Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 05:17 PM UTC

PDB ID	:	8PNG / pdb_00008png
Title	:	Crystal structure of the apo acyl-CoA dehydrogenase FadE2 (PA0508) from Pseudomonas aeruginosa
Authors	:	Wang, M.; Brear, P.; Welch, M.
Deposited on	:	2023-06-30
Resolution	:	1.94 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:

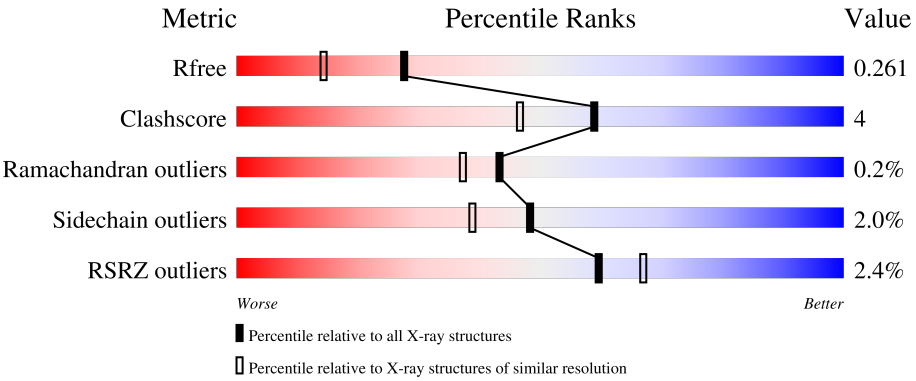
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

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}	180053	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (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 <=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	594	3% 88% 12%
1	B	594	2% 89% 10%

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	PEG	A	604	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 9714 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.

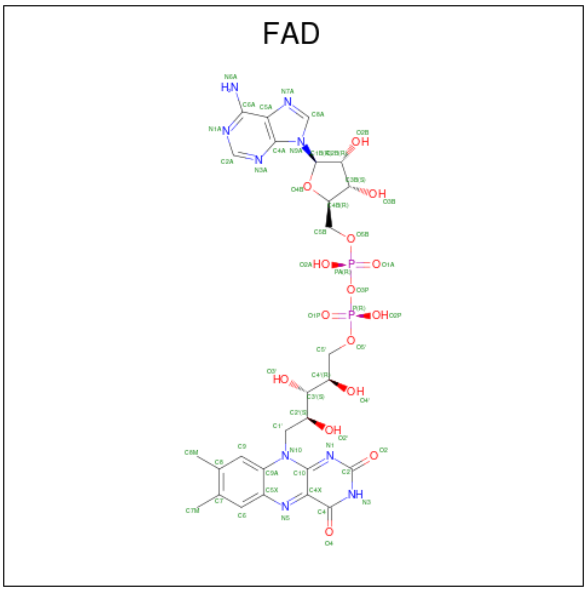
- Molecule 1 is a protein called Probable acyl-CoA dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	590	Total	C	N	O	S	0	1	0
			4469	2832	767	847	23			
1	A	594	Total	C	N	O	S	0	1	0
			4496	2848	773	851	24			

There are 4 discrepancies between the modelled and reference sequences:

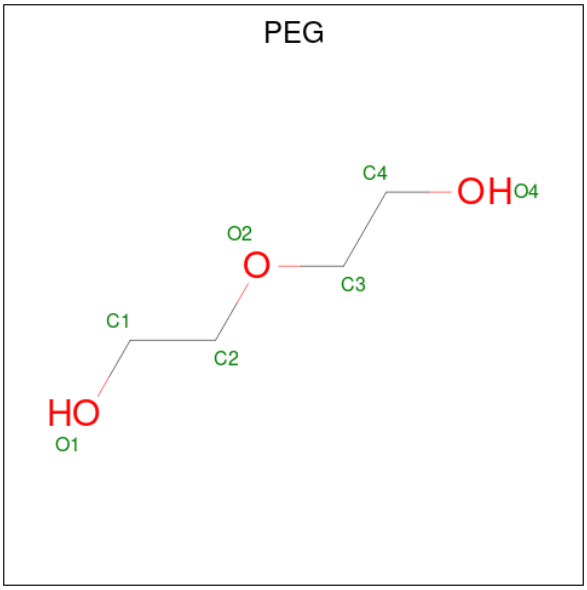
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP Q9I610
B	0	HIS	-	expression tag	UNP Q9I610
A	-1	GLY	-	expression tag	UNP Q9I610
A	0	HIS	-	expression tag	UNP Q9I610

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).



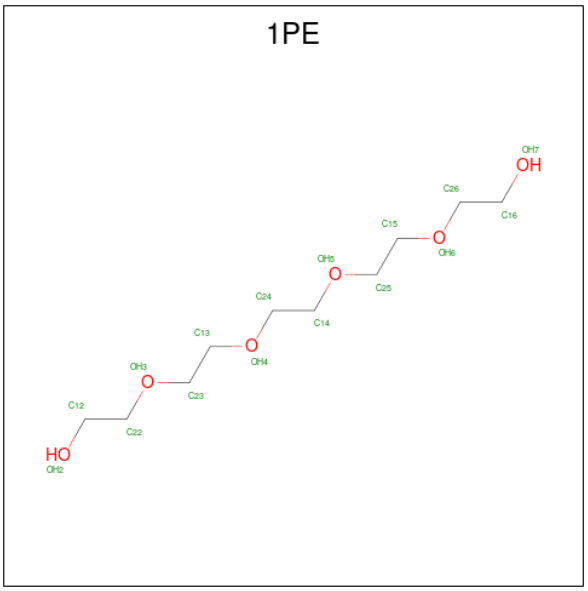
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



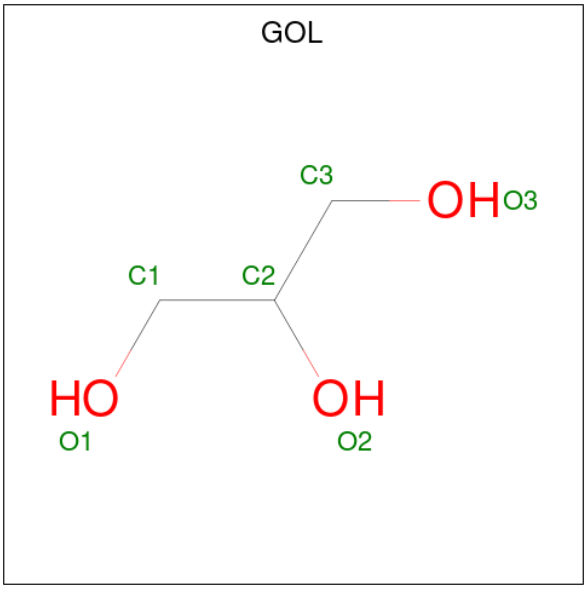
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	O		0	0
			7	4	3			
3	A	1	Total	C	O		0	0
			7	4	3			
3	A	1	Total	C	O		0	0
			7	4	3			
3	A	1	Total	C	O		0	0
			7	4	3			

- Molecule 4 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 16 10 6	0	0
4	A	1	Total C O 16 10 6	0	0
4	A	1	Total C O 16 10 6	0	0

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 12 6 6	0	1

- Molecule 6 is water.

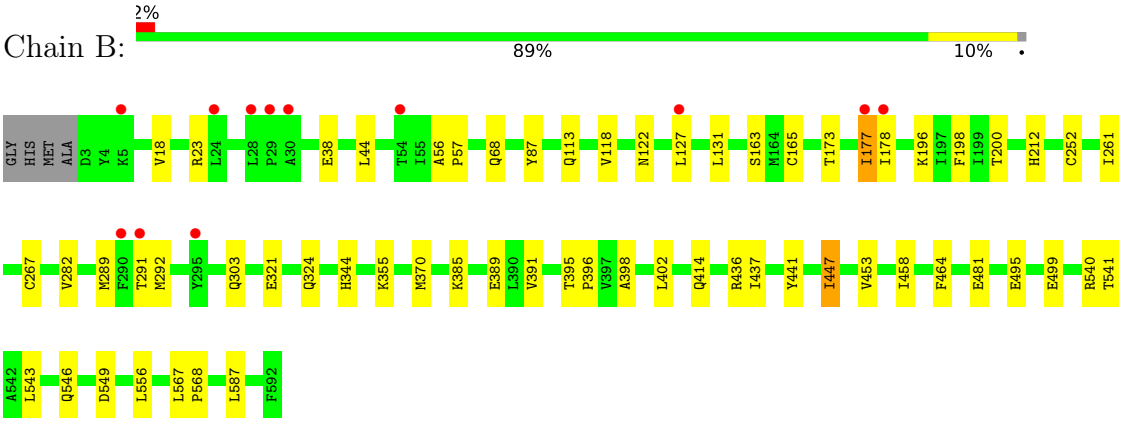
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	254	Total O 254 254	0	0
6	A	301	Total O 301 301	0	0

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.

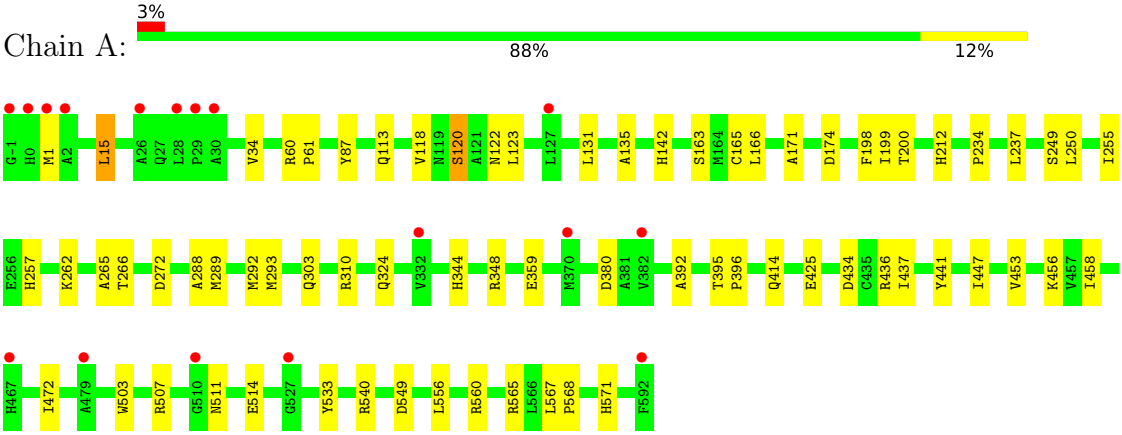
• Molecule 1: Probable acyl-CoA dehydrogenase

Chain B:



• Molecule 1: Probable acyl-CoA dehydrogenase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	61.85Å 64.40Å 286.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	62.91 – 1.94 62.91 – 1.94	Depositor EDS
% Data completeness (in resolution range)	99.9 (62.91-1.94) 99.9 (62.91-1.94)	Depositor EDS
R_{merge}	0.48	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.01 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.203 , 0.260 0.209 , 0.261	Depositor DCC
R_{free} test set	4238 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	30.6	Xtriage
Anisotropy	0.299	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 20.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.023 for k,h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	9714	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.72% of the height of the origin peak. No significant pseudotranslation is detected.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 1PE, PEG, GOL, 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	1.03	0/4592	1.45	1/6221 (0.0%)
1	B	1.03	0/4564	1.43	0/6184
All	All	1.03	0/9156	1.44	1/12405 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	549	ASP	CA-CB-CG	5.20	117.80	112.60

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	4496	0	4451	47	0
1	B	4469	0	4424	38	0
2	A	53	0	31	3	0
2	B	53	0	31	1	0
3	A	21	0	30	5	0
3	B	7	0	10	0	0
4	A	32	0	44	0	0
4	B	16	0	22	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	12	0	16	1	0
6	A	301	0	0	1	0
6	B	254	0	0	8	0
All	All	9714	0	9059	80	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 4.

All (80) 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:587:LEU:O	1:A:348:ARG:NH2	2.23	0.70
1:B:324:GLN:HE21	1:A:174:ASP:H	1.40	0.67
1:A:257:HIS:HA	3:A:604:PEG:H12	1.79	0.64
1:B:177:ILE:HD11	6:B:911:HOH:O	1.97	0.64
1:B:68:GLN:HG2	6:B:906:HOH:O	2.00	0.61
1:B:131:LEU:HD11	1:B:200:THR:HB	1.82	0.61
1:B:18:VAL:HA	1:B:541:THR:HG21	1.83	0.60
1:A:265:ALA:HA	3:A:604:PEG:H41	1.83	0.60
1:A:120:SER:O	1:A:310[B]:ARG:HG3	2.02	0.60
1:B:56:ALA:HB3	1:B:57:PRO:HD3	1.84	0.59
1:B:163:SER:OG	1:B:212:HIS:HD2	1.86	0.58
1:A:135:ALA:HA	1:A:292:MET:HE3	1.85	0.57
1:B:541:THR:HG22	6:B:935:HOH:O	2.04	0.56
1:A:131:LEU:HD11	1:A:200:THR:HG22	1.86	0.56
1:A:324:GLN:O	1:A:344:HIS:HE1	1.91	0.54
1:A:571:HIS:HD2	6:A:830:HOH:O	1.91	0.54
1:A:234:PRO:HG2	1:A:237:LEU:HD23	1.89	0.53
1:B:324:GLN:O	1:B:344:HIS:HE1	1.93	0.52
1:B:23:ARG:HD2	6:B:908:HOH:O	2.10	0.52
1:B:324:GLN:NE2	1:A:174:ASP:H	2.09	0.50
1:A:249:SER:OG	1:A:272:ASP:O	2.26	0.50
1:A:289:MET:O	1:A:293:MET:HG2	2.11	0.49
1:B:198:PHE:O	2:B:601:FAD:C4X	2.60	0.49
1:B:436:ARG:HE	1:A:414:GLN:NE2	2.11	0.49
1:A:556:LEU:O	1:A:560:ARG:HG3	2.13	0.49
1:B:324:GLN:HE22	1:A:171:ALA:HA	1.77	0.48
1:A:289:MET:HE2	1:A:292:MET:SD	2.54	0.48
1:B:173:THR:HG23	1:B:447:ILE:HG12	1.95	0.48
1:B:495:GLU:OE1	1:B:499:GLU:OE1	2.31	0.48
1:B:44:LEU:HD11	1:B:113:GLN:NE2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:872:HOH:O	1:A:565:ARG:HD2	2.14	0.47
1:A:131:LEU:HD11	1:A:200:THR:CG2	2.44	0.47
1:A:165:CYS:HA	1:A:199:ILE:HD12	1.96	0.47
1:B:395:THR:N	1:B:396:PRO:HD2	2.31	0.46
1:A:198:PHE:O	2:A:601:FAD:C4X	2.63	0.46
1:B:289:MET:HE2	1:B:292:MET:HE1	1.98	0.46
1:B:127:LEU:HD12	1:B:303:GLN:NE2	2.29	0.46
1:A:503:TRP:CZ2	1:A:507:ARG:HG3	2.50	0.46
1:A:60:ARG:HB2	1:A:61:PRO:HD3	1.97	0.46
1:B:398:ALA:O	1:B:402:LEU:HB2	2.16	0.46
1:B:87:TYR:OH	1:B:118:VAL:HG21	2.15	0.45
1:A:453:VAL:O	1:A:458:ILE:HG12	2.16	0.45
1:B:282:VAL:HG12	6:B:805:HOH:O	2.16	0.45
1:A:122:ASN:C	1:A:122:ASN:HD22	2.25	0.45
1:B:165:CYS:HB3	1:B:196:LYS:HG3	1.98	0.44
1:A:87:TYR:OH	1:A:118:VAL:HG21	2.16	0.44
1:A:198:PHE:HA	1:A:266:THR:HG22	1.99	0.44
1:A:250:LEU:HD12	1:A:250:LEU:C	2.43	0.44
1:A:15:LEU:HG	1:A:113:GLN:OE1	2.17	0.44
1:B:543:LEU:HG	1:B:556:LEU:HD21	2.00	0.44
1:A:447:ILE:HD11	2:A:601:FAD:C4A	2.48	0.44
1:B:173:THR:CG2	1:B:447:ILE:HG12	2.48	0.44
1:A:540:ARG:HG3	3:A:603:PEG:H41	1.99	0.44
2:A:601:FAD:H2'	2:A:601:FAD:H9	2.00	0.44
1:B:177:ILE:HD12	1:B:177:ILE:HA	1.79	0.43
1:A:163:SER:OG	1:A:212:HIS:HD2	2.02	0.43
1:B:453:VAL:O	1:B:458:ILE:HG12	2.18	0.43
1:A:434:ASP:O	1:A:437:ILE:HG22	2.18	0.43
1:A:567:LEU:N	1:A:568:PRO:CD	2.81	0.43
1:A:142:HIS:CD2	1:A:288:ALA:HA	2.53	0.43
1:A:262:LYS:O	3:A:604:PEG:H32	2.19	0.43
1:B:355:LYS:NZ	6:B:720:HOH:O	2.52	0.43
1:B:370:MET:HE2	1:B:370:MET:HB3	1.89	0.43
1:B:252:CYS:SG	1:B:267:CYS:HB3	2.58	0.43
1:B:291:THR:HG23	6:B:858:HOH:O	2.20	0.42
1:A:392:ALA:O	1:A:456:LYS:HE3	2.19	0.42
1:B:391:VAL:O	1:B:395:THR:HG23	2.19	0.42
1:A:359:GLU:OE2	5:A:605[A]:GOL:O2	2.34	0.42
1:B:414:GLN:NE2	1:A:436:ARG:HE	2.18	0.42
1:A:123:LEU:HD11	1:A:303:GLN:HB3	2.01	0.42
1:B:567:LEU:N	1:B:568:PRO:CD	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:511:ASN:HB3	1:A:514:GLU:HG2	2.02	0.41
1:A:395:THR:N	1:A:396:PRO:CD	2.83	0.41
1:A:503:TRP:CE2	1:A:507:ARG:HG3	2.56	0.41
1:A:255:ILE:HD12	3:A:604:PEG:H42	2.03	0.41
1:B:131:LEU:HD23	1:B:131:LEU:HA	1.92	0.41
1:A:380:ASP:OD1	1:A:380:ASP:C	2.64	0.41
1:A:166:LEU:N	1:A:166:LEU:HD23	2.37	0.40
1:A:472:ILE:HG12	1:A:533:TYR:CG	2.56	0.40
1:B:389:GLU:HG2	1:B:464:PHE:CE1	2.56	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	593/594 (100%)	572 (96%)	21 (4%)	0	100	100
1	B	589/594 (99%)	573 (97%)	14 (2%)	2 (0%)	36	30
All	All	1182/1188 (100%)	1145 (97%)	35 (3%)	2 (0%)	43	37

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	549	ASP
1	B	261	ILE

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	453/452 (100%)	447 (99%)	6 (1%)	61 54
1	B	451/452 (100%)	439 (97%)	12 (3%)	39 26
All	All	904/904 (100%)	886 (98%)	18 (2%)	48 39

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	38	GLU
1	B	122	ASN
1	B	177	ILE
1	B	178	ILE
1	B	321	GLU
1	B	385	LYS
1	B	437	ILE
1	B	441	TYR
1	B	447	ILE
1	B	481	GLU
1	B	540	ARG
1	B	546	GLN
1	A	1	MET
1	A	15	LEU
1	A	34	VAL
1	A	120	SER
1	A	425	GLU
1	A	441	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	122	ASN
1	B	212	HIS
1	B	303	GLN
1	B	324	GLN
1	B	344	HIS
1	B	414	GLN
1	B	420	HIS
1	A	70	ASN
1	A	122	ASN

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Mol	Chain	Res	Type
1	A	142	HIS
1	A	170	HIS
1	A	212	HIS
1	A	303	GLN
1	A	344	HIS
1	A	414	GLN
1	A	513	ASN
1	A	571	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)

11 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	$\#\|Z\| > 2$
4	1PE	B	603	-	15,15,15	0.25	0	14,14,14	0.19	0
4	1PE	A	606	-	15,15,15	0.24	0	14,14,14	0.16	0
2	FAD	A	601	-	58,58,58	0.64	0	85,89,89	0.62	1 (1%)
3	PEG	B	602	-	6,6,6	0.18	0	5,5,5	0.13	0
3	PEG	A	604	-	6,6,6	0.33	0	5,5,5	0.21	0
5	GOL	A	605[A]	-	5,5,5	0.16	0	5,5,5	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	1PE	A	607	-	15,15,15	0.23	0	14,14,14	0.12	0
3	PEG	A	603	-	6,6,6	0.20	0	5,5,5	0.16	0
3	PEG	A	602	-	6,6,6	0.18	0	5,5,5	0.16	0
5	GOL	A	605[B]	-	5,5,5	0.12	0	5,5,5	0.30	0
2	FAD	B	601	-	58,58,58	0.71	2 (3%)	85,89,89	0.82	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
4	1PE	B	603	-	-	5/13/13/13	-
4	1PE	A	606	-	-	3/13/13/13	-
2	FAD	A	601	-	-	1/34/50/50	0/6/6/6
3	PEG	B	602	-	-	3/4/4/4	-
3	PEG	A	604	-	-	1/4/4/4	-
5	GOL	A	605[A]	-	-	4/4/4/4	-
4	1PE	A	607	-	-	6/13/13/13	-
3	PEG	A	603	-	-	2/4/4/4	-
3	PEG	A	602	-	-	2/4/4/4	-
5	GOL	A	605[B]	-	-	4/4/4/4	-
2	FAD	B	601	-	-	6/34/50/50	0/6/6/6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	FAD	P-O3P	2.24	1.61	1.59
2	B	601	FAD	C1'-C2'	2.16	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	601	FAD	C4'-C3'-C2'	-3.21	108.22	113.57
2	B	601	FAD	C1'-C2'-C3'	2.63	116.78	109.66
2	A	601	FAD	C4-N3-C2	-2.37	121.43	125.64
2	B	601	FAD	C4-N3-C2	-2.11	121.90	125.64

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	FAD	C1'-C2'-C3'-O3'
2	B	601	FAD	C1'-C2'-C3'-C4'
2	A	601	FAD	C2'-C1'-N10-C10
5	A	605[A]	GOL	O1-C1-C2-C3
5	A	605[B]	GOL	O1-C1-C2-C3
5	A	605[B]	GOL	C1-C2-C3-O3
2	B	601	FAD	O2'-C2'-C3'-O3'
2	B	601	FAD	O2'-C2'-C3'-C4'
3	B	602	PEG	O1-C1-C2-O2
4	B	603	1PE	OH2-C12-C22-OH3
4	A	607	1PE	OH2-C12-C22-OH3
3	A	603	PEG	O2-C3-C4-O4
3	A	602	PEG	O1-C1-C2-O2
4	A	606	1PE	OH7-C16-C26-OH6
5	A	605[B]	GOL	O1-C1-C2-O2
5	A	605[B]	GOL	O2-C2-C3-O3
3	B	602	PEG	O2-C3-C4-O4
5	A	605[A]	GOL	O1-C1-C2-O2
5	A	605[A]	GOL	C1-C2-C3-O3
4	A	607	1PE	OH4-C13-C23-OH3
3	A	602	PEG	O2-C3-C4-O4
3	A	604	PEG	O2-C3-C4-O4
4	B	603	1PE	C15-C25-OH5-C14
4	B	603	1PE	C13-C23-OH3-C22
4	A	607	1PE	C13-C23-OH3-C22
3	B	602	PEG	C1-C2-O2-C3
4	A	607	1PE	C23-C13-OH4-C24
2	B	601	FAD	C4'-C5'-O5'-P
4	B	603	1PE	C25-C15-OH6-C26
4	B	603	1PE	C23-C13-OH4-C24
4	A	607	1PE	C14-C24-OH4-C13
3	A	603	PEG	C1-C2-O2-C3
5	A	605[A]	GOL	O2-C2-C3-O3
4	A	607	1PE	C25-C15-OH6-C26
4	A	606	1PE	C15-C25-OH5-C14
4	A	606	1PE	C16-C26-OH6-C15
2	B	601	FAD	PA-O3P-P-O2P

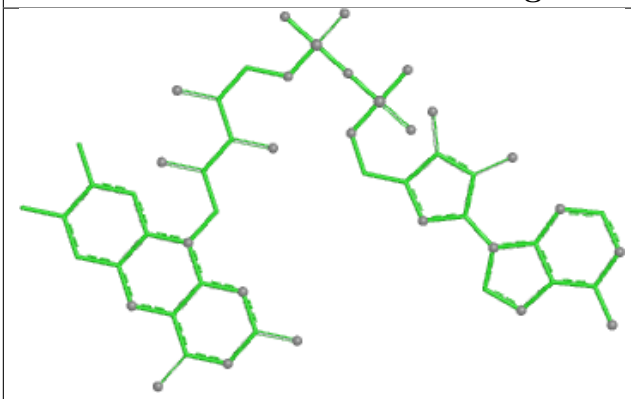
There are no ring outliers.

5 monomers are involved in 10 short contacts:

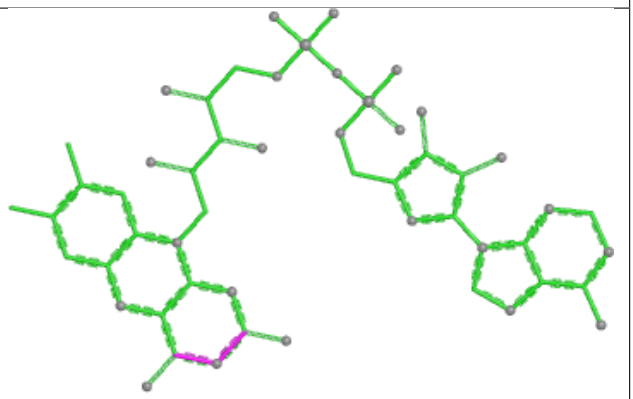
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	FAD	3	0
3	A	604	PEG	4	0
5	A	605[A]	GOL	1	0
3	A	603	PEG	1	0
2	B	601	FAD	1	0

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 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.

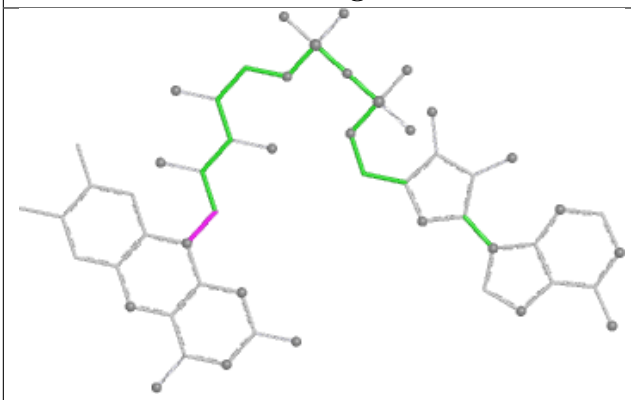
Ligand FAD A 601



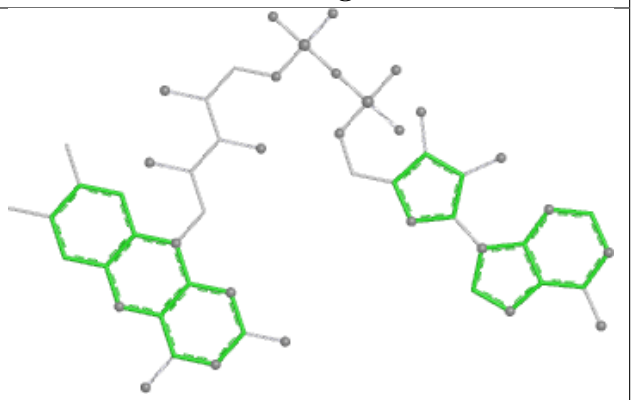
Bond lengths



Bond angles

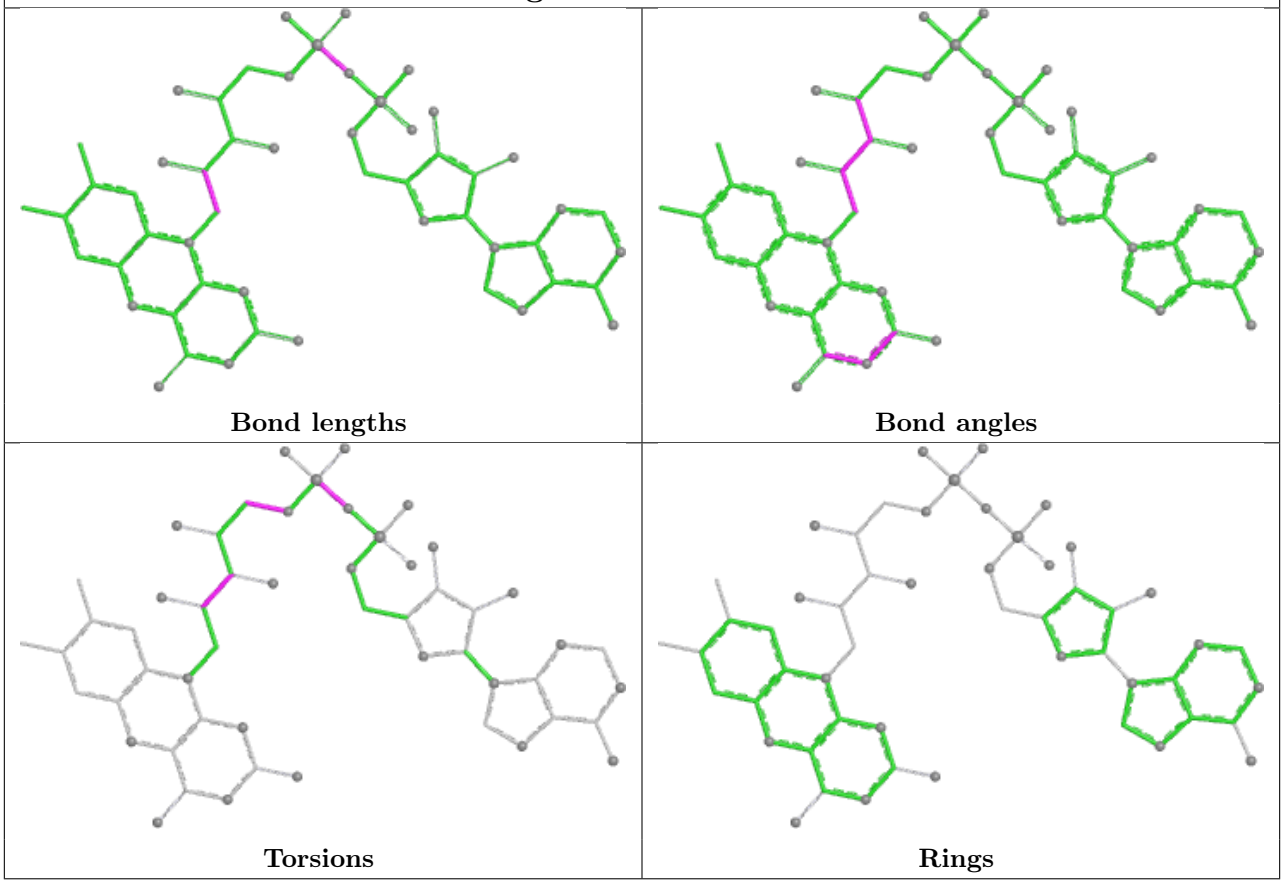


Torsions



Rings

Ligand FAD B 601



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{th} 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	594/594 (100%)	0.19	17 (2%)	53	60	15, 32, 50, 104	1 (0%)
1	B	590/594 (99%)	0.28	12 (2%)	65	72	17, 34, 54, 79	1 (0%)
All	All	1184/1188 (99%)	0.23	29 (2%)	59	67	15, 33, 52, 104	2 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	MET	4.8
1	A	-1	GLY	3.6
1	B	178	ILE	3.2
1	B	290	PHE	2.9
1	A	510	GLY	2.6
1	B	177	ILE	2.6
1	A	370	MET	2.5
1	A	28	LEU	2.5
1	A	479	ALA	2.5
1	A	0	HIS	2.4
1	A	26	ALA	2.4
1	A	29	PRO	2.4
1	B	30	ALA	2.3
1	A	592	PHE	2.3
1	B	5	LYS	2.3
1	B	127	LEU	2.3
1	A	30	ALA	2.3
1	B	54	THR	2.3
1	B	291	THR	2.2
1	B	24	LEU	2.2
1	B	28	LEU	2.2
1	B	295	TYR	2.1
1	A	467	HIS	2.1
1	A	527	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	127	LEU	2.1
1	A	2	ALA	2.1
1	B	29	PRO	2.0
1	A	332	VAL	2.0
1	A	382	VAL	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 oligosaccharides in this entry.

6.4 Ligands (i)

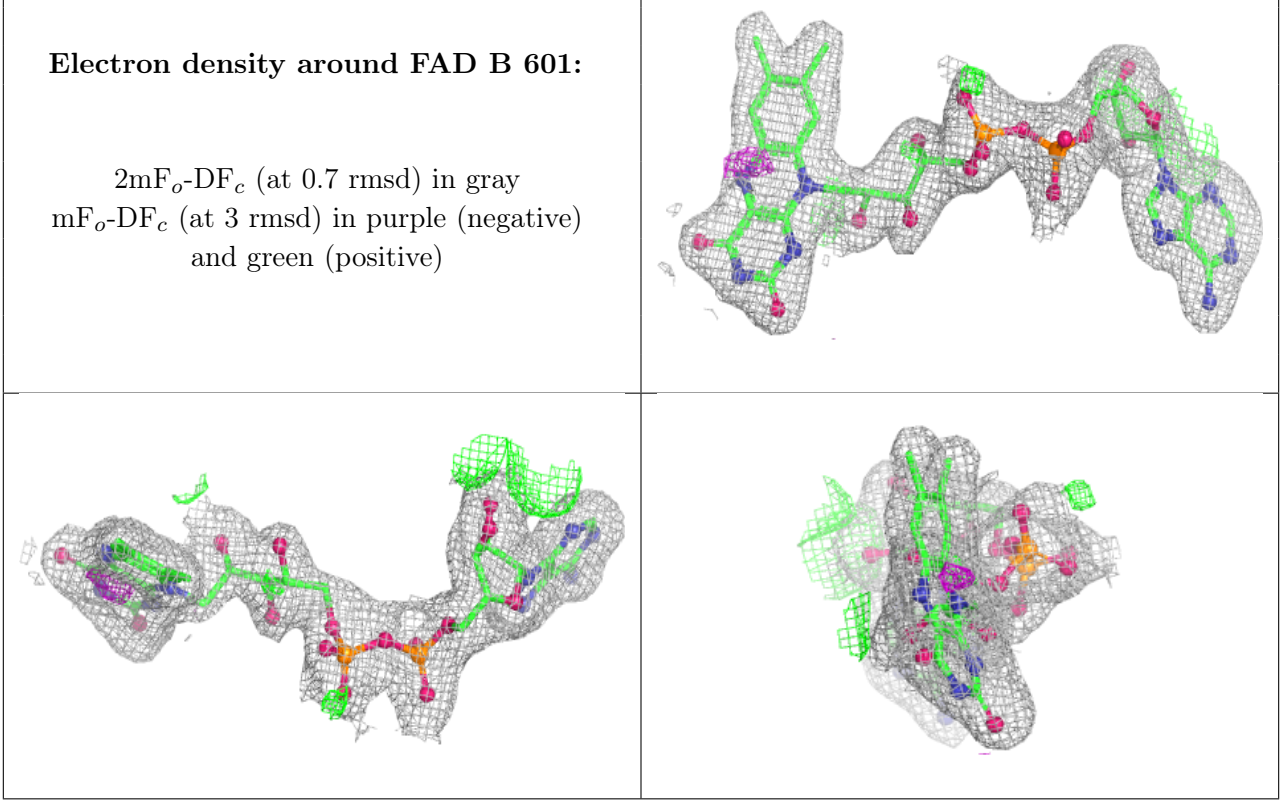
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
5	GOL	A	605[A]	6/6	0.64	0.18	26,32,33,35	6
5	GOL	A	605[B]	6/6	0.64	0.18	37,39,41,42	6
3	PEG	A	604	7/7	0.69	0.21	39,49,56,62	0
3	PEG	A	603	7/7	0.76	0.17	54,58,71,72	0
4	1PE	A	607	16/16	0.82	0.14	59,65,73,75	0
3	PEG	B	602	7/7	0.83	0.14	49,50,52,55	0
4	1PE	B	603	16/16	0.86	0.15	59,70,82,84	0
4	1PE	A	606	16/16	0.88	0.11	48,56,64,66	0
2	FAD	B	601	53/53	0.93	0.09	31,35,46,48	0
3	PEG	A	602	7/7	0.96	0.07	40,41,42,44	0
2	FAD	A	601	53/53	0.96	0.06	24,29,37,41	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.

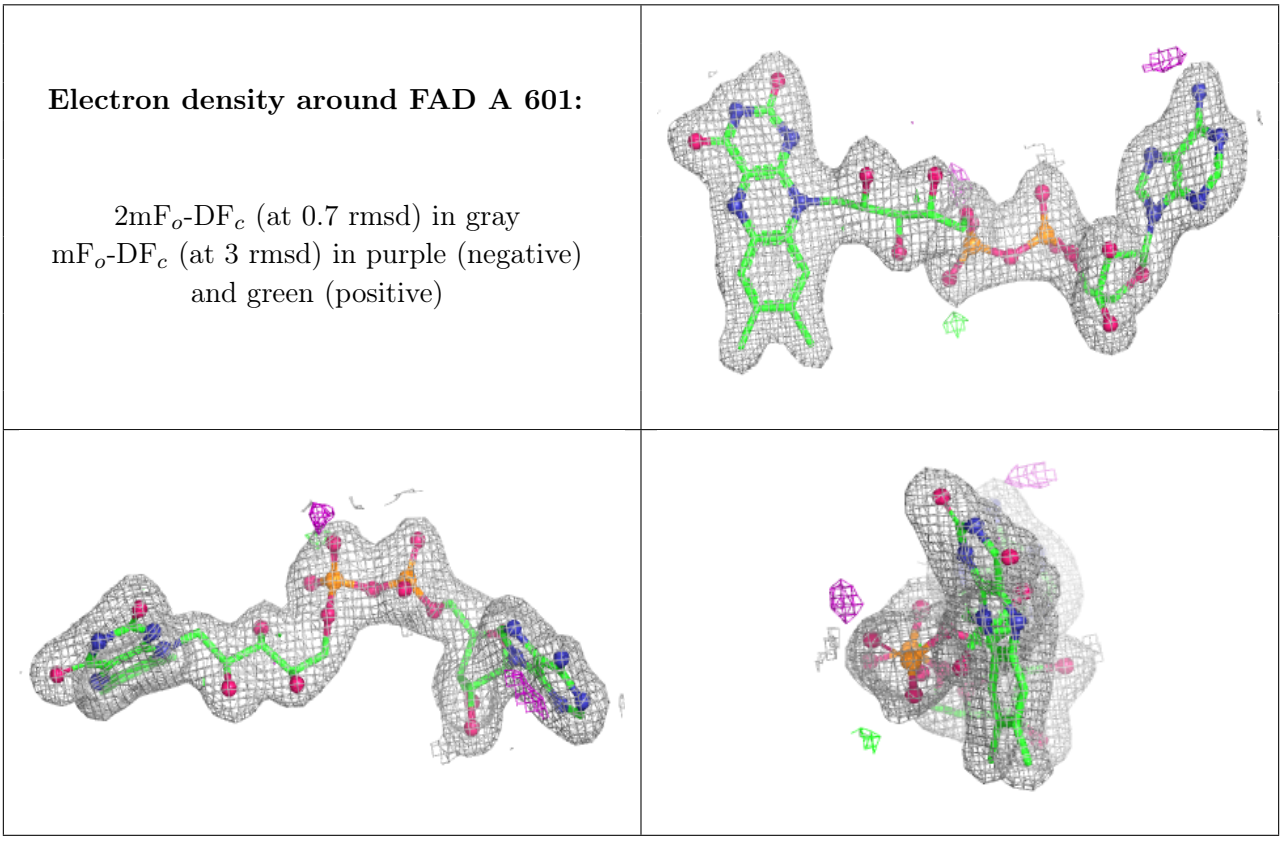
Electron density around FAD B 601:

$2mF_o$-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 601:

$2mF_o$-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.