



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 10:32 PM EDT

PDB ID : 3ZYV / pdb_00003zyv
Title : Crystal structure of the mouse liver Aldehyde Oxidase 3 (mAOX3)
Authors : Trincao, J.; Coelho, C.; Mahro, M.; Rodrigues, D.; Terao, M.; Garattini, E.;
Leimkuehler, S.; Romao, M.J.
Deposited on : 2011-08-27
Resolution : 2.54 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 : 2022.3.0, CSD as543be (2022)
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 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

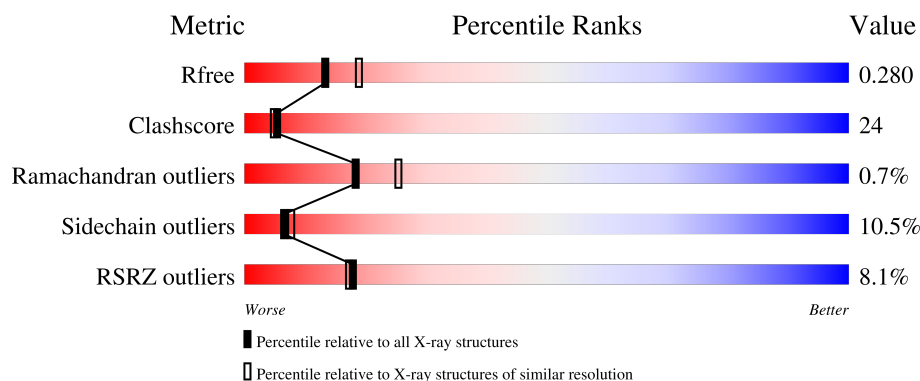
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.54 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	1335	7% 56% 33% 5% 6%
1	B	1335	7% 56% 33% 5% 5%
1	C	1335	7% 57% 31% 5% 7%
1	D	1335	9% 56% 33% 5% 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
3	FES	D	3002	-	-	X	-
5	MOS	A	3004	-	-	X	-
5	MOS	B	3004	-	-	X	-
5	MOS	C	3004	-	-	X	-
5	MOS	D	3004	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 38315 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.

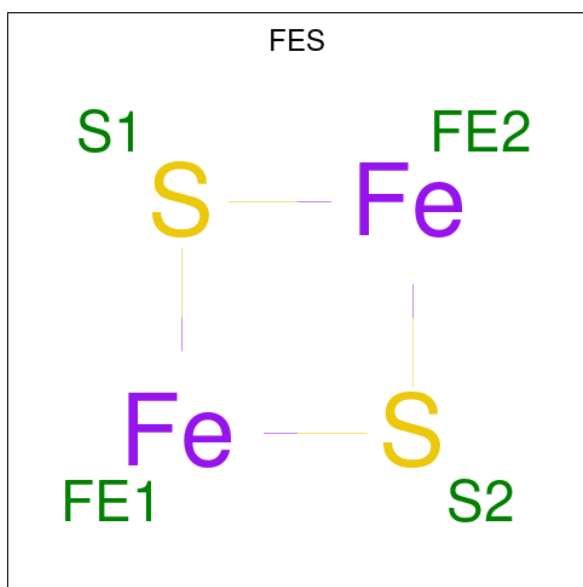
- Molecule 1 is a protein called AOX3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1253	Total	C	N	O	S	0	0	0
			9314	5905	1602	1747	60			
1	B	1262	Total	C	N	O	S	0	0	0
			9471	6016	1621	1774	60			
1	C	1244	Total	C	N	O	S	0	0	0
			9231	5865	1579	1728	59			
1	D	1257	Total	C	N	O	S	0	0	0
			9289	5892	1602	1739	56			

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

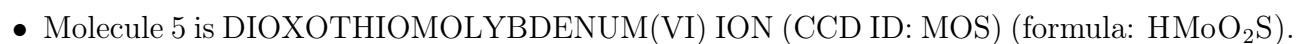
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		
2	B	1	Total	Na	0	0
			1	1		
2	C	1	Total	Na	0	0
			1	1		
2	D	1	Total	Na	0	0
			1	1		

- Molecule 3 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



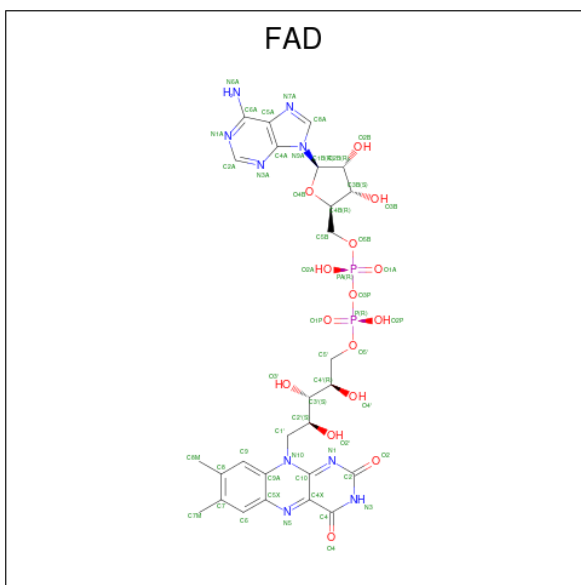
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	B	1	Total	Fe	S	0	0
			4	2	2		
3	B	1	Total	Fe	S	0	0
			4	2	2		
3	C	1	Total	Fe	S	0	0
			4	2	2		
3	C	1	Total	Fe	S	0	0
			4	2	2		
3	D	1	Total	Fe	S	0	0
			4	2	2		
3	D	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 4 is PHOSPHONIC ACIDMONO-(2-AMINO-5,6-DIMERCAPTO-4-OXO-3,7,8A, 9,10,10A-HEXAHYDRO-4H-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-7-YLMETHYL) ESTER (CCD ID: MTE) (formula: C₁₀H₁₄N₅O₆PS₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total 4	Mo 1	O 2	S 1	0	0
5	B	1	Total 4	Mo 1	O 2	S 1	0	0
5	C	1	Total 4	Mo 1	O 2	S 1	0	0
5	D	1	Total 4	Mo 1	O 2	S 1	0	0

- Molecule 6 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

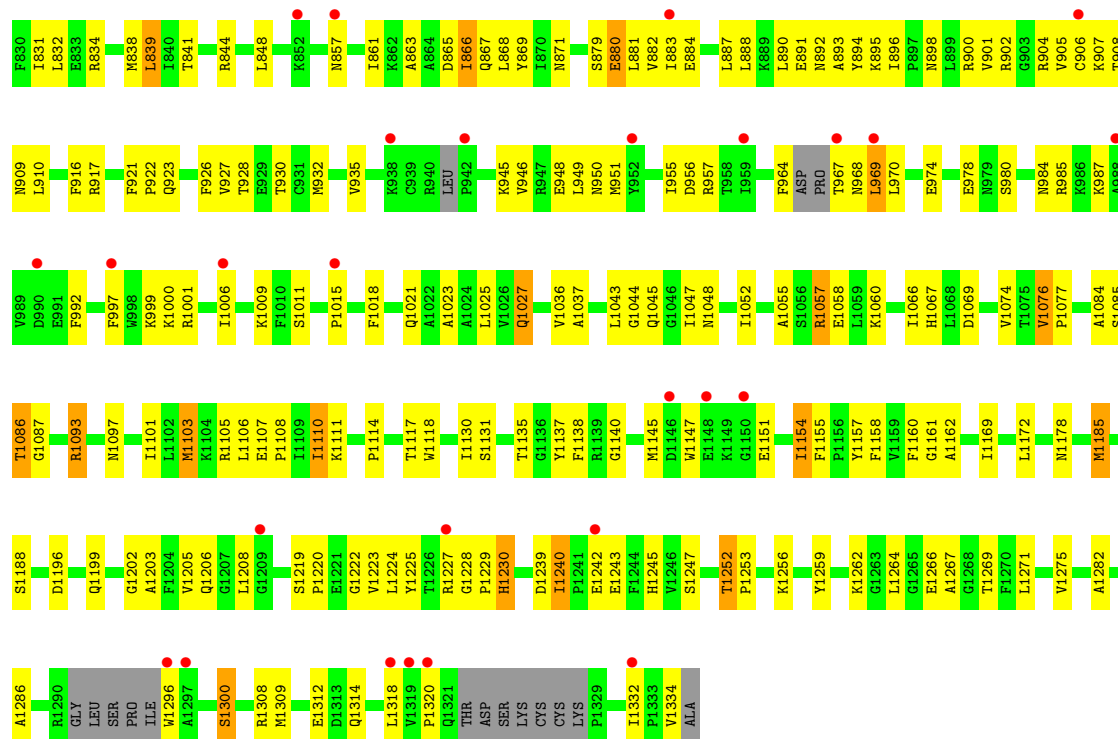
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	182	Total O 182 182	0	0
7	B	166	Total O 166 166	0	0

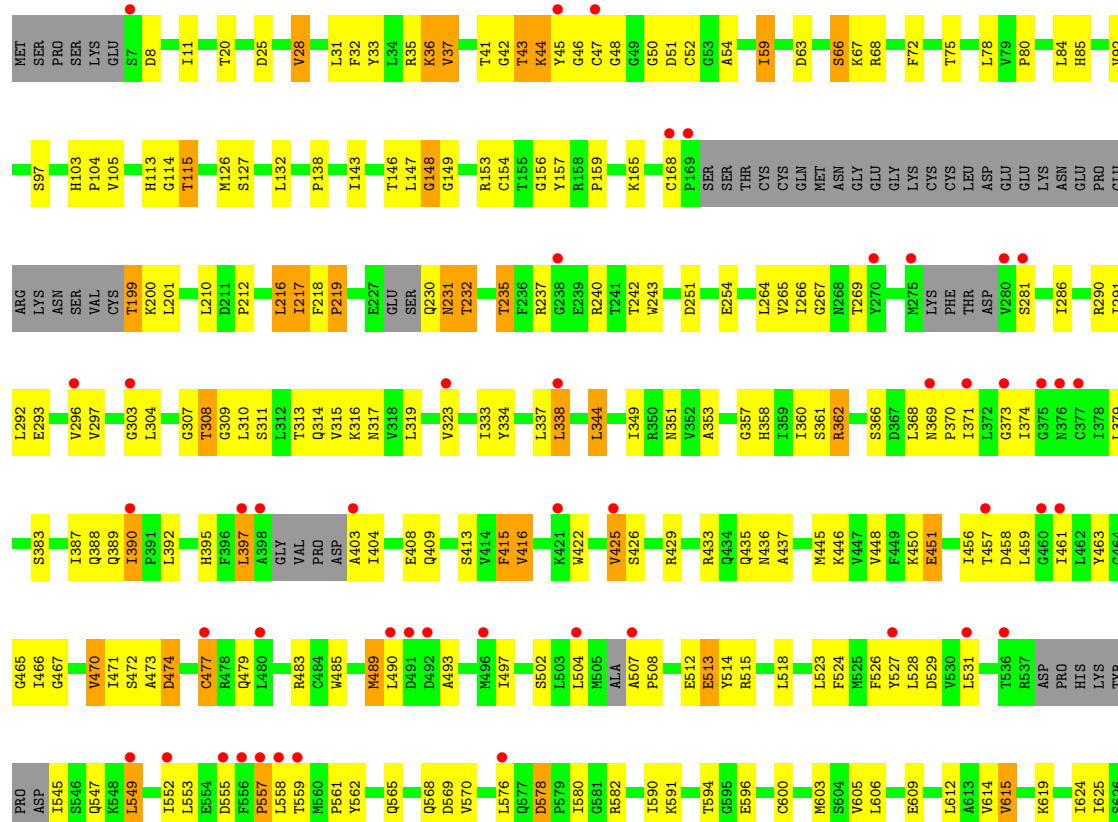
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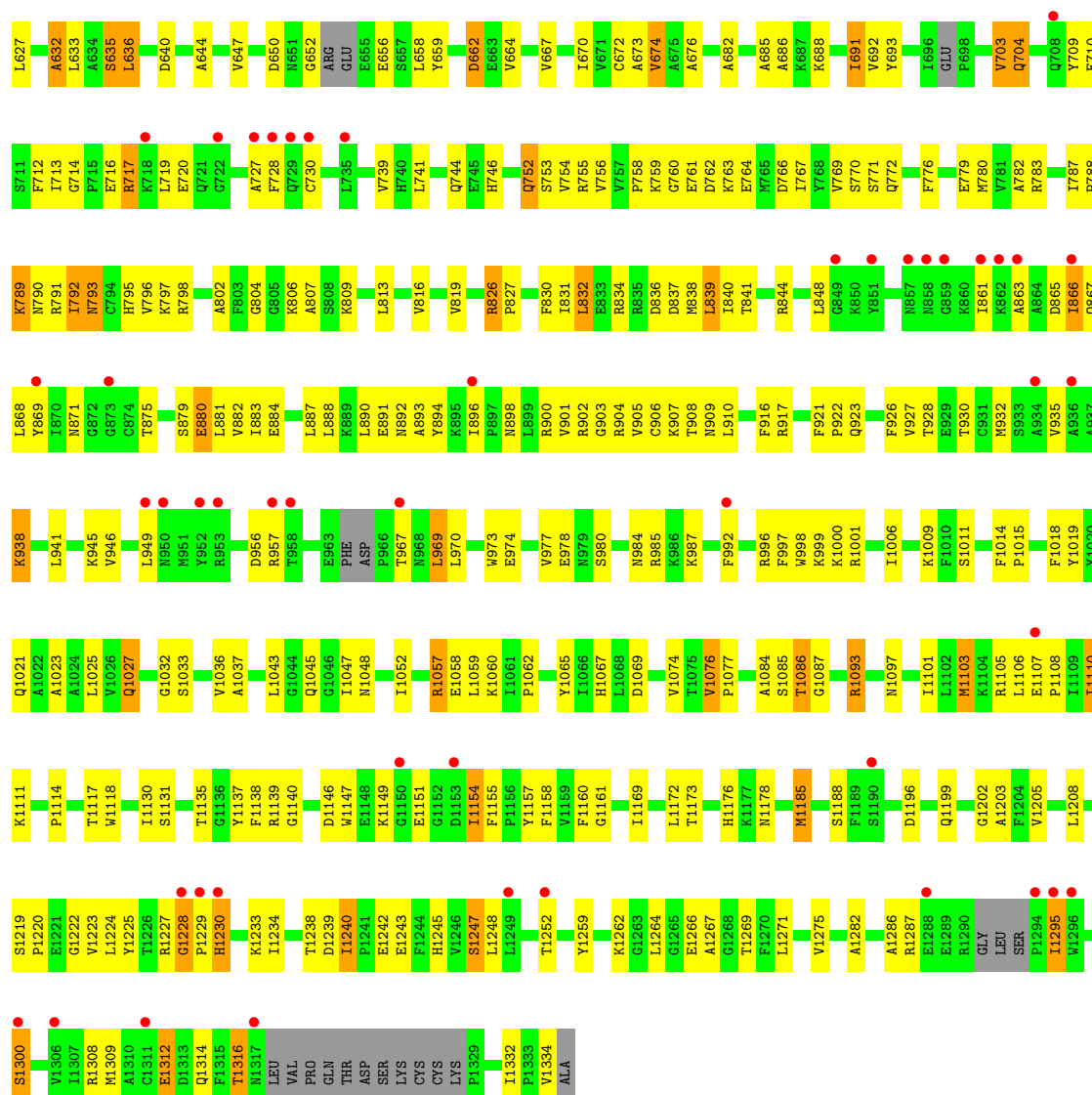
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	147	Total 147	O 147	0	0
7	D	155	Total 155	O 155	0	0

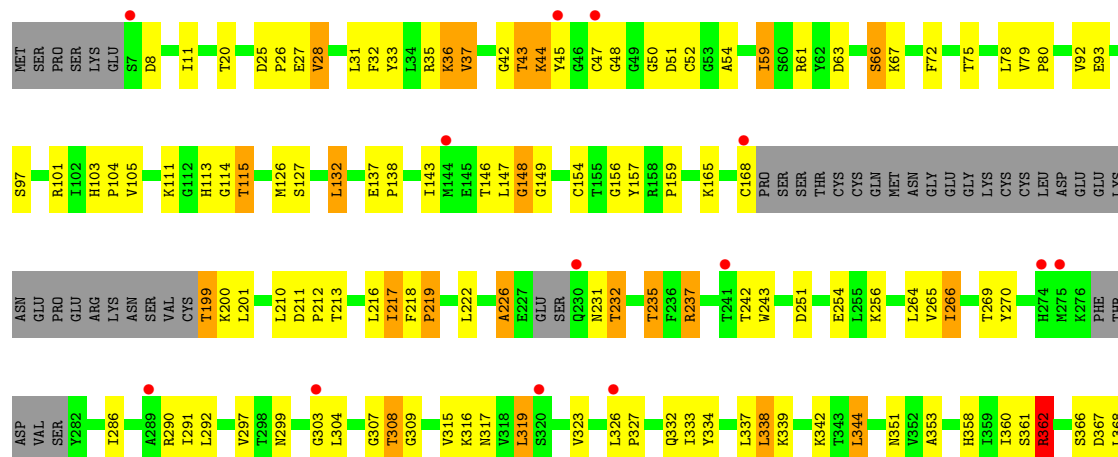


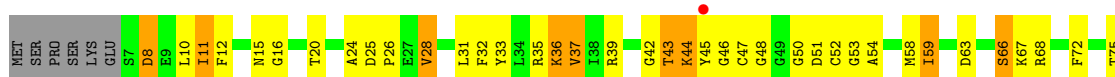
• Molecule 1: AOX3



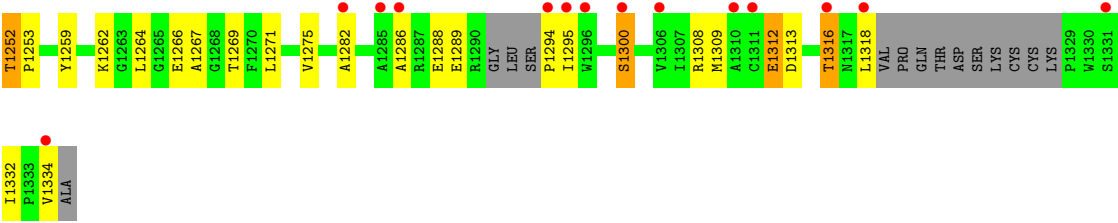


• Molecule 1: AOX3









4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	90.88Å 135.27Å 147.37Å 78.16° 77.72° 89.90°	Depositor
Resolution (Å)	49.91 – 2.54 49.91 – 2.54	Depositor EDS
% Data completeness (in resolution range)	75.0 (49.91-2.54) 75.0 (49.91-2.54)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.54Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.256 , 0.285 0.251 , 0.280	Depositor DCC
R_{free} test set	8336 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	35.6	Xtriage
Anisotropy	0.770	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 69.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.35$, $\langle L^2 \rangle = 0.18$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	38315	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.96% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FAD, NA, MTE, FES, MOS

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	0.40	0/9482	0.81	14/12869 (0.1%)
1	B	0.40	0/9650	0.82	16/13097 (0.1%)
1	C	0.39	0/9398	0.81	14/12757 (0.1%)
1	D	0.40	0/9460	0.80	12/12852 (0.1%)
All	All	0.40	0/37990	0.81	56/51575 (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
1	B	0	1
1	C	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	941	LEU	CA-C-N	10.62	131.32	120.38
1	B	941	LEU	C-N-CA	10.62	131.32	120.38
1	B	826	ARG	N-CA-C	8.57	115.70	108.07
1	C	619	LYS	CB-CG-CD	8.54	130.95	111.30
1	B	558	LEU	N-CA-C	-8.30	93.99	108.69

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	557	PRO	Peptide
1	B	557	PRO	Peptide
1	C	226	ALA	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	9314	0	9046	454	0
1	B	9471	0	9271	465	0
1	C	9231	0	8962	429	0
1	D	9289	0	8958	462	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	8	0	0	1	0
3	B	8	0	0	1	0
3	C	8	0	0	1	0
3	D	8	0	0	2	0
4	A	24	0	10	4	0
4	B	24	0	10	1	0
4	C	24	0	10	3	0
4	D	24	0	10	3	0
5	A	4	0	0	2	0
5	B	4	0	0	2	0
5	C	4	0	0	2	0
5	D	4	0	0	2	0
6	A	53	0	31	8	0
6	B	53	0	31	14	0
6	C	53	0	31	20	0
6	D	53	0	31	15	0
7	A	182	0	0	93	0
7	B	166	0	0	67	0
7	C	147	0	0	56	0
7	D	155	0	0	92	0
All	All	38315	0	36401	1775	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 24.

The worst 5 of 1775 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)
6:B:3005:FAD:H9	6:B:3005:FAD:O2'	1.48	1.12
1:A:308:THR:HG21	6:A:3005:FAD:N6A	1.62	1.11
1:B:308:THR:HG21	6:B:3005:FAD:N6A	1.67	1.09
1:A:496:MET:SD	7:A:2076:HOH:O	2.12	1.07
1:D:12:PHE:HB3	7:D:2002:HOH:O	1.55	1.06

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	1221/1335 (92%)	1123 (92%)	89 (7%)	9 (1%)	18	25
1	B	1238/1335 (93%)	1137 (92%)	93 (8%)	8 (1%)	21	29
1	C	1210/1335 (91%)	1111 (92%)	88 (7%)	11 (1%)	14	20
1	D	1231/1335 (92%)	1120 (91%)	104 (8%)	7 (1%)	21	29
All	All	4900/5340 (92%)	4491 (92%)	374 (8%)	35 (1%)	18	25

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	398	ALA
1	B	762	ASP
1	C	398	ALA
1	C	474	ASP
1	A	762	ASP

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	958/1129 (85%)	856 (89%)	102 (11%)	6	7
1	B	988/1129 (88%)	879 (89%)	109 (11%)	6	6
1	C	948/1129 (84%)	853 (90%)	95 (10%)	7	9
1	D	941/1129 (83%)	845 (90%)	96 (10%)	7	8
All	All	3835/4516 (85%)	3433 (90%)	402 (10%)	6	8

5 of 402 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	242	THR
1	C	1047	ILE
1	D	1288	GLU
1	C	319	LEU
1	C	619	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1097	ASN
1	D	752	GLN
1	C	587	GLN
1	D	721	GLN
1	D	1091	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 4 are monoatomic - leaving 20 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
6	FAD	C	3005	-	58,58,58	1.46	10 (17%)	85,89,89	1.54	16 (18%)
6	FAD	D	3005	-	58,58,58	1.44	8 (13%)	85,89,89	1.56	15 (17%)
6	FAD	A	3005	-	58,58,58	1.44	9 (15%)	85,89,89	1.56	16 (18%)
6	FAD	B	3005	-	58,58,58	1.45	9 (15%)	85,89,89	1.69	21 (24%)
5	MOS	A	3004	4	0,3,3	-	-	-		
5	MOS	B	3004	4	0,3,3	-	-	-		
5	MOS	C	3004	4	0,3,3	-	-	-		
3	FES	B	3002	1	0,4,4	-	-	-		
3	FES	A	3001	1	0,4,4	-	-	-		
4	MTE	D	3003	5	21,26,26	1.55	2 (9%)	19,40,40	1.93	5 (26%)
3	FES	B	3001	1	0,4,4	-	-	-		
5	MOS	D	3004	4	0,3,3	-	-	-		
3	FES	C	3001	1	0,4,4	-	-	-		
3	FES	A	3002	1	0,4,4	-	-	-		
3	FES	D	3002	1	0,4,4	-	-	-		
3	FES	D	3001	1	0,4,4	-	-	-		
3	FES	C	3002	1	0,4,4	-	-	-		
4	MTE	C	3003	5	21,26,26	1.55	3 (14%)	19,40,40	2.43	6 (31%)
4	MTE	B	3003	5	21,26,26	1.53	2 (9%)	19,40,40	2.25	7 (36%)
4	MTE	A	3003	5	21,26,26	1.50	2 (9%)	19,40,40	2.06	6 (31%)

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	FES	D	3001	1	-	-	0/1/1/1
4	MTE	D	3003	5	-	4/6/34/34	0/3/3/3
6	FAD	C	3005	-	-	17/34/50/50	0/6/6/6
6	FAD	D	3005	-	-	12/34/50/50	0/6/6/6
6	FAD	A	3005	-	-	8/34/50/50	0/6/6/6
6	FAD	B	3005	-	-	17/34/50/50	0/6/6/6
3	FES	B	3002	1	-	-	0/1/1/1
3	FES	A	3001	1	-	-	0/1/1/1
3	FES	C	3002	1	-	-	0/1/1/1
4	MTE	C	3003	5	-	0/6/34/34	0/3/3/3
3	FES	C	3001	1	-	-	0/1/1/1
3	FES	A	3002	1	-	-	0/1/1/1
4	MTE	B	3003	5	-	2/6/34/34	0/3/3/3
3	FES	B	3001	1	-	-	0/1/1/1
3	FES	D	3002	1	-	-	0/1/1/1
4	MTE	A	3003	5	-	0/6/34/34	0/3/3/3

The worst 5 of 45 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	3003	MTE	C9-C10	5.63	1.48	1.38
6	B	3005	FAD	C9A-C5X	5.35	1.49	1.41
6	C	3005	FAD	C9A-C5X	5.30	1.49	1.41
4	C	3003	MTE	C9-C10	5.28	1.47	1.38
4	A	3003	MTE	C9-C10	5.24	1.47	1.38

The worst 5 of 92 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	3003	MTE	O3'-C7-C6	-7.24	104.14	108.96
6	A	3005	FAD	C5A-C4A-N3A	-5.98	118.48	126.72
6	D	3005	FAD	C5A-C4A-N3A	-5.95	118.53	126.72
6	C	3005	FAD	C5A-C4A-N3A	-5.54	119.08	126.72
6	B	3005	FAD	C5A-C4A-N3A	-5.51	119.13	126.72

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	3003	MTE	C4'-O4'-P-O1P
4	D	3003	MTE	C4'-O4'-P-O2P

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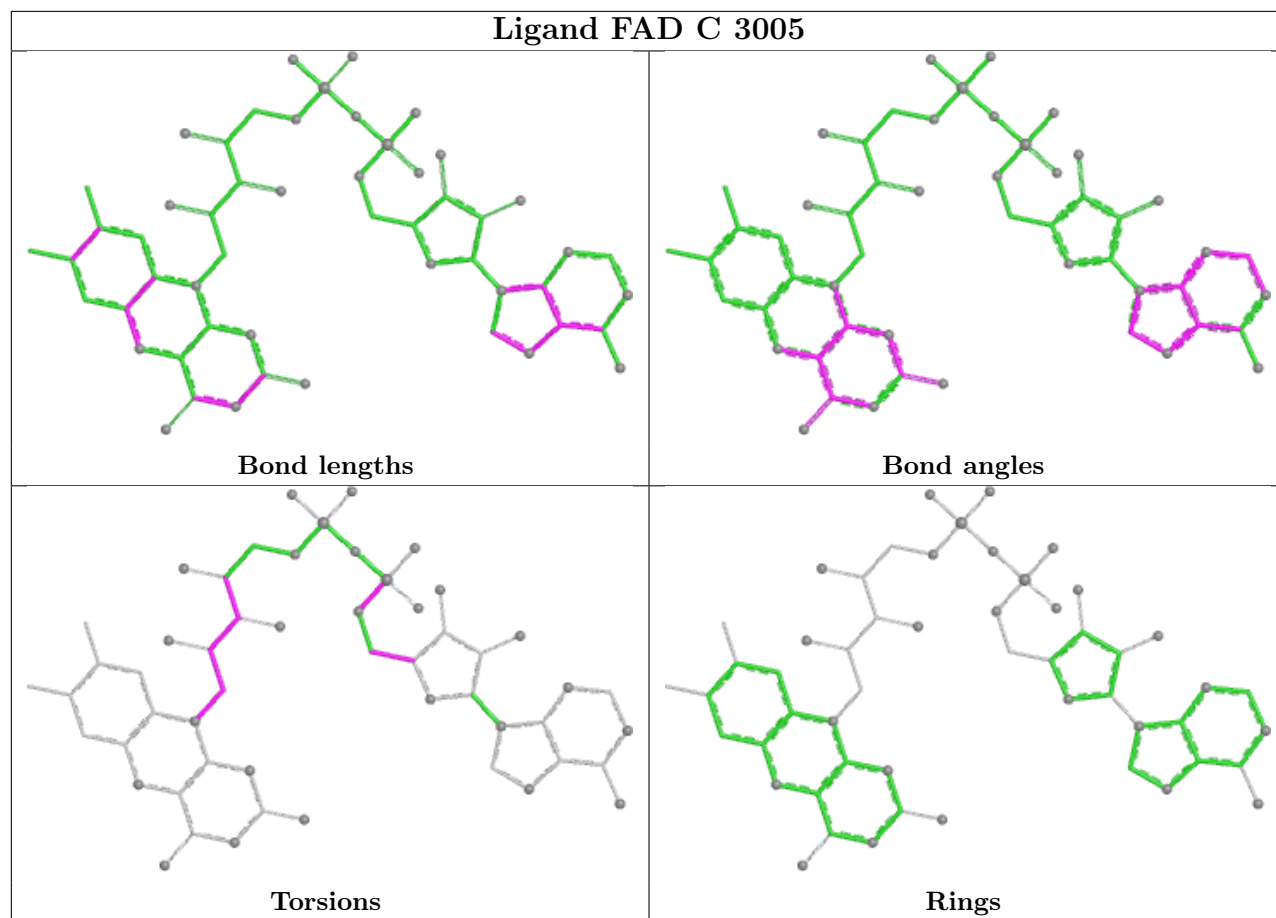
Mol	Chain	Res	Type	Atoms
4	D	3003	MTE	C4'-O4'-P-O3P
6	A	3005	FAD	C5B-O5B-PA-O2A
6	B	3005	FAD	C5B-O5B-PA-O1A

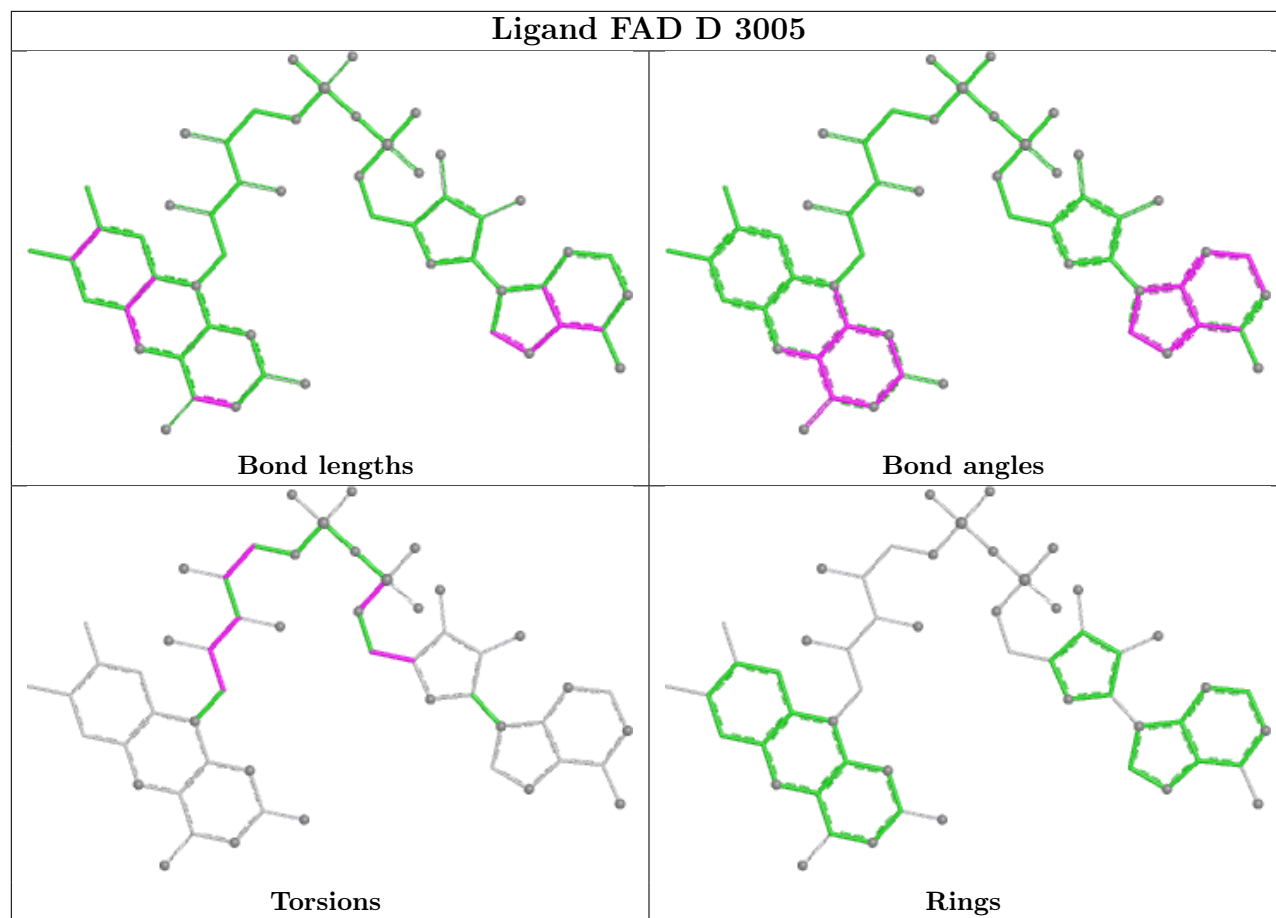
There are no ring outliers.

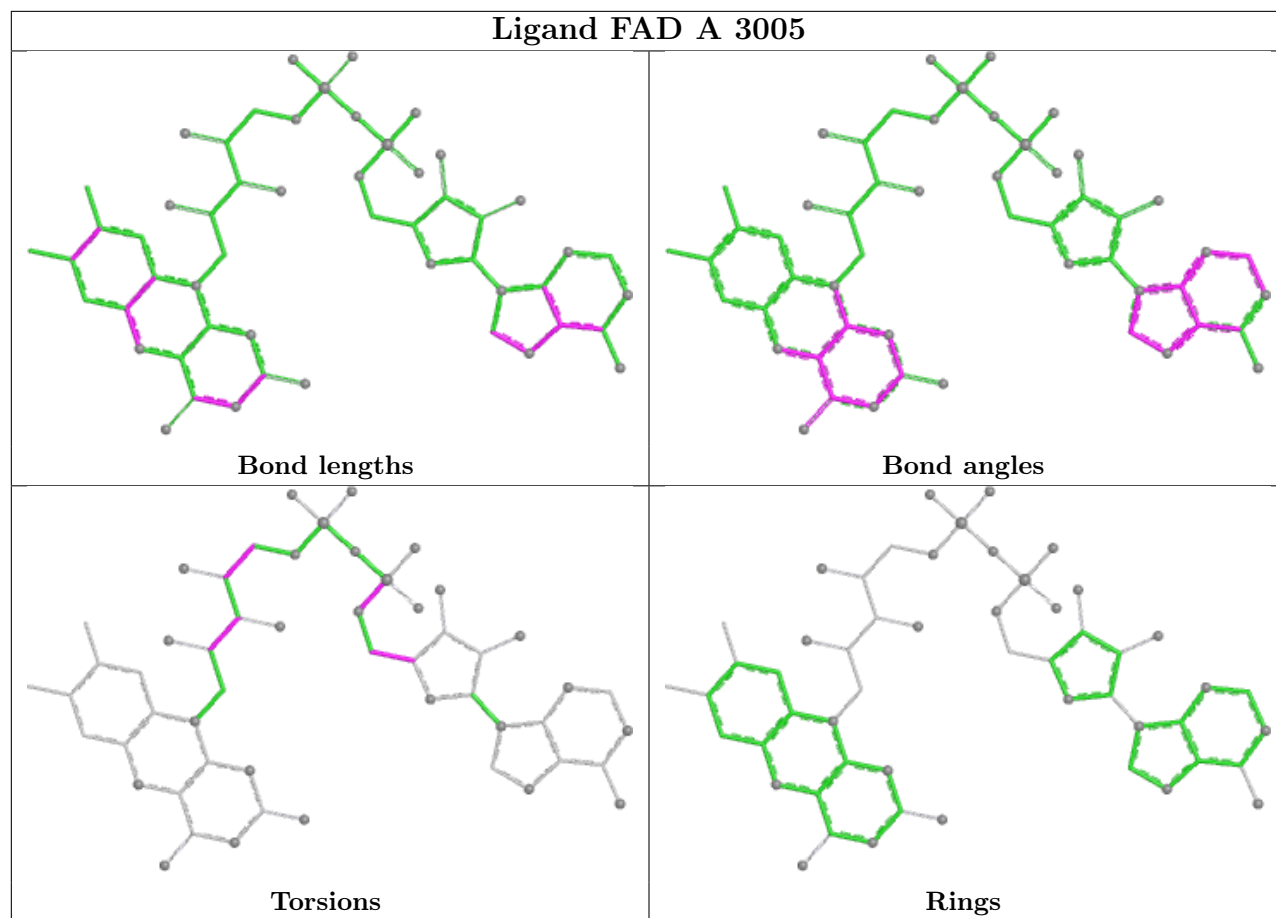
16 monomers are involved in 81 short contacts:

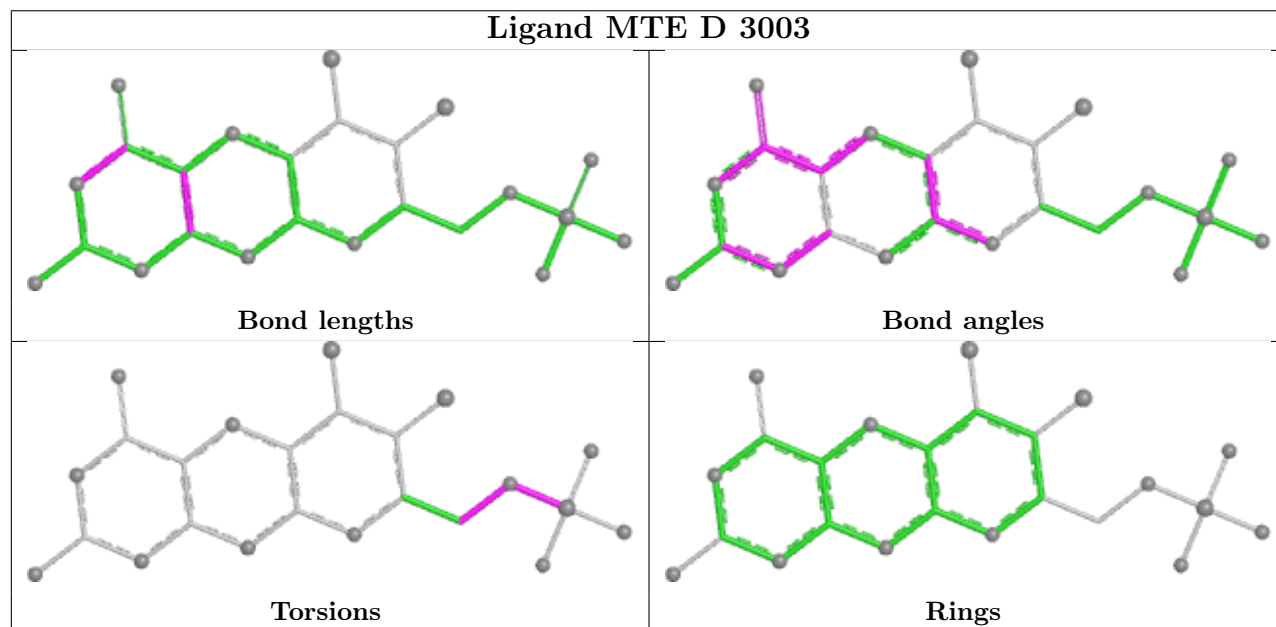
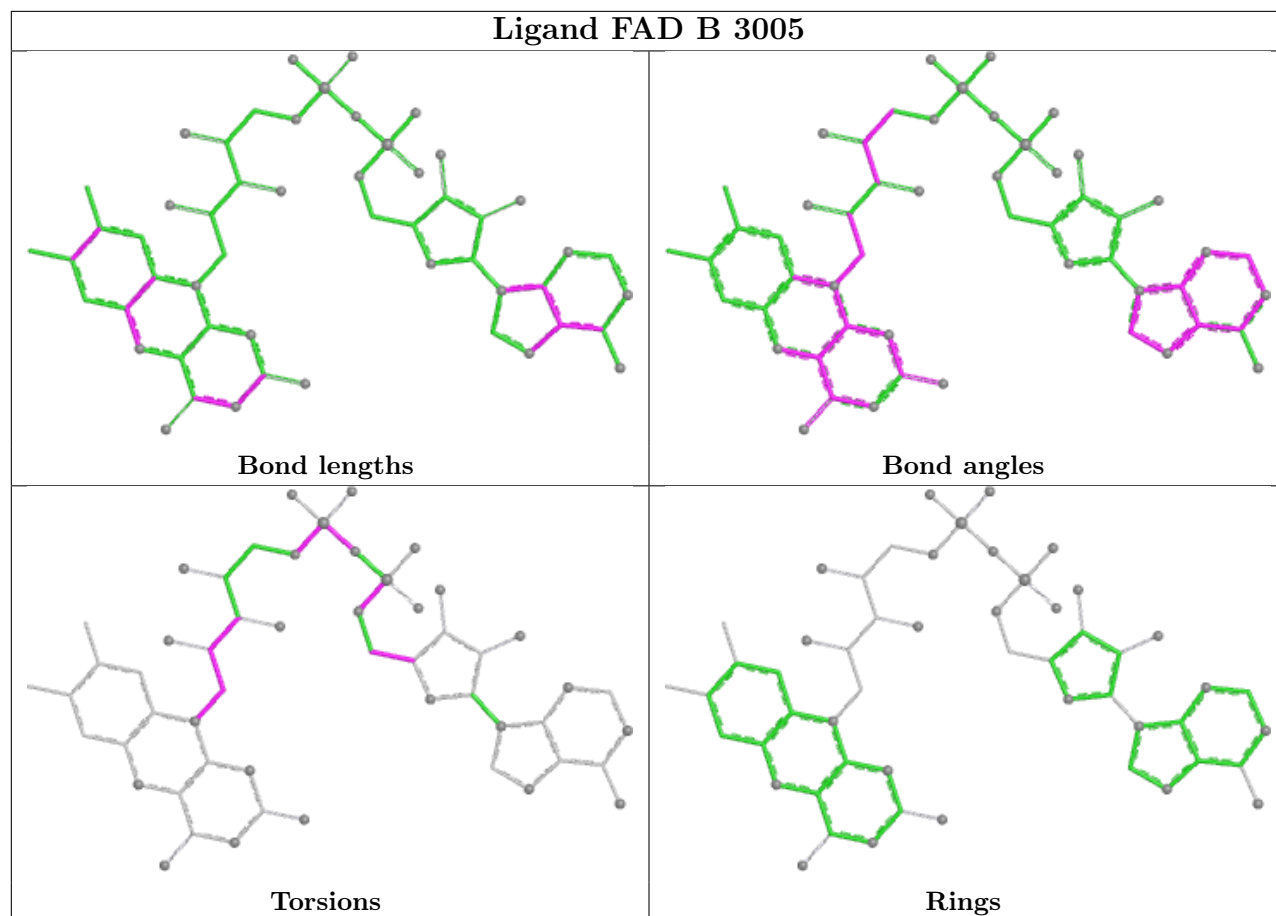
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	3005	FAD	20	0
6	D	3005	FAD	15	0
6	A	3005	FAD	8	0
6	B	3005	FAD	14	0
5	A	3004	MOS	2	0
5	B	3004	MOS	2	0
5	C	3004	MOS	2	0
3	B	3002	FES	1	0
4	D	3003	MTE	3	0
5	D	3004	MOS	2	0
3	A	3002	FES	1	0
3	D	3002	FES	2	0
3	C	3002	FES	1	0
4	C	3003	MTE	3	0
4	B	3003	MTE	1	0
4	A	3003	MTE	4	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.

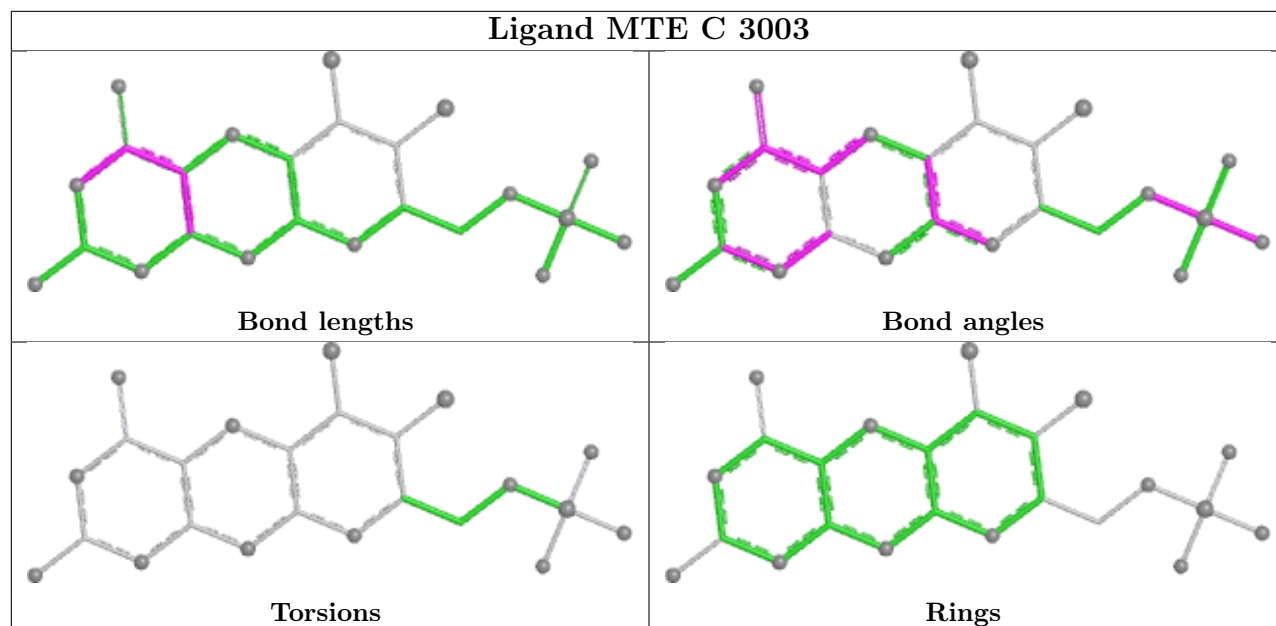




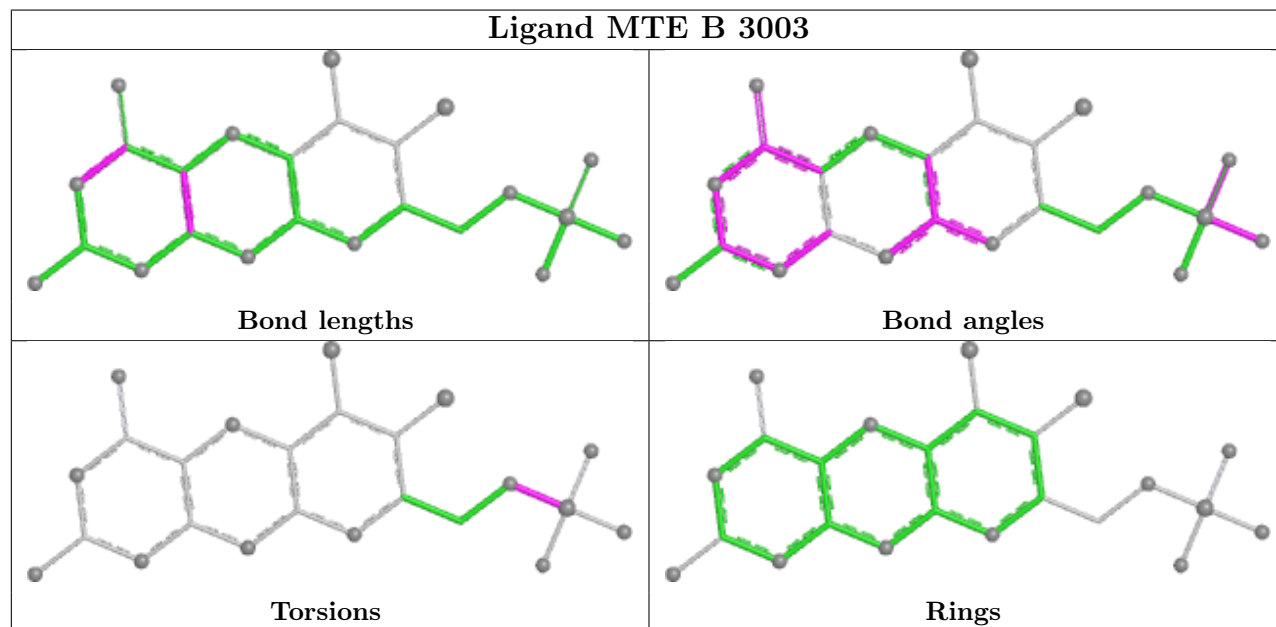


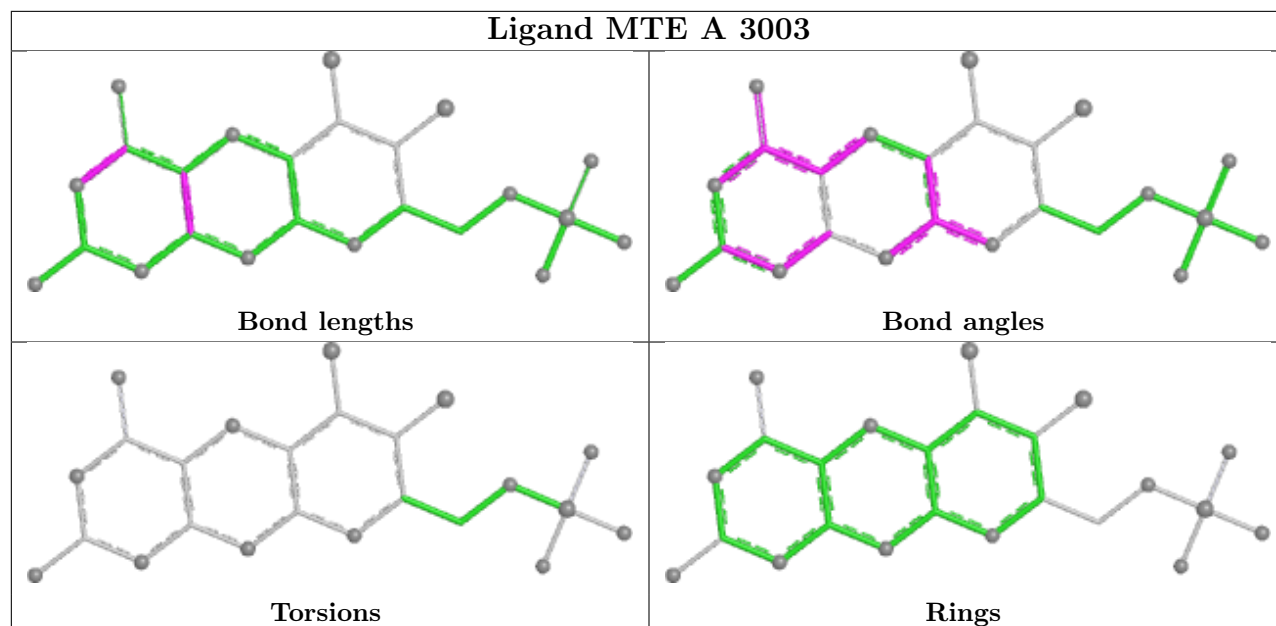


Ligand MTE C 3003



Ligand MTE B 3003





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	1253/1335 (93%)	0.62	95 (7%) 20 19	12, 40, 70, 88	0
1	B	1262/1335 (94%)	0.63	95 (7%) 20 19	10, 39, 67, 87	0
1	C	1244/1335 (93%)	0.72	95 (7%) 20 19	18, 43, 73, 99	0
1	D	1257/1335 (94%)	0.84	122 (9%) 13 12	20, 45, 79, 97	0
All	All	5016/5340 (93%)	0.70	407 (8%) 18 17	10, 42, 73, 99	0

The worst 5 of 407 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	477	CYS	5.5
1	D	278	THR	5.4
1	B	403	ALA	4.8
1	D	398	ALA	4.5
1	B	857	ASN	4.5

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 [i](#)

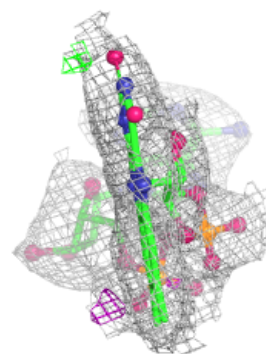
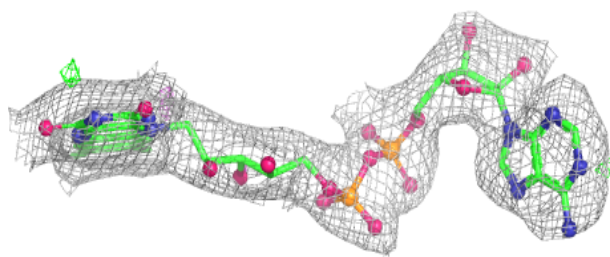
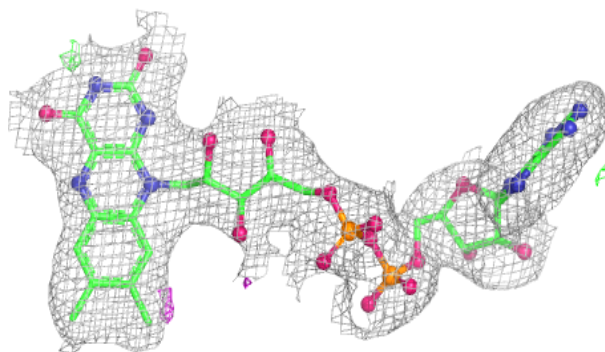
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NA	C	2337	1/1	0.86	0.12	50,50,50,50	0
2	NA	A	2337	1/1	0.90	0.09	26,26,26,26	0
2	NA	D	2337	1/1	0.93	0.08	17,17,17,17	0
6	FAD	D	3005	53/53	0.93	0.09	6,33,46,53	0
6	FAD	C	3005	53/53	0.94	0.10	9,31,49,50	0
6	FAD	B	3005	53/53	0.94	0.09	7,31,43,51	0
6	FAD	A	3005	53/53	0.95	0.08	9,28,45,49	0
4	MTE	B	3003	24/24	0.95	0.09	15,35,49,67	0
2	NA	B	2337	1/1	0.96	0.06	12,12,12,12	0
4	MTE	D	3003	24/24	0.96	0.08	13,33,49,53	0
4	MTE	A	3003	24/24	0.96	0.08	12,27,37,42	0
4	MTE	C	3003	24/24	0.97	0.08	7,32,46,61	0
5	MOS	D	3004	4/4	0.97	0.10	42,55,69,77	0
5	MOS	B	3004	4/4	0.98	0.09	42,55,69,77	0
3	FES	C	3001	4/4	0.98	0.04	24,24,31,39	0
3	FES	A	3001	4/4	0.99	0.03	19,20,23,26	0
5	MOS	A	3004	4/4	0.99	0.07	42,55,69,77	0
3	FES	C	3002	4/4	0.99	0.07	29,33,36,38	0
5	MOS	C	3004	4/4	0.99	0.09	42,55,69,77	0
3	FES	D	3001	4/4	0.99	0.02	15,23,23,26	0
3	FES	D	3002	4/4	0.99	0.03	15,24,25,41	0
3	FES	A	3002	4/4	0.99	0.04	16,23,33,38	0
3	FES	B	3001	4/4	0.99	0.02	7,20,22,26	0
3	FES	B	3002	4/4	0.99	0.03	20,21,34,38	0

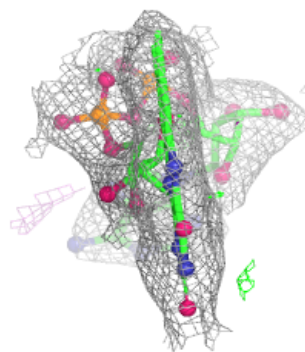
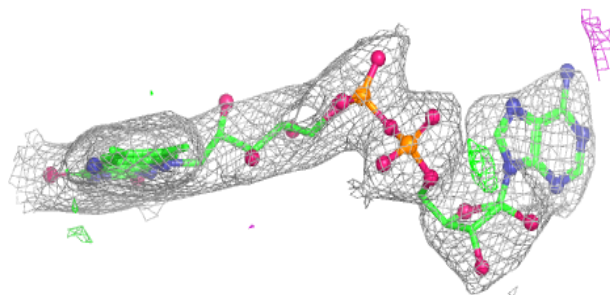
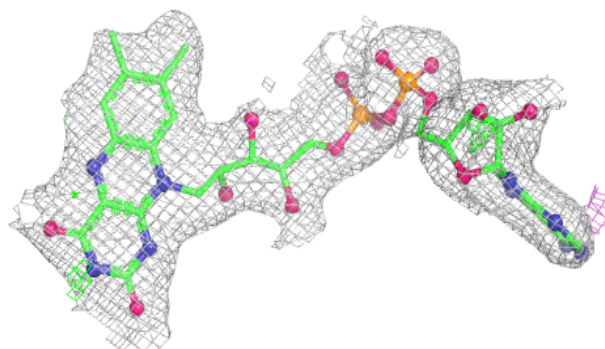
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FAD D 3005:

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

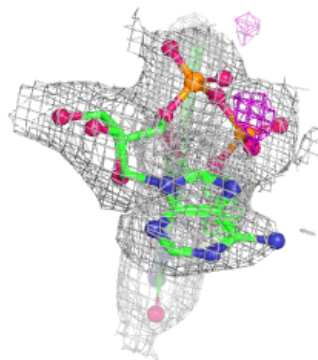
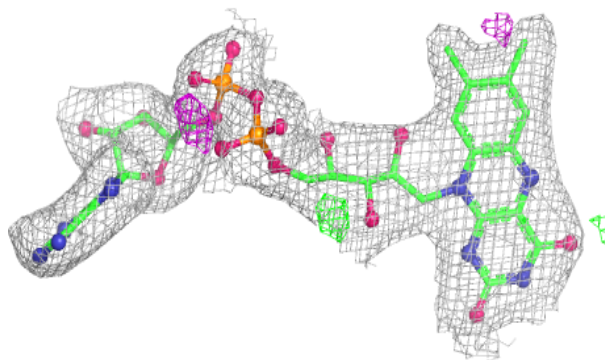
**Electron density around FAD C 3005:**

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

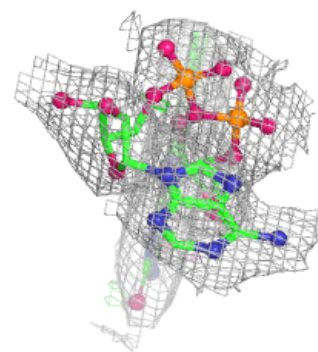
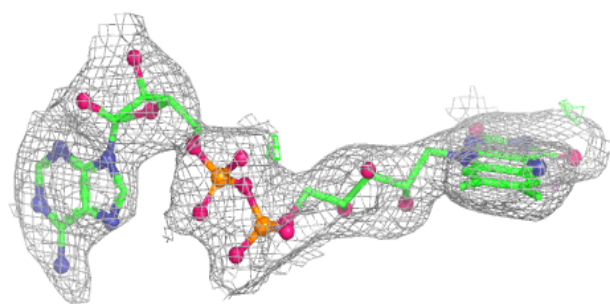
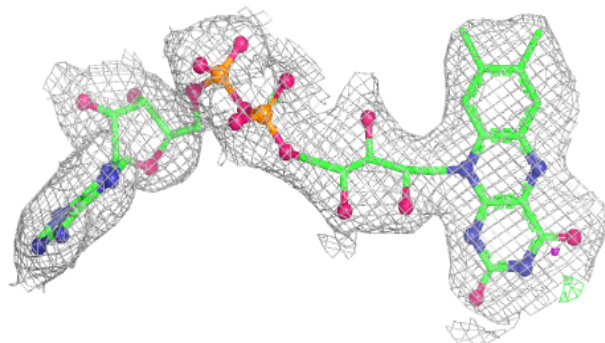


Electron density around FAD B 3005:

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

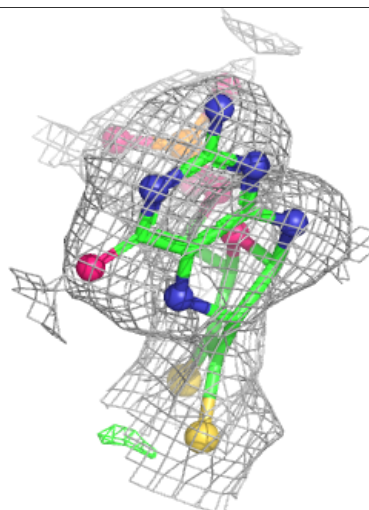
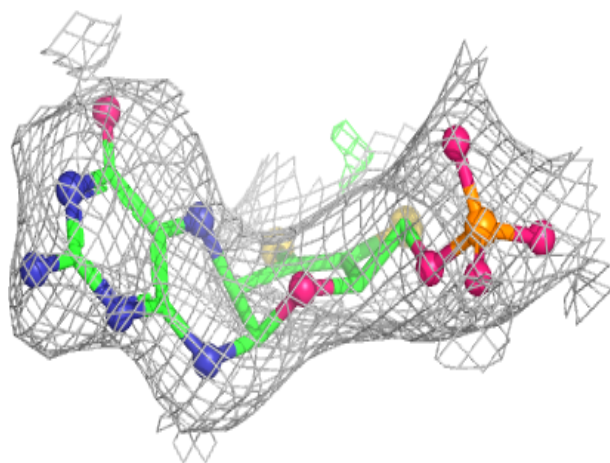
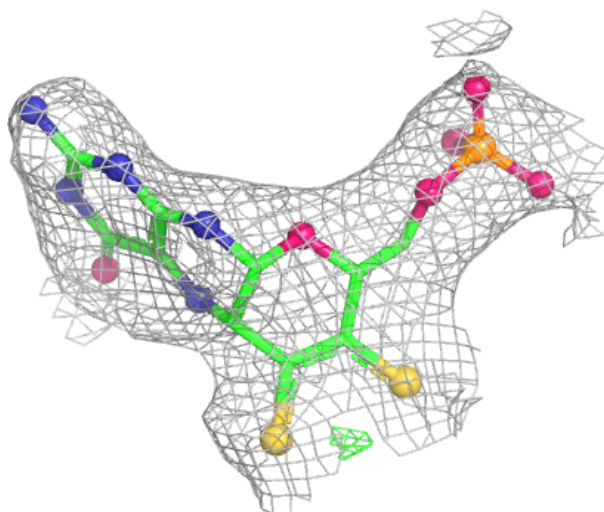
**Electron density around FAD A 3005:**

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



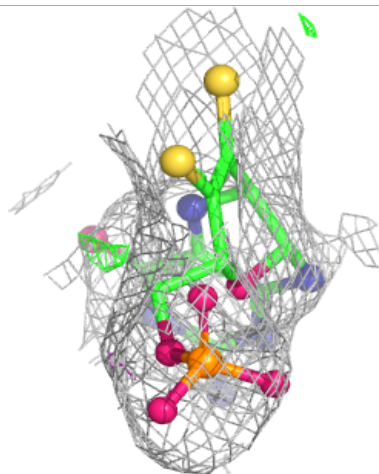
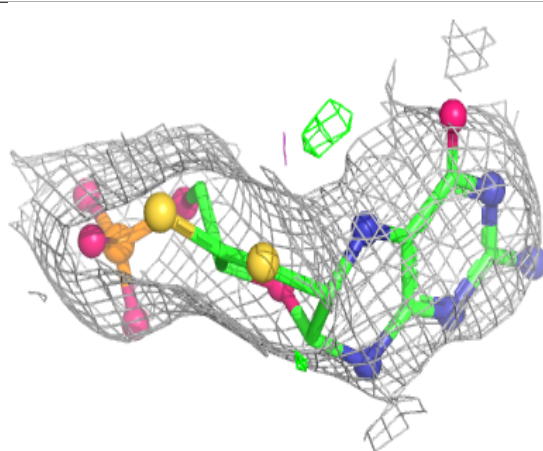
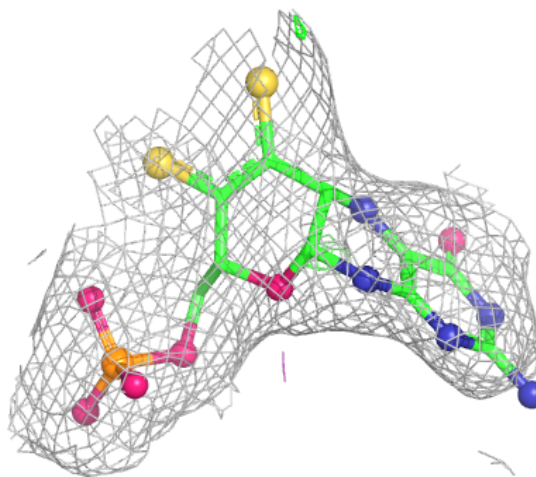
Electron density around MTE B 3003:

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



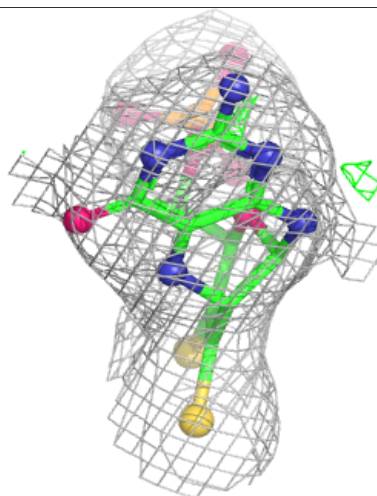
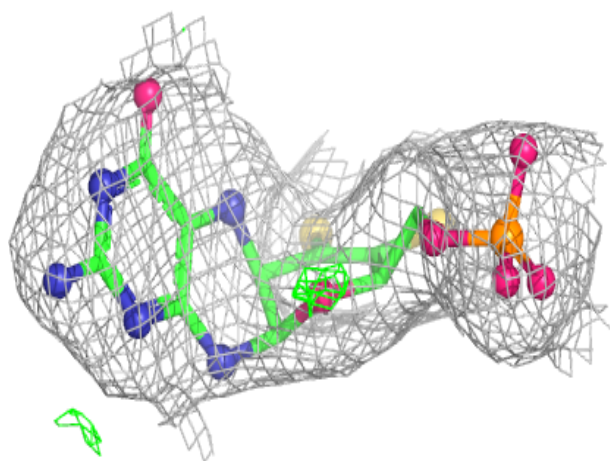
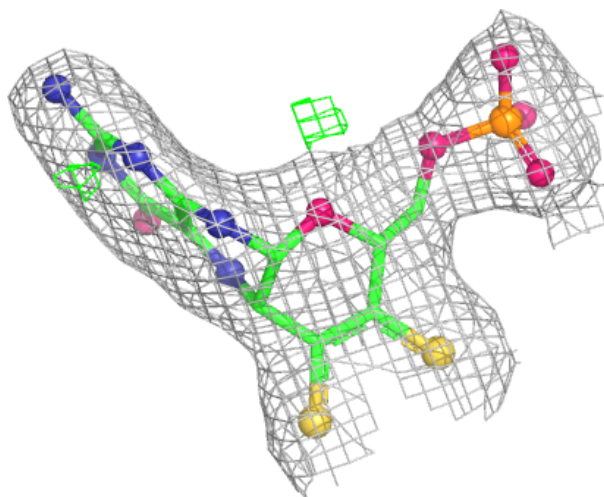
Electron density around MTE D 3003:

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



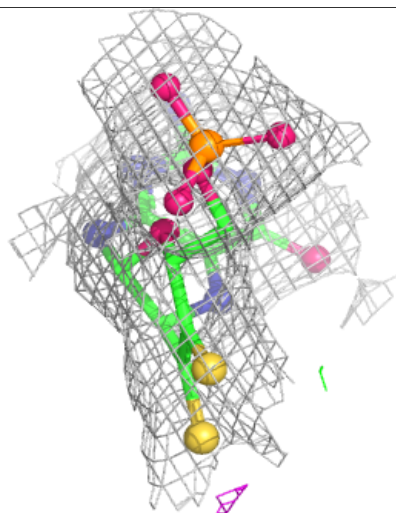
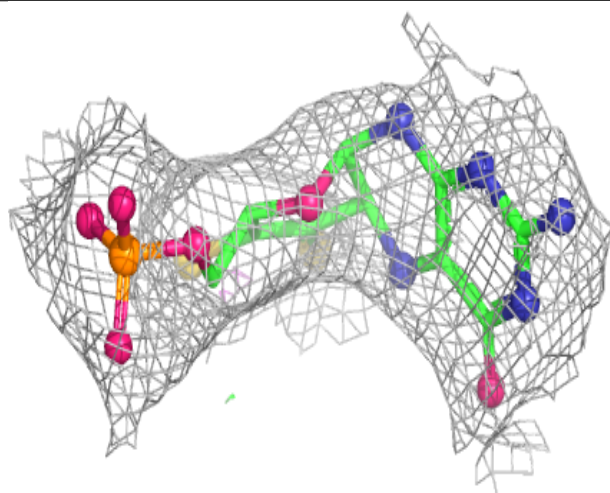
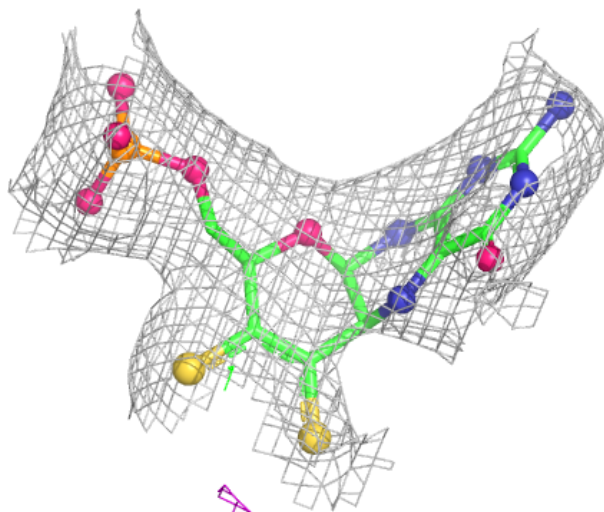
Electron density around MTE A 3003:

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



Electron density around MTE C 3003:

$2mF_o-DF_c$ (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.