



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 5, 2026 – 06:22 PM JST

PDB ID : 7DQX / pdb_00007dqx
Title : Crystal structure of xanthine dehydrogenase family protein
Authors : Lei, W.
Deposited on : 2020-12-24
Resolution : 3.44 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

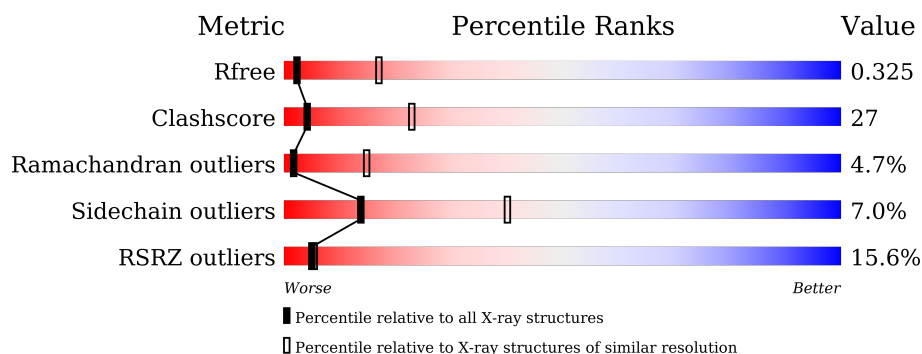
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.44 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}	180053	1736 (3.50-3.38)
Clashscore	190562	1808 (3.50-3.38)
Ramachandran outliers	187476	1776 (3.50-3.38)
Sidechain outliers	187428	1777 (3.50-3.38)
RSRZ outliers	180081	1736 (3.50-3.38)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	794	19% 52% 35% 7% ..
1	D	794	19% 52% 37% 7% ..
2	B	296	8% 65% 26% 5% ..
3	C	160	7% 65% 32% ..
3	F	160	9% 72% 22% ..
4	E	296	7% 65% 26% 6% ..

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
8	FES	C	201	-	-	X	-
8	FES	C	202	-	-	X	-
8	FES	F	201	-	-	X	-
8	FES	F	202	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 18678 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 6-hydroxypseudooxynicotine dehydrogenase complex subunit gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	765	Total	C	N	O	S	1	0	0
			5831	3665	1028	1122	16			
1	D	770	Total	C	N	O	S	1	0	0
			5867	3694	1027	1129	17			

- Molecule 2 is a protein called 6-hydroxypseudooxynicotine dehydrogenase complex subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	287	Total	C	N	O	S	0	0	0
			2135	1337	392	401	5			

- Molecule 3 is a protein called 6-hydroxypseudooxynicotine dehydrogenase complex subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	160	Total	C	N	O	S	0	0	0
			1229	750	227	240	12			
3	F	160	Total	C	N	O	S	0	0	0
			1229	750	227	240	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	53	ILE	LEU	conflict	UNP O87682
C	136	LEU	ILE	conflict	UNP O87682
F	53	ILE	LEU	conflict	UNP O87682
F	136	LEU	ILE	conflict	UNP O87682

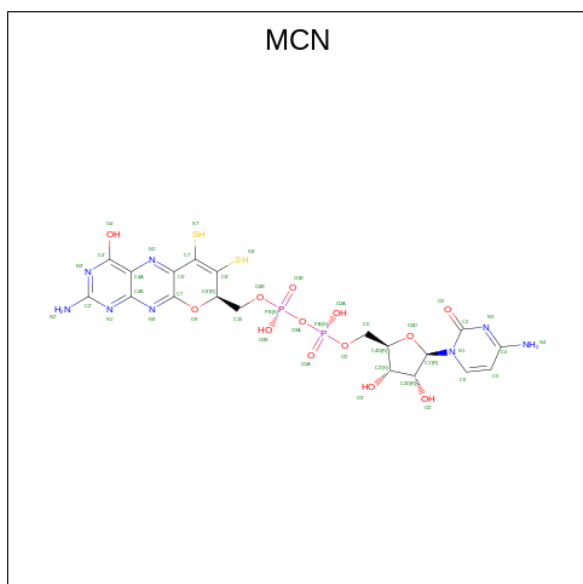
- Molecule 4 is a protein called 6-hydroxypseudooxynicotine dehydrogenase complex subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	293	Total	C	N	O	S	0	0	0
			2175	1361	400	409	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	201	LEU	ILE	conflict	UNP O87681

- Molecule 5 is PTERIN CYTOSINE DINUCLEOTIDE (CCD ID: MCN) (formula: $C_{19}H_{22}N_8O_{13}P_2S_2$).

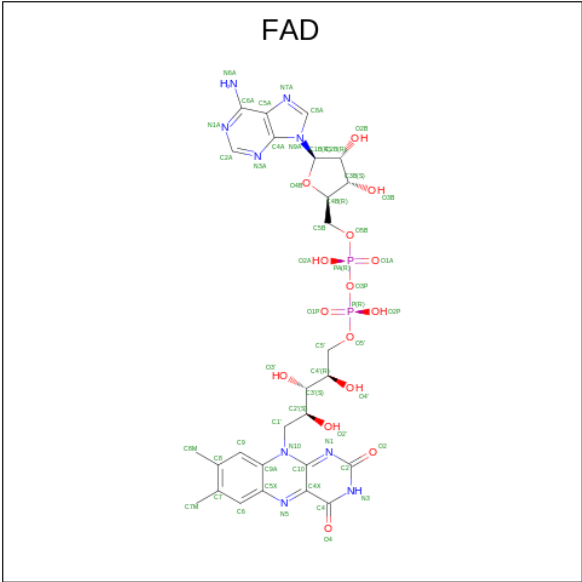


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total 44	C 19	N 8	O 13	P 2	S 2	0	0
5	D	1	Total 44	C 19	N 8	O 13	P 2	S 2	0	0

- Molecule 6 is MOLYBDENUM ATOM (CCD ID: MO) (formula: Mo).

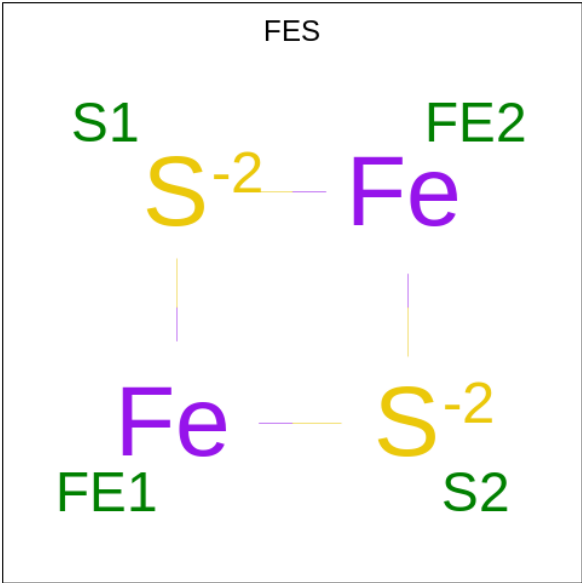
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mo	0	0
			1	1		
6	D	1	Total	Mo	0	0
			1	1		

- Molecule 7 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

- Molecule 8 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



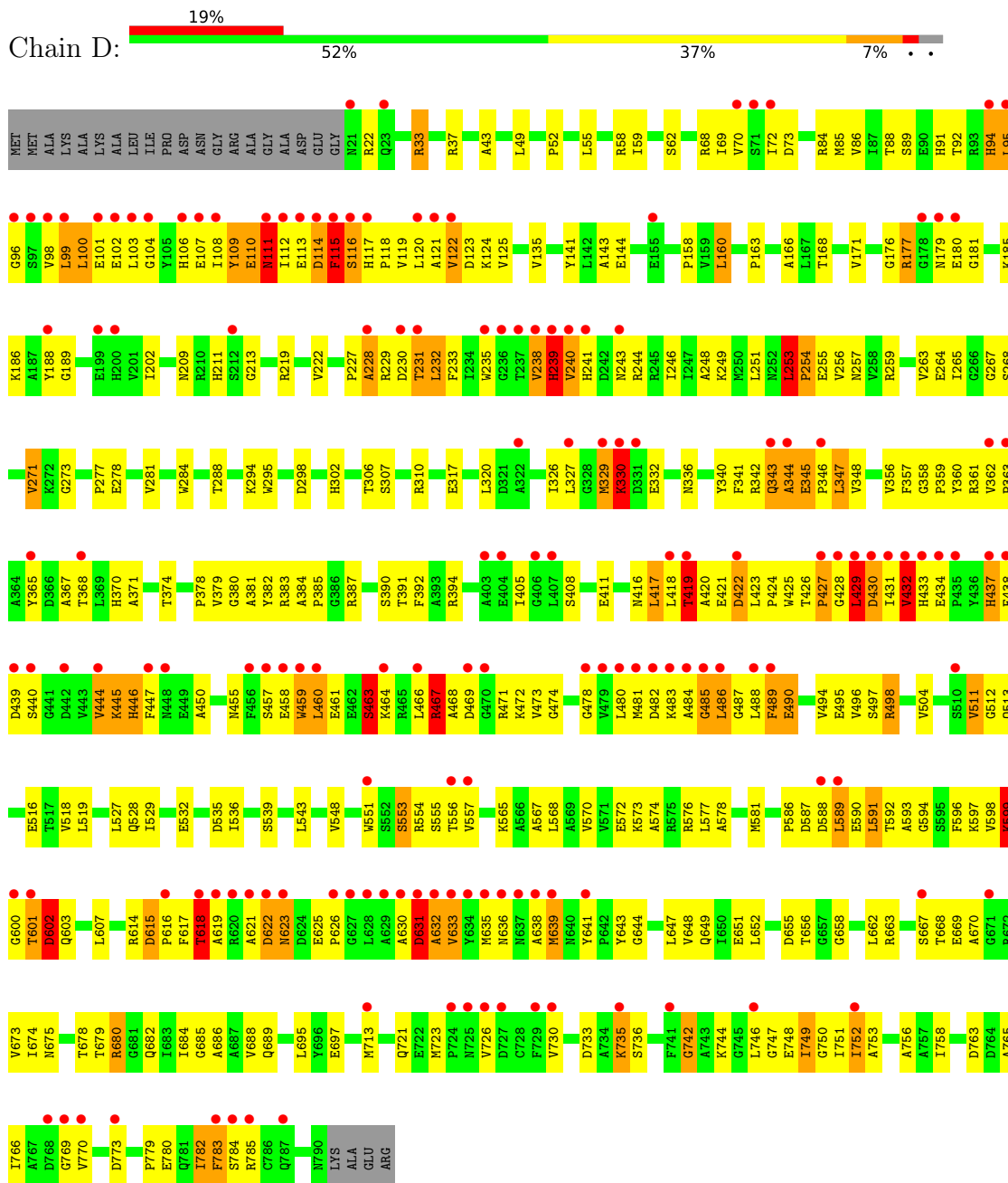
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	Fe	S	0	0
			4	2	2		
8	C	1	Total	Fe	S	0	0
			4	2	2		

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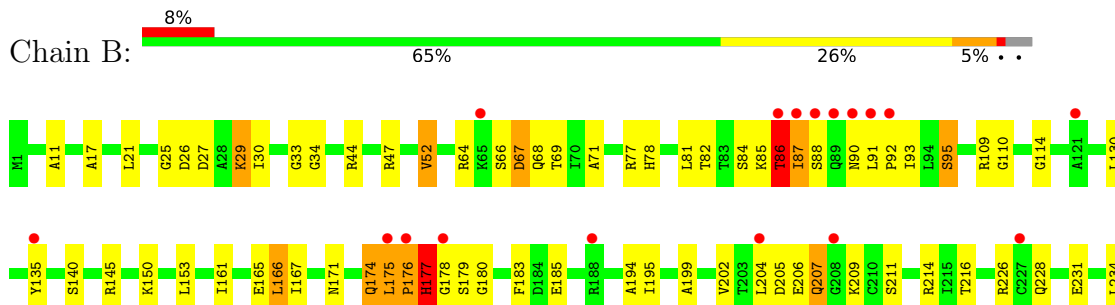
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	F	1	Total	Fe	S	0	0
			4	2	2		
8	F	1	Total	Fe	S	0	0
			4	2	2		

- Chain D:

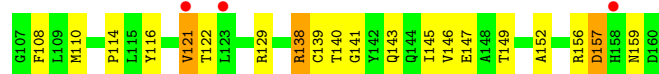


- Chain B:

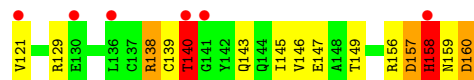
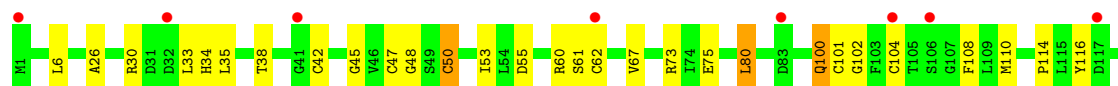




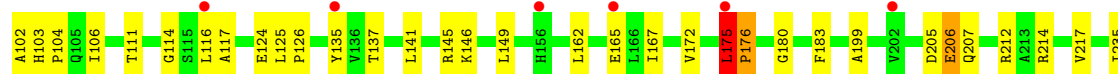
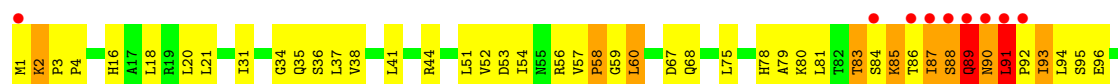
- Molecule 3: 6-hydroxypseudooxynicotine dehydrogenase complex subunit beta



- Molecule 3: 6-hydroxypseudooxynicotine dehydrogenase complex subunit beta



- Molecule 4: 6-hydroxypseudooxynicotine dehydrogenase complex subunit alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	112.86Å 126.79Å 294.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	147.24 – 3.44 147.24 – 3.44	Depositor EDS
% Data completeness (in resolution range)	93.7 (147.24-3.44) 93.7 (147.24-3.44)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 3.48Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.287 , 0.326 0.286 , 0.325	Depositor DCC
R_{free} test set	2706 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	76.2	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 55.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	18678	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.39% 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: FES, MO, MCN, 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	0.59	0/5947	1.00	25/8084 (0.3%)
1	D	0.60	0/5986	1.02	25/8142 (0.3%)
2	B	0.62	0/2170	0.97	9/2950 (0.3%)
3	C	0.59	0/1247	0.90	4/1689 (0.2%)
3	F	0.62	0/1247	0.84	3/1689 (0.2%)
4	E	0.63	0/2211	0.94	7/3006 (0.2%)
All	All	0.60	0/18808	0.98	73/25560 (0.3%)

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	9
1	D	0	10
2	B	0	2
3	C	0	1
3	F	0	2
4	E	0	2
All	All	0	26

There are no bond length outliers.

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	34	HIS	N-CA-C	-12.30	95.52	112.25
1	D	426	THR	CA-C-N	10.44	132.89	119.84
1	D	426	THR	C-N-CA	10.44	132.89	119.84
1	D	104	GLY	N-CA-C	-9.58	103.08	114.48

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	331	ASP	N-CA-C	8.99	123.80	109.86

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	114	ASP	Peptide
1	A	115	PHE	Peptide
1	A	243	ASN	Peptide
1	A	330	LYS	Peptide
1	A	466	LEU	Peptide

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	5831	0	5717	371	0
1	D	5867	0	5754	409	0
2	B	2135	0	2188	97	0
3	C	1229	0	1187	47	0
3	F	1229	0	1187	45	0
4	E	2175	0	2219	82	0
5	A	44	0	17	14	0
5	D	44	0	17	15	0
6	A	1	0	0	0	0
6	D	1	0	0	0	0
7	B	53	0	31	11	0
7	E	53	0	31	9	0
8	C	8	0	0	6	0
8	F	8	0	0	6	0
All	All	18678	0	18348	1015	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 27.

The worst 5 of 1015 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:486:LEU:HD13	1:A:554:ARG:HB2	1.23	1.20
1:D:588:ASP:HB3	1:D:598:VAL:HA	1.23	1.18
1:A:439:ASP:HA	1:A:440:SER:CB	1.75	1.16
1:A:490:GLU:HG3	1:A:554:ARG:HH12	1.07	1.11
1:A:485:GLY:HA2	1:A:486:LEU:HB2	1.12	1.11

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	761/794 (96%)	612 (80%)	101 (13%)	48 (6%)	1	10
1	D	768/794 (97%)	616 (80%)	113 (15%)	39 (5%)	1	13
2	B	285/296 (96%)	250 (88%)	26 (9%)	9 (3%)	3	22
3	C	158/160 (99%)	129 (82%)	26 (16%)	3 (2%)	6	30
3	F	158/160 (99%)	135 (85%)	21 (13%)	2 (1%)	9	37
4	E	291/296 (98%)	251 (86%)	27 (9%)	13 (4%)	2	15
All	All	2421/2500 (97%)	1993 (82%)	314 (13%)	114 (5%)	2	15

5 of 114 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	98	VAL
1	A	118	PRO
1	A	229	ARG
1	A	258	VAL

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	602/632 (95%)	560 (93%)	42 (7%)	14	40
1	D	607/632 (96%)	560 (92%)	47 (8%)	12	38
2	B	225/234 (96%)	209 (93%)	16 (7%)	13	39
3	C	138/138 (100%)	131 (95%)	7 (5%)	21	49
3	F	138/138 (100%)	130 (94%)	8 (6%)	18	45
4	E	228/234 (97%)	213 (93%)	15 (7%)	15	42
All	All	1938/2008 (96%)	1803 (93%)	135 (7%)	14	40

5 of 135 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	496	VAL
1	D	589	LEU
1	D	735	LYS
2	B	150	LYS
2	B	95	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
4	E	118	HIS
1	D	343	GLN
4	E	174	GLN
3	F	144	GLN
1	D	637	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	MCN	A	801	6	41,48,48	1.32	2 (4%)	49,74,74	1.54	8 (16%)
8	FES	C	201	3	0,4,4	-	-	-	-	-
7	FAD	B	301	-	56,58,58	1.48	10 (17%)	81,89,89	1.78	17 (20%)
7	FAD	E	301	-	56,58,58	1.51	10 (17%)	81,89,89	1.68	16 (19%)
8	FES	F	201	3	0,4,4	-	-	-	-	-
5	MCN	D	801	6	41,48,48	1.30	3 (7%)	49,74,74	1.64	6 (12%)
8	FES	C	202	3	0,4,4	-	-	-	-	-
8	FES	F	202	3	0,4,4	-	-	-	-	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MCN	A	801	6	-	13/22/54/54	0/5/5/5
8	FES	C	201	3	-	-	0/1/1/1
7	FAD	B	301	-	-	21/34/50/50	0/6/6/6
7	FAD	E	301	-	-	12/34/50/50	0/6/6/6
8	FES	F	201	3	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MCN	D	801	6	-	15/22/54/54	0/5/5/5
8	FES	C	202	3	-	-	0/1/1/1
8	FES	F	202	3	-	-	0/1/1/1

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	E	301	FAD	C9A-C5X	5.31	1.50	1.41
7	B	301	FAD	C9A-C5X	5.26	1.50	1.41
5	A	801	MCN	C4A-C4B	4.83	1.49	1.40
5	D	801	MCN	C4A-C4B	4.75	1.48	1.40
7	E	301	FAD	C5A-C4A	4.70	1.47	1.39

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	301	FAD	C5A-C4A-N3A	-6.50	118.28	126.75
7	E	301	FAD	C5A-C4A-N3A	-6.00	118.93	126.75
7	B	301	FAD	N3A-C4A-N9A	5.62	136.34	127.08
5	D	801	MCN	C2'-N1'-C4B	5.06	121.14	115.36
5	A	801	MCN	C2'-N1'-C4B	4.90	120.96	115.36

There are no chirality outliers.

5 of 61 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	801	MCN	O4D-C4D-C5'-O5'
5	A	801	MCN	C5'-O5'-PA-O1A
5	A	801	MCN	O3B-C10-C9'-C8'
5	A	801	MCN	O3B-C10-C9'-O9'
5	D	801	MCN	O4D-C4D-C5'-O5'

There are no ring outliers.

8 monomers are involved in 61 short contacts:

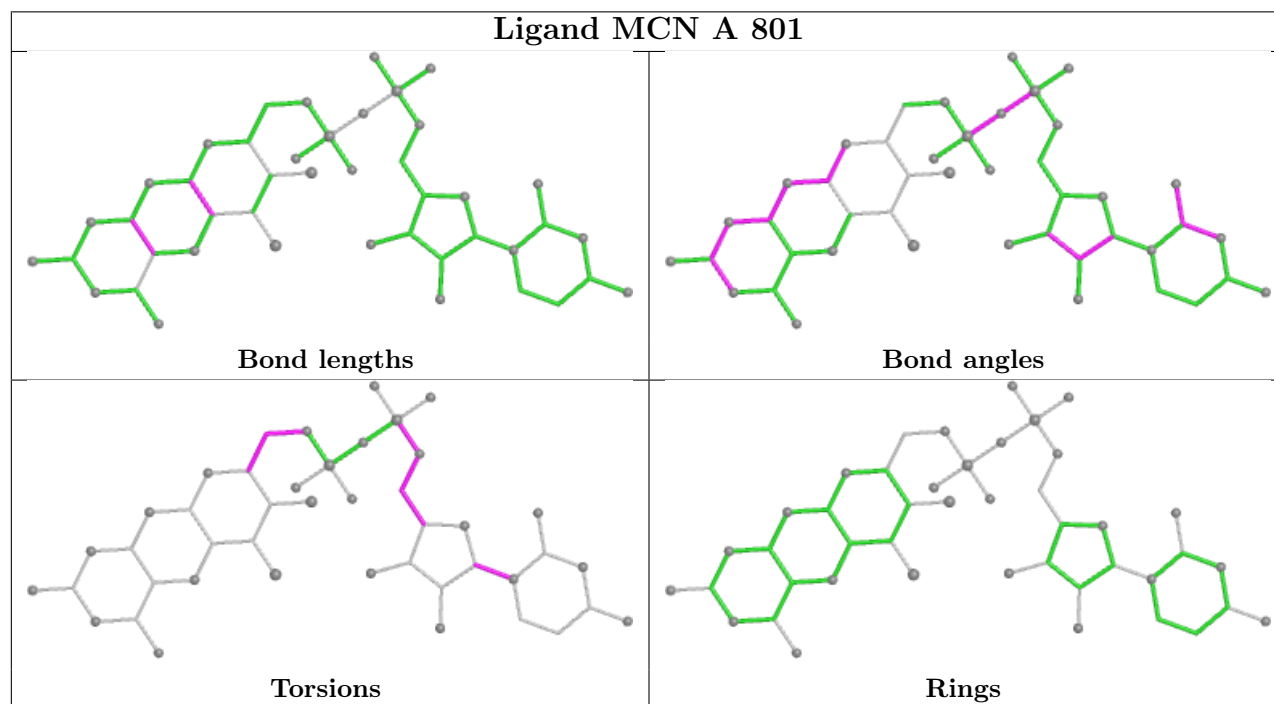
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	801	MCN	14	0
8	C	201	FES	3	0
7	B	301	FAD	11	0
7	E	301	FAD	9	0
8	F	201	FES	3	0

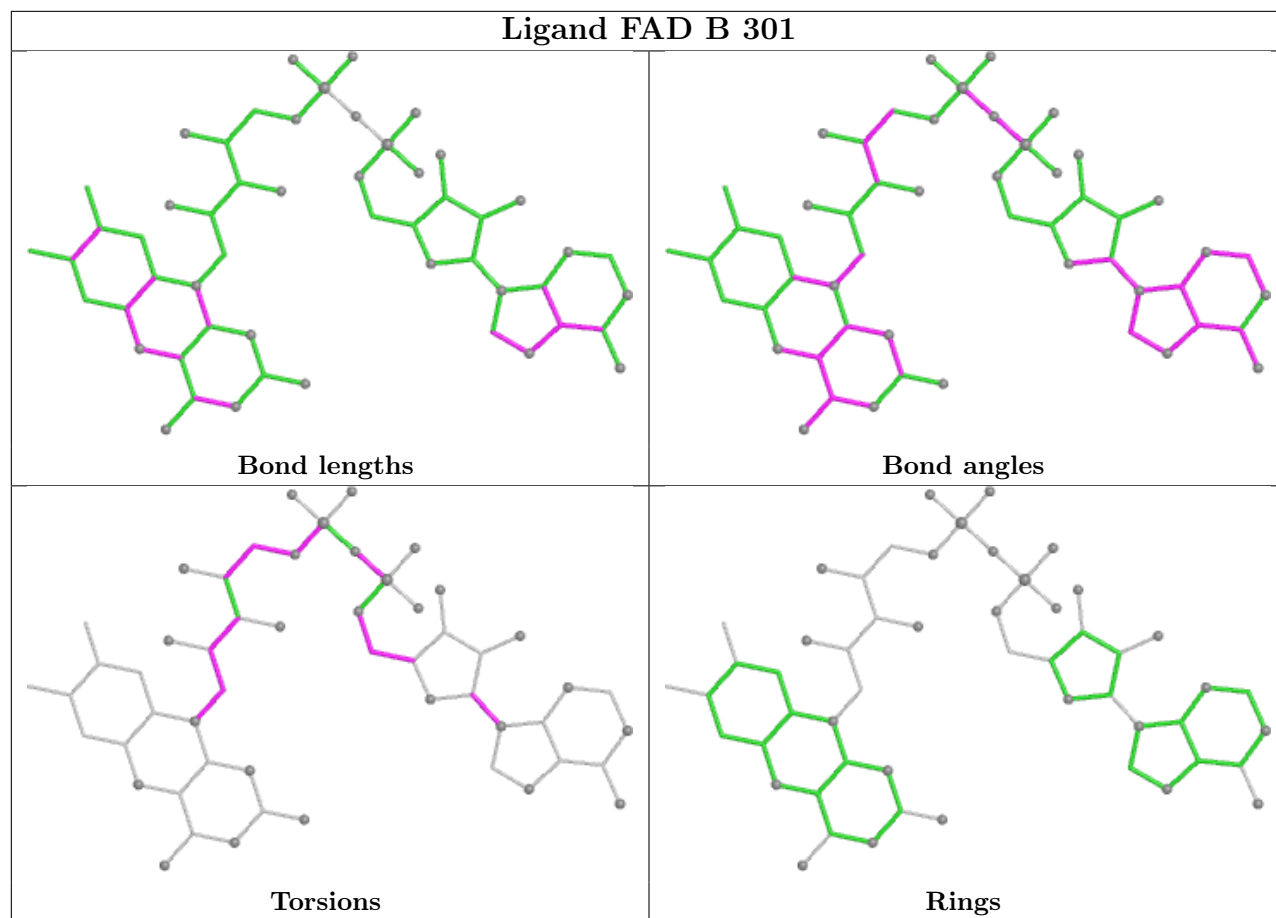
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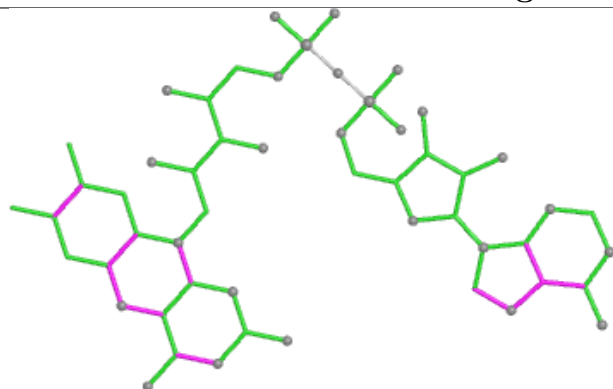
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	801	MCN	15	0
8	C	202	FES	3	0
8	F	202	FES	3	0

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

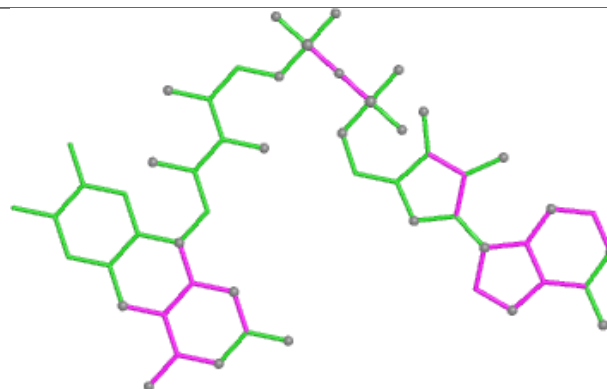




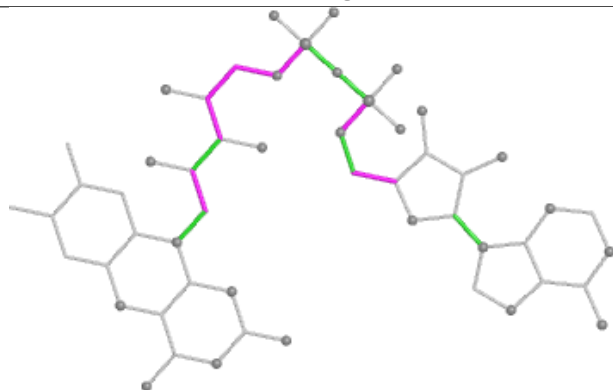
Ligand FAD E 301



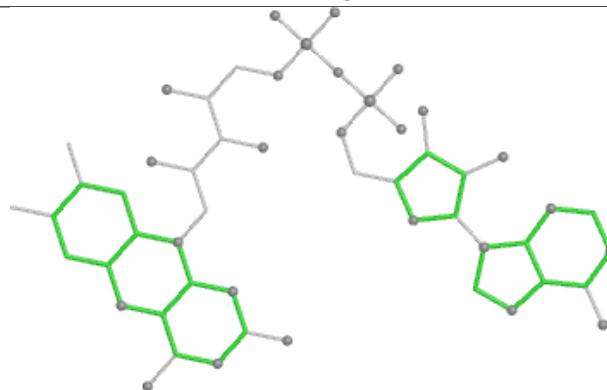
Bond lengths



Bond angles

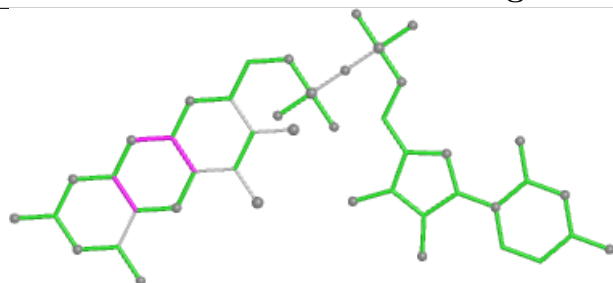


Torsions

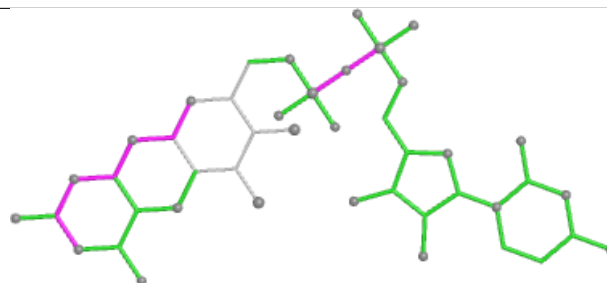


Rings

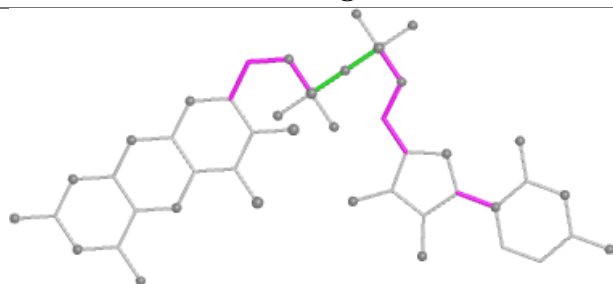
Ligand MCN D 801



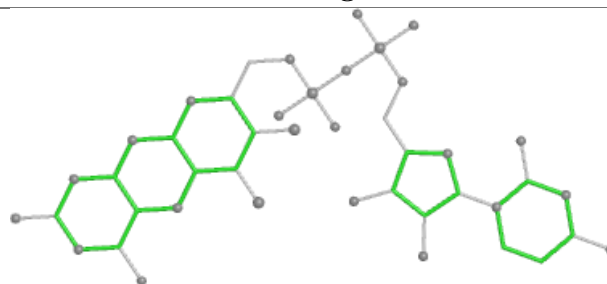
Bond lengths



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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	765/794 (96%)	1.14	154 (20%) 3 3	38, 60, 104, 150	1 (0%)
1	D	770/794 (96%)	1.21	154 (20%) 3 3	43, 64, 107, 148	1 (0%)
2	B	287/296 (96%)	0.79	24 (8%) 17 13	51, 71, 102, 116	0
3	C	160/160 (100%)	0.72	11 (6%) 23 17	38, 58, 89, 124	0
3	F	160/160 (100%)	0.77	14 (8%) 15 12	46, 56, 92, 137	0
4	E	293/296 (98%)	0.73	22 (7%) 20 15	43, 66, 92, 145	0
All	All	2435/2500 (97%)	1.02	379 (15%) 5 5	38, 63, 103, 150	2 (0%)

The worst 5 of 379 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	430	ASP	11.0
1	D	428	GLY	8.6
1	A	482	ASP	7.7
1	D	237	THR	7.5
1	D	239	HIS	7.2

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

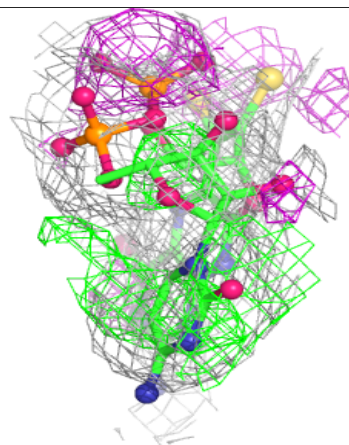
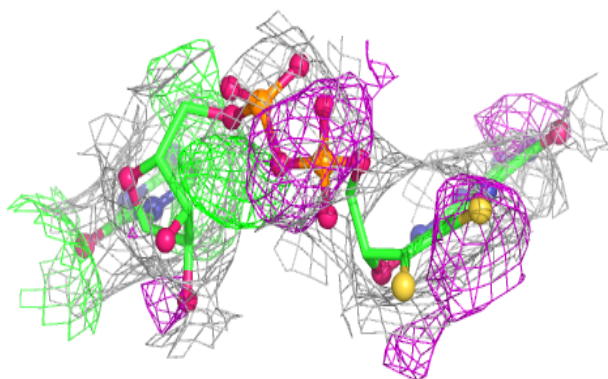
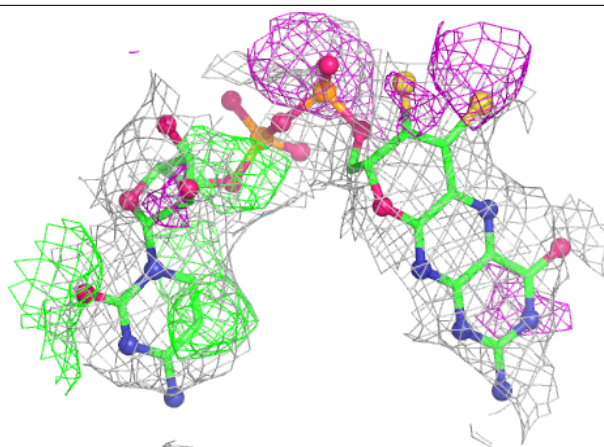
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MCN	D	801	44/44	0.68	0.21	54,74,89,93	0
5	MCN	A	801	44/44	0.73	0.18	53,69,82,87	0
6	MO	D	802	1/1	0.76	0.21	105,105,105,105	0
6	MO	A	802	1/1	0.88	0.19	96,96,96,96	0
8	FES	F	202	4/4	0.89	0.13	46,48,50,51	0
7	FAD	E	301	53/53	0.90	0.13	50,57,63,64	0
7	FAD	B	301	53/53	0.91	0.12	57,60,70,71	0
8	FES	C	201	4/4	0.92	0.10	64,64,65,66	0
8	FES	C	202	4/4	0.95	0.08	43,47,47,49	0
8	FES	F	201	4/4	0.96	0.07	54,55,57,58	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.

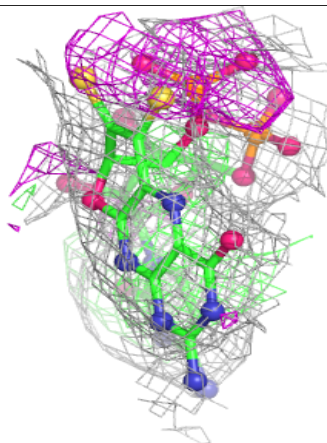
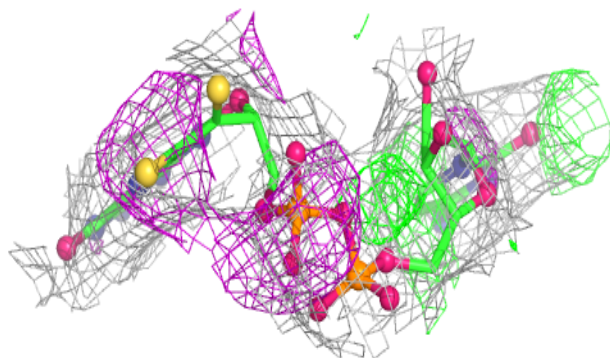
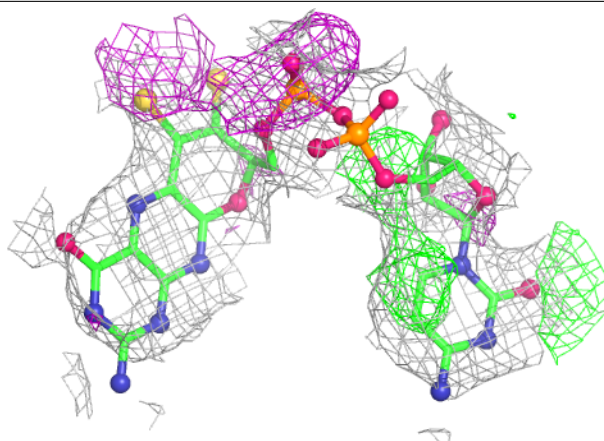
Electron density around MCN D 801:

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

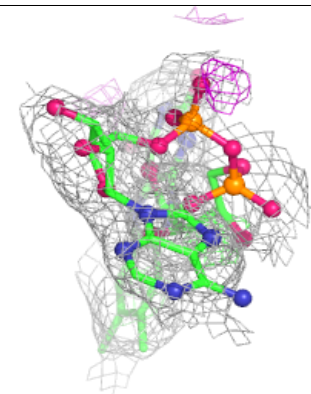
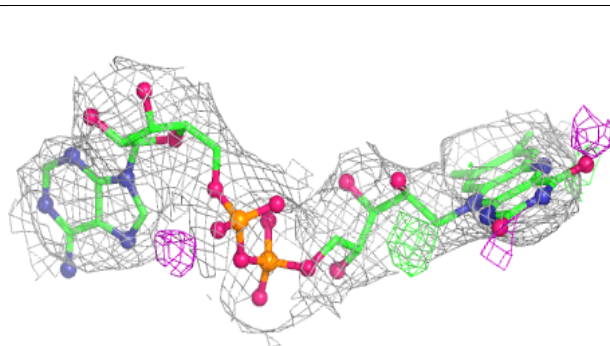
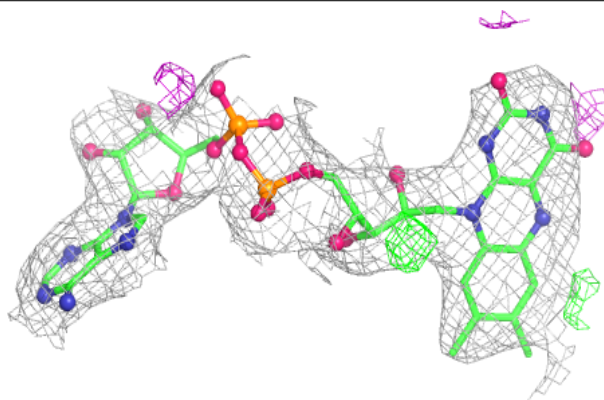


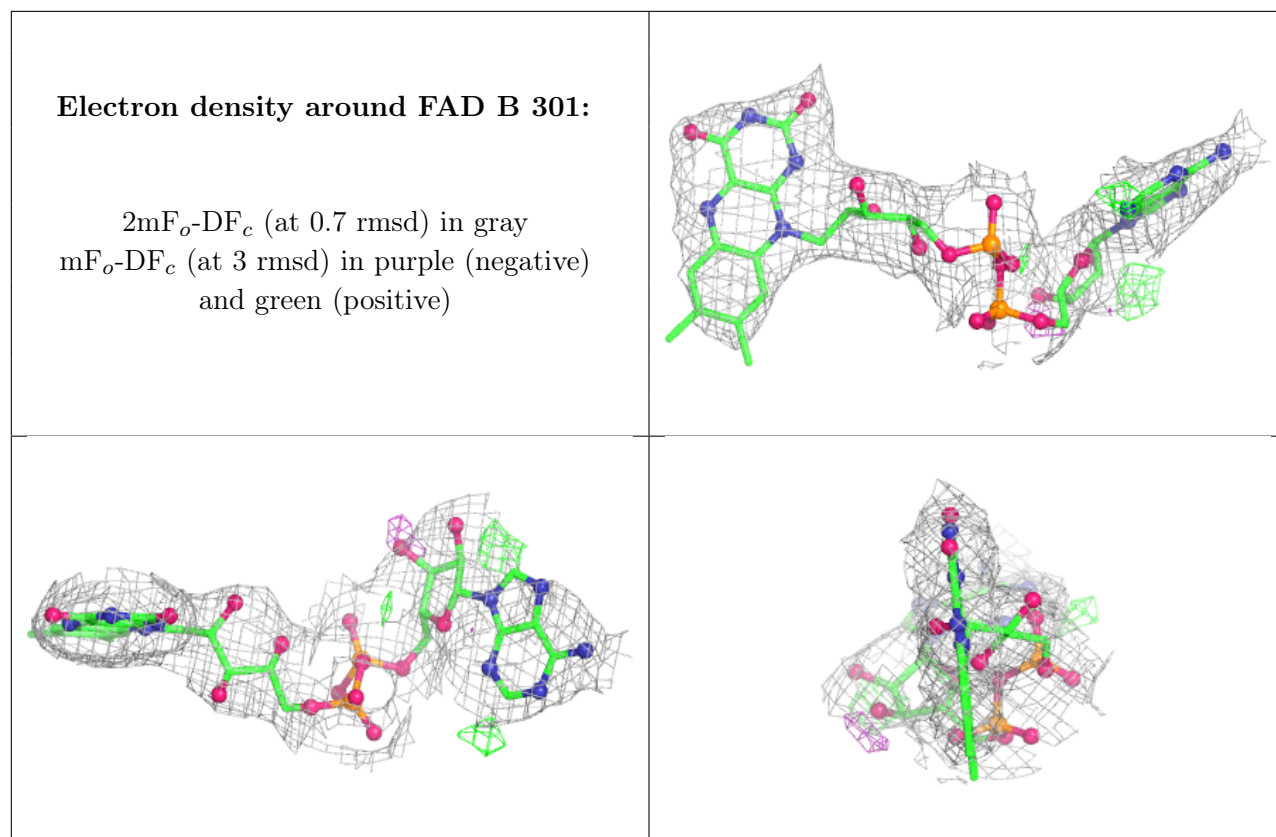
Electron density around MCN A 801:

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

**Electron density around FAD E 301:**

$2mF_o-DF_c$ (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.