W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

May 16, 2020 – 05:09 am BST

PDB ID	:	3BDJ
Title	:	Crystal Structure of Bovine Milk Xanthine Dehydrogenase with a Covalently Bound Oxipurinol Inhibitor
Authors	:	Eger, B.T.; Okamoto, K.; Nishino, T.; Pai, E.F.; Nishino, T.
Deposited on	:	2007-11-14
Resolution	:	2.00 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 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	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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.
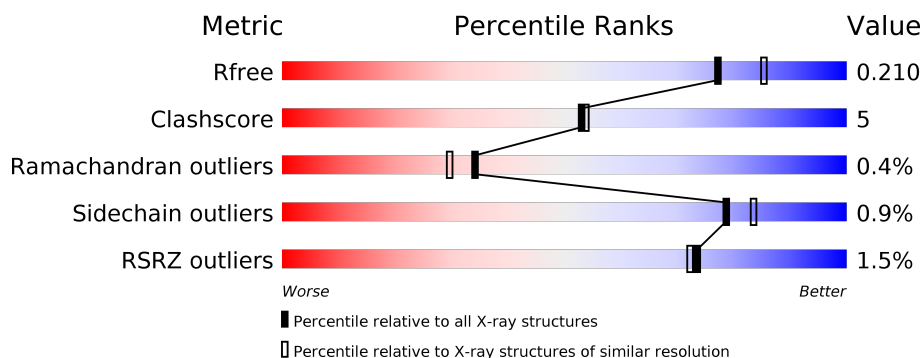
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	1332	84% ... 12% ··
1	B	1332	83% ... 13% ·

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	B	4002	-	-	X	-

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 21626 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 Xanthine dehydrogenase/oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1286	Total	C	N	O	S	0	0	0
			9991	6354	1712	1865	60			
1	B	1286	Total	C	N	O	S	0	0	0
			9991	6354	1712	1865	60			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	552	HIS	ASP	SEE REMARK 999	UNP P80457
B	552	HIS	ASP	SEE REMARK 999	UNP P80457

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Ca	0	0
			1	1		
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).

FES

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		

- 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 (three-letter code: MTE) (formula: $C_{10}H_{14}N_5O_6PS_2$).
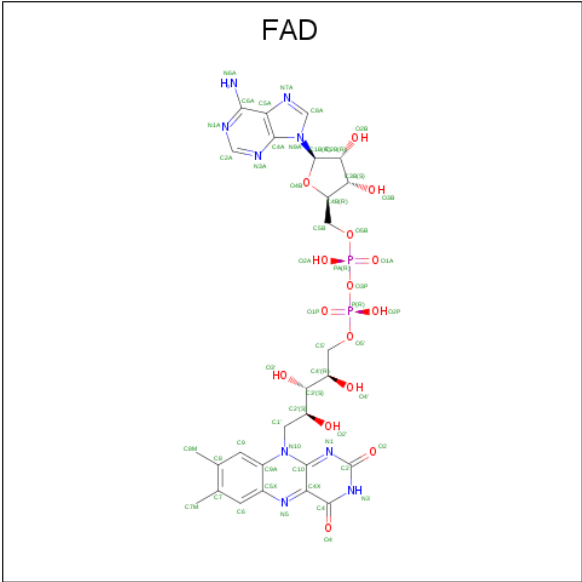

MTE
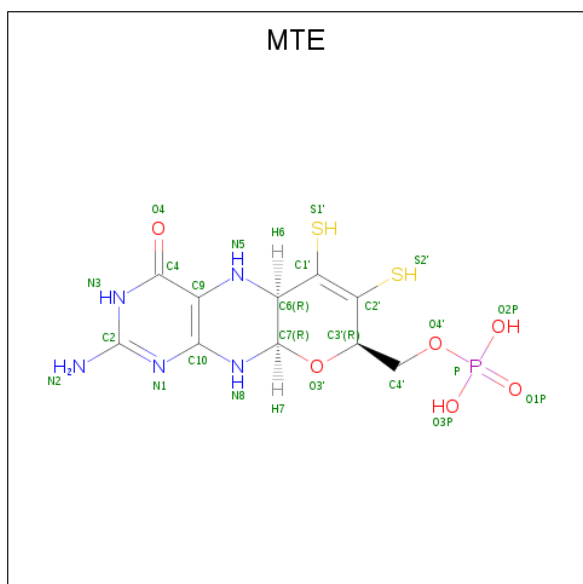
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
4	B	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		

- Molecule 5 is Oxo(sulfanyl)molybdenum(IV) ION (three-letter code: MOW) (formula: $HMoOS$).
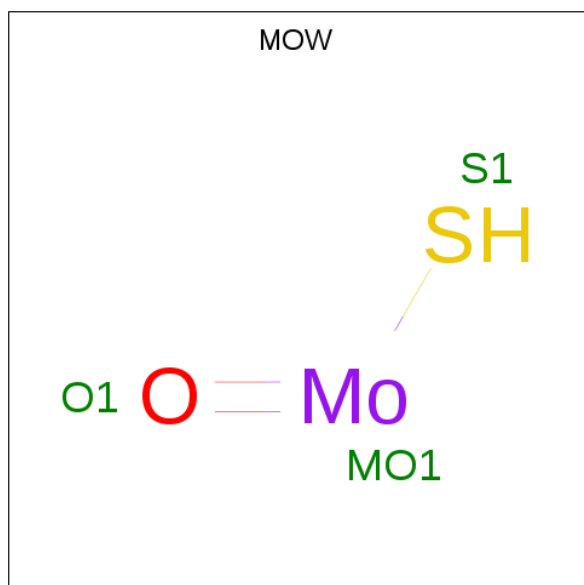
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	Mo	O	S	0	0
			3	1	1	1		
5	B	1	Total	Mo	O	S	0	0
			3	1	1	1		

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

FAD

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

• Molecule 7 is Oxypurinol (three-letter code: 141) (formula: $C_5H_4N_4O_2$).

141
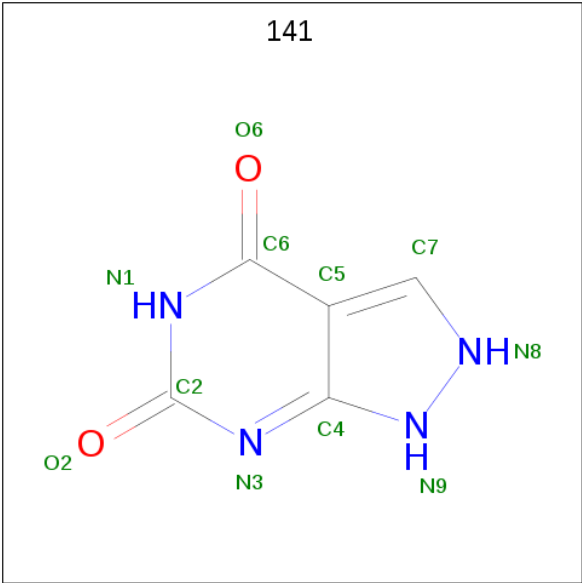
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			11	5	4	2		
7	B	1	Total	C	N	O	0	0
			11	5	4	2		

• Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total 6	C 3	O 3	0	0
8	A	1	Total 6	C 3	O 3	0	0
8	A	1	Total 6	C 3	O 3	0	0
8	B	1	Total 6	C 3	O 3	0	0
8	B	1	Total 6	C 3	O 3	0	0
8	B	1	Total 6	C 3	O 3	0	0
8	B	1	Total 6	C 3	O 3	0	0

• Molecule 9 is CARBONATE ION (three-letter code: CO3) (formula: CO_3).
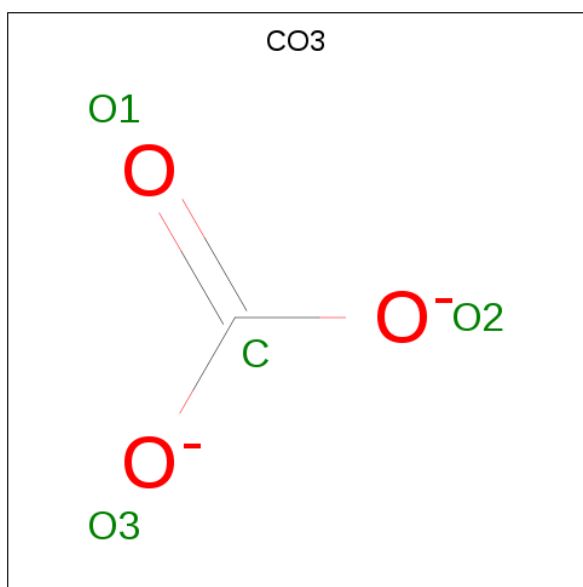
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total C O			0	0
			4	1	3		
9	B	1	Total C O			0	0
			4	1	3		

• Molecule 10 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	706	Total O		0	0
			706	706		
10	B	688	Total O		0	0
			688	688		

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Xanthine dehydrogenase/oxidase

- Molecule 1: Xanthine dehydrogenase/oxidase
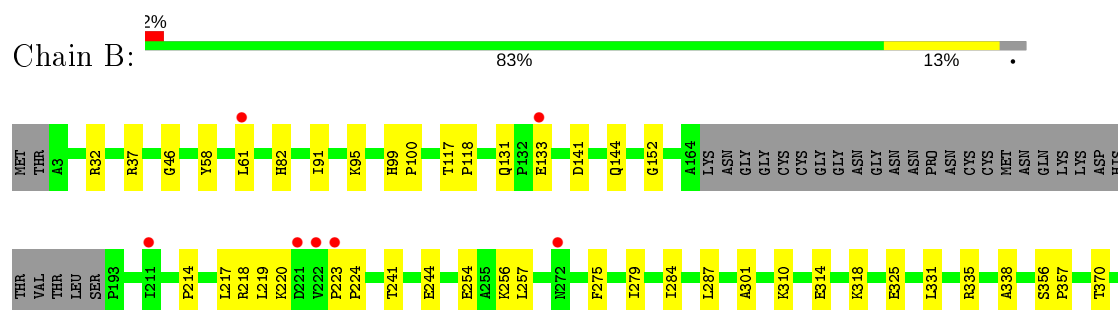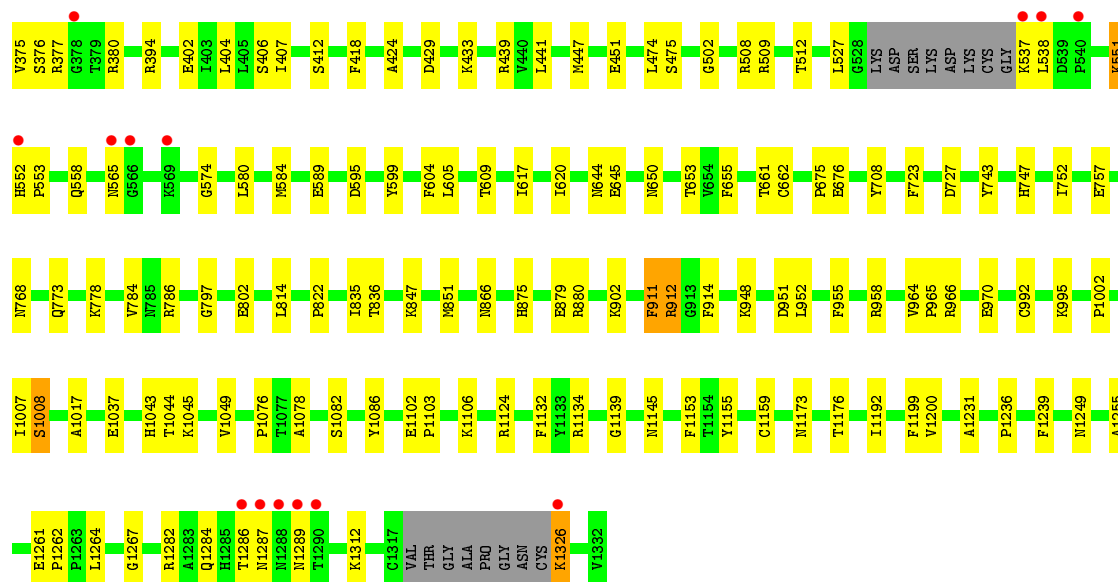
4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	166.52Å 124.07Å 148.80Å 90.00° 91.01° 90.00°	Depositor
Resolution (Å)	19.96 – 2.00 19.96 – 2.00	Depositor EDS
% Data completeness (in resolution range)	89.6 (19.96-2.00) 89.2 (19.96-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	1.29 (at 1.99Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.191 , 0.224 0.180 , 0.210	Depositor DCC
R_{free} test set	2424 reflections (1.26%)	wwPDB-VP
Wilson B-factor (Å^2)	16.7	Xtriage
Anisotropy	0.575	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 59.4	EDS
L-test for twinning [2]	$<|L|> = 0.49, <L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	21626	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.11% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CO3, 141, CA, MOW, FES, FAD, MTE

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	0.33	0/10210	0.60	0/13818
1	B	0.32	0/10210	0.60	0/13818
All	All	0.33	0/20420	0.60	0/27636

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (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	9991	0	9991	106	0
1	B	9991	0	9991	117	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	8	0	0	1	0
3	B	8	0	0	2	0
4	A	24	0	10	1	0
4	B	24	0	10	1	0
5	A	3	0	0	1	0
5	B	3	0	0	1	0
6	A	53	0	31	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	53	0	31	0	0
7	A	11	0	3	2	0
7	B	11	0	3	2	0
8	A	18	0	24	0	0
8	B	24	0	32	1	0
9	A	4	0	0	0	0
9	B	4	0	0	0	0
10	A	706	0	0	4	0
10	B	688	0	0	4	0
All	All	21626	0	20126	216	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 5.

The worst 5 of 216 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:757:GLU:H	1:B:584:MET:HE3	1.21	1.01
1:B:551:LYS:HD2	1:B:551:LYS:H	1.33	0.92
1:B:1326:LYS:HZ2	1:B:1326:LYS:N	1.68	0.91
1:B:131:GLN:HE21	1:B:133:GLU:H	1.18	0.90
1:B:404:LEU:HD21	1:B:407:ILE:HD11	1.53	0.88

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	1278/1332 (96%)	1238 (97%)	35 (3%)	5 (0%)	34	30
1	B	1278/1332 (96%)	1232 (96%)	41 (3%)	5 (0%)	34	30
All	All	2556/2664 (96%)	2470 (97%)	76 (3%)	10 (0%)	34	30

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1008	SER
1	B	1008	SER
1	A	912	ARG
1	B	1139	GLY
1	A	1139	GLY

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	1091/1128 (97%)	1080 (99%)	11 (1%)	76	81
1	B	1091/1128 (97%)	1082 (99%)	9 (1%)	81	86
All	All	2182/2256 (97%)	2162 (99%)	20 (1%)	78	83

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1239	PHE
1	A	1326	LYS
1	B	911	PHE
1	A	1002	PRO
1	A	1145	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1284	GLN
1	B	351	ASN
1	B	1284	GLN
1	B	130	ASN
1	B	131	GLN

5.3.3   RNA (i)

There are no RNA molecules in this entry.

5.4   Non-standard residues in protein, DNA, RNA chains (i)

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

5.5   Carbohydrates (i)

There are no carbohydrates in this entry.

5.6   Ligand geometry (i)

Of 23 ligands modelled in this entry, 2 are monoatomic - leaving 21 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
3	FES	B	4001	1	0,4,4	0.00	-	-		
6	FAD	A	3005	-	51,58,58	3.37	20 (39%)	60,89,89	2.79	16 (26%)
3	FES	A	3001	1	0,4,4	0.00	-	-		
6	FAD	B	4005	-	51,58,58	3.37	19 (37%)	60,89,89	2.79	16 (26%)
7	141	B	5102	-	10,12,12	1.84	2 (20%)	4,17,17	12.10	4 (100%)
8	GOL	B	5004	-	5,5,5	0.64	0	5,5,5	0.36	0
8	GOL	B	5003	-	5,5,5	0.61	0	5,5,5	0.37	0
4	MTE	B	4003	5	21,26,26	2.59	8 (38%)	21,40,40	3.32	7 (33%)
8	GOL	A	5006	-	5,5,5	0.64	0	5,5,5	0.34	0
4	MTE	A	3003	5	21,26,26	2.60	8 (38%)	21,40,40	3.32	8 (38%)
9	CO3	A	5201	-	0,3,3	0.00	-	0,3,3	0.00	-
7	141	A	5101	-	10,12,12	1.88	2 (20%)	4,17,17	12.04	4 (100%)
8	GOL	A	5005	-	5,5,5	0.67	0	5,5,5	0.43	0
8	GOL	B	5001	-	5,5,5	0.64	0	5,5,5	0.32	0
5	MOW	B	4004	4	0,2,2	0.00	-	-		
3	FES	A	3002	1	0,4,4	0.00	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z|>2$	Counts	RMSZ	$\#|Z|>2$
5	MOW	A	3004	4	0,2,2	0.00	-	-		
3	FES	B	4002	1	0,4,4	0.00	-	-		
8	GOL	B	5002	-	5,5,5	0.61	0	5,5,5	0.45	0
8	GOL	A	5007	-	5,5,5	0.67	0	5,5,5	0.27	0
9	CO3	B	5202	-	0,3,3	0.00	-	0,3,3	0.00	-

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	B	4001	1	-	-	0/1/1/1
6	FAD	A	3005	-	-	6/30/50/50	0/6/6/6
3	FES	A	3001	1	-	-	0/1/1/1
6	FAD	B	4005	-	-	6/30/50/50	0/6/6/6
7	141	B	5102	-	-	-	0/2/2/2
8	GOL	B	5004	-	-	2/4/4/4	-
8	GOL	B	5003	-	-	2/4/4/4	-
4	MTE	B	4003	5	-	1/6/34/34	0/3/3/3
8	GOL	A	5006	-	-	0/4/4/4	-
4	MTE	A	3003	5	-	1/6/34/34	0/3/3/3
7	141	A	5101	-	-	-	0/2/2/2
8	GOL	A	5005	-	-	4/4/4/4	-
8	GOL	B	5001	-	-	0/4/4/4	-
3	FES	A	3002	1	-	-	0/1/1/1
3	FES	B	4002	1	-	-	0/1/1/1
8	GOL	B	5002	-	-	4/4/4/4	-
8	GOL	A	5007	-	-	0/4/4/4	-

The worst 5 of 59 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	4005	FAD	C4X-C10	12.32	1.51	1.38
6	A	3005	FAD	C4X-C10	12.20	1.51	1.38
6	A	3005	FAD	C9A-N10	9.60	1.51	1.38
6	B	4005	FAD	C9A-N10	9.37	1.51	1.38
6	B	4005	FAD	O4B-C1B	7.66	1.51	1.41

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	B	5102	141	C5-C6-N1	-18.72	111.35	124.40
7	A	5101	141	C5-C6-N1	-18.58	111.45	124.40
7	B	5102	141	C6-N1-C2	14.40	127.30	115.14
7	A	5101	141	C6-N1-C2	14.34	127.25	115.14
6	A	3005	FAD	C4-N3-C2	11.06	124.48	115.14

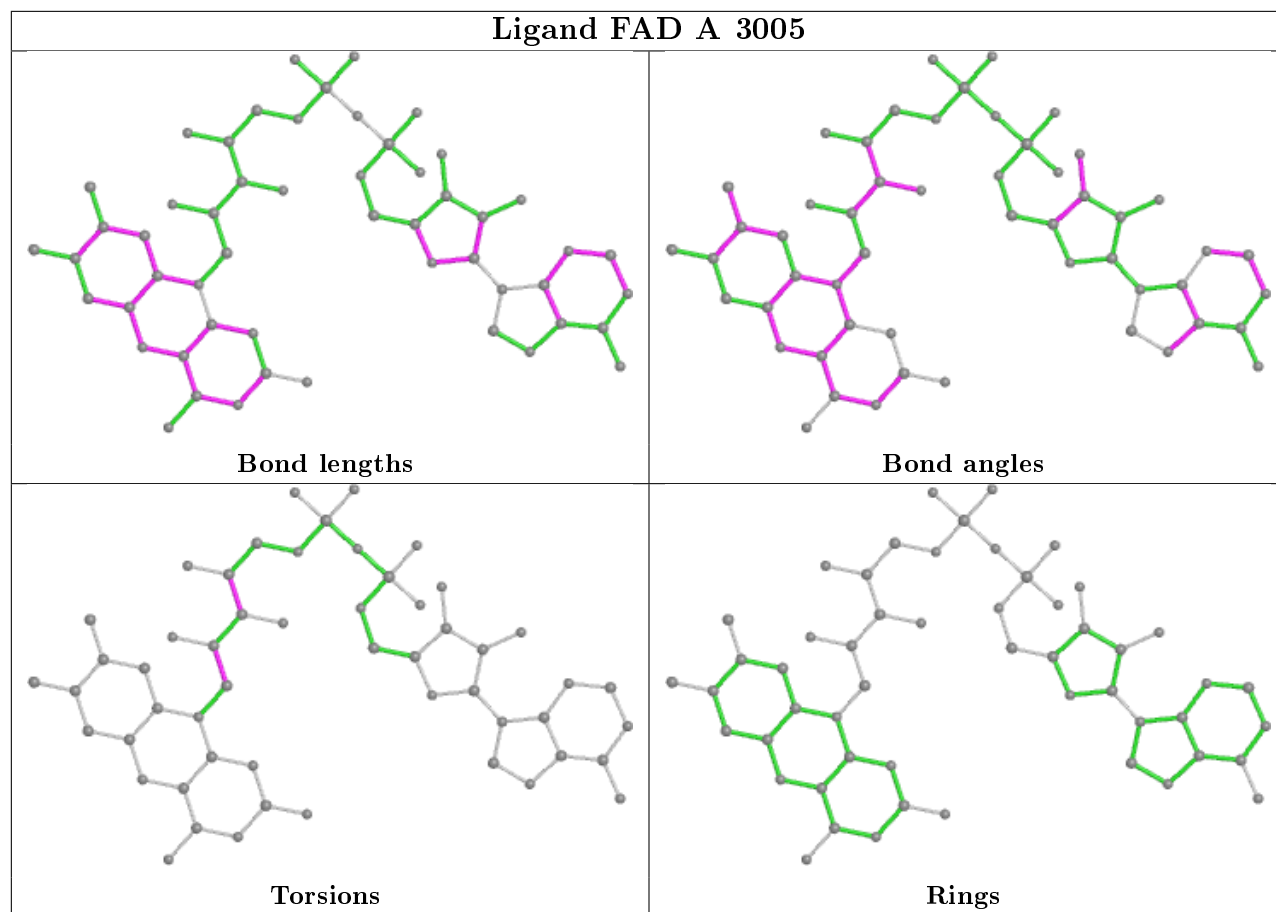There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	B	5002	GOL	O1-C1-C2-C3
8	B	5002	GOL	C1-C2-C3-O3
8	A	5005	GOL	O1-C1-C2-O2
8	A	5005	GOL	O1-C1-C2-C3
6	A	3005	FAD	N10-C1'-C2'-O2'

There are no ring outliers.

10 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	3005	FAD	1	0
7	B	5102	141	2	0
8	B	5003	GOL	1	0
4	B	4003	MTE	1	0
4	A	3003	MTE	1	0
7	A	5101	141	2	0
5	B	4004	MOW	1	0
3	A	3002	FES	1	0
5	A	3004	MOW	1	0
3	B	4002	FES	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 FAD A 3005

Bond lengths

Bond angles

Torsions

Rings

Ligand FAD B 4005

Bond lengths

Bond angles

Torsions

Rings

Ligand MTE B 4003

Bond lengths

Bond angles

Torsions

Rings

Ligand MTE A 3003

Bond lengths

Bond angles

Torsions

Rings
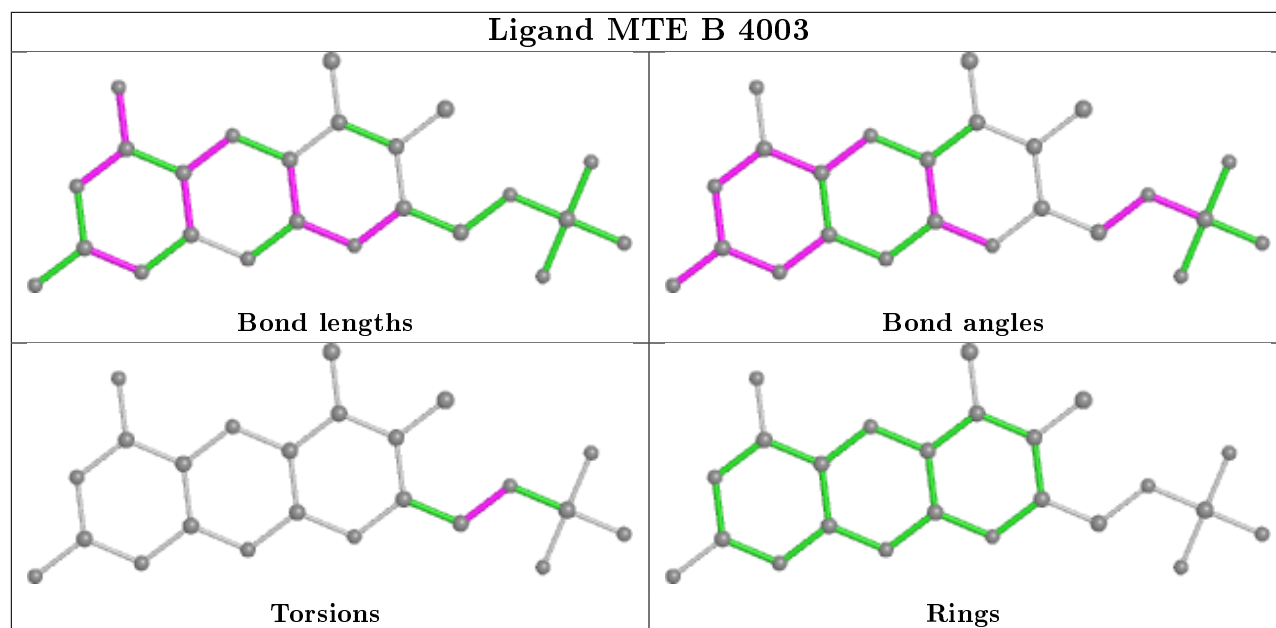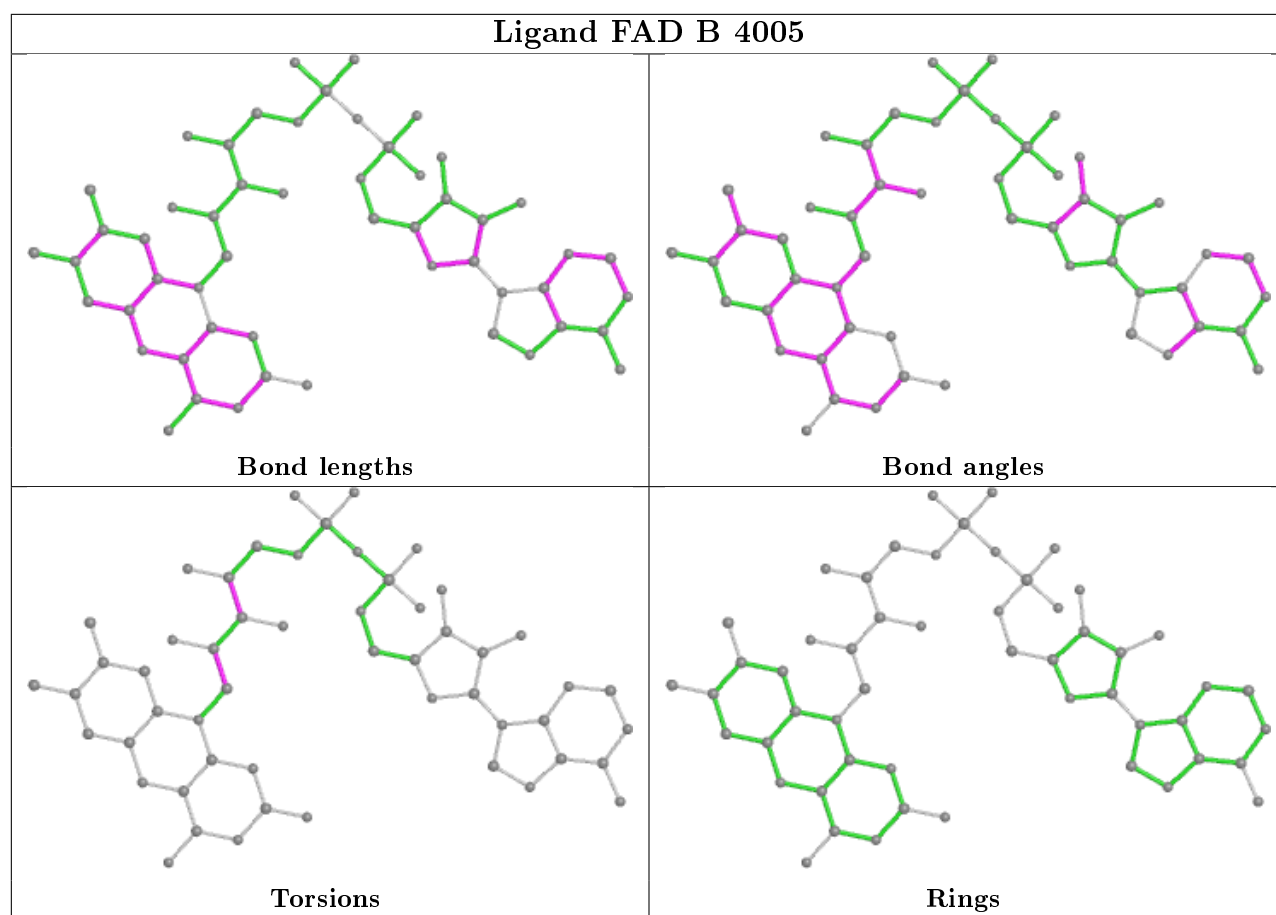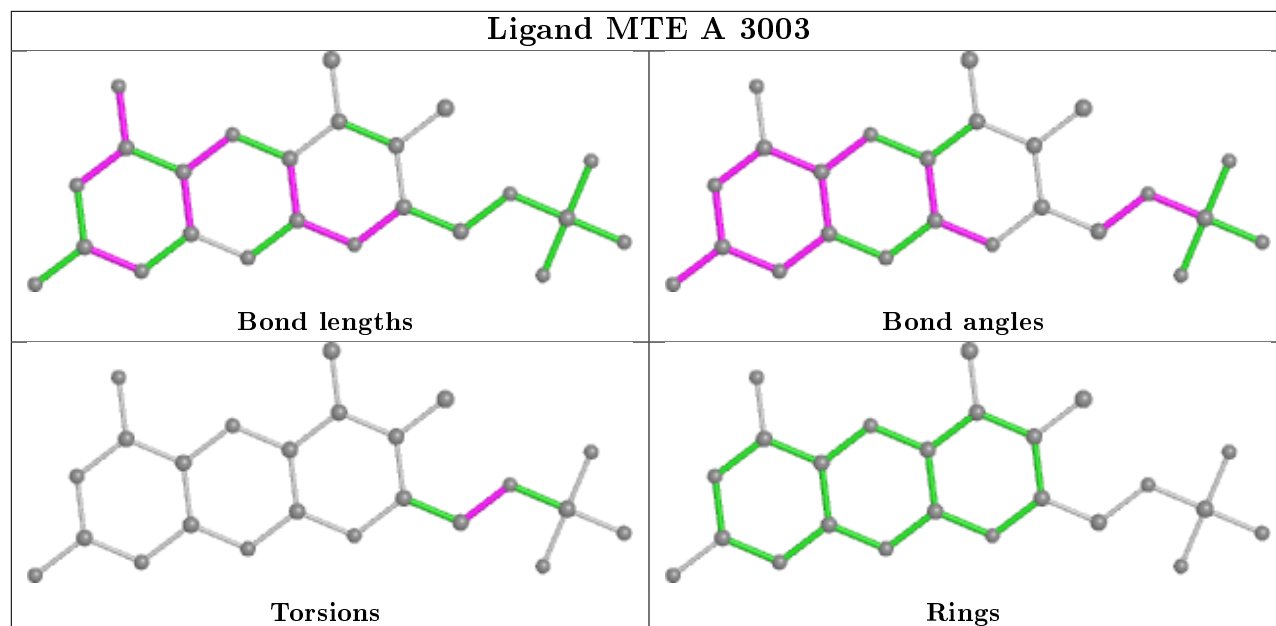
5.7 Other polymers (i)

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	1286/1332 (96%)	-0.31	17 (1%)	77	76	10, 19, 34, 57	0
1	B	1286/1332 (96%)	-0.29	21 (1%)	72	70	8, 19, 34, 56	0
All	All	2572/2664 (96%)	-0.30	38 (1%)	73	72	8, 19, 34, 57	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	565	ASN	7.3
1	B	1288	ASN	6.5
1	B	537	LYS	5.5
1	A	1288	ASN	5.3
1	B	566	GLY	5.1

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 carbohydrates 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(Å^2)	Q<0.9
8	GOL	B	5004	6/6	0.90	0.15	21,28,29,34	0
8	GOL	B	5002	6/6	0.92	0.15	20,23,25,25	0
8	GOL	B	5001	6/6	0.93	0.11	24,26,28,29	0
8	GOL	A	5005	6/6	0.93	0.12	18,19,19,20	0
8	GOL	A	5006	6/6	0.93	0.13	28,28,29,31	0
8	GOL	B	5003	6/6	0.93	0.15	29,30,31,33	0
8	GOL	A	5007	6/6	0.96	0.11	22,26,27,27	0
6	FAD	B	4005	53/53	0.97	0.08	12,15,20,22	0
7	141	B	5102	11/11	0.98	0.07	13,15,16,16	0
4	MTE	A	3003	24/24	0.98	0.07	10,12,15,17	0
4	MTE	B	4003	24/24	0.98	0.09	9,13,16,18	0
9	CO3	B	5202	4/4	0.98	0.07	14,15,15,17	0
7	141	A	5101	11/11	0.98	0.07	12,14,15,16	0
6	FAD	A	3005	53/53	0.98	0.08	12,16,20,23	0
3	FES	A	3001	4/4	0.99	0.05	11,11,13,13	0
2	CA	B	5302	1/1	0.99	0.03	15,15,15,15	0
9	CO3	A	5201	4/4	0.99	0.07	12,13,13,15	0
3	FES	B	4001	4/4	1.00	0.04	11,12,12,14	0
3	FES	A	3002	4/4	1.00	0.03	11,11,11,12	0
2	CA	A	5301	1/1	1.00	0.04	15,15,15,15	0
3	FES	B	4002	4/4	1.00	0.04	11,12,12,12	0
5	MOW	B	4004	3/3	1.00	0.03	13,13,14,16	0
5	MOW	A	3004	3/3	1.00	0.03	14,14,15,15	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.
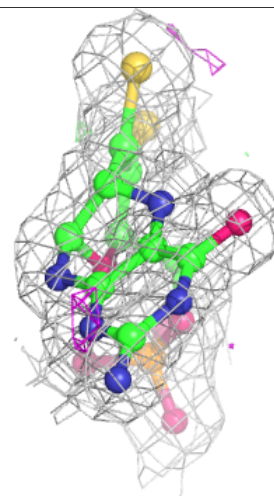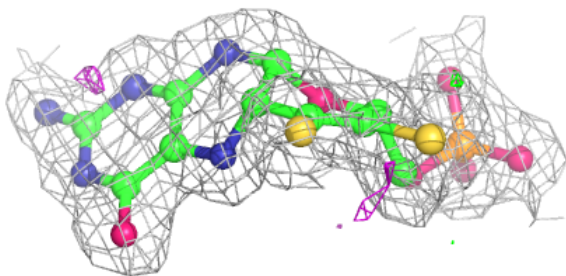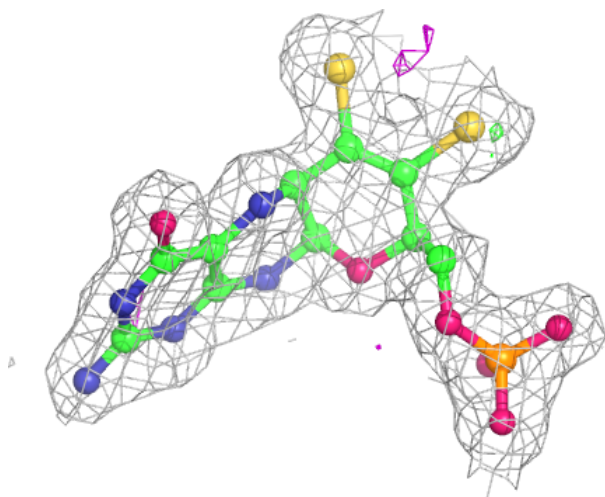
Electron density around FAD B 4005:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
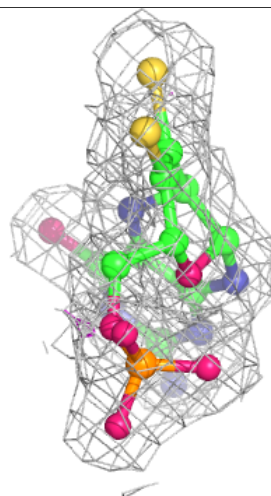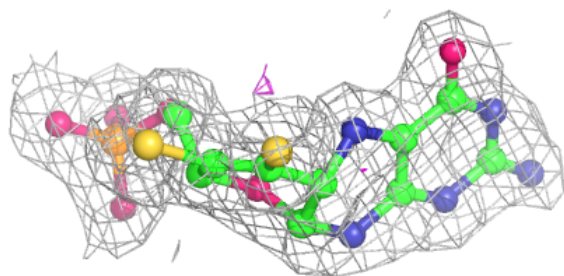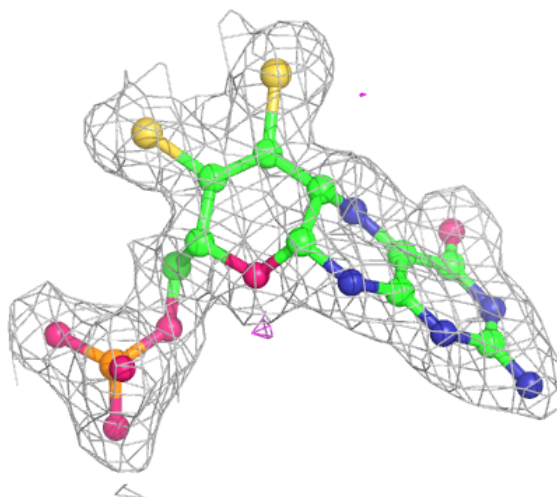mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
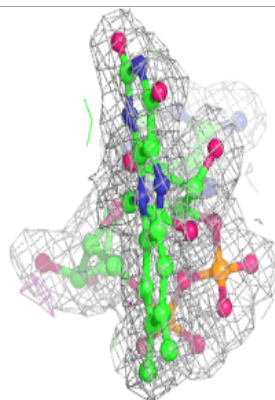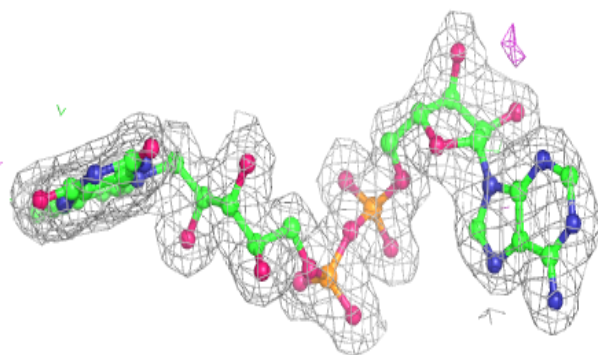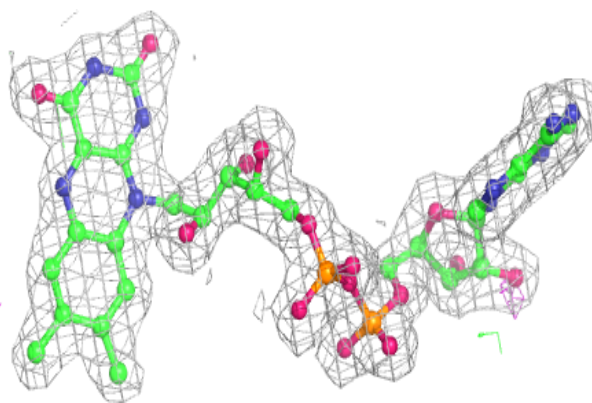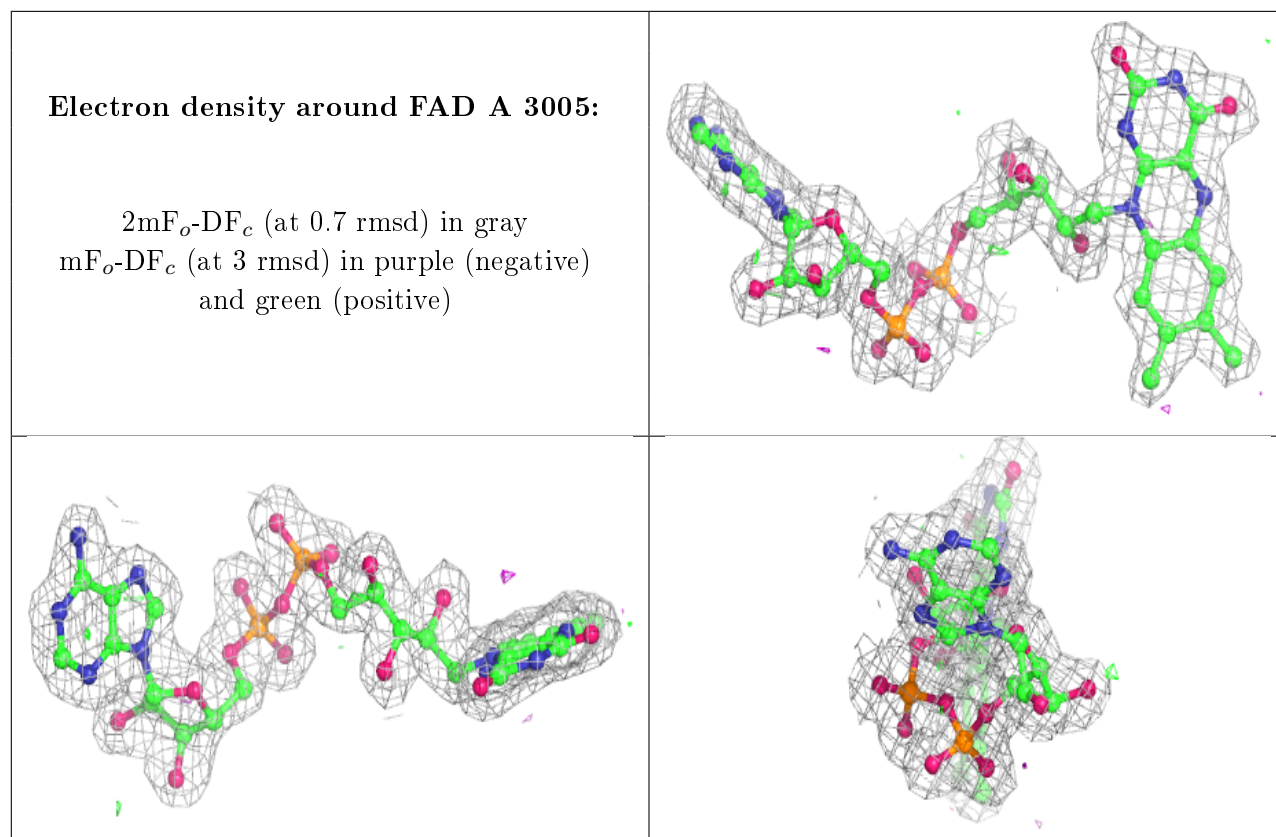
Electron density around MTE A 3003:

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

Electron density around MTE B 4003:

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

Electron density around FAD A 3005:

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

6.5 Other polymers ⓘ

There are no such residues in this entry.