



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 04:35 AM BST

PDB ID : 6LQ5  
Title : Crystal Structure of E447A Acyl-CoA Dehydrogenase FadE5 mutant from *Mycobacteria smegmatis* in complex with C16CoA  
Authors : Liu, X.; Chen, X.B.  
Deposited on : 2020-01-13  
Resolution : 1.90 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](mailto: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.

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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) : 1.13  
EDS : 2.13.1  
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) : 2.13.1

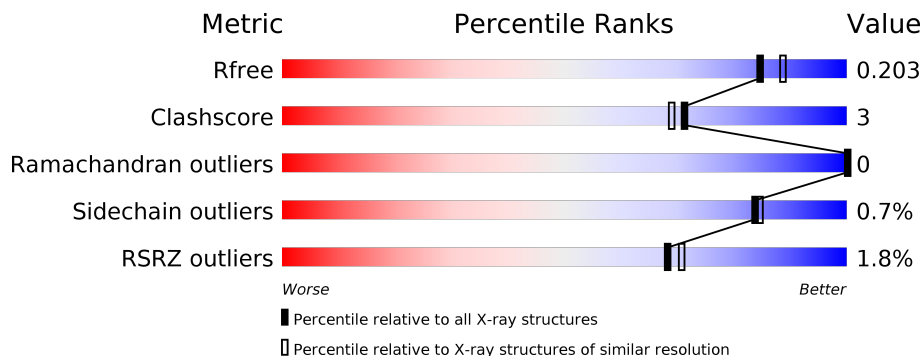
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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  $\geq 3$ , 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.

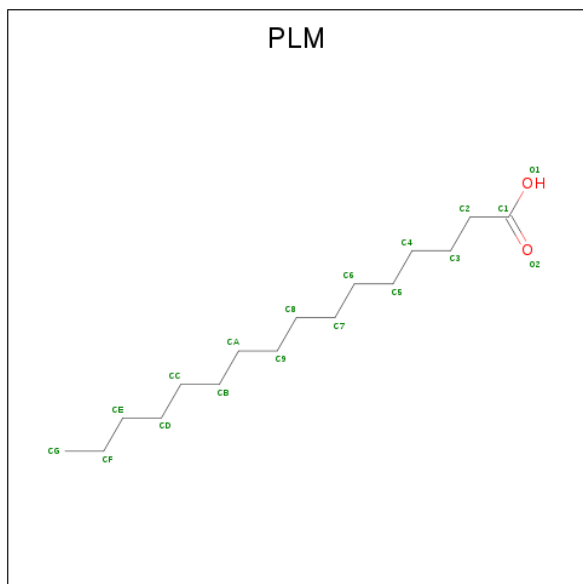
Mol	Chain	Length	Quality of chain
1	A	611	 2% 91% 8%
1	B	611	 2% 93% 6%



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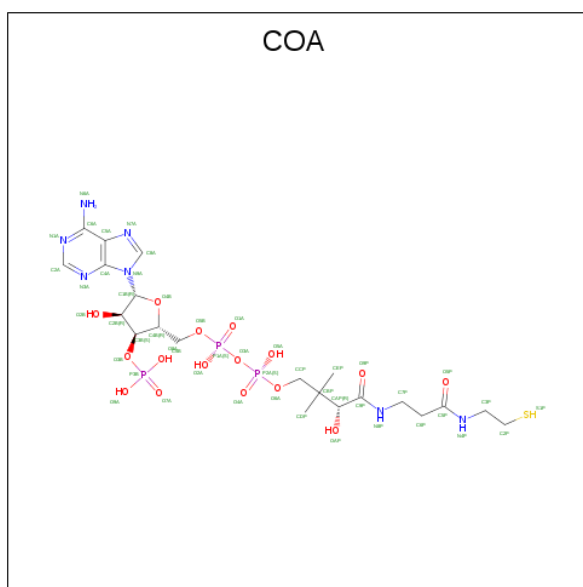
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	B	1	53	27	9	15	2	0	0

- Molecule 3 is PALMITIC ACID (three-letter code: PLM) (formula:  $C_{16}H_{32}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	17	16	1	0	0
3	B	1	17	16	1	0	0

- Molecule 4 is COENZYME A (three-letter code: COA) (formula:  $C_{21}H_{36}N_7O_{16}P_3S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
4	A	1	48	21	7	16	3	1	0	0
4	B	1	48	21	7	16	3	1	0	0

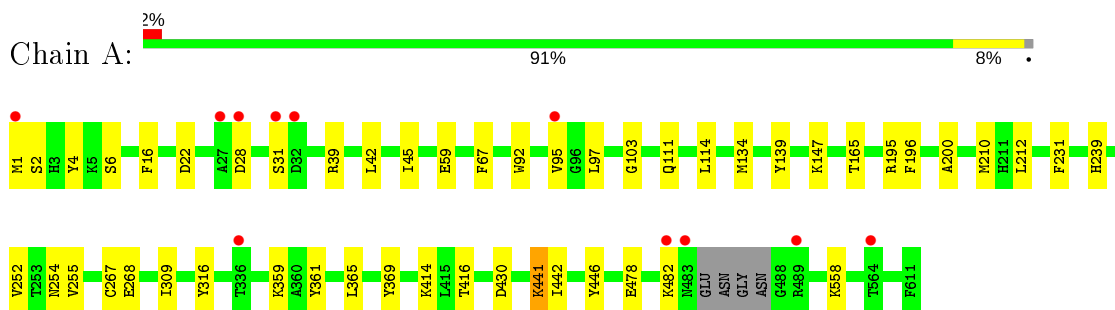
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	553	553	553	0	0
5	B	588	588	588	0	0

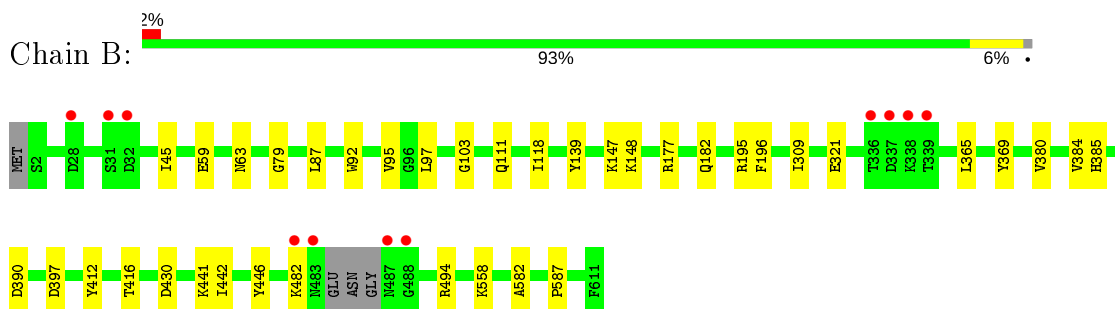
### 3 Residue-property plots [i](#)

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: Acyl-CoA dehydrogenase



- Molecule 1: Acyl-CoA dehydrogenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.21Å 206.79Å 74.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.66 – 1.90 19.66 – 1.90	Depositor EDS
% Data completeness (in resolution range)	93.6 (19.66-1.90) 93.6 (19.66-1.90)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.66 (at 1.90Å)	Xtrriage
Refinement program	PHENIX 1.14_3260	Depositor
R, $R_{free}$	0.154 , 0.202 0.156 , 0.203	Depositor DCC
$R_{free}$ test set	5530 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.6	Xtrriage
Anisotropy	0.428	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 56.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	10666	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: COA, PLM, 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	0.64	0/4738	0.66	1/6411 (0.0%)
1	B	0.68	1/4735 (0.0%)	0.67	2/6408 (0.0%)
All	All	0.66	1/9473 (0.0%)	0.66	3/12819 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	321	GLU	CG-CD	5.03	1.59	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	177	ARG	NE-CZ-NH2	-5.54	117.53	120.30
1	A	195	ARG	NE-CZ-NH2	-5.47	117.57	120.30
1	B	195	ARG	NE-CZ-NH2	-5.23	117.69	120.30

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	4646	0	4579	36	0
1	B	4643	0	4569	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	53	0	31	6	0
2	B	53	0	31	5	0
3	A	17	0	31	2	0
3	B	17	0	31	1	0
4	A	48	0	30	1	0
4	B	48	0	30	0	0
5	A	553	0	0	6	0
5	B	588	0	0	10	0
All	All	10666	0	9332	65	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 3.

All (65) 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:442:ILE:HD11	2:A:701:FAD:HM83	1.56	0.88
1:B:148:LYS:HD3	5:B:810:HOH:O	1.82	0.79
1:B:442:ILE:HD11	2:B:701:FAD:HM83	1.69	0.75
1:B:442:ILE:CD1	2:B:701:FAD:HM83	2.17	0.73
1:A:442:ILE:CD1	2:A:701:FAD:HM83	2.22	0.69
1:A:95:VAL:HG12	1:A:111:GLN:HG3	1.77	0.66
1:B:482:LYS:NZ	5:B:807:HOH:O	2.30	0.65
1:B:397:ASP:OD2	5:B:801:HOH:O	2.15	0.63
1:B:494:ARG:NH2	5:B:805:HOH:O	2.28	0.61
1:A:558:LYS:NZ	5:A:810:HOH:O	2.34	0.59
1:A:59:GLU:OE1	5:A:801:HOH:O	2.17	0.59
1:B:45:ILE:HD12	1:B:92:TRP:CE3	2.38	0.59
1:A:139:TYR:CZ	1:A:147:LYS:HD3	2.40	0.56
1:B:148:LYS:CD	5:B:810:HOH:O	2.48	0.55
1:A:196:PHE:O	2:A:701:FAD:C4X	2.56	0.54
1:A:254:ASN:ND2	5:A:804:HOH:O	2.24	0.54
1:B:309:ILE:HG12	1:B:365:LEU:HB3	1.91	0.53
1:A:252:VAL:HG13	1:A:267:CYS:HB3	1.90	0.52
1:A:67:PHE:HB2	1:A:255:VAL:HG23	1.91	0.52
1:B:442:ILE:HD13	2:B:701:FAD:HM83	1.91	0.52
1:B:139:TYR:CZ	1:B:147:LYS:HD3	2.44	0.52
1:A:210:MET:HE2	1:A:212:LEU:HD21	1.91	0.51
1:A:92:TRP:O	1:A:95:VAL:HG23	2.10	0.51
1:A:134:MET:HE1	3:A:702:PLM:HB2	1.92	0.51
1:A:200:ALA:HB3	1:A:267:CYS:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:ILE:HD11	1:B:118:ILE:HD11	1.93	0.50
1:A:416:THR:HG23	1:B:441:LYS:HE2	1.92	0.50
1:A:268:GLU:OE1	5:A:802:HOH:O	2.20	0.50
1:A:134:MET:CE	3:A:702:PLM:HB2	2.42	0.49
1:B:196:PHE:O	2:B:701:FAD:C4X	2.61	0.49
1:B:412:TYR:CE1	1:B:441:LYS:HD2	2.47	0.49
1:A:239:HIS:HD2	5:A:1198:HOH:O	1.96	0.48
1:A:16:PHE:HE2	1:A:39:ARG:HD2	1.78	0.48
1:A:482:LYS:HE2	1:A:482:LYS:HA	1.94	0.48
1:B:148:LYS:HE3	5:B:968:HOH:O	2.12	0.48
1:A:45:ILE:HD12	1:A:92:TRP:CE3	2.49	0.48
1:A:42:LEU:HD23	1:A:114:LEU:HD23	1.96	0.47
1:B:59:GLU:OE1	1:B:79:GLY:HA3	2.16	0.46
1:B:63:ASN:ND2	5:B:804:HOH:O	2.24	0.46
1:B:95:VAL:HG12	1:B:111:GLN:HG3	1.98	0.46
1:B:87:LEU:HD11	1:B:118:ILE:HD13	1.99	0.45
1:B:390:ASP:OD2	5:B:802:HOH:O	2.21	0.44
1:A:254:ASN:ND2	5:A:815:HOH:O	2.41	0.44
1:B:582:ALA:O	1:B:587:PRO:HD3	2.18	0.43
1:B:196:PHE:HB3	2:B:701:FAD:C9A	2.48	0.43
1:A:316:TYR:CZ	1:A:359:LYS:HB2	2.53	0.43
1:A:361:TYR:CE2	1:A:414:LYS:HE3	2.54	0.43
1:B:97:LEU:O	1:B:103:GLY:HA3	2.18	0.43
1:B:182:GLN:NE2	5:B:827:HOH:O	2.52	0.43
1:A:4:TYR:CE2	1:A:6:SER:HB3	2.54	0.43
1:A:309:ILE:HG12	1:A:365:LEU:HB3	2.01	0.42
1:A:441:LYS:HE3	1:B:416:THR:HG23	2.01	0.42
1:B:384:VAL:HG23	1:B:385:HIS:CD2	2.54	0.42
1:A:478:GLU:O	1:A:482:LYS:HG2	2.20	0.42
1:A:28:ASP:O	1:A:31:SER:OG	2.25	0.42
3:B:702:PLM:HC1	3:B:702:PLM:H92	1.88	0.42
1:A:165:THR:OG1	2:A:701:FAD:H1'1	2.19	0.42
1:A:1:MET:HB3	1:A:2:SER:H	1.61	0.41
1:B:558:LYS:NZ	5:B:830:HOH:O	2.52	0.41
1:A:210:MET:HE3	1:A:231:PHE:CE1	2.56	0.41
1:B:380:VAL:O	1:B:384:VAL:HG22	2.21	0.41
1:A:196:PHE:HB3	2:A:701:FAD:C9A	2.51	0.41
1:A:97:LEU:HB3	1:A:103:GLY:HA3	2.02	0.41
1:A:22:ASP:OD1	1:A:22:ASP:N	2.54	0.40
2:A:701:FAD:C2	4:A:703:COA:S1P	3.09	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	603/611 (99%)	591 (98%)	12 (2%)	0	100	100
1	B	603/611 (99%)	594 (98%)	9 (2%)	0	100	100
All	All	1206/1222 (99%)	1185 (98%)	21 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	474/478 (99%)	470 (99%)	4 (1%)	81	82
1	B	473/478 (99%)	470 (99%)	3 (1%)	86	87
All	All	947/956 (99%)	940 (99%)	7 (1%)	84	84

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	369	TYR
1	A	430	ASP
1	A	441	LYS
1	A	446	TYR
1	B	369	TYR
1	B	430	ASP
1	B	446	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	254	ASN
1	A	519	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

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	PLM	A	702	4	16,16,17	0.83	0	15,15,17	0.44	0
2	FAD	A	701	-	51,58,58	1.24	4 (7%)	60,89,89	2.23	8 (13%)
4	COA	B	703	3	41,50,50	4.05	12 (29%)	52,75,75	1.35	5 (9%)
4	COA	A	703	3	41,50,50	4.00	10 (24%)	52,75,75	1.34	5 (9%)
2	FAD	B	701	-	51,58,58	1.24	5 (9%)	60,89,89	2.23	8 (13%)
3	PLM	B	702	4	16,16,17	0.79	0	15,15,17	0.82	0

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	PLM	A	702	4	-	7/13/14/15	-
2	FAD	A	701	-	-	4/30/50/50	0/6/6/6
4	COA	B	703	3	-	3/44/64/64	0/3/3/3
4	COA	A	703	3	-	7/44/64/64	0/3/3/3
2	FAD	B	701	-	-	2/30/50/50	0/6/6/6
3	PLM	B	702	4	-	6/13/14/15	-

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	703	COA	O4B-C1B	15.76	1.63	1.41
4	A	703	COA	C2B-C1B	-15.19	1.30	1.53
4	B	703	COA	C2B-C1B	-15.00	1.31	1.53
4	A	703	COA	O4B-C1B	14.61	1.61	1.41
4	A	703	COA	O4B-C4B	-6.90	1.29	1.45
4	A	703	COA	C9P-N8P	6.90	1.48	1.33
4	B	703	COA	C9P-N8P	6.88	1.48	1.33
2	B	701	FAD	C4X-C10	6.02	1.44	1.38
4	B	703	COA	O4B-C4B	-5.60	1.32	1.45
2	A	701	FAD	C4X-C10	5.60	1.44	1.38
4	A	703	COA	C5P-N4P	5.59	1.46	1.33
4	B	703	COA	C5P-N4P	5.24	1.45	1.33
4	A	703	COA	O2B-C2B	4.29	1.53	1.43
4	B	703	COA	O2B-C2B	4.19	1.52	1.43
4	B	703	COA	P3B-O3B	4.17	1.67	1.59
4	A	703	COA	P3B-O3B	3.95	1.66	1.59
2	A	701	FAD	C4-N3	3.61	1.39	1.33
4	B	703	COA	C6A-N6A	3.44	1.46	1.34
4	A	703	COA	C6A-N6A	3.34	1.46	1.34
2	B	701	FAD	C9A-N10	2.68	1.42	1.38
4	B	703	COA	O9P-C9P	-2.55	1.18	1.23
2	A	701	FAD	C4-C4X	2.45	1.45	1.41
2	B	701	FAD	C4-N3	2.34	1.37	1.33
4	A	703	COA	OAP-CAP	-2.32	1.38	1.42
4	A	703	COA	O5P-C5P	-2.32	1.18	1.23
2	B	701	FAD	C10-N1	-2.30	1.30	1.33
4	B	703	COA	OAP-CAP	-2.29	1.38	1.42
2	A	701	FAD	C9A-N10	2.24	1.41	1.38
2	B	701	FAD	P-O2P	-2.17	1.45	1.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	703	COA	P2A-O6A	2.17	1.68	1.59
4	B	703	COA	C6P-C5P	2.07	1.55	1.51

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	FAD	C4-N3-C2	12.59	125.78	115.14
2	B	701	FAD	C4-N3-C2	12.21	125.45	115.14
2	A	701	FAD	C4X-C4-N3	-7.30	113.44	123.43
2	B	701	FAD	C4X-C4-N3	-6.82	114.10	123.43
4	A	703	COA	N3A-C2A-N1A	-5.04	120.81	128.68
2	B	701	FAD	C10-C4X-N5	4.84	124.60	121.26
2	A	701	FAD	C10-C4X-N5	4.45	124.33	121.26
4	B	703	COA	N3A-C2A-N1A	-4.22	122.08	128.68
2	B	701	FAD	C4X-C10-N10	-4.06	116.12	120.30
4	B	703	COA	C3P-N4P-C5P	-3.64	116.09	122.84
2	B	701	FAD	C1'-N10-C9A	3.51	121.06	118.29
2	A	701	FAD	C4-C4X-C10	-3.45	117.67	119.95
2	A	701	FAD	C4X-C10-N10	-3.41	116.80	120.30
2	B	701	FAD	C4-C4X-C10	-3.18	117.85	119.95
4	A	703	COA	C6P-C7P-N8P	-3.07	105.70	111.90
2	A	701	FAD	C1'-N10-C9A	2.79	120.49	118.29
4	B	703	COA	C6P-C7P-N8P	-2.55	106.74	111.90
4	B	703	COA	C7P-N8P-C9P	-2.50	118.14	122.59
2	B	701	FAD	C5A-C6A-N6A	2.46	124.09	120.35
4	A	703	COA	C3P-N4P-C5P	-2.24	118.67	122.84
4	A	703	COA	C1B-N9A-C4A	-2.21	122.75	126.64
4	B	703	COA	C7P-C6P-C5P	-2.21	108.67	112.36
4	A	703	COA	C5B-C4B-C3B	-2.21	107.08	114.40
2	A	701	FAD	C5A-C6A-N6A	2.20	123.69	120.35
2	B	701	FAD	O2'-C2'-C1'	2.07	114.57	109.59
2	A	701	FAD	O2'-C2'-C1'	2.04	114.50	109.59

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	703	COA	CAP-CBP-CCP-O6A
3	B	702	PLM	C9-CA-CB-CC
3	A	702	PLM	C4-C5-C6-C7
3	B	702	PLM	CC-CD-CE-CF
3	A	702	PLM	C6-C7-C8-C9

*Continued on next page...*

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Mol	Chain	Res	Type	Atoms
2	A	701	FAD	O2'-C2'-C3'-C4'
3	A	702	PLM	C5-C6-C7-C8
3	A	702	PLM	CC-CD-CE-CF
3	B	702	PLM	C8-C9-CA-CB
2	A	701	FAD	O2'-C2'-C3'-O3'
3	A	702	PLM	C8-C9-CA-CB
3	A	702	PLM	C3-C4-C5-C6
3	B	702	PLM	C5-C6-C7-C8
4	A	703	COA	P2A-O3A-P1A-O1A
2	B	701	FAD	O2'-C2'-C3'-C4'
3	B	702	PLM	C7-C8-C9-CA
4	A	703	COA	O9P-C9P-CAP-OAP
4	A	703	COA	CDP-CBP-CCP-O6A
4	A	703	COA	CEP-CBP-CCP-O6A
2	B	701	FAD	O2'-C2'-C3'-O3'
4	B	703	COA	C2P-C3P-N4P-C5P
4	A	703	COA	C2P-C3P-N4P-C5P
4	B	703	COA	CEP-CBP-CCP-O6A
3	A	702	PLM	CD-CE-CF-CG
2	A	701	FAD	C5B-O5B-PA-O3P
4	A	703	COA	P2A-O3A-P1A-O2A
2	A	701	FAD	C5B-O5B-PA-O1A
4	B	703	COA	CDP-CBP-CCP-O6A
3	B	702	PLM	C6-C7-C8-C9

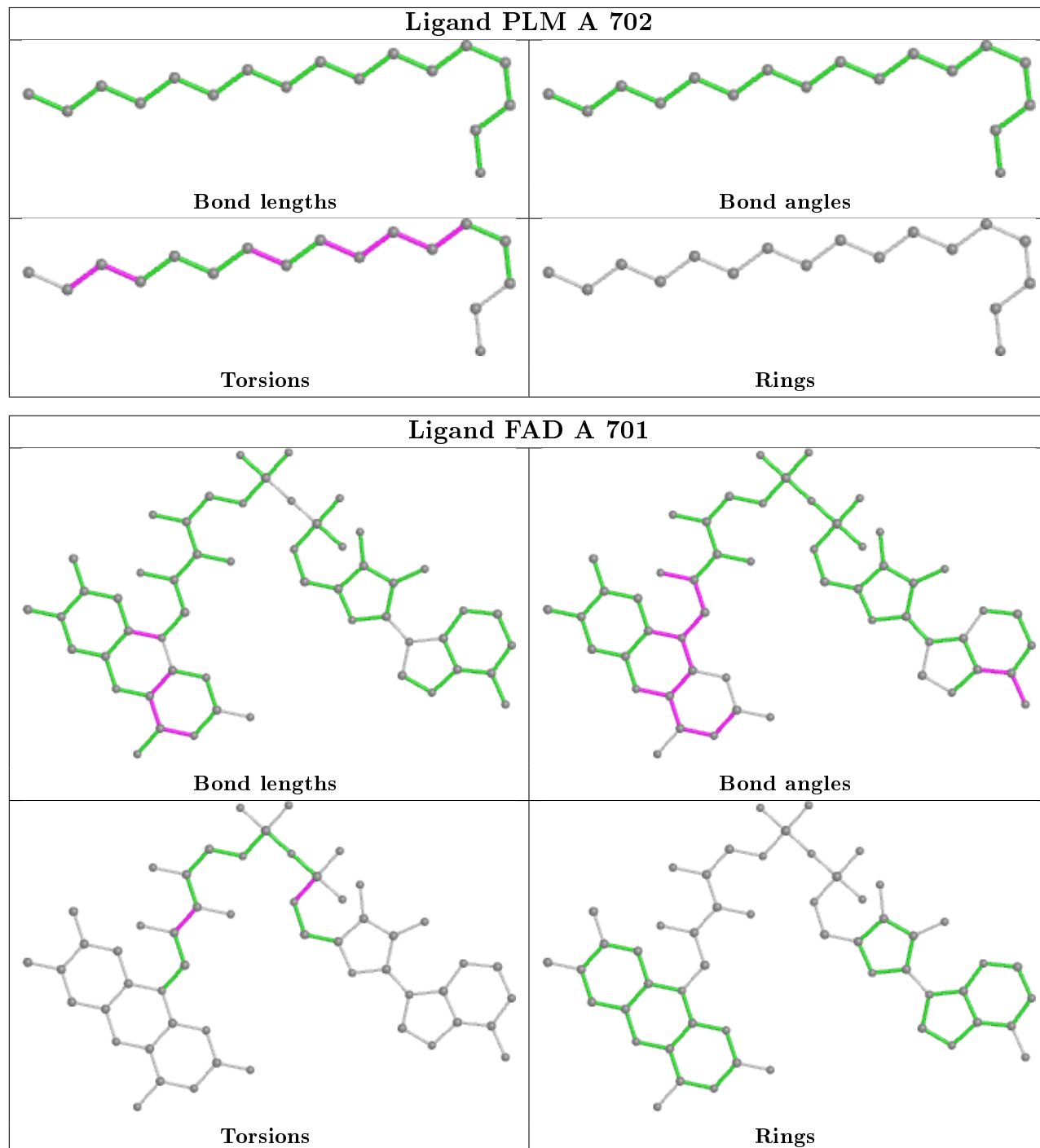
There are no ring outliers.

5 monomers are involved in 14 short contacts:

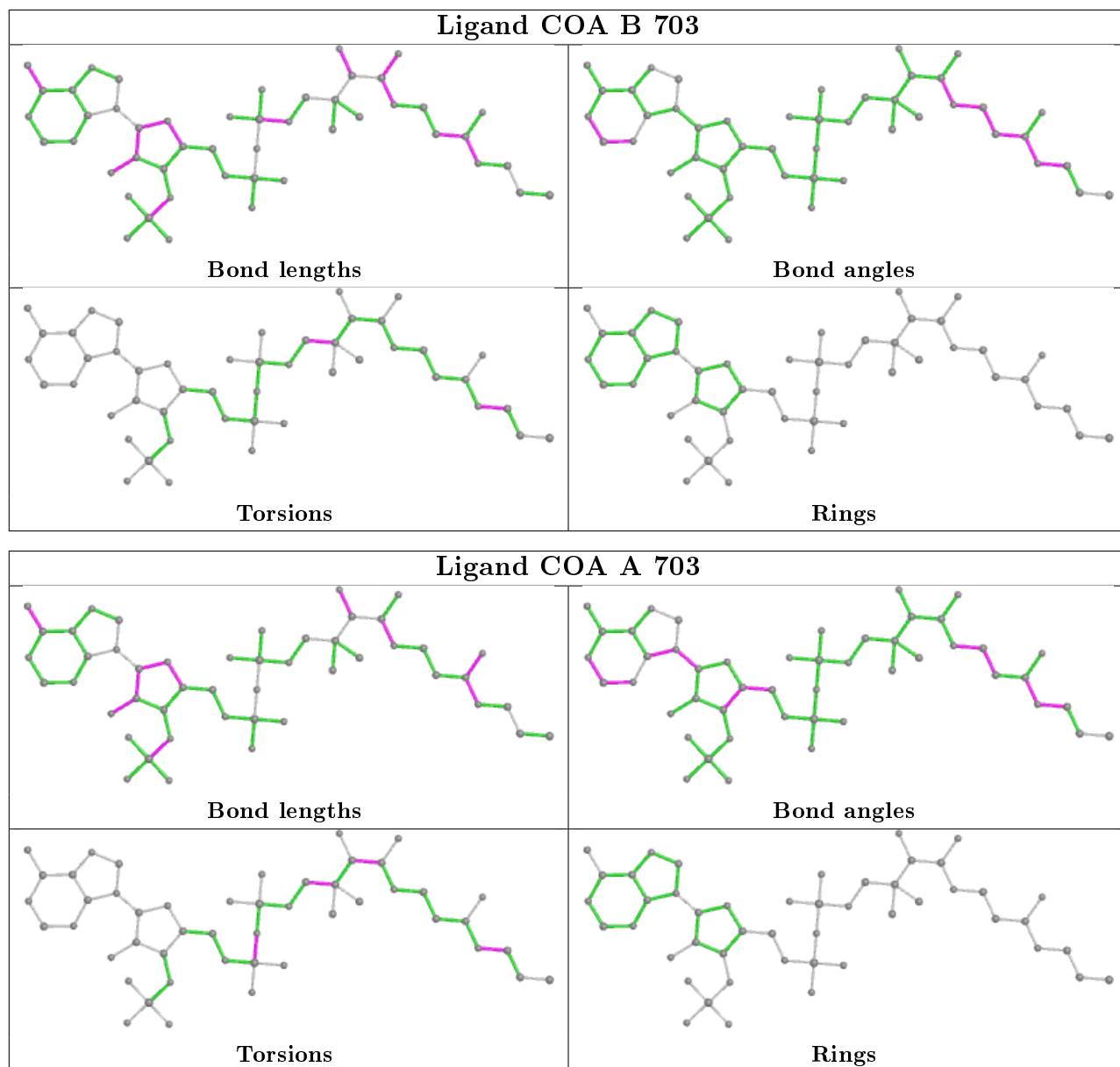
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	702	PLM	2	0
2	A	701	FAD	6	0
4	A	703	COA	1	0
2	B	701	FAD	5	0
3	B	702	PLM	1	0

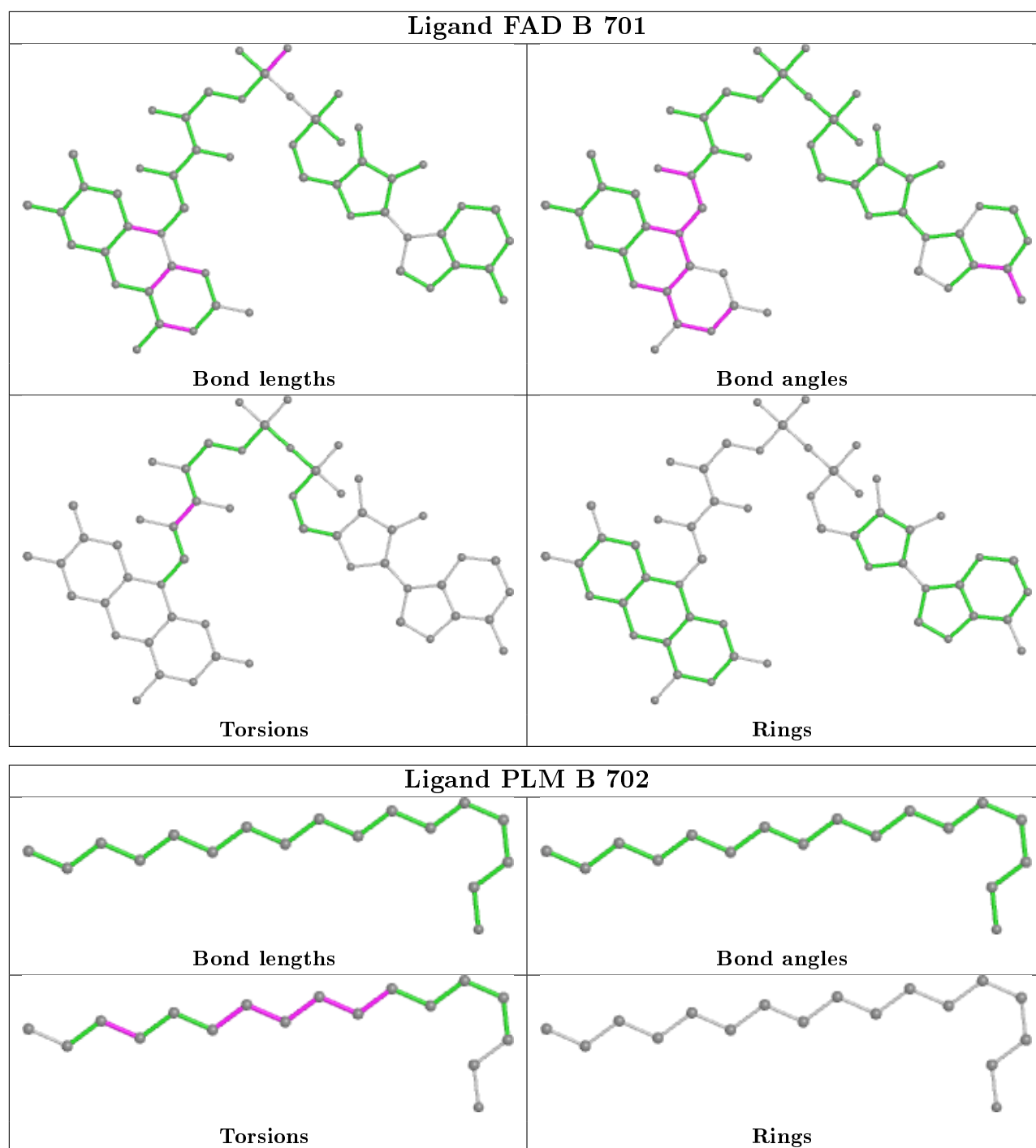
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	607/611 (99%)	-0.02	11 (1%) 68 71	14, 21, 38, 61	0
1	B	607/611 (99%)	-0.10	11 (1%) 68 71	13, 20, 35, 56	0
All	All	1214/1222 (99%)	-0.06	22 (1%) 68 71	13, 20, 37, 61	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	MET	7.0
1	A	27	ALA	4.7
1	A	32	ASP	4.0
1	B	336	THR	3.8
1	A	28	ASP	3.8
1	B	32	ASP	3.5
1	B	338	LYS	3.4
1	A	31	SER	3.3
1	B	31	SER	3.0
1	B	488	GLY	2.9
1	A	489	ARG	2.9
1	A	482	LYS	2.9
1	A	336	THR	2.8
1	B	483	ASN	2.7
1	A	95	VAL	2.6
1	A	564	THR	2.5
1	B	337	ASP	2.5
1	B	339	THR	2.4
1	A	483	ASN	2.4
1	B	482	LYS	2.3
1	B	487	ASN	2.2
1	B	28	ASP	2.2

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

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

## 6.3 Carbohydrates [i](#)

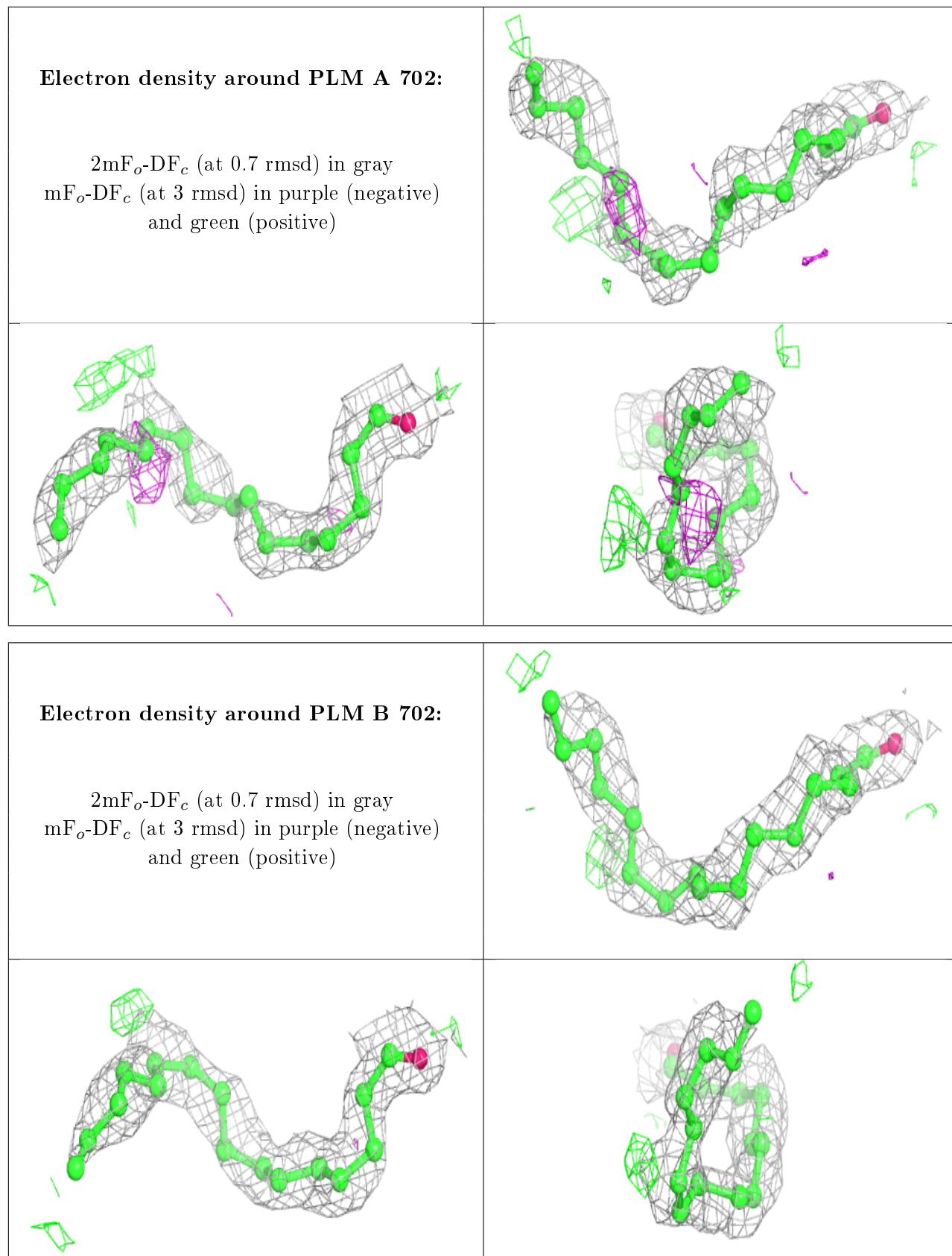
There are no monosaccharides in this entry.

## 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, 95<sup>th</sup> 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.

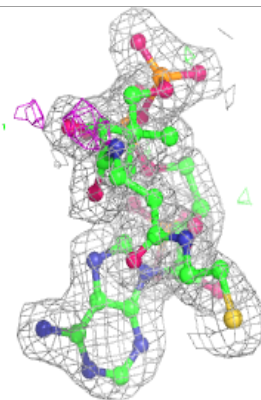
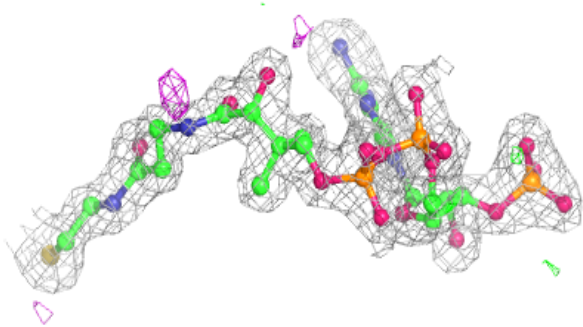
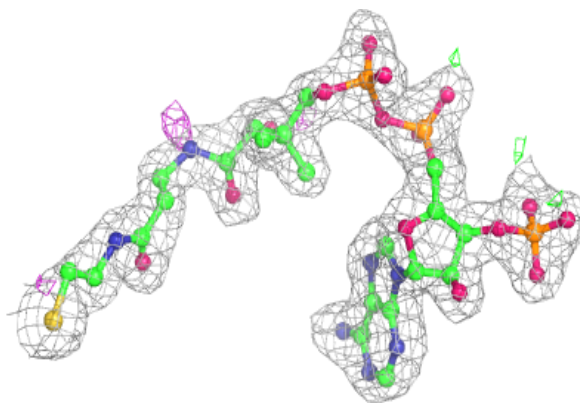
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	PLM	A	702	17/18	0.88	0.15	26,37,50,55	0
3	PLM	B	702	17/18	0.90	0.16	21,33,47,51	0
4	COA	A	703	48/48	0.94	0.12	20,26,33,36	0
2	FAD	B	701	53/53	0.94	0.10	15,19,24,25	0
4	COA	B	703	48/48	0.94	0.11	19,24,30,32	0
2	FAD	A	701	53/53	0.95	0.10	15,20,25,31	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.

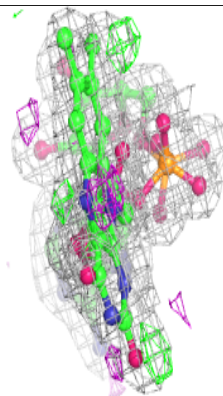
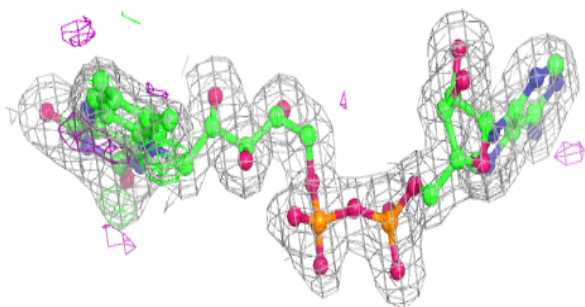
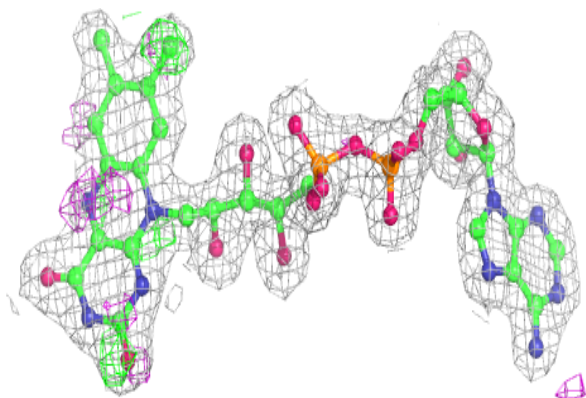


**Electron density around COA A 703:**

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

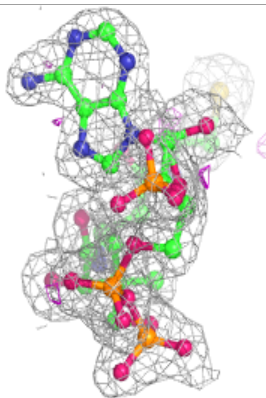
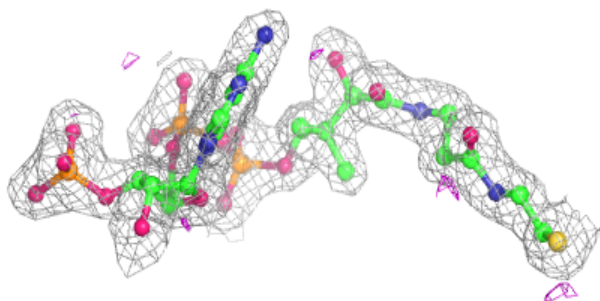
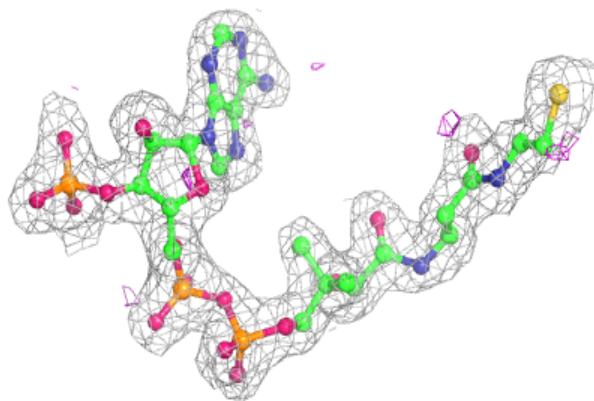
**Electron density around FAD B 701:**

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

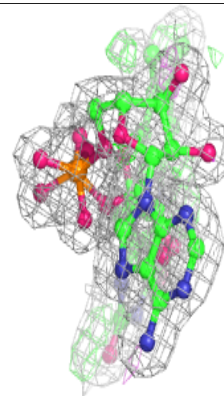
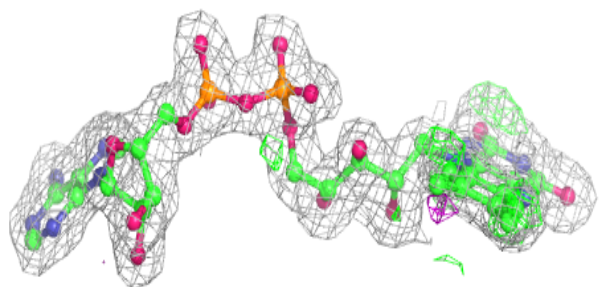
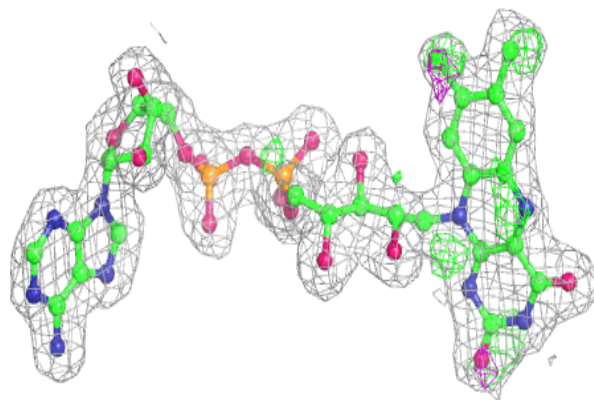


**Electron density around COA B 703:**

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

**Electron density around FAD A 701:**

$2mF_o-DF_c$  (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.