



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 30, 2021 – 12:50 PM EDT

PDB ID : 7JXK
Title : EGFR kinase (T790M/V948R) in complex with PF-06747775 and JBJ-04-125-02
Authors : Beyett, T.S.; Eck, M.J.
Deposited on : 2020-08-27
Resolution : 3.10 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 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 : 2.23.1
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) : 2.23.1

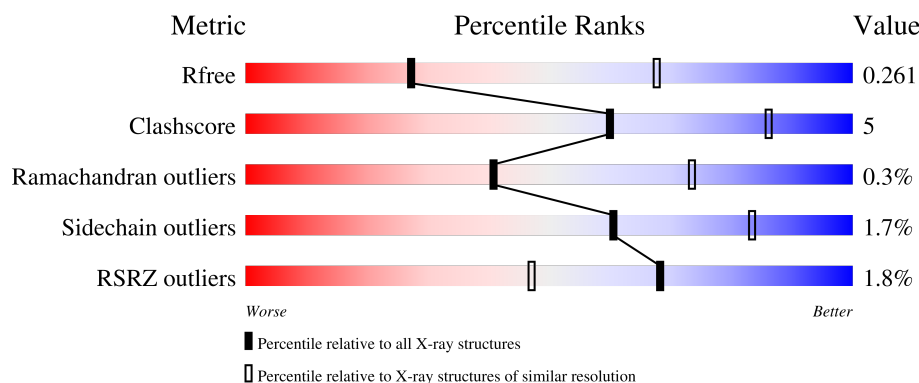
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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.



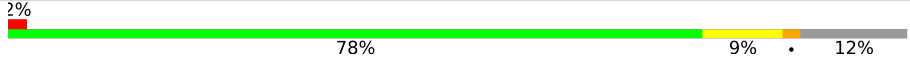
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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	331	<div> <div>0%</div> <div>77% 12% 11%</div> </div>
1	B	331	<div> <div>3%</div> <div>76% 11% 12%</div> </div>
1	C	331	<div> <div>2%</div> <div>75% 13% 12%</div> </div>
1	D	331	<div> <div>2%</div> <div>78% 11% 11%</div> </div>
1	E	331	<div> <div>77% 9% 13%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	331	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: a small red segment at the beginning labeled '2%', a large green segment labeled '78%', a small yellow segment labeled '9%', and a small grey segment at the end labeled '12%'. The segments are separated by thin white lines.

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14507 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 Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	294	Total	C	N	O	S	0	1	0
			2377	1528	404	425	20			
1	A	293	Total	C	N	O	S	0	1	0
			2369	1522	403	424	20			
1	C	292	Total	C	N	O	S	0	1	0
			2361	1518	401	422	20			
1	F	292	Total	C	N	O	S	0	1	0
			2360	1516	401	423	20			
1	E	287	Total	C	N	O	S	0	1	0
			2314	1488	391	416	19			
1	B	290	Total	C	N	O	S	0	1	0
			2347	1507	399	421	20			

There are 30 discrepancies between the modelled and reference sequences:

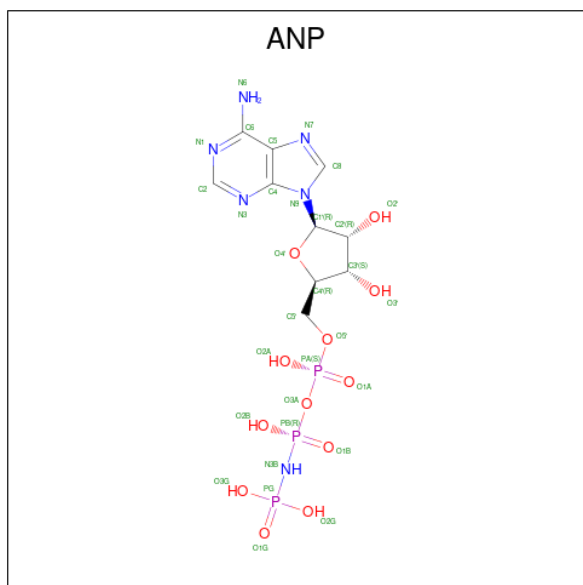
Chain	Residue	Modelled	Actual	Comment	Reference
D	692	GLY	-	expression tag	UNP P00533
D	693	SER	-	expression tag	UNP P00533
D	694	THR	-	expression tag	UNP P00533
D	790	MET	THR	engineered mutation	UNP P00533
D	948	ARG	VAL	engineered mutation	UNP P00533
A	692	GLY	-	expression tag	UNP P00533
A	693	SER	-	expression tag	UNP P00533
A	694	THR	-	expression tag	UNP P00533
A	790	MET	THR	engineered mutation	UNP P00533
A	948	ARG	VAL	engineered mutation	UNP P00533
C	692	GLY	-	expression tag	UNP P00533
C	693	SER	-	expression tag	UNP P00533
C	694	THR	-	expression tag	UNP P00533
C	790	MET	THR	engineered mutation	UNP P00533
C	948	ARG	VAL	engineered mutation	UNP P00533
F	692	GLY	-	expression tag	UNP P00533
F	693	SER	-	expression tag	UNP P00533

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Chain	Residue	Modelled	Actual	Comment	Reference
F	694	THR	-	expression tag	UNP P00533
F	790	MET	THR	engineered mutation	UNP P00533
F	948	ARG	VAL	engineered mutation	UNP P00533
E	692	GLY	-	expression tag	UNP P00533
E	693	SER	-	expression tag	UNP P00533
E	694	THR	-	expression tag	UNP P00533
E	790	MET	THR	engineered mutation	UNP P00533
E	948	ARG	VAL	engineered mutation	UNP P00533
B	692	GLY	-	expression tag	UNP P00533
B	693	SER	-	expression tag	UNP P00533
B	694	THR	-	expression tag	UNP P00533
B	790	MET	THR	engineered mutation	UNP P00533
B	948	ARG	VAL	engineered mutation	UNP P00533

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).

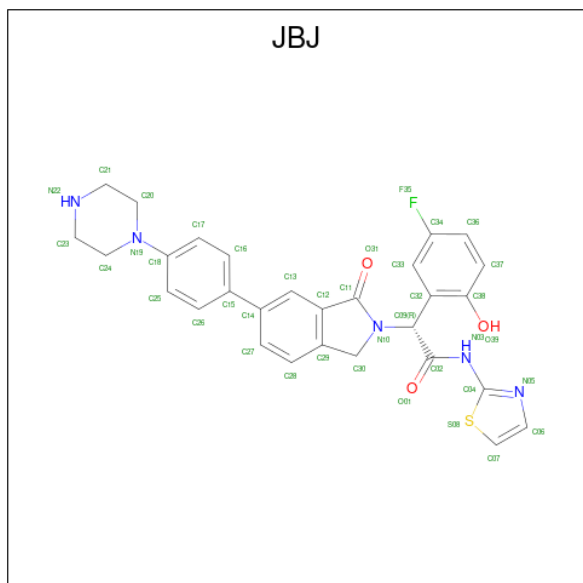


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	D	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

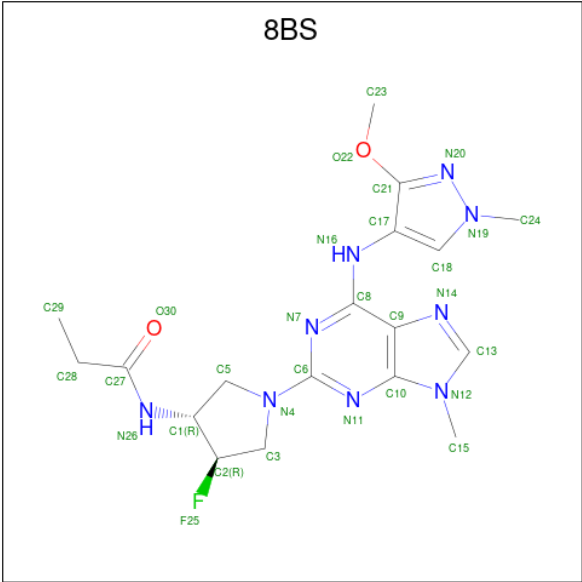
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0

- Molecule 4 is (2R)-2-(5-fluoro-2-hydroxyphenyl)-2-{1-oxo-6-[4-(piperazin-1-yl)phenyl]-1,3-dihydro-2H-isoindol-2-yl}-N-(1,3-thiazol-2-yl)acetamide (three-letter code: JBJ) (formula: C₂₉H₂₆FN₅O₃S) (labeled as "Ligand of Interest" by depositor).

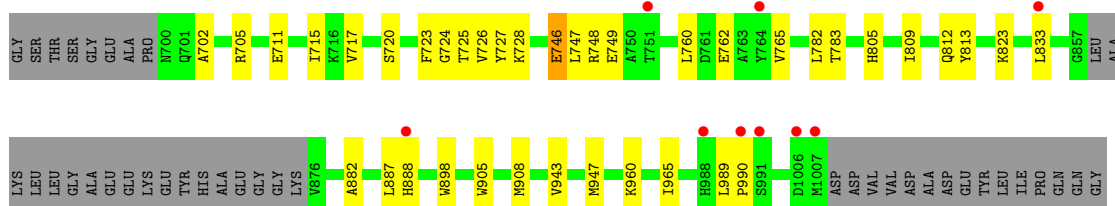


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	D	1	Total 39	C 29	F 1	N 5	O 3	S 1	0	0
4	A	1	Total 39	C 29	F 1	N 5	O 3	S 1	0	0
4	C	1	Total 39	C 29	F 1	N 5	O 3	S 1	0	0
4	F	1	Total 39	C 29	F 1	N 5	O 3	S 1	0	0
4	E	1	Total 39	C 29	F 1	N 5	O 3	S 1	0	0

- Molecule 5 is N-[(3R,4R)-4-fluoro-1-{6-[(3-methoxy-1-methyl-1H-pyrazol-4-yl)amino]-9-methyl-9H-purin-2-yl}pyrrolidin-3-yl]propanamide (three-letter code: 8BS) (formula: C₁₈H₂₄FN₉O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	F	N	O	0	0
			30	18	1	9	2		
5	C	1	Total	C	F	N	O	0	0
			30	18	1	9	2		
5	F	1	Total	C	F	N	O	0	0
			30	18	1	9	2		
5	E	1	Total	C	F	N	O	0	0
			30	18	1	9	2		



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	66.85Å 87.37Å 91.31Å 62.06° 85.58° 73.33°	Depositor
Resolution (Å)	80.48 – 3.10 80.48 – 3.10	Depositor EDS
% Data completeness (in resolution range)	90.8 (80.48-3.10) 90.8 (80.48-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 3.13Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.222 , 0.261 0.222 , 0.261	Depositor DCC
R_{free} test set	1453 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	67.0	Xtriage
Anisotropy	0.570	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	14507	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 27.78 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.0690e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ANP, 8BS, JBJ

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	0.30	0/2424	0.51	0/3276
1	B	0.28	0/2402	0.50	0/3247
1	C	0.30	0/2416	0.50	0/3265
1	D	0.27	0/2432	0.49	0/3287
1	E	0.26	0/2367	0.48	0/3199
1	F	0.28	0/2415	0.52	1/3265 (0.0%)
All	All	0.28	0/14456	0.50	1/19539 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	782	LEU	CB-CG-CD1	-5.20	102.17	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2369	0	2418	21	0
1	B	2347	0	2390	24	0
1	C	2361	0	2412	28	0
1	D	2377	0	2430	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2314	0	2359	23	0
1	F	2360	0	2405	23	0
2	B	31	0	13	1	0
2	D	31	0	13	1	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
4	A	39	0	0	0	0
4	C	39	0	0	1	0
4	D	39	0	0	0	0
4	E	39	0	0	2	0
4	F	39	0	0	3	0
5	A	30	0	0	0	0
5	C	30	0	0	0	0
5	E	30	0	0	1	0
5	F	30	0	0	0	0
All	All	14507	0	14440	132	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 5.

The worst 5 of 132 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:F:755:ALA:HB1	4:F:1102:JBJ:N22	2.03	0.73
1:E:723:PHE:HB3	1:E:747:LEU:HD22	1.78	0.65
1:D:830:ASP:HB3	1:C:717:VAL:HG11	1.81	0.62
1:A:832:ARG:HH22	1:B:724:GLY:C	2.04	0.60
1:F:905:TRP:HD1	1:F:947:MET:HE1	1.66	0.60

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	290/331 (88%)	282 (97%)	7 (2%)	1 (0%)	41	73
1	B	287/331 (87%)	277 (96%)	9 (3%)	1 (0%)	41	73
1	C	289/331 (87%)	277 (96%)	10 (4%)	2 (1%)	22	57
1	D	291/331 (88%)	282 (97%)	7 (2%)	2 (1%)	22	57
1	E	282/331 (85%)	275 (98%)	7 (2%)	0	100	100
1	F	289/331 (87%)	278 (96%)	11 (4%)	0	100	100
All	All	1728/1986 (87%)	1671 (97%)	51 (3%)	6 (0%)	41	73

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	859	ALA
1	D	721	GLY
1	C	753	PRO
1	D	783	THR
1	A	1006	ASP

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	263/290 (91%)	257 (98%)	6 (2%)	50	77
1	B	261/290 (90%)	257 (98%)	4 (2%)	65	85
1	C	262/290 (90%)	253 (97%)	9 (3%)	37	69
1	D	264/290 (91%)	264 (100%)	0	100	100
1	E	257/290 (89%)	257 (100%)	0	100	100
1	F	262/290 (90%)	255 (97%)	7 (3%)	44	74
All	All	1569/1740 (90%)	1543 (98%)	26 (2%)	60	83

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1007	MET

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Mol	Chain	Res	Type
1	F	749	GLU
1	B	783	THR
1	F	748	ARG
1	F	751	THR

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

Mol	Chain	Res	Type
1	E	982	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 2 are monoatomic - leaving 11 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$
5	8BS	E	1101	1	26,33,33	2.82	12 (46%)	21,48,48	2.95	8 (38%)
4	JBj	D	1103	-	42,44,44	1.85	11 (26%)	52,63,63	4.49	15 (28%)
5	8BS	A	1101	1	26,33,33	2.01	9 (34%)	21,48,48	2.14	6 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	JBJ	C	1102	-	42,44,44	2.64	15 (35%)	52,63,63	4.13	16 (30%)
2	ANP	D	1101	3	29,33,33	1.11	4 (13%)	31,52,52	1.07	3 (9%)
5	8BS	C	1101	1	26,33,33	2.20	11 (42%)	21,48,48	2.52	7 (33%)
4	JBJ	A	1102	-	42,44,44	2.76	15 (35%)	52,63,63	4.09	16 (30%)
5	8BS	F	1101	1	26,33,33	2.57	11 (42%)	21,48,48	2.78	11 (52%)
2	ANP	B	1101	3	29,33,33	1.08	4 (13%)	31,52,52	0.98	2 (6%)
4	JBJ	E	1102	-	42,44,44	2.69	16 (38%)	52,63,63	3.91	13 (25%)
4	JBJ	F	1102	-	42,44,44	2.58	15 (35%)	52,63,63	3.99	17 (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	8BS	E	1101	1	-	3/12/28/28	0/4/4/4
4	JBJ	D	1103	-	-	6/22/44/44	0/6/6/6
5	8BS	A	1101	1	-	6/12/28/28	0/4/4/4
4	JBJ	C	1102	-	-	3/22/44/44	0/6/6/6
2	ANP	D	1101	3	-	4/14/38/38	0/3/3/3
5	8BS	C	1101	1	-	4/12/28/28	0/4/4/4
4	JBJ	A	1102	-	-	4/22/44/44	0/6/6/6
5	8BS	F	1101	1	-	5/12/28/28	0/4/4/4
2	ANP	B	1101	3	-	2/14/38/38	0/3/3/3
4	JBJ	E	1102	-	-	0/22/44/44	0/6/6/6
4	JBJ	F	1102	-	-	0/22/44/44	0/6/6/6

The worst 5 of 123 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1102	JBJ	C09-C02	8.23	1.63	1.54
4	E	1102	JBJ	C09-C02	7.83	1.62	1.54
4	A	1102	JBJ	C09-C02	7.71	1.62	1.54
5	E	1101	8BS	C6-N4	7.34	1.49	1.35
4	F	1102	JBJ	C30-N10	7.34	1.52	1.46

The worst 5 of 114 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1103	JBj	C30-N10-C11	-19.70	105.02	113.12
4	A	1102	JBj	C30-N10-C11	-18.49	105.51	113.12
4	F	1102	JBj	C30-N10-C11	-18.43	105.54	113.12
4	C	1102	JBj	C30-N10-C11	-18.18	105.64	113.12
4	E	1102	JBj	C30-N10-C11	-18.01	105.71	113.12

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

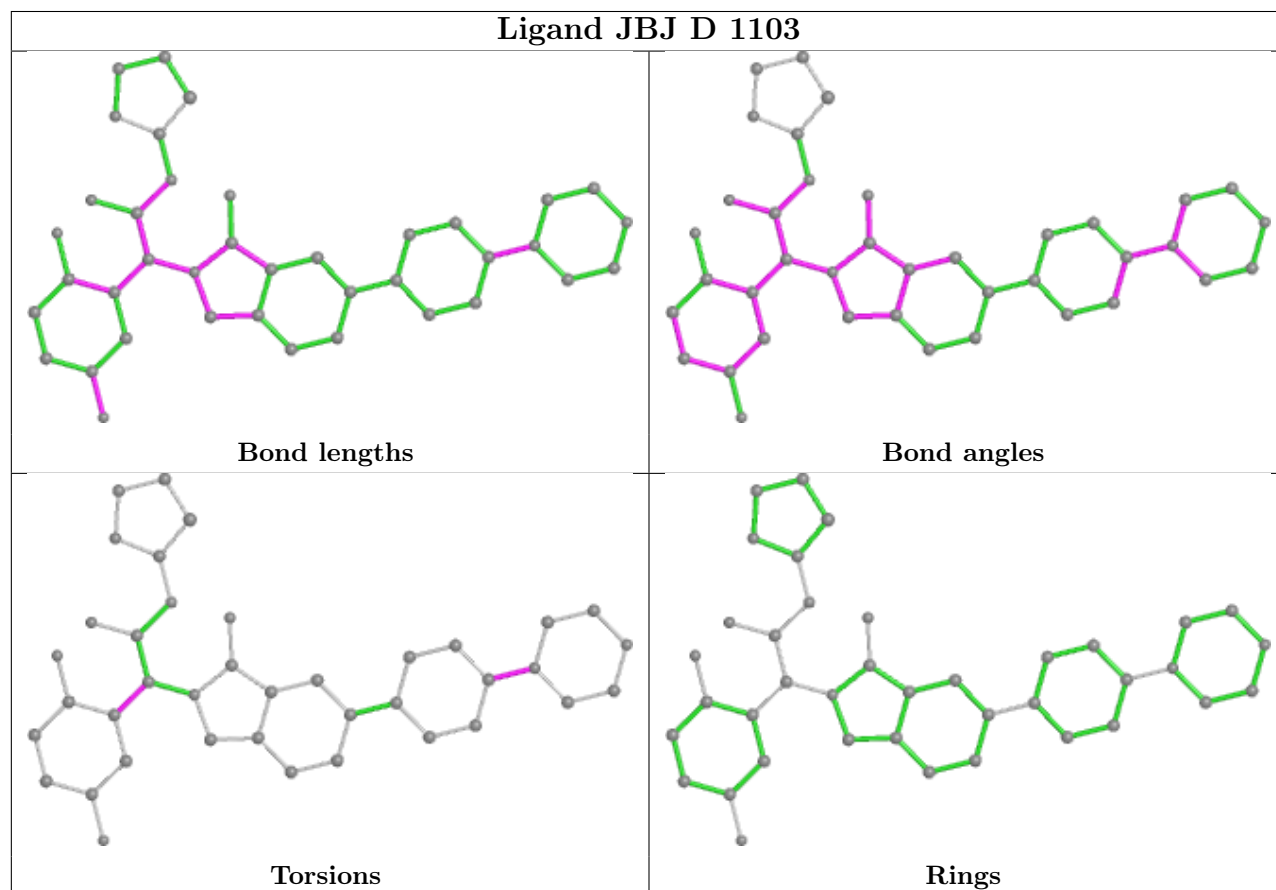
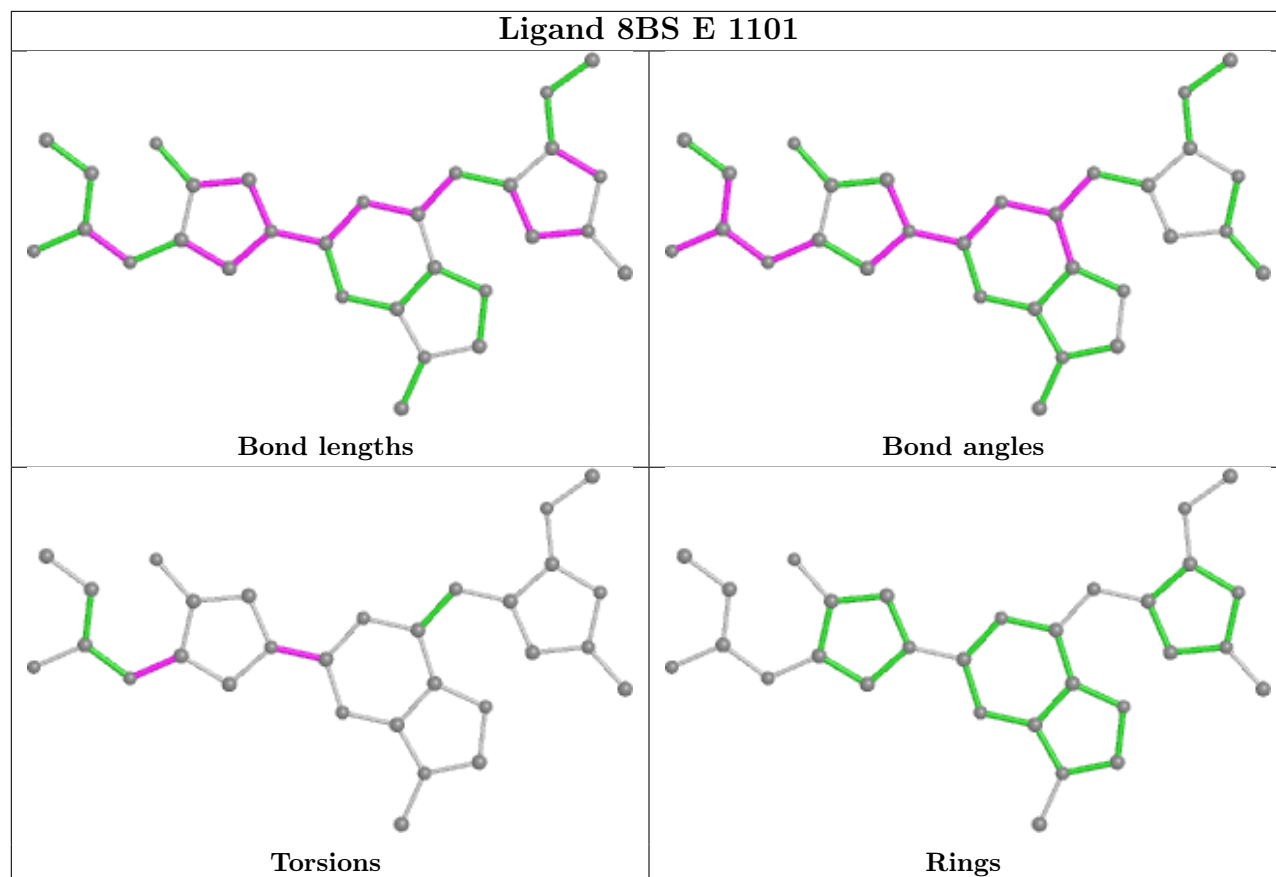
Mol	Chain	Res	Type	Atoms
2	D	1101	ANP	PB-N3B-PG-O1G
2	D	1101	ANP	C5'-O5'-PA-O1A
2	B	1101	ANP	PB-N3B-PG-O1G
5	A	1101	8BS	N7-C6-N4-C5
5	A	1101	8BS	N11-C6-N4-C5

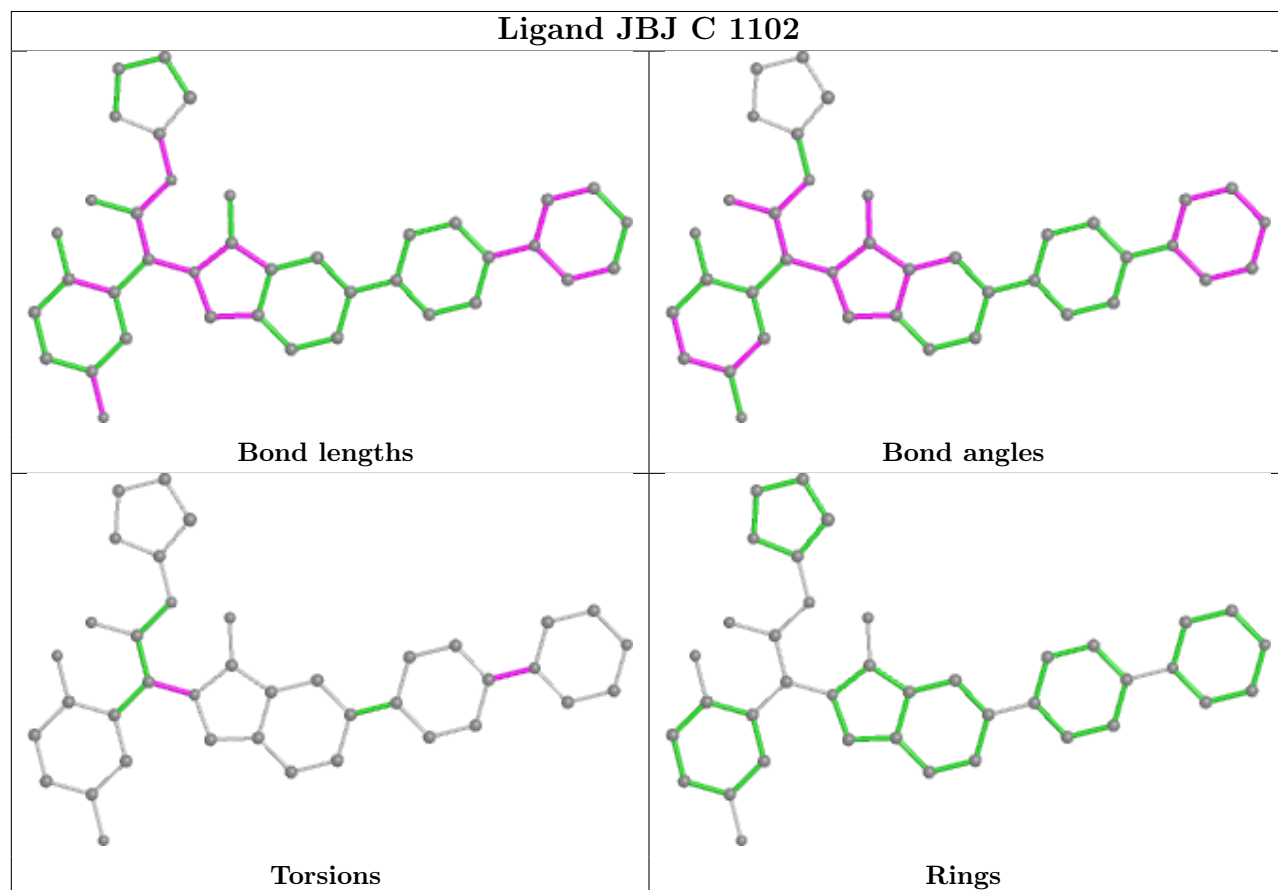
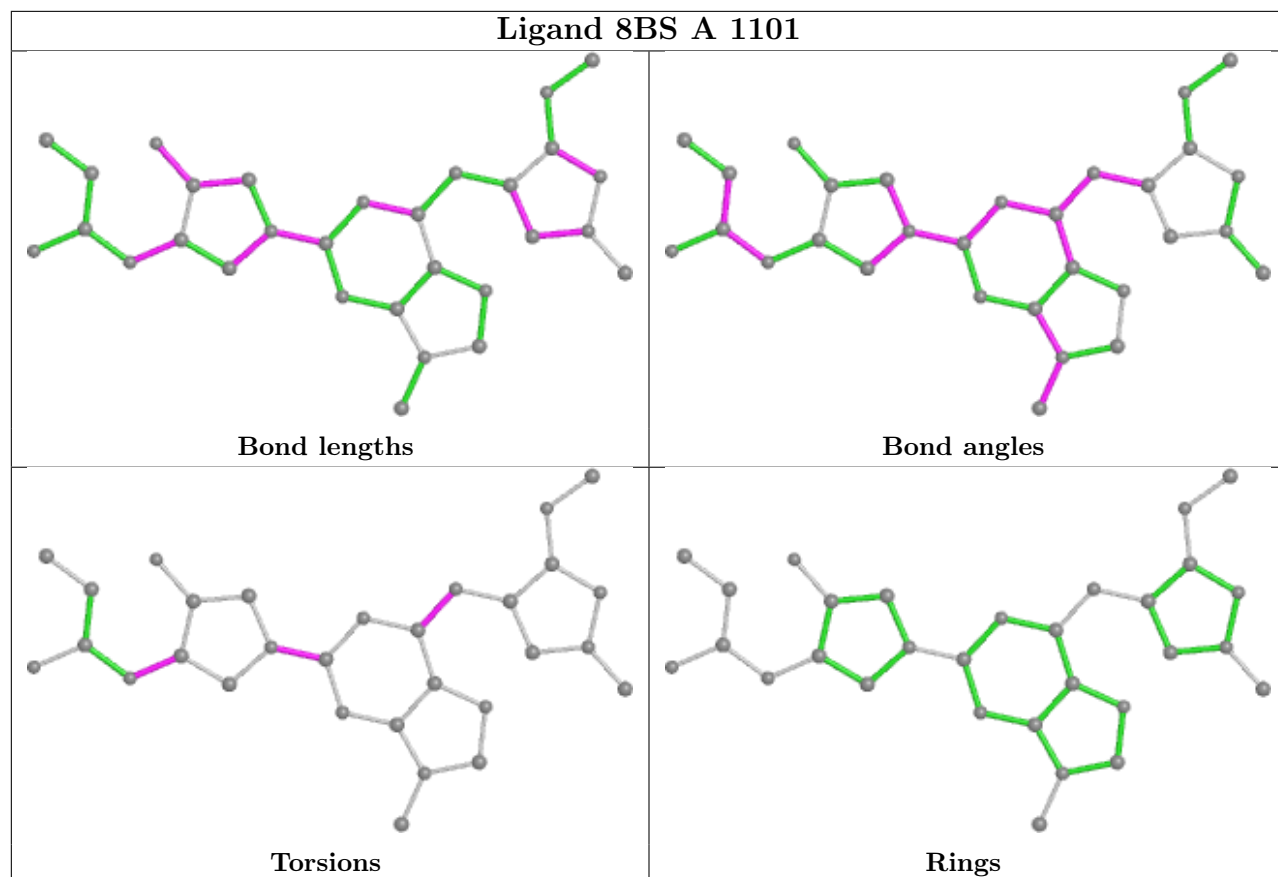
There are no ring outliers.

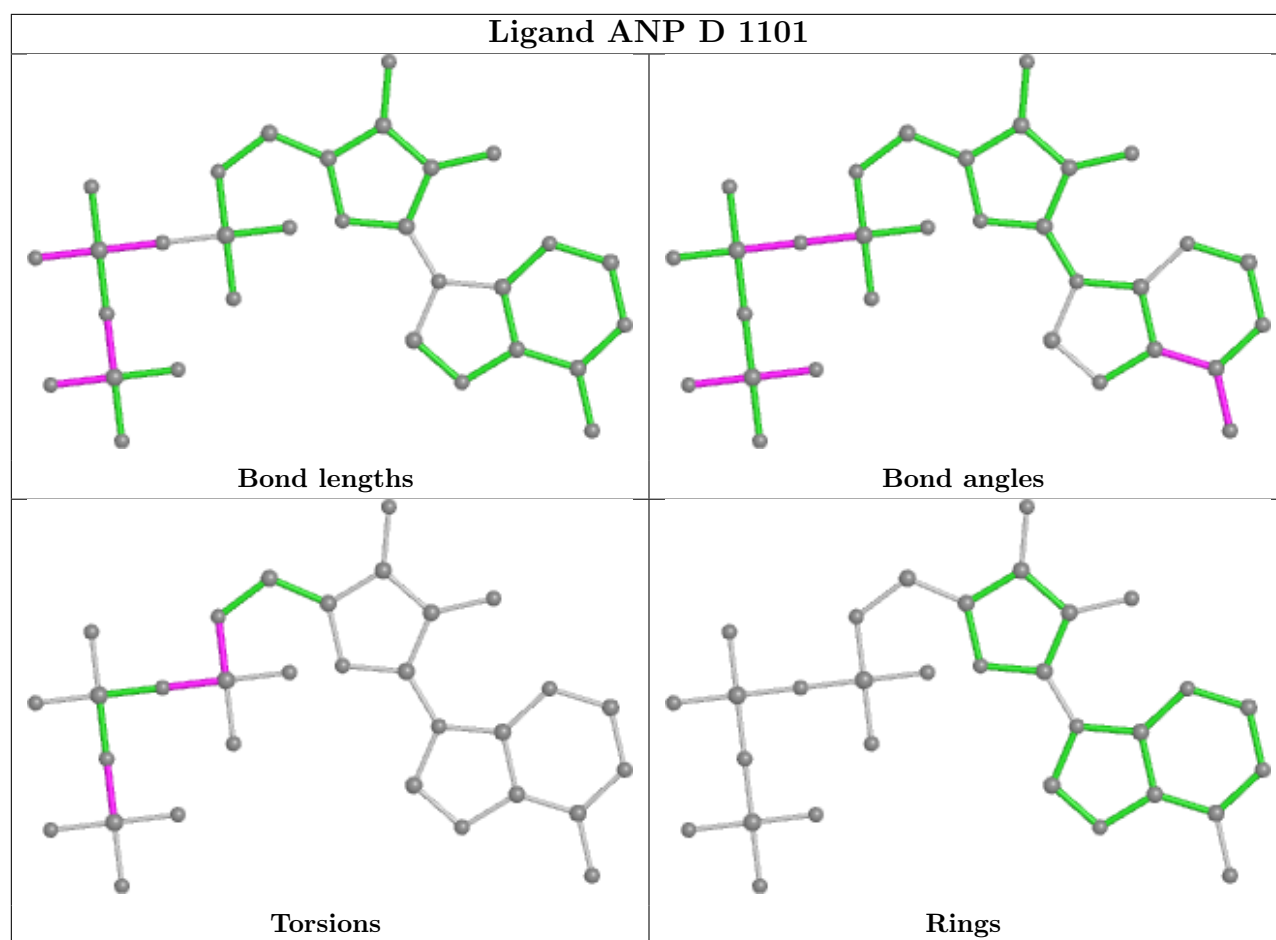
6 monomers are involved in 9 short contacts:

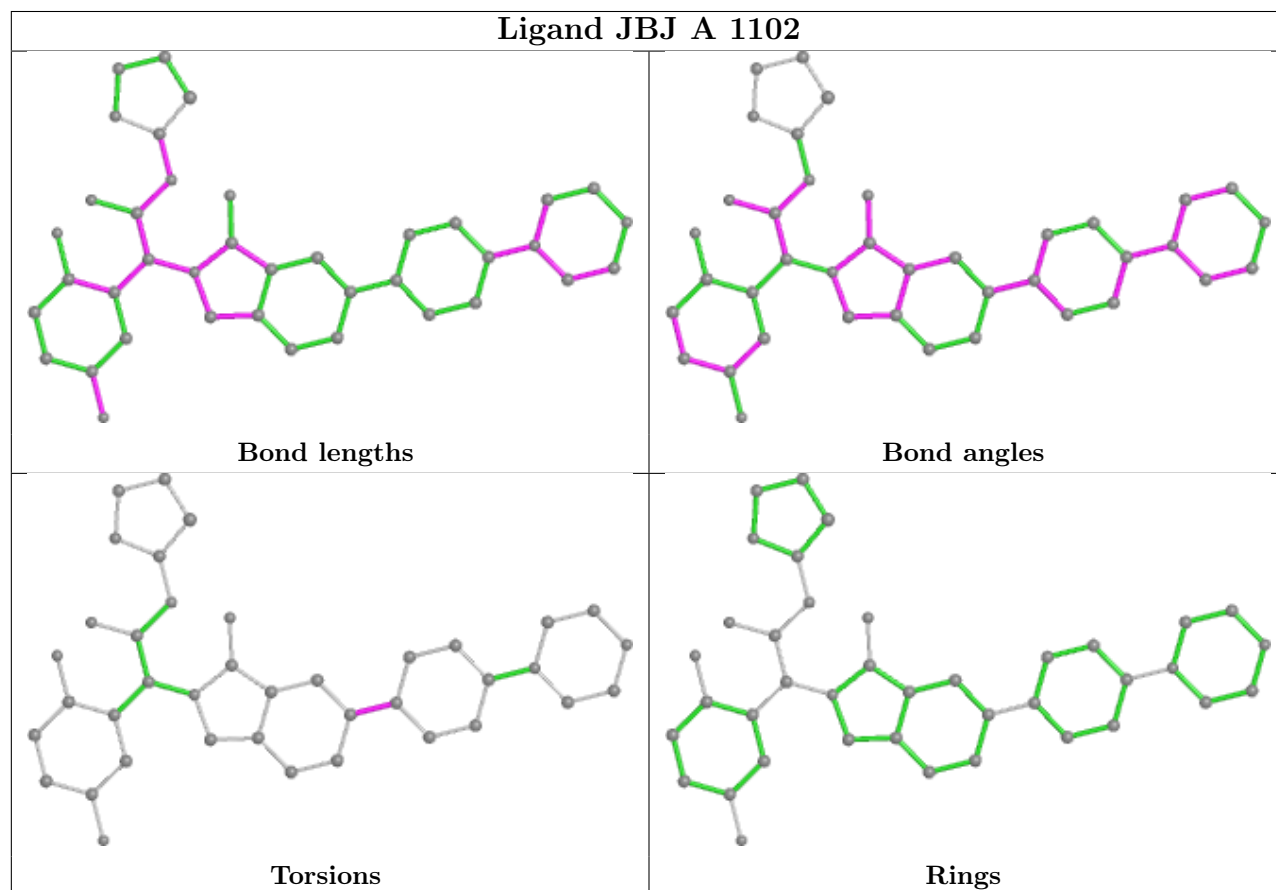
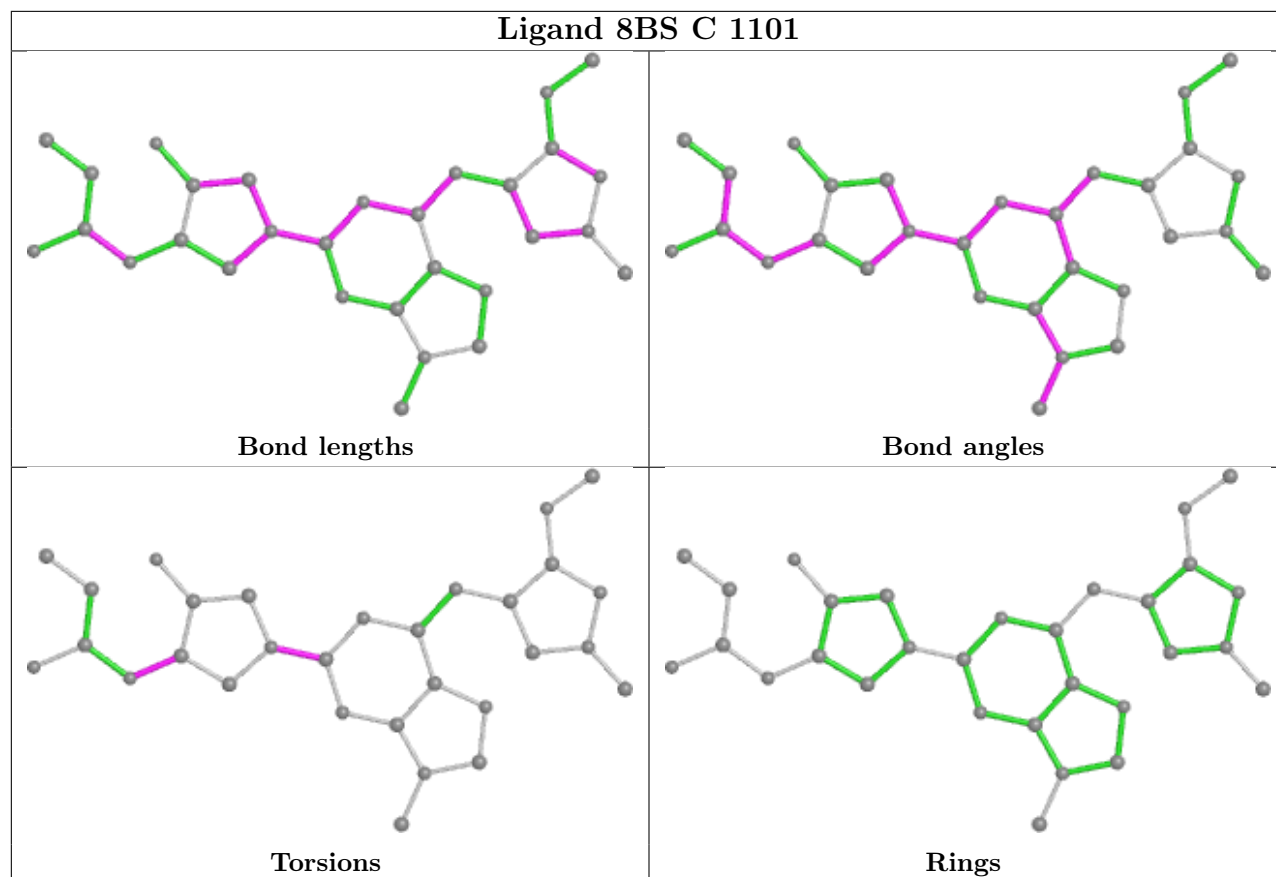
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	1101	8BS	1	0
4	C	1102	JBj	1	0
2	D	1101	ANP	1	0
2	B	1101	ANP	1	0
4	E	1102	JBj	2	0
4	F	1102	JBj	3	0

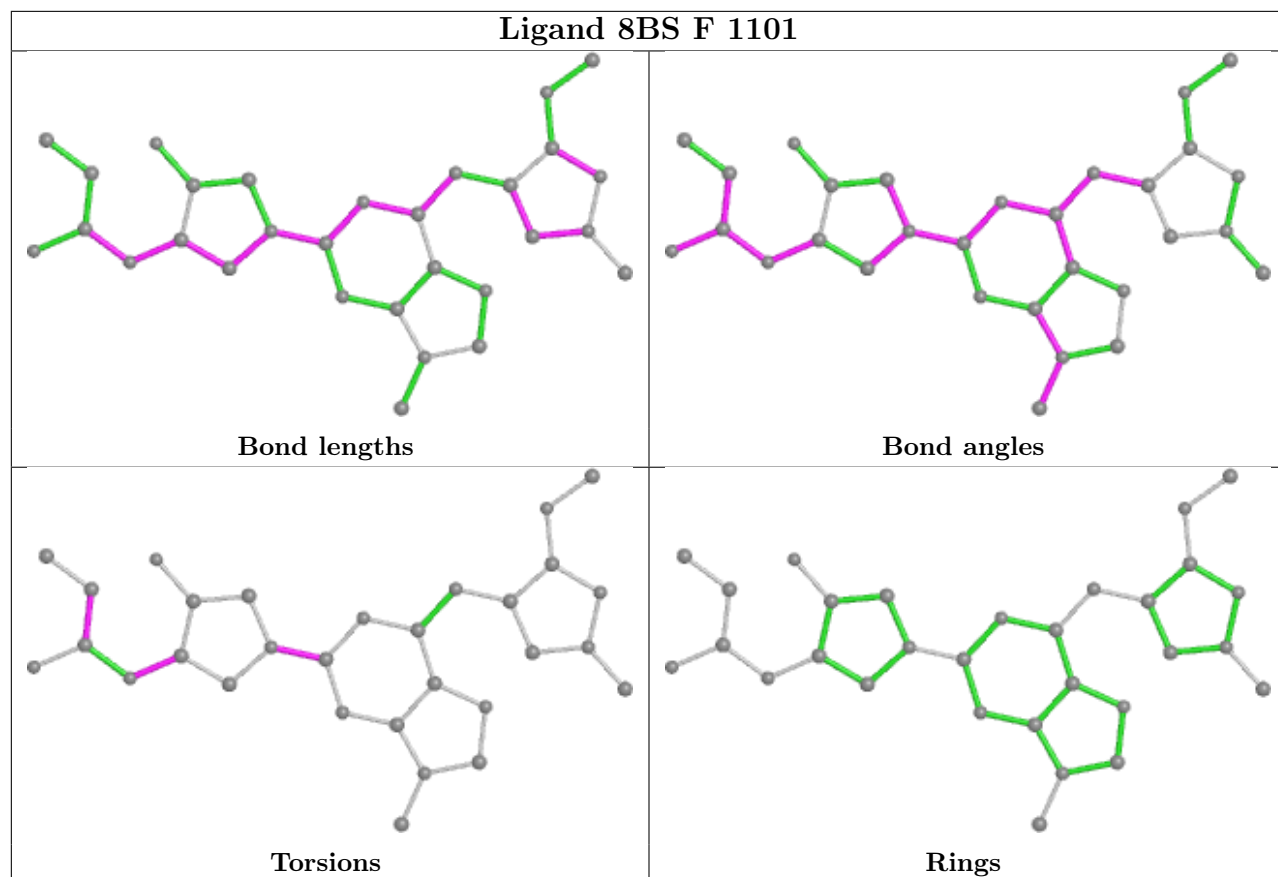
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

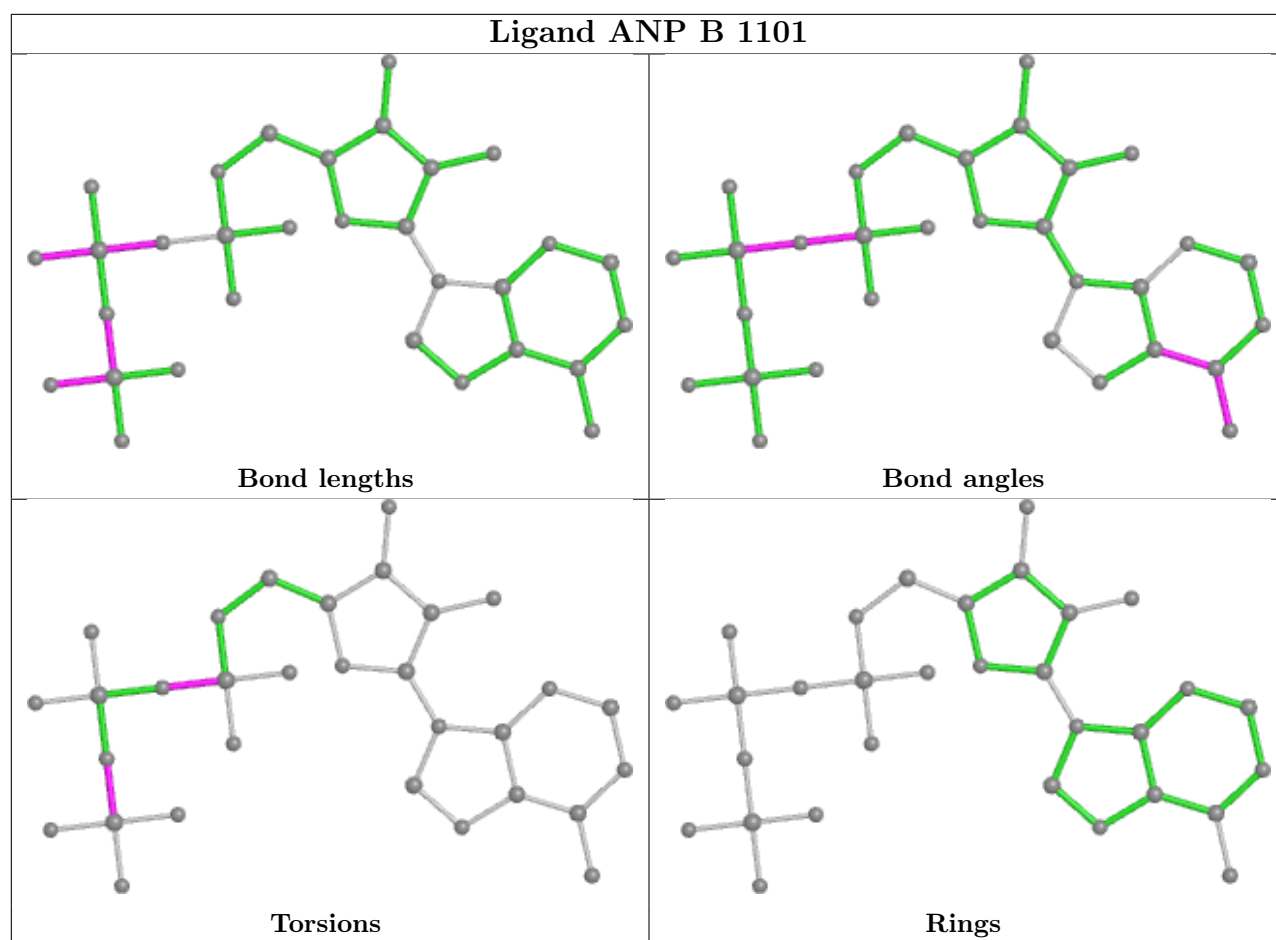


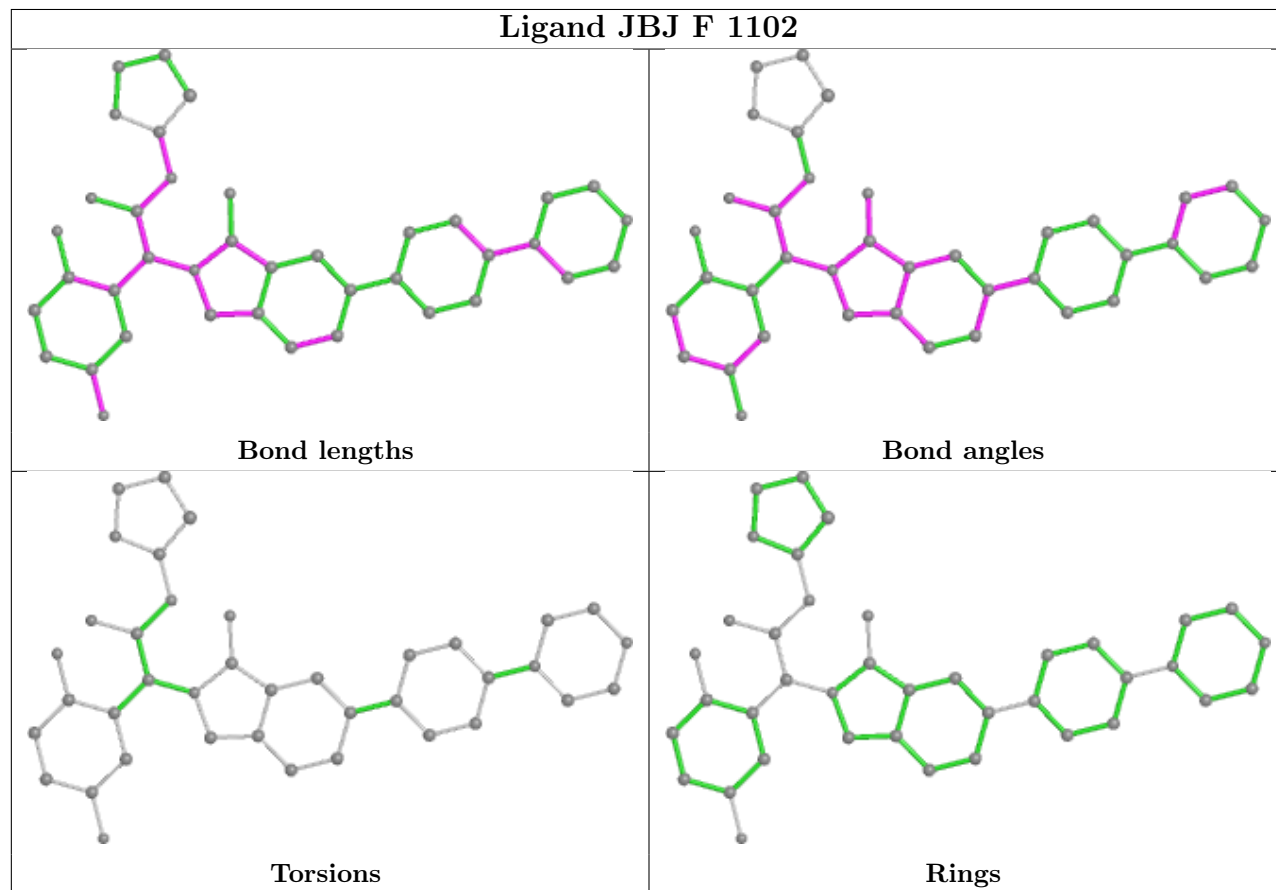
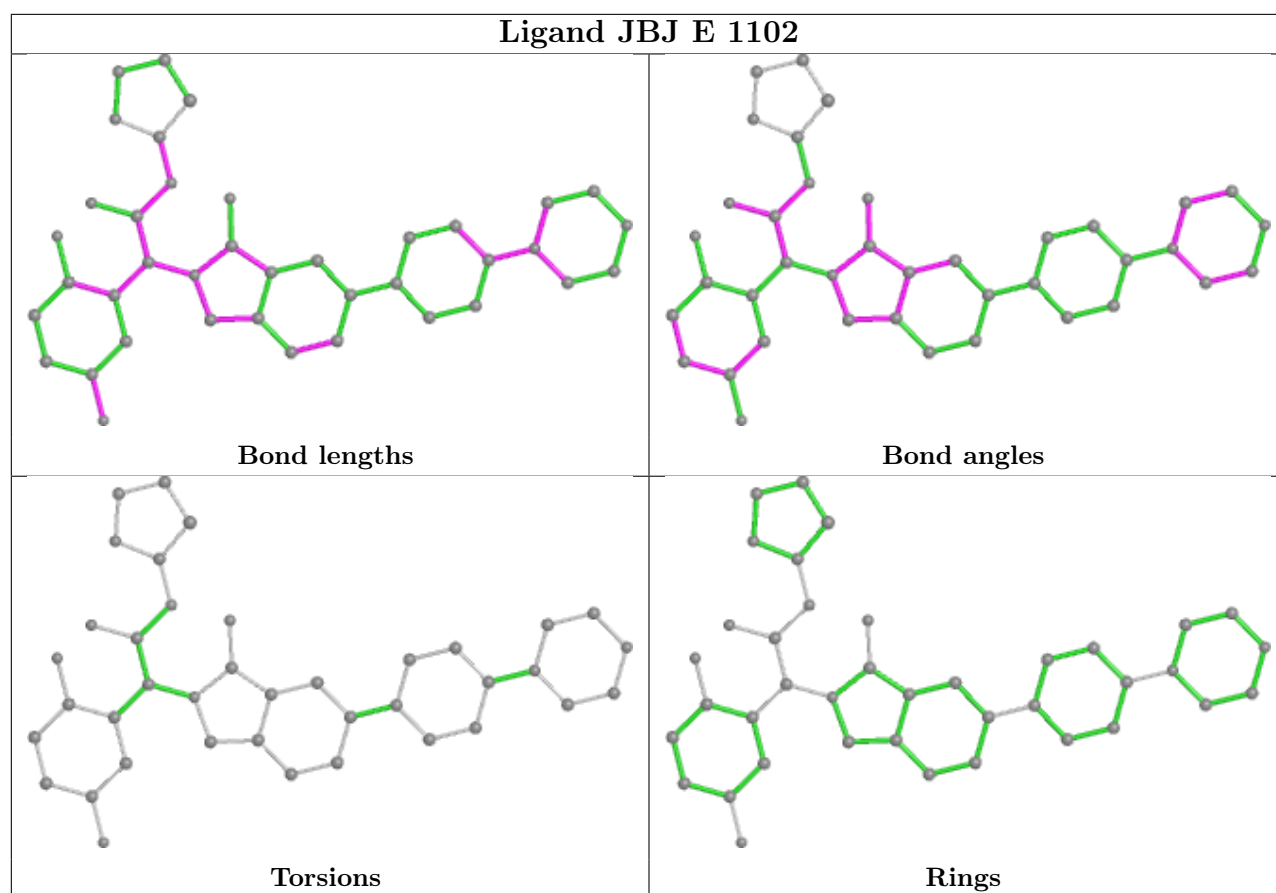












5.7 Other polymers [i](#)

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	293/331 (88%)	-0.27	3 (1%) 82 67	32, 62, 97, 113	0
1	B	290/331 (87%)	0.06	9 (3%) 49 26	44, 93, 136, 188	0
1	C	292/331 (88%)	-0.02	7 (2%) 59 37	48, 84, 126, 148	0
1	D	294/331 (88%)	-0.25	6 (2%) 65 44	31, 63, 98, 120	0
1	E	287/331 (86%)	-0.16	1 (0%) 94 88	43, 80, 120, 138	0
1	F	292/331 (88%)	-0.11	5 (1%) 70 49	39, 65, 95, 108	0
All	All	1748/1986 (88%)	-0.12	31 (1%) 68 47	31, 72, 120, 188	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	747	LEU	4.4
1	F	990	PRO	3.5
1	D	861	LEU	3.3
1	B	991	SER	3.3
1	A	982	GLN	3.1

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

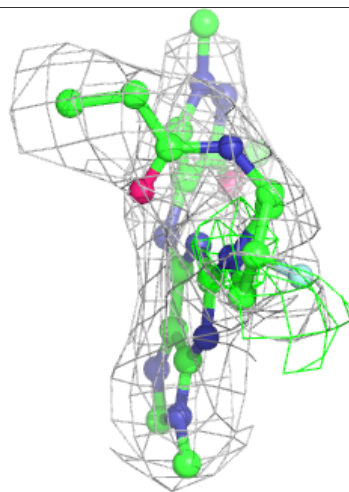
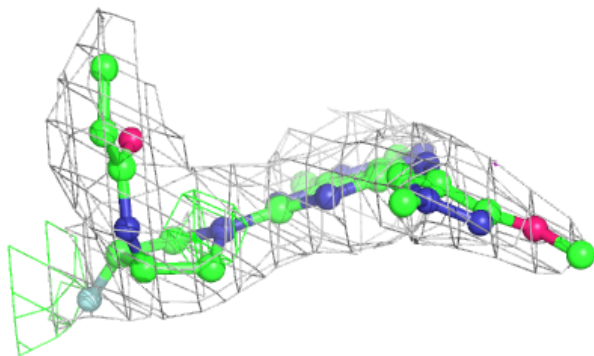
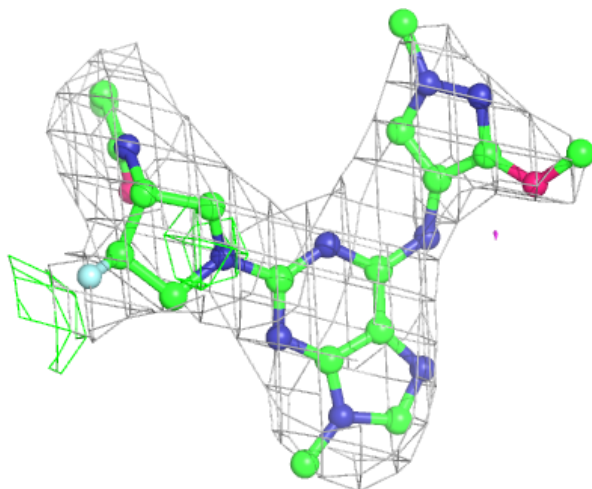
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	8BS	E	1101	30/30	0.82	0.25	84,98,106,107	0
2	ANP	B	1101	31/31	0.86	0.22	49,75,110,130	0
5	8BS	C	1101	30/30	0.89	0.27	88,105,118,122	0
4	JBj	C	1102	39/39	0.90	0.28	64,76,118,121	0
5	8BS	F	1101	30/30	0.90	0.24	85,97,109,116	0
5	8BS	A	1101	30/30	0.90	0.23	59,71,81,87	0
4	JBj	F	1102	39/39	0.92	0.25	57,67,93,96	0
2	ANP	D	1101	31/31	0.93	0.16	41,53,79,86	0
4	JBj	E	1102	39/39	0.93	0.30	59,71,117,124	0
4	JBj	A	1102	39/39	0.94	0.25	55,65,106,111	0
4	JBj	D	1103	39/39	0.94	0.24	58,69,107,116	0
3	MG	B	1102	1/1	0.95	0.07	83,83,83,83	0
3	MG	D	1102	1/1	0.95	0.08	57,57,57,57	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.

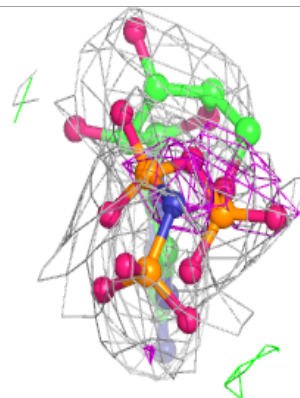
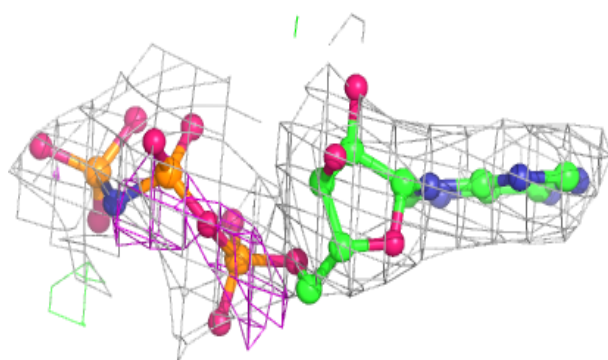
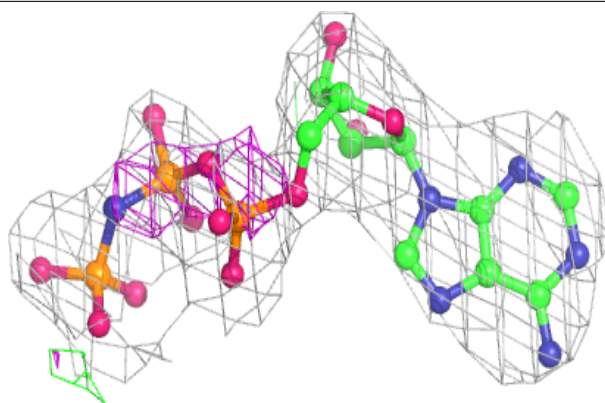
Electron density around 8BS E 1101:

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



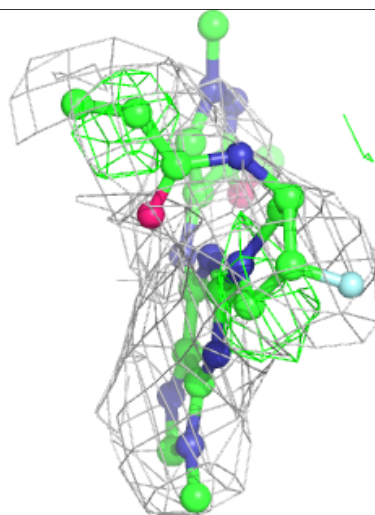
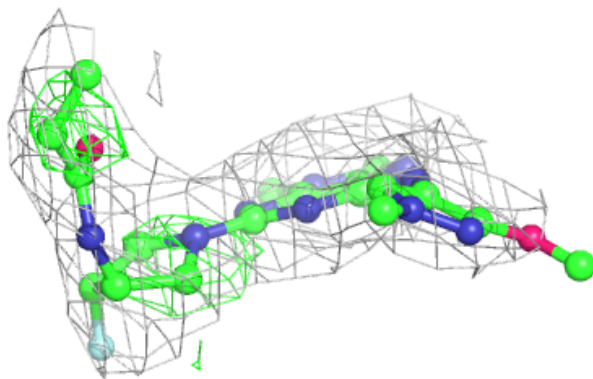
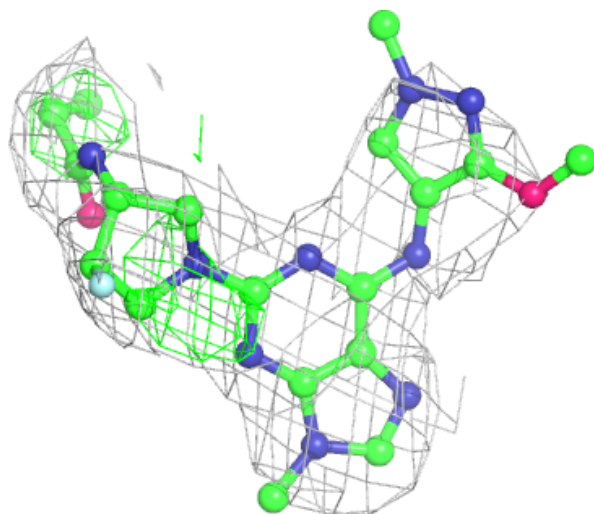
Electron density around ANP B 1101:

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



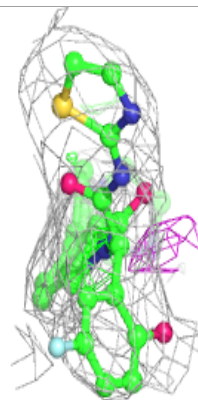
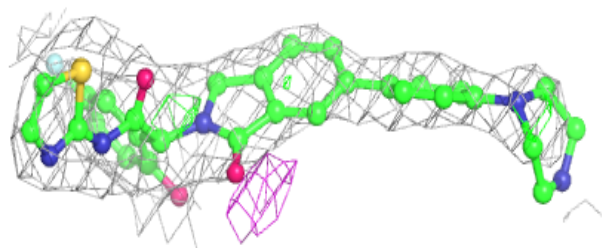
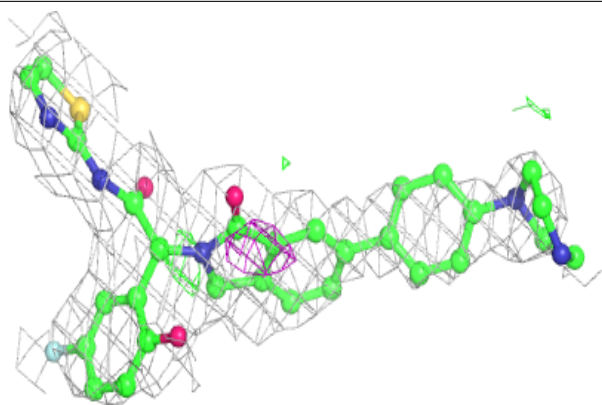
Electron density around 8BS C 1101:

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



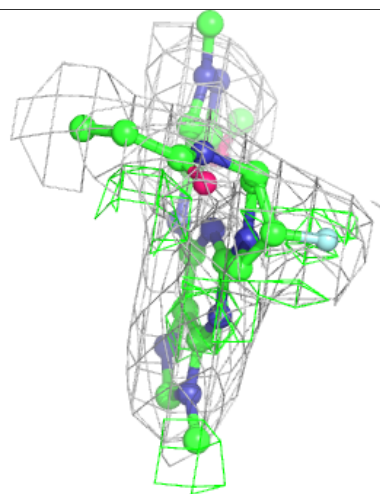
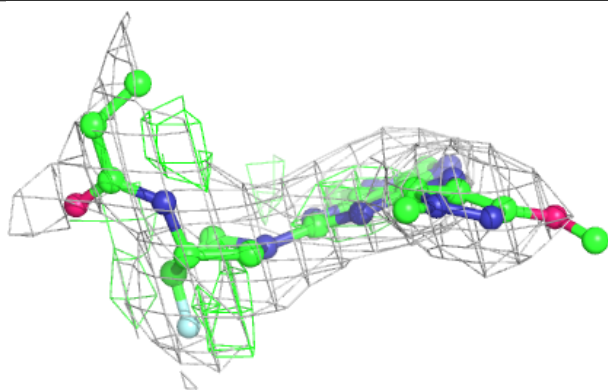
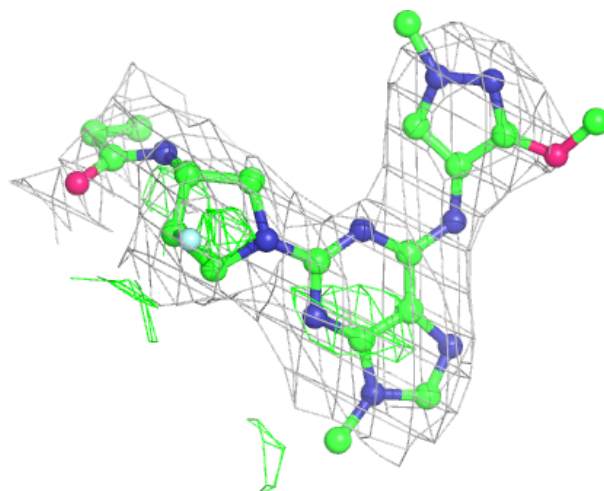
Electron density around JBJ C 1102:

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



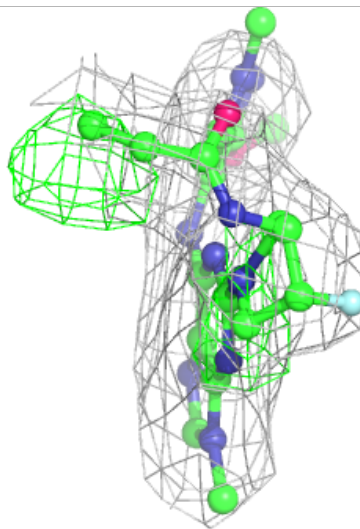
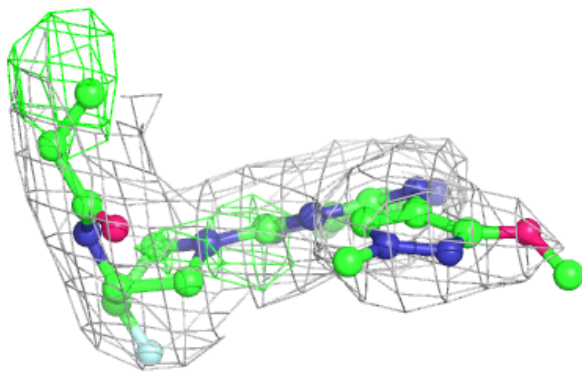
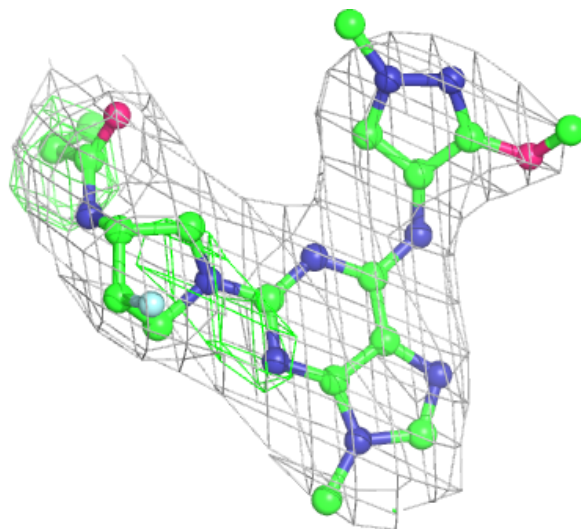
Electron density around 8BS F 1101:

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



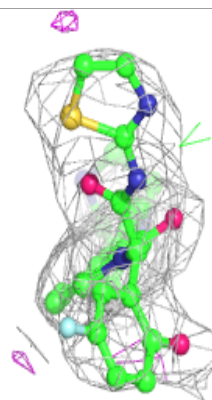
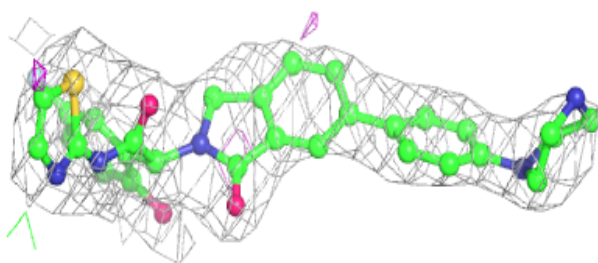
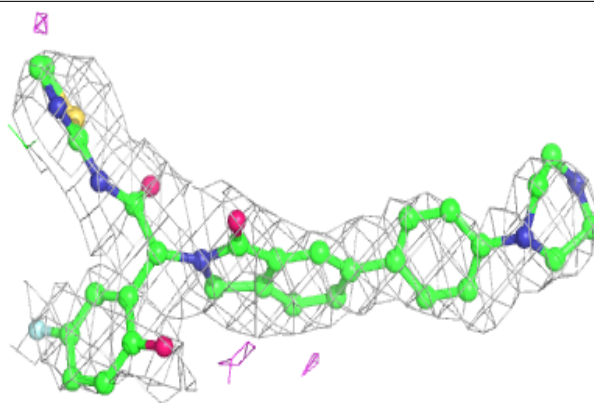
Electron density around 8BS A 1101:

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

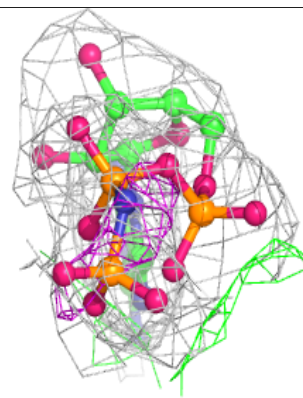
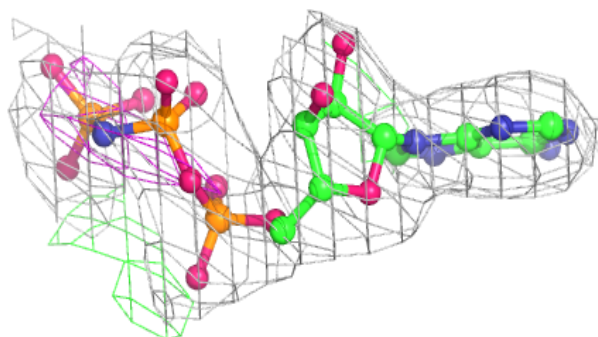
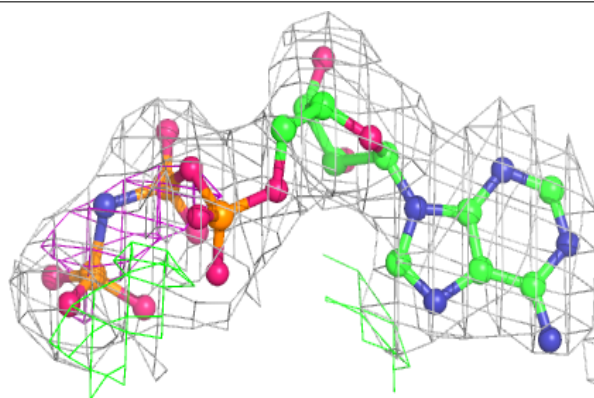


Electron density around JBJ F 1102:

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

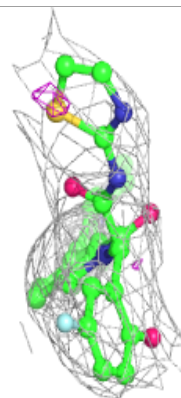
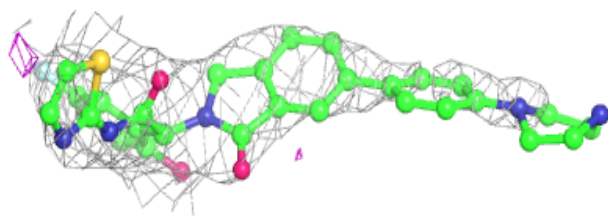
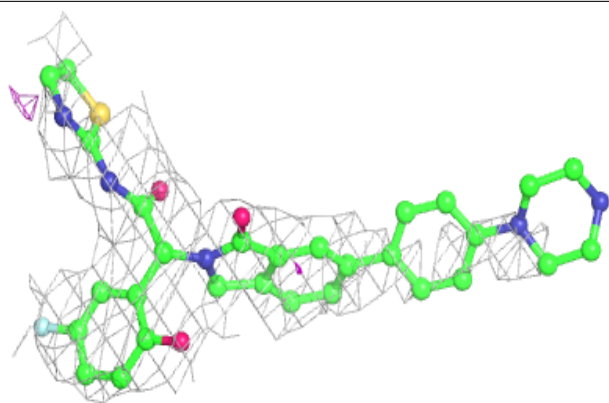
**Electron density around ANP D 1101:**

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

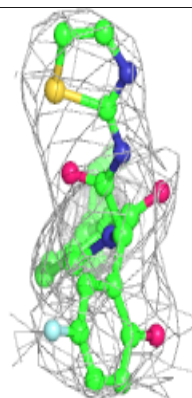
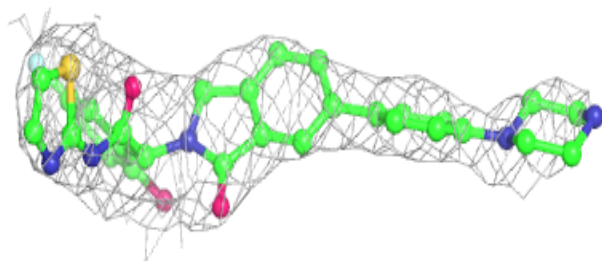
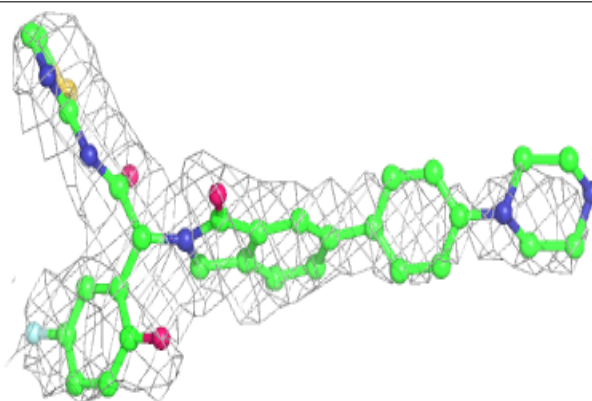


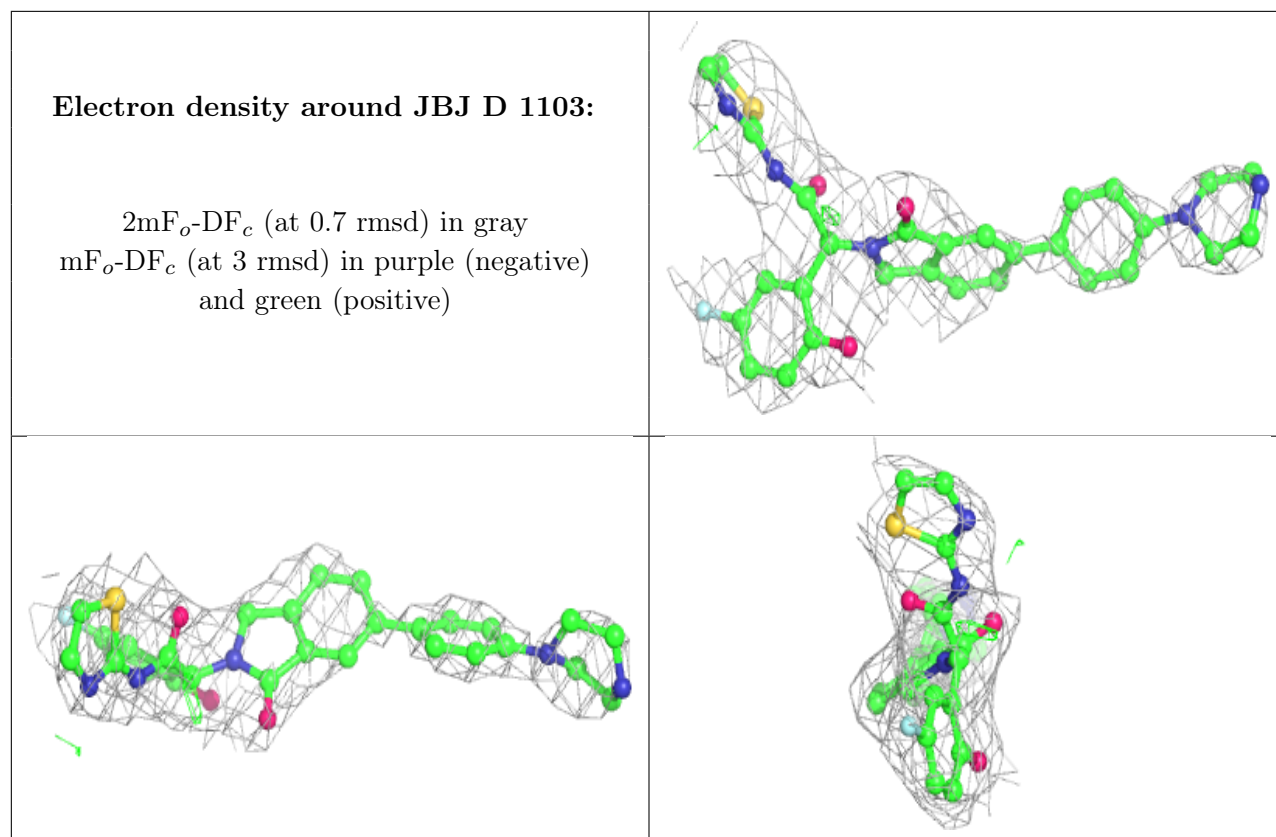
Electron density around JBJ E 1102:

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

**Electron density around JBJ A 1102:**

$2mF_o-DF_c$ (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.