wwPDB X-ray Structure Validation Summary Report (i)

Aug 27, 2023 – 12:42 AM EDT

PDB ID	:	3FNF
Title	:	Crystal structure of InhA bound to triclosan derivative
Authors	:	Wang, F.
Deposited on	:	2008-12-24
Resolution	:	2.30 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

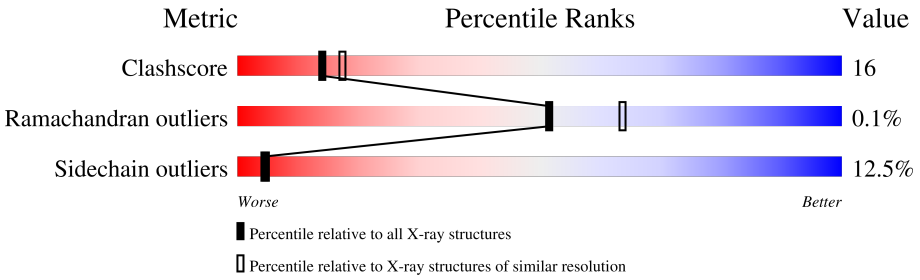
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.30 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))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	269	71% 24% 5%
1	B	269	67% 19% 7% 7%
1	C	269	71% 21% . . .
1	D	269	67% 25% . .

2 Entry composition (i)

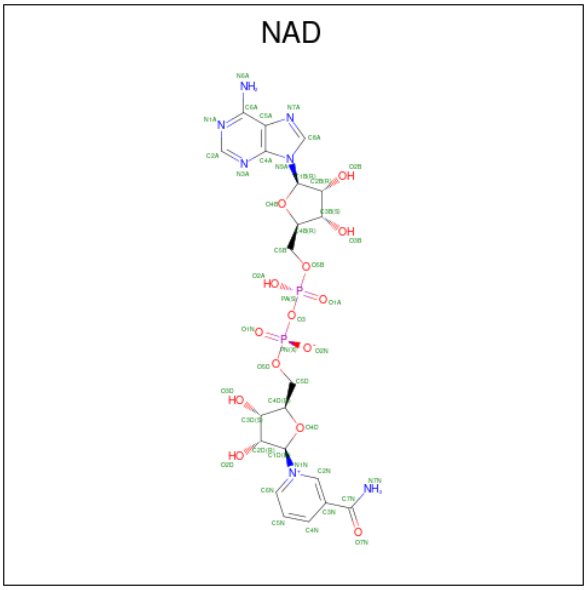
There are 4 unique types of molecules in this entry. The entry contains 8260 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Enoyl-[acyl-carrier-protein] reductase [NADH].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	268	Total	C	N	O	S	0	0	0
			1994	1263	348	373	10			
1	B	249	Total	C	N	O	S	0	0	0
			1866	1183	327	346	10			
1	C	261	Total	C	N	O	S	0	0	0
			1953	1238	341	364	10			
1	D	257	Total	C	N	O	S	0	0	0
			1926	1221	337	358	10			

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

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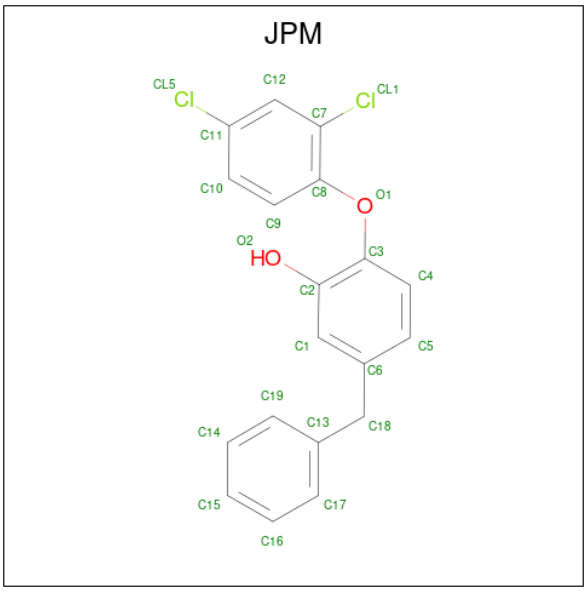
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is 5-benzyl-2-(2,4-dichlorophenoxy)phenol (three-letter code: JPM) (formula: $C_{19}H_{14}Cl_2O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	Cl	O	0	0
			23	19	2	2		
3	B	1	Total	C	Cl	O	0	0
			23	19	2	2		
3	C	1	Total	C	Cl	O	0	0
			23	19	2	2		
3	D	1	Total	C	Cl	O	0	0
			23	19	2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	68	Total	O	0	0
			68	68		
4	B	64	Total	O	0	0
			64	64		
4	C	63	Total	O	0	0
			63	63		

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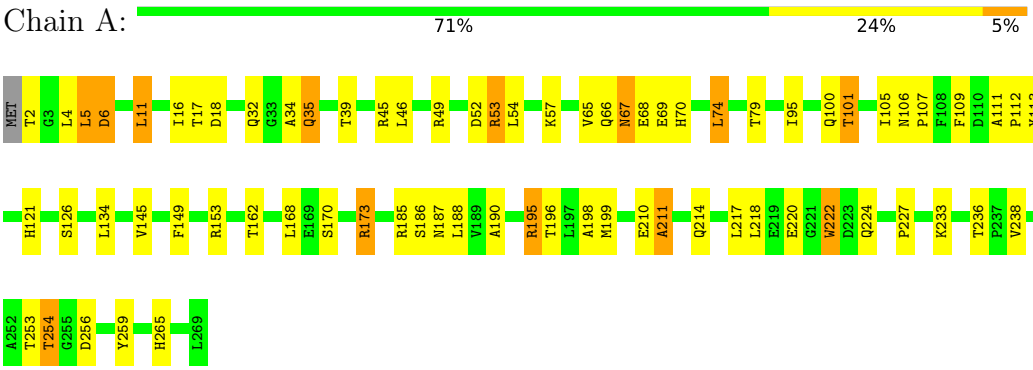
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	58	Total O 58 58	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

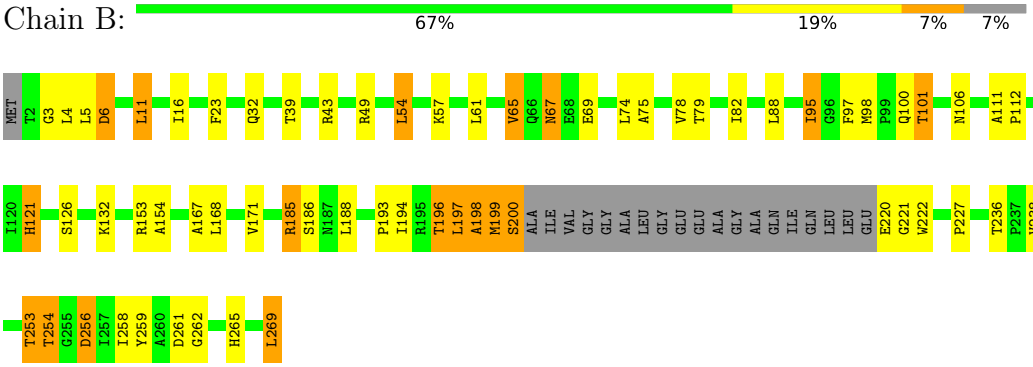
• Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADH]

Chain A:



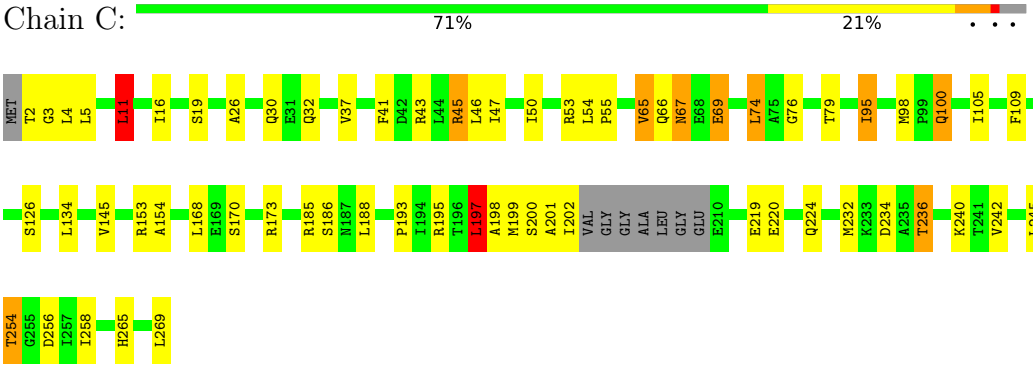
• Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADH]

Chain B:



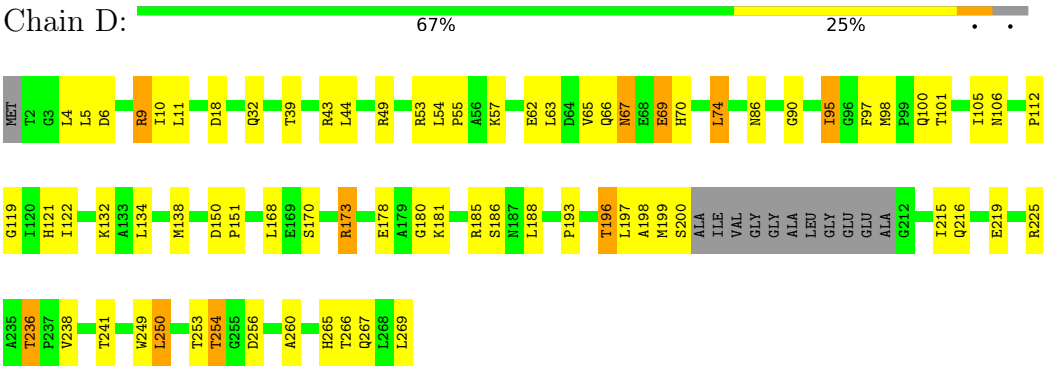
• Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADH]

Chain C:



• Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADH]

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	125.65Å 92.38Å 102.41Å 90.00° 106.51° 90.00°	Depositor
Resolution (Å)	19.85 – 2.30 40.16 – 1.21	Depositor EDS
% Data completeness (in resolution range)	98.8 (19.85-2.30) 2.1 (40.16-1.21)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$	-	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.200 , 0.260 0.581 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	(Not available)	Xtriage
Anisotropy	(Not available)	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 5.7	EDS
L-test for twinning[1]	$< \|L\| >$ = (Not available), $< L^2 >$ = (Not available)	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.41	EDS
Total number of atoms	8260	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *(Not available)*

[1]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: NAD, JPM

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	0.69	0/2032	0.83	3/2758 (0.1%)
1	B	0.67	0/1903	0.80	4/2582 (0.2%)
1	C	0.65	0/1990	0.82	4/2700 (0.1%)
1	D	0.61	0/1963	0.78	2/2663 (0.1%)
All	All	0.65	0/7888	0.81	13/10703 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	173	ARG	NE-CZ-NH2	-9.48	115.56	120.30
1	C	11	LEU	CA-CB-CG	7.45	132.43	115.30
1	C	269	LEU	CA-CB-CG	7.24	131.96	115.30
1	C	173	ARG	NE-CZ-NH2	-7.02	116.79	120.30
1	B	11	LEU	CA-CB-CG	6.84	131.04	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	211	ALA	Peptide

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	1994	0	2008	74	0
1	B	1866	0	1877	63	0
1	C	1953	0	1967	65	0
1	D	1926	0	1940	68	0
2	A	44	0	26	2	0
2	B	44	0	26	2	0
2	C	44	0	26	1	0
2	D	44	0	26	3	0
3	A	23	0	13	0	0
3	B	23	0	13	2	0
3	C	23	0	13	1	0
3	D	23	0	13	3	0
4	A	68	0	0	6	0
4	B	64	0	0	5	0
4	C	63	0	0	9	0
4	D	58	0	0	3	0
All	All	8260	0	7948	250	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 16.

The worst 5 of 250 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:B:16:ILE:HG23	1:B:197:LEU:CD2	1.73	1.18
1:B:197:LEU:H	1:B:197:LEU:HD12	1.15	1.09
1:B:106:ASN:HB2	4:B:304:HOH:O	1.50	1.08
1:A:211:ALA:HA	1:A:214:GLN:HB2	1.36	1.05
1:C:186:SER:H	1:C:254:THR:HG22	1.25	0.97

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	266/269 (99%)	251 (94%)	14 (5%)	1 (0%)	34 42
1	B	245/269 (91%)	229 (94%)	16 (6%)	0	100 100
1	C	257/269 (96%)	242 (94%)	15 (6%)	0	100 100
1	D	253/269 (94%)	235 (93%)	18 (7%)	0	100 100
All	All	1021/1076 (95%)	957 (94%)	63 (6%)	1 (0%)	51 64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	195	ARG

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	203/205 (99%)	177 (87%)	26 (13%)	4 4
1	B	192/205 (94%)	166 (86%)	26 (14%)	4 4
1	C	200/205 (98%)	179 (90%)	21 (10%)	7 8
1	D	198/205 (97%)	172 (87%)	26 (13%)	4 4
All	All	793/820 (97%)	694 (88%)	99 (12%)	4 5

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	54	LEU
1	C	253	THR
1	C	67	ASN
1	C	168	LEU
1	D	9	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	86	ASN
1	C	187	ASN
1	D	265	HIS
1	C	121	HIS
1	C	265	HIS

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)

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	$\#\|Z\|>2$
3	JPM	C	420	-	25,25,25	2.81	3 (12%)	34,34,34	1.22	4 (11%)
2	NAD	B	310	-	42,48,48	1.76	4 (9%)	50,73,73	1.48	6 (12%)
3	JPM	D	430	-	25,25,25	3.01	2 (8%)	34,34,34	1.09	4 (11%)
3	JPM	A	400	-	25,25,25	2.91	4 (16%)	34,34,34	1.34	5 (14%)
3	JPM	B	410	-	25,25,25	2.93	2 (8%)	34,34,34	1.28	3 (8%)
2	NAD	C	320	-	42,48,48	1.71	4 (9%)	50,73,73	1.48	5 (10%)
2	NAD	D	330	-	42,48,48	1.73	3 (7%)	50,73,73	1.58	6 (12%)
2	NAD	A	300	-	42,48,48	1.82	4 (9%)	50,73,73	1.55	6 (12%)

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	JPM	C	420	-	-	0/8/8/8	0/3/3/3
2	NAD	B	310	-	-	10/26/62/62	0/5/5/5
3	JPM	D	430	-	-	0/8/8/8	0/3/3/3
3	JPM	A	400	-	-	0/8/8/8	0/3/3/3
3	JPM	B	410	-	-	1/8/8/8	0/3/3/3
2	NAD	C	320	-	-	6/26/62/62	0/5/5/5
2	NAD	D	330	-	-	10/26/62/62	0/5/5/5
2	NAD	A	300	-	-	5/26/62/62	0/5/5/5

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	410	JPM	C11-CL5	-10.72	1.51	1.74
3	D	430	JPM	C11-CL5	-10.43	1.51	1.74
3	A	400	JPM	C11-CL5	-10.41	1.51	1.74
3	C	420	JPM	C11-CL5	-10.35	1.52	1.74
3	D	430	JPM	C7-CL1	-9.93	1.50	1.73

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	310	NAD	N3A-C2A-N1A	-6.45	118.60	128.68
2	A	300	NAD	N3A-C2A-N1A	-6.20	118.99	128.68
2	C	320	NAD	N3A-C2A-N1A	-6.20	118.99	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	330	NAD	N3A-C2A-N1A	-5.66	119.83	128.68
2	D	330	NAD	C3N-C7N-N7N	4.74	123.44	117.75

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	300	NAD	C5D-O5D-PN-O1N
2	A	300	NAD	C5D-O5D-PN-O2N
2	B	310	NAD	C5B-O5B-PA-O1A
2	B	310	NAD	PN-O3-PA-O5B
2	B	310	NAD	C5D-O5D-PN-O1N

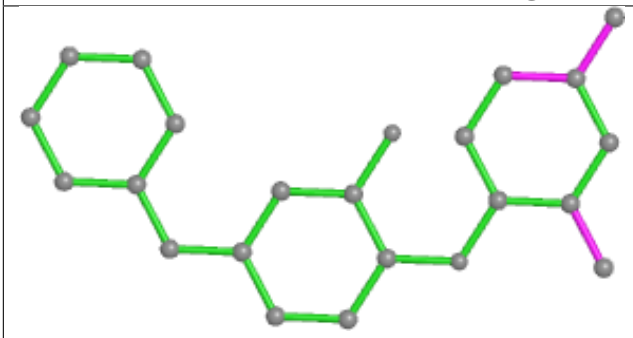
There are no ring outliers.

7 monomers are involved in 14 short contacts:

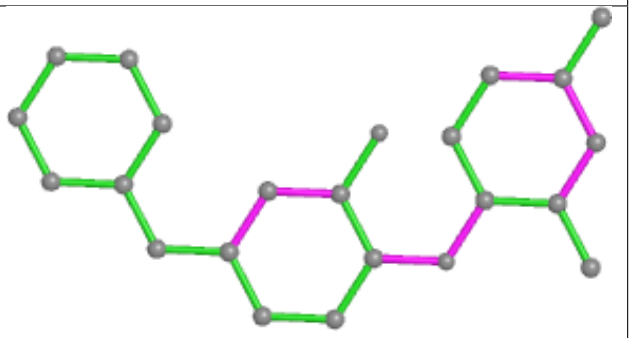
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	420	JPM	1	0
2	B	310	NAD	2	0
3	D	430	JPM	3	0
3	B	410	JPM	2	0
2	C	320	NAD	1	0
2	D	330	NAD	3	0
2	A	300	NAD	2	0

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

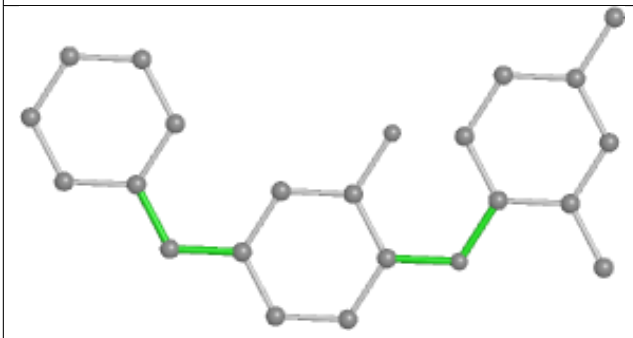
Ligand JPM C 420



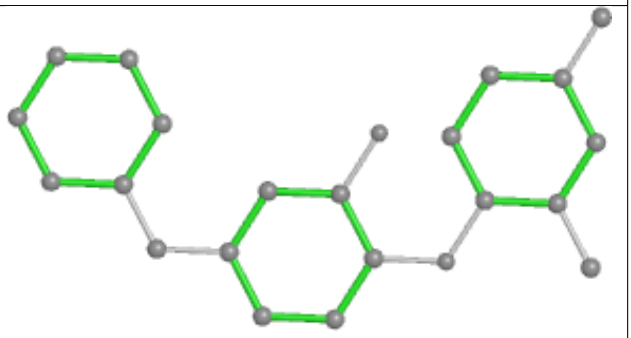
Bond lengths



Bond angles

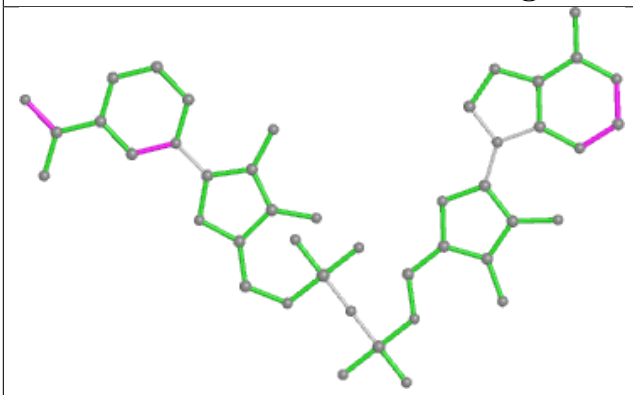


Torsions

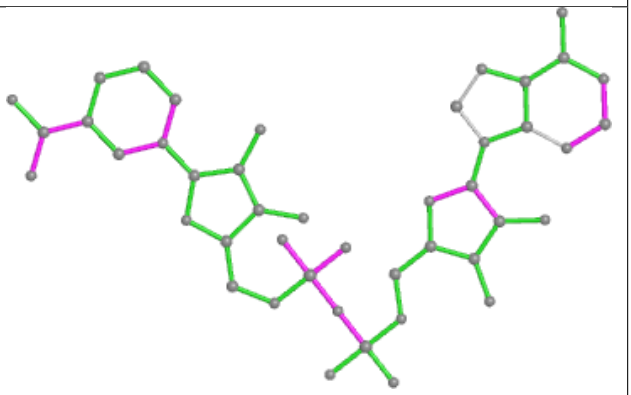


Rings

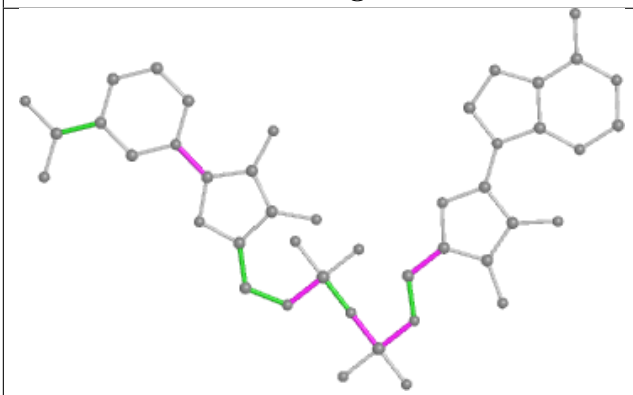
Ligand NAD B 310



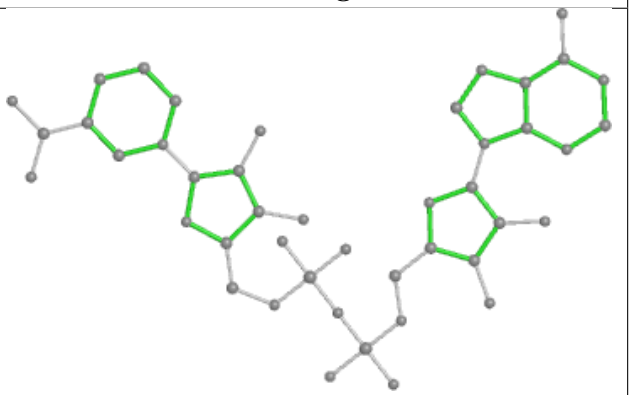
Bond lengths



Bond angles

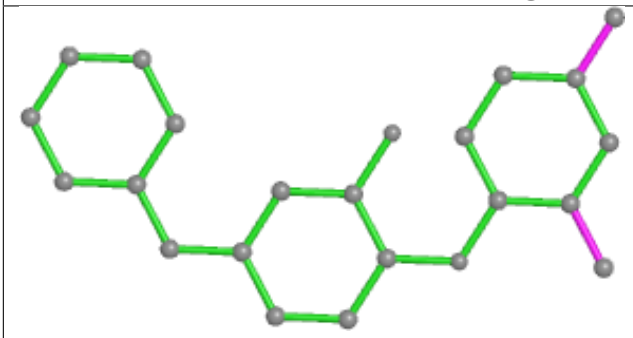


Torsions

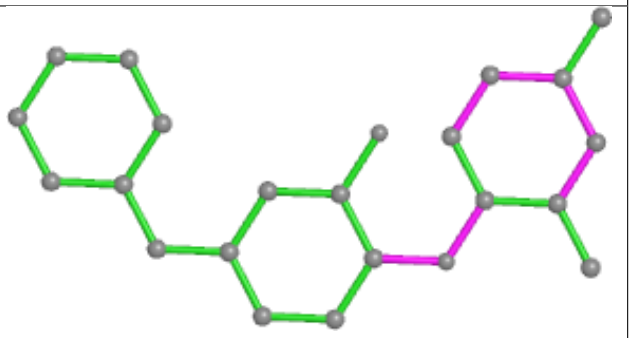


Rings

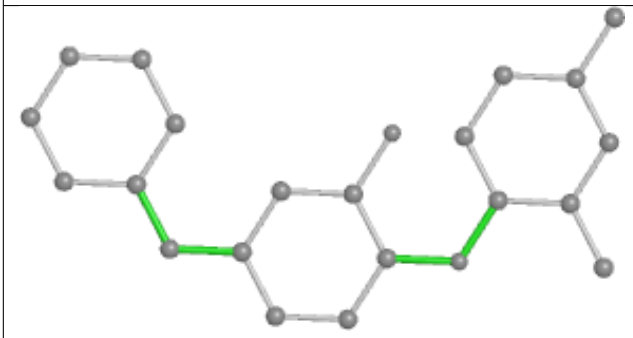
Ligand JPM D 430



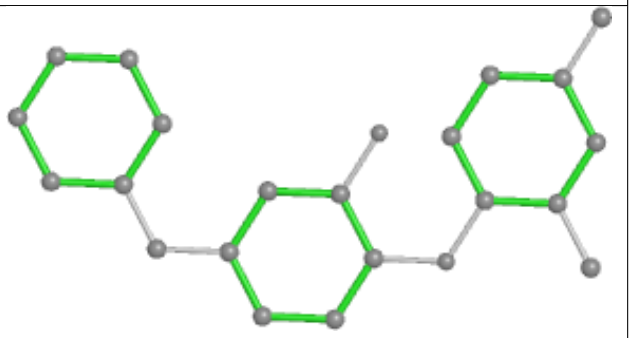
Bond lengths



Bond angles

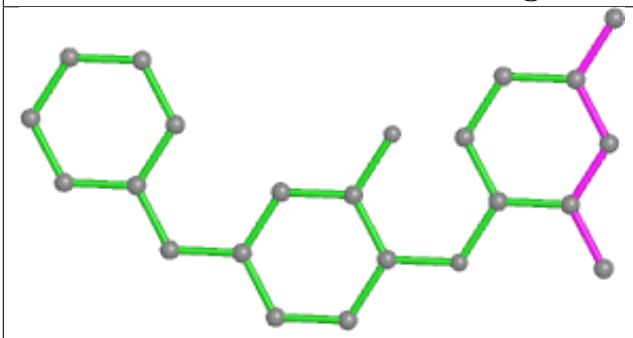


Torsions

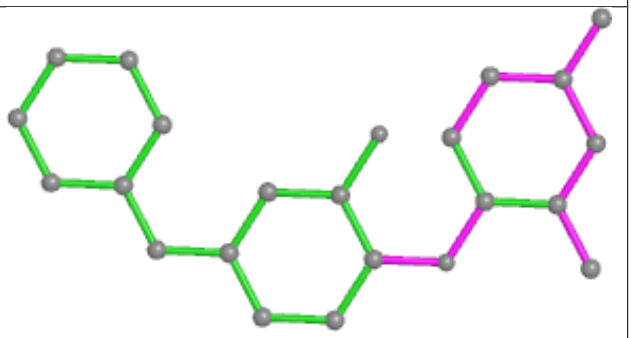


Rings

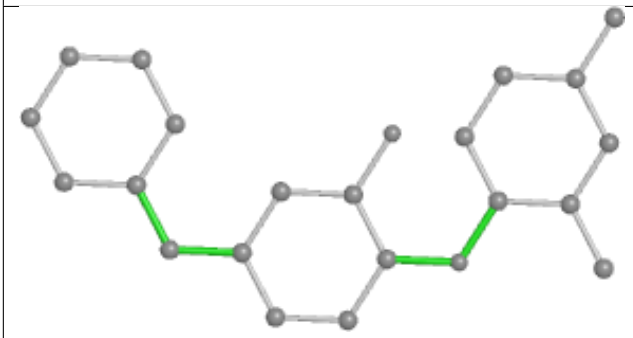
Ligand JPM A 400



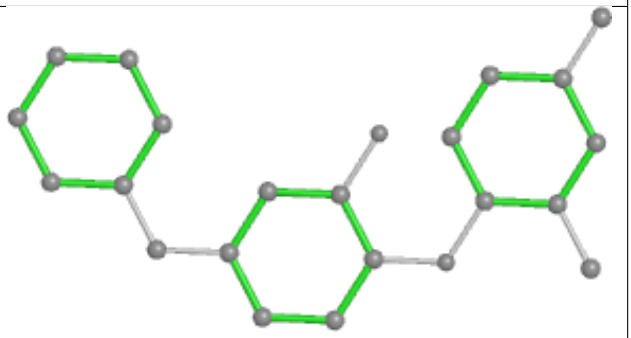
Bond lengths



Bond angles

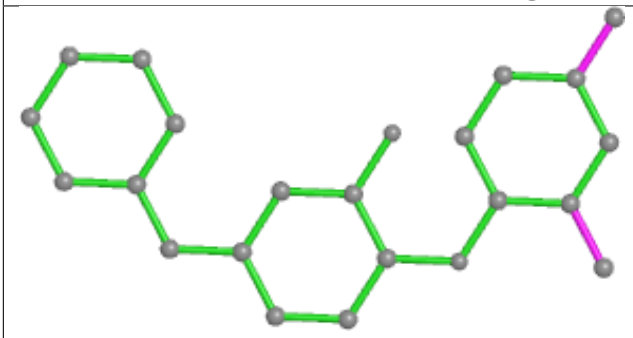


Torsions

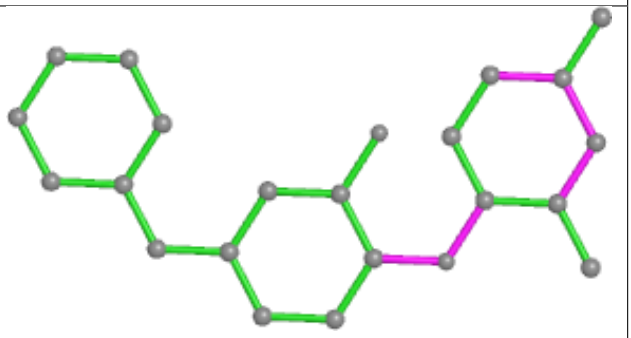


Rings

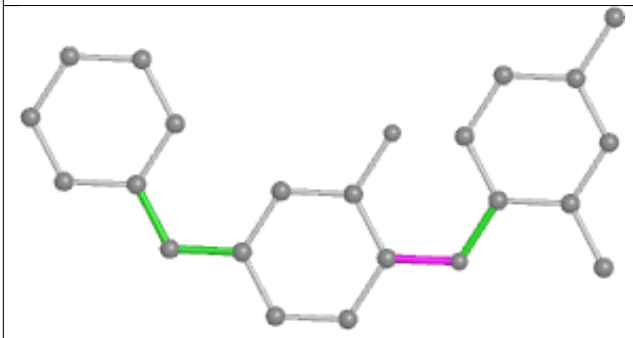
Ligand JPM B 410



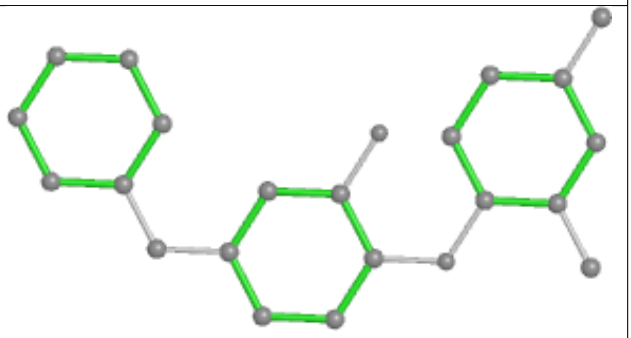
Bond lengths



Bond angles

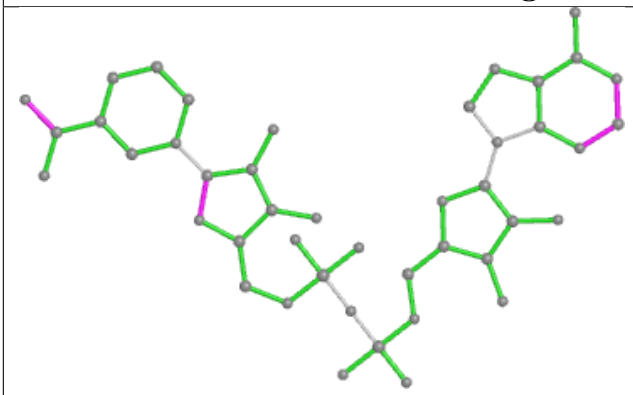


Torsions

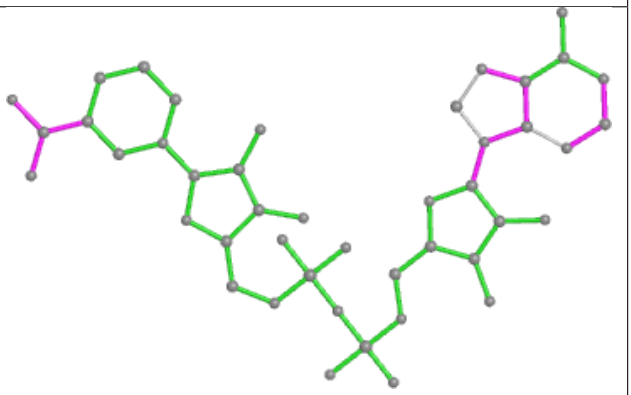


Rings

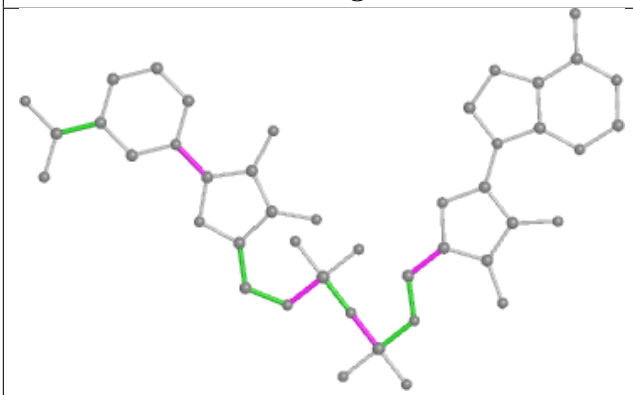
Ligand NAD C 320



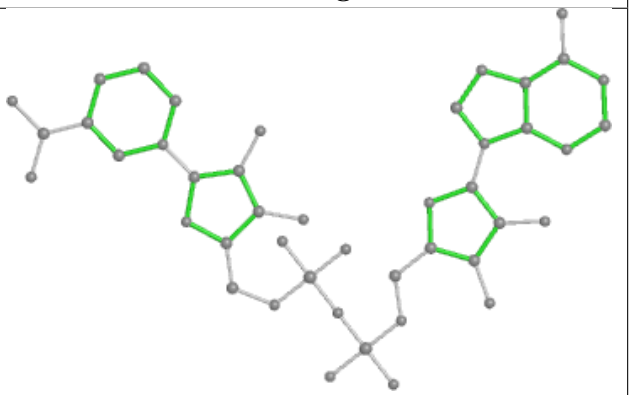
Bond lengths



Bond angles

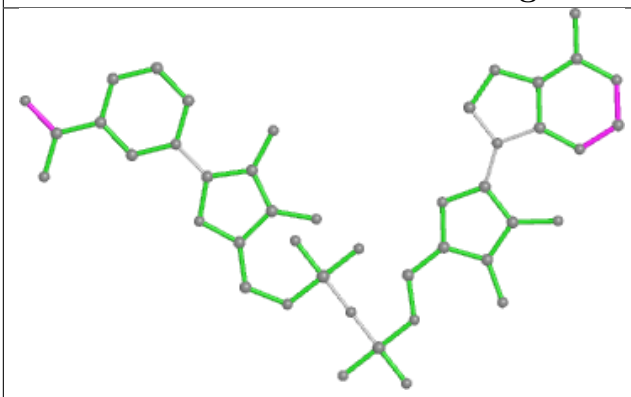


Torsions

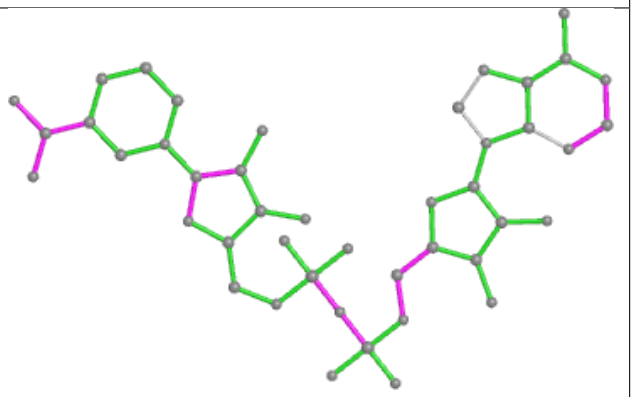


Rings

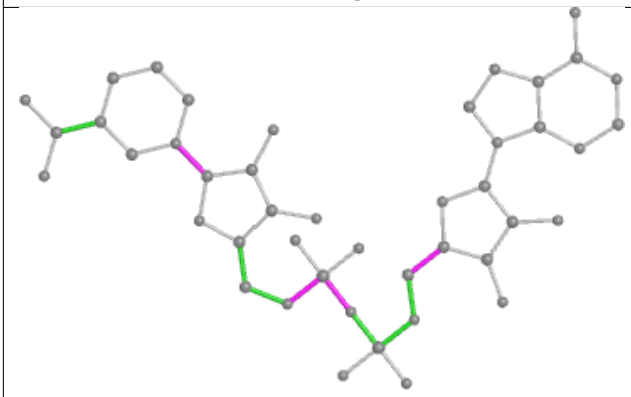
Ligand NAD D 330



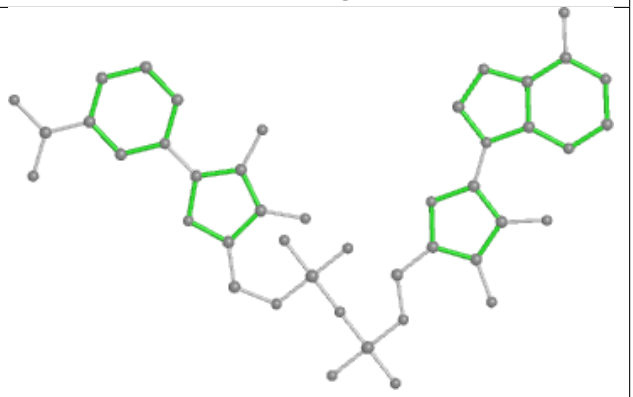
Bond lengths



Bond angles

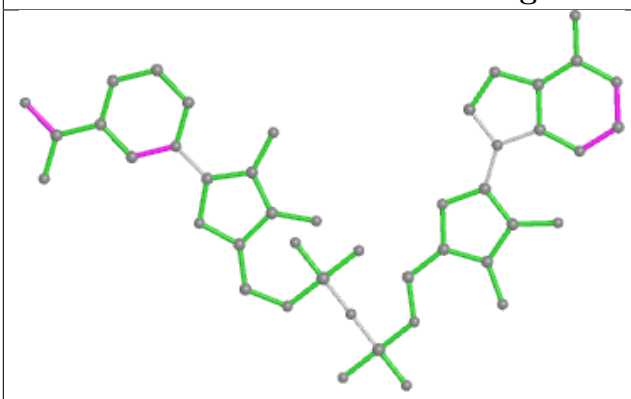


Torsions

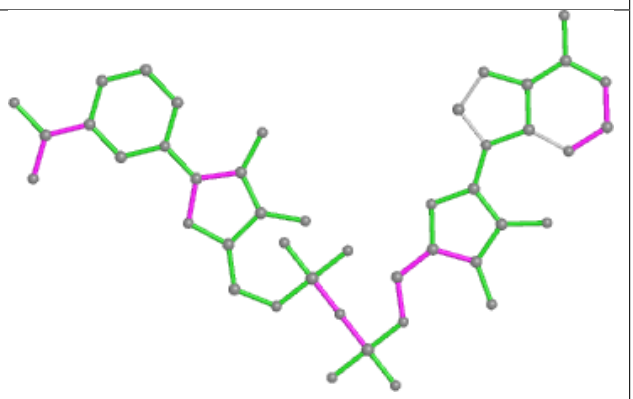


Rings

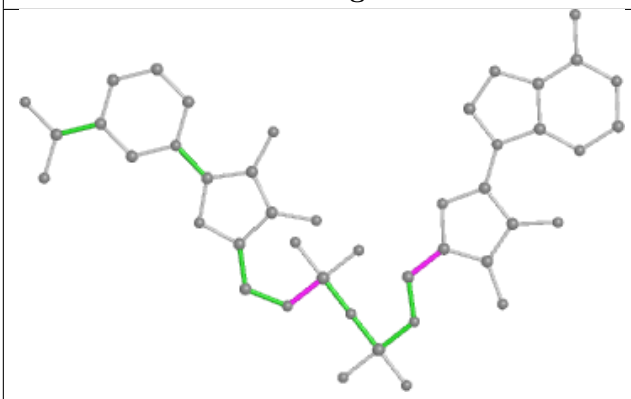
Ligand NAD A 300



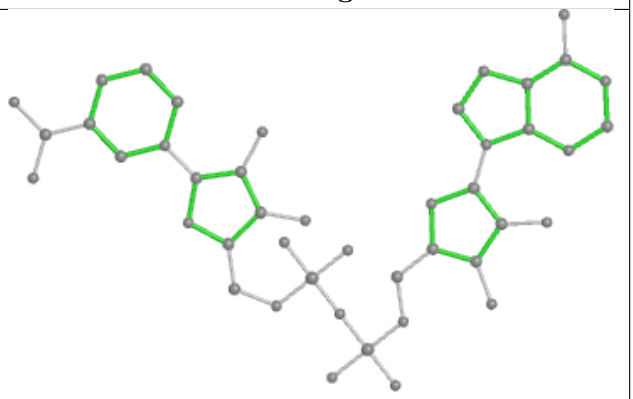
Bond lengths



Bond angles



Torsions



Rings

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

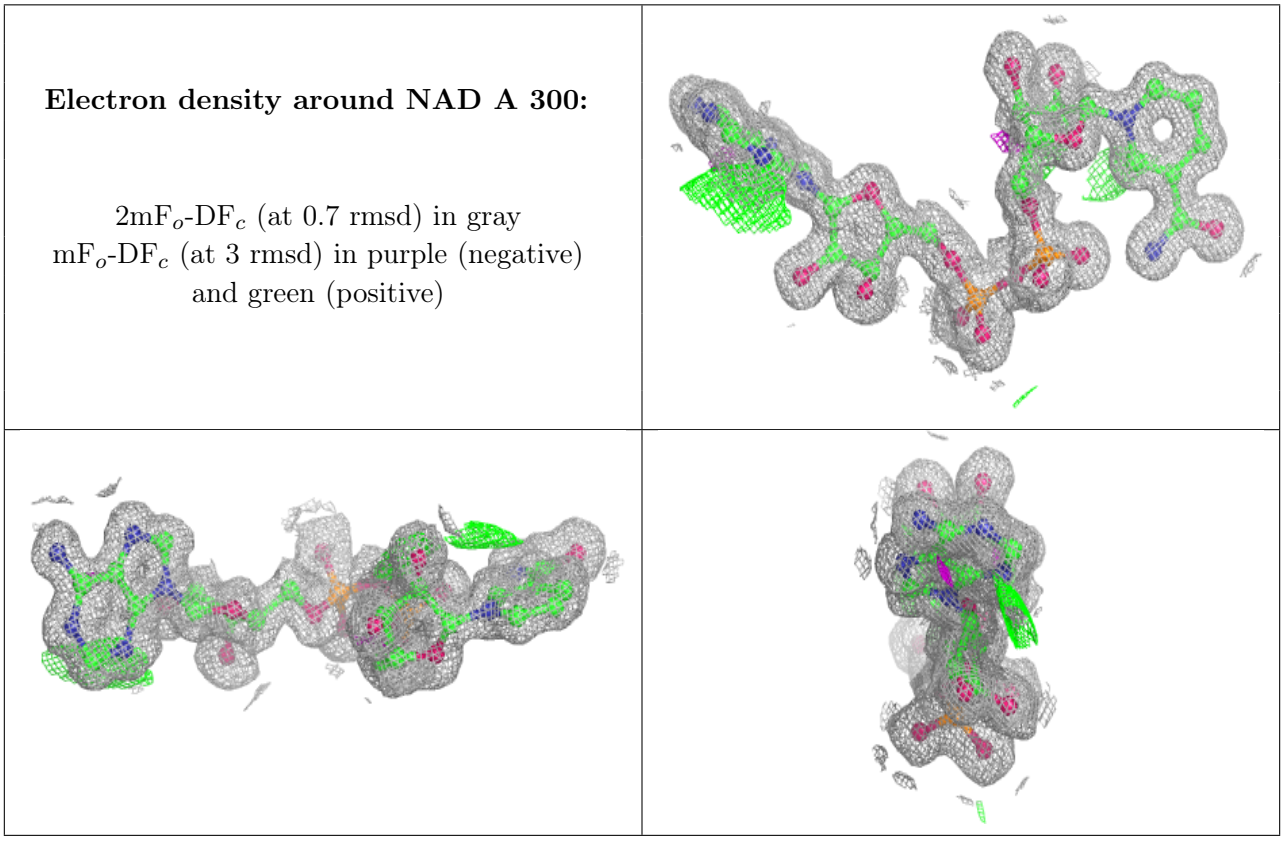
6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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.

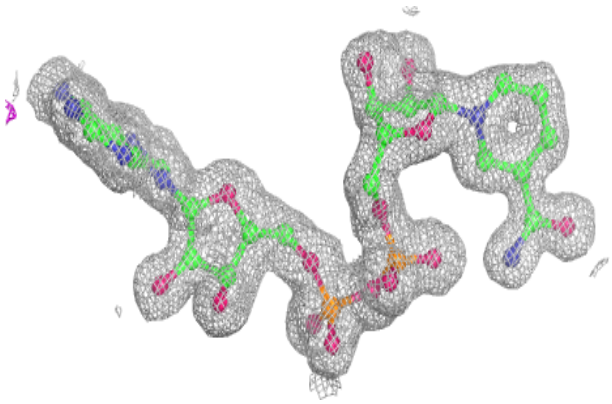
Electron density around NAD A 300:

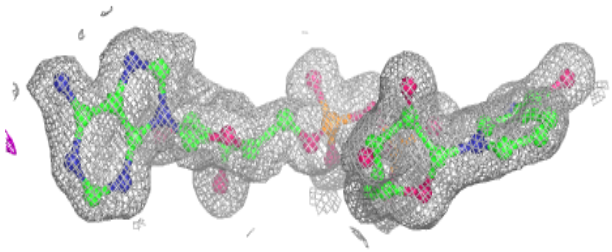
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

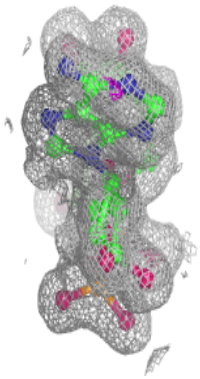


Electron density around NAD B 310:

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

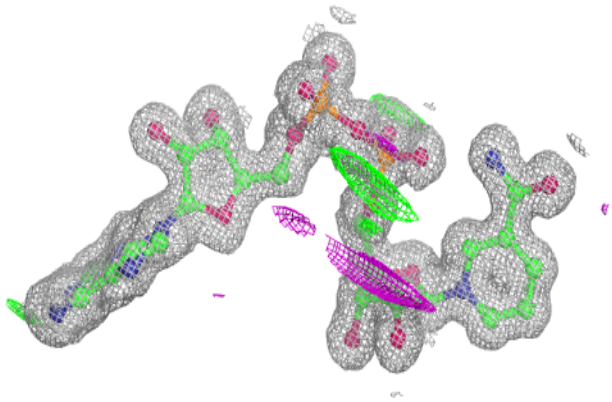


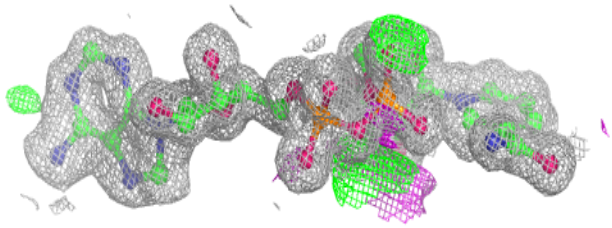


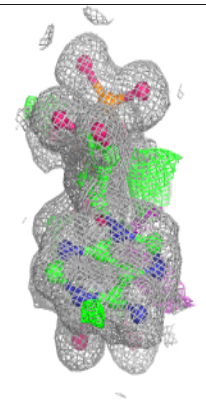


Electron density around NAD C 320:

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

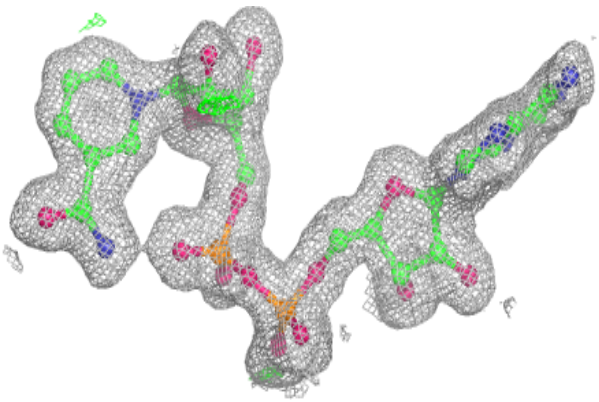


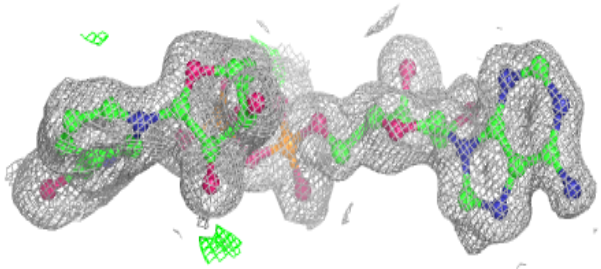


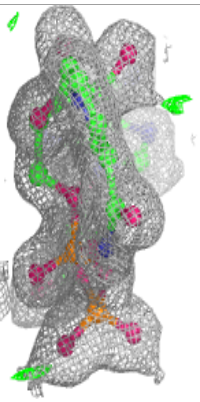


Electron density around NAD D 330:

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

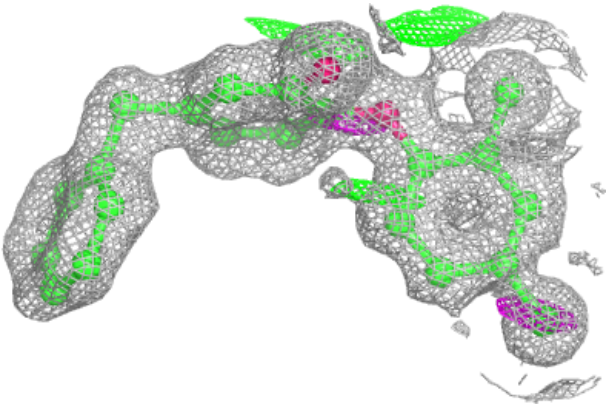


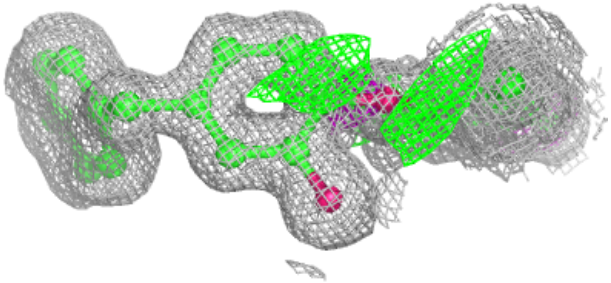


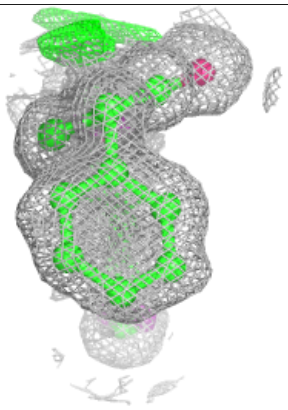


Electron density around JPM A 400:

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

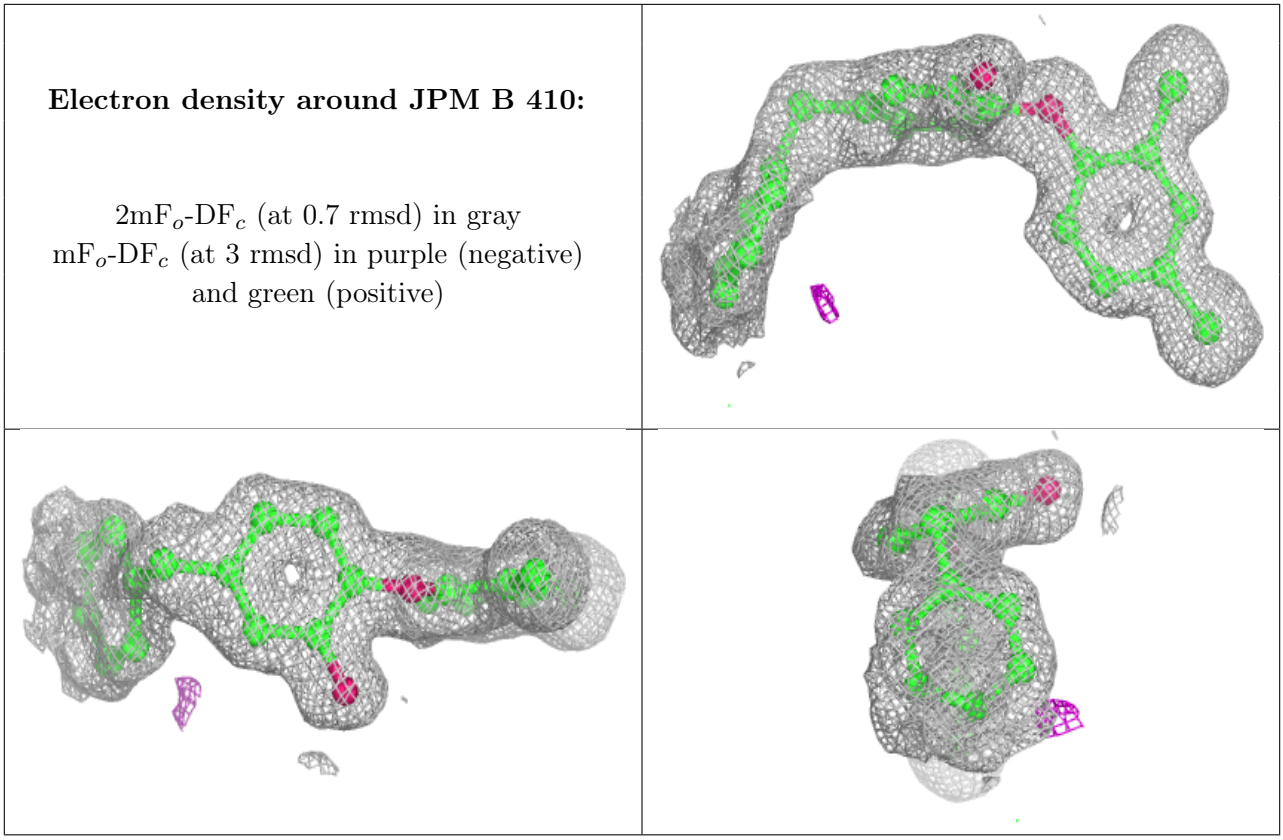






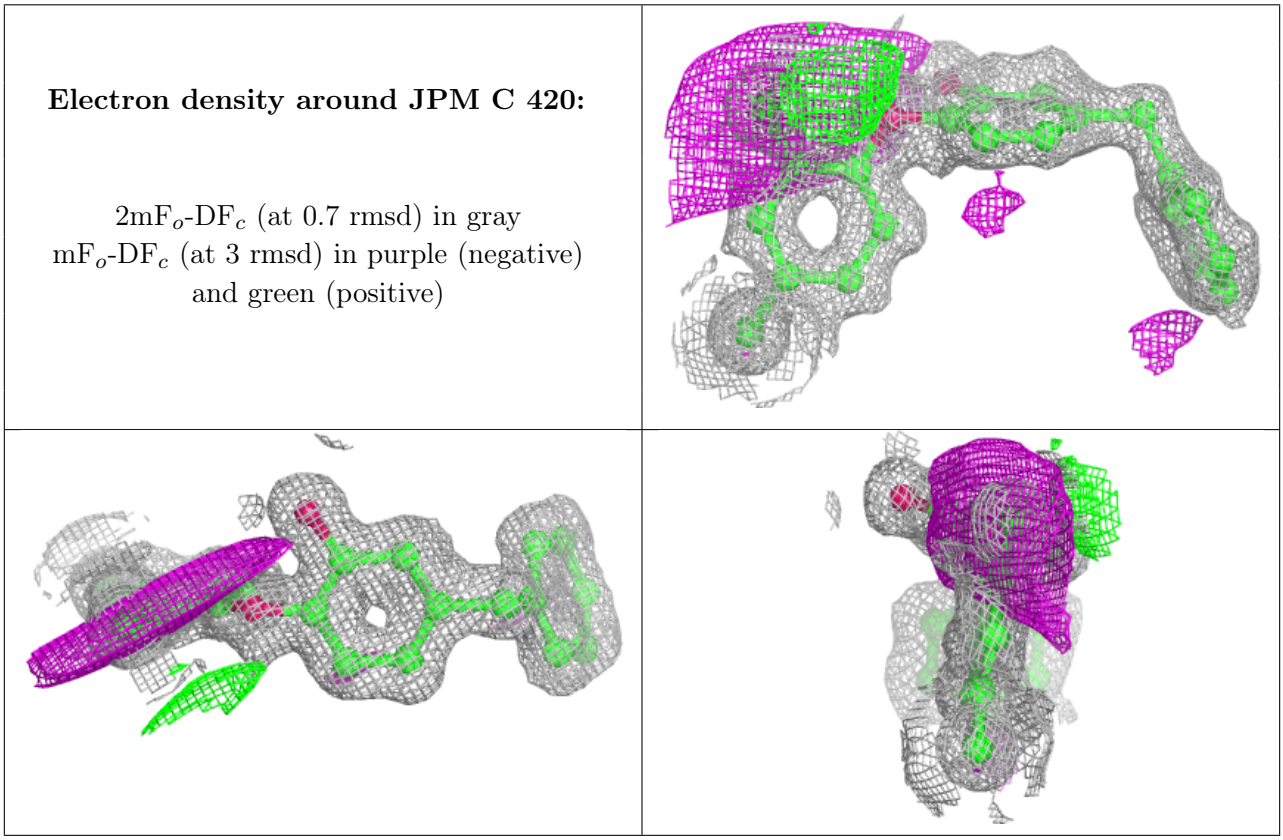
Electron density around JPM B 410:

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



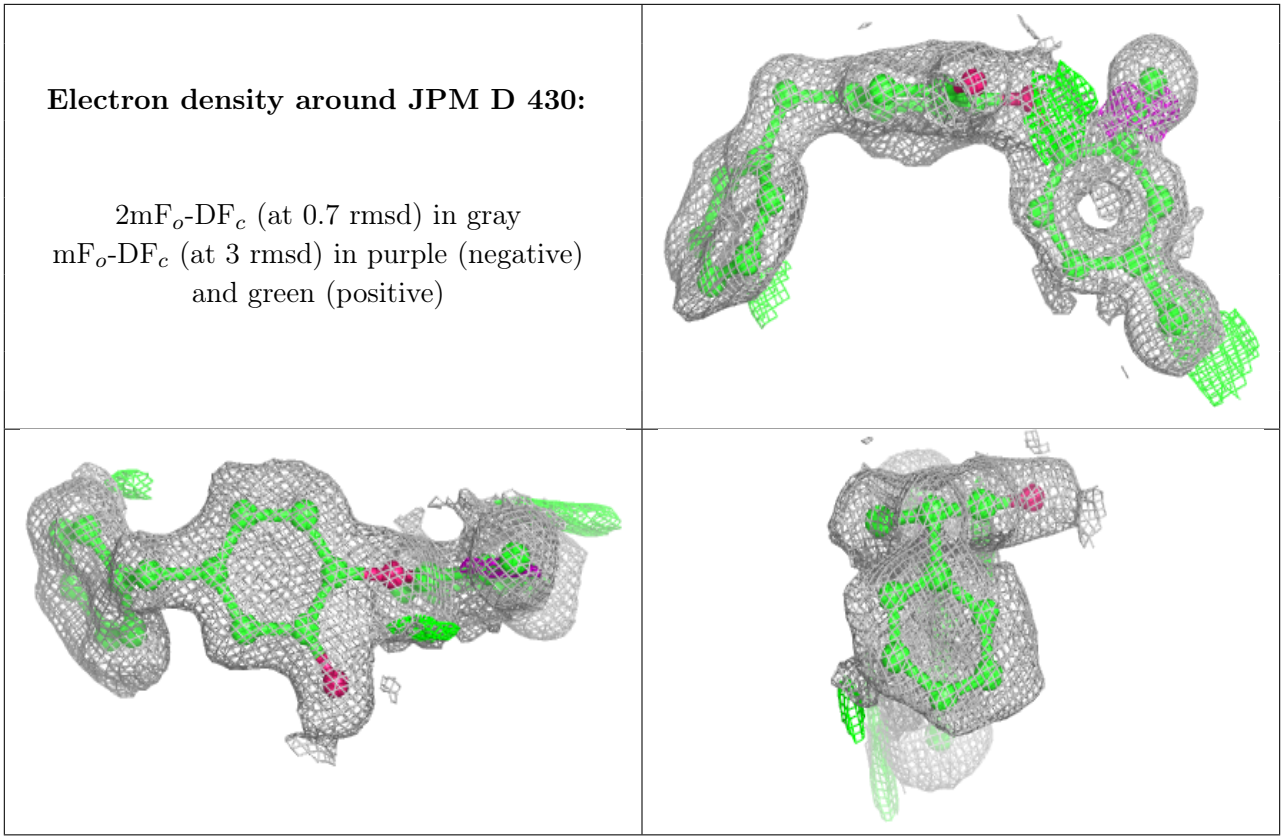
Electron density around JPM C 420:

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



Electron density around JPM D 430:

$2mF_o$-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)

Unable to reproduce the depositors R factor - this section is therefore empty.