



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 06:25 am BST

PDB ID : 6BL0
Title : Novel Modes of Inhibition of Wild-Type IDH1:Direct Covalent Modification of His315 with Cmpd11
Authors : Jakob, C.G.; Qiu, W.
Deposited on : 2017-11-09
Resolution : 2.17 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 2.11
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

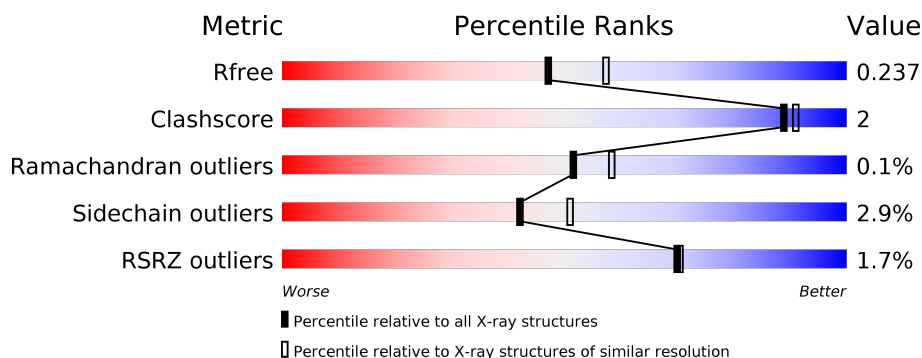
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.17 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	6864 (2.20-2.16)
Clashscore	141614	7689 (2.20-2.16)
Ramachandran outliers	138981	7564 (2.20-2.16)
Sidechain outliers	138945	7564 (2.20-2.16)
RSRZ outliers	127900	6738 (2.20-2.16)

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 $\leq 5\%$. 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	425	<div> <div>92%</div> <div>6% •</div> </div>
1	B	425	<div> <div>3%</div> <div>90%</div> <div>8% •</div> </div>
1	C	425	<div> <div>%</div> <div>90%</div> <div>7% ••</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10615 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 Isocitrate dehydrogenase [NADP] cytoplasmic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	416	Total	C	N	O	S	0	0	0
			3288	2090	558	622	18			
1	B	416	Total	C	N	O	S	0	0	0
			3292	2093	559	622	18			
1	C	416	Total	C	N	O	S	0	0	0
			3292	2093	559	622	18			

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	415	SER	-	expression tag	UNP O75874
A	416	LEU	-	expression tag	UNP O75874
A	417	GLU	-	expression tag	UNP O75874
A	418	HIS	-	expression tag	UNP O75874
A	419	HIS	-	expression tag	UNP O75874
A	420	HIS	-	expression tag	UNP O75874
A	421	HIS	-	expression tag	UNP O75874
A	422	HIS	-	expression tag	UNP O75874
A	423	HIS	-	expression tag	UNP O75874
A	424	HIS	-	expression tag	UNP O75874
A	425	HIS	-	expression tag	UNP O75874
B	415	SER	-	expression tag	UNP O75874
B	416	LEU	-	expression tag	UNP O75874
B	417	GLU	-	expression tag	UNP O75874
B	418	HIS	-	expression tag	UNP O75874
B	419	HIS	-	expression tag	UNP O75874
B	420	HIS	-	expression tag	UNP O75874
B	421	HIS	-	expression tag	UNP O75874
B	422	HIS	-	expression tag	UNP O75874
B	423	HIS	-	expression tag	UNP O75874
B	424	HIS	-	expression tag	UNP O75874
B	425	HIS	-	expression tag	UNP O75874
C	415	SER	-	expression tag	UNP O75874

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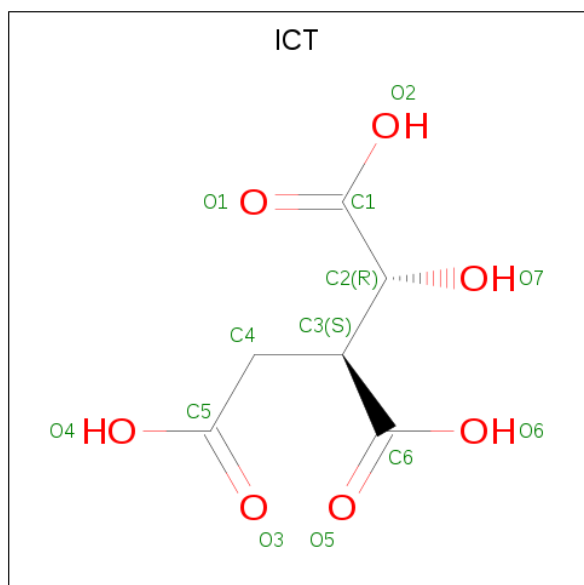
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Chain	Residue	Modelled	Actual	Comment	Reference
C	416	LEU	-	expression tag	UNP O75874
C	417	GLU	-	expression tag	UNP O75874
C	418	HIS	-	expression tag	UNP O75874
C	419	HIS	-	expression tag	UNP O75874
C	420	HIS	-	expression tag	UNP O75874
C	421	HIS	-	expression tag	UNP O75874
C	422	HIS	-	expression tag	UNP O75874
C	423	HIS	-	expression tag	UNP O75874
C	424	HIS	-	expression tag	UNP O75874
C	425	HIS	-	expression tag	UNP O75874

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mg 2 2	0	0
2	C	1	Total Mg 1 1	0	0

- Molecule 3 is ISOCITRIC ACID (three-letter code: ICT) (formula: C₆H₈O₇).



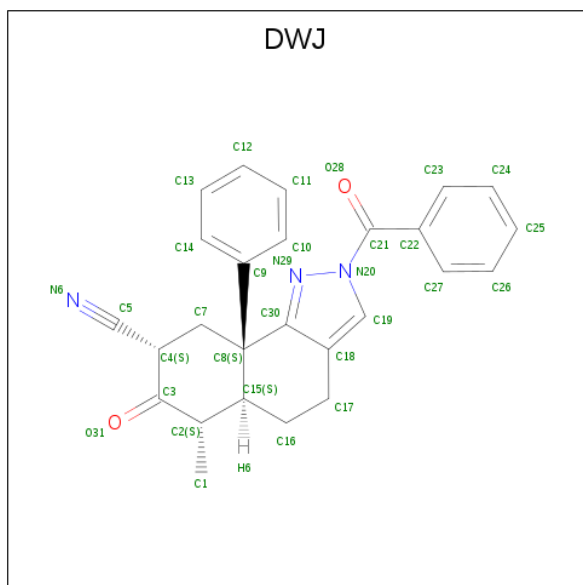
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 13 6 7	0	0
3	A	1	Total C O 13 6 7	0	0

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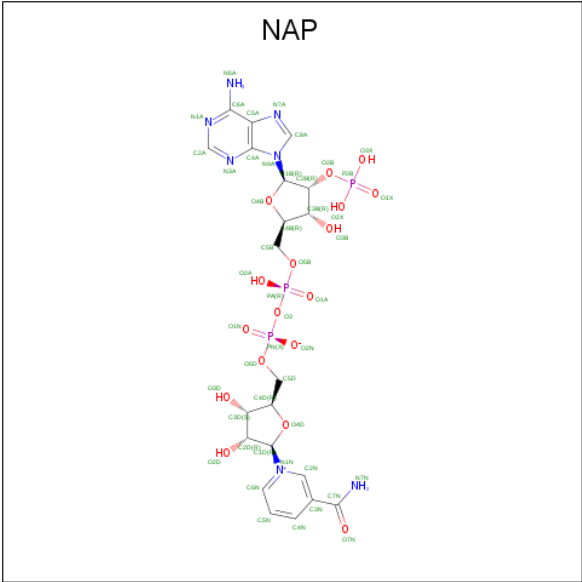
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is (5a*S*,6*S*,8*S*,9a*S*)-2-(benzenecarbonyl)-6-methyl-7-oxo-9a-phenyl-4,5,5a,6,7,8,9,9a-octahydro-2*H*-benzo[*g*]indazole-8-carbonitrile (three-letter code: DWJ) (formula: C₂₆H₂₃N₃O₂) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			31	26	3	2		

- Molecule 5 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
5	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

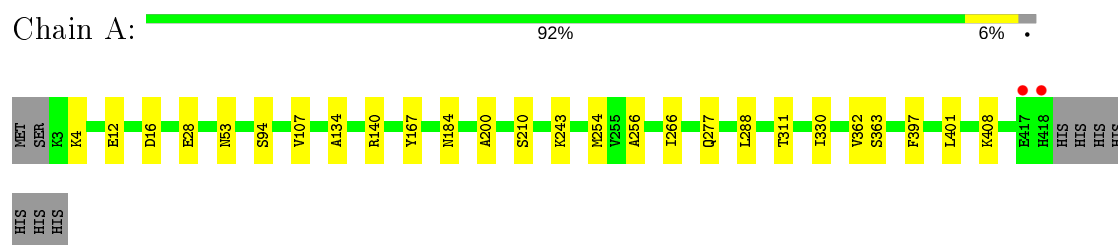
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	143	Total	O	0	0
			143	143		
6	B	173	Total	O	0	0
			173	173		
6	C	258	Total	O	0	0
			258	258		

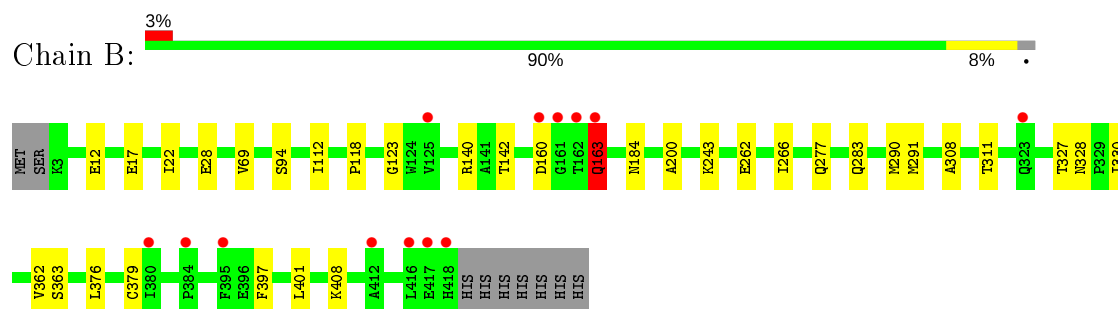
3 Residue-property plots [i](#)

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.

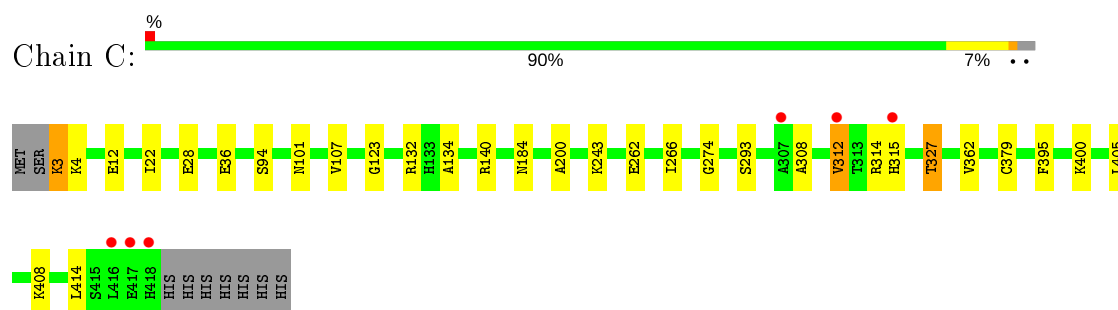
- Molecule 1: Isocitrate dehydrogenase [NADP] cytoplasmic



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4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	98.19Å 274.33Å 115.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	137.16 – 2.17 137.16 – 2.17	Depositor EDS
% Data completeness (in resolution range)	99.9 (137.16-2.17) 99.9 (137.16-2.17)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 2.16Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.196 , 0.227 0.202 , 0.237	Depositor DCC
R_{free} test set	4105 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	45.6	Xtriage
Anisotropy	0.243	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 48.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10615	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DWJ, NAP, MG, ICT

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	0.48	0/3357	0.64	0/4529
1	B	0.50	0/3361	0.66	0/4533
1	C	0.54	0/3361	0.66	0/4533
All	All	0.51	0/10079	0.66	0/13595

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	3288	0	3244	11	0
1	B	3292	0	3255	16	0
1	C	3292	0	3255	13	0
2	A	2	0	0	0	0
2	C	1	0	0	0	0
3	A	26	0	8	1	0
3	C	13	0	4	1	0
4	A	31	0	0	0	0
5	B	48	0	25	1	0
5	C	48	0	25	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	143	0	0	0	0
6	B	173	0	0	0	0
6	C	258	0	0	2	0
All	All	10615	0	9816	38	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 2.

All (38) 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:C:101:ASN:HB3	6:C:790:HOH:O	1.35	1.23
1:A:167:TYR:HB3	1:B:142:THR:HG21	1.81	0.60
1:C:22:ILE:HD11	1:C:327:THR:HB	1.83	0.60
3:A:505:ICT:H2	5:B:501:NAP:C4N	2.32	0.60
1:C:4:LYS:HD2	1:C:36:GLU:HG3	1.86	0.57
1:A:277:GLN:HE22	1:B:277:GLN:HE22	1.54	0.55
3:C:501:ICT:H2	5:C:502:NAP:C4N	2.37	0.53
1:C:107:VAL:HG23	1:C:134:ALA:HB2	1.91	0.52
1:A:362:VAL:HG23	1:A:408:LYS:HD2	1.92	0.51
1:B:362:VAL:HG23	1:B:408:LYS:HD2	1.92	0.51
1:C:362:VAL:HG23	1:C:408:LYS:HD2	1.93	0.51
1:B:112:ILE:HD13	1:B:330:ILE:HG22	1.95	0.48
1:A:107:VAL:HG23	1:A:134:ALA:HB2	1.96	0.48
1:B:291:MET:HE2	1:B:308:ALA:HB3	1.95	0.48
1:B:397:PHE:CE2	1:B:401:LEU:HD11	2.48	0.48
1:C:293:SER:HB2	1:C:308:ALA:HB2	1.96	0.48
1:C:200:ALA:HA	1:C:266:ILE:HG13	1.97	0.47
1:A:397:PHE:CE2	1:A:401:LEU:HD11	2.51	0.46
1:B:330:ILE:HD12	1:B:363:SER:HB3	1.98	0.46
1:B:118:PRO:HD2	1:B:379:CYS:HB3	1.99	0.45
1:B:17:GLU:HB2	1:B:311:THR:HB	1.99	0.45
1:B:290:MET:HG3	1:B:376:LEU:HD21	1.99	0.45
1:A:200:ALA:HA	1:A:266:ILE:HG13	2.00	0.44
1:A:53:ASN:ND2	1:C:395:PHE:HB3	2.32	0.44
1:C:132:ARG:HG3	1:C:274:GLY:HA3	1.99	0.44
1:A:330:ILE:HD12	1:A:363:SER:HB3	2.00	0.43
1:B:328:ASN:OD1	1:B:330:ILE:HG12	2.18	0.43
1:B:22:ILE:HD11	1:B:327:THR:HB	2.00	0.42
1:A:210:SER:HB3	1:A:254:MET:HG2	2.02	0.42
1:B:200:ALA:HA	1:B:266:ILE:HG13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:123:GLY:O	1:C:262:GLU:HA	2.20	0.42
1:C:362:VAL:HG21	1:C:405:LEU:HA	2.02	0.42
1:B:123:GLY:O	1:B:262:GLU:HA	2.21	0.41
1:B:163:GLN:HB3	1:C:3:LYS:HB3	2.03	0.41
1:A:16:ASP:HB2	1:A:311:THR:HG21	2.03	0.40
1:A:256:ALA:O	1:B:283:GLN:HG2	2.21	0.40
5:C:502:NAP:C2A	6:C:698:HOH:O	2.69	0.40
1:C:312:VAL:HB	1:C:315:HIS:HB2	2.03	0.40

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	414/425 (97%)	401 (97%)	13 (3%)	0	100	100
1	B	414/425 (97%)	397 (96%)	16 (4%)	1 (0%)	47	52
1	C	414/425 (97%)	401 (97%)	13 (3%)	0	100	100
All	All	1242/1275 (97%)	1199 (96%)	42 (3%)	1 (0%)	51	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	163	GLN

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	349/361 (97%)	341 (98%)	8 (2%)	50 60
1	B	350/361 (97%)	341 (97%)	9 (3%)	46 55
1	C	350/361 (97%)	337 (96%)	13 (4%)	34 40
All	All	1049/1083 (97%)	1019 (97%)	30 (3%)	42 51

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LYS
1	A	12	GLU
1	A	28	GLU
1	A	94	SER
1	A	140	ARG
1	A	184	ASN
1	A	243	LYS
1	A	288	LEU
1	B	12	GLU
1	B	28	GLU
1	B	69	VAL
1	B	94	SER
1	B	140	ARG
1	B	160	ASP
1	B	163	GLN
1	B	184	ASN
1	B	243	LYS
1	C	3	LYS
1	C	12	GLU
1	C	28	GLU
1	C	94	SER
1	C	140	ARG
1	C	184	ASN
1	C	243	LYS
1	C	312	VAL
1	C	314	ARG
1	C	327	THR
1	C	379	CYS
1	C	400	LYS
1	C	414	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	GLN
1	B	185	GLN
1	B	277	GLN
1	B	323	GLN
1	C	185	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 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	$\# Z > 2$
3	ICT	C	501	2	2,12,12	0.54	0	5,16,16	2.52	4 (80%)
3	ICT	A	505	2	2,12,12	0.09	0	5,16,16	1.93	2 (40%)
5	NAP	C	502	-	45,52,52	0.83	1 (2%)	56,80,80	0.93	4 (7%)
5	NAP	B	501	-	45,52,52	0.84	1 (2%)	56,80,80	0.92	2 (3%)
4	DWJ	A	504	1	31,35,35	0.72	1 (3%)	37,52,52	1.78	7 (18%)
3	ICT	A	502	2	2,12,12	0.36	0	5,16,16	3.04	2 (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	ICT	C	501	2	-	1/6/16/16	-
3	ICT	A	505	2	-	0/6/16/16	-
5	NAP	C	502	-	-	9/31/67/67	0/5/5/5
5	NAP	B	501	-	-	10/31/67/67	0/5/5/5
4	DWJ	A	504	1	-	2/10/50/50	0/5/5/5
3	ICT	A	502	2	-	2/6/16/16	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	501	NAP	C2N-N1N	4.32	1.40	1.35
5	C	502	NAP	C2N-N1N	4.06	1.39	1.35
4	A	504	DWJ	N29-N20	-2.11	1.35	1.39

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	ICT	C1-C2-C3	-4.92	106.71	112.25
4	A	504	DWJ	C7-C4-C3	4.74	117.39	108.09
3	A	502	ICT	C4-C3-C6	-4.18	107.04	112.70
4	A	504	DWJ	C2-C3-C4	4.18	121.33	113.47
4	A	504	DWJ	C16-C15-C8	4.09	117.06	110.43
3	C	501	ICT	C4-C3-C6	-4.08	107.18	112.70
3	A	505	ICT	C4-C3-C6	-3.40	108.09	112.70
4	A	504	DWJ	C7-C8-C9	2.99	116.93	111.03
4	A	504	DWJ	C22-C21-N20	2.97	124.20	119.52
4	A	504	DWJ	C9-C8-C30	-2.85	105.49	110.95
4	A	504	DWJ	C7-C8-C30	-2.50	108.46	114.77
5	C	502	NAP	C5A-C6A-N6A	2.31	123.87	120.35
5	C	502	NAP	O2A-PA-O5B	-2.29	97.10	107.75
3	C	501	ICT	O7-C2-C3	2.27	114.91	108.56
5	B	501	NAP	C5A-C6A-N6A	2.26	123.78	120.35
3	C	501	ICT	C4-C3-C2	-2.24	104.00	110.29
5	B	501	NAP	C2N-N1N-C1D	-2.23	114.17	119.14
3	C	501	ICT	C1-C2-C3	-2.11	109.87	112.25
3	A	505	ICT	O7-C2-C3	2.10	114.44	108.56
5	C	502	NAP	C2N-N1N-C1D	-2.05	114.57	119.14
5	C	502	NAP	O3B-C3B-C2B	2.04	116.96	111.17

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	502	NAP	C5B-O5B-PA-O1A
5	C	502	NAP	C5D-O5D-PN-O1N
5	C	502	NAP	C5D-O5D-PN-O2N
5	C	502	NAP	O4D-C1D-N1N-C2N
5	C	502	NAP	O4D-C1D-N1N-C6N
5	C	502	NAP	C2D-C1D-N1N-C2N
5	B	501	NAP	C5B-O5B-PA-O3
5	B	501	NAP	C5D-O5D-PN-O1N
5	B	501	NAP	C5D-O5D-PN-O2N
5	B	501	NAP	O4D-C1D-N1N-C2N
5	B	501	NAP	O4D-C1D-N1N-C6N
5	B	501	NAP	C2D-C1D-N1N-C2N
3	C	501	ICT	C1-C2-C3-C6
5	C	502	NAP	C5B-O5B-PA-O3
5	B	501	NAP	C5B-O5B-PA-O1A
5	B	501	NAP	C5B-O5B-PA-O2A
3	A	502	ICT	O7-C2-C3-C6
3	A	502	ICT	C1-C2-C3-C6
4	A	504	DWJ	C30-C8-C9-C10
4	A	504	DWJ	C30-C8-C9-C14
5	C	502	NAP	C5D-O5D-PN-O3
5	C	502	NAP	C2D-C1D-N1N-C6N
5	B	501	NAP	C5D-O5D-PN-O3
5	B	501	NAP	C2D-C1D-N1N-C6N

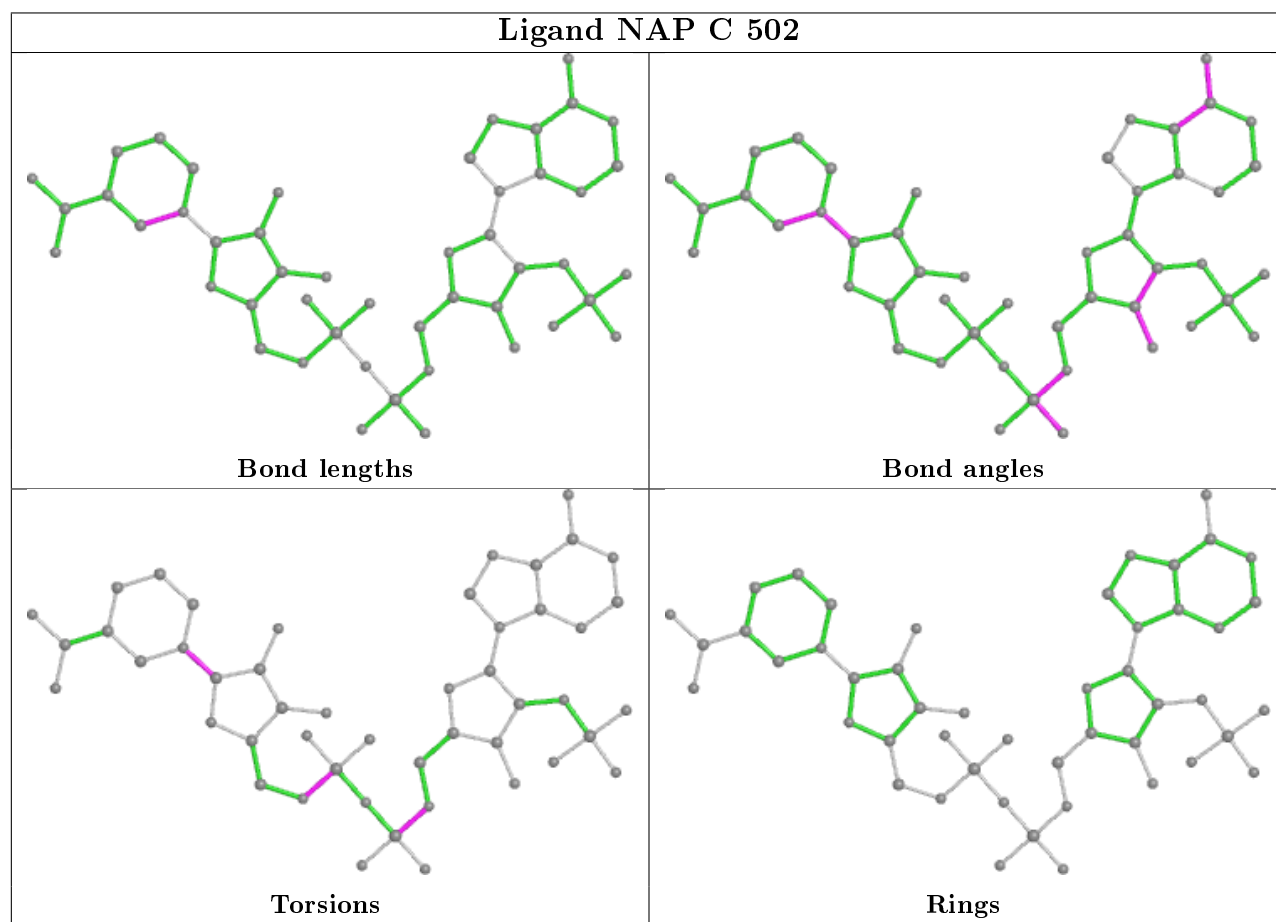
There are no ring outliers.

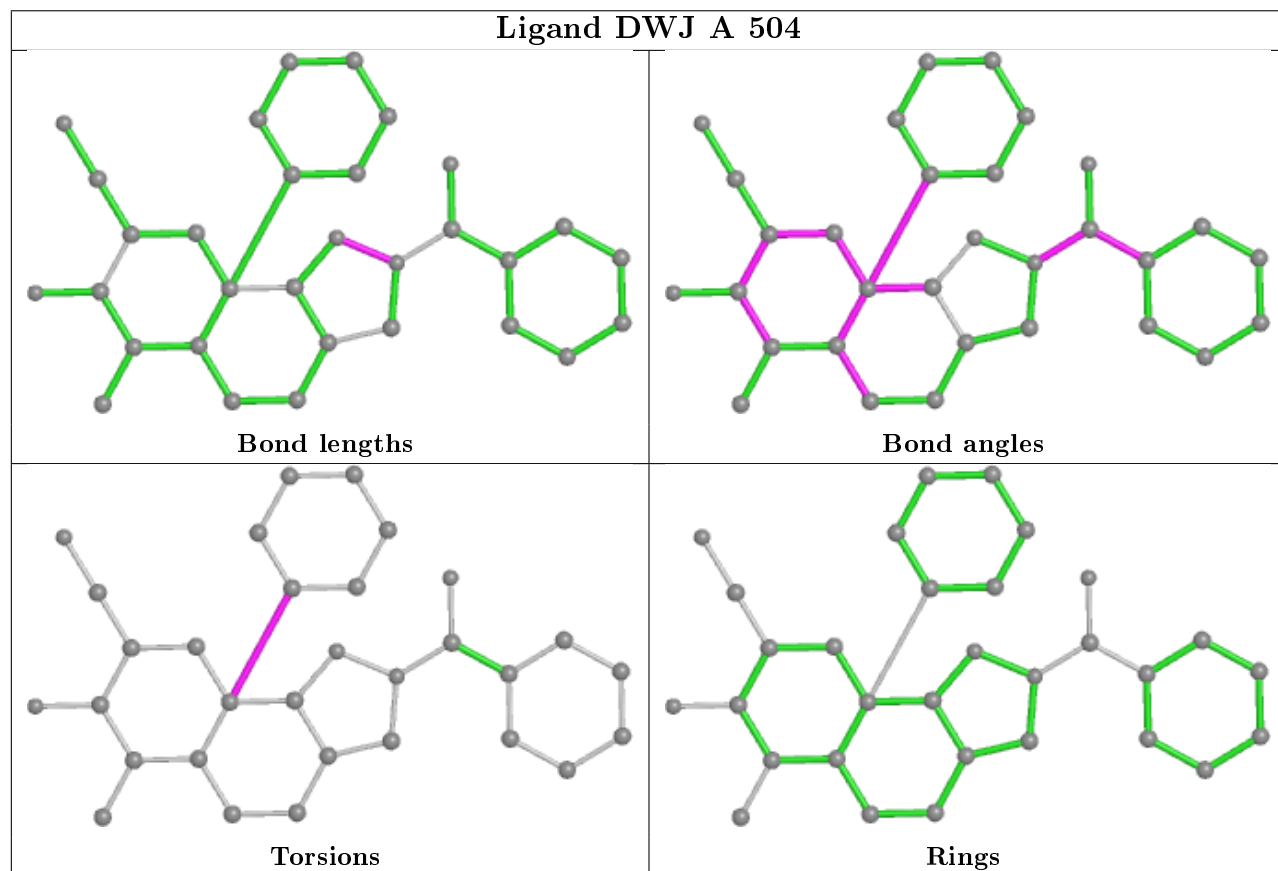
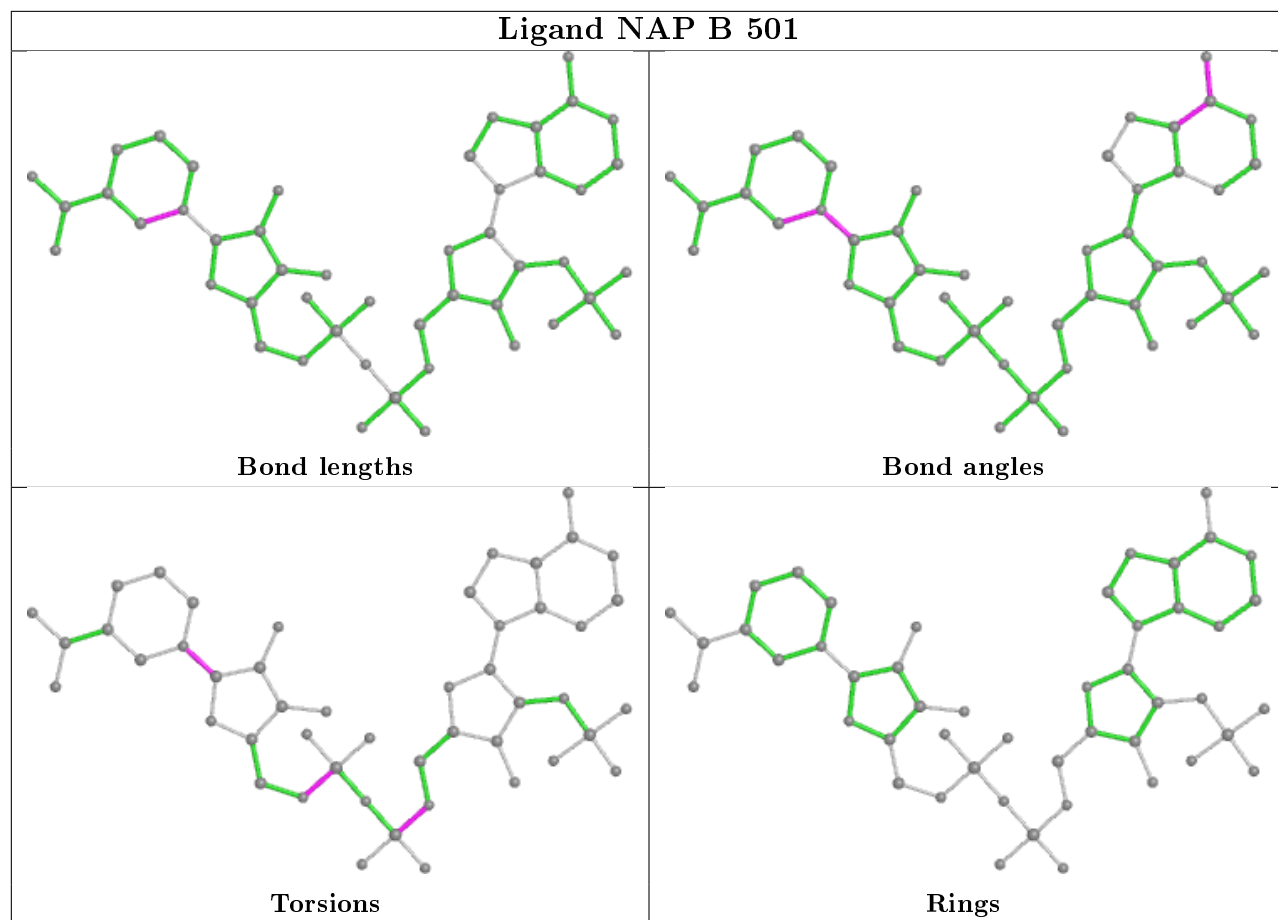
4 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	501	ICT	1	0
3	A	505	ICT	1	0
5	C	502	NAP	2	0
5	B	501	NAP	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 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

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	416/425 (97%)	0.07	2 (0%) 91 91	33, 55, 82, 131	0
1	B	416/425 (97%)	0.11	13 (3%) 49 50	32, 54, 82, 170	0
1	C	416/425 (97%)	0.01	6 (1%) 75 75	28, 42, 74, 138	0
All	All	1248/1275 (97%)	0.06	21 (1%) 70 70	28, 51, 81, 170	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	418	HIS	8.2
1	B	416	LEU	7.3
1	C	418	HIS	4.9
1	A	418	HIS	4.2
1	B	162	THR	4.1
1	A	417	GLU	3.8
1	B	160	ASP	3.5
1	C	307	ALA	3.3
1	B	417	GLU	3.1
1	B	163	GLN	2.8
1	B	161	GLY	2.7
1	B	125	VAL	2.7
1	B	412	ALA	2.6
1	B	384	PRO	2.5
1	B	380	ILE	2.4
1	C	417	GLU	2.4
1	B	395	PHE	2.2
1	C	315	HIS	2.1
1	C	416	LEU	2.1
1	B	323	GLN	2.0
1	C	312	VAL	2.0

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 ⓘ

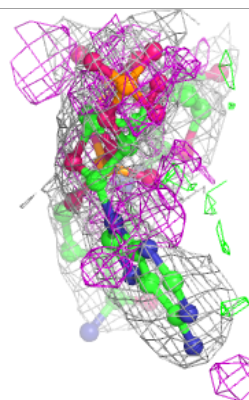
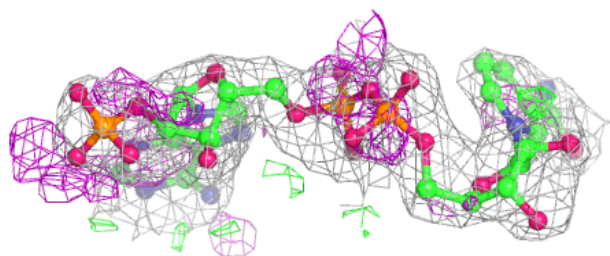
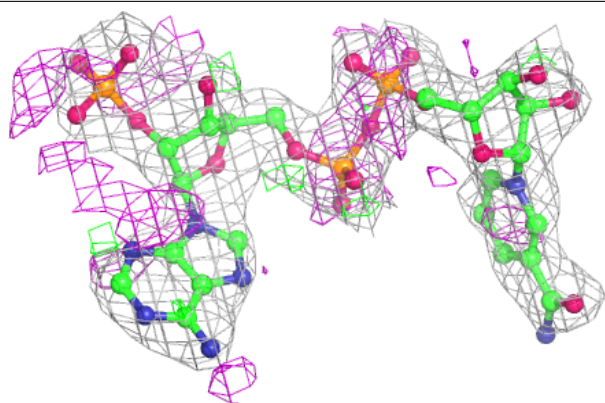
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MG	A	501	1/1	0.88	0.12	49,49,49,49	0
3	ICT	A	502	13/13	0.90	0.14	53,58,63,69	0
5	NAP	C	502	48/48	0.93	0.21	44,61,69,74	0
3	ICT	A	505	13/13	0.94	0.13	42,48,54,59	0
4	DWJ	A	504	31/31	0.96	0.10	55,58,64,64	0
2	MG	A	503	1/1	0.96	0.03	42,42,42,42	0
5	NAP	B	501	48/48	0.96	0.13	43,55,64,66	0
3	ICT	C	501	13/13	0.96	0.13	40,46,55,64	0
2	MG	C	500	1/1	0.98	0.10	37,37,37,37	0

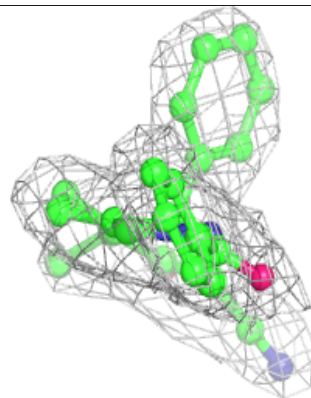
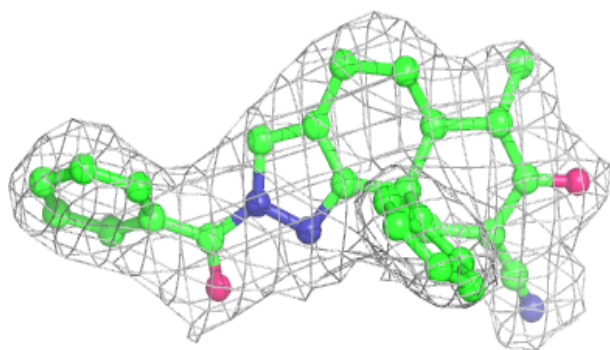
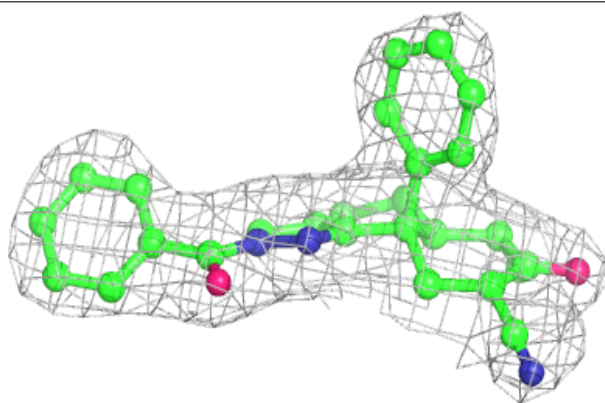
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

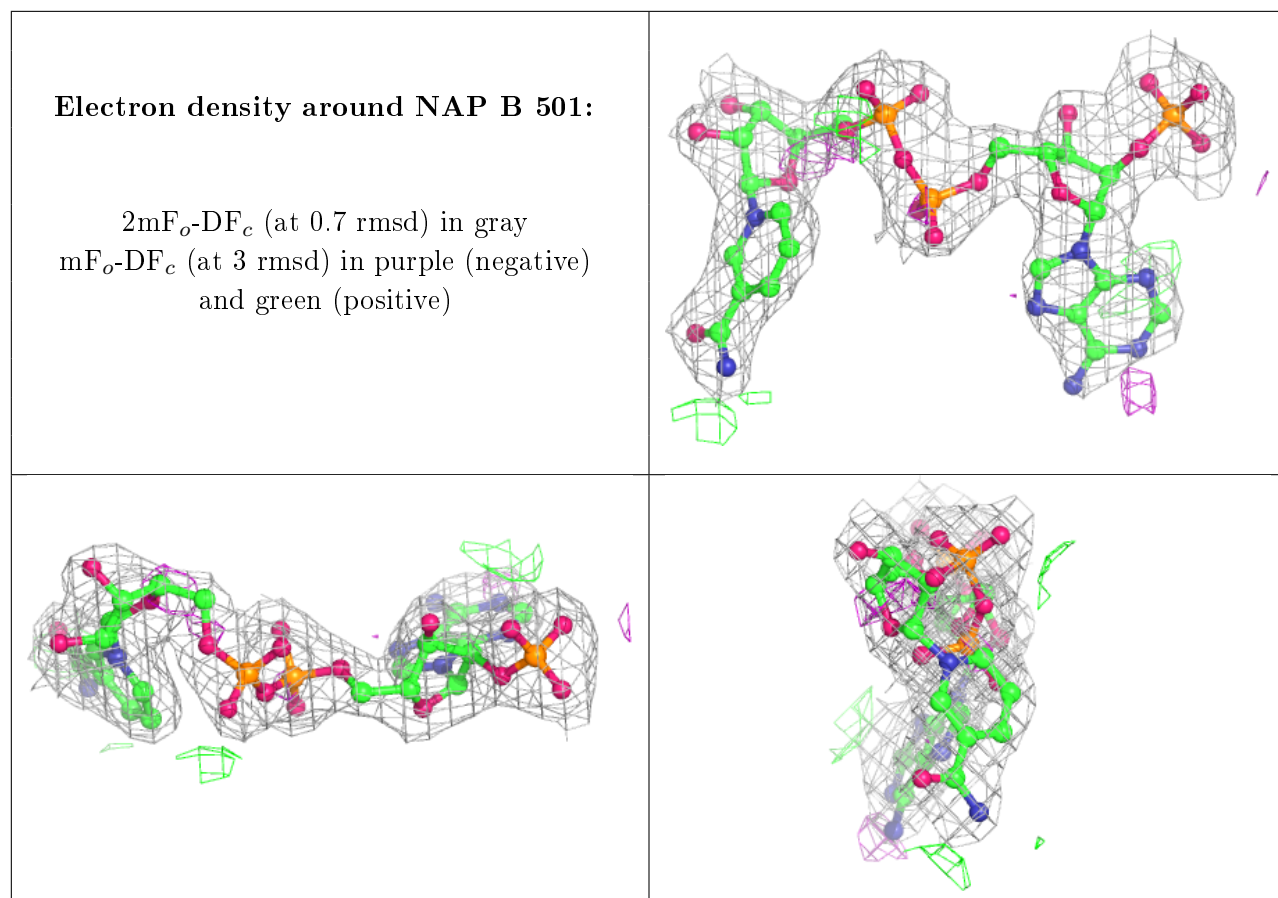
Electron density around NAP C 502:

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

**Electron density around DWJ A 504:**

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





6.5 Other polymers ⓘ

There are no such residues in this entry.