



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 8, 2025 – 12:09 PM JST

PDB ID : 9UDB / pdb_00009udb
Title : Crystal structure of MonCI in complex with farnesyl acetate
Authors : Deng, Y.M.; Chen, X.
Deposited on : 2025-04-06
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

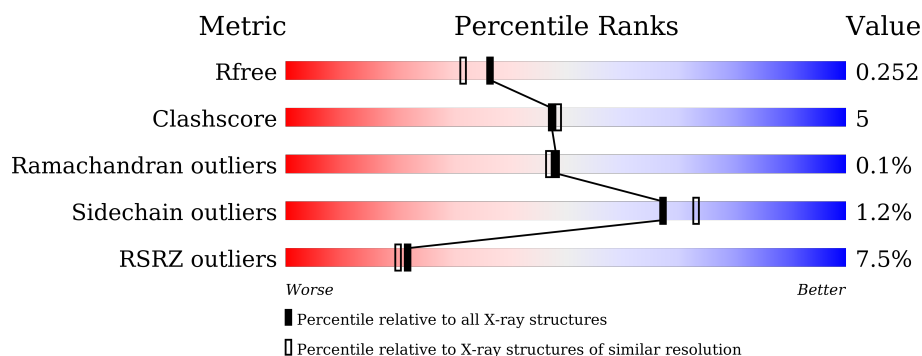
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (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 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	511	<div> <div>4%</div> <div>87% 5% 8%</div> </div>
1	B	511	<div> <div>10%</div> <div>75% 16% 8%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7374 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 MonCI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	471	Total	C	N	O	S	0	0	0
			3575	2233	661	672	9			
1	B	470	Total	C	N	O	S	0	0	0
			3570	2230	660	671	9			

There are 30 discrepancies between the modelled and reference sequences:

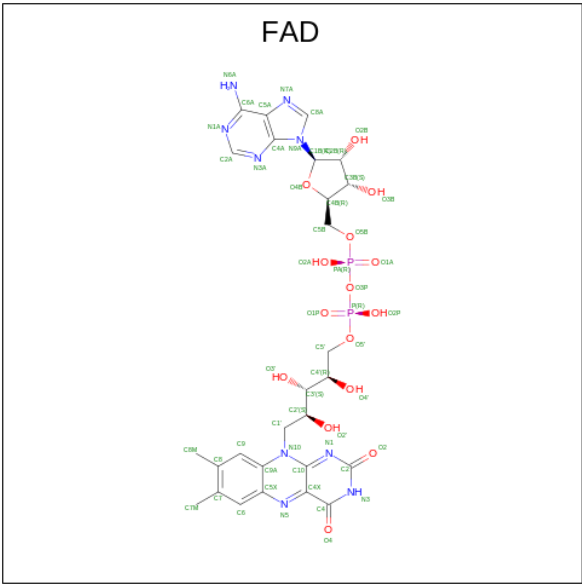
Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	initiating methionine	UNP Q846W9
A	-13	ASN	-	expression tag	UNP Q846W9
A	-12	HIS	-	expression tag	UNP Q846W9
A	-11	LYS	-	expression tag	UNP Q846W9
A	-10	VAL	-	expression tag	UNP Q846W9
A	-9	HIS	-	expression tag	UNP Q846W9
A	-8	HIS	-	expression tag	UNP Q846W9
A	-7	HIS	-	expression tag	UNP Q846W9
A	-6	HIS	-	expression tag	UNP Q846W9
A	-5	HIS	-	expression tag	UNP Q846W9
A	-4	HIS	-	expression tag	UNP Q846W9
A	-3	ILE	-	expression tag	UNP Q846W9
A	-2	GLU	-	expression tag	UNP Q846W9
A	-1	GLY	-	expression tag	UNP Q846W9
A	0	ARG	-	expression tag	UNP Q846W9
B	-14	MET	-	initiating methionine	UNP Q846W9
B	-13	ASN	-	expression tag	UNP Q846W9
B	-12	HIS	-	expression tag	UNP Q846W9
B	-11	LYS	-	expression tag	UNP Q846W9
B	-10	VAL	-	expression tag	UNP Q846W9
B	-9	HIS	-	expression tag	UNP Q846W9
B	-8	HIS	-	expression tag	UNP Q846W9
B	-7	HIS	-	expression tag	UNP Q846W9
B	-6	HIS	-	expression tag	UNP Q846W9
B	-5	HIS	-	expression tag	UNP Q846W9

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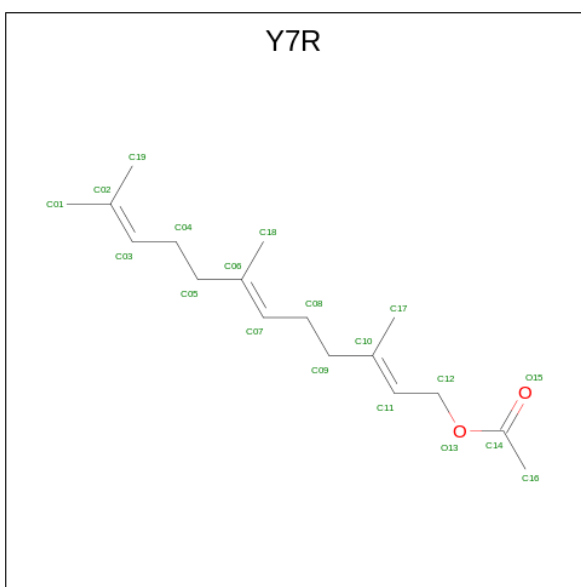
Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	HIS	-	expression tag	UNP Q846W9
B	-3	ILE	-	expression tag	UNP Q846W9
B	-2	GLU	-	expression tag	UNP Q846W9
B	-1	GLY	-	expression tag	UNP Q846W9
B	0	ARG	-	expression tag	UNP Q846W9

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is (2E,6E)-3,7,11-trimethyldodeca-2,6,10-trien-1-yl acetate (CCD ID: Y7R) (formula: C₁₇H₂₈O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	C O	0	0
			19	17 2		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	90	Total	O	0	0
			90	90		
5	B	13	Total	O	0	0
			13	13		

- Molecule 1: MonCl



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.26Å 52.56Å 145.13Å 90.00° 92.76° 90.00°	Depositor
Resolution (Å)	19.47 – 2.00 19.47 – 2.00	Depositor EDS
% Data completeness (in resolution range)	93.7 (19.47-2.00) 93.5 (19.47-2.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 2.01Å)	Xtriage
Refinement program	PHENIX (1.16_3549: ???)	Depositor
R, R_{free}	0.219 , 0.251 0.220 , 0.252	Depositor DCC
R_{free} test set	3313 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	44.3	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 43.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7374	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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: Y7R, FAD, CL

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	0.27	0/3645	0.48	0/4965
1	B	0.30	0/3640	0.53	0/4958
All	All	0.29	0/7285	0.51	0/9923

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

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	3575	0	3565	15	0
1	B	3570	0	3560	63	0
2	A	53	0	31	2	0
2	B	53	0	31	4	0
3	A	19	0	0	0	0
4	A	1	0	0	0	0
5	A	90	0	0	0	0
5	B	13	0	0	0	0
All	All	7374	0	7187	79	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.

All (79) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:THR:OG1	1:B:183:SER:HB2	1.66	0.96
1:B:211:ARG:CG	1:B:295:VAL:HG22	2.10	0.82
1:B:137:ARG:HG2	1:B:162:LEU:HB2	1.60	0.82
1:B:211:ARG:CD	1:B:295:VAL:HG22	2.10	0.81
1:B:212:LEU:HD11	1:B:250:ARG:HB3	1.70	0.73
1:B:316:ASP:HA	1:B:365:THR:HG21	1.70	0.72
1:B:220:THR:HG21	1:B:249:GLY:HA2	1.81	0.63
1:B:54:ARG:HH21	1:B:54:ARG:HG2	1.62	0.62
1:B:54:ARG:HD3	1:B:296:PHE:CD1	2.34	0.61
1:B:362:ARG:HG3	1:B:364:GLY:H	1.66	0.61
1:B:8:HIS:HE1	1:B:170:LEU:HD21	1.66	0.60
1:B:211:ARG:HH11	1:B:291:PRO:HB3	1.68	0.59
1:B:160:ARG:HH12	1:B:167:GLN:HE21	1.50	0.58
1:B:226:VAL:HB	1:B:282:LEU:HD21	1.85	0.58
1:A:208:TYR:OH	1:A:330:PRO:HD2	2.05	0.56
1:B:232:ASP:N	1:B:232:ASP:OD1	2.37	0.56
1:B:10:VAL:HG21	1:B:170:LEU:HD22	1.89	0.55
1:B:211:ARG:CD	1:B:295:VAL:CG2	2.82	0.54
1:B:255:LEU:HG	1:B:270:PHE:CZ	2.42	0.54
1:B:426:LYS:N	1:B:426:LYS:HD2	2.23	0.53
1:B:211:ARG:HD3	1:B:295:VAL:HG22	1.88	0.53
1:A:37:ARG:HG3	1:A:162:LEU:HD11	1.91	0.53
1:A:330:PRO:HB3	2:A:501:FAD:C6	2.39	0.53
1:B:46:HIS:CD2	1:B:54:ARG:HG3	2.44	0.52
1:A:184:ARG:NH2	1:A:187:GLN:OE1	2.42	0.51
1:B:330:PRO:HB3	2:B:700:FAD:C6	2.40	0.51
1:B:259:ARG:NH2	1:B:392:ASN:O	2.44	0.51
1:A:428:SER:O	1:A:432:THR:HG23	2.11	0.51
1:B:366:ARG:O	1:B:370:LYS:HG3	2.11	0.50
1:A:23:HIS:HB2	1:A:126:ALA:HB1	1.93	0.50
1:B:154:VAL:HG23	1:B:315:PRO:HB2	1.94	0.49
1:B:267:GLU:CD	1:B:267:GLU:H	2.15	0.49
1:B:362:ARG:HG2	1:B:365:THR:H	1.78	0.48
1:A:330:PRO:HB3	2:A:501:FAD:C5X	2.42	0.48
1:B:6:PRO:O	1:B:29:VAL:HG13	2.14	0.48
1:B:208:TYR:OH	1:B:330:PRO:HD2	2.13	0.48
1:B:47:ARG:NH1	2:B:700:FAD:O3B	2.46	0.48
1:B:57:HIS:HA	2:B:700:FAD:O4	2.13	0.47
1:B:229:ALA:HA	1:B:240:PHE:HD1	1.79	0.47
1:A:232:ASP:OD1	1:A:232:ASP:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:54:ARG:HD3	1:B:296:PHE:CE1	2.49	0.47
1:B:74:THR:HA	1:B:125:GLN:NE2	2.30	0.46
1:B:38:ASP:OD2	1:B:49:GLY:N	2.47	0.46
1:B:242:VAL:HG21	1:B:244:TYR:CZ	2.51	0.45
1:B:303:ASN:OD1	1:B:329:ASN:N	2.47	0.45
1:A:243:VAL:HG23	1:A:282:LEU:HD22	1.99	0.45
1:B:328:PHE:O	1:B:330:PRO:HD3	2.16	0.45
1:B:129:ALA:HB3	1:B:132:ILE:HG13	1.98	0.44
1:B:211:ARG:HG2	1:B:295:VAL:HG22	1.95	0.44
1:B:5:ARG:HG3	1:B:5:ARG:NH2	2.31	0.44
1:A:95:LEU:HB2	1:A:100:TRP:CZ3	2.53	0.44
1:B:180:GLY:O	1:B:183:SER:HB3	2.16	0.44
1:B:95:LEU:HB2	1:B:100:TRP:CZ3	2.53	0.44
1:B:470:GLU:O	1:B:474:VAL:HG13	2.17	0.44
1:B:5:ARG:HG3	1:B:5:ARG:HH21	1.82	0.43
1:B:424:SER:OG	1:B:458:ARG:HG2	2.17	0.43
1:B:417:ILE:HG21	1:B:444:LEU:HD13	2.01	0.43
1:A:349:GLU:OE2	1:A:352:ARG:NH2	2.52	0.43
1:B:93:VAL:HG13	1:B:466:PRO:HD2	2.01	0.43
1:B:36:GLU:OE2	1:B:37:ARG:N	2.52	0.43
1:B:100:TRP:CZ2	1:B:465:PRO:HG3	2.53	0.42
1:B:95:LEU:HD13	1:B:100:TRP:CE2	2.55	0.42
1:A:421:SER:HB3	1:A:431:VAL:HG21	2.00	0.42
1:B:74:THR:HA	1:B:125:GLN:HE22	1.85	0.42
1:B:211:ARG:HD3	1:B:295:VAL:CG2	2.48	0.42
1:A:56:ALA:HB1	1:A:244:TYR:HD2	1.85	0.42
1:A:252:LEU:HD12	1:A:252:LEU:HA	1.90	0.42
1:B:10:VAL:HG21	1:B:170:LEU:CD2	2.49	0.42
1:B:354:VAL:HB	1:B:355:GLN:H	1.70	0.42
1:B:350:PHE:O	1:B:354:VAL:HG22	2.21	0.41
1:B:230:ALA:HB3	1:B:239:ARG:O	2.20	0.41
1:B:147:GLY:HA2	1:B:152:GLY:HA3	2.03	0.41
1:B:471:GLU:O	1:B:474:VAL:HG22	2.21	0.41
1:A:263:LEU:HD23	1:A:263:LEU:HA	1.93	0.41
2:B:700:FAD:H9	2:B:700:FAD:H1'1	1.91	0.41
1:B:8:HIS:HE1	1:B:170:LEU:CD2	2.34	0.40
1:B:334:HIS:HE1	1:B:382:LEU:HD22	1.86	0.40
1:B:137:ARG:NE	1:B:163:ASP:OD1	2.54	0.40
1:B:421:SER:HB3	1:B:431:VAL:HG21	2.04	0.40

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	467/511 (91%)	461 (99%)	6 (1%)	0	100	100
1	B	466/511 (91%)	456 (98%)	9 (2%)	1 (0%)	44	42
All	All	933/1022 (91%)	917 (98%)	15 (2%)	1 (0%)	48	47

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	354	VAL

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	367/401 (92%)	366 (100%)	1 (0%)	91	94
1	B	367/401 (92%)	359 (98%)	8 (2%)	47	51
All	All	734/802 (92%)	725 (99%)	9 (1%)	67	73

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	235	ARG
1	B	48	LYS
1	B	119	ASP
1	B	183	SER
1	B	211	ARG

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Mol	Chain	Res	Type
1	B	267	GLU
1	B	366	ARG
1	B	412	ARG
1	B	426	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	46	HIS
1	B	125	GLN
1	B	167	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	Y7R	A	502	-	18,18,18	0.99	1 (5%)	21,21,21	1.60	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FAD	B	700	-	53,58,58	0.46	0	68,89,89	0.53	2 (2%)
2	FAD	A	501	-	53,58,58	0.48	0	68,89,89	0.54	1 (1%)

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	Y7R	A	502	-	-	9/18/18/18	-
2	FAD	B	700	-	-	7/30/50/50	0/6/6/6
2	FAD	A	501	-	-	5/30/50/50	0/6/6/6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	Y7R	O13-C12	-2.03	1.40	1.46

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	Y7R	C18-C06-C05	3.53	121.22	115.27
3	A	502	Y7R	C12-C11-C10	-3.15	120.59	126.04
3	A	502	Y7R	C17-C10-C09	2.78	119.95	115.27
2	A	501	FAD	C5A-C6A-N6A	2.38	123.98	120.35
2	B	700	FAD	P-O3P-PA	-2.26	125.06	132.83
2	B	700	FAD	C5A-C6A-N6A	2.25	123.77	120.35
3	A	502	Y7R	C19-C02-C01	2.06	119.15	114.60

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	FAD	C5'-O5'-P-O3P
3	A	502	Y7R	C04-C05-C06-C07
3	A	502	Y7R	C04-C05-C06-C18
3	A	502	Y7R	C07-C08-C09-C10
3	A	502	Y7R	C11-C12-O13-C14
3	A	502	Y7R	C03-C04-C05-C06
3	A	502	Y7R	C16-C14-O13-C12

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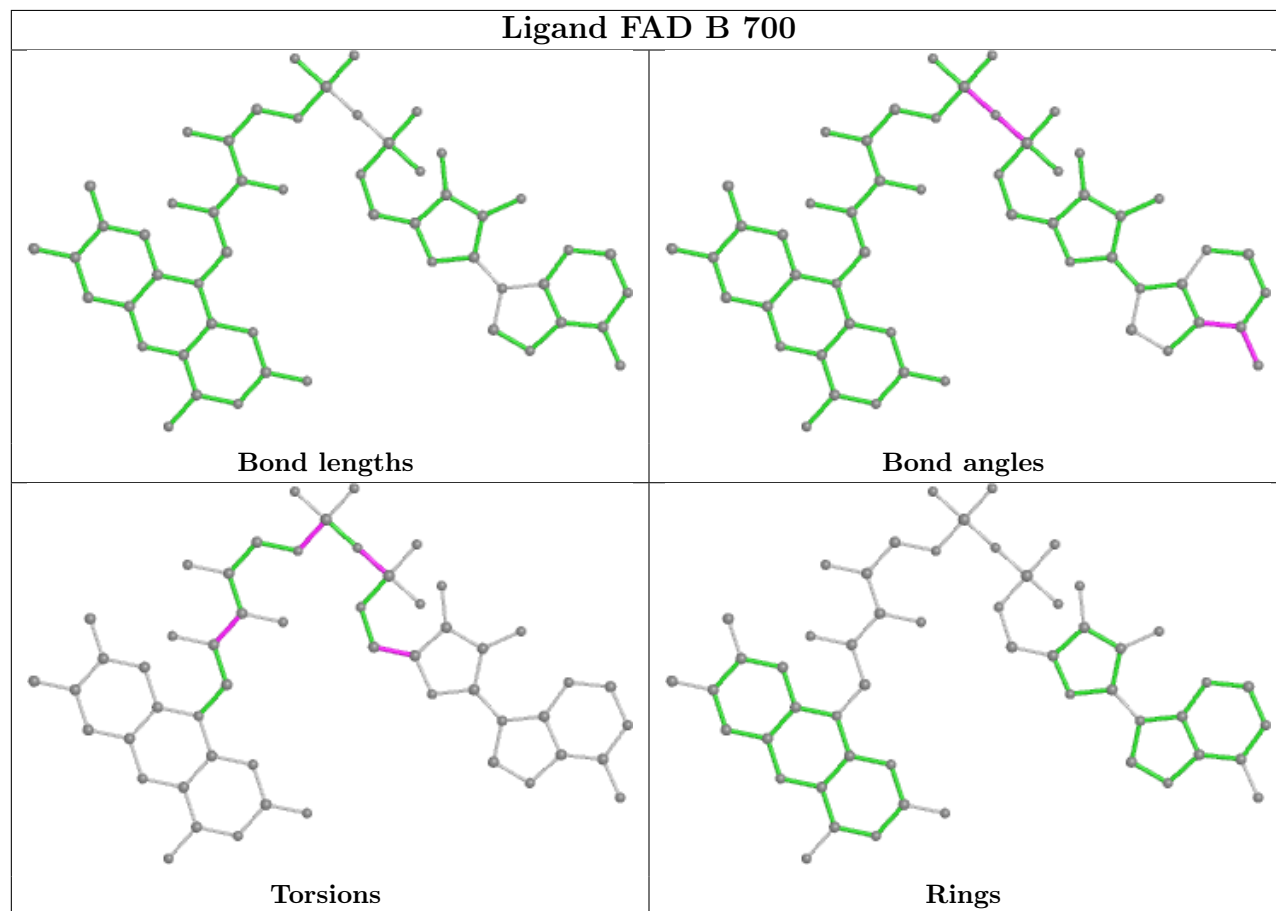
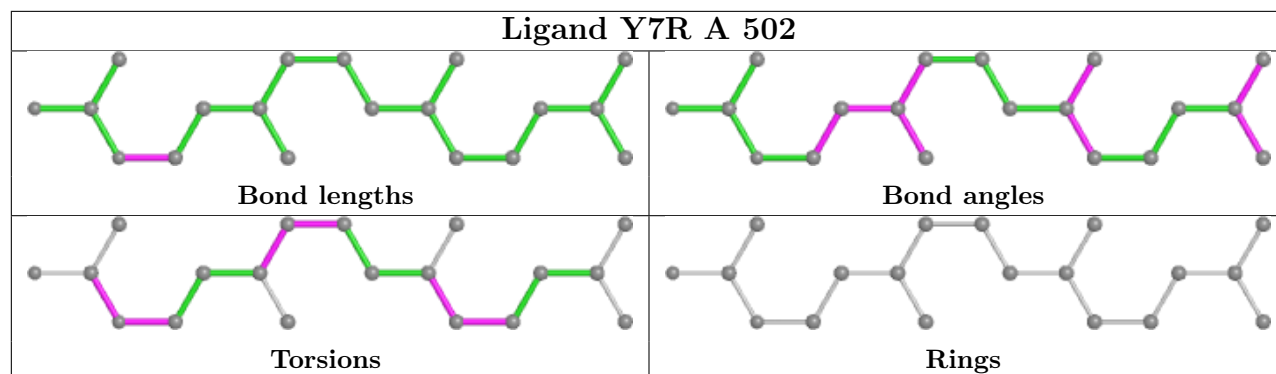
Mol	Chain	Res	Type	Atoms
2	A	501	FAD	PA-O3P-P-O5'
2	A	501	FAD	P-O3P-PA-O2A
2	A	501	FAD	C5'-O5'-P-O2P
3	A	502	Y7R	O15-C14-O13-C12
2	B	700	FAD	O2'-C2'-C3'-C4'
2	B	700	FAD	O2'-C2'-C3'-O3'
2	B	700	FAD	P-O3P-PA-O2A
3	A	502	Y7R	C08-C09-C10-C17
2	B	700	FAD	C5'-O5'-P-O3P
3	A	502	Y7R	C08-C09-C10-C11
2	B	700	FAD	C5'-O5'-P-O2P
2	A	501	FAD	O4B-C4B-C5B-O5B
2	B	700	FAD	O4B-C4B-C5B-O5B
2	B	700	FAD	C1'-C2'-C3'-O3'

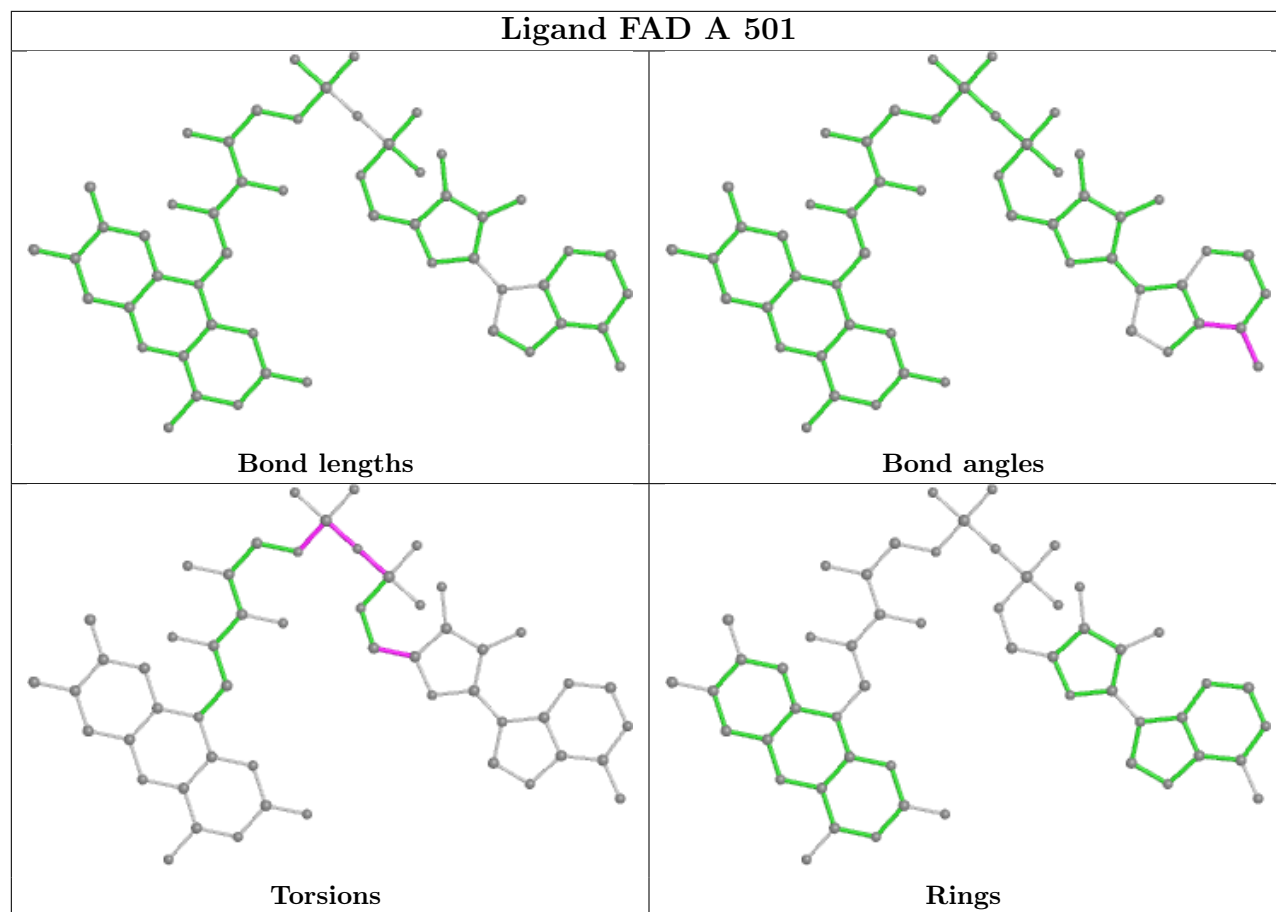
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	700	FAD	4	0
2	A	501	FAD	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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	471/511 (92%)	0.12	18 (3%)	44 42	28, 43, 67, 109	0
1	B	470/511 (91%)	0.92	53 (11%)	11 10	40, 70, 110, 142	0
All	All	941/1022 (92%)	0.52	71 (7%)	22 20	28, 53, 100, 142	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	234	VAL	5.9
1	B	149	GLY	5.2
1	B	230	ALA	5.1
1	A	230	ALA	4.8
1	B	354	VAL	4.8
1	B	35	VAL	4.3
1	B	159	VAL	4.3
1	B	152	GLY	4.1
1	B	219	ALA	3.7
1	B	234	VAL	3.7
1	B	405	VAL	3.6
1	B	150	SER	3.6
1	B	231	ASP	3.5
1	B	208	TYR	3.4
1	B	479	ALA	3.4
1	A	354	VAL	3.3
1	A	480	ALA	3.3
1	B	363	ALA	3.2
1	A	479	ALA	3.1
1	B	211	ARG	3.1
1	B	212	LEU	3.0
1	A	363	ALA	2.9
1	B	146	SER	2.8
1	B	232	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	362	ARG	2.8
1	B	413	PHE	2.7
1	B	145	GLY	2.7
1	B	14	ALA	2.7
1	B	118	LEU	2.7
1	B	265	THR	2.6
1	B	475	VAL	2.6
1	A	355	GLN	2.5
1	B	404	GLY	2.5
1	B	190	ALA	2.5
1	A	454	ARG	2.5
1	B	189	LEU	2.4
1	B	406	ASP	2.4
1	A	478	ASP	2.4
1	B	473	ALA	2.4
1	B	403	ILE	2.4
1	B	162	LEU	2.3
1	A	232	ASP	2.3
1	B	144	THR	2.3
1	B	296	PHE	2.3
1	A	353	SER	2.3
1	B	218	GLY	2.3
1	B	292	LEU	2.3
1	B	39	ALA	2.3
1	B	474	VAL	2.2
1	A	145	GLY	2.2
1	B	148	GLY	2.2
1	B	267	GLU	2.2
1	A	146	SER	2.2
1	A	229	ALA	2.2
1	B	192	LEU	2.2
1	B	300	SER	2.2
1	B	4	THR	2.1
1	A	208	TYR	2.1
1	B	248	GLY	2.1
1	B	50	VAL	2.1
1	B	362	ARG	2.1
1	A	149	GLY	2.1
1	B	355	GLN	2.1
1	B	155	THR	2.1
1	B	125	GLN	2.1
1	B	295	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	263	LEU	2.1
1	A	407	THR	2.1
1	B	244	TYR	2.0
1	B	24	VAL	2.0
1	B	161	ASP	2.0

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](#)

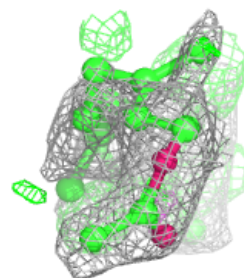
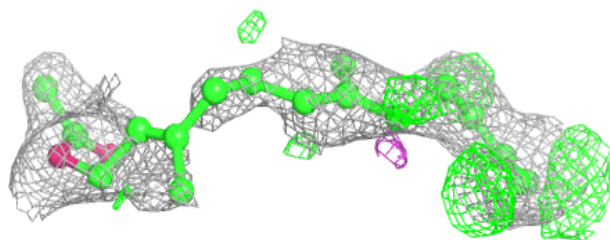
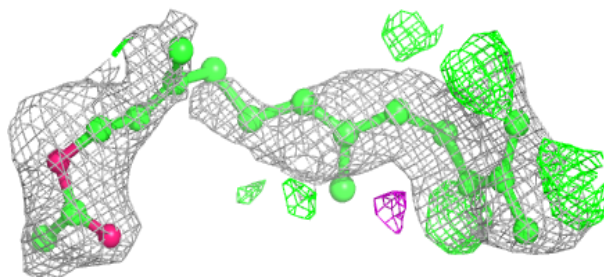
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	Y7R	A	502	19/19	0.70	0.22	74,82,89,90	0
2	FAD	B	700	53/53	0.91	0.10	57,65,77,77	0
2	FAD	A	501	53/53	0.96	0.07	30,35,41,42	0
4	CL	A	503	1/1	0.98	0.04	42,42,42,42	0

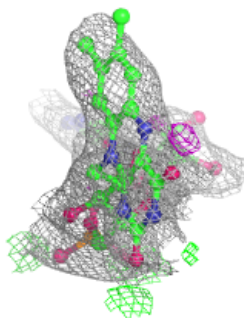
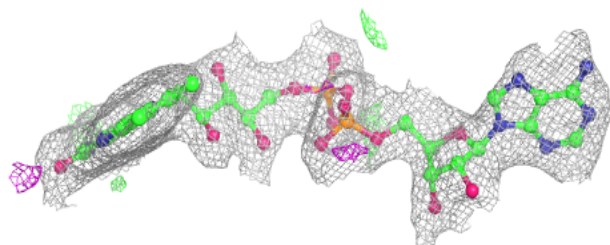
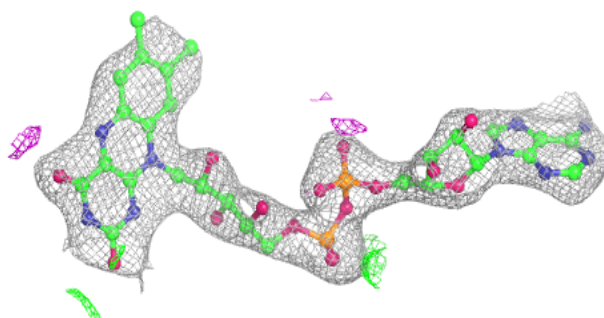
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around Y7R A 502:

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

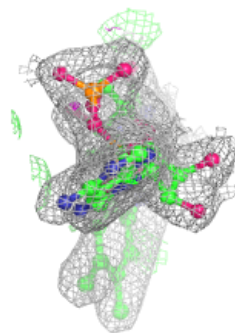
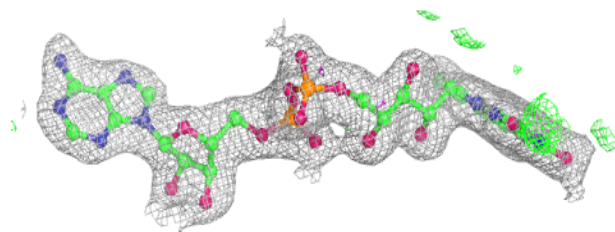
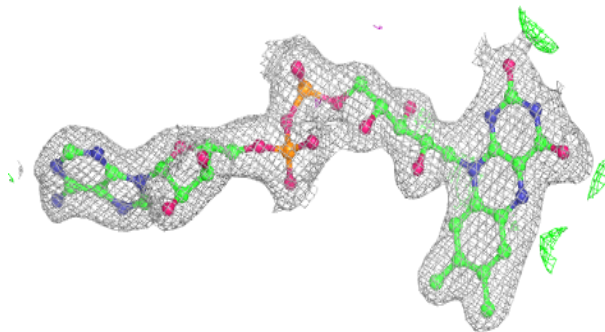
**Electron density around FAD B 700:**

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



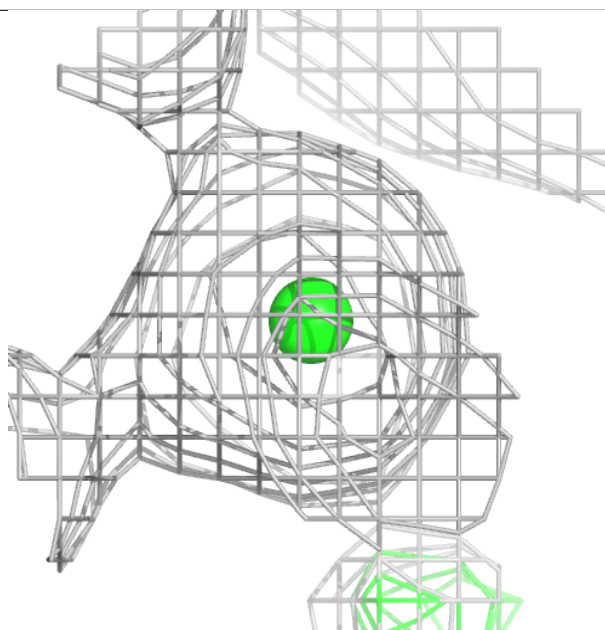
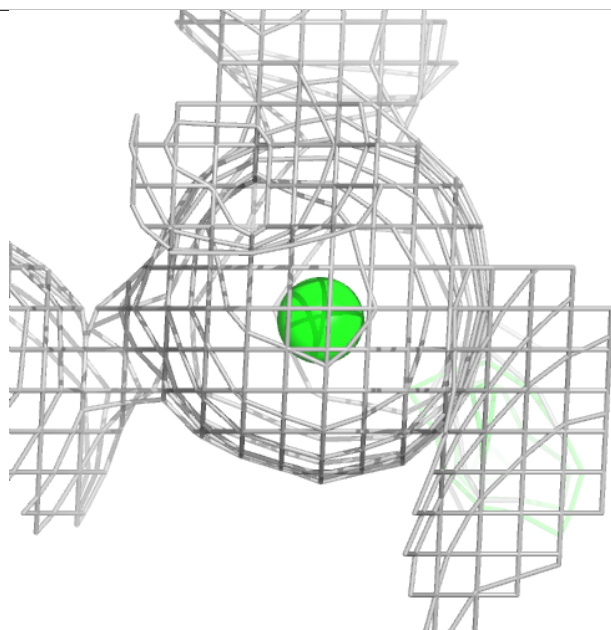
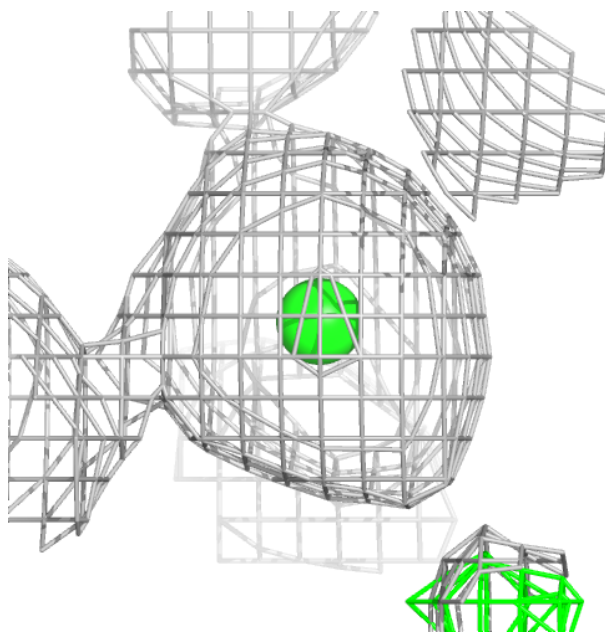
Electron density around FAD A 501:

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



Electron density around CL A 503:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.