <div>90%</div> <div>10%</div> </div>
1	E	205	<div> <div>86%</div> <div>13%</div> </div>
1	F	205	<div> <div>3%</div> <div>89%</div> <div>11%</div> </div>

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
1	G	205	
1	H	205	
1	I	205	
1	J	205	

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
2	NAG	A	1206	X	-	-	-
2	NAG	B	1206	X	-	-	-
2	NAG	C	1206	X	-	-	X
2	NAG	D	1208	X	-	-	-
2	NAG	F	1206	X	-	-	-
2	NAG	J	1206	X	-	-	-
5	NA	I	1208	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 18055 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 SOLUBLE ACETYLCHOLINE RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	1	0
			1644	1042	269	324	9			
1	B	205	Total	C	N	O	S	0	1	0
			1645	1042	269	325	9			
1	C	205	Total	C	N	O	S	0	0	0
			1640	1039	269	323	9			
1	D	205	Total	C	N	O	S	0	0	0
			1640	1039	269	323	9			
1	E	205	Total	C	N	O	S	0	0	0
			1640	1039	269	323	9			
1	F	205	Total	C	N	O	S	0	0	0
			1640	1039	269	323	9			
1	G	205	Total	C	N	O	S	0	0	0
			1640	1039	269	323	9			
1	H	205	Total	C	N	O	S	0	0	0
			1640	1039	269	323	9			
1	I	205	Total	C	N	O	S	0	1	0
			1645	1042	269	325	9			
1	J	205	Total	C	N	O	S	0	1	0
			1648	1044	272	323	9			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	41	VAL	ALA	conflict	UNP Q8WSF8
A	53	TRP	TYR	engineered mutation	UNP Q8WSF8
A	55	ARG	GLN	conflict	UNP Q8WSF8
A	136	VAL	ALA	conflict	UNP Q8WSF8
B	41	VAL	ALA	conflict	UNP Q8WSF8
B	53	TRP	TYR	engineered mutation	UNP Q8WSF8
B	55	ARG	GLN	conflict	UNP Q8WSF8
B	136	VAL	ALA	conflict	UNP Q8WSF8
C	41	VAL	ALA	conflict	UNP Q8WSF8

*Continued on next page...*

*Continued from previous page...*

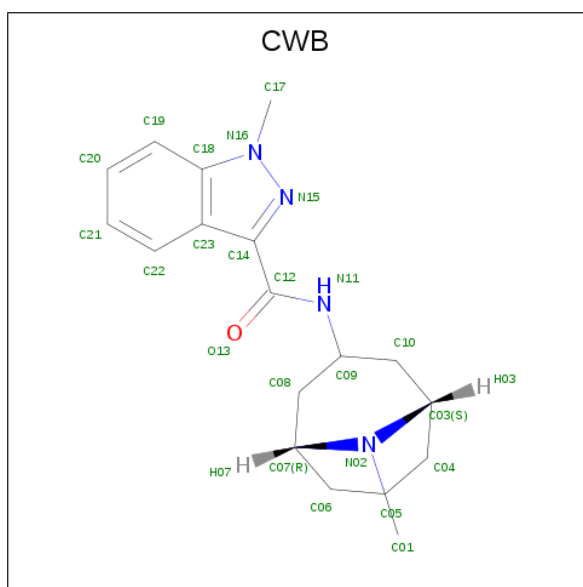
Chain	Residue	Modelled	Actual	Comment	Reference
C	53	TRP	TYR	engineered mutation	UNP Q8WSF8
C	55	ARG	GLN	conflict	UNP Q8WSF8
C	136	VAL	ALA	conflict	UNP Q8WSF8
D	41	VAL	ALA	conflict	UNP Q8WSF8
D	53	TRP	TYR	engineered mutation	UNP Q8WSF8
D	55	ARG	GLN	conflict	UNP Q8WSF8
D	136	VAL	ALA	conflict	UNP Q8WSF8
E	41	VAL	ALA	conflict	UNP Q8WSF8
E	53	TRP	TYR	engineered mutation	UNP Q8WSF8
E	55	ARG	GLN	conflict	UNP Q8WSF8
E	136	VAL	ALA	conflict	UNP Q8WSF8
F	41	VAL	ALA	conflict	UNP Q8WSF8
F	53	TRP	TYR	engineered mutation	UNP Q8WSF8
F	55	ARG	GLN	conflict	UNP Q8WSF8
F	136	VAL	ALA	conflict	UNP Q8WSF8
G	41	VAL	ALA	conflict	UNP Q8WSF8
G	53	TRP	TYR	engineered mutation	UNP Q8WSF8
G	55	ARG	GLN	conflict	UNP Q8WSF8
G	136	VAL	ALA	conflict	UNP Q8WSF8
H	41	VAL	ALA	conflict	UNP Q8WSF8
H	53	TRP	TYR	engineered mutation	UNP Q8WSF8
H	55	ARG	GLN	conflict	UNP Q8WSF8
H	136	VAL	ALA	conflict	UNP Q8WSF8
I	41	VAL	ALA	conflict	UNP Q8WSF8
I	53	TRP	TYR	engineered mutation	UNP Q8WSF8
I	55	ARG	GLN	conflict	UNP Q8WSF8
I	136	VAL	ALA	conflict	UNP Q8WSF8
J	41	VAL	ALA	conflict	UNP Q8WSF8
J	53	TRP	TYR	engineered mutation	UNP Q8WSF8
J	55	ARG	GLN	conflict	UNP Q8WSF8
J	136	VAL	ALA	conflict	UNP Q8WSF8

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		
2	E	1	Total	C	N	O	0	0
			14	8	1	5		
2	F	1	Total	C	N	O	0	0
			14	8	1	5		
2	H	1	Total	C	N	O	0	0
			14	8	1	5		
2	I	1	Total	C	N	O	0	0
			14	8	1	5		
2	J	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is 1-methyl-N-[(1R,5S)-9-methyl-9-azabicyclo[3.3.1]nonan-3-yl]indazole-3-carboxamide (three-letter code: CWB) (formula: C<sub>18</sub>H<sub>24</sub>N<sub>4</sub>O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			23	18	4	1		
3	B	1	Total	C	N	O	0	0
			23	18	4	1		
3	C	1	Total	C	N	O	0	0
			23	18	4	1		
3	D	1	Total	C	N	O	0	0
			23	18	4	1		
3	E	1	Total	C	N	O	0	0
			23	18	4	1		
3	F	1	Total	C	N	O	0	0
			23	18	4	1		
3	G	1	Total	C	N	O	0	0
			23	18	4	1		
3	H	1	Total	C	N	O	0	0
			23	18	4	1		
3	I	1	Total	C	N	O	0	0
			23	18	4	1		
3	J	1	Total	C	N	O	0	0
			23	18	4	1		

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		
4	C	1	Total	O	P	0	0
			5	4	1		
4	E	1	Total	O	P	0	0
			5	4	1		
4	G	1	Total	O	P	0	0
			5	4	1		
4	H	1	Total	O	P	0	0
			5	4	1		

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	I	1	Total	Na	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	189	Total	O	0	0
			189	189		
6	B	157	Total	O	0	0
			157	157		
6	C	123	Total	O	0	0
			123	123		

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	168	Total 168	O 168	0	0
6	E	152	Total 152	O 152	0	0
6	F	66	Total 66	O 66	0	0
6	G	63	Total 63	O 63	0	0
6	H	80	Total 80	O 80	0	0
6	I	130	Total 130	O 130	0	0
6	J	123	Total 123	O 123	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: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain A: 




#### • Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain B: 




#### • Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain C: 




#### • Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain D: 




#### • Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

Chain E: 

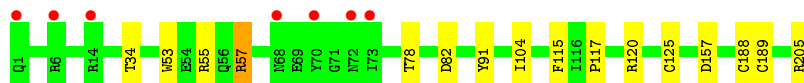


#### • Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

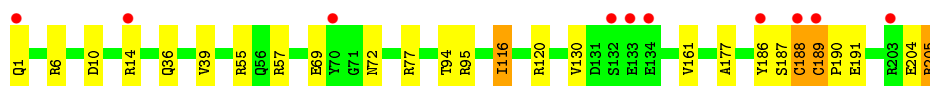
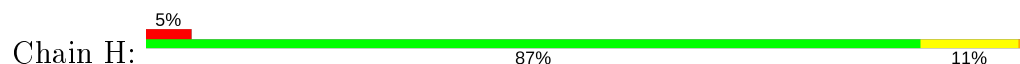
Chain F: 



- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR



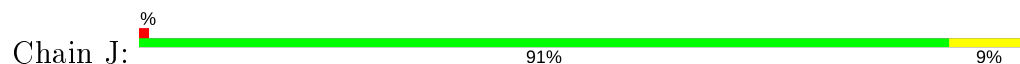
- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR



- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR



- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.09 Å 138.90 Å 119.89 Å 90.00° 91.07° 90.00°	Depositor
Resolution (Å)	48.91 – 2.40 48.91 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.91-2.40) 99.7 (48.91-2.40)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.95 (at 2.39 Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.170 , 0.226 0.168 , 0.221	Depositor DCC
$R_{free}$ test set	5294 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.6	Xtriage
Anisotropy	0.432	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 61.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	18055	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% 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: NA, PO4, CWB, NAG

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	0.28	0/1688	0.45	0/2304
1	B	0.34	0/1689	0.45	0/2305
1	C	0.34	0/1681	0.45	0/2294
1	D	0.35	0/1681	0.46	0/2294
1	E	0.37	0/1681	0.47	0/2294
1	F	0.24	0/1681	0.42	0/2294
1	G	0.24	0/1681	0.41	0/2294
1	H	0.25	0/1681	0.43	0/2294
1	I	0.34	0/1689	0.45	0/2305
1	J	0.26	0/1692	0.44	0/2308
All	All	0.31	0/16844	0.44	0/22986

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	1644	0	1584	7	0
1	B	1645	0	1581	11	0
1	C	1640	0	1577	14	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1640	0	1577	9	0
1	E	1640	0	1577	17	0
1	F	1640	0	1577	13	0
1	G	1640	0	1578	13	0
1	H	1640	0	1578	21	0
1	I	1645	0	1581	8	0
1	J	1648	0	1590	12	0
2	A	14	0	13	0	0
2	B	14	0	13	0	0
2	C	14	0	13	0	0
2	D	14	0	13	1	0
2	E	14	0	13	0	0
2	F	14	0	13	1	0
2	H	14	0	13	0	0
2	I	14	0	13	0	0
2	J	14	0	13	2	0
3	A	23	0	24	0	0
3	B	23	0	24	0	0
3	C	23	0	24	0	0
3	D	23	0	24	0	0
3	E	23	0	24	1	0
3	F	23	0	24	2	0
3	G	23	0	24	1	0
3	H	23	0	24	0	0
3	I	23	0	24	0	0
3	J	23	0	24	0	0
4	A	5	0	0	1	0
4	C	5	0	0	0	0
4	E	5	0	0	0	0
4	G	5	0	0	0	0
4	H	5	0	0	1	0
5	I	1	0	0	0	0
6	A	189	0	0	3	0
6	B	157	0	0	6	0
6	C	123	0	0	4	0
6	D	168	0	0	3	0
6	E	152	0	0	0	0
6	F	66	0	0	3	0
6	G	63	0	0	2	0
6	H	80	0	0	5	0
6	I	130	0	0	4	0
6	J	123	0	0	3	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	18055	0	16157	120	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 4.

The worst 5 of 120 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:J:1206:NAG:O7	2:J:1206:NAG:O3	1.96	0.83
6:D:2165:HOH:O	2:F:1206:NAG:O4	2.03	0.76
1:H:6:ARG:NH2	1:H:69:GLU:O	2.21	0.74
1:H:10:ASP:HA	1:H:14:ARG:HD3	1.71	0.72
1:J:55[B]:ARG:NH2	6:J:2024:HOH:O	2.27	0.66

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	204/205 (100%)	201 (98%)	3 (2%)	0	100	100
1	B	204/205 (100%)	198 (97%)	6 (3%)	0	100	100
1	C	203/205 (99%)	200 (98%)	3 (2%)	0	100	100
1	D	203/205 (99%)	197 (97%)	6 (3%)	0	100	100
1	E	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
1	F	203/205 (99%)	200 (98%)	3 (2%)	0	100	100
1	G	203/205 (99%)	196 (97%)	7 (3%)	0	100	100
1	H	203/205 (99%)	196 (97%)	7 (3%)	0	100	100
1	I	204/205 (100%)	200 (98%)	4 (2%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	204/205 (100%)	200 (98%)	4 (2%)	0	100	100
All	All	2034/2050 (99%)	1986 (98%)	48 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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	189/188 (100%)	184 (97%)	5 (3%)	46	66
1	B	189/188 (100%)	184 (97%)	5 (3%)	46	66
1	C	188/188 (100%)	182 (97%)	6 (3%)	39	59
1	D	188/188 (100%)	183 (97%)	5 (3%)	44	65
1	E	188/188 (100%)	181 (96%)	7 (4%)	34	53
1	F	188/188 (100%)	182 (97%)	6 (3%)	39	59
1	G	188/188 (100%)	186 (99%)	2 (1%)	73	87
1	H	188/188 (100%)	181 (96%)	7 (4%)	34	53
1	I	189/188 (100%)	186 (98%)	3 (2%)	62	79
1	J	189/188 (100%)	188 (100%)	1 (0%)	88	95
All	All	1884/1880 (100%)	1837 (98%)	47 (2%)	47	67

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	31	LEU
1	E	158	THR
1	I	57	ARG
1	E	116	ILE
1	E	205	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:



Mol	Chain	Res	Type
1	E	98	GLN
1	F	1	GLN
1	G	119	GLN
1	J	13	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 25 ligands modelled in this entry, 1 is monoatomic - leaving 24 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	$\# Z  > 2$
4	PO4	G	1208	-	4,4,4	0.87	0	6,6,6	0.43	0
3	CWB	A	1207	-	22,26,26	2.41	8 (36%)	27,38,38	3.27	11 (40%)
2	NAG	I	1206	1	14,14,15	0.99	1 (7%)	17,19,21	1.57	4 (23%)
3	CWB	C	1207	-	22,26,26	2.39	7 (31%)	27,38,38	3.07	10 (37%)
4	PO4	C	1208	-	4,4,4	0.95	0	6,6,6	0.33	0
2	NAG	E	1209	1	14,14,15	1.18	1 (7%)	17,19,21	2.44	6 (35%)
2	NAG	A	1206	1	14,14,15	0.89	0	17,19,21	1.88	6 (35%)
3	CWB	F	1207	-	22,26,26	2.40	7 (31%)	27,38,38	2.89	9 (33%)
3	CWB	G	1207	-	22,26,26	2.37	7 (31%)	27,38,38	3.15	11 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	PO4	A	1208	-	4,4,4	0.89	0	6,6,6	0.47	0
2	NAG	B	1206	1	14,14,15	0.66	0	17,19,21	1.29	3 (17%)
2	NAG	F	1206	1	14,14,15	0.85	1 (7%)	17,19,21	1.83	5 (29%)
2	NAG	H	1206	1	14,14,15	0.30	0	17,19,21	0.61	0
3	CWB	I	1207	-	22,26,26	2.37	8 (36%)	27,38,38	3.65	13 (48%)
3	CWB	J	1207	-	22,26,26	2.43	7 (31%)	27,38,38	2.11	6 (22%)
3	CWB	E	1207	-	22,26,26	2.39	7 (31%)	27,38,38	3.11	11 (40%)
4	PO4	H	1208	-	4,4,4	0.88	0	6,6,6	0.42	0
3	CWB	B	1207	-	22,26,26	2.37	8 (36%)	27,38,38	3.13	10 (37%)
2	NAG	D	1208	1	14,14,15	0.68	0	17,19,21	2.22	5 (29%)
2	NAG	C	1206	1	14,14,15	0.37	0	17,19,21	1.32	1 (5%)
2	NAG	J	1206	1	14,14,15	0.52	0	17,19,21	1.85	4 (23%)
3	CWB	D	1207	-	22,26,26	2.42	8 (36%)	27,38,38	3.40	11 (40%)
4	PO4	E	1208	-	4,4,4	0.87	0	6,6,6	0.43	0
3	CWB	H	1207	-	22,26,26	2.50	9 (40%)	27,38,38	2.69	11 (40%)

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
3	CWB	G	1207	-	-	0/4/30/30	0/5/4/4
3	CWB	A	1207	-	-	0/4/30/30	0/5/4/4
2	NAG	I	1206	1	-	2/6/23/26	0/1/1/1
3	CWB	C	1207	-	-	0/4/30/30	0/5/4/4
3	CWB	D	1207	-	-	0/4/30/30	0/5/4/4
2	NAG	D	1208	1	1/1/5/7	5/6/23/26	0/1/1/1
3	CWB	H	1207	-	-	1/4/30/30	0/5/4/4
3	CWB	J	1207	-	-	2/4/30/30	0/5/4/4
2	NAG	B	1206	1	1/1/5/7	4/6/23/26	0/1/1/1
2	NAG	C	1206	1	1/1/5/7	3/6/23/26	0/1/1/1
2	NAG	F	1206	1	1/1/5/7	5/6/23/26	0/1/1/1
3	CWB	B	1207	-	-	0/4/30/30	0/5/4/4
2	NAG	E	1209	1	-	2/6/23/26	0/1/1/1
2	NAG	J	1206	1	1/1/5/7	3/6/23/26	0/1/1/1
2	NAG	H	1206	1	-	5/6/23/26	0/1/1/1
3	CWB	I	1207	-	-	3/4/30/30	0/5/4/4

Continued on next page...

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1206	1	1/1/5/7	4/6/23/26	0/1/1/1
3	CWB	E	1207	-	-	0/4/30/30	0/5/4/4
3	CWB	F	1207	-	-	1/4/30/30	0/5/4/4

The worst 5 of 79 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	1207	CWB	C10-C09	-6.36	1.42	1.52
3	J	1207	CWB	C10-C09	-6.18	1.43	1.52
3	E	1207	CWB	C10-C09	-6.08	1.43	1.52
3	C	1207	CWB	C10-C09	-6.01	1.43	1.52
3	F	1207	CWB	C12-N11	5.98	1.47	1.34

The worst 5 of 137 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	1207	CWB	C01-N02-C07	14.09	124.55	113.16
3	D	1207	CWB	C01-N02-C03	10.85	121.93	113.16
3	E	1207	CWB	C01-N02-C03	9.93	121.19	113.16
3	C	1207	CWB	C01-N02-C03	9.34	120.70	113.16
3	A	1207	CWB	C08-C09-C10	9.25	119.28	111.13

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1206	NAG	C1
2	B	1206	NAG	C1
2	F	1206	NAG	C1
2	D	1208	NAG	C1
2	C	1206	NAG	C1

5 of 40 torsion outliers are listed below:

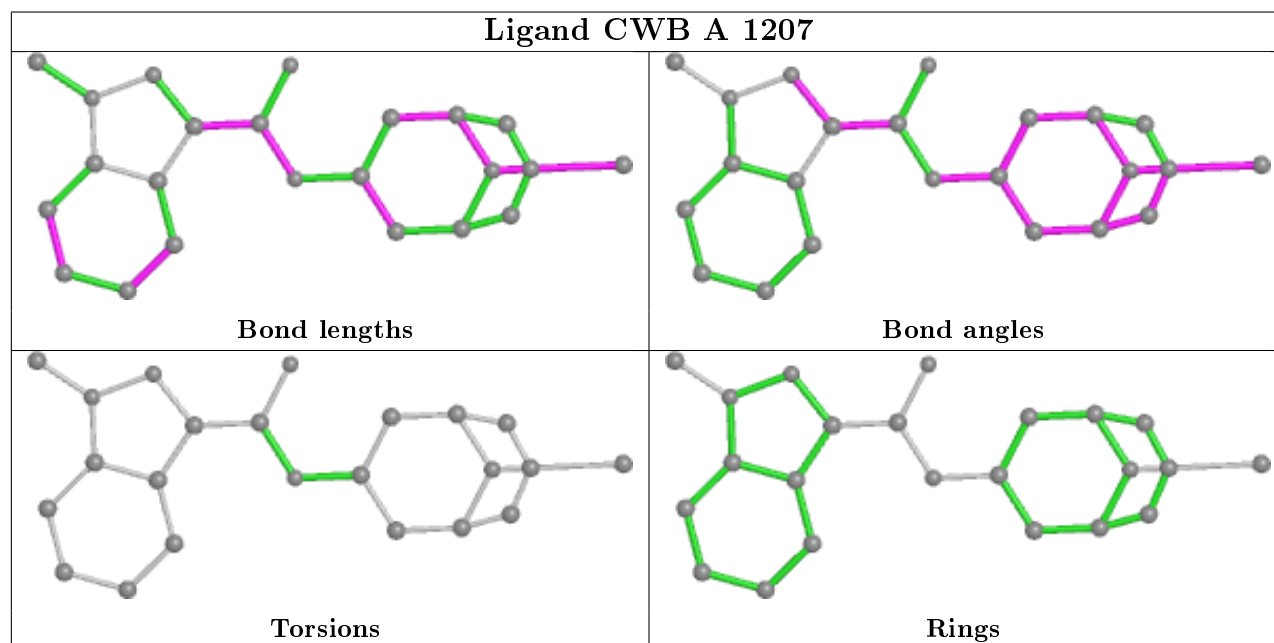
Mol	Chain	Res	Type	Atoms
2	B	1206	NAG	C8-C7-N2-C2
2	B	1206	NAG	O7-C7-N2-C2
2	F	1206	NAG	C3-C2-N2-C7
2	F	1206	NAG	C8-C7-N2-C2
2	F	1206	NAG	O7-C7-N2-C2

There are no ring outliers.

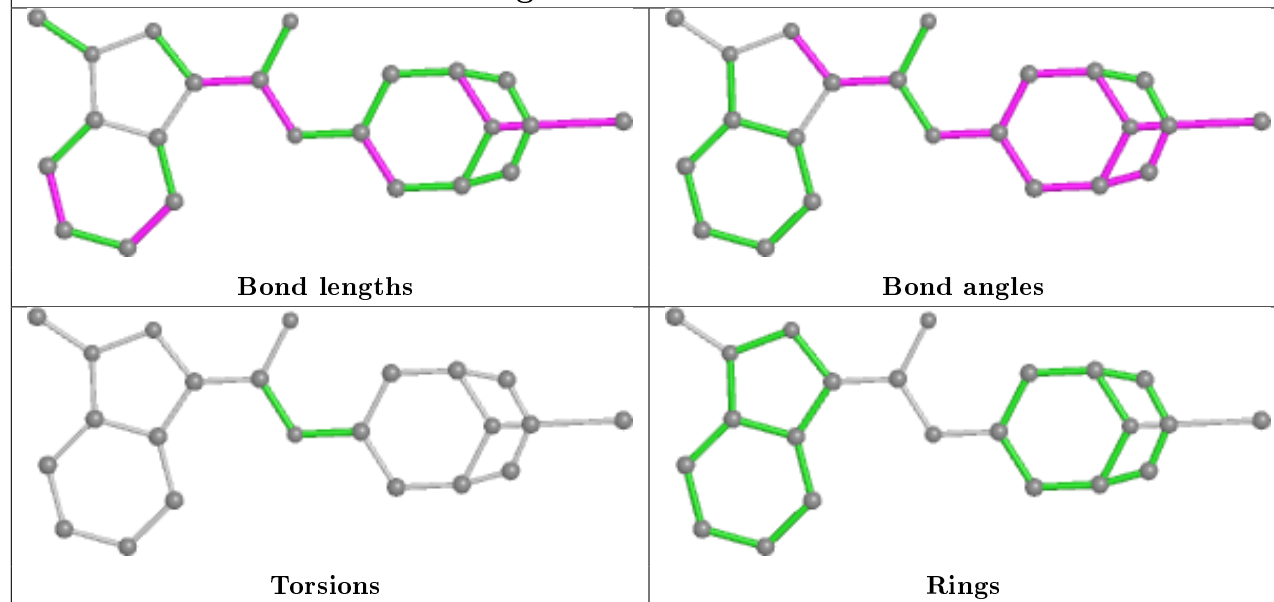
8 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	1207	CWB	2	0
3	G	1207	CWB	1	0
4	A	1208	PO4	1	0
2	F	1206	NAG	1	0
3	E	1207	CWB	1	0
4	H	1208	PO4	1	0
2	D	1208	NAG	1	0
2	J	1206	NAG	2	0

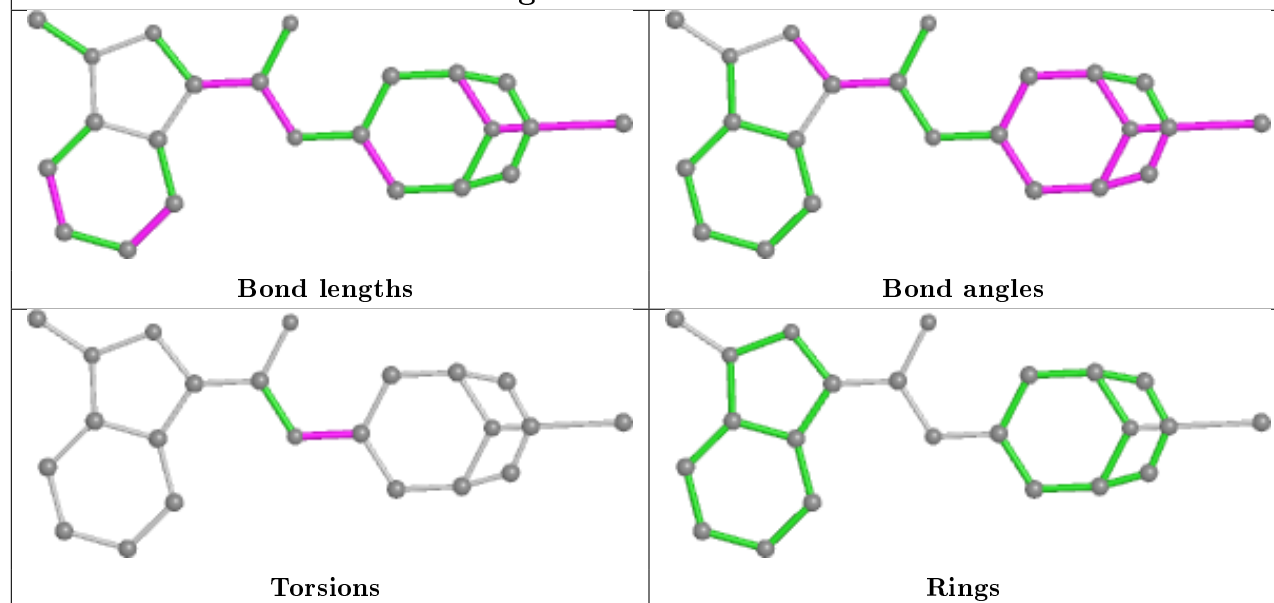
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



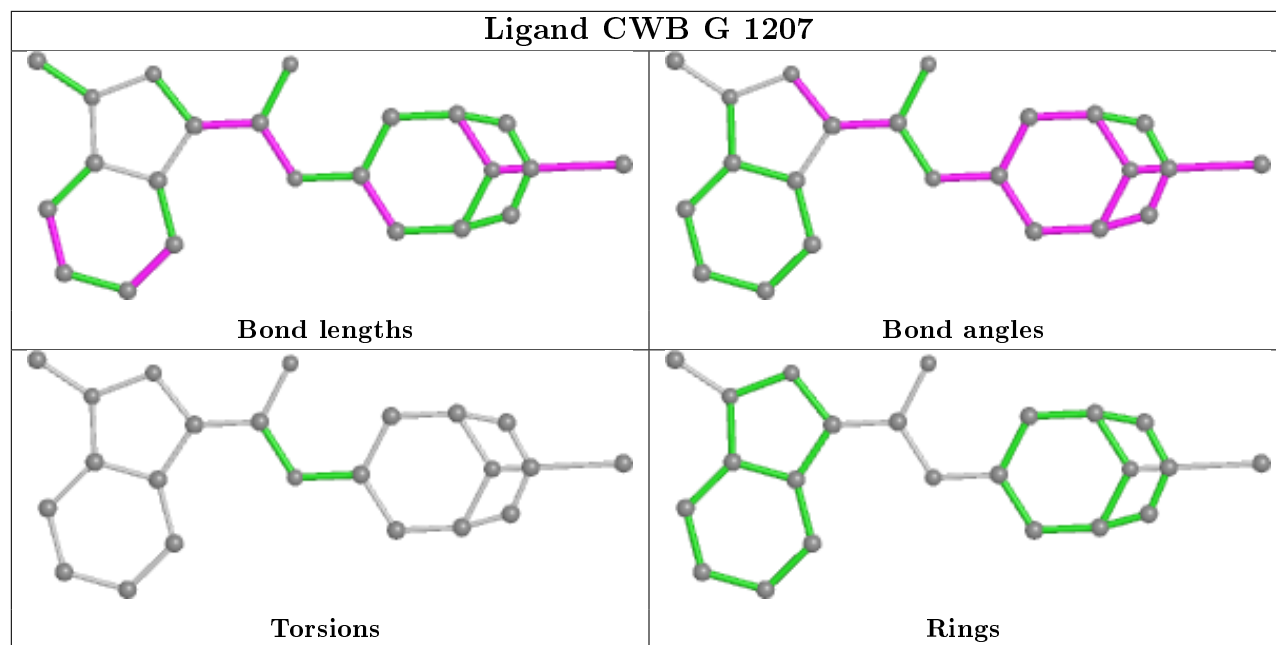
## Ligand CWB C 1207



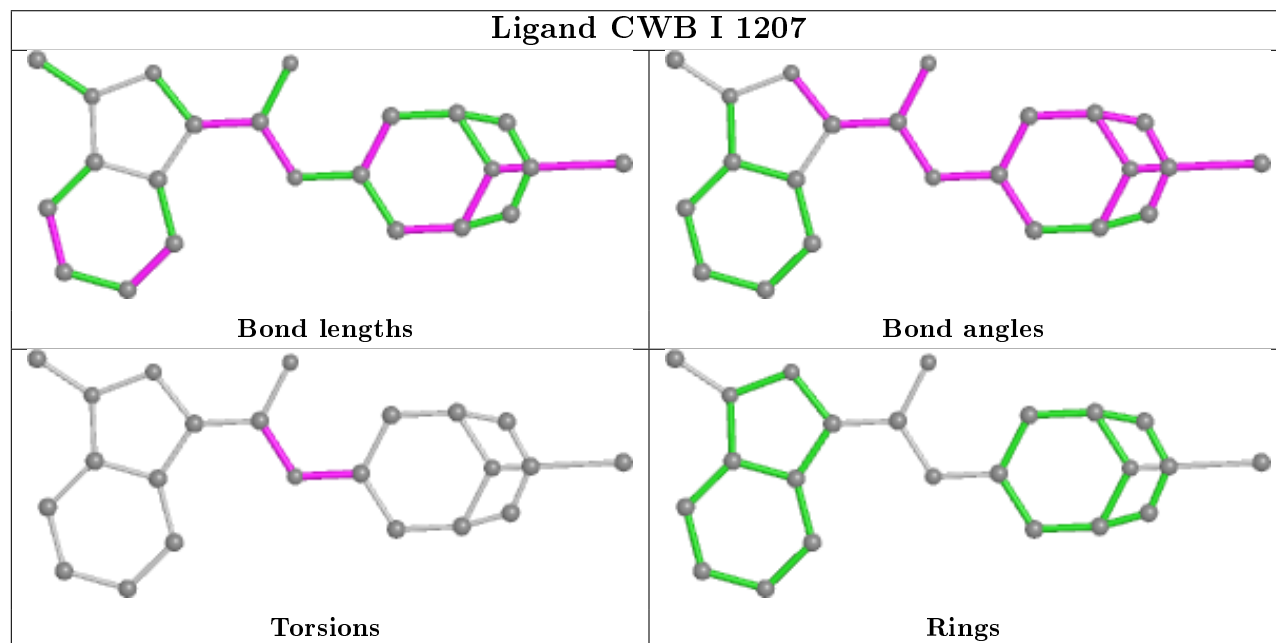
## Ligand CWB F 1207



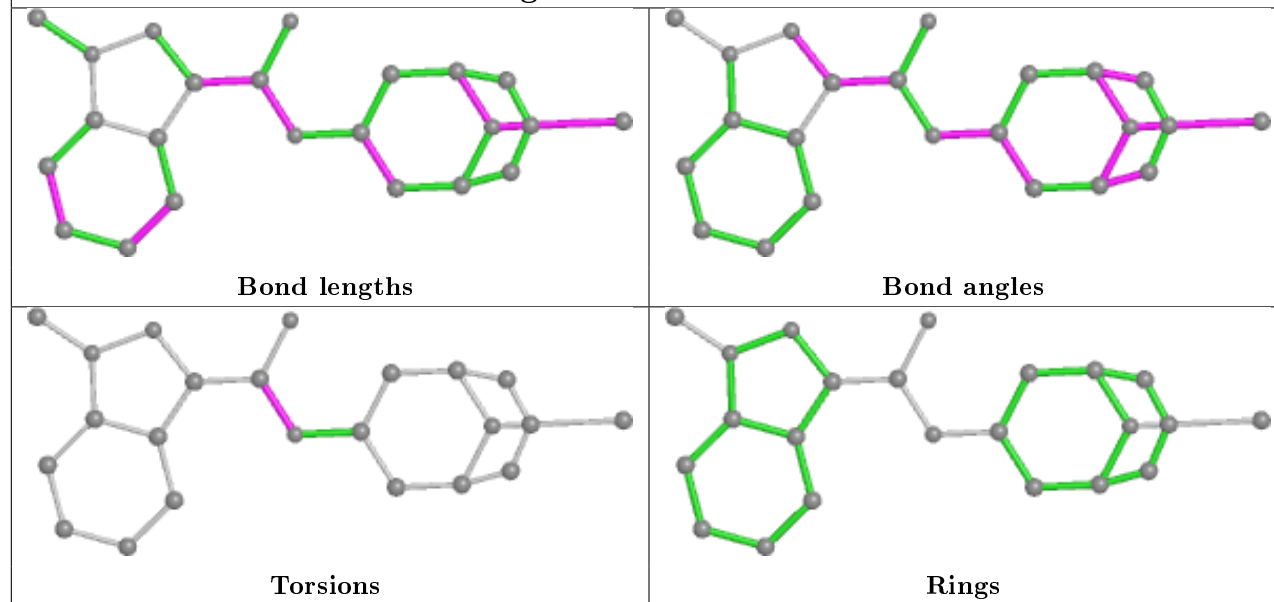
## Ligand CWB G 1207



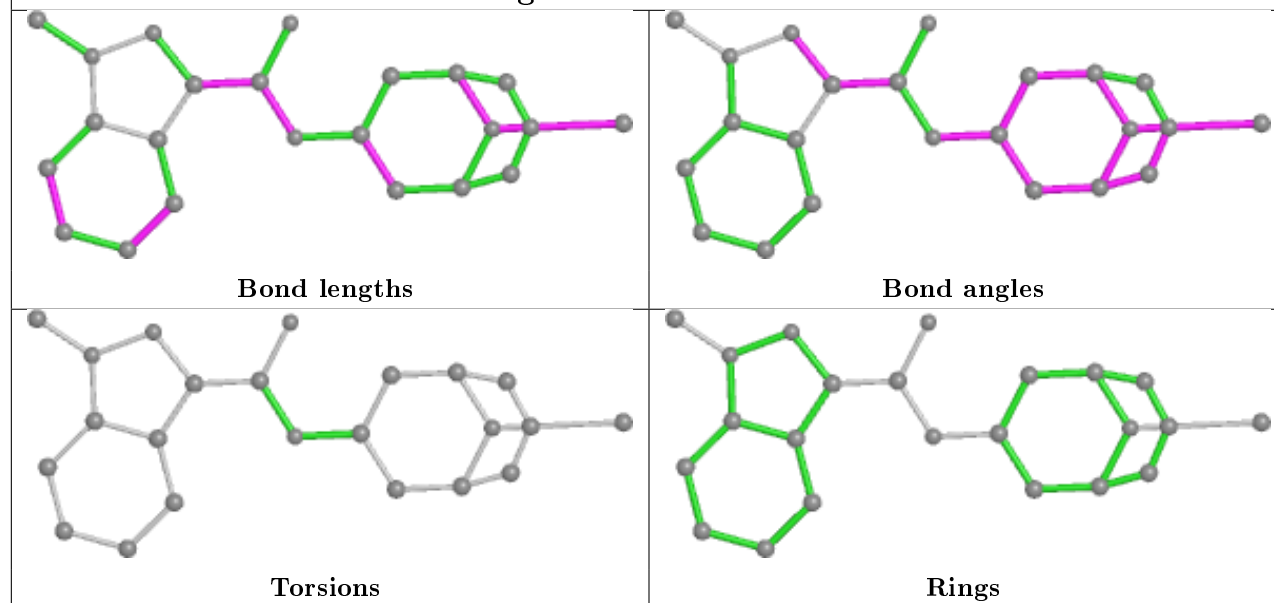
## Ligand CWB I 1207



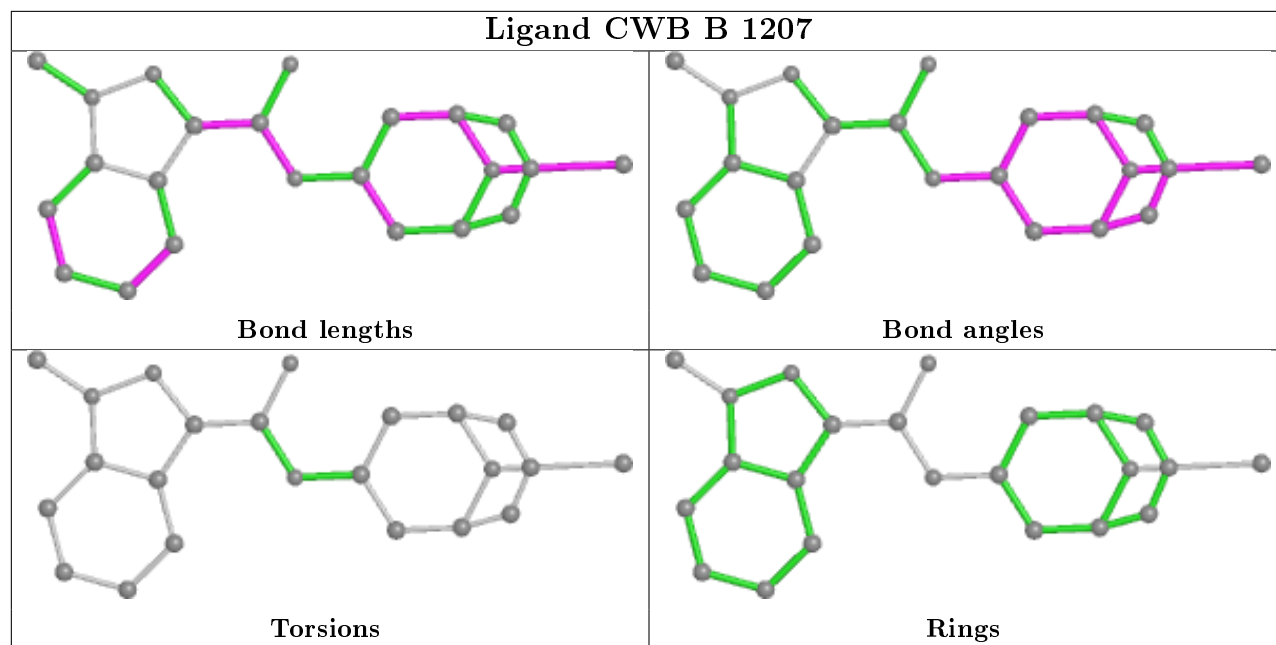
## Ligand CWB J 1207



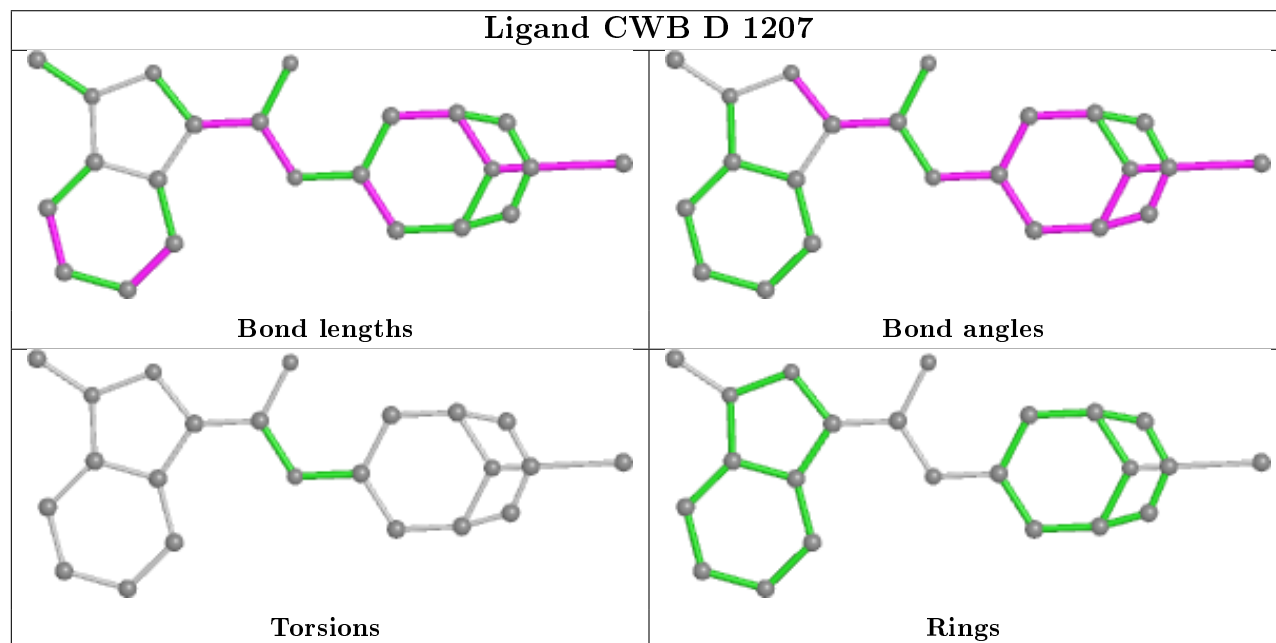
## Ligand CWB E 1207



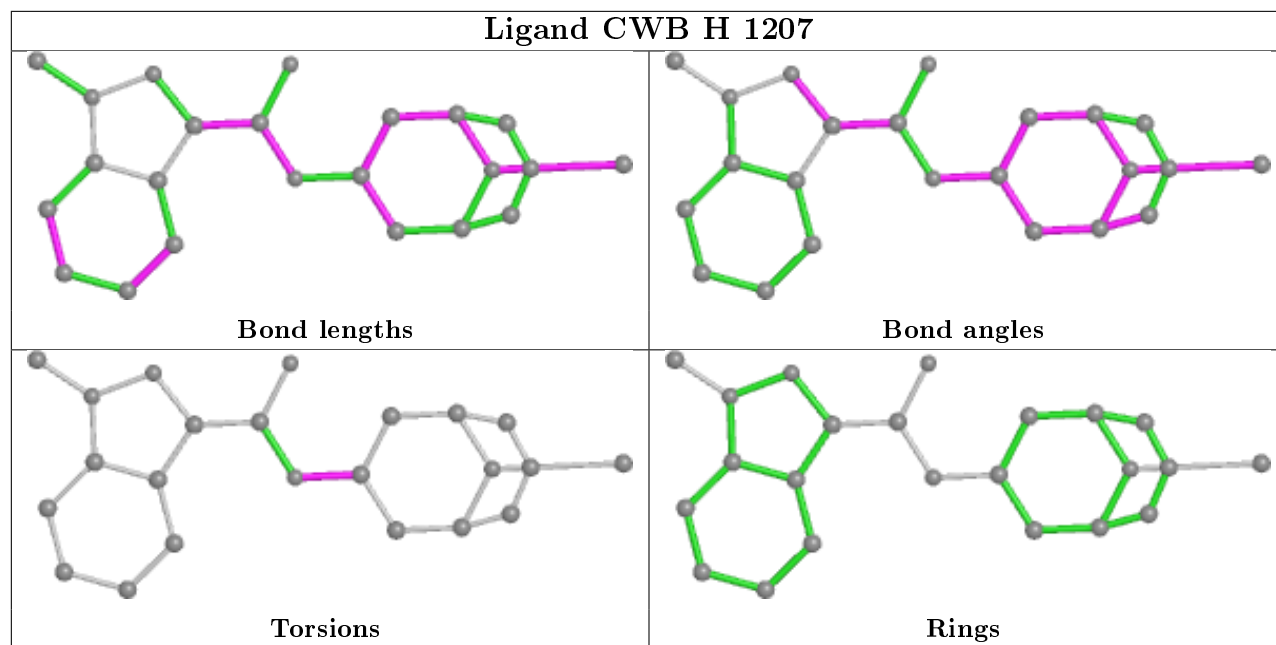
## Ligand CWB B 1207



## Ligand CWB D 1207







## 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, 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	205/205 (100%)	-0.54	1 (0%) 91 89	19, 34, 64, 112	0
1	B	205/205 (100%)	-0.41	1 (0%) 91 89	18, 34, 65, 115	0
1	C	205/205 (100%)	-0.37	1 (0%) 91 89	23, 38, 69, 104	0
1	D	205/205 (100%)	-0.51	0 100 100	14, 34, 70, 107	0
1	E	205/205 (100%)	-0.47	0 100 100	17, 31, 59, 96	0
1	F	205/205 (100%)	0.04	6 (2%) 51 50	35, 59, 112, 157	0
1	G	205/205 (100%)	-0.05	7 (3%) 45 44	33, 59, 98, 119	0
1	H	205/205 (100%)	-0.09	10 (4%) 29 28	27, 51, 102, 139	0
1	I	205/205 (100%)	-0.41	1 (0%) 91 89	24, 40, 72, 113	0
1	J	205/205 (100%)	-0.40	2 (0%) 82 80	24, 41, 76, 140	0
All	All	2050/2050 (100%)	-0.32	29 (1%) 75 73	14, 42, 84, 157	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	14	ARG	4.8
1	H	14	ARG	4.1
1	G	72	ASN	3.8
1	G	68	ASN	3.5
1	H	188	CYS	3.4

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

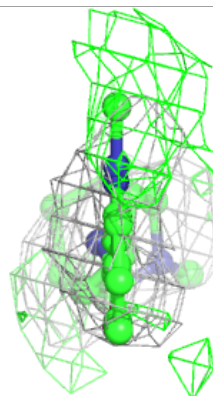
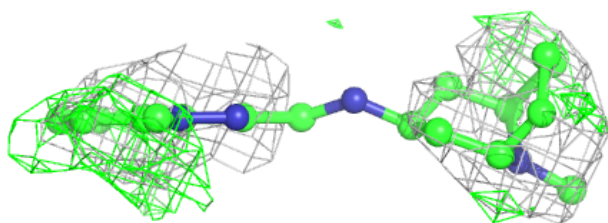
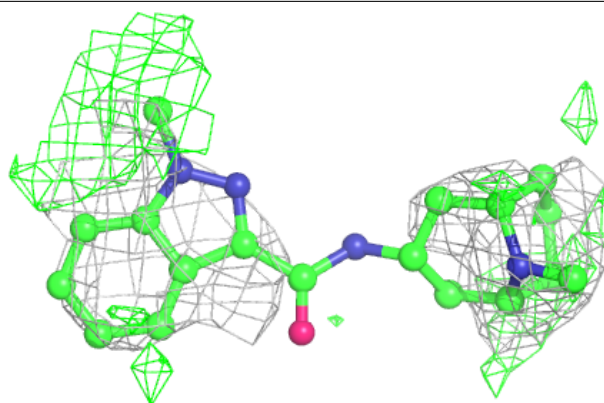
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
4	PO4	G	1208	5/5	0.60	0.30	135,136,139,142	0
3	CWB	J	1207	23/23	0.65	0.27	125,141,152,154	0
5	NA	I	1208	1/1	0.68	0.52	83,83,83,83	0
2	NAG	F	1206	14/15	0.71	0.22	104,107,110,115	0
2	NAG	C	1206	14/15	0.71	0.49	102,114,121,122	0
2	NAG	H	1206	14/15	0.75	0.30	67,90,101,108	0
2	NAG	A	1206	14/15	0.77	0.21	66,78,85,86	0
2	NAG	D	1208	14/15	0.77	0.30	87,101,106,110	0
4	PO4	H	1208	5/5	0.78	0.25	124,128,129,130	0
3	CWB	F	1207	23/23	0.78	0.24	77,104,117,120	0
2	NAG	B	1206	14/15	0.80	0.27	86,95,103,103	0
4	PO4	A	1208	5/5	0.81	0.23	98,107,108,111	0
2	NAG	J	1206	14/15	0.81	0.35	86,98,103,104	0
2	NAG	I	1206	14/15	0.82	0.26	67,77,87,87	0
2	NAG	E	1209	14/15	0.86	0.19	57,67,78,81	0
3	CWB	H	1207	23/23	0.86	0.20	64,83,103,104	0
3	CWB	A	1207	23/23	0.93	0.14	30,42,51,57	0
3	CWB	I	1207	23/23	0.94	0.14	28,37,49,53	0
4	PO4	C	1208	5/5	0.94	0.10	89,94,100,101	0
3	CWB	G	1207	23/23	0.95	0.11	23,39,44,47	0
3	CWB	C	1207	23/23	0.96	0.13	10,31,37,47	0
3	CWB	E	1207	23/23	0.96	0.13	17,28,37,47	0
4	PO4	E	1208	5/5	0.97	0.11	73,75,83,90	0
3	CWB	B	1207	23/23	0.97	0.12	16,25,31,40	0
3	CWB	D	1207	23/23	0.98	0.12	10,24,33,34	0

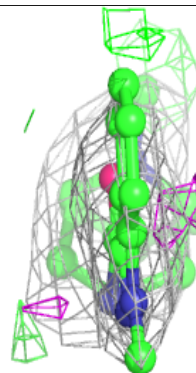
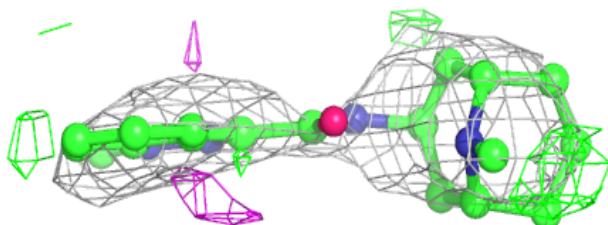
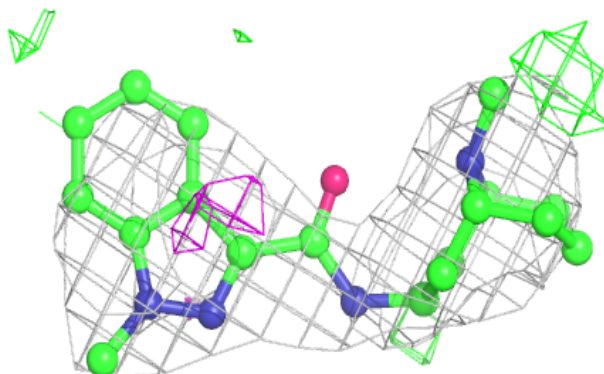
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around CWB J 1207:**

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

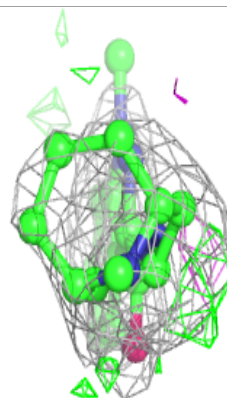
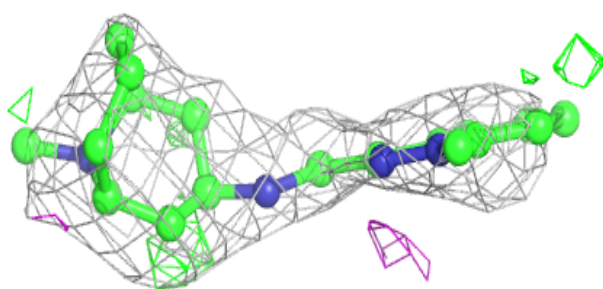
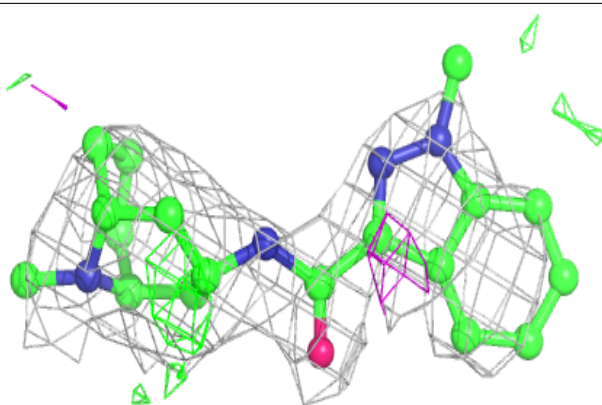
**Electron density around CWB F 1207:**

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

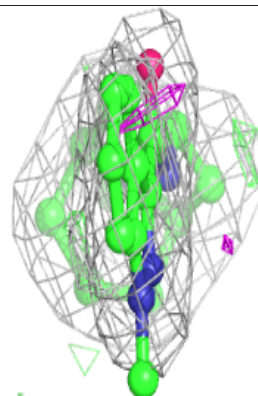
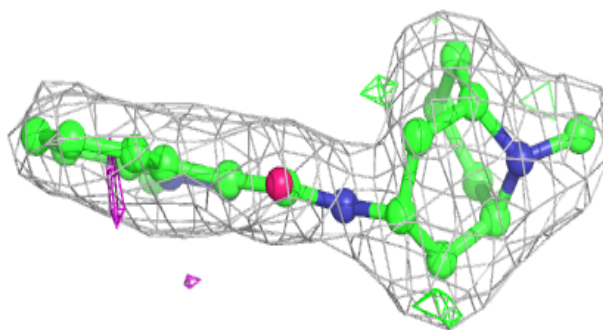
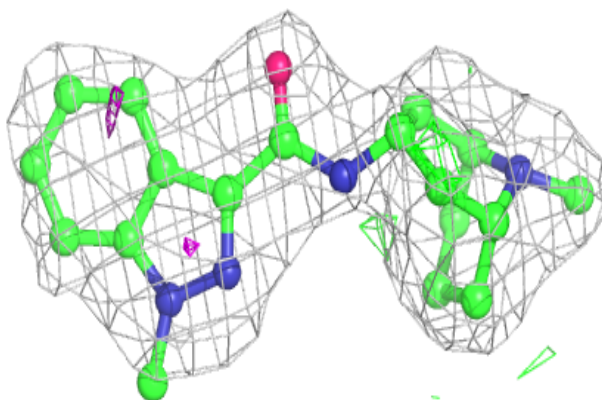


**Electron density around CWB H 1207:**

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

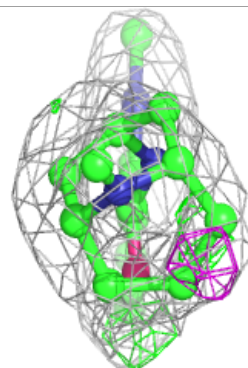
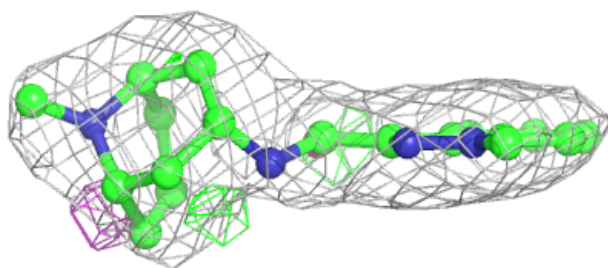
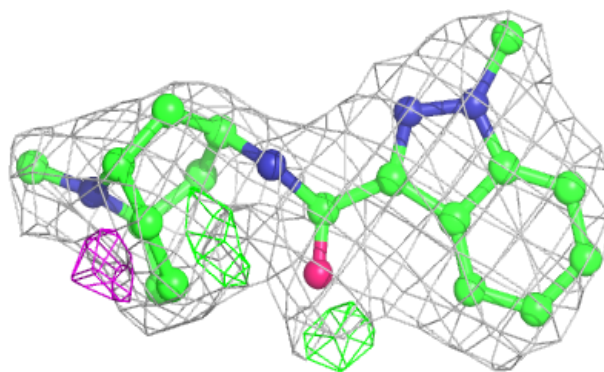
**Electron density around CWB A 1207:**

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

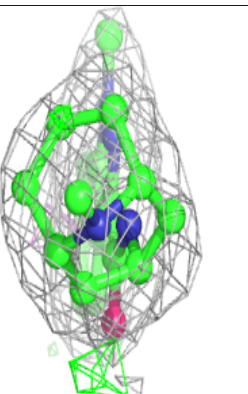
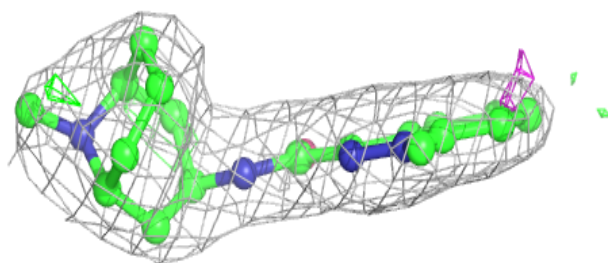
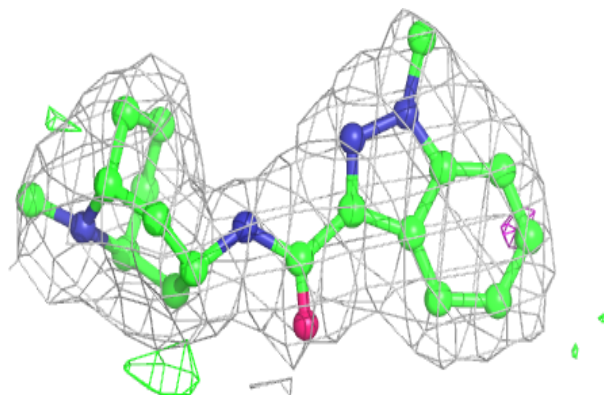


**Electron density around CWB I 1207:**

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

**Electron density around CWB G 1207:**

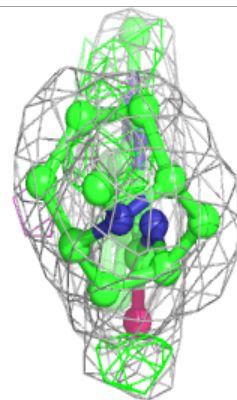
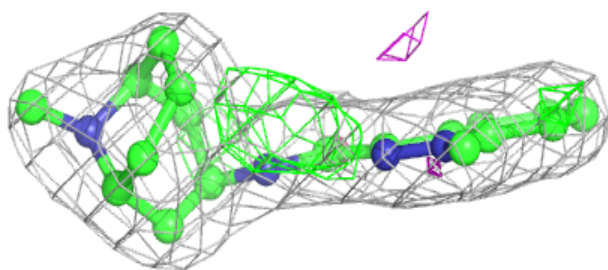
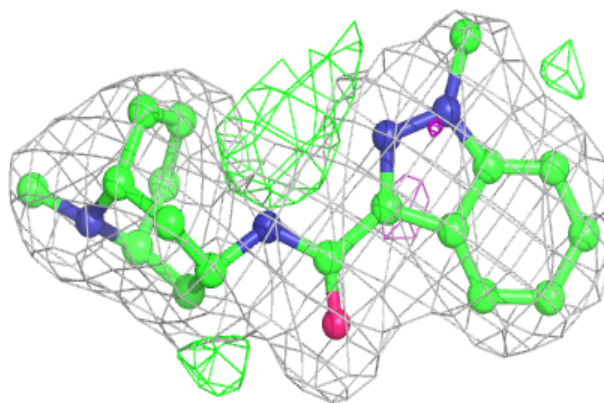
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



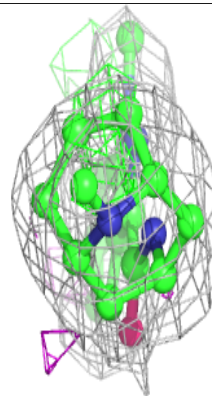
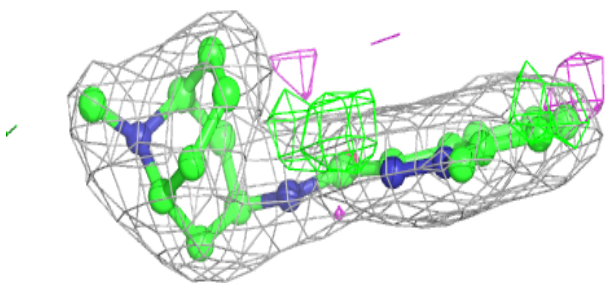
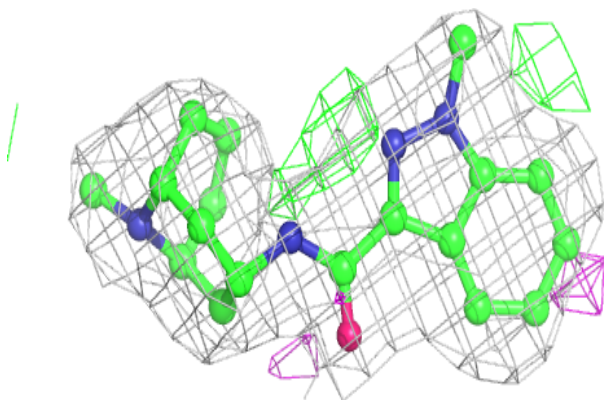


**Electron density around CWB C 1207:**

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

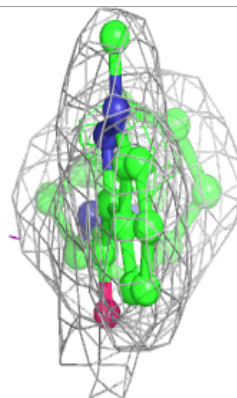
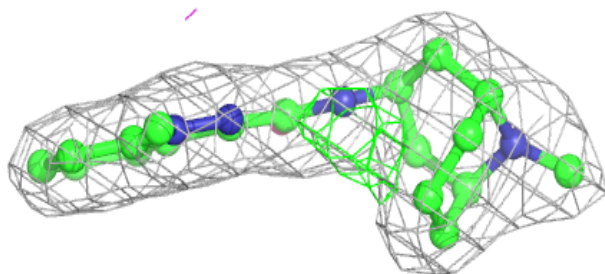
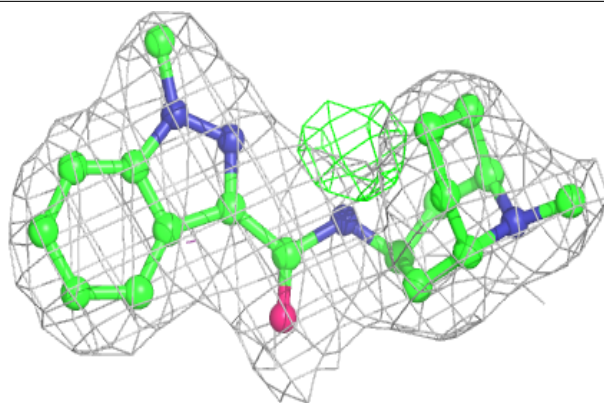
**Electron density around CWB E 1207:**

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

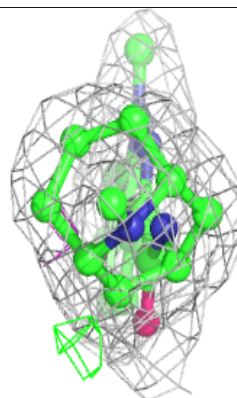
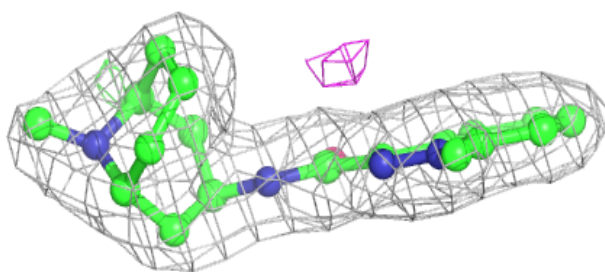
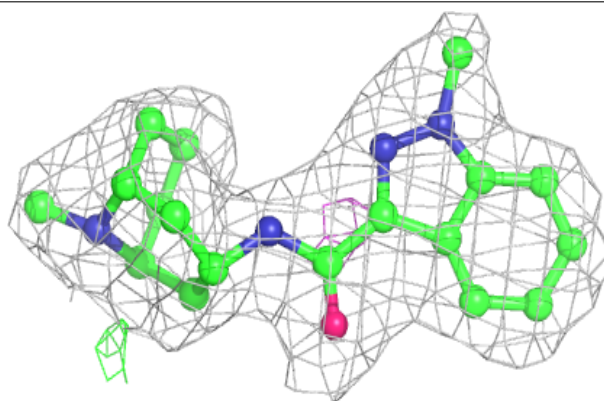


**Electron density around CWB B 1207:**

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

**Electron density around CWB D 1207:**

$2mF_o-DF_c$  (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.