



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 15, 2024 – 11:07 PM EST

PDB ID : 1V97
Title : Crystal Structure of Bovine Milk Xanthine Dehydrogenase FYX-051 bound form
Authors : Okamoto, K.; Matsumoto, K.; Hille, R.; Eger, B.T.; Pai, E.F.; Nishino, T.
Deposited on : 2004-01-21
Resolution : 1.94 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.21
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.004 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

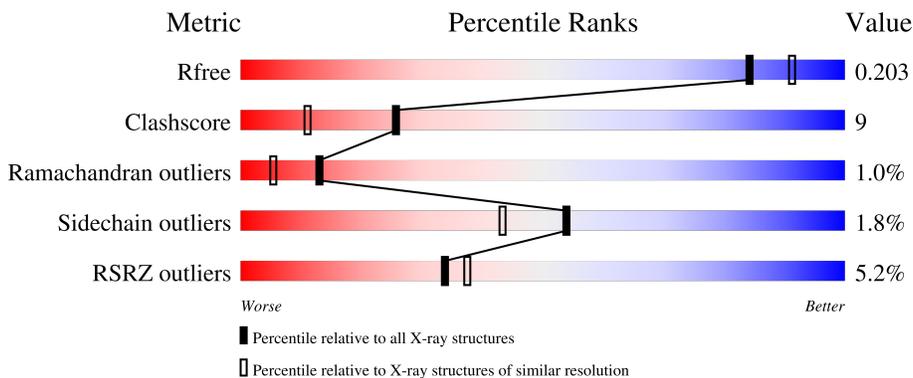
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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}	164625	1306 (1.94-1.94)
Clashscore	180529	1400 (1.94-1.94)
Ramachandran outliers	177936	1387 (1.94-1.94)
Sidechain outliers	177891	1387 (1.94-1.94)
RSRZ outliers	164620	1306 (1.94-1.94)

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	1332	 5% 80% 16% ..
1	B	1332	 5% 80% 16% ..

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	MOS	A	3004	-	-	X	-
5	MOS	B	4004	-	-	X	-
8	ACY	A	3007	-	-	X	-
8	ACY	B	4007	-	-	X	-
9	GOL	A	5001	-	X	-	-
9	GOL	A	5003	-	X	-	-
9	GOL	A	5005	-	X	-	-
9	GOL	A	5007	-	X	-	-
9	GOL	B	5002	-	X	-	-
9	GOL	B	5004	-	X	-	-
9	GOL	B	5006	-	X	-	-
9	GOL	B	5008	-	X	-	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 22481 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.

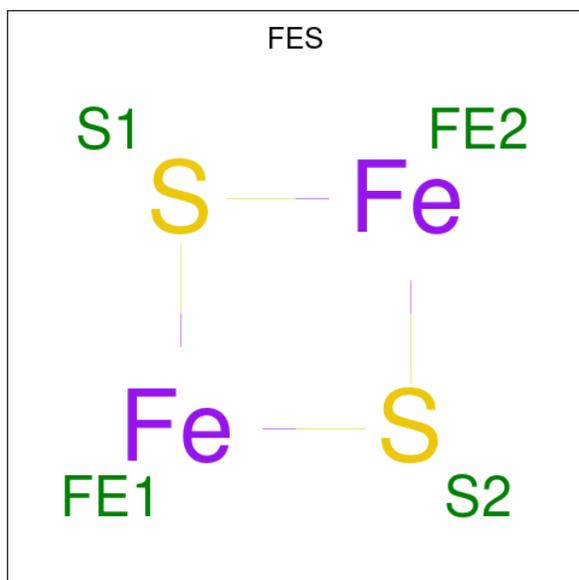
- Molecule 1 is a protein called Xanthine dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1298	10071	6401	1727	1882	61	0	0	0
1	B	1296	10054	6391	1724	1878	61	0	0	0

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

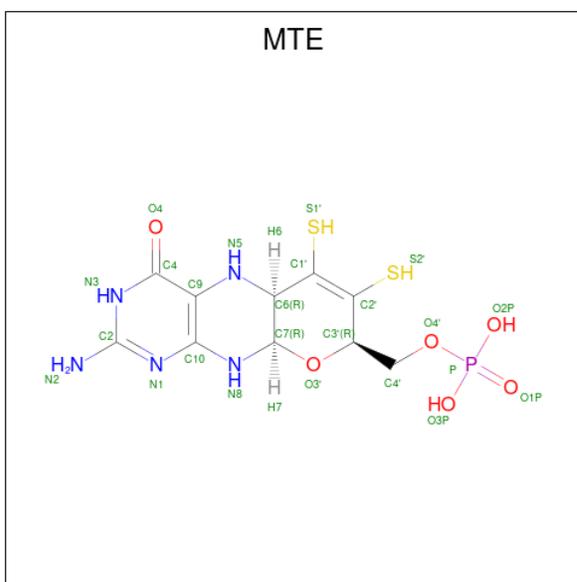
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		

- Molecule 3 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



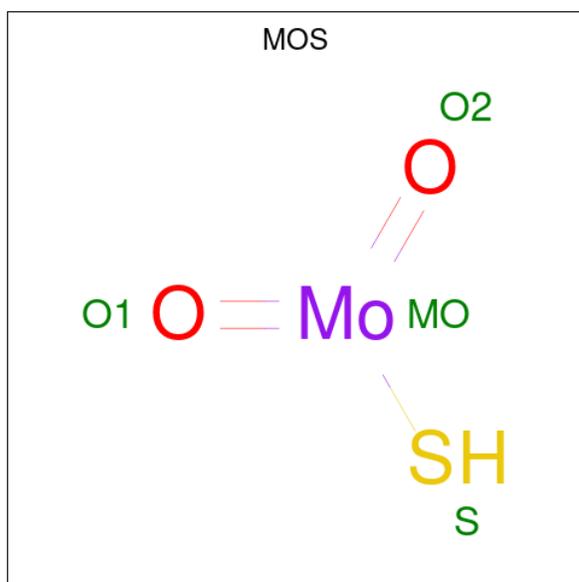
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	B	1	Total	Fe	S	0	0
			4	2	2		
3	B	1	Total	Fe	S	0	0
			4	2	2		

- 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: C₁₀H₁₄N₅O₆PS₂).



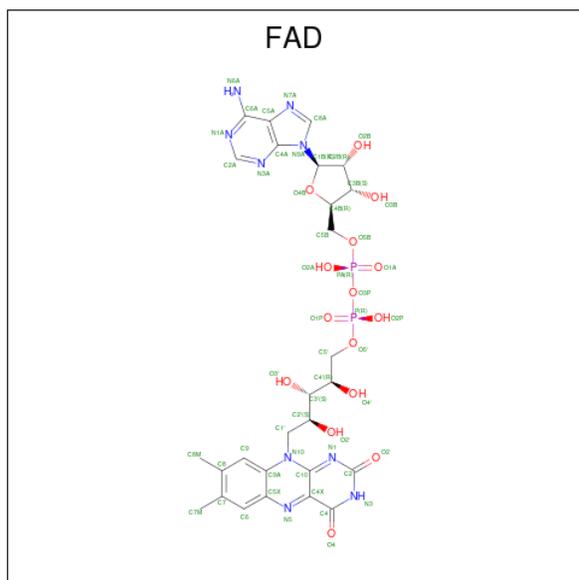
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
4	A	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		
4	B	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		

- Molecule 5 is DIOXOTHIO MOLYBDENUM(VI) ION (three-letter code: MOS) (formula: HMoO₂S).



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

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



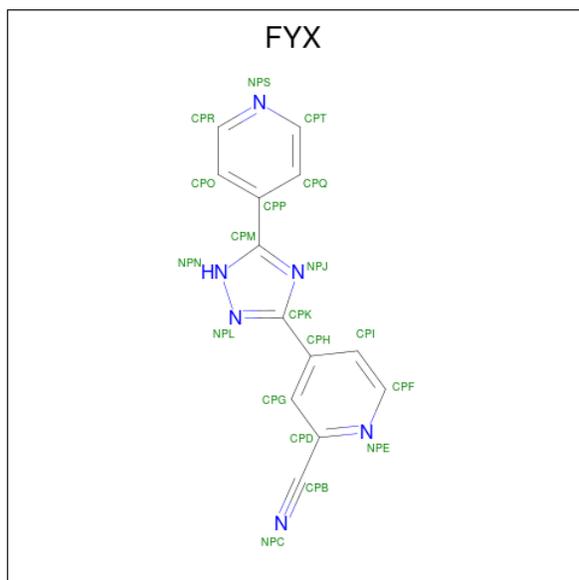
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
6	A	1	53	27	9	15	2	0	0

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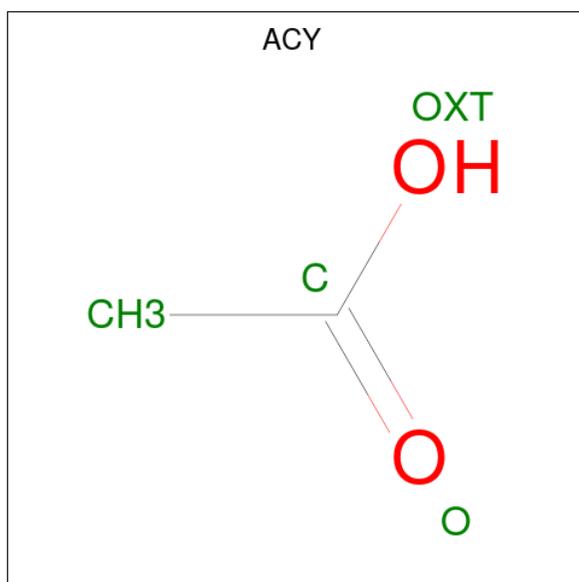
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
6	B	1	53	27	9	15	2	0	0

- Molecule 7 is 4-(5-PYRIDIN-4-YL-1H-1,2,4-TRIAZOL-3-YL)PYRIDINE-2-CARBONITRILE (three-letter code: FYX) (formula: C₁₃H₈N₆).



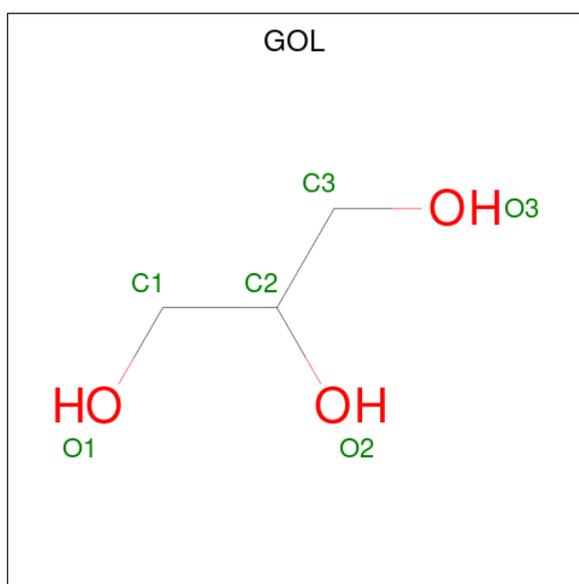
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	N		
7	A	1	19	13	6	0	0
7	B	1	19	13	6	0	0

- Molecule 8 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			4	2	2		
8	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 9 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

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

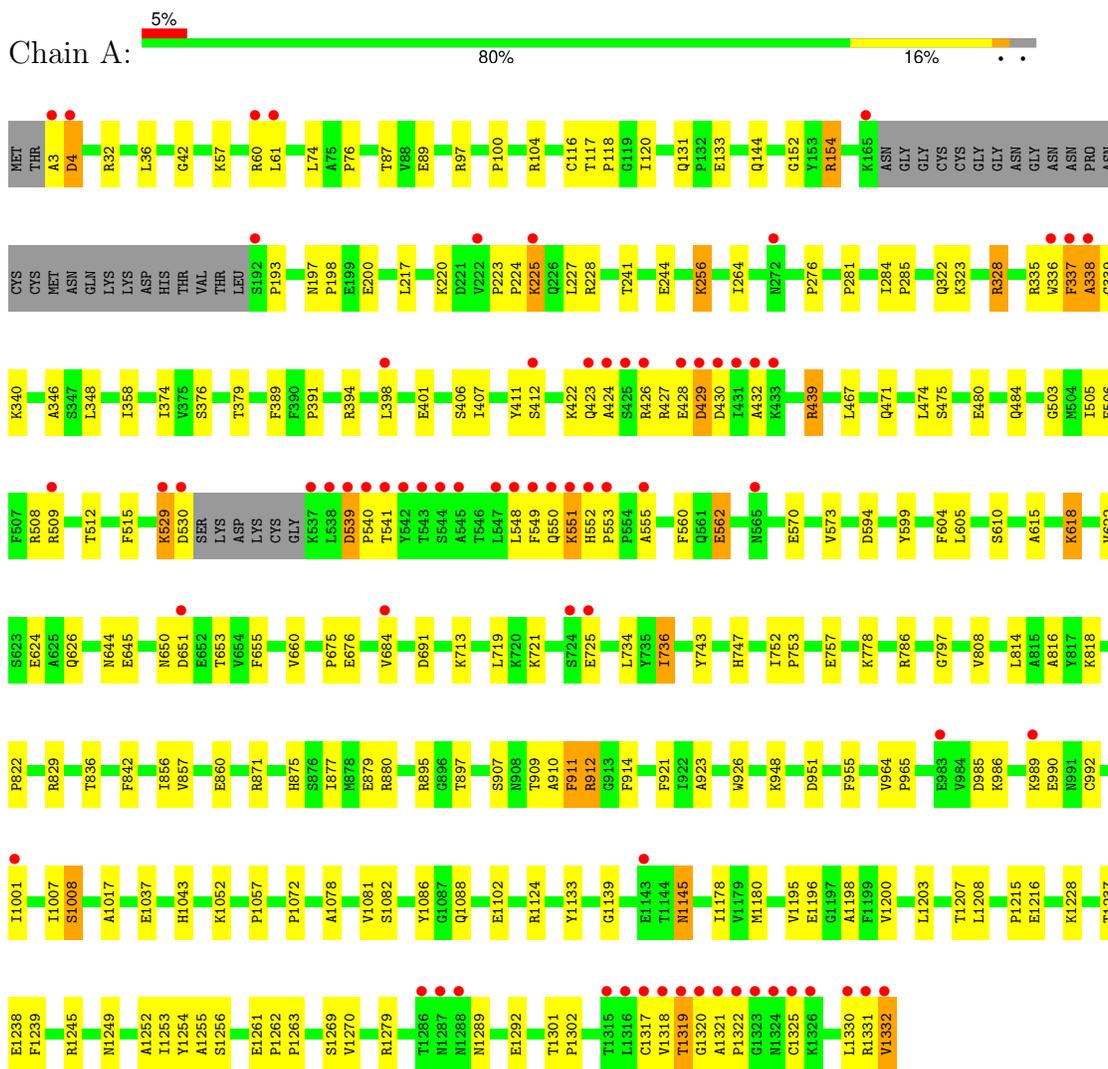
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1061	Total 1061	O 1061	0	0
10	B	1021	Total 1021	O 1021	0	0

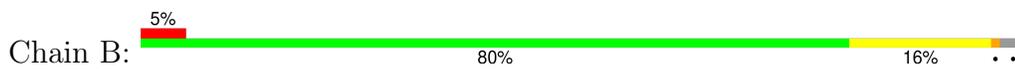
3 Residue-property plots

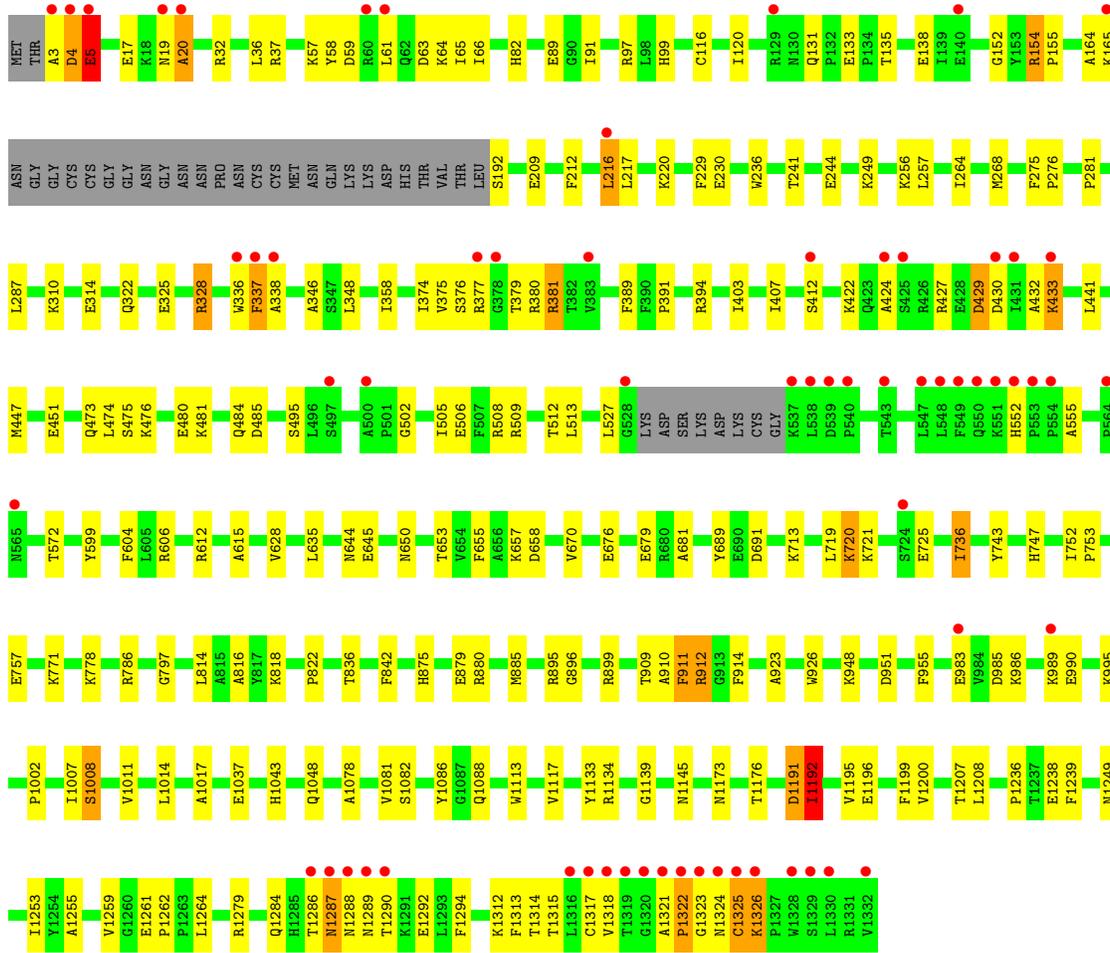
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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



- Molecule 1: Xanthine dehydrogenase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	167.99Å 124.61Å 146.93Å 90.00° 90.99° 90.00°	Depositor
Resolution (Å)	40.00 – 1.94 40.00 – 1.94	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.00-1.94) 96.4 (40.00-1.94)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.10 (at 1.94Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.178 , 0.208 0.173 , 0.203	Depositor DCC
R_{free} test set	6405 reflections (2.99%)	wwPDB-VP
Wilson B-factor (Å ²)	17.0	Xtrriage
Anisotropy	0.123	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 52.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	22481	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.07% 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: MTE, FYX, MOS, CA, GOL, ACY, FES, 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	0.31	0/10292	0.60	0/13931
1	B	0.31	0/10275	0.62	4/13909 (0.0%)
All	All	0.31	0/20567	0.61	4/27840 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1192	ILE	N-CA-CB	-9.77	88.34	110.80
1	B	1191	ASP	N-CA-C	7.02	129.96	111.00
1	B	5	GLU	N-CA-C	6.78	129.29	111.00
1	B	1192	ILE	N-CA-C	-5.30	96.70	111.00

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	10071	0	10071	183	0
1	B	10054	0	10053	200	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	8	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	8	0	0	0	0
4	A	24	0	10	1	0
4	B	24	0	10	1	0
5	A	4	0	0	2	0
5	B	4	0	0	2	0
6	A	53	0	31	3	0
6	B	53	0	31	3	0
7	A	19	0	7	0	0
7	B	19	0	7	0	0
8	A	4	0	3	3	0
8	B	4	0	3	4	0
9	A	24	0	16	5	0
9	B	24	0	15	3	0
10	A	1061	0	0	16	0
10	B	1021	0	0	14	0
All	All	22481	0	20257	383	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 9.

The worst 5 of 383 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:340:LYS:NZ	10:A:6066:HOH:O	1.60	1.25
1:A:1088:GLN:NE2	9:A:5007:GOL:O3	1.86	1.08
1:A:3:ALA:HB1	1:A:228:ARG:H	1.17	1.06
1:B:1286:THR:HG22	1:B:1287:ASN:H	1.28	0.98
1:B:229:PHE:HA	10:B:5161:HOH:O	1.65	0.95

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	1292/1332 (97%)	1235 (96%)	43 (3%)	14 (1%)	12	4
1	B	1290/1332 (97%)	1235 (96%)	42 (3%)	13 (1%)	13	5
All	All	2582/2664 (97%)	2470 (96%)	85 (3%)	27 (1%)	13	5

5 of 27 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	ASP
1	A	1008	SER
1	A	1322	PRO
1	B	4	ASP
1	B	5	GLU

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	1100/1128 (98%)	1078 (98%)	22 (2%)	50	38
1	B	1098/1128 (97%)	1081 (98%)	17 (2%)	60	52
All	All	2198/2256 (97%)	2159 (98%)	39 (2%)	54	43

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	381	ARG
1	B	983	GLU
1	B	433	LYS
1	B	736	ILE
1	B	1192	ILE

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

Mol	Chain	Res	Type
1	B	146	ASN

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Mol	Chain	Res	Type
1	B	473	GLN
1	B	1287	ASN
1	B	351	ASN
1	B	552	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 2 are monoatomic - leaving 22 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$
9	GOL	A	5003	-	5,5,5	5.24	4 (80%)	5,5,5	6.77	3 (60%)
8	ACY	A	3007	-	3,3,3	1.21	0	3,3,3	1.68	1 (33%)
3	FES	A	3001	1	0,4,4	-	-	-	-	-
3	FES	B	4002	1	0,4,4	-	-	-	-	-
9	GOL	B	5002	-	5,5,5	5.25	4 (80%)	5,5,5	6.77	3 (60%)
7	FYX	B	4006	5	19,21,21	2.43	8 (42%)	15,28,28	3.23	8 (53%)
6	FAD	B	4005	-	54,58,58	1.80	16 (29%)	71,89,89	2.19	20 (28%)
3	FES	A	3002	1	0,4,4	-	-	-	-	-
5	MOS	A	3004	7,4	0,3,3	-	-	-	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	GOL	B	5006	-	5,5,5	5.25	4 (80%)	5,5,5	6.77	3 (60%)
4	MTE	A	3003	5	19,26,26	5.93	10 (52%)	20,40,40	2.99	8 (40%)
8	ACY	B	4007	-	3,3,3	1.16	0	3,3,3	1.71	1 (33%)
9	GOL	A	5007	-	5,5,5	5.25	4 (80%)	5,5,5	6.77	3 (60%)
3	FES	B	4001	1	0,4,4	-	-	-	-	-
9	GOL	B	5008	-	5,5,5	5.25	4 (80%)	5,5,5	6.77	3 (60%)
7	FYX	A	3006	5	19,21,21	2.47	8 (42%)	15,28,28	3.23	8 (53%)
4	MTE	B	4003	5	19,26,26	5.93	12 (63%)	20,40,40	2.76	7 (35%)
9	GOL	B	5004	-	5,5,5	5.25	4 (80%)	5,5,5	6.77	3 (60%)
9	GOL	A	5001	-	5,5,5	5.24	4 (80%)	5,5,5	6.77	3 (60%)
6	FAD	A	3005	-	54,58,58	1.84	17 (31%)	71,89,89	2.10	21 (29%)
9	GOL	A	5005	-	5,5,5	5.24	4 (80%)	5,5,5	6.77	3 (60%)
5	MOS	B	4004	7,4	0,3,3	-	-	-	-	-

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
9	GOL	B	5008	-	-	2/4/4/4	-
9	GOL	A	5003	-	-	2/4/4/4	-
6	FAD	B	4005	-	-	2/30/50/50	0/6/6/6
3	FES	A	3001	1	-	-	0/1/1/1
3	FES	B	4002	1	-	-	0/1/1/1
9	GOL	B	5002	-	-	2/4/4/4	-
3	FES	A	3002	1	-	-	0/1/1/1
7	FYX	A	3006	5	-	0/0/10/10	0/3/3/3
7	FYX	B	4006	5	-	0/0/10/10	0/3/3/3
4	MTE	B	4003	5	-	3/6/34/34	0/3/3/3
9	GOL	B	5004	-	-	2/4/4/4	-
9	GOL	B	5006	-	-	2/4/4/4	-
4	MTE	A	3003	5	-	3/6/34/34	0/3/3/3
9	GOL	A	5007	-	-	2/4/4/4	-
9	GOL	A	5001	-	-	2/4/4/4	-
6	FAD	A	3005	-	-	1/30/50/50	0/6/6/6
9	GOL	A	5005	-	-	2/4/4/4	-
3	FES	B	4001	1	-	-	0/1/1/1

The worst 5 of 103 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	4003	MTE	C7-C6	19.33	1.69	1.53
4	A	3003	MTE	C7-C6	18.98	1.68	1.53
4	A	3003	MTE	C9-C10	11.06	1.61	1.41
4	B	4003	MTE	C9-C10	11.02	1.61	1.41
9	B	5006	GOL	C3-C2	-9.90	1.14	1.51

The worst 5 of 98 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	5008	GOL	O3-C3-C2	13.82	172.58	110.38
9	A	5003	GOL	O3-C3-C2	13.81	172.56	110.38
9	A	5001	GOL	O3-C3-C2	13.81	172.55	110.38
9	A	5007	GOL	O3-C3-C2	13.81	172.54	110.38
9	B	5002	GOL	O3-C3-C2	13.81	172.54	110.38

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	3003	MTE	C4'-O4'-P-O3P
4	B	4003	MTE	C4'-O4'-P-O2P
4	B	4003	MTE	C4'-O4'-P-O3P
9	A	5001	GOL	O2-C2-C3-O3
9	A	5003	GOL	O2-C2-C3-O3

There are no ring outliers.

13 monomers are involved in 27 short contacts:

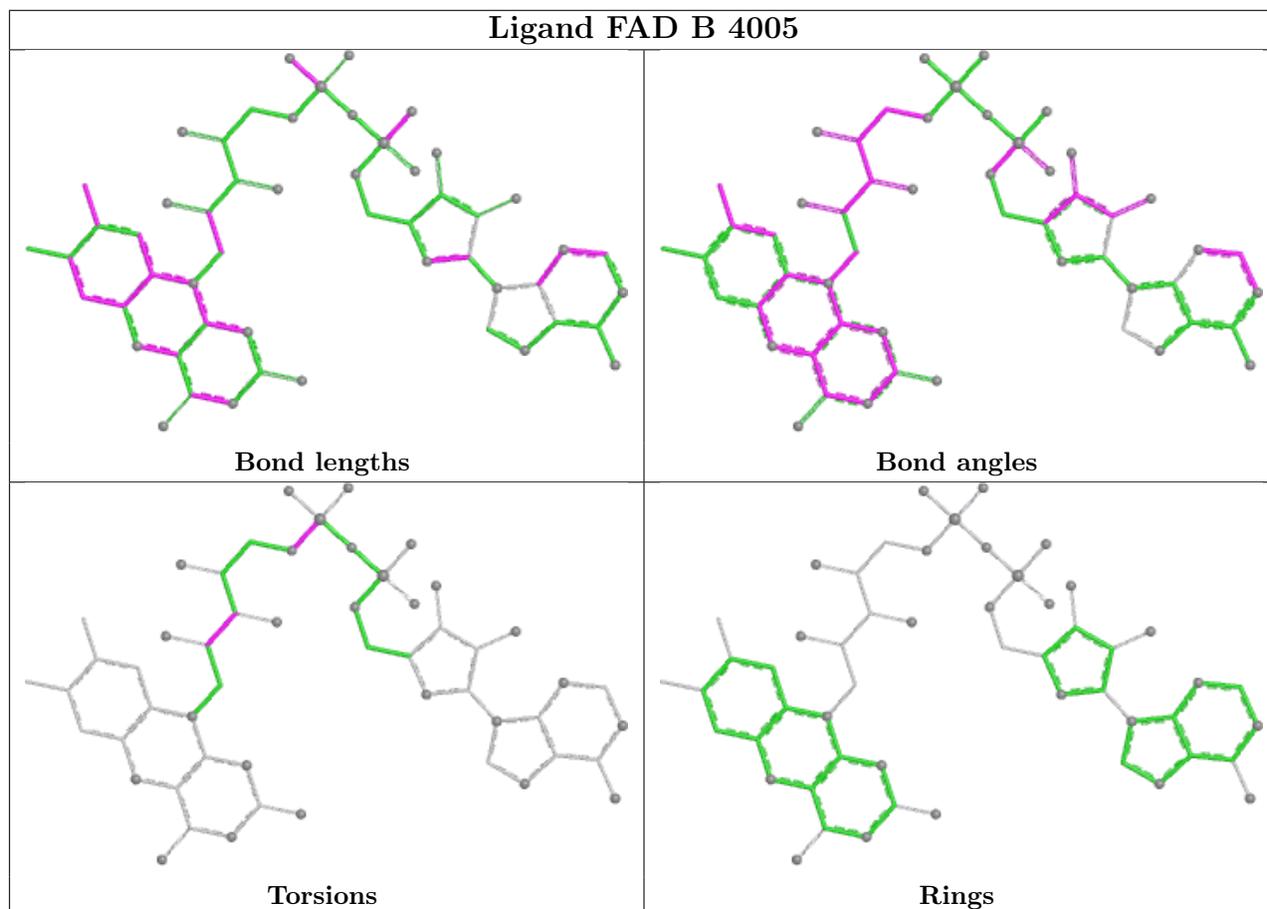
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	5003	GOL	1	0
8	A	3007	ACY	3	0
6	B	4005	FAD	3	0
5	A	3004	MOS	2	0
4	A	3003	MTE	1	0
8	B	4007	ACY	4	0
9	A	5007	GOL	3	0
9	B	5008	GOL	2	0
4	B	4003	MTE	1	0
9	B	5004	GOL	1	0
9	A	5001	GOL	1	0

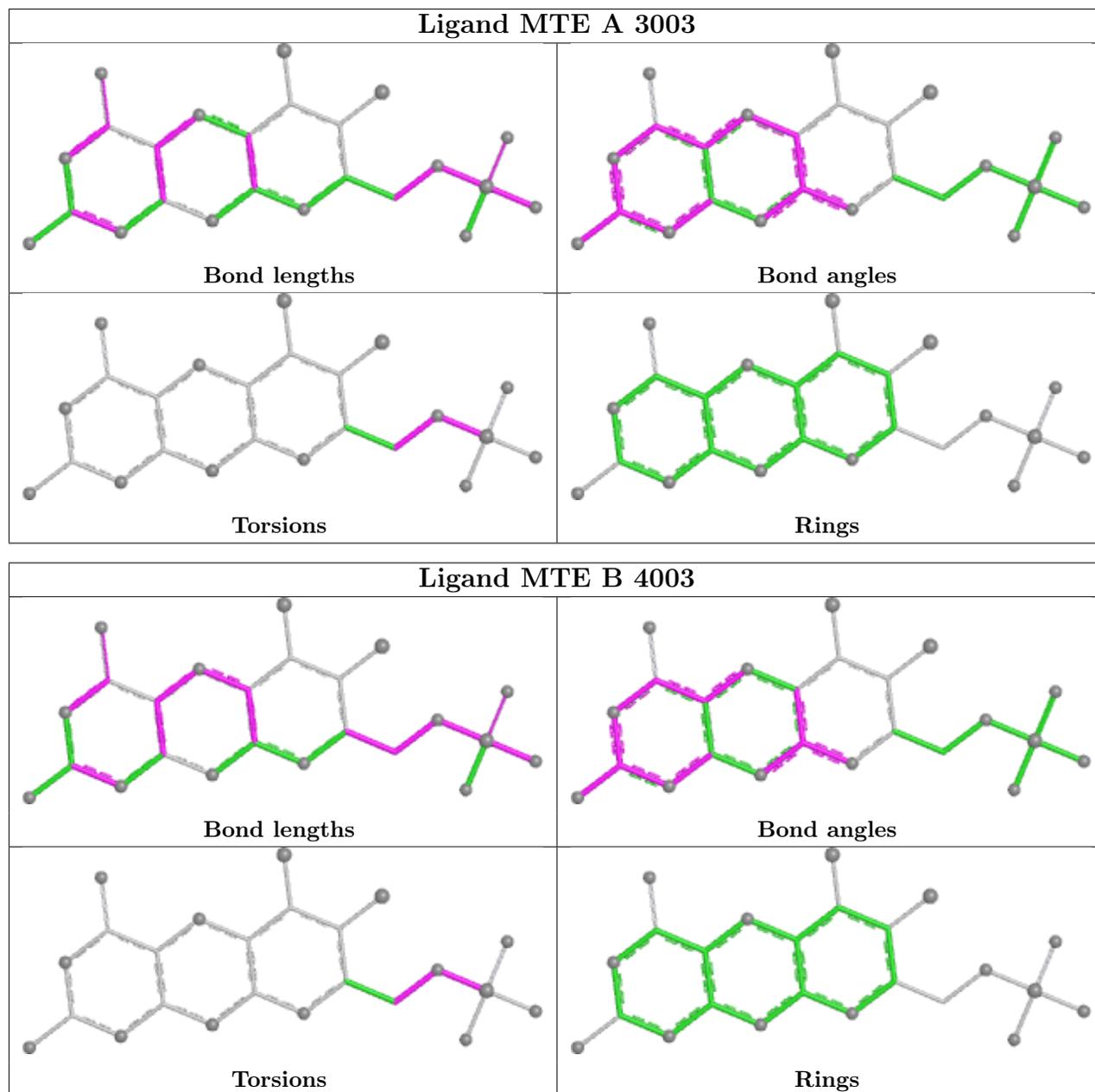
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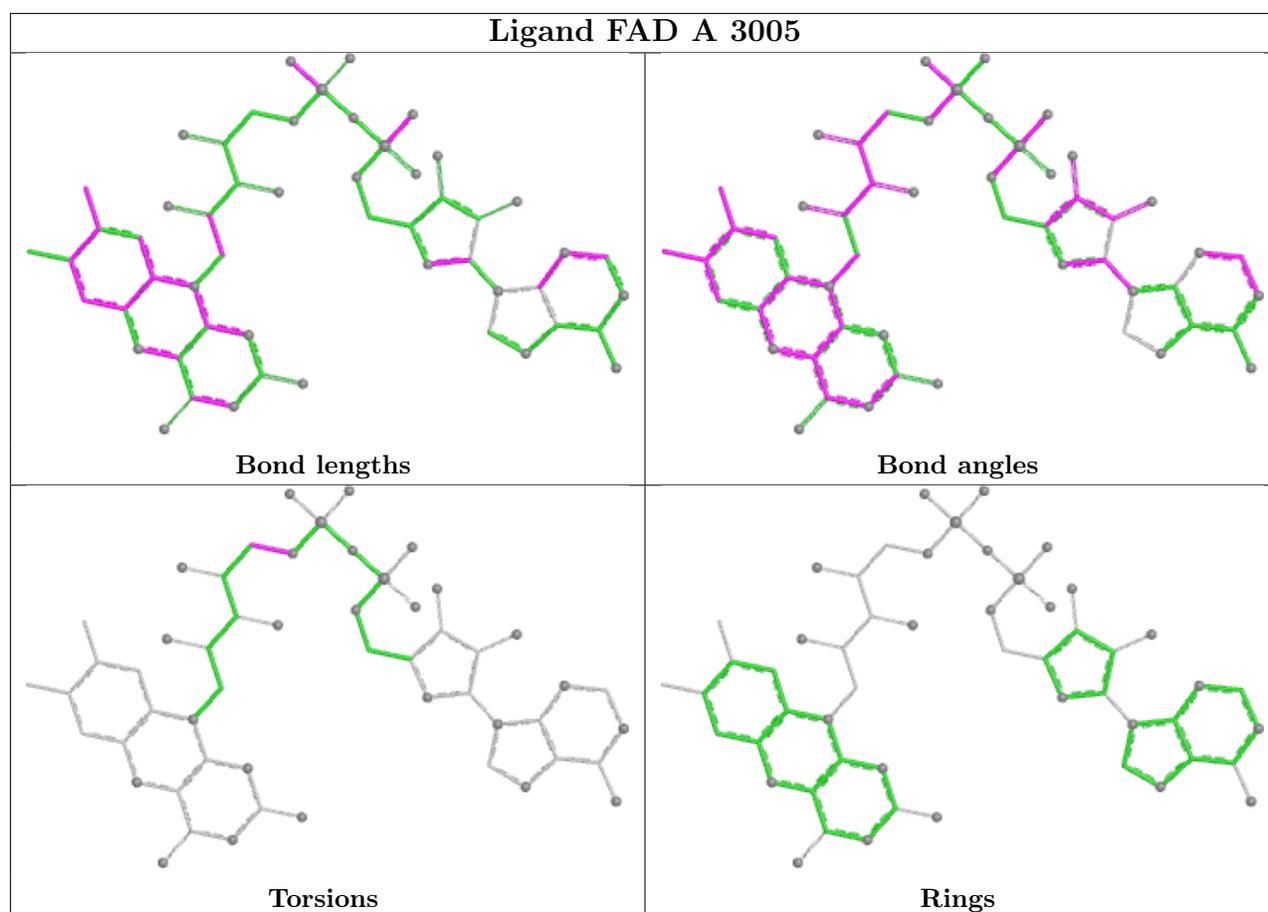
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	3005	FAD	3	0
5	B	4004	MOS	2	0

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 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.







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	1298/1332 (97%)	-0.09	71 (5%) 32 35	9, 18, 39, 61	0
1	B	1296/1332 (97%)	-0.08	64 (4%) 36 40	9, 19, 38, 61	0
All	All	2594/2664 (97%)	-0.08	135 (5%) 34 37	9, 18, 39, 61	0

The worst 5 of 135 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	ALA	10.7
1	B	1322	PRO	7.7
1	A	431	ILE	7.7
1	A	1332	VAL	7.5
1	A	1318	VAL	7.4

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 monosaccharides in this entry.

6.4 Ligands [i](#)

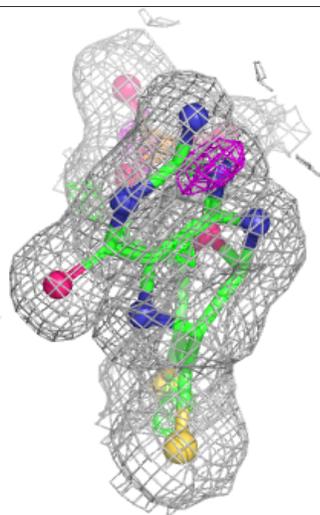
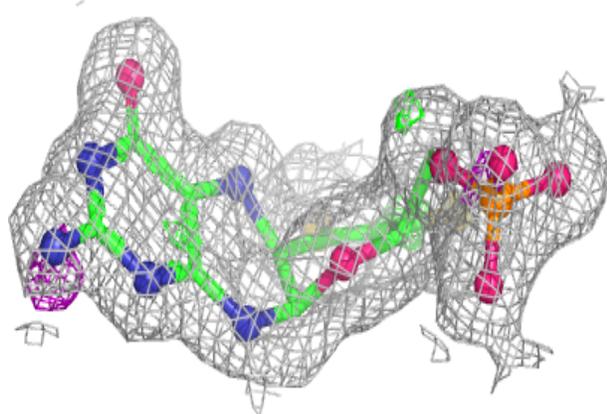
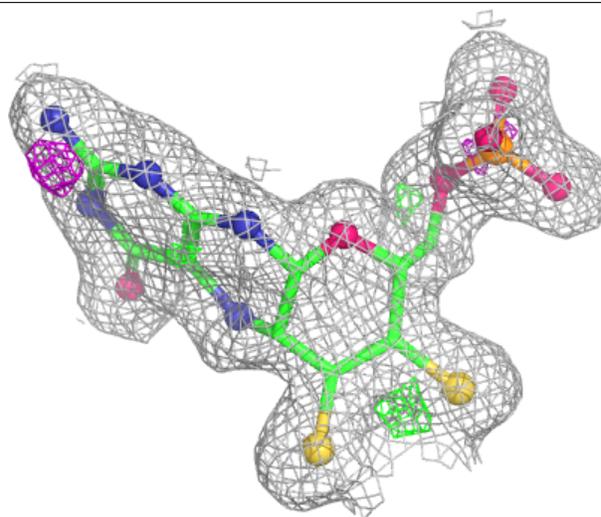
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
9	GOL	A	5007	6/6	0.65	0.22	40,42,43,45	0
9	GOL	B	5008	6/6	0.66	0.24	42,43,45,46	0
9	GOL	B	5004	6/6	0.71	0.23	34,38,41,42	0
9	GOL	B	5006	6/6	0.81	0.16	31,35,37,40	0
9	GOL	A	5001	6/6	0.81	0.16	23,29,30,36	0
9	GOL	A	5003	6/6	0.82	0.17	29,34,35,37	0
9	GOL	A	5005	6/6	0.82	0.15	29,34,38,41	0
9	GOL	B	5002	6/6	0.85	0.12	24,29,31,31	0
7	FYX	B	4006	19/19	0.93	0.08	14,18,24,27	0
7	FYX	A	3006	19/19	0.94	0.07	15,18,27,27	0
8	ACY	A	3007	4/4	0.96	0.05	4,9,13,13	0
8	ACY	B	4007	4/4	0.96	0.05	7,13,13,16	0
4	MTE	A	3003	24/24	0.97	0.06	8,12,15,17	0
6	FAD	A	3005	53/53	0.97	0.06	12,16,20,24	0
6	FAD	B	4005	53/53	0.97	0.06	12,17,21,23	0
4	MTE	B	4003	24/24	0.98	0.06	9,11,15,16	0
3	FES	A	3001	4/4	0.99	0.03	11,11,11,11	0
3	FES	A	3002	4/4	0.99	0.02	11,11,12,12	0
3	FES	B	4001	4/4	0.99	0.02	11,11,12,12	0
3	FES	B	4002	4/4	0.99	0.03	11,12,12,12	0
2	CA	A	3008	1/1	0.99	0.03	12,12,12,12	0
5	MOS	B	4004	4/4	1.00	0.02	10,13,14,15	0
2	CA	B	4008	1/1	1.00	0.02	16,16,16,16	0
5	MOS	A	3004	4/4	1.00	0.02	12,14,15,16	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.

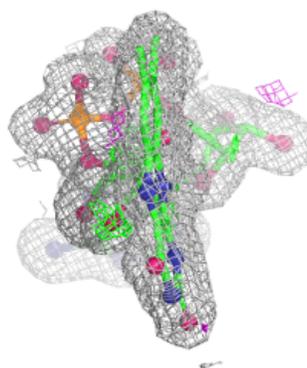
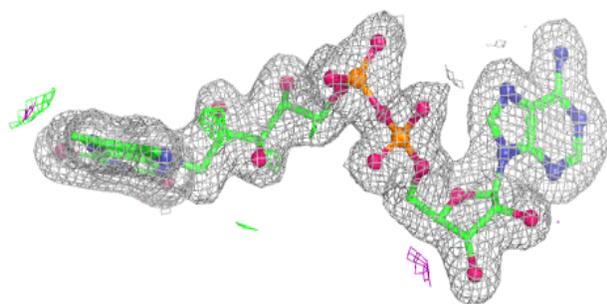
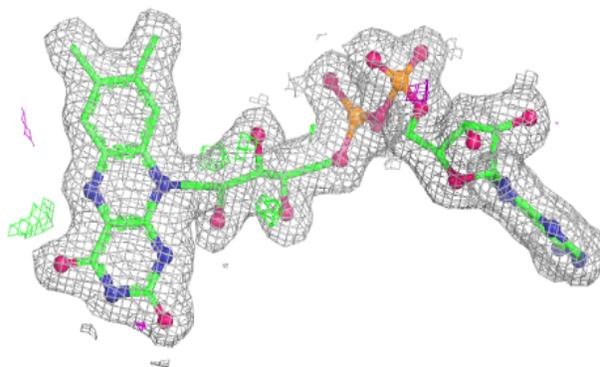
Electron density around MTE A 3003:

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

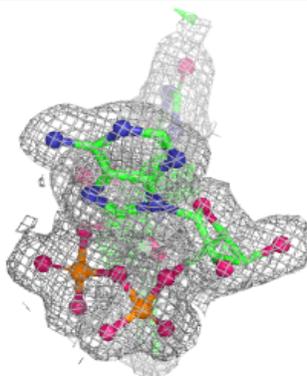
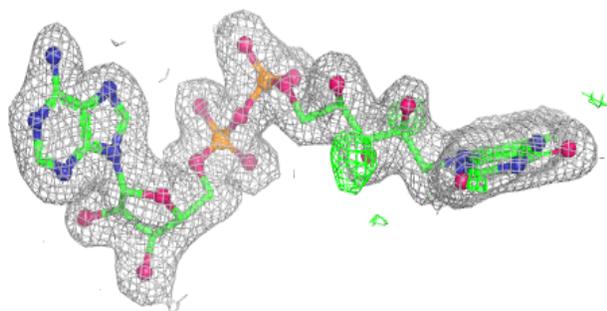
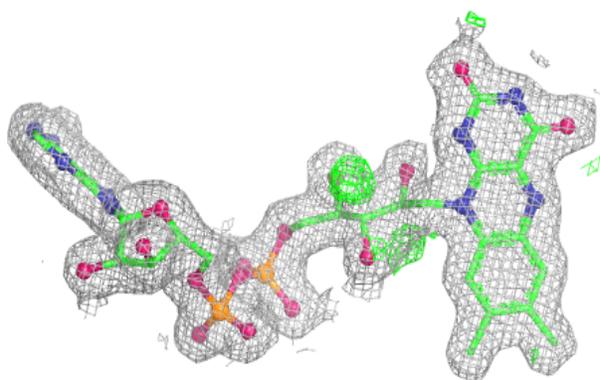


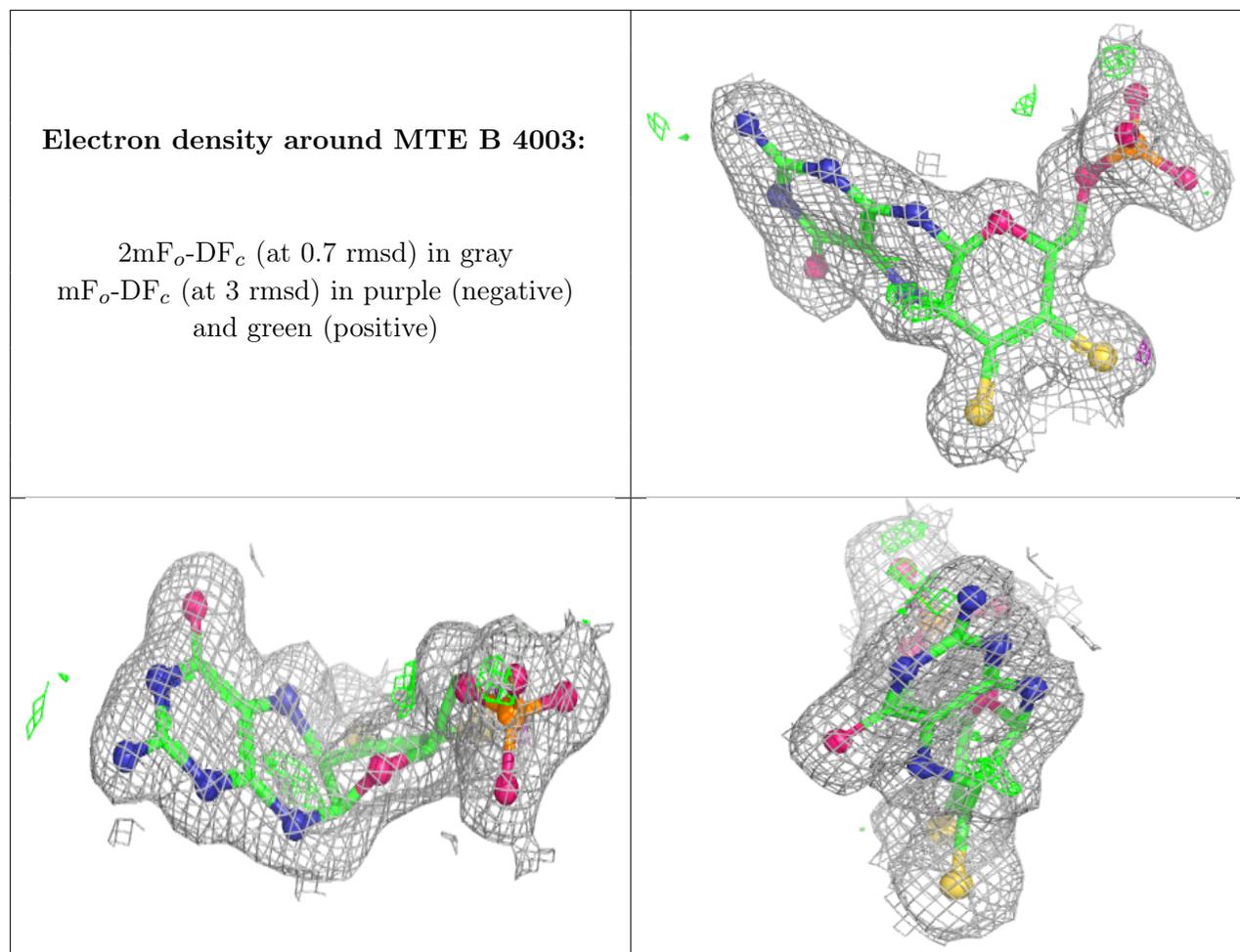
Electron density around FAD A 3005:

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

**Electron density around 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.