



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:01 PM UTC

PDB ID : 9Q1G / pdb_00009q1g
Title : Blimp-1 with compound 5
Authors : Watson, E.R.
Deposited on : 2025-08-13
Resolution : 3.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

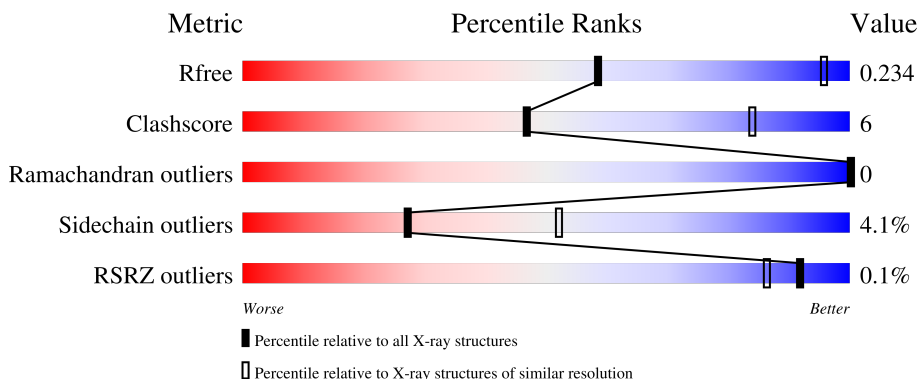
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.






Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1131 (3.80-3.60)
Clashscore	190562	1171 (3.80-3.60)
Ramachandran outliers	187476	1129 (3.80-3.60)
Sidechain outliers	187428	1126 (3.80-3.60)
RSRZ outliers	180081	1130 (3.80-3.60)

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	188	69% 13% 18%
1	B	188	69% 13% 17%
1	C	188	72% 11% 17%
1	D	188	70% 13% 17%
1	E	188	68% 15% 17%

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Mol	Chain	Length	Quality of chain
1	F	188	 70% 13% • 17%
1	G	188	 70% 15% 15%
1	H	188	 70% 13% • 16%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 10520 atoms, of which 128 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 PR domain zinc finger protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	155	1249	808	208	226	7	0	2	0
1	B	156	1277	822	214	234	7	0	2	0
1	C	156	1277	823	214	233	7	0	2	0
1	D	156	1273	818	216	232	7	0	2	0
1	E	156	1278	825	211	235	7	0	2	0
1	F	156	1278	825	211	235	7	0	2	0
1	G	160	1305	839	218	241	7	0	2	0
1	H	158	1287	834	211	235	7	8	2	0

There are 16 discrepancies between the modelled and reference sequences:

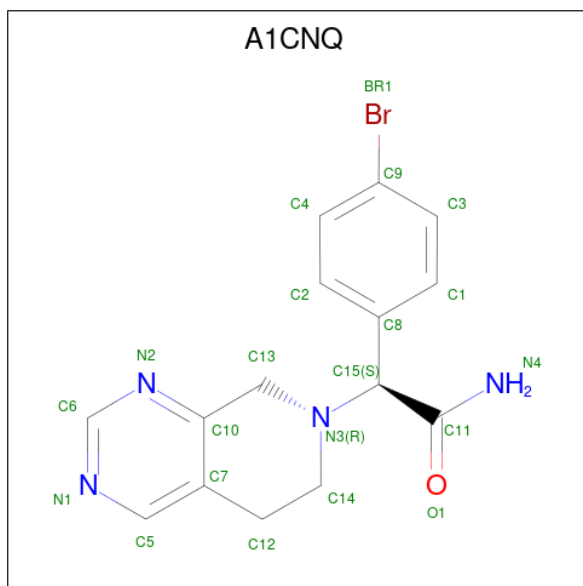
Chain	Residue	Modelled	Actual	Comment	Reference
A	36	GLY	-	expression tag	UNP O75626
A	37	SER	-	expression tag	UNP O75626
B	36	GLY	-	expression tag	UNP O75626
B	37	SER	-	expression tag	UNP O75626
C	36	GLY	-	expression tag	UNP O75626
C	37	SER	-	expression tag	UNP O75626
D	36	GLY	-	expression tag	UNP O75626
D	37	SER	-	expression tag	UNP O75626
E	36	GLY	-	expression tag	UNP O75626
E	37	SER	-	expression tag	UNP O75626
F	36	GLY	-	expression tag	UNP O75626
F	37	SER	-	expression tag	UNP O75626
G	36	GLY	-	expression tag	UNP O75626

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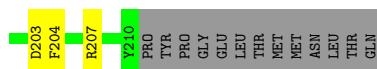
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Chain	Residue	Modelled	Actual	Comment	Reference
G	37	SER	-	expression tag	UNP O75626
H	36	GLY	-	expression tag	UNP O75626
H	37	SER	-	expression tag	UNP O75626

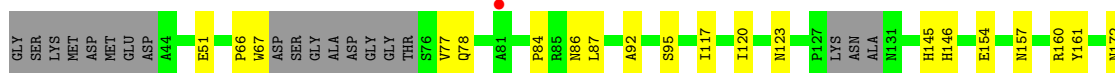
- Molecule 2 is (2S)-2-(4-bromophenyl)-2-(5,8-dihydropyrido[3,4-d]pyrimidin-7(6H)-yl)acetamide (CCD ID: A1CNQ) (formula: C₁₅H₁₅BrN₄O) (labeled as "Ligand of Interest" by depositor).



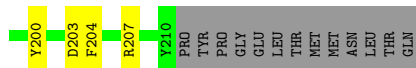
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	Br	C	H	N	O		
2	A	1	Total	Br	C	H	N	O	16	0
			37	1	15	16	4	1		
2	B	1	Total	Br	C	H	N	O	16	0
			37	1	15	16	4	1		
2	C	1	Total	Br	C	H	N	O	16	0
			37	1	15	16	4	1		
2	D	1	Total	Br	C	H	N	O	16	0
			37	1	15	16	4	1		
2	E	1	Total	Br	C	H	N	O	16	0
			37	1	15	16	4	1		
2	F	1	Total	Br	C	H	N	O	16	0
			37	1	15	16	4	1		
2	G	1	Total	Br	C	H	N	O	16	0
			37	1	15	16	4	1		
2	H	1	Total	Br	C	H	N	O	16	0
			37	1	15	16	4	1		



- Molecule 1: PR domain zinc finger protein 1



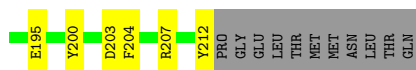
- Molecule 1: PR domain zinc finger protein 1



- Molecule 1: PR domain zinc finger protein 1



- Molecule 1: PR domain zinc finger protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	243.42Å 47.87Å 180.66Å 90.00° 129.18° 90.00°	Depositor
Resolution (Å)	38.09 – 3.70 38.09 – 3.70	Depositor EDS
% Data completeness (in resolution range)	77.4 (38.09-3.70) 77.2 (38.09-3.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 3.66Å)	Xtrriage
Refinement program	BUSTER 2.11.8 (10-JUL-2024)	Depositor
R, R_{free}	0.216 , 0.253 0.224 , 0.234	Depositor DCC
R_{free} test set	660 reflections (3.71%)	wwPDB-VP
Wilson B-factor (Å ²)	66.9	Xtrriage
Anisotropy	0.445	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 140.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	10520	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: A1CNQ

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	0.58	0/1287	0.92	0/1756
1	B	0.57	0/1314	0.91	2/1788 (0.1%)
1	C	0.53	0/1315	0.89	0/1790
1	D	0.56	0/1310	0.90	0/1783
1	E	0.55	0/1316	0.90	0/1792
1	F	0.54	0/1316	0.90	0/1792
1	G	0.56	0/1343	0.92	2/1828 (0.1%)
1	H	0.57	0/1327	0.92	1/1810 (0.1%)
All	All	0.56	0/10528	0.91	5/14339 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	211	PRO	N-CA-CB	7.46	109.27	103.30
1	G	213	PRO	N-CA-CB	6.17	109.78	103.00
1	H	122	THR	N-CA-C	5.57	118.87	112.97
1	B	157	ASN	CA-C-N	5.19	128.98	120.63
1	B	157	ASN	C-N-CA	5.19	128.98	120.63

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	1249	0	1139	16	0
1	B	1277	0	1186	17	0
1	C	1277	0	1180	11	0
1	D	1273	0	1175	14	0
1	E	1278	0	1182	16	0
1	F	1278	0	1182	17	0
1	G	1305	0	1194	16	0
1	H	1287	0	1181	14	0
2	A	21	16	0	0	0
2	B	21	16	0	0	0
2	C	21	16	0	0	0
2	D	21	16	0	0	0
2	E	21	16	0	0	0
2	F	21	16	0	0	0
2	G	21	16	0	0	0
2	H	21	16	0	0	0
All	All	10392	128	9419	112	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 6.

The worst 5 of 112 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:G:120:ILE:HG23	1:G:146:HIS:CD2	2.19	0.77
1:D:120:ILE:HG23	1:D:146:HIS:CD2	2.20	0.77
1:E:120:ILE:HG23	1:E:146:HIS:CD2	2.20	0.76
1:C:120:ILE:HG23	1:C:146:HIS:CD2	2.22	0.74
1:H:120:ILE:HG23	1:H:146:HIS:CD2	2.22	0.74

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	151/188 (80%)	143 (95%)	8 (5%)	0	100	100
1	B	152/188 (81%)	143 (94%)	9 (6%)	0	100	100
1	C	152/188 (81%)	143 (94%)	9 (6%)	0	100	100
1	D	152/188 (81%)	144 (95%)	8 (5%)	0	100	100
1	E	152/188 (81%)	142 (93%)	10 (7%)	0	100	100
1	F	152/188 (81%)	145 (95%)	7 (5%)	0	100	100
1	G	156/188 (83%)	148 (95%)	8 (5%)	0	100	100
1	H	154/188 (82%)	144 (94%)	10 (6%)	0	100	100
All	All	1221/1504 (81%)	1152 (94%)	69 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	125/164 (76%)	118 (94%)	7 (6%)	19	46
1	B	132/164 (80%)	128 (97%)	4 (3%)	36	57
1	C	131/164 (80%)	126 (96%)	5 (4%)	29	53
1	D	130/164 (79%)	124 (95%)	6 (5%)	24	49
1	E	132/164 (80%)	126 (96%)	6 (4%)	24	49
1	F	132/164 (80%)	128 (97%)	4 (3%)	36	57
1	G	133/164 (81%)	128 (96%)	5 (4%)	29	53
1	H	131/164 (80%)	126 (96%)	5 (4%)	29	53
All	All	1046/1312 (80%)	1004 (96%)	42 (4%)	27	52

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	78	GLN
1	G	154	GLU

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Mol	Chain	Res	Type
1	F	120	ILE
1	G	43	ASP
1	H	77	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	193	ASN
1	G	194	GLN
1	H	193	ASN
1	H	78	GLN
1	G	193	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 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	$\# Z > 2$
2	A1CNQ	H	501	-	23,23,23	0.82	1 (4%)	25,32,32	0.45	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	A1CNQ	G	501	-	23,23,23	0.86	2 (8%)	25,32,32	0.42	0
2	A1CNQ	D	501	-	23,23,23	0.84	2 (8%)	25,32,32	0.43	0
2	A1CNQ	C	501	-	23,23,23	0.83	2 (8%)	25,32,32	0.46	0
2	A1CNQ	F	501	-	23,23,23	0.84	1 (4%)	25,32,32	0.38	0
2	A1CNQ	E	501	-	23,23,23	0.83	1 (4%)	25,32,32	0.50	0
2	A1CNQ	A	501	-	23,23,23	0.83	1 (4%)	25,32,32	0.42	0
2	A1CNQ	B	501	-	23,23,23	0.85	2 (8%)	25,32,32	0.42	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	A1CNQ	H	501	-	-	4/12/21/21	0/3/3/3
2	A1CNQ	G	501	-	-	4/12/21/21	0/3/3/3
2	A1CNQ	D	501	-	-	4/12/21/21	0/3/3/3
2	A1CNQ	C	501	-	-	4/12/21/21	0/3/3/3
2	A1CNQ	F	501	-	-	4/12/21/21	0/3/3/3
2	A1CNQ	E	501	-	-	4/12/21/21	0/3/3/3
2	A1CNQ	A	501	-	-	4/12/21/21	0/3/3/3
2	A1CNQ	B	501	-	-	4/12/21/21	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	501	A1CNQ	C15-N3	3.36	1.53	1.47
2	B	501	A1CNQ	C15-N3	3.29	1.53	1.47
2	D	501	A1CNQ	C15-N3	3.26	1.53	1.47
2	F	501	A1CNQ	C15-N3	3.25	1.53	1.47
2	E	501	A1CNQ	C15-N3	3.24	1.53	1.47

There are no bond angle outliers.

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	A1CNQ	N4-C11-C15-N3

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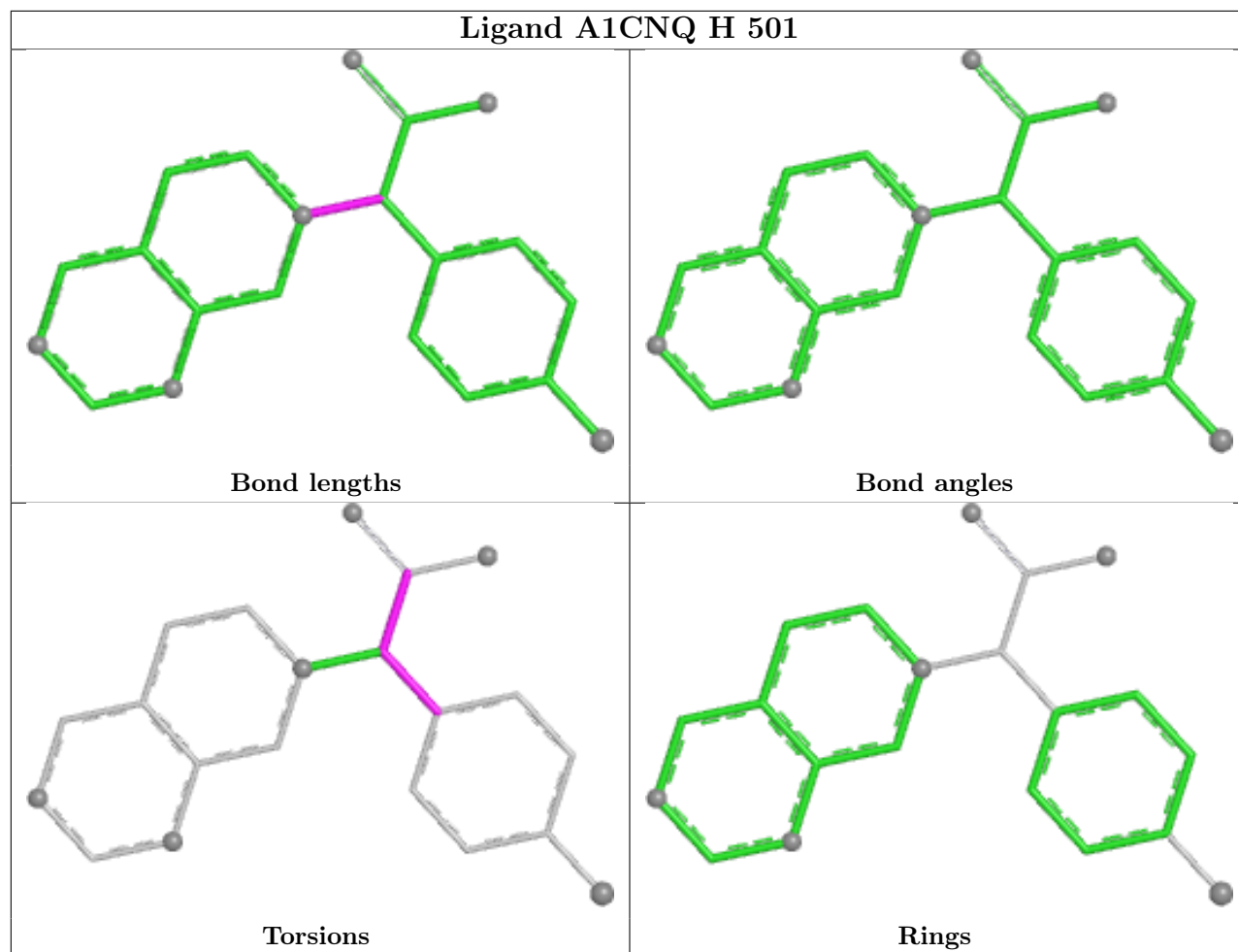
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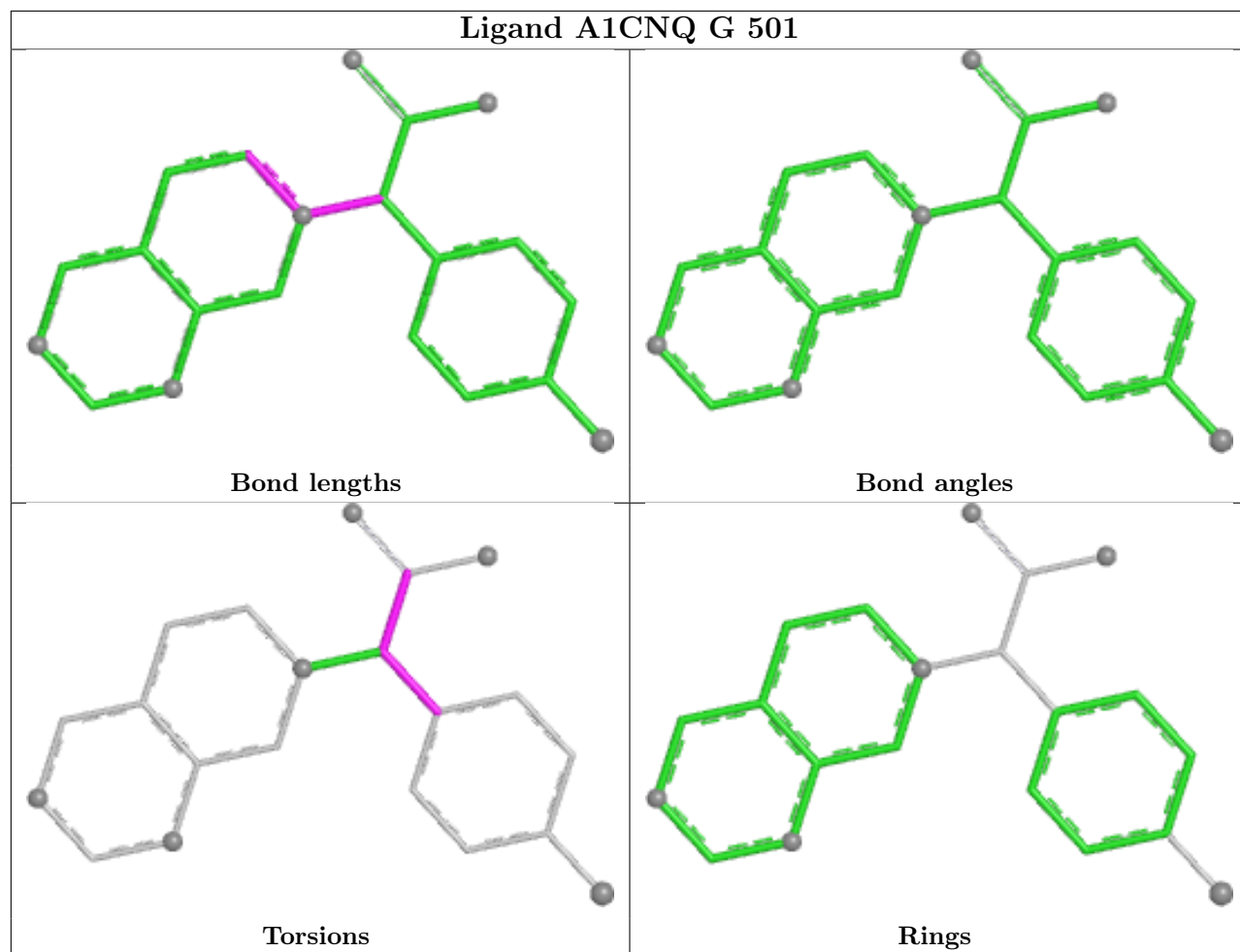
Mol	Chain	Res	Type	Atoms
2	A	501	A1CNQ	O1-C11-C15-N3
2	C	501	A1CNQ	N4-C11-C15-N3
2	C	501	A1CNQ	O1-C11-C15-N3
2	D	501	A1CNQ	N4-C11-C15-N3

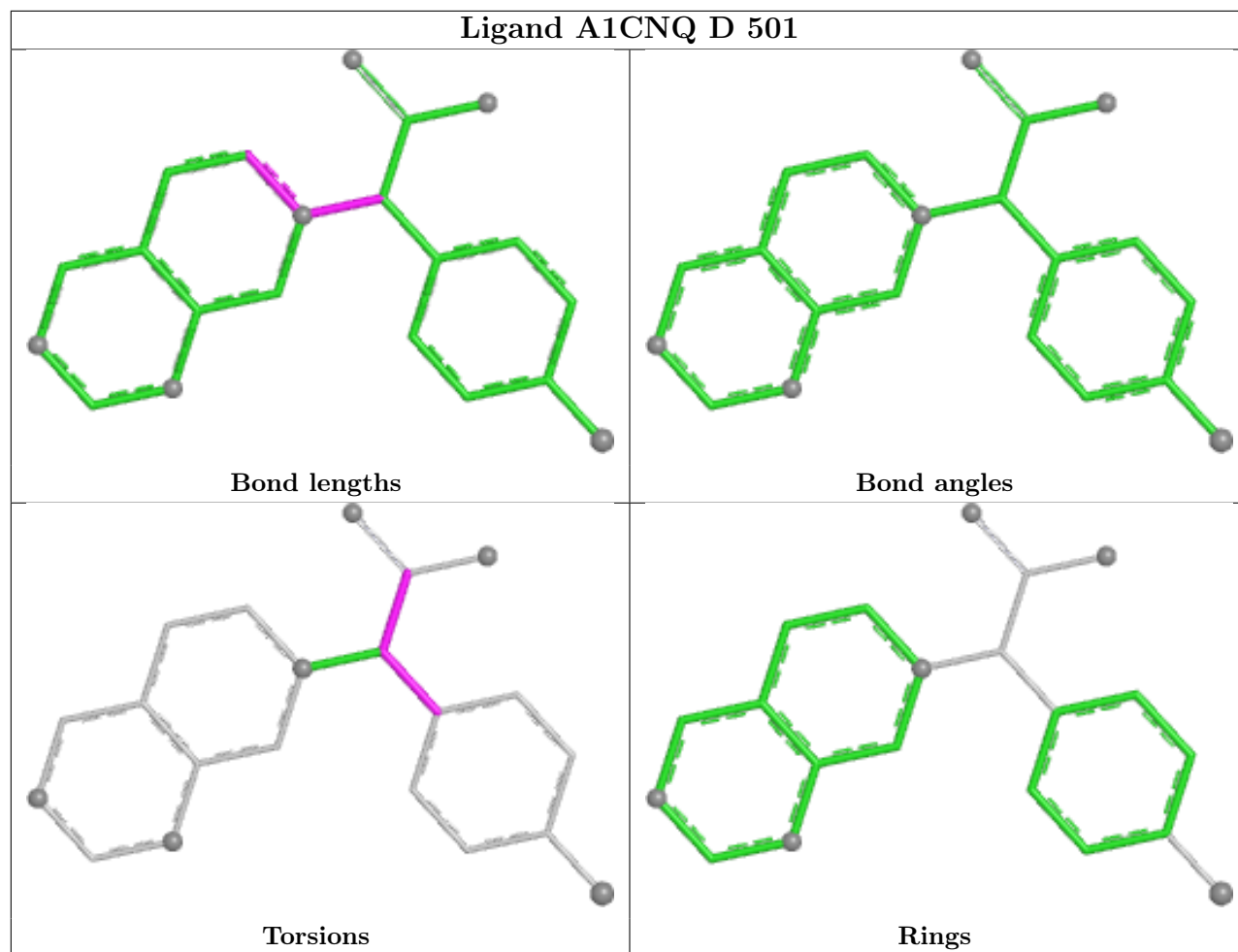
There are no ring outliers.

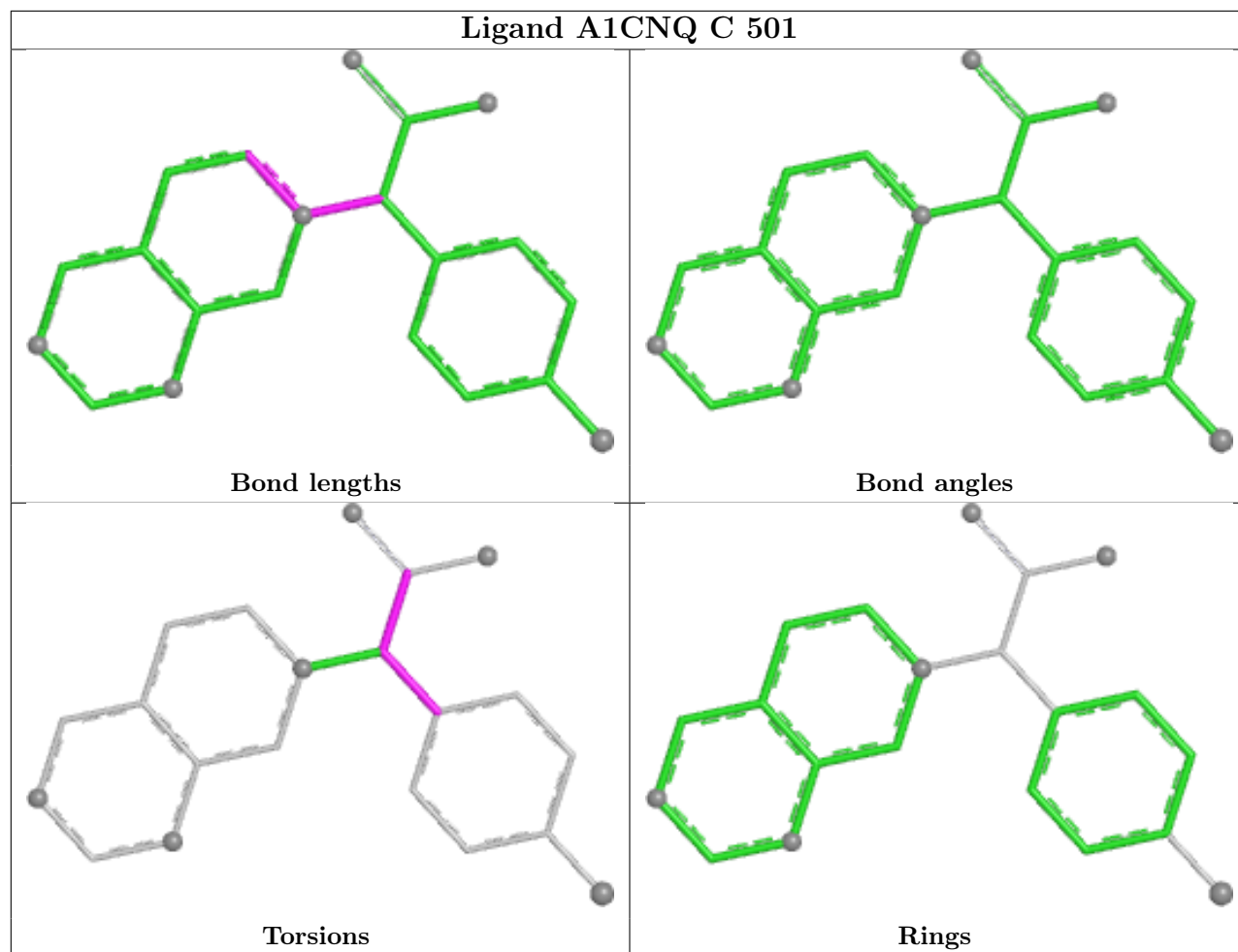
No monomer is involved in short contacts.

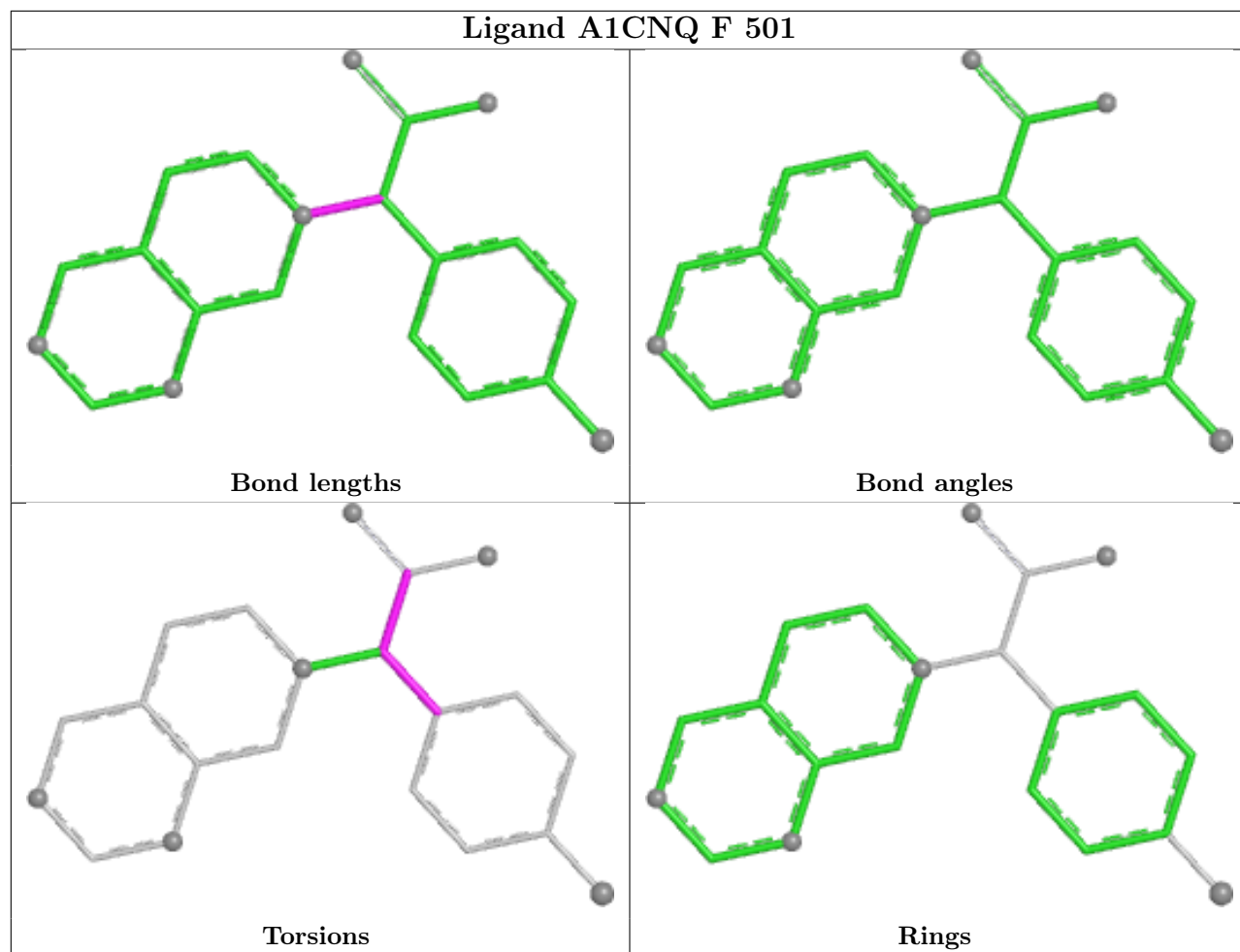
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

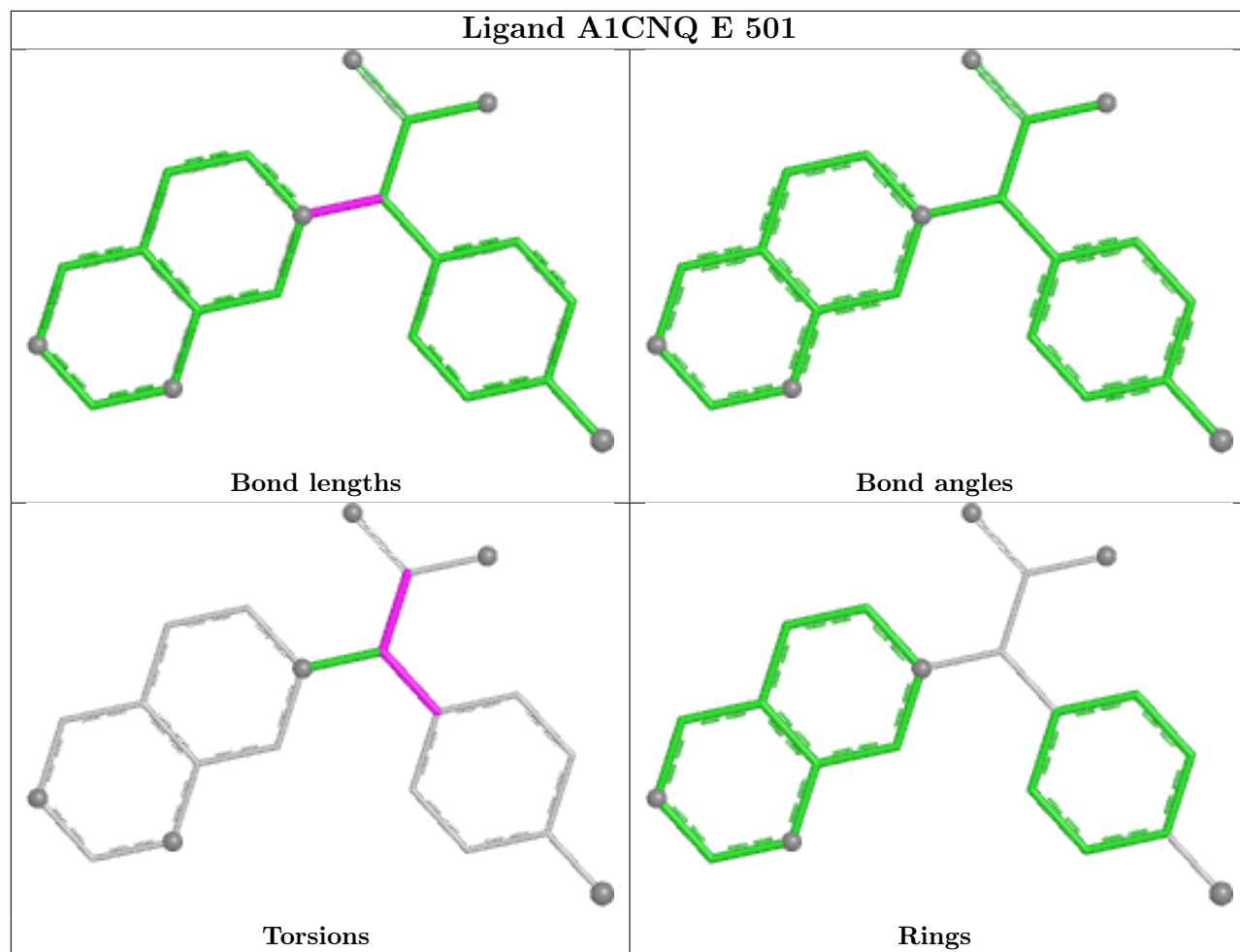


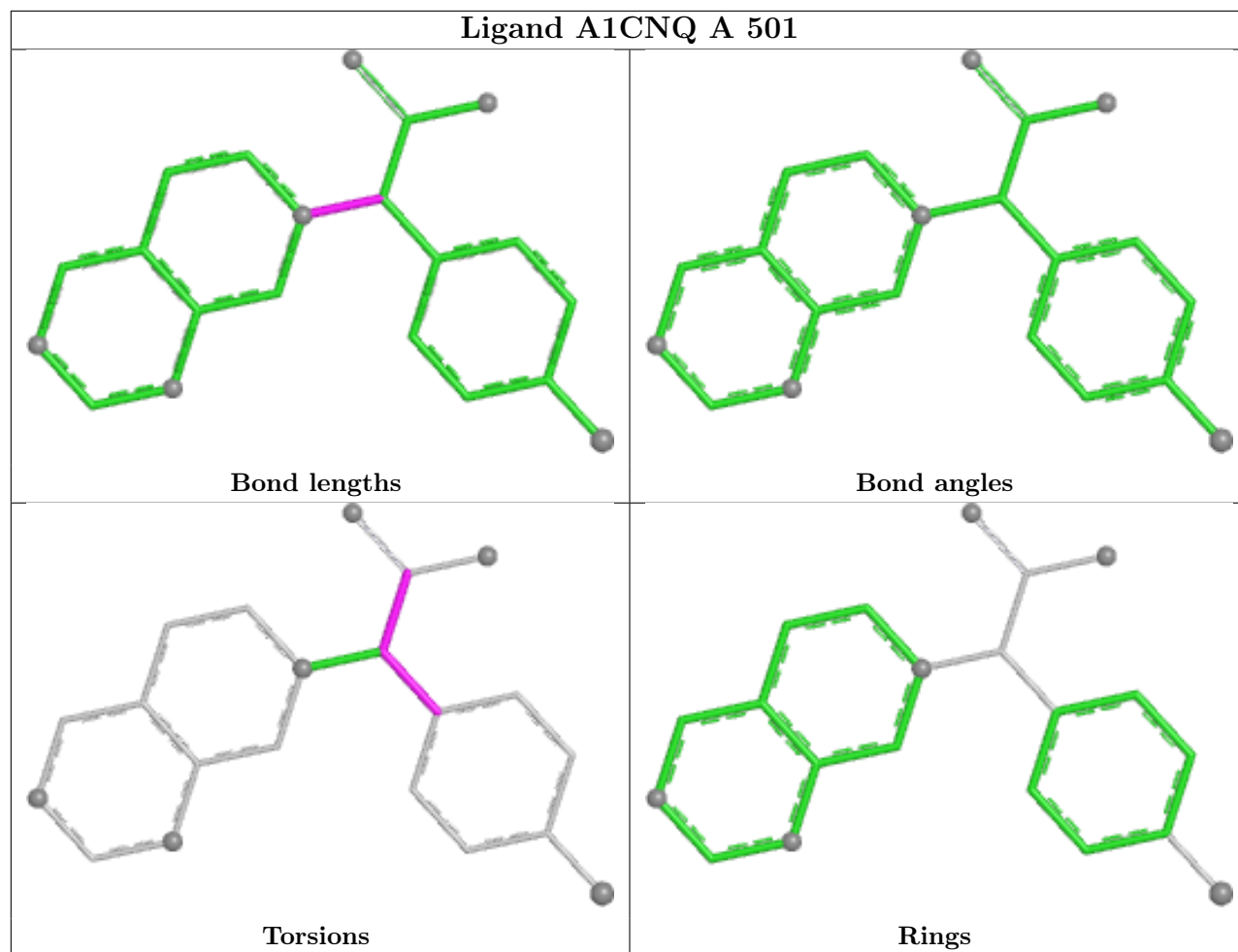


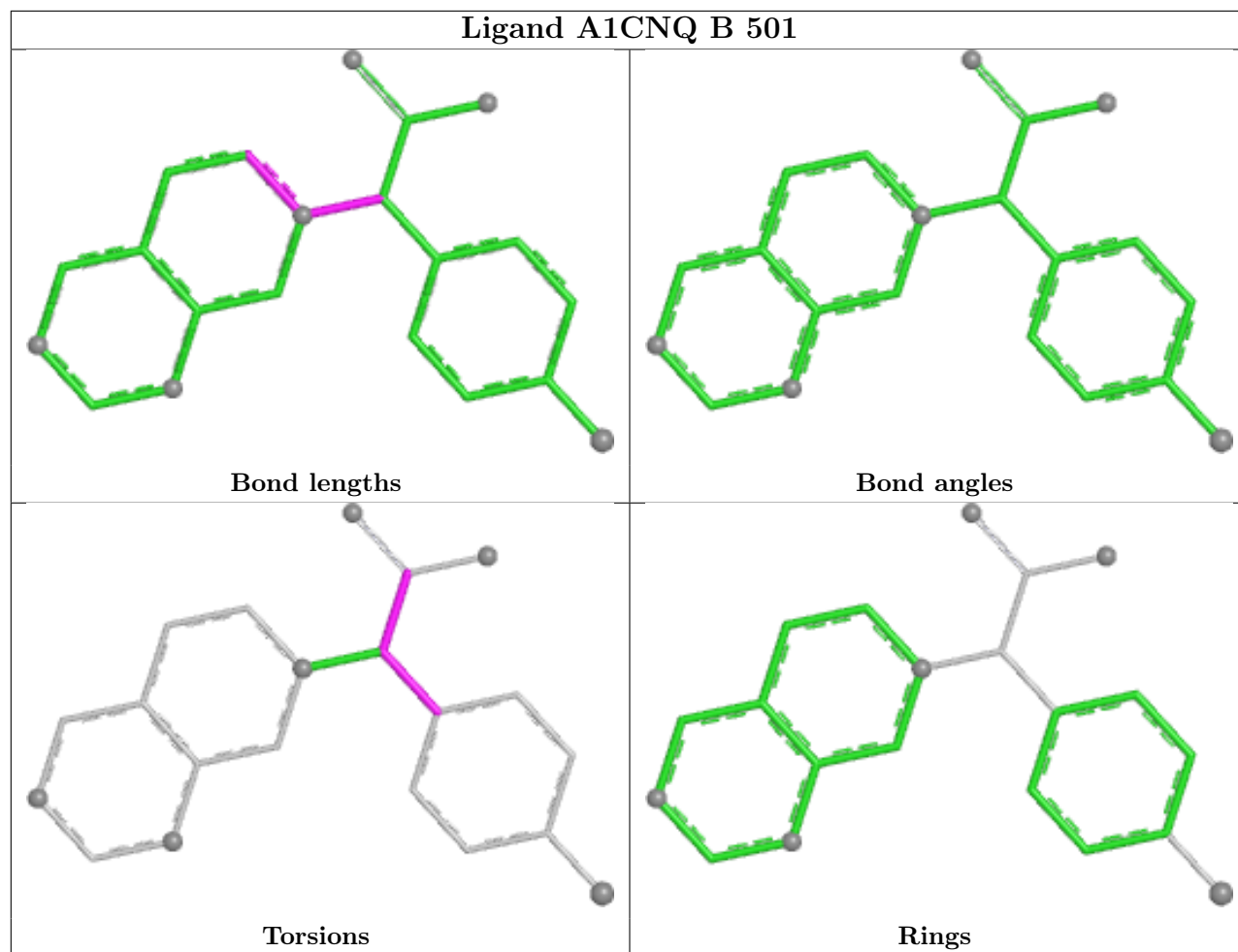












5.7 Other polymers [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	155/188 (82%)	-0.34	0 100 100	25, 76, 119, 183	2 (1%)
1	B	156/188 (82%)	-0.34	0 100 100	23, 89, 164, 218	2 (1%)
1	C	156/188 (82%)	-0.22	0 100 100	35, 113, 186, 222	2 (1%)
1	D	156/188 (82%)	-0.37	0 100 100	38, 93, 139, 196	2 (1%)
1	E	156/188 (82%)	-0.29	1 (0%) 85 66	25, 94, 188, 249	2 (1%)
1	F	156/188 (82%)	-0.44	0 100 100	34, 82, 133, 169	2 (1%)
1	G	160/188 (85%)	-0.31	0 100 100	38, 89, 176, 243	2 (1%)
1	H	157/188 (83%)	-0.25	0 100 100	52, 99, 175, 259	1 (0%)
All	All	1252/1504 (83%)	-0.32	1 (0%) 92 86	23, 91, 171, 259	15 (1%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	81	ALA	2.6

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 oligosaccharides in this entry.

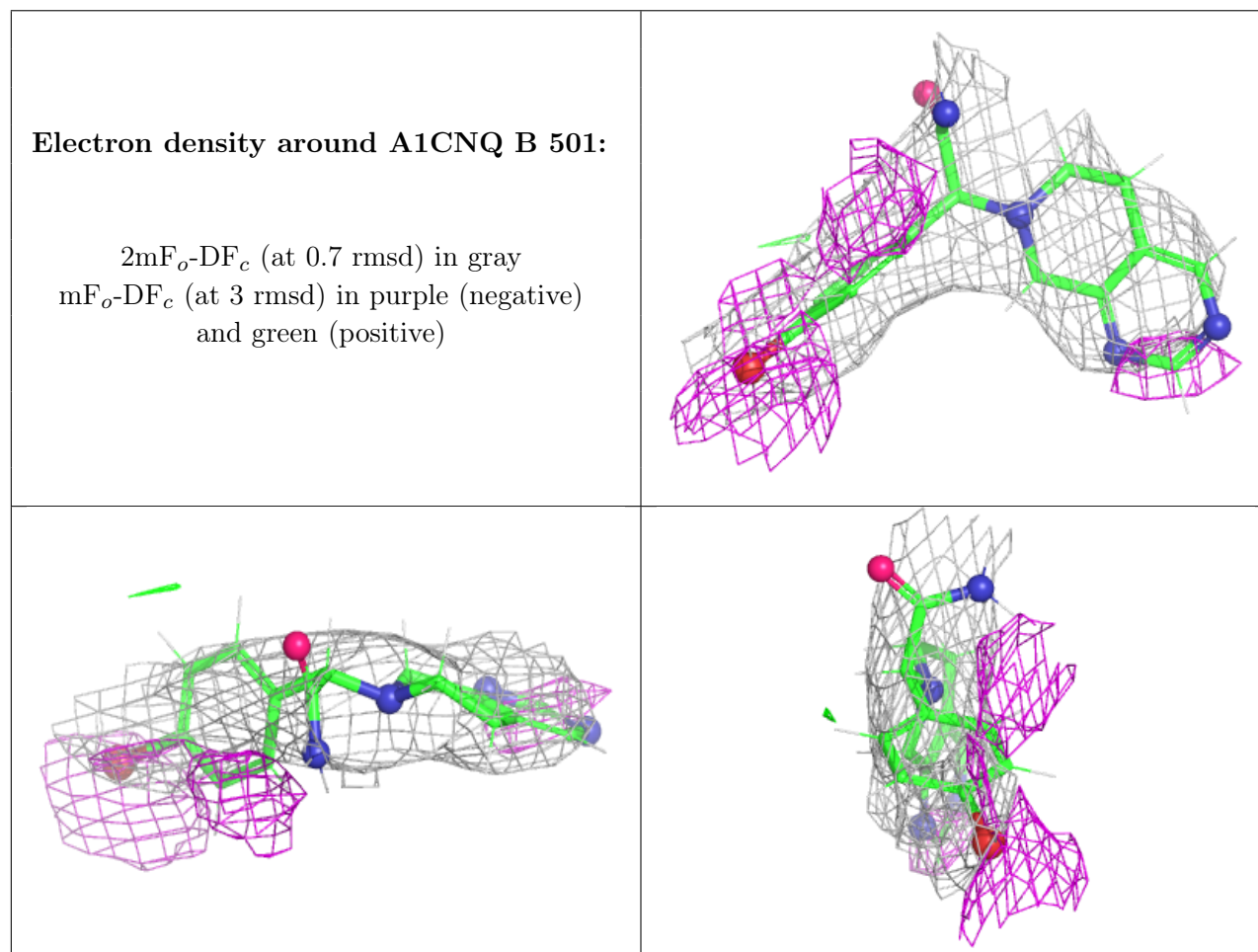
6.4 Ligands [i](#)

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.

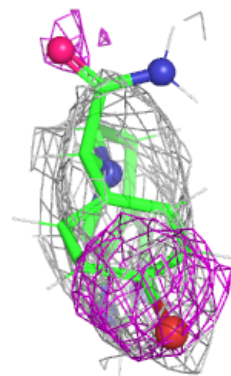
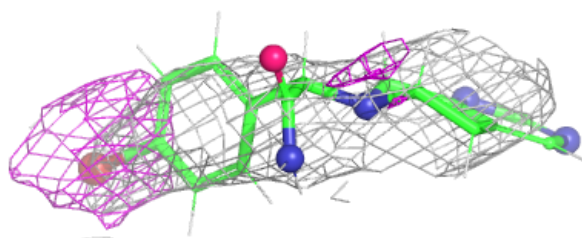
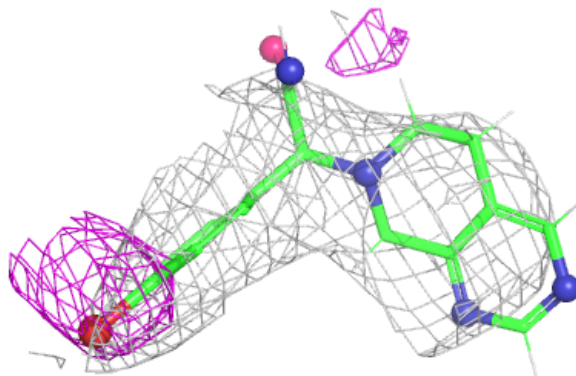
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	A1CNQ	B	501	21/21	0.87	0.12	59,79,102,145	16
2	A1CNQ	H	501	21/21	0.88	0.12	75,95,110,142	16
2	A1CNQ	D	501	21/21	0.89	0.11	78,90,114,122	16
2	A1CNQ	G	501	21/21	0.90	0.11	68,99,112,142	16
2	A1CNQ	E	501	21/21	0.90	0.11	92,104,129,140	16
2	A1CNQ	F	501	21/21	0.93	0.10	51,68,93,101	16
2	A1CNQ	C	501	21/21	0.94	0.08	84,104,118,177	16
2	A1CNQ	A	501	21/21	0.97	0.07	42,65,80,85	16

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.



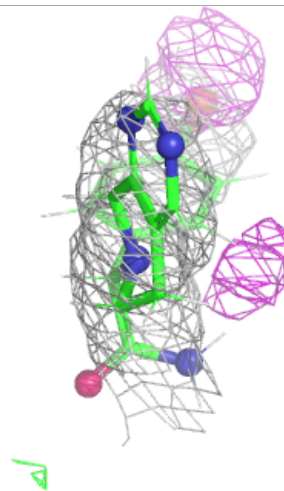
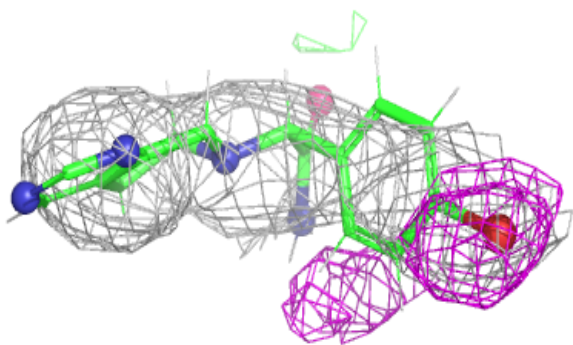
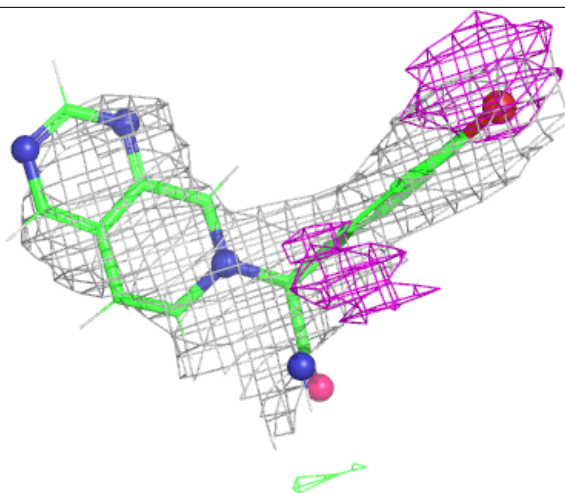
Electron density around A1CNQ H 501:

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



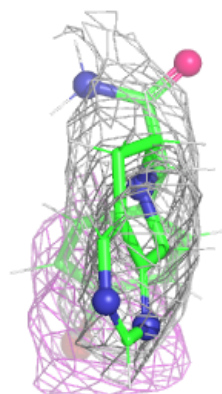
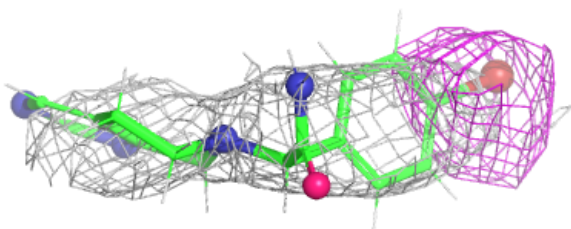
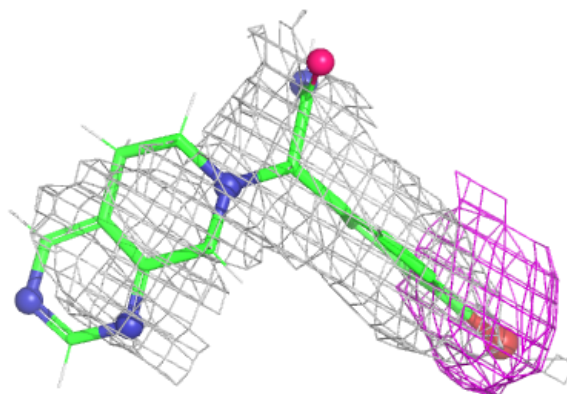
Electron density around A1CNQ D 501:

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

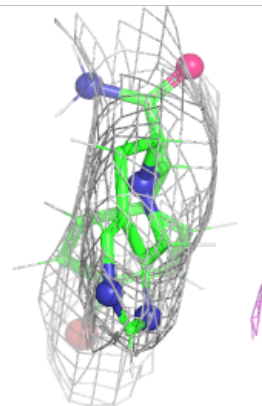
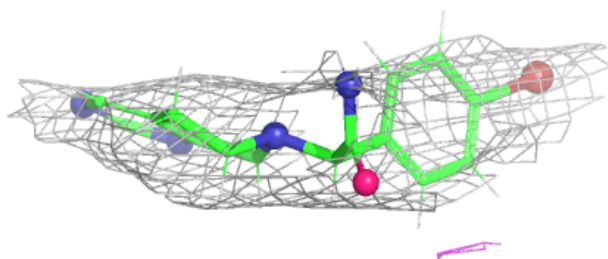


Electron density around A1CNQ G 501:

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

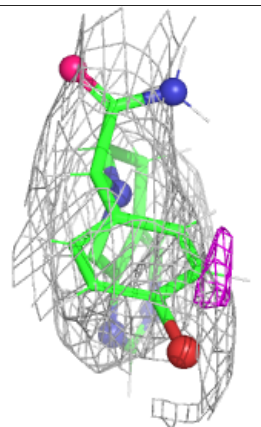
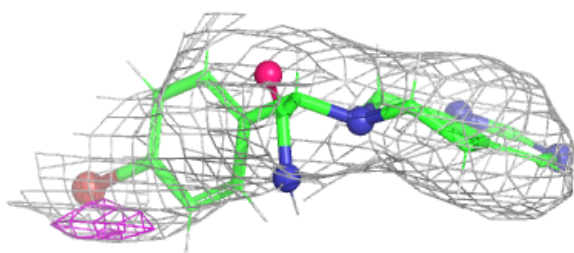
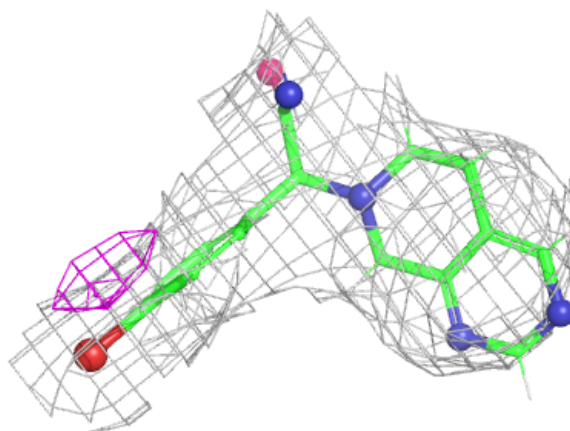
**Electron density around A1CNQ E 501:**

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



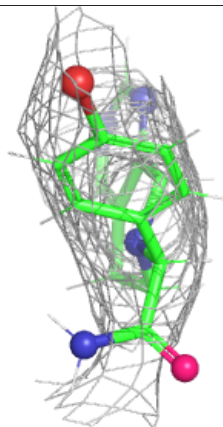
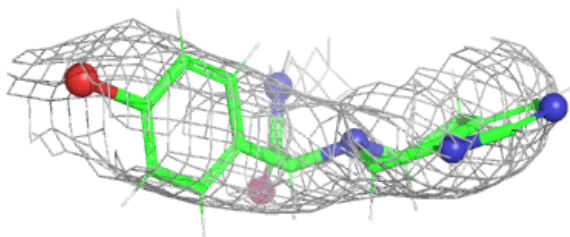
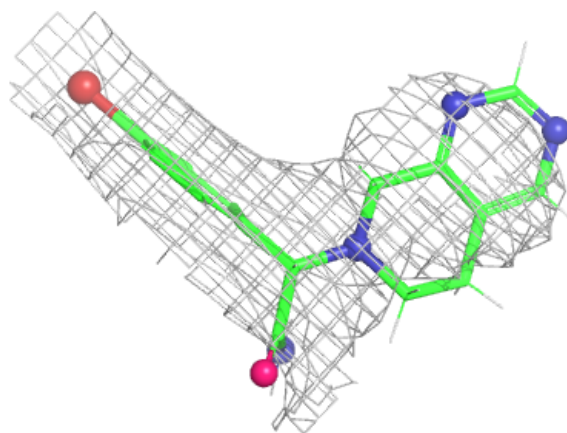
Electron density around A1CNQ F 501:

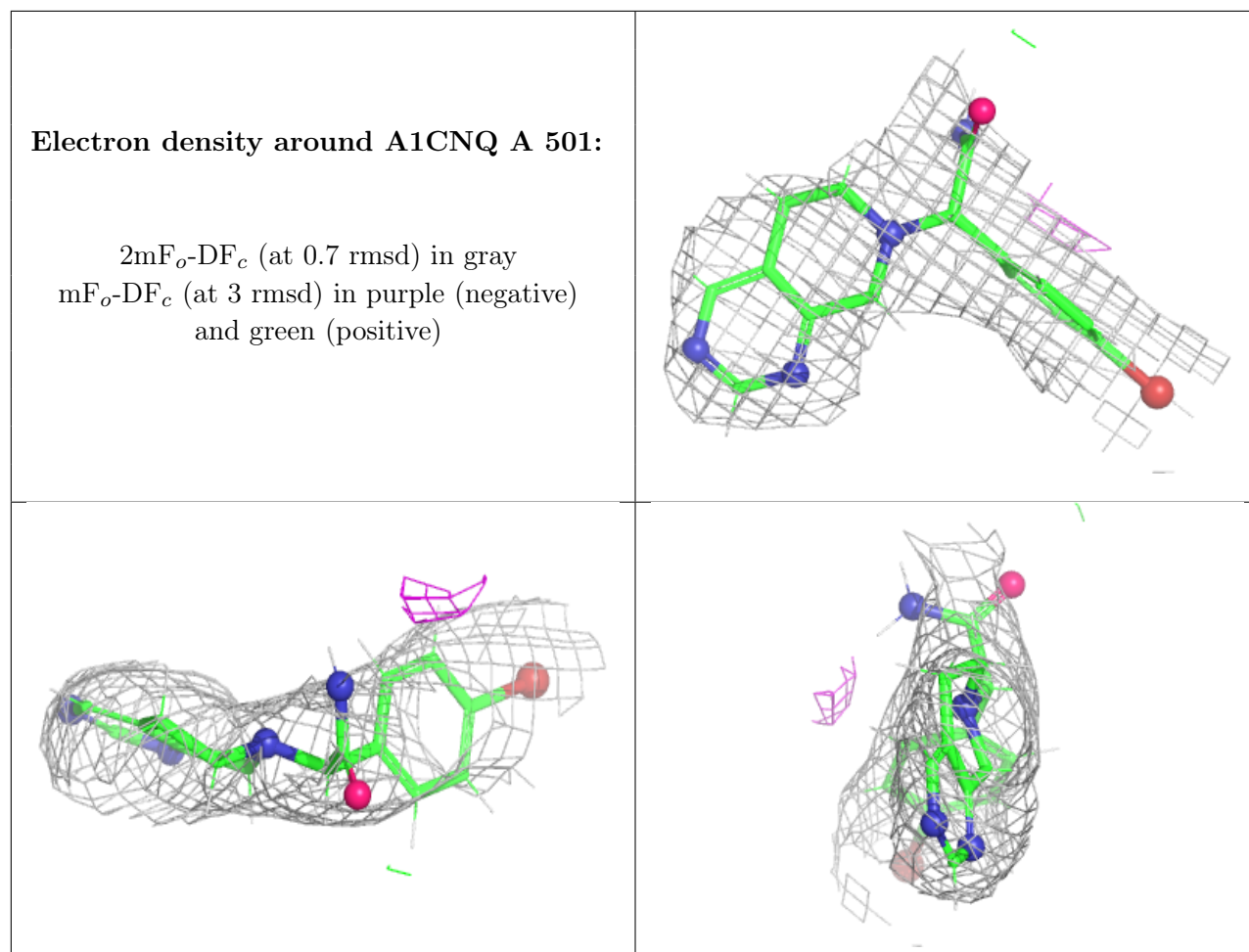
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around A1CNQ C 501:

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





6.5 Other polymers [i](#)

There are no such residues in this entry.