wwPDB X-ray Structure Validation Summary Report (i)

Jun 17, 2024 – 06:47 PM EDT

PDB ID	:	5URH
Title	:	CYPOR/D632A with NADP+
Authors	:	Xia, C.; Kim, J.J.
Deposited on	:	2017-02-10
Resolution	:	2.50 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:

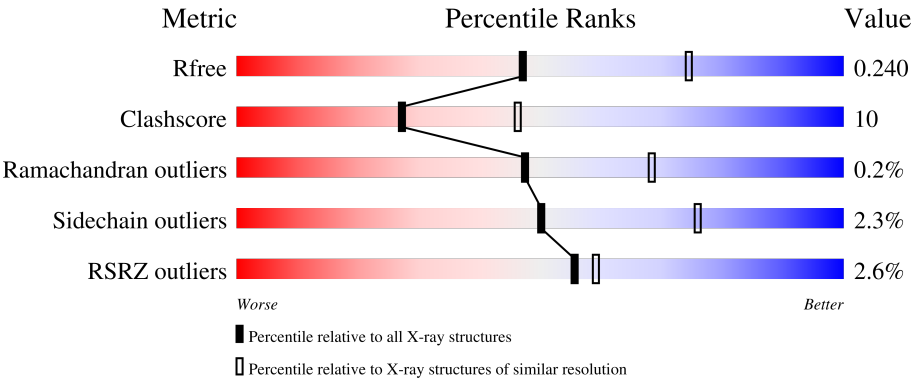
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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% 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	622	77% 20% .
1	B	622	5% 70% 27% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PO4	A	704	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 10276 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.

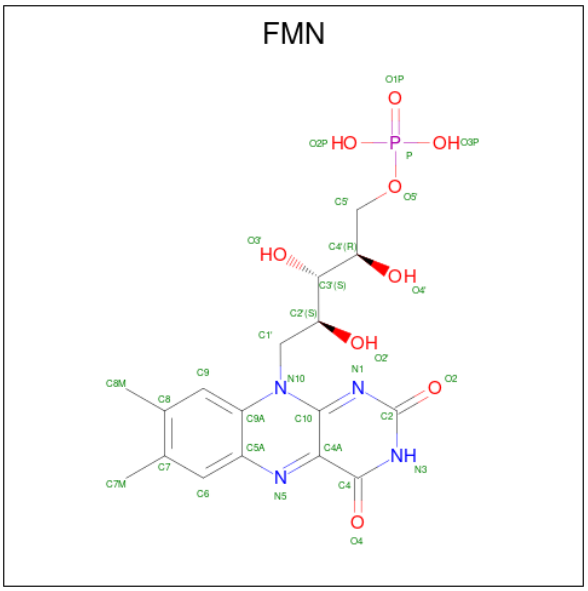
- Molecule 1 is a protein called NADPH–cytochrome P450 reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	609	Total	C	N	O	S	0	0	0
			4860	3084	833	920	23			
1	B	606	Total	C	N	O	S	0	0	1
			4822	3060	830	909	23			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	632	ALA	ASP	engineered mutation	UNP P00388
B	632	ALA	ASP	engineered mutation	UNP P00388

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

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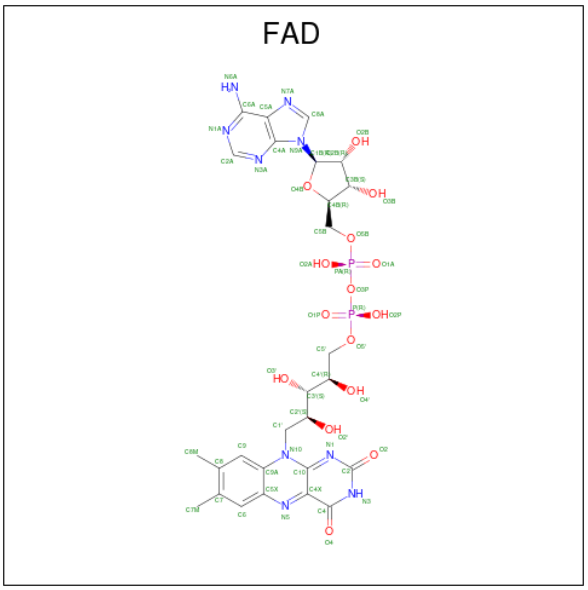
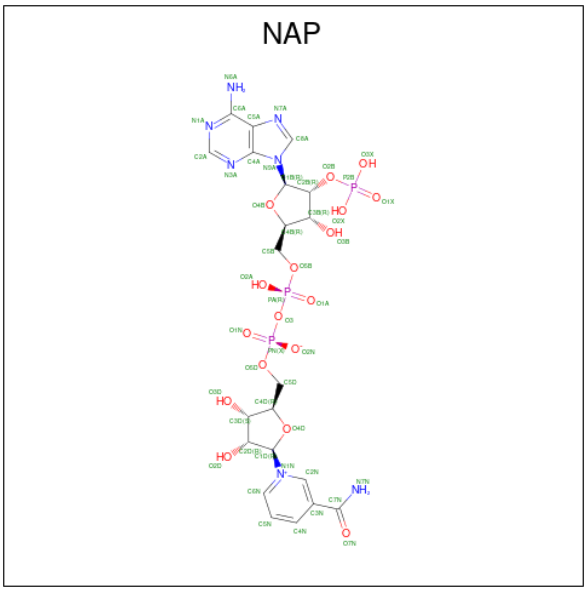
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



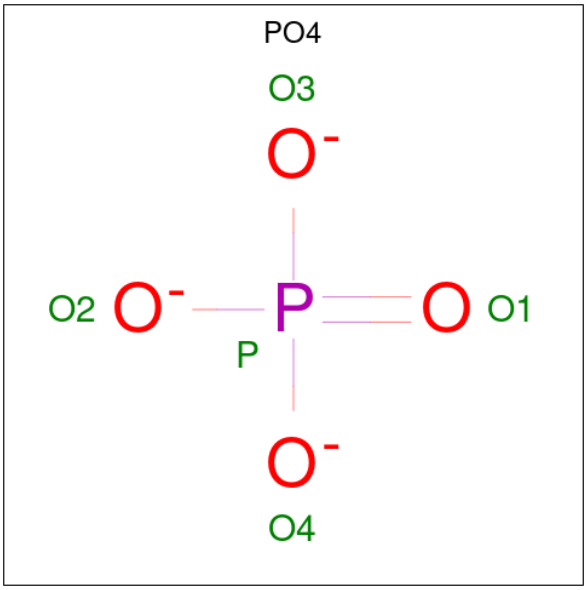
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			40	15	6	16	3		
4	B	1	Total	C	N	O	P	0	0
			40	15	6	16	3		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	O	P		0	0
			5	4	1			
5	B	1	Total	O	P		0	0
			5	4	1			

- Molecule 6 is water.

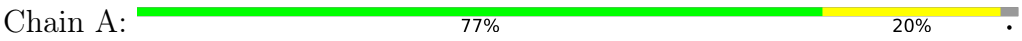
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	180	Total O 180 180	0	0
6	B	156	Total O 156 156	0	0

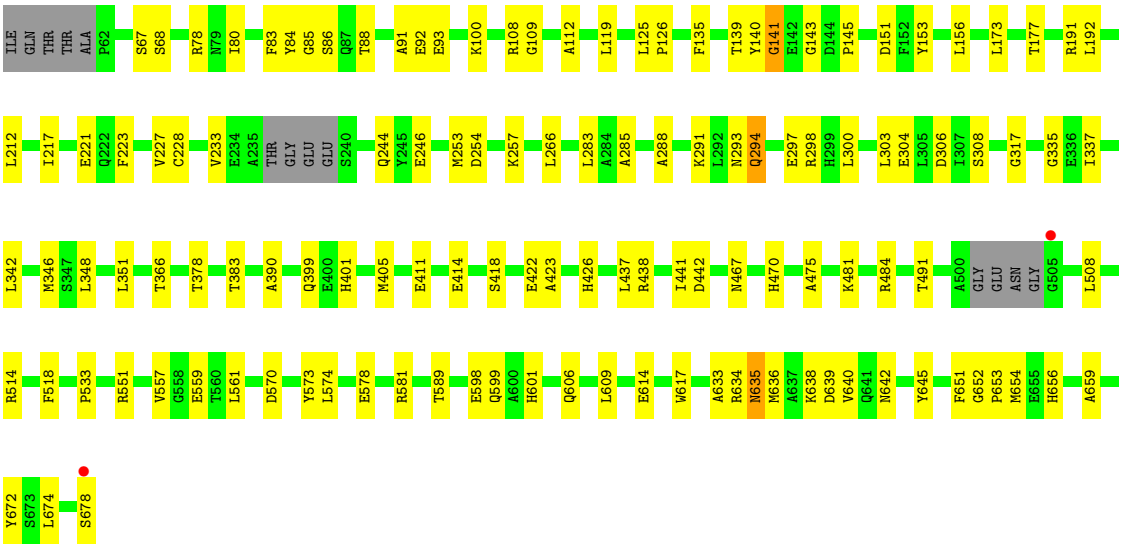
3 Residue-property plots (i)

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 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: NADPH–cytochrome P450 reductase

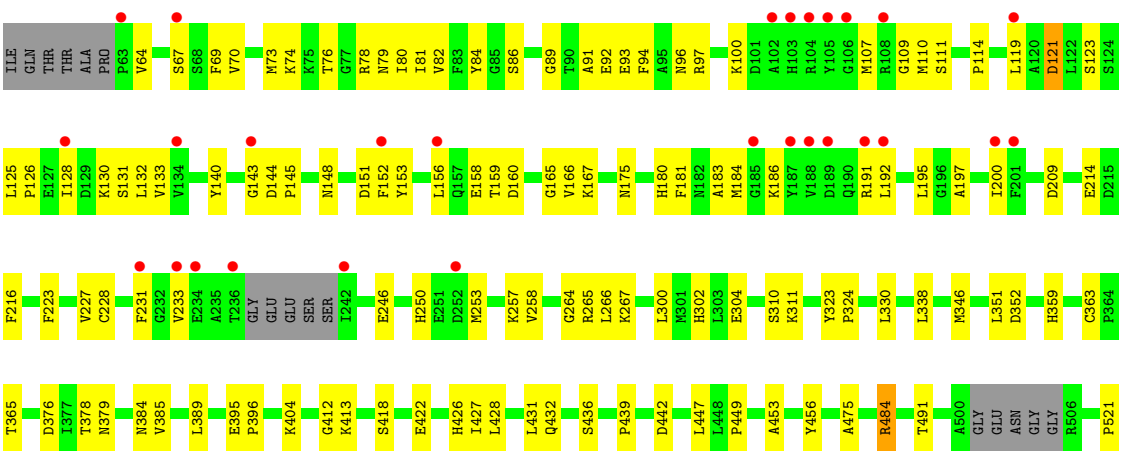
Chain A:

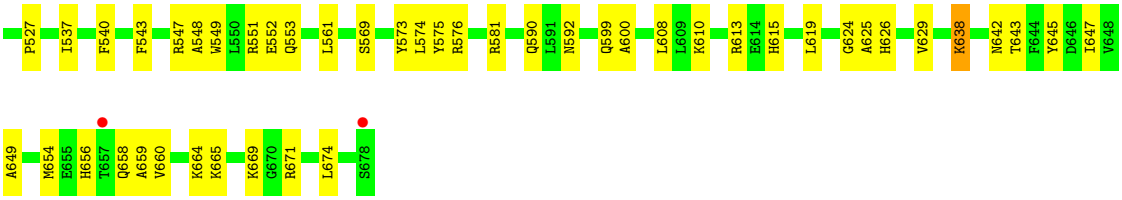




• Molecule 1: NADPH–cytochrome P450 reductase

Chain B:




P527
I537
F540
F543
R547
A548
W549
L550
R551
E552
Q553
L561
S569
Y573
L574
Y575
R576
R581
Q590
L591
N592
Q599
A600
L608
L609
K610
R613
E614
H615
L619
G624
A625
H626
V629
K638
N642
T643
F644
Y645
D646
I647
V648

A649
M654
E655
H656
T657
Q658
A659
V660
K664
K665
K669
G670
R671
L674
S678

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	101.68Å 116.21Å 118.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.95 – 2.50 46.95 – 2.48	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.95-2.50) 99.1 (46.95-2.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.38 (at 2.48Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.204 , 0.251 0.196 , 0.240	Depositor DCC
R_{free} test set	2465 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å^2)	41.0	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 36.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.012 for -h,l,k	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	10276	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.33% 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: PO4, NAP, FMN, FAD

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	0.39	0/4975	0.60	1/6729 (0.0%)
1	B	0.36	0/4937	0.62	6/6681 (0.1%)
All	All	0.37	0/9912	0.61	7/13410 (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	B	0	1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	158	GLU	CB-CA-C	-8.38	93.65	110.40
1	B	158	GLU	N-CA-C	7.27	130.63	111.00
1	B	67	SER	CB-CA-C	5.97	121.44	110.10
1	B	159	THR	CB-CA-C	-5.61	96.45	111.60
1	B	160	ASP	N-CA-CB	-5.42	100.85	110.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	456	TYR	Sidechain

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	4860	0	4703	79	0
1	B	4822	0	4652	117	0
2	A	31	0	19	1	0
2	B	31	0	19	0	0
3	A	53	0	31	1	0
3	B	53	0	31	0	0
4	A	40	0	19	3	0
4	B	40	0	19	0	0
5	A	5	0	0	1	0
5	B	5	0	0	0	0
6	A	180	0	0	4	0
6	B	156	0	0	1	0
All	All	10276	0	9493	196	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 10.

The worst 5 of 196 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:86:SER:HB2	1:B:91:ALA:HB3	1.46	0.93
1:A:639:ASP:C	1:A:640:VAL:CA	2.42	0.88
1:B:70:VAL:HG23	1:B:121:ASP:HB3	1.57	0.86
1:B:561:LEU:HD22	1:B:590:GLN:HB2	1.60	0.84
1:A:633:ALA:HB3	1:A:678:SER:HA	1.60	0.83

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	599/622 (96%)	577 (96%)	20 (3%)	2 (0%)	41 61
1	B	598/622 (96%)	555 (93%)	43 (7%)	0	100 100
All	All	1197/1244 (96%)	1132 (95%)	63 (5%)	2 (0%)	47 68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	141	GLY
1	A	635	ASN

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	516/530 (97%)	503 (98%)	13 (2%)	47 73
1	B	508/530 (96%)	497 (98%)	11 (2%)	52 77
All	All	1024/1060 (97%)	1000 (98%)	24 (2%)	50 76

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	151	ASP
1	B	346	MET
1	B	330	LEU
1	B	396	PRO
1	A	570	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	465	HIS

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Mol	Chain	Res	Type
1	B	635	ASN
1	A	486	ASN
1	B	194	GLN
1	B	222	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)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	FMN	B	701	-	33,33,33	2.63	13 (39%)	48,50,50	1.64	13 (27%)
5	PO4	B	704	-	4,4,4	1.62	0	6,6,6	0.44	0
4	NAP	A	703	-	36,43,52	1.47	5 (13%)	44,67,80	1.49	4 (9%)
4	NAP	B	703	-	36,43,52	1.47	5 (13%)	44,67,80	1.47	4 (9%)
2	FMN	A	701	-	33,33,33	2.62	12 (36%)	48,50,50	1.61	14 (29%)
3	FAD	B	702	-	53,58,58	2.13	11 (20%)	68,89,89	1.55	12 (17%)
5	PO4	A	704	-	4,4,4	1.64	0	6,6,6	0.43	0
3	FAD	A	702	-	53,58,58	2.14	11 (20%)	68,89,89	1.51	11 (16%)

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	FMN	B	701	-	-	0/18/18/18	0/3/3/3
4	NAP	A	703	-	-	4/23/59/67	0/4/4/5
4	NAP	B	703	-	-	3/23/59/67	0/4/4/5
2	FMN	A	701	-	-	0/18/18/18	0/3/3/3
3	FAD	B	702	-	-	1/30/50/50	0/6/6/6
3	FAD	A	702	-	-	0/30/50/50	0/6/6/6

The worst 5 of 57 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	702	FAD	C8A-N7A	7.57	1.48	1.34
3	B	702	FAD	C8A-N7A	7.56	1.48	1.34
2	B	701	FMN	C8M-C8	-6.34	1.38	1.51
2	A	701	FMN	C8M-C8	-6.20	1.38	1.51
2	A	701	FMN	C4A-N5	5.93	1.42	1.30

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	702	FAD	N3A-C2A-N1A	-7.35	117.19	128.68
3	A	702	FAD	N3A-C2A-N1A	-7.30	117.27	128.68
4	A	703	NAP	N3A-C2A-N1A	-6.92	117.86	128.68
4	B	703	NAP	N3A-C2A-N1A	-6.87	117.93	128.68
2	B	701	FMN	C9A-C5A-N5	3.85	126.62	122.43

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	703	NAP	C5D-O5D-PN-O1N
4	A	703	NAP	C5D-O5D-PN-O3
4	A	703	NAP	C5D-O5D-PN-O2N
4	B	703	NAP	PA-O3-PN-O1N
4	A	703	NAP	C2B-O2B-P2B-O1X

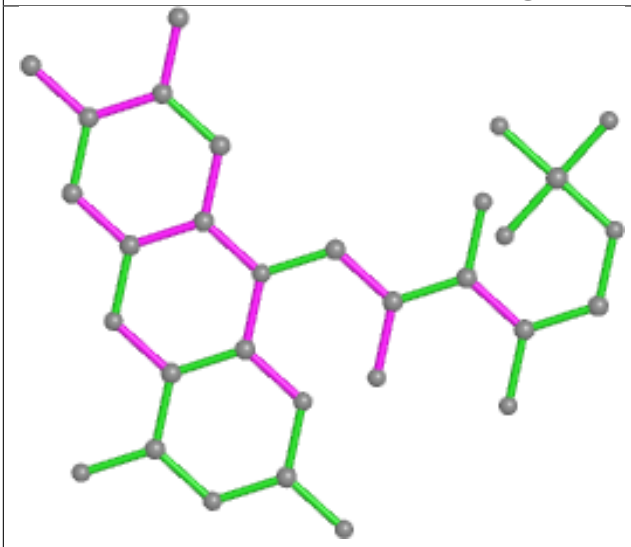
There are no ring outliers.

4 monomers are involved in 6 short contacts:

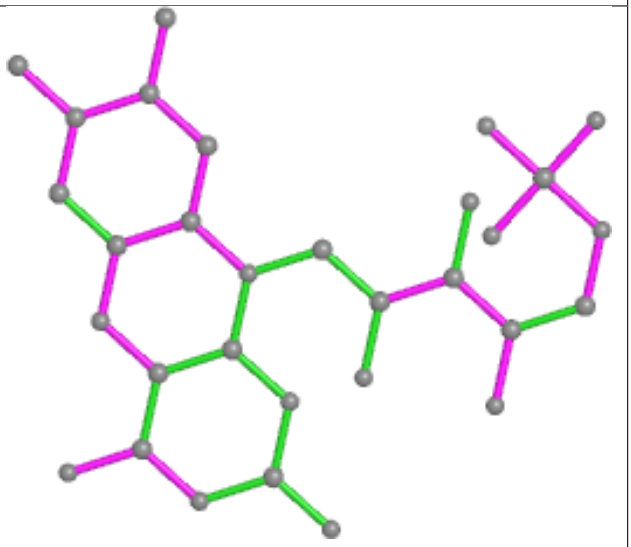
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	703	NAP	3	0
2	A	701	FMN	1	0
5	A	704	PO4	1	0
3	A	702	FAD	1	0

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.

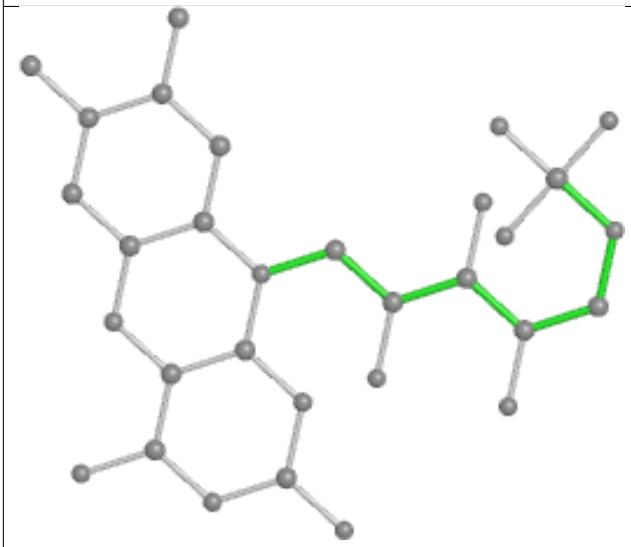
Ligand FMN B 701



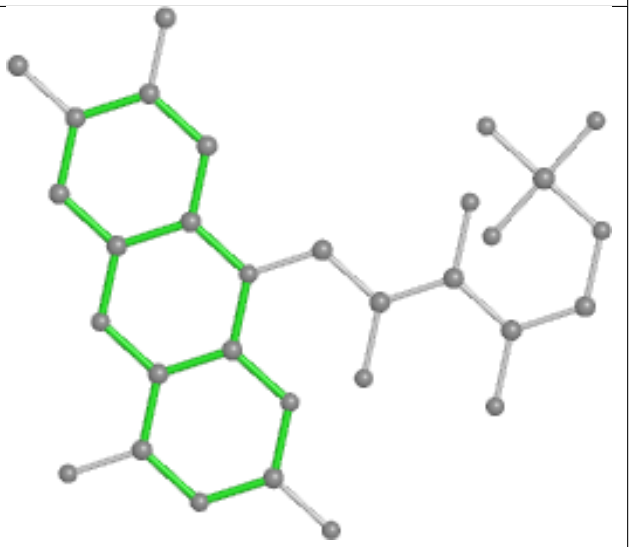
Bond lengths



Bond angles

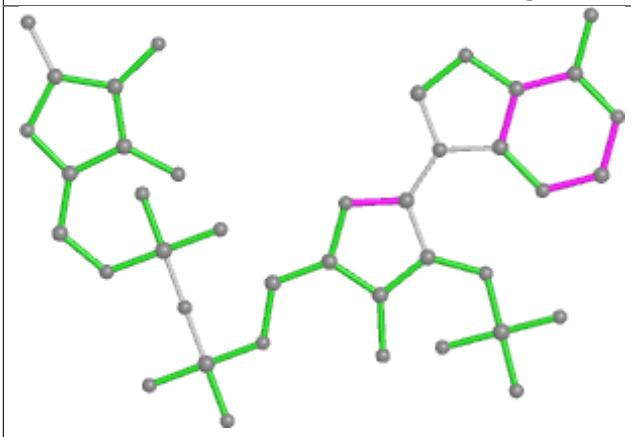


Torsions

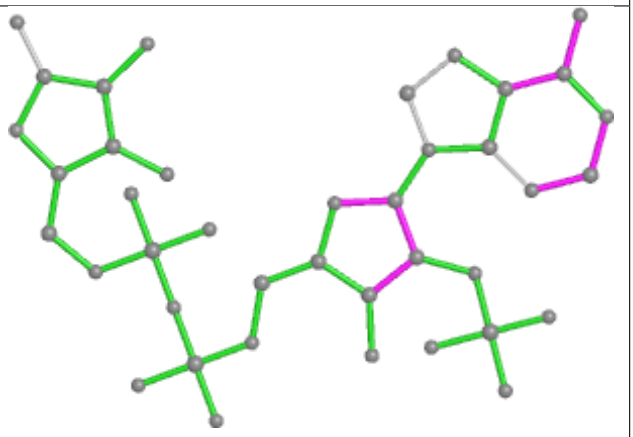


Rings

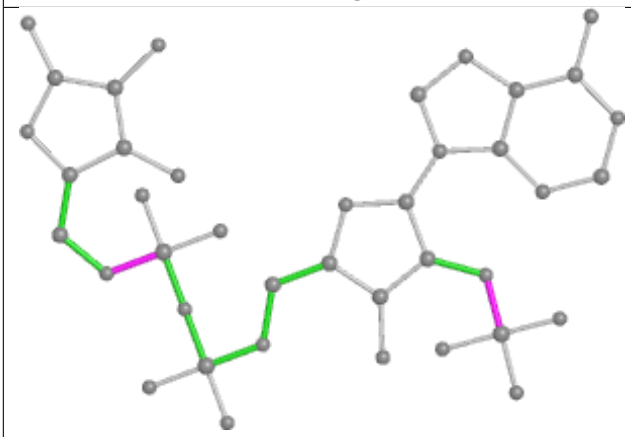
Ligand NAP A 703



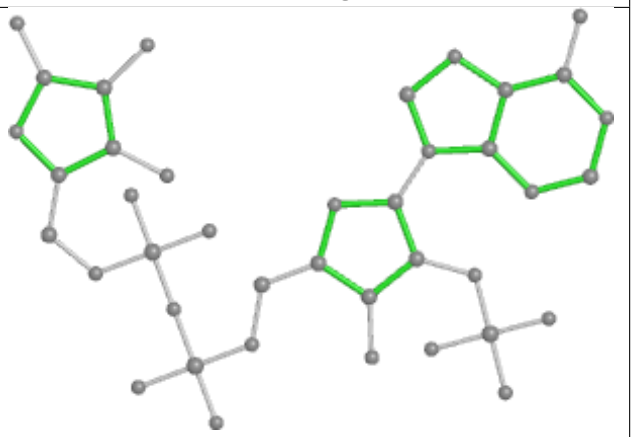
Bond lengths



Bond angles

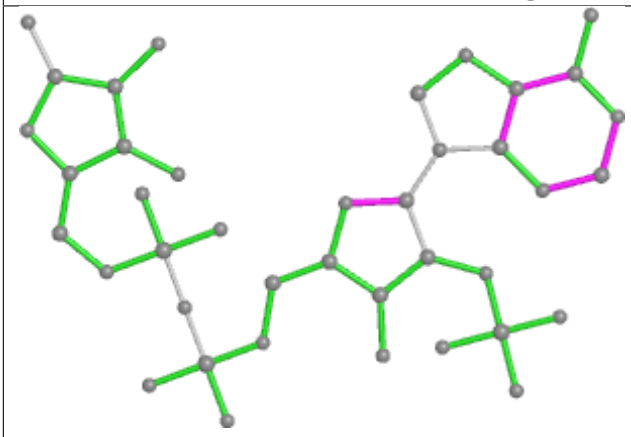


Torsions

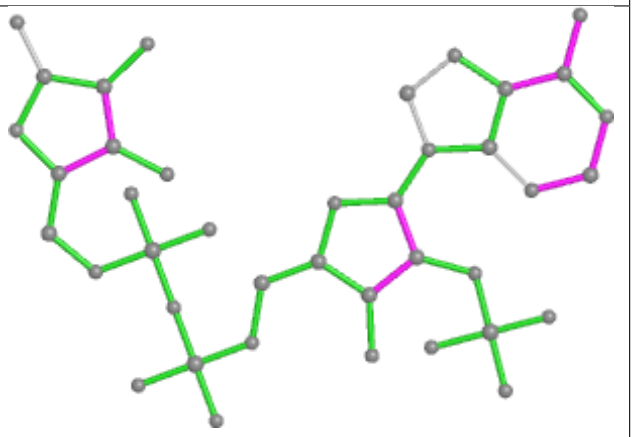


Rings

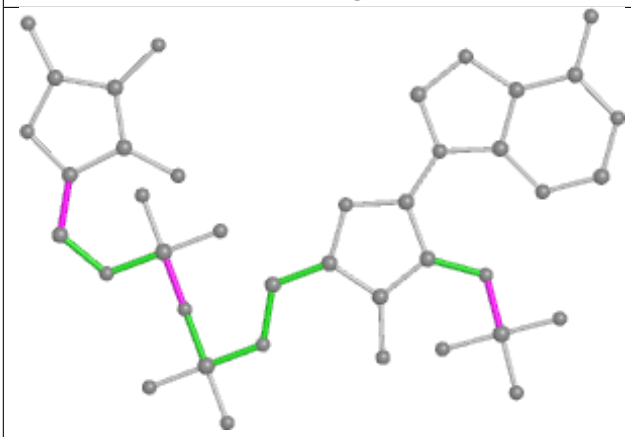
Ligand NAP B 703



Bond lengths



Bond angles



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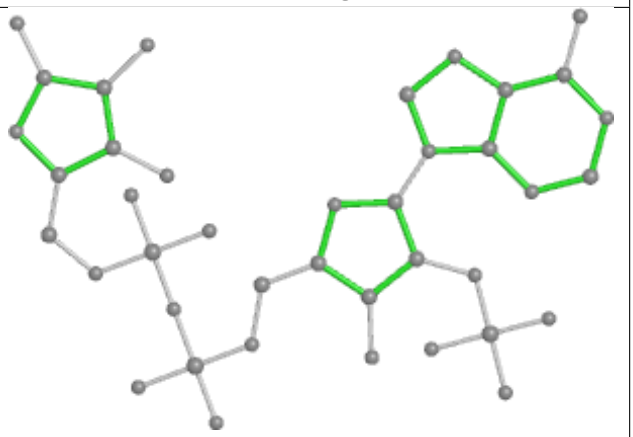
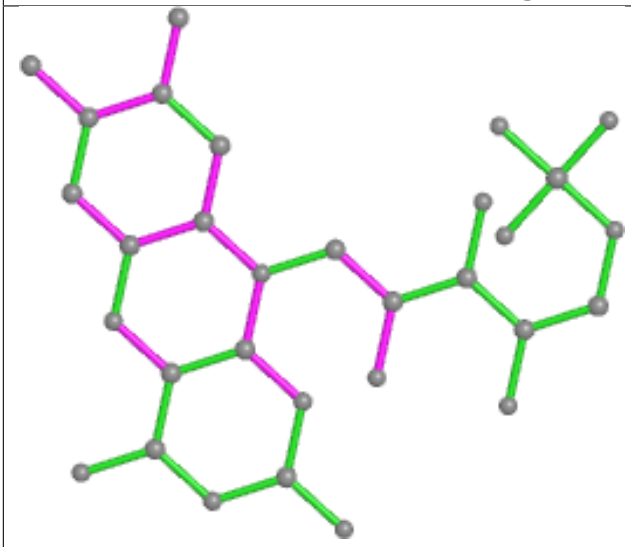
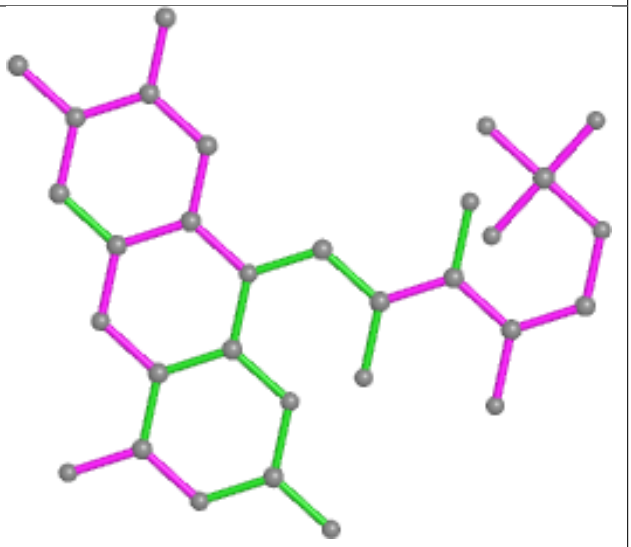


Rings

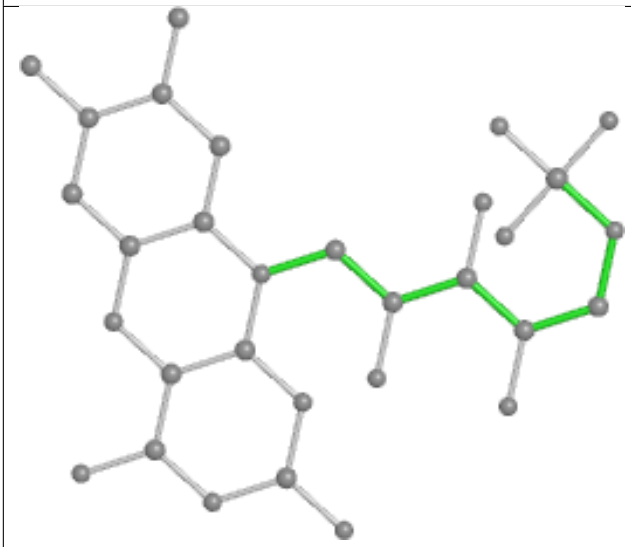
Ligand FMN A 701



Bond lengths



Bond angles



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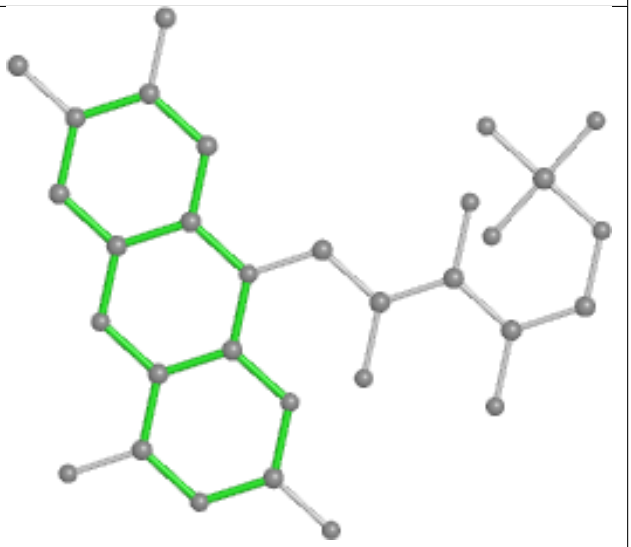
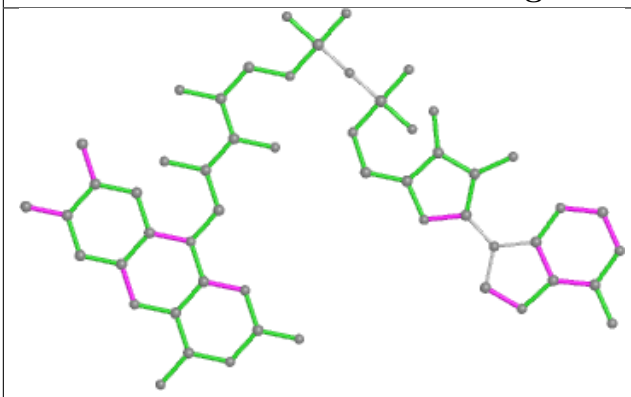
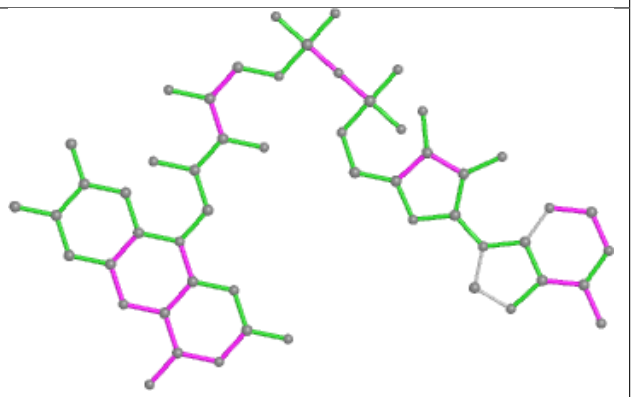


Rings

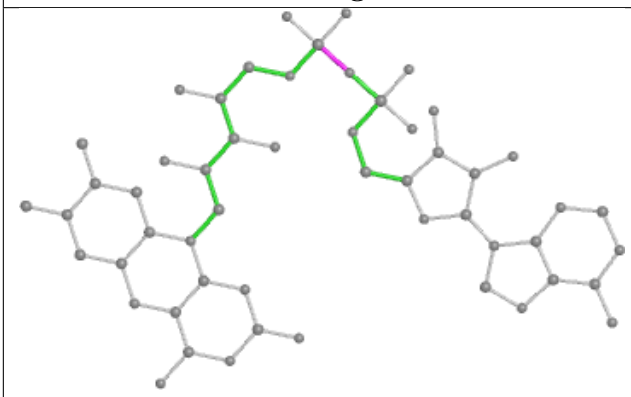
Ligand FAD B 702



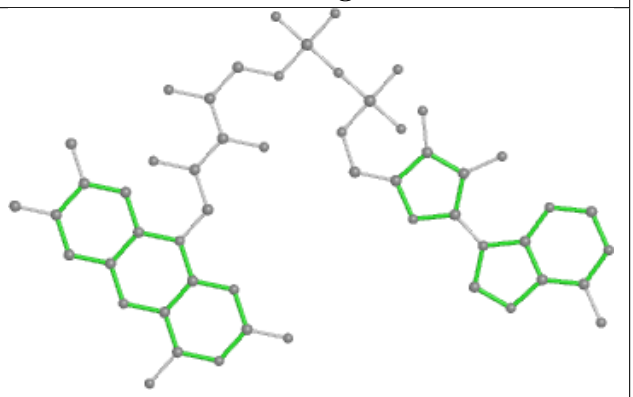
Bond lengths



Bond angles

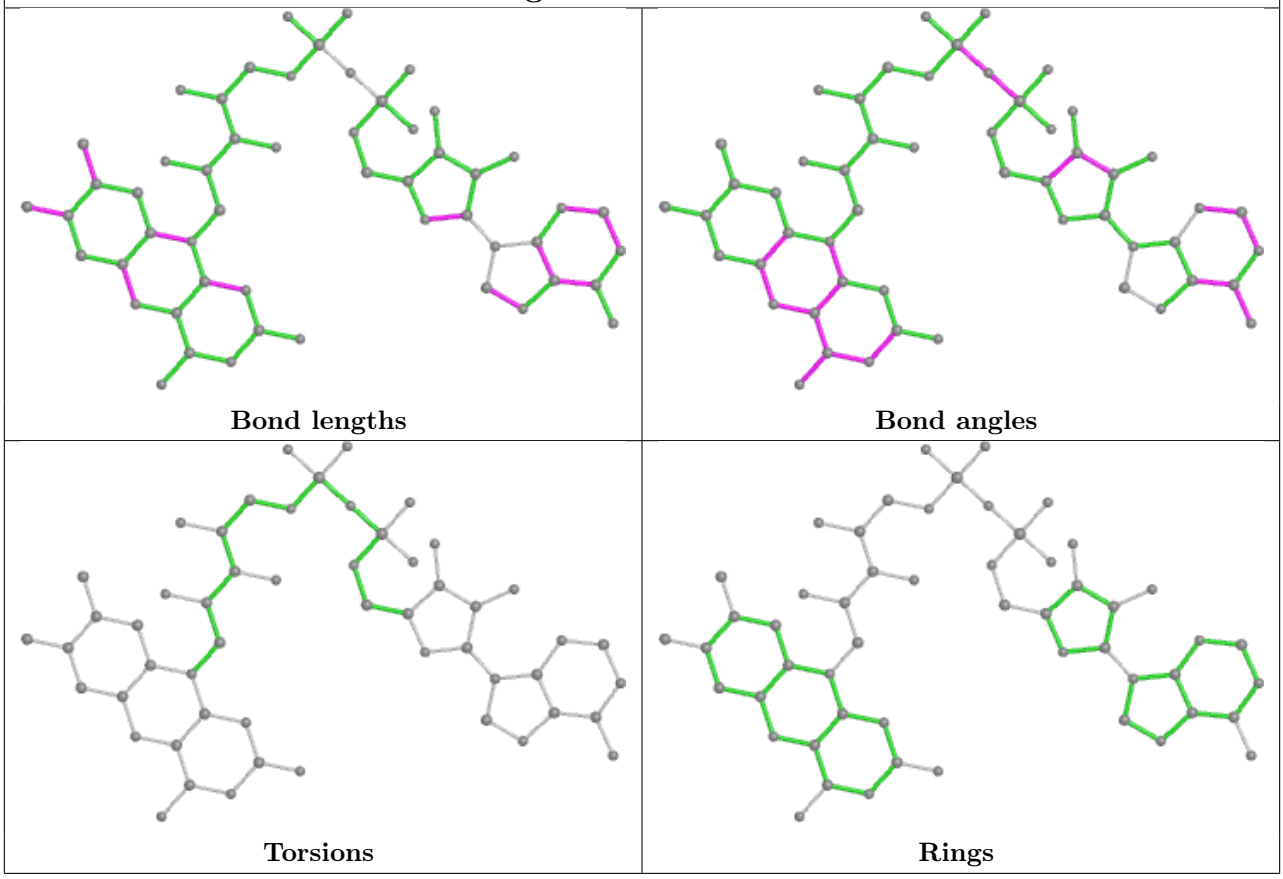


Torsions



Rings

Ligand FAD A 702



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	609/622 (97%)	-0.31	2 (0%)	94	94	22, 39, 59, 75	0
1	B	606/622 (97%)	0.12	30 (4%)	28	30	19, 49, 92, 100	0
All	All	1215/1244 (97%)	-0.09	32 (2%)	56	59	19, 43, 88, 100	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	156	LEU	4.5
1	B	242	ILE	3.6
1	B	233	VAL	3.6
1	B	104	ARG	3.5
1	B	187	TYR	3.5

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 monosaccharides in this entry.

6.4 Ligands

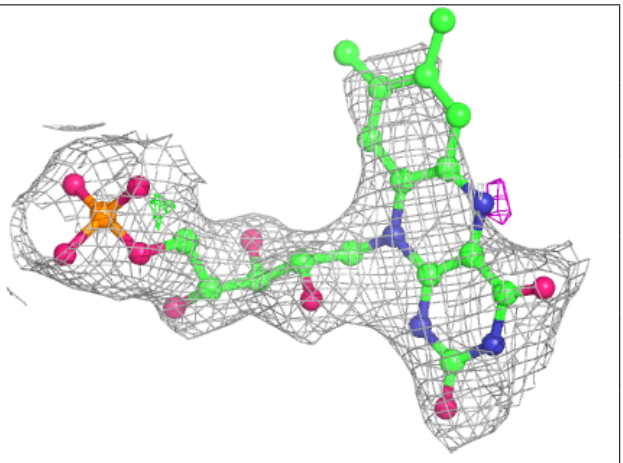
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

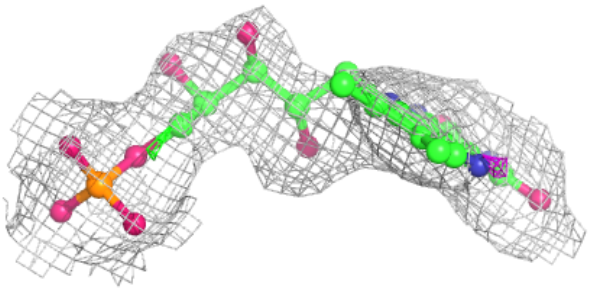
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	PO4	A	704	5/5	0.38	0.47	160,160,160,161	0
5	PO4	B	704	5/5	0.90	0.15	96,96,97,97	0
2	FMN	B	701	31/31	0.92	0.18	65,83,86,86	0
2	FMN	A	701	31/31	0.96	0.14	31,44,49,51	0
4	NAP	B	703	40/48	0.97	0.15	31,37,78,85	0
3	FAD	A	702	53/53	0.97	0.13	24,28,44,46	0
4	NAP	A	703	40/48	0.97	0.14	27,34,80,86	0
3	FAD	B	702	53/53	0.98	0.13	16,23,35,36	0

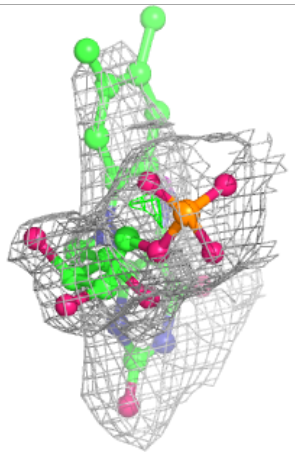
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FMN B 701:

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

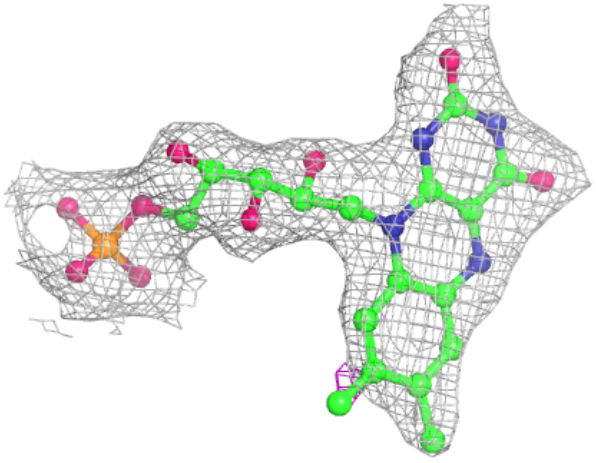


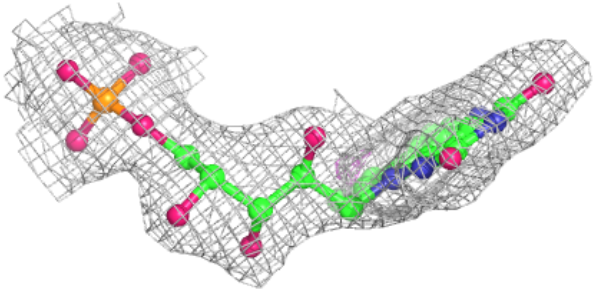


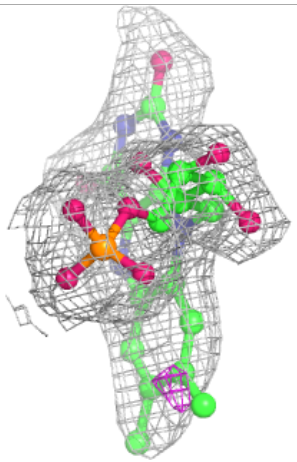


Electron density around FMN A 701:

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

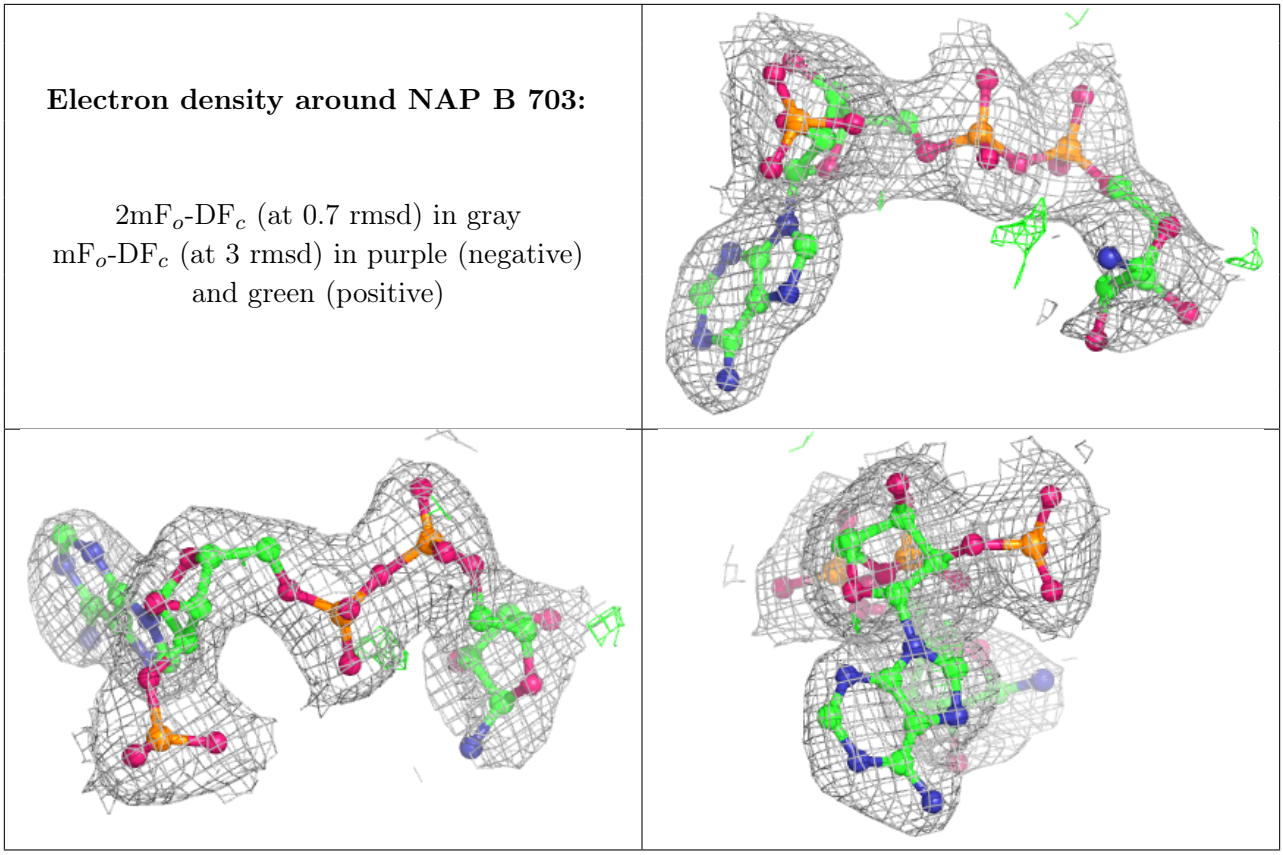






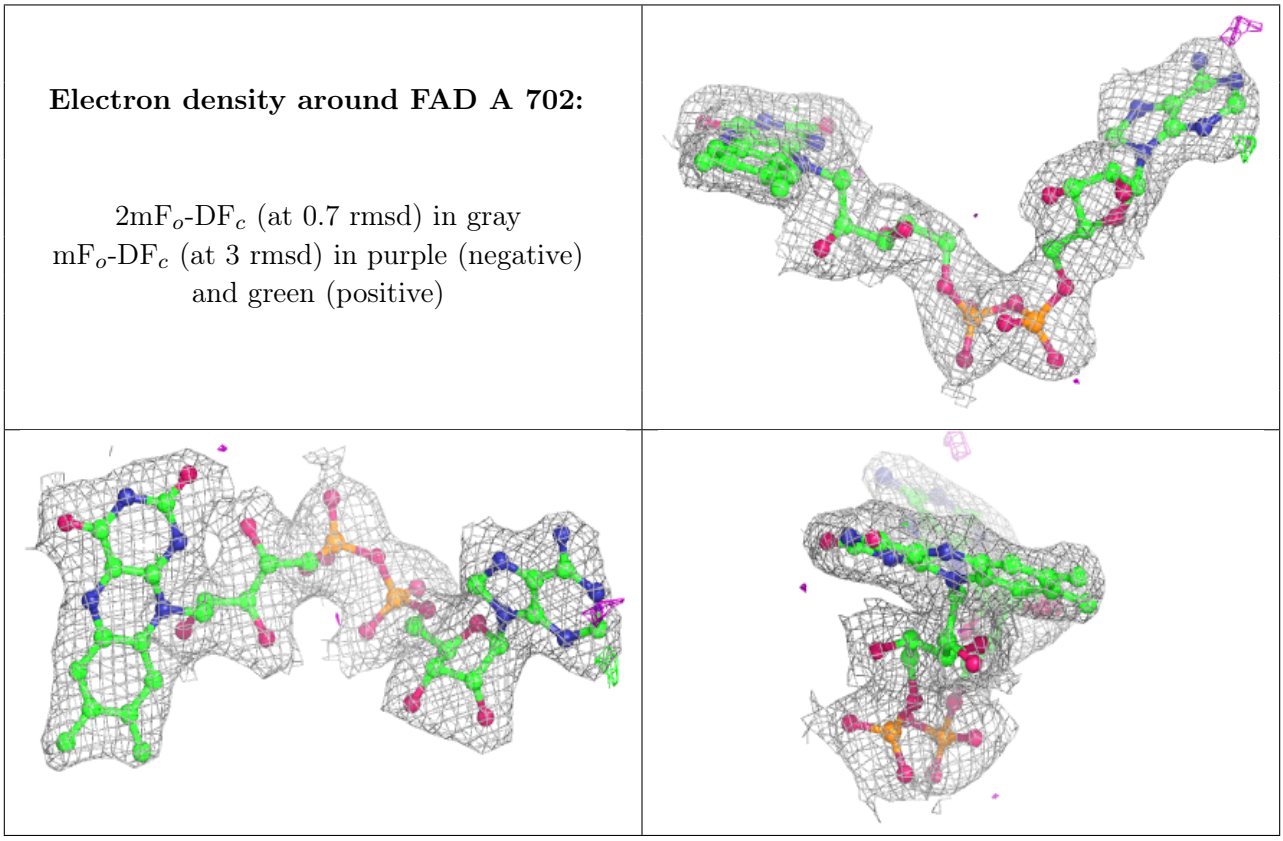
Electron density around NAP B 703:

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



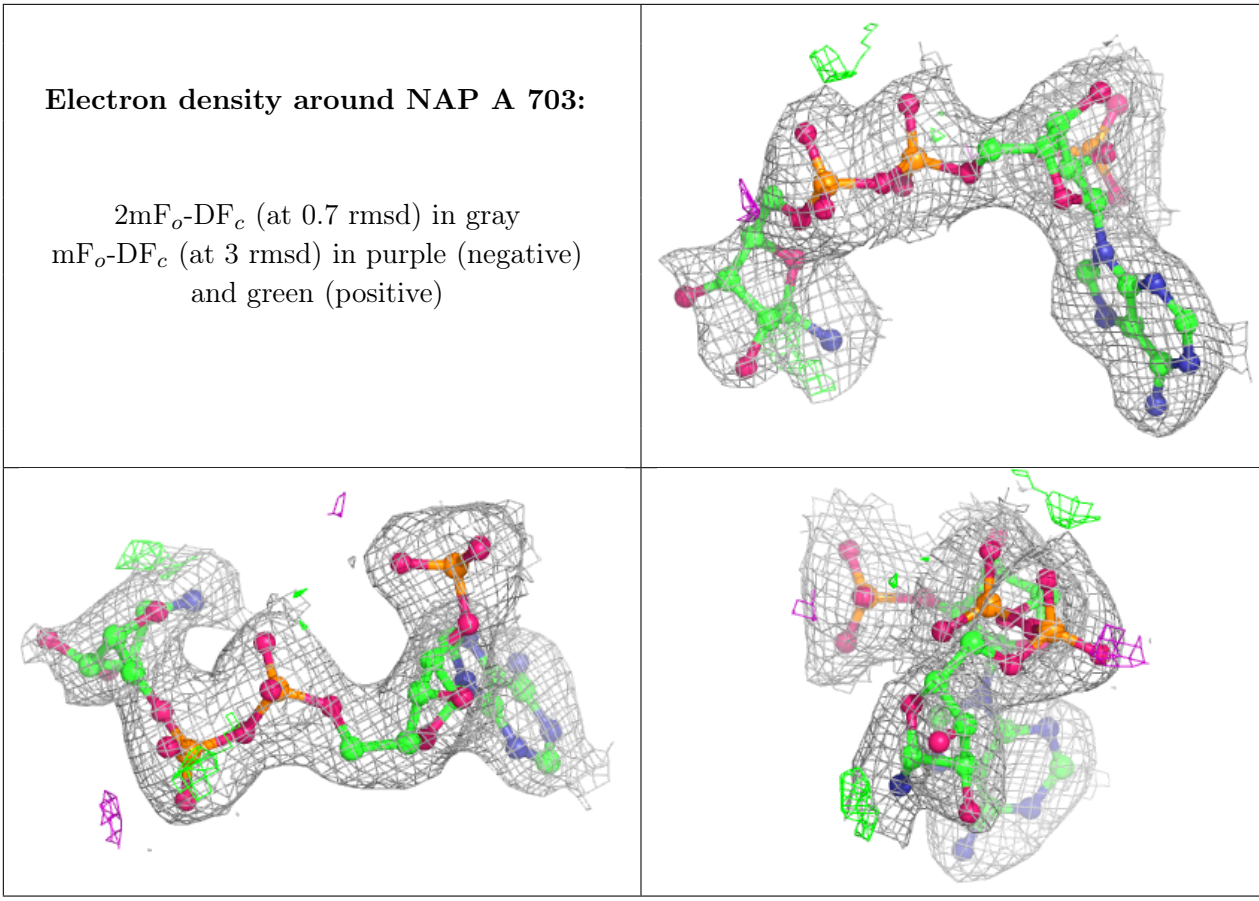
Electron density around FAD A 702:

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



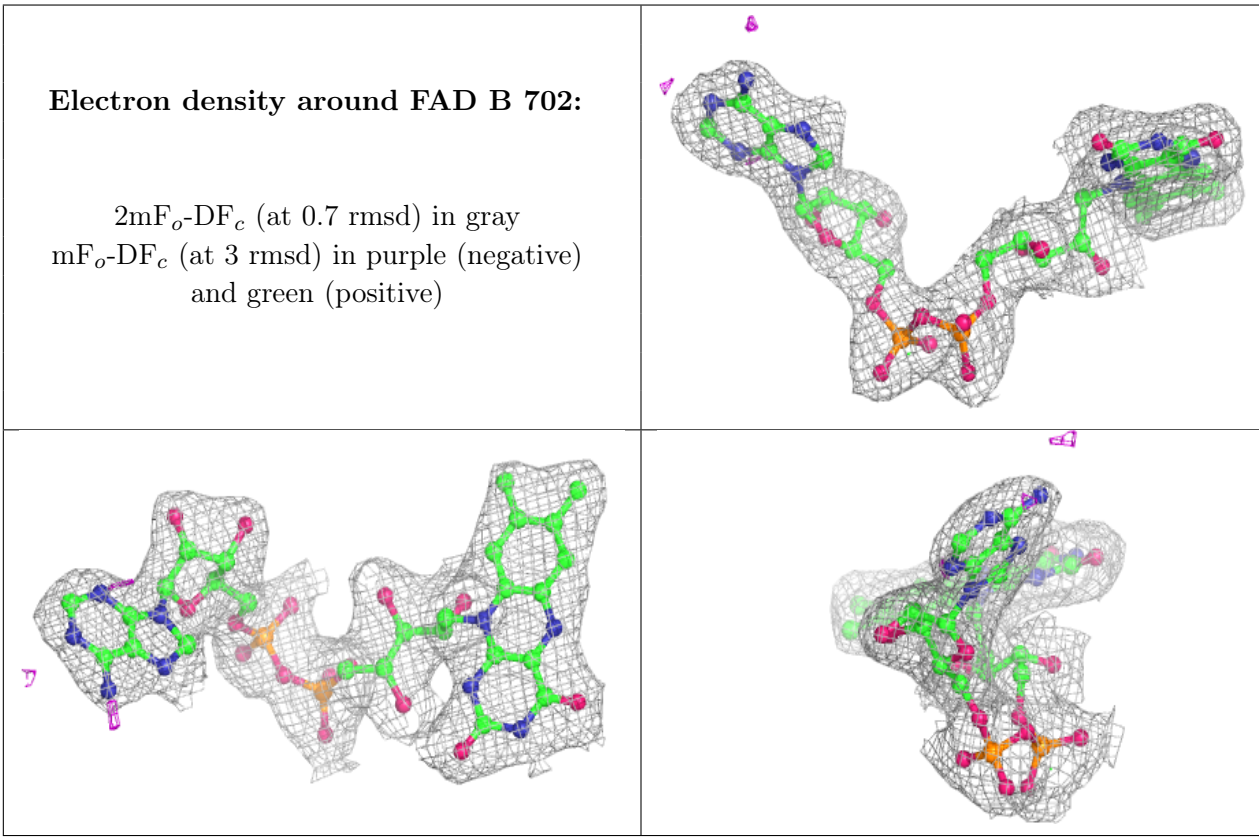
Electron density around NAP A 703:

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



Electron density around FAD B 702:

$2mF_o$-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.