wwPDB X-ray Structure Validation Summary Report (i)

May 22, 2020 – 03:22 pm BST

PDB ID	:	5DHU
Title	:	Crystal structure of NAD kinase 1 from Listeria monocytogenes in complex with a novel inhibitor
Authors	:	Gelin, M.; Paoletti, J.; Assairi, L.; Huteau, V.; Pochet, S.; Labesse, G.
Deposited on	:	2015-08-31
Resolution	:	2.33 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

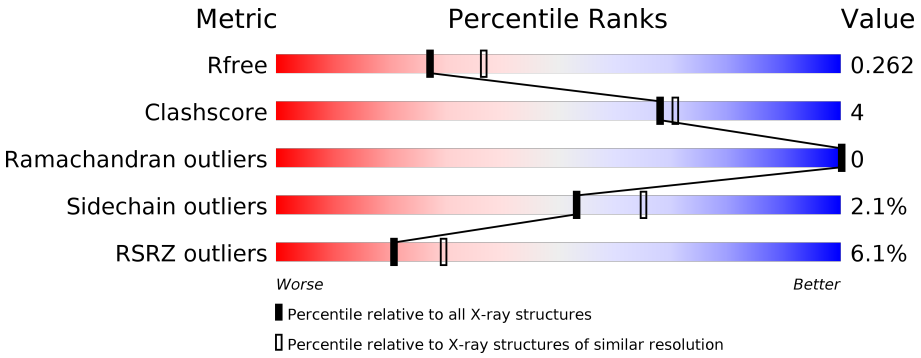
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.33 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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 >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	272	3% 89% 7% .
1	B	272	6% 78% 18% .
1	C	272	8% 87% 6% 7%
1	D	272	7% 80% 10% 10%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8425 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 NAD kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	263	Total	C	N	O	S	0	1	0
			2065	1323	345	388	9			
1	B	262	Total	C	N	O	S	0	2	0
			2107	1352	354	392	9			
1	C	254	Total	C	N	O	S	0	0	0
			1981	1271	332	369	9			
1	D	244	Total	C	N	O	S	0	0	0
			1894	1211	323	352	8			

There are 32 discrepancies between the modelled and reference sequences:

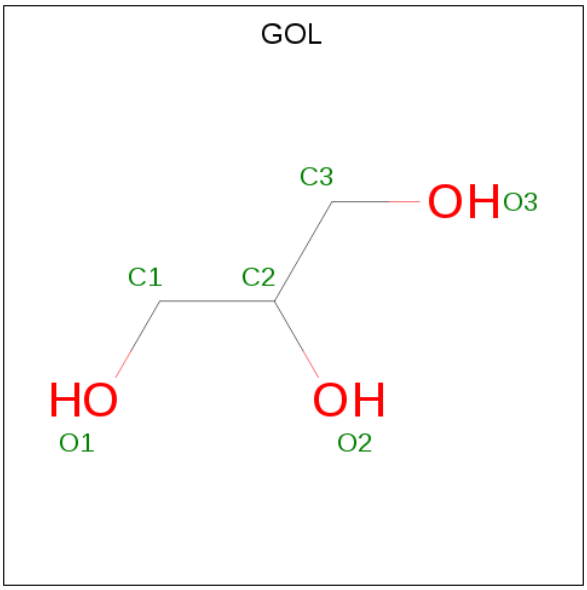
Chain	Residue	Modelled	Actual	Comment	Reference
A	265	LEU	-	expression tag	UNP Q8Y8D7
A	266	GLU	-	expression tag	UNP Q8Y8D7
A	267	HIS	-	expression tag	UNP Q8Y8D7
A	268	HIS	-	expression tag	UNP Q8Y8D7
A	269	HIS	-	expression tag	UNP Q8Y8D7
A	270	HIS	-	expression tag	UNP Q8Y8D7
A	271	HIS	-	expression tag	UNP Q8Y8D7
A	272	HIS	-	expression tag	UNP Q8Y8D7
B	265	LEU	-	expression tag	UNP Q8Y8D7
B	266	GLU	-	expression tag	UNP Q8Y8D7
B	267	HIS	-	expression tag	UNP Q8Y8D7
B	268	HIS	-	expression tag	UNP Q8Y8D7
B	269	HIS	-	expression tag	UNP Q8Y8D7
B	270	HIS	-	expression tag	UNP Q8Y8D7
B	271	HIS	-	expression tag	UNP Q8Y8D7
B	272	HIS	-	expression tag	UNP Q8Y8D7
C	265	LEU	-	expression tag	UNP Q8Y8D7
C	266	GLU	-	expression tag	UNP Q8Y8D7
C	267	HIS	-	expression tag	UNP Q8Y8D7
C	268	HIS	-	expression tag	UNP Q8Y8D7
C	269	HIS	-	expression tag	UNP Q8Y8D7

Continued on next page...

Continued from previous page...

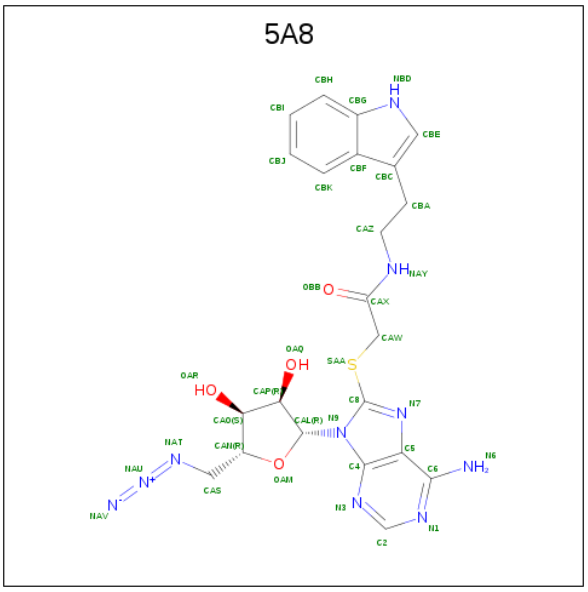
Chain	Residue	Modelled	Actual	Comment	Reference
C	270	HIS	-	expression tag	UNP Q8Y8D7
C	271	HIS	-	expression tag	UNP Q8Y8D7
C	272	HIS	-	expression tag	UNP Q8Y8D7
D	265	LEU	-	expression tag	UNP Q8Y8D7
D	266	GLU	-	expression tag	UNP Q8Y8D7
D	267	HIS	-	expression tag	UNP Q8Y8D7
D	268	HIS	-	expression tag	UNP Q8Y8D7
D	269	HIS	-	expression tag	UNP Q8Y8D7
D	270	HIS	-	expression tag	UNP Q8Y8D7
D	271	HIS	-	expression tag	UNP Q8Y8D7
D	272	HIS	-	expression tag	UNP Q8Y8D7

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



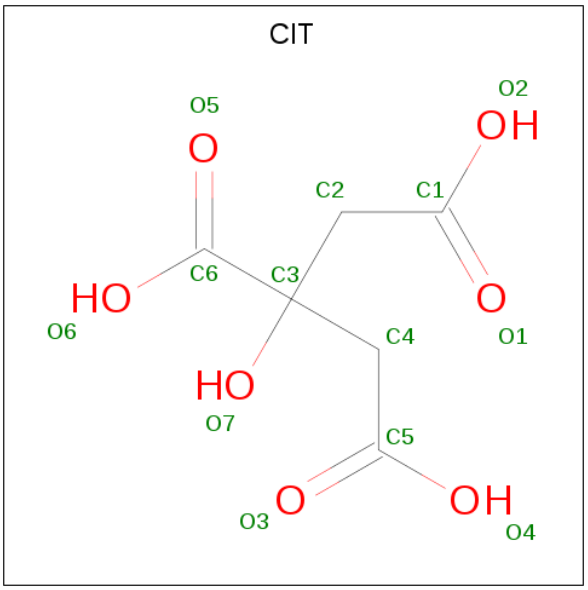
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	6	3	3	0	0

- Molecule 3 is 5'-azido-5'-deoxy-8-[(2-{[2-(1H-indol-3-yl)ethyl]amino}-2-oxoethyl)sulfanyl]adenosine (three-letter code: 5A8) (formula: $C_{22}H_{24}N_{10}O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			37	22	10	4	1		
3	B	1	Total	C	N	O	S	0	0
			37	22	10	4	1		
3	C	1	Total	C	N	O	S	0	0
			37	22	10	4	1		
3	D	1	Total	C	N	O	S	0	0
			37	22	10	4	1		

- Molecule 4 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 13 6 7	0	0

- Molecule 5 is water.

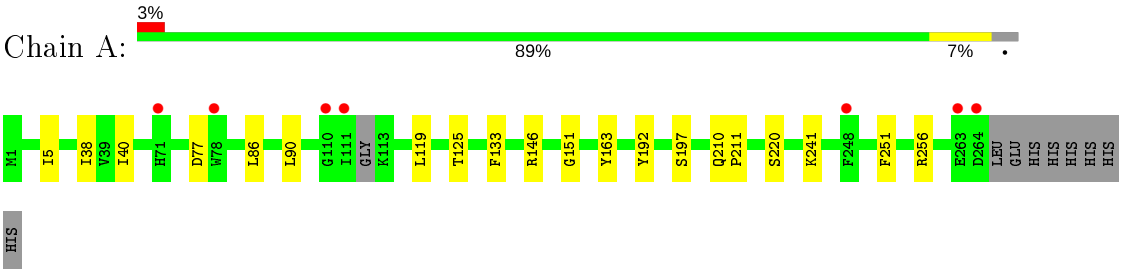
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	74	Total O 74 74	0	0
5	B	34	Total O 34 34	0	0
5	C	53	Total O 53 53	0	0
5	D	50	Total O 50 50	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

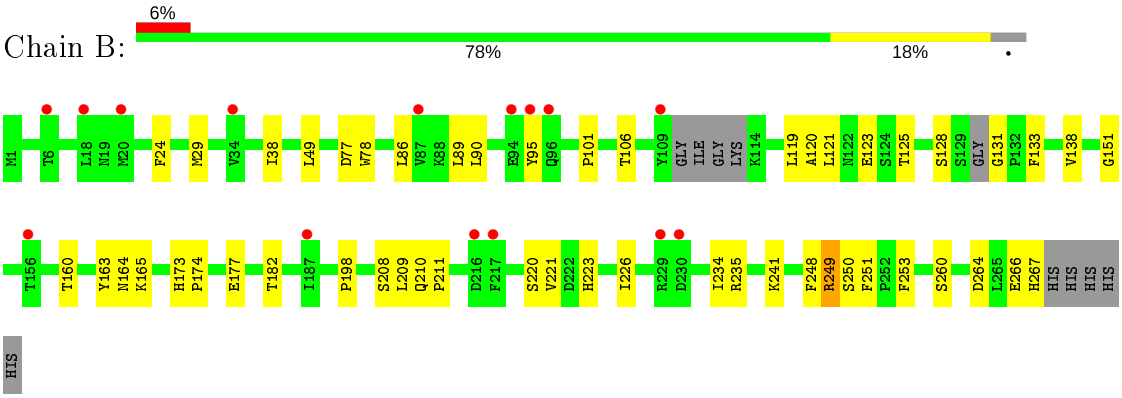
- Molecule 1: NAD kinase 1

Chain A:



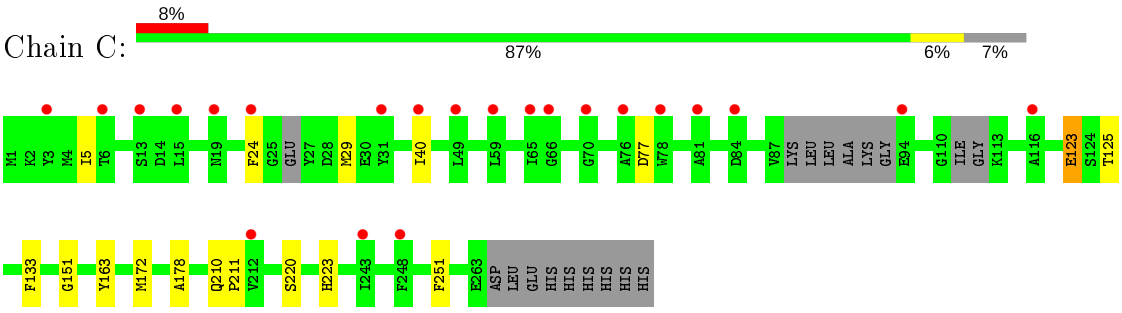
- Molecule 1: NAD kinase 1

Chain B:



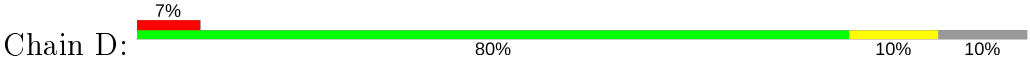
- Molecule 1: NAD kinase 1

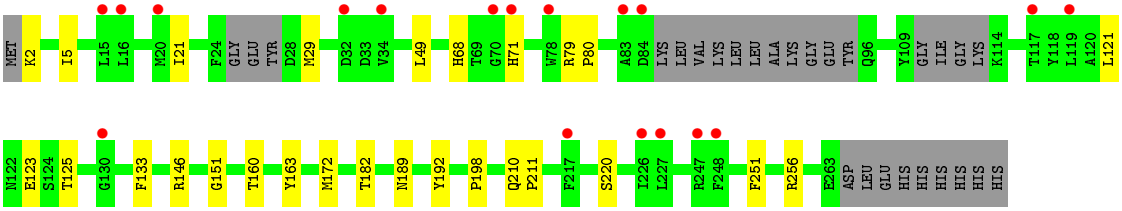
Chain C:



- Molecule 1: NAD kinase 1

Chain D:




MET K2 I5 L15 L16 M20 I21 F24 GLY GLU TYR D28 M29 D32 D33 V34 L49 H68 T69 G70 H71 W78 R79 P80 A83 D84 LYS LEU VAL LYS LEU LEU ALA LYS GLY GLU TYR Q96 Y109 GLY ILE GLY LYS K114 T117 Y118 L119 A120 L121
N122 E123 S124 T125 G130 F133 R146 G151 T160 Y163 M172 T182 N189 Y192 P198 Q210 P211 F217 S220 I226 L227 R247 F248 F251 R256 E263 ASP LEU GLU HIS HIS HIS HIS HIS HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	66.92Å 119.34Å 67.75Å 90.00° 100.37° 90.00°	Depositor
Resolution (Å)	47.45 – 2.33 59.67 – 2.33	Depositor EDS
% Data completeness (in resolution range)	92.2 (47.45-2.33) 92.1 (59.67-2.33)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.03	Depositor
$< I/\sigma(I) >$ [1]	2.30 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.225 , 0.259 0.228 , 0.262	Depositor DCC
R_{free} test set	1279 reflections (3.11%)	wwPDB-VP
Wilson B-factor (Å^2)	47.6	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 51.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.028 for l,-k,h	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8425	wwPDB-VP
Average B, all atoms (Å^2)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.65% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CIT, 5A8

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	0.21	0/2120	0.35	0/2869
1	B	0.21	0/2160	0.34	0/2917
1	C	0.21	0/2029	0.35	0/2747
1	D	0.21	0/1939	0.34	0/2624
All	All	0.21	0/8248	0.35	0/11157

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

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	2065	0	1988	10	0
1	B	2107	0	2058	28	0
1	C	1981	0	1885	9	0
1	D	1894	0	1803	12	0
2	A	6	0	8	0	0
3	A	37	0	0	0	0
3	B	37	0	0	0	0
3	C	37	0	0	1	0
3	D	37	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	13	0	5	3	0
5	A	74	0	0	1	0
5	B	34	0	0	0	0
5	C	53	0	0	0	0
5	D	50	0	0	2	0
All	All	8425	0	7747	60	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 60 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:A:38:ILE:HD13	1:A:90:LEU:HD22	1.74	0.69
4:B:301:CIT:O4	4:B:301:CIT:O7	2.13	0.67
1:B:38:ILE:HD13	1:B:90:LEU:HD22	1.76	0.66
1:A:256:ARG:NH2	5:A:402:HOH:O	2.31	0.63
1:A:125:THR:OG1	1:A:220:SER:OG	2.19	0.59

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	260/272 (96%)	246 (95%)	14 (5%)	0	100	100
1	B	258/272 (95%)	245 (95%)	13 (5%)	0	100	100
1	C	246/272 (90%)	231 (94%)	15 (6%)	0	100	100
1	D	236/272 (87%)	220 (93%)	16 (7%)	0	100	100
All	All	1000/1088 (92%)	942 (94%)	58 (6%)	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	220/237 (93%)	217 (99%)	3 (1%)	67	78
1	B	228/237 (96%)	221 (97%)	7 (3%)	40	49
1	C	208/237 (88%)	205 (99%)	3 (1%)	67	78
1	D	199/237 (84%)	193 (97%)	6 (3%)	41	50
All	All	855/948 (90%)	836 (98%)	19 (2%)	53	63

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	249[B]	ARG
1	C	123	GLU
1	D	79	ARG
1	B	249[A]	ARG
1	D	123	GLU

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

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

6 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	GOL	A	301	-	5,5,5	0.37	0	5,5,5	0.26	0
4	CIT	B	301	-	3,12,12	1.46	0	3,17,17	1.98	2 (66%)
3	5A8	D	301	-	37,41,41	1.64	8 (21%)	35,58,58	2.25	4 (11%)
3	5A8	B	302	-	37,41,41	2.08	15 (40%)	35,58,58	1.68	7 (20%)
3	5A8	A	302	-	37,41,41	2.12	12 (32%)	35,58,58	1.24	2 (5%)
3	5A8	C	301	-	37,41,41	2.18	13 (35%)	35,58,58	1.85	5 (14%)

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	GOL	A	301	-	-	2/4/4/4	-
4	CIT	B	301	-	-	6/6/16/16	-
3	5A8	D	301	-	-	4/13/35/35	0/5/5/5
3	5A8	B	302	-	-	5/13/35/35	0/5/5/5
3	5A8	A	302	-	-	3/13/35/35	0/5/5/5
3	5A8	C	301	-	-	5/13/35/35	0/5/5/5

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	5A8	C8-N9	-6.76	1.29	1.36
3	C	301	5A8	C8-N9	-6.11	1.30	1.36
3	B	302	5A8	C8-N9	-5.45	1.31	1.36
3	D	301	5A8	NAU-NAT	4.43	1.35	1.23
3	C	301	5A8	C4-N3	-3.99	1.30	1.35

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	301	5A8	OAM-CAN-CAS	10.53	120.08	109.09
3	C	301	5A8	OAM-CAN-CAS	-6.73	102.08	109.09
3	C	301	5A8	N3-C2-N1	-5.41	120.22	128.68
3	B	302	5A8	N3-C2-N1	-5.01	120.84	128.68
3	D	301	5A8	N3-C2-N1	-3.98	122.46	128.68

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	GOL	O1-C1-C2-C3
4	B	301	CIT	C1-C2-C3-O7
4	B	301	CIT	C1-C2-C3-C4
4	B	301	CIT	C1-C2-C3-C6
4	B	301	CIT	C2-C3-C4-C5

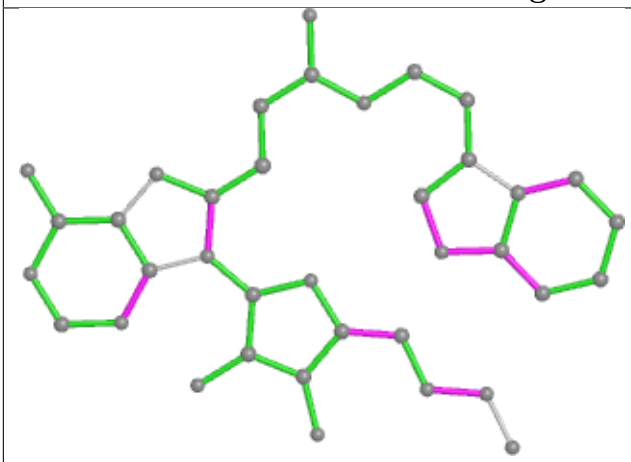
There are no ring outliers.

3 monomers are involved in 5 short contacts:

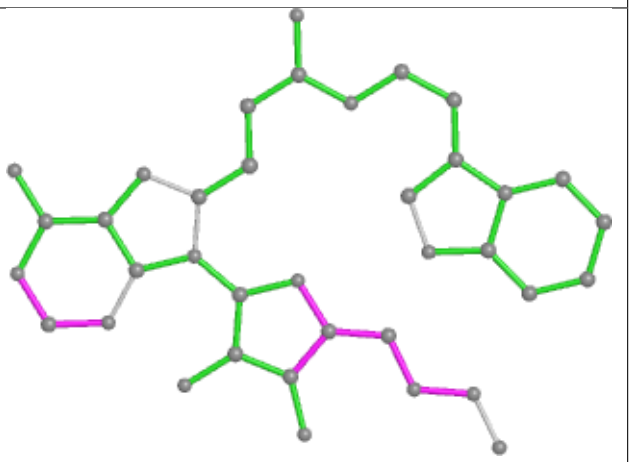
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	301	CIT	3	0
3	D	301	5A8	1	0
3	C	301	5A8	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

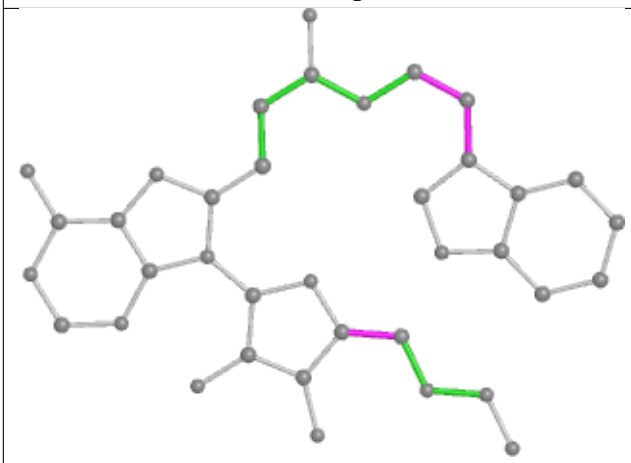
Ligand 5A8 D 301



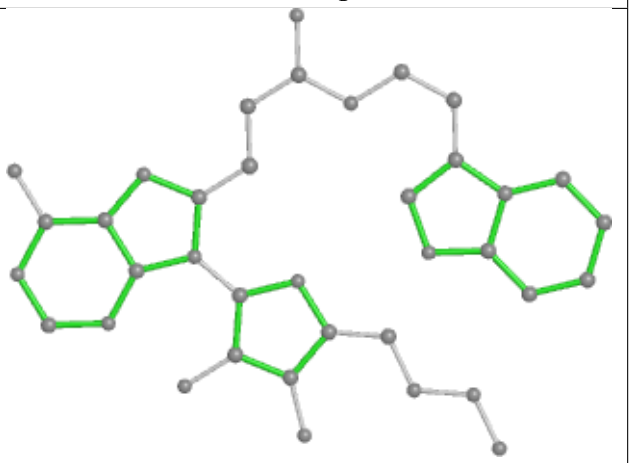
Bond lengths



Bond angles

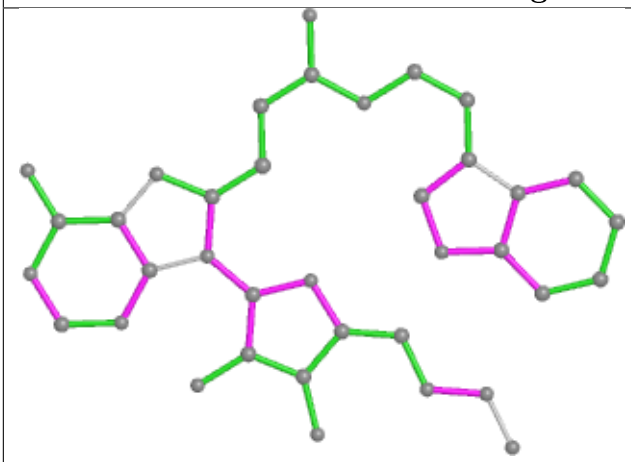


Torsions

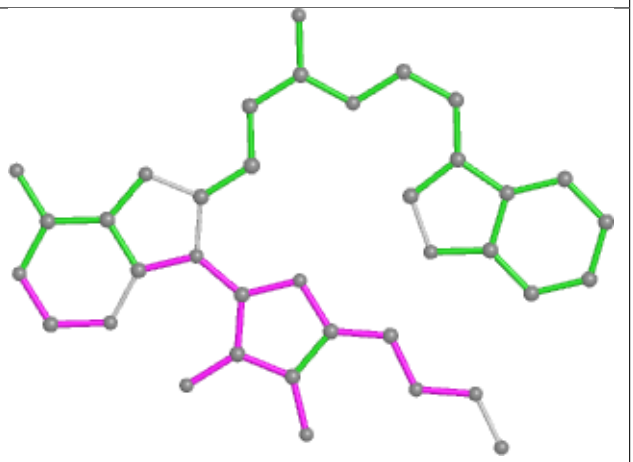


Rings

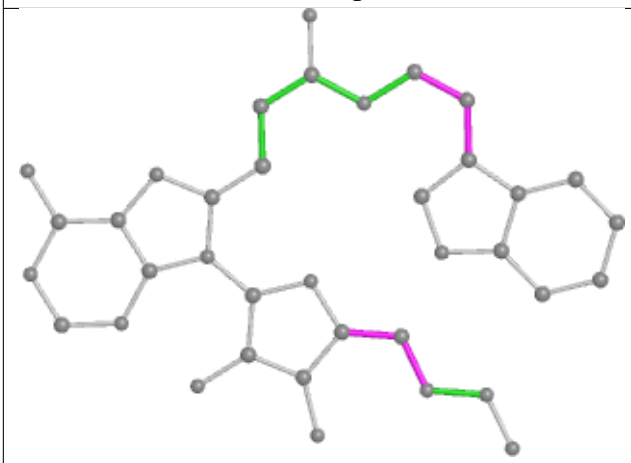
Ligand 5A8 B 302



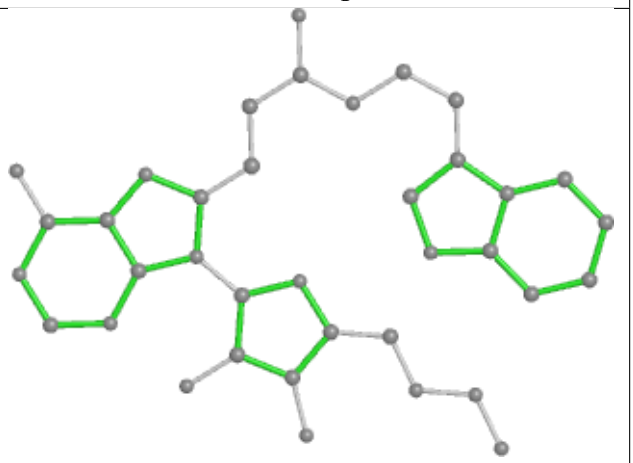
Bond lengths



Bond angles

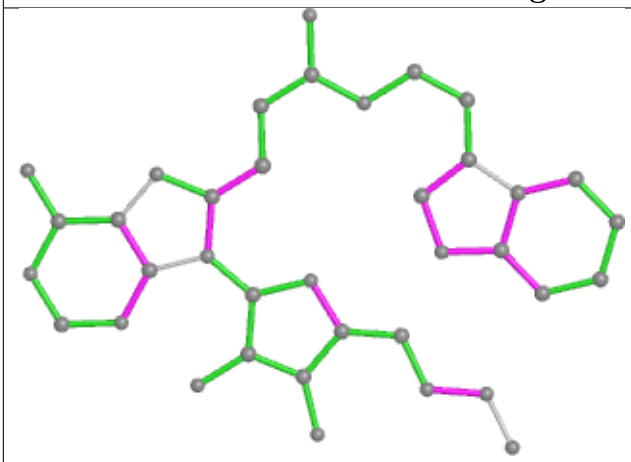


Torsions

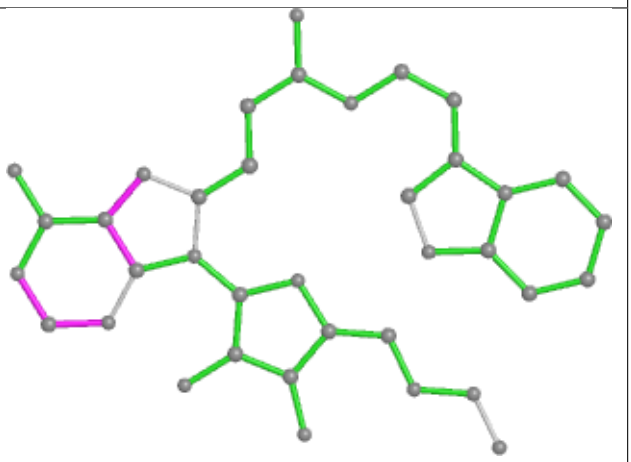


Rings

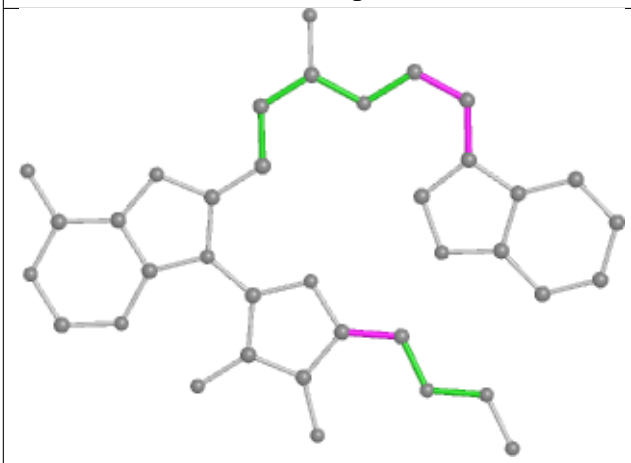
Ligand 5A8 A 302



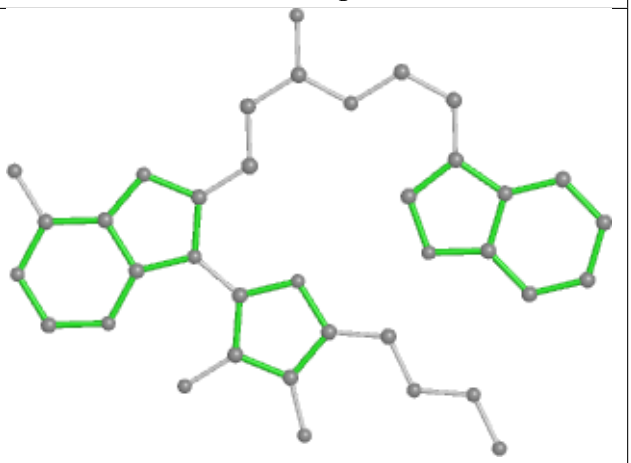
Bond lengths



Bond angles

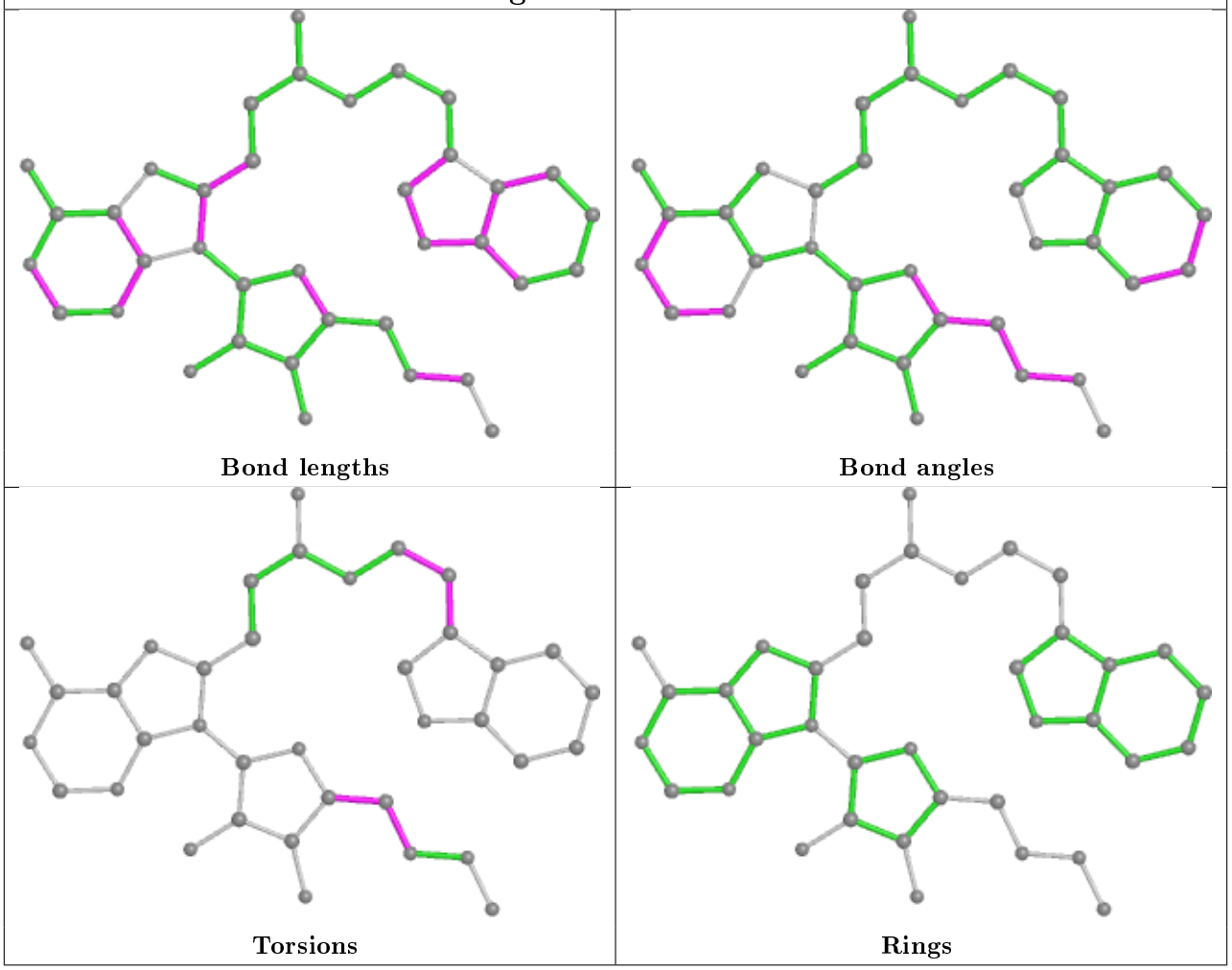


Torsions



Rings

Ligand 5A8 C 301



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

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^{th} 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	263/272 (96%)	0.42	7 (2%)	54	64	27, 52, 90, 134	46 (17%)
1	B	262/272 (96%)	0.64	15 (5%)	23	33	31, 70, 106, 131	52 (19%)
1	C	254/272 (93%)	0.70	22 (8%)	10	15	33, 70, 121, 136	40 (15%)
1	D	244/272 (89%)	0.74	18 (7%)	14	21	35, 72, 122, 156	37 (15%)
All	All	1023/1088 (94%)	0.62	62 (6%)	21	30	27, 66, 117, 156	175 (17%)

The worst 5 of 62 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	248	PHE	6.5
1	A	264	ASP	5.3
1	C	40	ILE	4.9
1	B	20	MET	4.4
1	A	111	ILE	4.3

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 carbohydrates in this entry.

6.4 Ligands

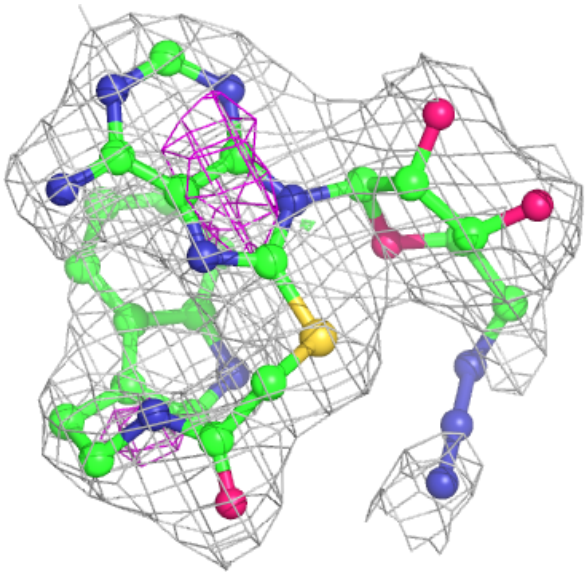
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

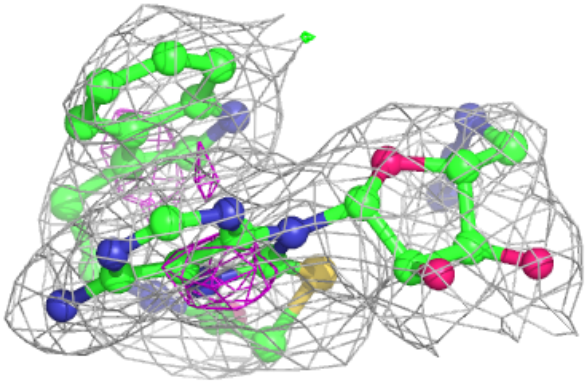
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	CIT	B	301	13/13	0.80	0.34	57,60,65,65	13
3	5A8	D	301	37/37	0.83	0.23	51,60,68,77	4
2	GOL	A	301	6/6	0.84	0.32	81,81,81,82	0
3	5A8	B	302	37/37	0.89	0.15	50,57,64,67	5
3	5A8	C	301	37/37	0.92	0.15	38,44,59,59	5
3	5A8	A	302	37/37	0.93	0.15	33,44,55,57	5

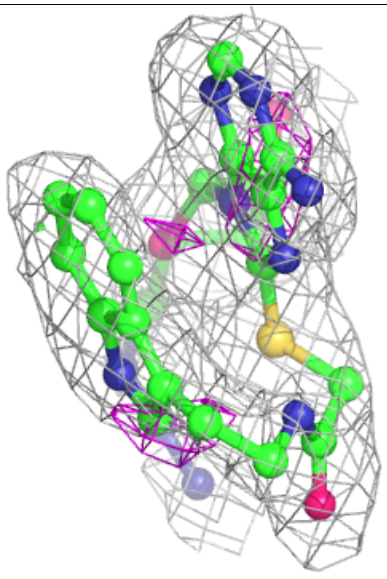
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 5A8 D 301:

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

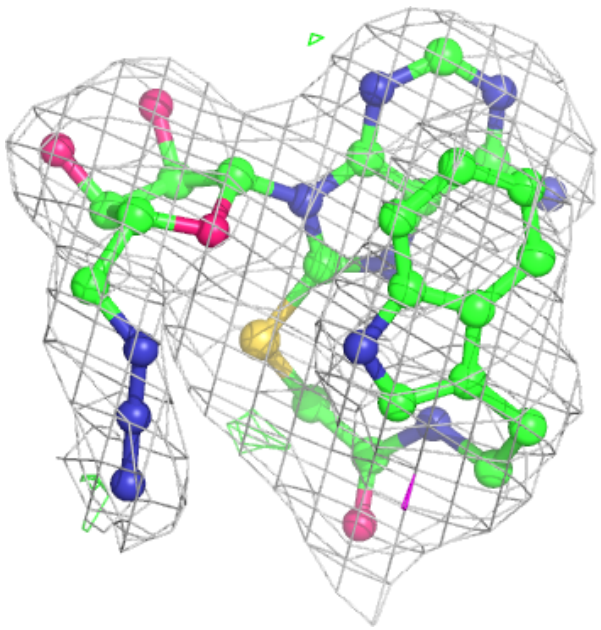


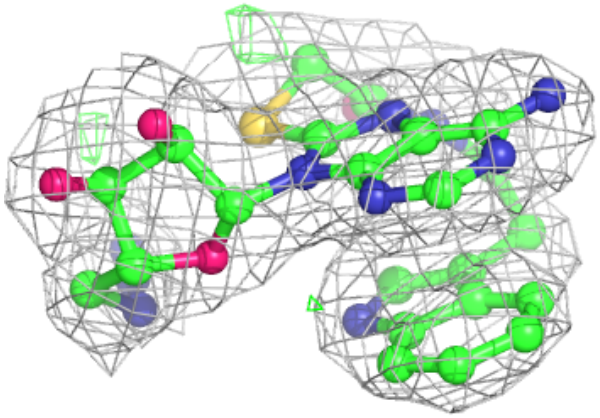


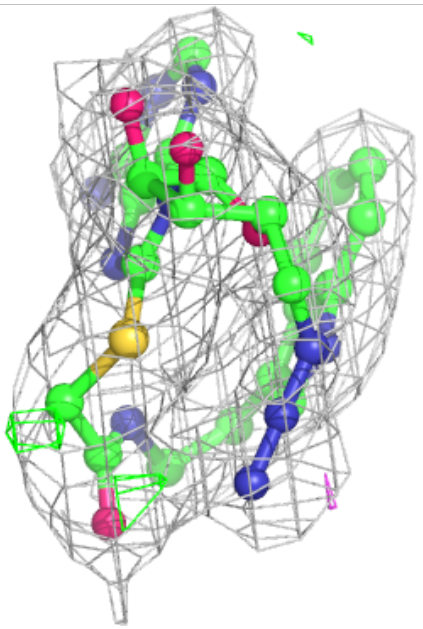


Electron density around 5A8 B 302:

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

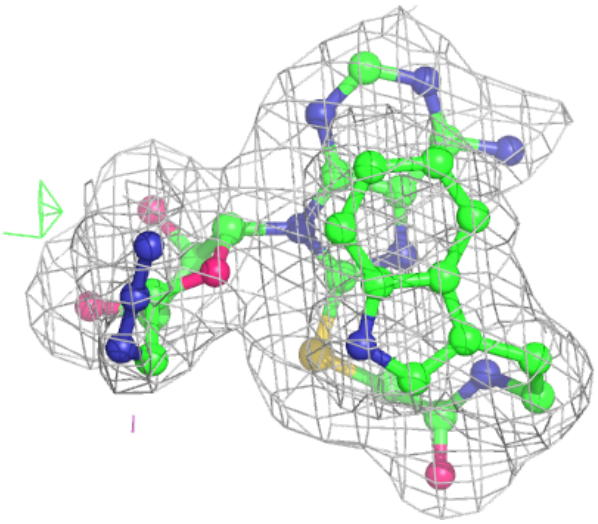


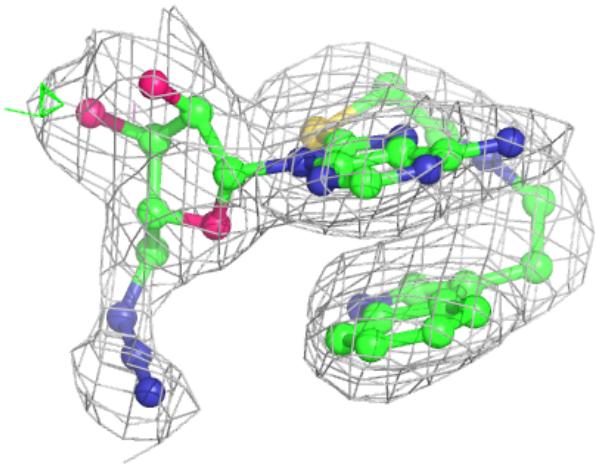


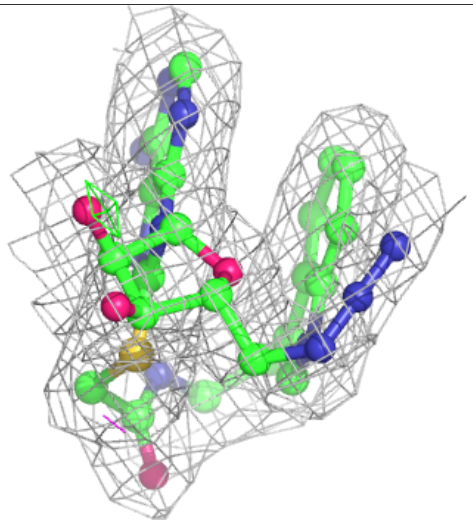


Electron density around 5A8 C 301:

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

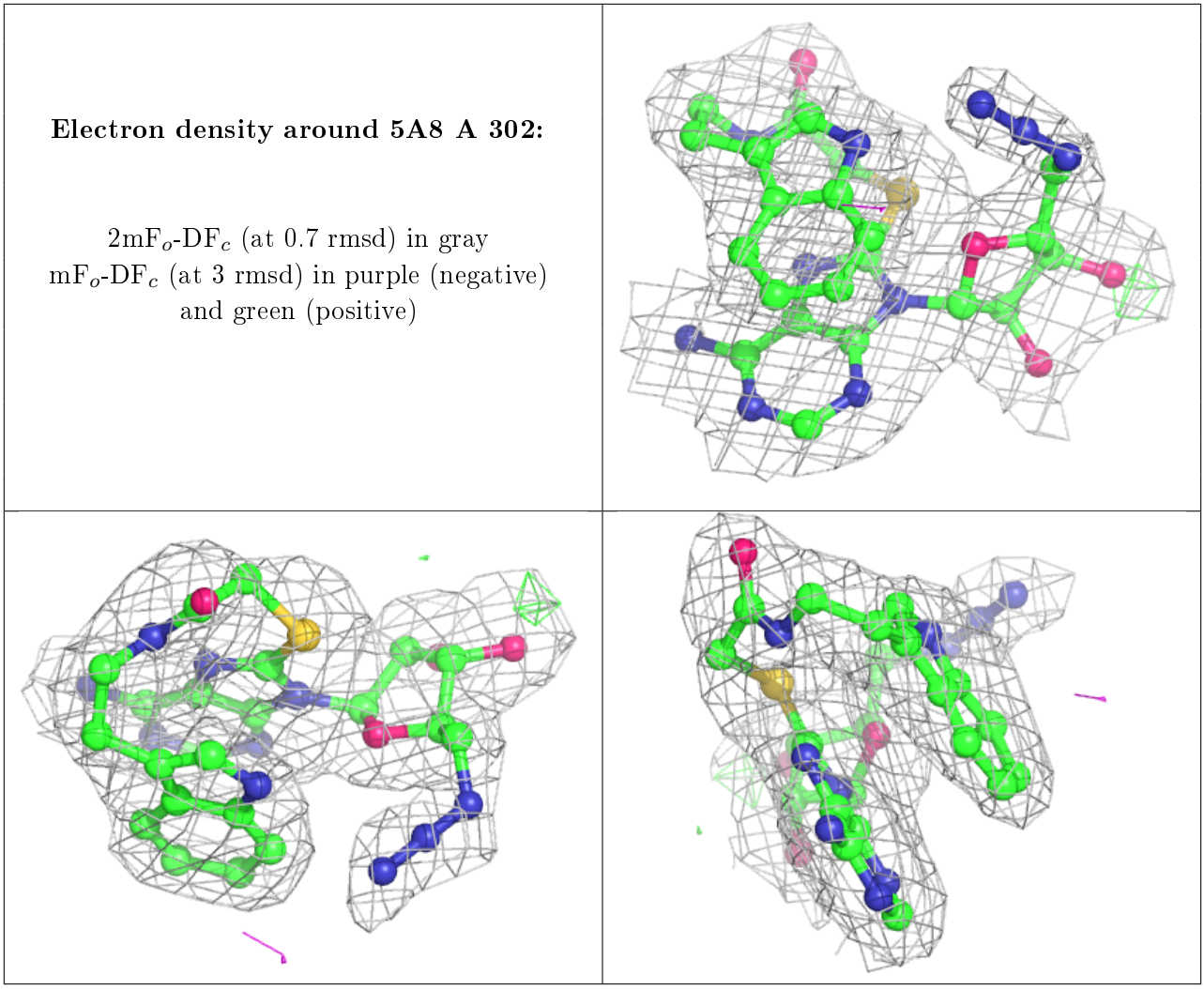






Electron density around 5A8 A 302:

$2mF_o$-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.