Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 10:21 pm BST

PDB ID	:	1JQI
Title	:	Crystal Structure of Rat Short Chain Acyl-CoA Dehydrogenase Complexed With Acetoacetyl-CoA
Authors	:	Battaile, K.P.; Molin-Case, J.; Paschke, R.; Wang, M.; Bennett, D.; Vockley, J.; Kim, J.-J.P.
Deposited on	:	2001-08-07
Resolution	:	2.25 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 following versions of software and data (see references ⓘ) were used in the production of this report:

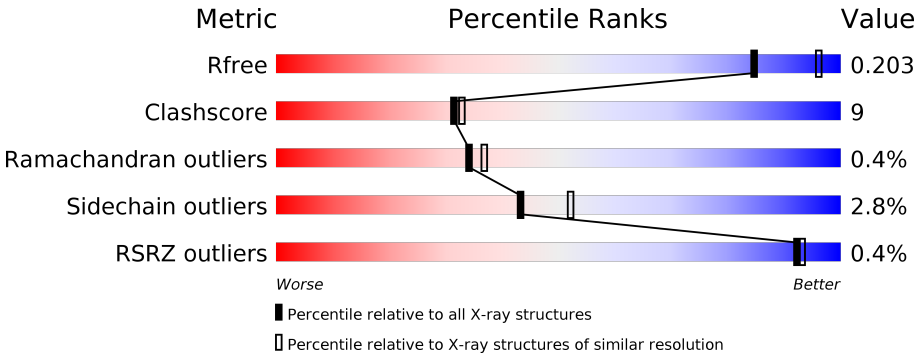
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance

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

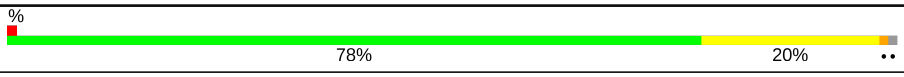
The reported resolution of this entry is 2.25 Å.

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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	388	
1	B	388	

2 Entry composition

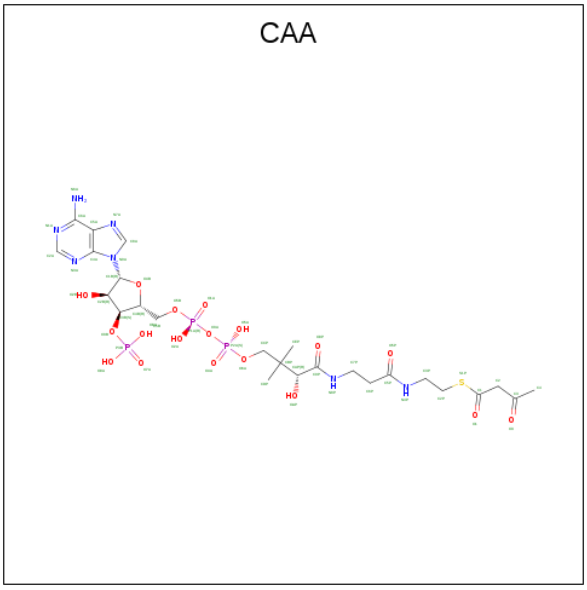
There are 4 unique types of molecules in this entry. The entry contains 6328 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 short chain acyl-CoA dehydrogenase.

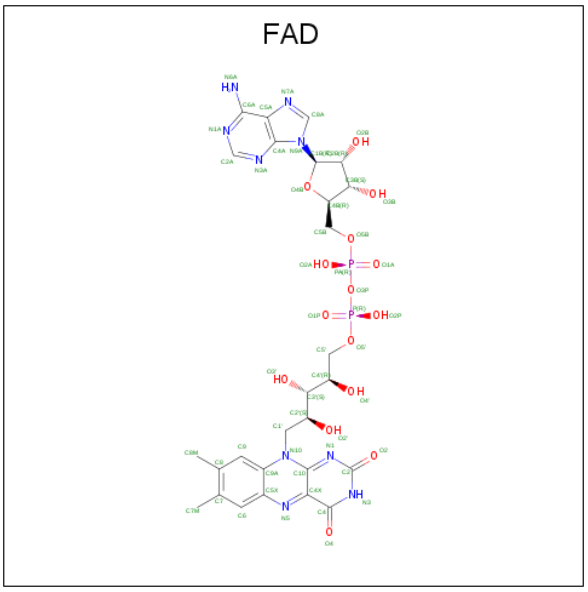
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	384	Total	C	N	O	S	0	0	0
			2927	1844	505	560	18			
1	B	384	Total	C	N	O	S	0	0	0
			2927	1844	505	560	18			

- Molecule 2 is ACETOACETYL-COENZYME A (three-letter code: CAA) (formula: $C_{25}H_{40}N_7O_{18}P_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			54	25	7	18	3	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

- Molecule 4 is water.

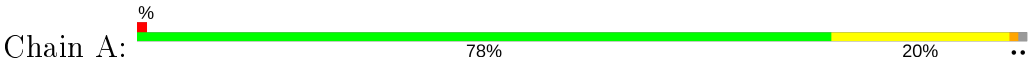
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	105	Total	O	0	0
			105	105		
4	B	155	Total	O	0	0
			155	155		

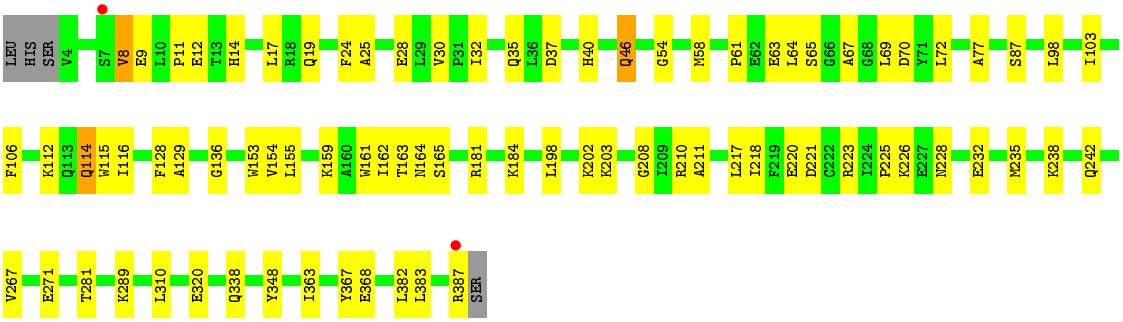
3 Residue-property plots (i)

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

- Molecule 1: short chain acyl-CoA dehydrogenase

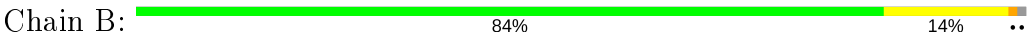
Chain A:

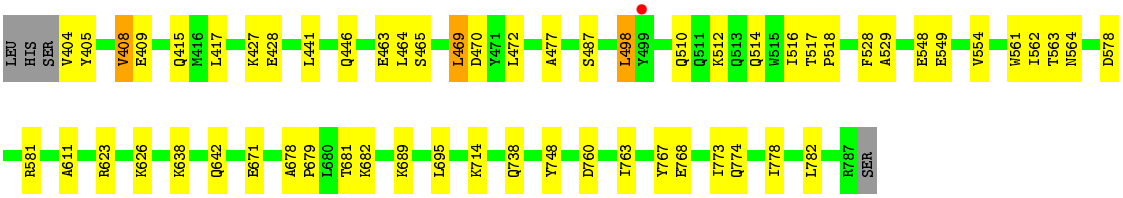




- Molecule 1: short chain acyl-CoA dehydrogenase

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α, β, γ	143.61Å 143.61Å 77.46Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.89 – 2.25 29.89 – 2.10	Depositor EDS
% Data completeness (in resolution range)	83.2 (29.89-2.25) 78.0 (29.89-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.66 (at 2.10Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.168 , 0.206 0.158 , 0.203	Depositor DCC
R_{free} test set	3234 reflections (7.70%)	wwPDB-VP
Wilson B-factor (Å^2)	23.6	Xtriage
Anisotropy	0.225	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 62.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6328	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% 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: CAA, 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	0/2978	0.55	0/4023
1	B	0.32	0/2978	0.57	0/4023
All	All	0.32	0/5956	0.56	0/8046

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	2927	0	2946	64	0
1	B	2927	0	2946	48	0
2	A	54	0	36	2	0
2	B	54	0	36	2	0
3	A	53	0	31	3	0
3	B	53	0	31	3	0
4	A	105	0	0	3	0
4	B	155	0	0	2	0
All	All	6328	0	6026	109	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.

All (109) 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:8:VAL:HG13	1:A:9:GLU:H	1.23	1.02
1:B:408:VAL:HG13	1:B:409:GLU:H	1.29	0.95
1:A:289:LYS:NZ	1:A:338:GLN:HE22	1.76	0.82
1:A:103:ILE:HB	1:A:116:ILE:HD11	1.64	0.79
1:B:463:GLU:HG3	4:B:1246:HOH:O	1.84	0.78
1:B:417:LEU:HD11	1:B:477:ALA:HB2	1.67	0.76
1:B:638:LYS:HE2	1:B:642:GLN:NE2	2.00	0.75
1:A:129:ALA:HB1	1:A:159:LYS:HG2	1.68	0.75
1:B:510:GLN:HE21	1:B:514:GLN:HG3	1.52	0.74
1:A:289:LYS:HZ2	1:A:338:GLN:HE22	1.32	0.74
1:A:8:VAL:HG13	1:A:9:GLU:N	2.01	0.71
1:A:46:GLN:NE2	1:A:46:GLN:H	1.90	0.69
1:B:763:ILE:HD11	3:B:799:FAD:HM83	1.74	0.69
1:A:363:ILE:HD11	3:A:399:FAD:HM83	1.75	0.68
1:B:446:GLN:H	1:B:446:GLN:NE2	1.92	0.67
1:A:11:PRO:HB2	1:A:14:HIS:HD2	1.60	0.67
1:B:404:VAL:HG12	1:B:405:TYR:H	1.60	0.67
1:B:408:VAL:HG13	1:B:409:GLU:N	2.07	0.67
1:B:498:LEU:HB3	1:B:528:PHE:HB2	1.76	0.66
1:A:17:LEU:HD11	1:A:77:ALA:HB2	1.75	0.66
1:B:638:LYS:HE2	1:B:642:GLN:HE22	1.59	0.66
1:A:154:VAL:HG22	1:A:223:ARG:HG2	1.79	0.65
1:A:225:PRO:HG2	1:A:228:ASN:OD1	1.97	0.65
1:B:689:LYS:HE3	1:B:738:GLN:NE2	2.12	0.64
1:B:548:GLU:HG2	4:B:1115:HOH:O	1.98	0.63
1:A:368:GLU:HG2	2:A:400:CAA:H2'2	1.80	0.62
1:A:218:ILE:N	1:A:218:ILE:HD12	2.14	0.62
1:A:220:GLU:O	1:A:220:GLU:HG3	1.99	0.62
1:A:220:GLU:HG2	4:A:1108:HOH:O	2.01	0.60
1:A:202:LYS:HD3	1:A:203:LYS:N	2.19	0.57
1:B:763:ILE:CD1	3:B:799:FAD:HM83	2.33	0.57
1:A:202:LYS:HD3	1:A:203:LYS:H	1.68	0.57
1:A:363:ILE:CD1	3:A:399:FAD:HM83	2.34	0.56
1:B:768:GLU:HG2	2:B:800:CAA:H2'2	1.87	0.56
1:A:161:TRP:O	3:A:399:FAD:C4X	2.54	0.56
1:A:162:ILE:HG13	1:A:217:LEU:HG	1.88	0.56
1:B:682:LYS:HA	1:B:682:LYS:NZ	2.21	0.56
1:A:40:HIS:HB2	4:A:1258:HOH:O	2.05	0.56
1:A:163:THR:O	1:A:164:ASN:HB2	2.05	0.55
1:B:563:THR:O	1:B:564:ASN:HB2	2.05	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:348:TYR:CZ	1:B:763:ILE:HB	2.42	0.55
1:B:561:TRP:O	3:B:799:FAD:C4X	2.54	0.55
1:B:671:GLU:HG2	1:B:681:THR:HG21	1.88	0.55
1:A:87:SER:CB	1:A:211:ALA:HB3	2.37	0.55
1:A:25:ALA:O	1:A:30:VAL:HG23	2.07	0.54
1:B:626:LYS:HB3	1:B:626:LYS:NZ	2.22	0.54
1:B:682:LYS:HA	1:B:682:LYS:HZ2	1.72	0.54
1:A:37:ASP:OD2	1:A:210:ARG:HD3	2.08	0.53
1:B:714:LYS:HD2	1:B:714:LYS:N	2.23	0.53
1:B:554:VAL:HG22	1:B:623:ARG:HG2	1.90	0.52
1:A:112:LYS:O	1:A:116:ILE:HB	2.09	0.52
1:A:98:LEU:HB3	1:A:128:PHE:HB2	1.91	0.52
1:A:24:PHE:CE1	1:A:28:GLU:HG3	2.43	0.52
1:A:232:GLU:O	1:A:235:MET:HB2	2.09	0.52
1:A:46:GLN:HE21	1:A:46:GLN:H	1.57	0.52
1:A:64:LEU:O	1:A:65:SER:HB2	2.09	0.52
1:B:517:THR:HB	1:B:518:PRO:HD3	1.92	0.52
1:A:155:LEU:HD12	1:A:155:LEU:N	2.26	0.50
1:B:512:LYS:O	1:B:516:ILE:HB	2.10	0.50
1:B:695:LEU:HD23	1:B:695:LEU:C	2.32	0.50
1:A:383:LEU:O	1:A:387:ARG:HG2	2.10	0.50
1:B:549:GLU:HG3	1:B:554:VAL:CG2	2.41	0.50
1:A:238:LYS:O	1:A:242:GLN:HG3	2.12	0.50
1:A:106:PHE:HZ	1:A:242:GLN:NE2	2.10	0.49
1:A:63:GLU:H	1:A:63:GLU:CD	2.15	0.49
1:B:529:ALA:HA	1:B:562:ILE:HD12	1.93	0.49
1:A:162:ILE:HB	1:A:165:SER:HB3	1.95	0.48
1:B:581:ARG:HG2	1:B:581:ARG:HH11	1.79	0.48
1:B:760:ASP:O	1:B:763:ILE:HG22	2.14	0.48
1:B:464:LEU:O	1:B:465:SER:HB2	2.15	0.47
1:A:106:PHE:HZ	1:A:242:GLN:HE21	1.62	0.47
1:A:58:MET:HA	1:A:67:ALA:HB3	1.96	0.47
1:A:267:VAL:O	1:A:271:GLU:HG3	2.15	0.47
1:B:408:VAL:CG1	1:B:409:GLU:H	2.13	0.47
1:B:638:LYS:HG2	1:B:642:GLN:HE21	1.80	0.47
1:B:487:SER:CB	1:B:611:ALA:HB3	2.45	0.46
1:B:768:GLU:HG2	2:B:800:CAA:C2	2.46	0.46
1:A:129:ALA:HB1	1:A:159:LYS:CG	2.42	0.46
1:B:774:GLN:O	1:B:778:ILE:HG13	2.16	0.46
1:A:363:ILE:HB	1:B:748:TYR:CZ	2.50	0.45
1:B:678:ALA:HB1	1:B:679:PRO:CD	2.47	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:184:LYS:HB2	1:A:184:LYS:HE3	1.85	0.44
1:A:289:LYS:NZ	1:A:338:GLN:NE2	2.55	0.44
1:A:289:LYS:HZ3	1:A:338:GLN:HE22	1.62	0.44
1:A:368:GLU:HG2	2:A:400:CAA:C2	2.45	0.44
1:A:54:GLY:HA2	4:A:1136:HOH:O	2.17	0.44
1:A:61:PRO:HG2	1:A:64:LEU:HD23	1.99	0.44
1:A:271:GLU:HG2	1:A:281:THR:HG21	2.01	0.43
1:B:510:GLN:NE2	1:B:514:GLN:HG3	2.27	0.43
1:A:208:GLY:HA3	1:B:748:TYR:OH	2.18	0.43
1:A:153:TRP:CD1	1:A:226:LYS:HA	2.54	0.42
1:A:310:LEU:CD1	1:A:320:GLU:HG2	2.50	0.42
1:B:469:LEU:HB3	1:B:470:ASP:H	1.61	0.42
1:A:289:LYS:HD3	1:A:338:GLN:NE2	2.35	0.42
1:A:46:GLN:NE2	1:A:46:GLN:N	2.64	0.42
1:B:427:LYS:HD2	1:B:428:GLU:HG2	2.01	0.42
1:B:549:GLU:HG3	1:B:554:VAL:HG21	2.00	0.42
1:A:114:GLN:HG3	1:A:115:TRP:CD1	2.54	0.41
1:A:114:GLN:HE21	1:A:114:GLN:HB2	1.66	0.41
1:A:40:HIS:CD2	1:A:40:HIS:N	2.87	0.41
1:A:382:LEU:C	1:A:382:LEU:HD13	2.41	0.41
1:A:387:ARG:HG3	1:A:387:ARG:HH11	1.85	0.41
1:B:446:GLN:N	1:B:446:GLN:NE2	2.66	0.41
1:B:578:ASP:HB3	1:B:581:ARG:HD3	2.02	0.41
1:B:404:VAL:HG12	1:B:405:TYR:N	2.32	0.40
1:A:69:LEU:HB3	1:A:70:ASP:H	1.76	0.40
1:A:155:LEU:CD1	1:A:155:LEU:N	2.85	0.40
1:A:32:ILE:O	1:A:35:GLN:HG2	2.20	0.40
1:B:549:GLU:HG3	1:B:554:VAL:HG23	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	382/388 (98%)	365 (96%)	15 (4%)	2 (0%)	29 29
1	B	382/388 (98%)	368 (96%)	13 (3%)	1 (0%)	41 46
All	All	764/776 (98%)	733 (96%)	28 (4%)	3 (0%)	34 37

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	VAL
1	B	408	VAL
1	A	136	GLY

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	307/311 (99%)	298 (97%)	9 (3%)	42 51
1	B	307/311 (99%)	299 (97%)	8 (3%)	46 55
All	All	614/622 (99%)	597 (97%)	17 (3%)	43 52

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	GLU
1	A	19	GLN
1	A	46	GLN
1	A	72	LEU
1	A	114	GLN
1	A	181	ARG
1	A	198	LEU
1	A	221	ASP
1	A	367	TYR
1	B	415	GLN
1	B	441	LEU
1	B	469	LEU
1	B	472	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	498	LEU
1	B	767	TYR
1	B	773	ILE
1	B	782	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	HIS
1	A	46	GLN
1	A	114	GLN
1	A	242	GLN
1	A	274	HIS
1	A	313	ASN
1	A	338	GLN
1	B	414	HIS
1	B	415	GLN
1	B	446	GLN
1	B	510	GLN
1	B	513	GLN
1	B	616	ASN
1	B	642	GLN
1	B	713	ASN
1	B	738	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

4 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	FAD	B	799	-	51,58,58	1.71	8 (15%)	60,89,89	2.58	13 (21%)
3	FAD	A	399	-	51,58,58	1.74	8 (15%)	60,89,89	2.67	14 (23%)
2	CAA	B	800	-	47,56,56	1.34	6 (12%)	60,83,83	1.72	9 (15%)
2	CAA	A	400	-	47,56,56	1.35	7 (14%)	60,83,83	1.76	9 (15%)

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	FAD	B	799	-	-	0/30/50/50	0/6/6/6
3	FAD	A	399	-	-	0/30/50/50	0/6/6/6
2	CAA	B	800	-	-	4/50/71/71	0/3/3/3
2	CAA	A	400	-	-	5/50/71/71	0/3/3/3

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	399	FAD	C9A-N10	6.30	1.47	1.38
3	B	799	FAD	C9A-N10	6.02	1.46	1.38
3	B	799	FAD	C4-N3	4.41	1.40	1.33
3	A	399	FAD	C10-N1	4.28	1.38	1.33
3	B	799	FAD	C10-N1	4.24	1.38	1.33
2	A	400	CAA	O4B-C1B	4.05	1.46	1.41
2	B	800	CAA	O4B-C1B	3.95	1.46	1.41
3	A	399	FAD	C4-N3	3.83	1.39	1.33
3	A	399	FAD	C4X-N5	3.67	1.38	1.33
3	B	799	FAD	C4-C4X	3.55	1.47	1.41
3	A	399	FAD	C4-C4X	3.51	1.47	1.41

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	399	FAD	C4X-C10	3.47	1.42	1.38
2	B	800	CAA	C4A-N3A	3.40	1.40	1.35
2	A	400	CAA	C4A-N3A	3.35	1.40	1.35
3	B	799	FAD	C4X-N5	3.10	1.37	1.33
2	B	800	CAA	OAP-CAP	2.99	1.47	1.42
2	A	400	CAA	OAP-CAP	2.95	1.47	1.42
3	B	799	FAD	C4X-C10	2.91	1.41	1.38
2	A	400	CAA	C9P-N8P	2.78	1.39	1.33
2	B	800	CAA	C9P-N8P	2.61	1.39	1.33
2	A	400	CAA	C5P-N4P	2.47	1.39	1.33
3	A	399	FAD	C1'-N10	-2.43	1.45	1.48
3	B	799	FAD	C8A-N7A	-2.42	1.30	1.34
2	B	800	CAA	C5P-N4P	2.31	1.38	1.33
3	A	399	FAD	C8A-N7A	-2.24	1.30	1.34
3	B	799	FAD	C1'-N10	-2.23	1.45	1.48
2	B	800	CAA	C8A-N7A	-2.16	1.30	1.34
2	A	400	CAA	C8A-N7A	-2.13	1.30	1.34
2	A	400	CAA	C2A-N3A	2.02	1.35	1.32

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	399	FAD	C4-N3-C2	13.65	126.66	115.14
3	B	799	FAD	C4-N3-C2	12.81	125.95	115.14
3	A	399	FAD	C10-C4X-N5	8.65	127.24	121.26
3	B	799	FAD	C10-C4X-N5	8.54	127.17	121.26
2	A	400	CAA	O1-C1-S1P	-7.26	113.18	122.61
2	B	800	CAA	O1-C1-S1P	-6.93	113.61	122.61
2	A	400	CAA	C2-C1-S1P	-6.75	105.29	113.69
2	B	800	CAA	C2-C1-S1P	-6.49	105.61	113.69
3	A	399	FAD	C4X-C4-N3	-5.88	115.39	123.43
3	B	799	FAD	C4X-C4-N3	-5.79	115.51	123.43
3	B	799	FAD	C4X-C10-N10	-4.79	115.38	120.30
3	A	399	FAD	C4X-C10-N10	-4.77	115.40	120.30
3	A	399	FAD	C4-C4X-C10	-4.31	117.10	119.95
3	B	799	FAD	C4-C4X-C10	-4.21	117.16	119.95
2	A	400	CAA	CEP-CBP-CAP	3.60	115.06	108.82
2	B	800	CAA	CEP-CBP-CAP	3.51	114.90	108.82
3	B	799	FAD	C5X-C9A-N10	-3.37	115.27	117.72
3	A	399	FAD	C5X-C9A-N10	-3.20	115.40	117.72
2	B	800	CAA	C6P-C7P-N8P	-3.12	105.61	111.90
3	A	399	FAD	C6-C5X-N5	-3.11	115.62	119.05

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	799	FAD	C6-C5X-N5	-2.93	115.83	119.05
2	A	400	CAA	C6P-C7P-N8P	-2.85	106.13	111.90
3	A	399	FAD	C9A-C5X-N5	2.81	126.76	122.36
3	B	799	FAD	C9A-C5X-N5	2.77	126.69	122.36
3	A	399	FAD	C4-C4X-N5	-2.57	115.66	118.60
3	B	799	FAD	C4-C4X-N5	-2.56	115.67	118.60
2	A	400	CAA	O1-C1-C2	-2.45	119.11	123.35
2	A	400	CAA	C2P-S1P-C1	2.44	109.48	101.87
3	A	399	FAD	C5A-C6A-N6A	2.38	123.97	120.35
3	A	399	FAD	O3'-C3'-C2'	-2.36	103.12	108.81
3	B	799	FAD	C5A-C6A-N6A	2.34	123.90	120.35
3	A	399	FAD	P-O3P-PA	-2.30	124.94	132.83
2	B	800	CAA	O3B-P3B-O7A	-2.28	100.58	109.39
2	B	800	CAA	O1-C1-C2	-2.22	119.50	123.35
2	A	400	CAA	O3B-P3B-O7A	-2.21	100.86	109.39
2	B	800	CAA	C2P-S1P-C1	2.20	108.73	101.87
3	B	799	FAD	C1'-N10-C10	2.18	120.36	118.41
3	B	799	FAD	O3'-C3'-C2'	-2.17	103.57	108.81
2	A	400	CAA	O9A-P3B-O8A	2.16	115.88	107.64
2	A	400	CAA	C3P-N4P-C5P	-2.13	118.88	122.84
2	B	800	CAA	O9A-P3B-O8A	2.13	115.77	107.64
3	A	399	FAD	C4X-N5-C5X	-2.11	114.66	116.77
3	B	799	FAD	P-O3P-PA	-2.09	125.64	132.83
2	B	800	CAA	C6P-C5P-N4P	-2.07	112.94	116.42
3	A	399	FAD	C1'-N10-C10	2.06	120.25	118.41

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	800	CAA	C5P-C6P-C7P-N8P
2	B	800	CAA	O1-C1-S1P-C2P
2	A	400	CAA	C5P-C6P-C7P-N8P
2	A	400	CAA	O1-C1-S1P-C2P
2	A	400	CAA	O1-C1-C2-C3
2	B	800	CAA	O1-C1-C2-C3
2	B	800	CAA	P1A-O3A-P2A-O4A
2	A	400	CAA	P1A-O3A-P2A-O4A
2	A	400	CAA	O9P-C9P-CAP-OAP

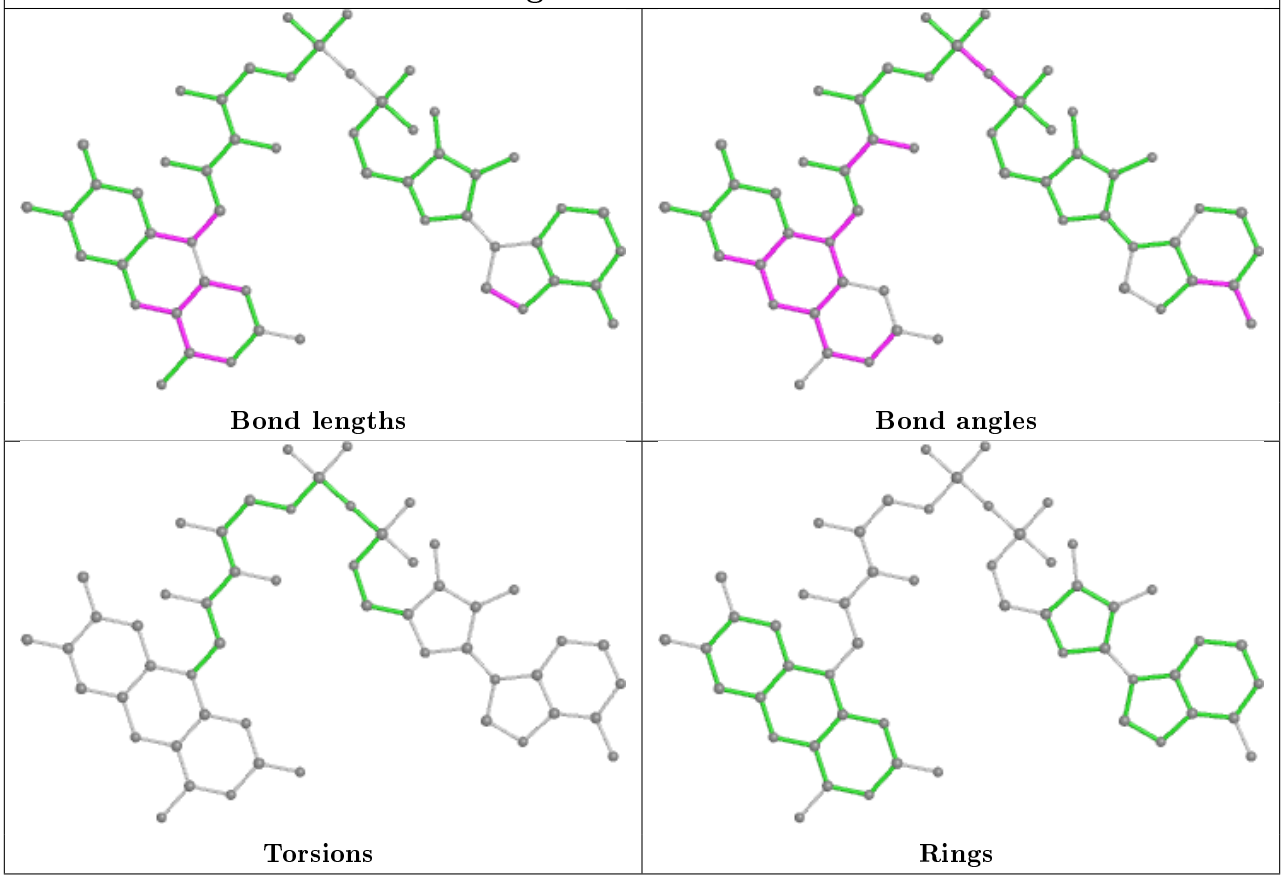
There are no ring outliers.

4 monomers are involved in 10 short contacts:

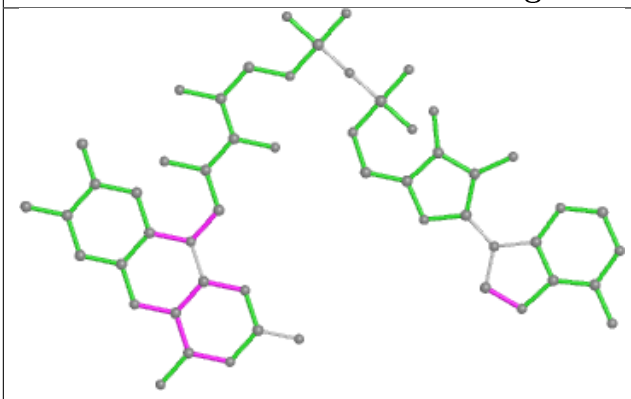
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	799	FAD	3	0
3	A	399	FAD	3	0
2	B	800	CAA	2	0
2	A	400	CAA	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

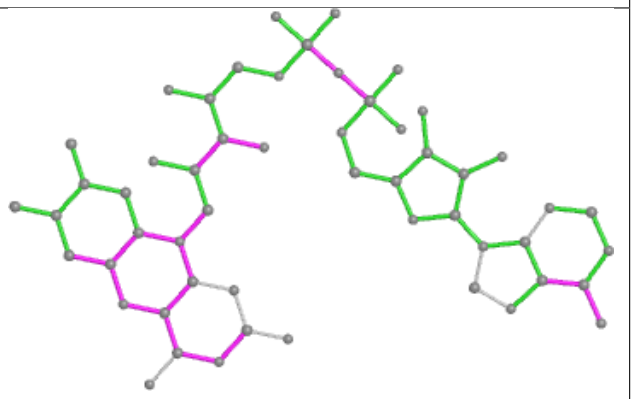
Ligand FAD B 799



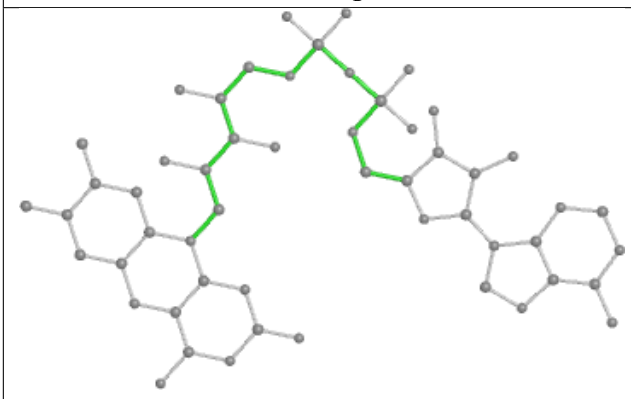
Ligand FAD A 399



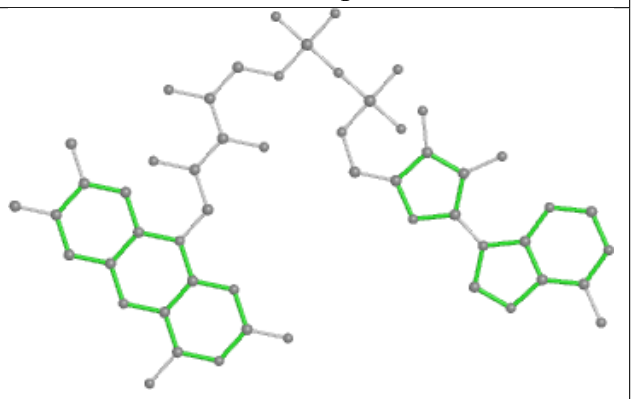
Bond lengths



Bond angles

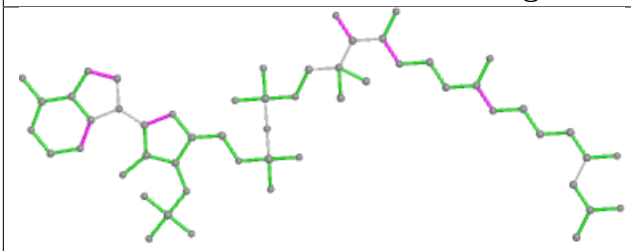


Torsions

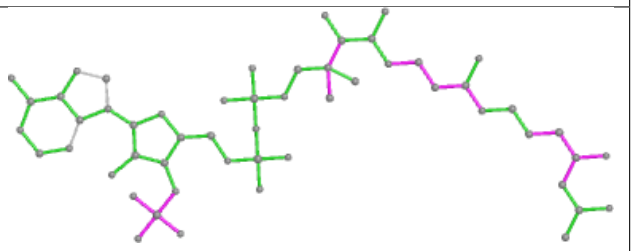


Rings

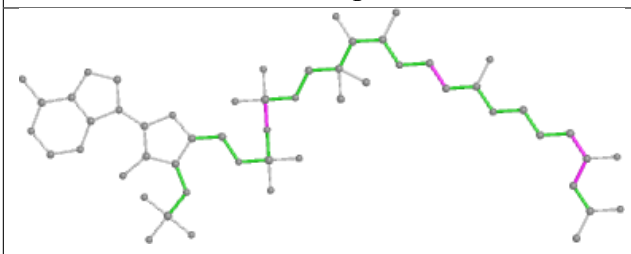
Ligand CAA B 800



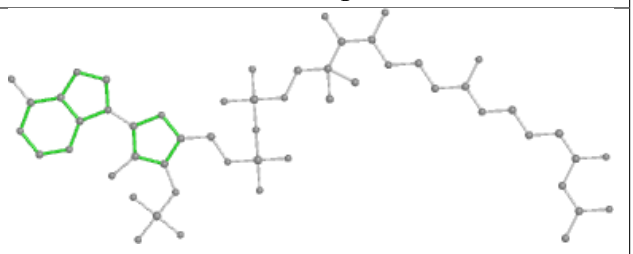
Bond lengths



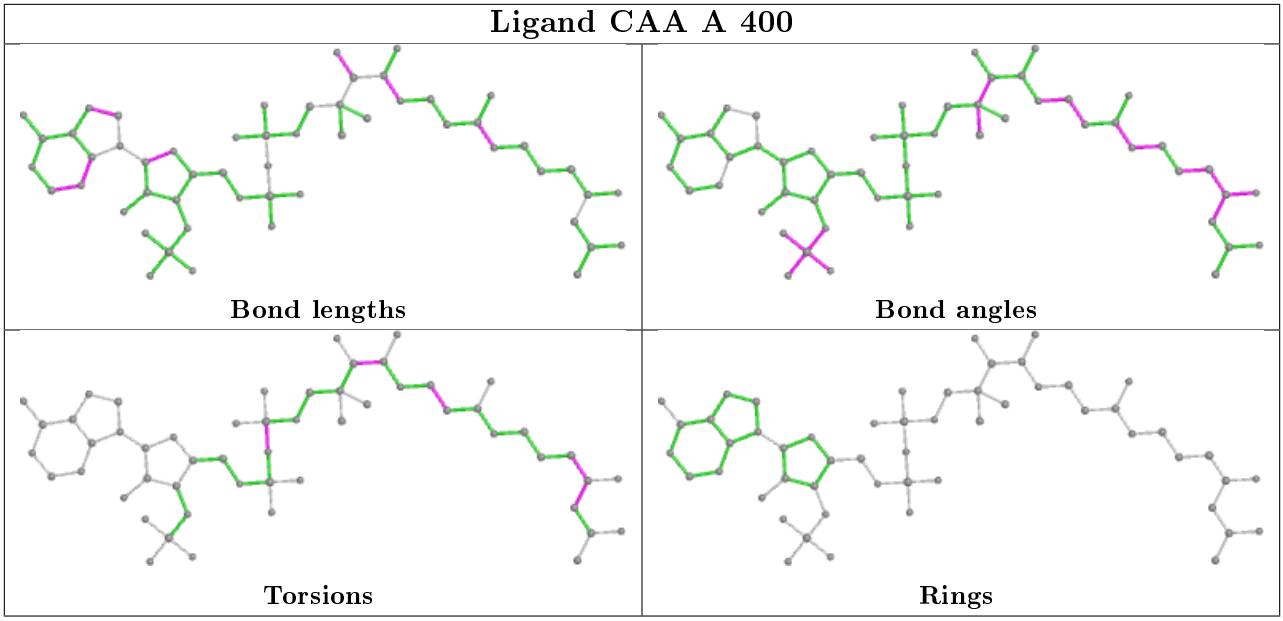
Bond angles



Torsions



Rings



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	384/388 (98%)	-0.66	2 (0%)	91	91	14, 26, 49, 64	0
1	B	384/388 (98%)	-0.78	1 (0%)	94	94	13, 22, 44, 64	0
All	All	768/776 (98%)	-0.72	3 (0%)	92	93	13, 24, 46, 64	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	499	TYR	3.5
1	A	387	ARG	3.1
1	A	7	SER	2.4

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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
2	CAA	A	400	54/54	0.78	0.21	31,62,86,90	0
2	CAA	B	800	54/54	0.88	0.16	25,38,74,75	0

Continued on next page...

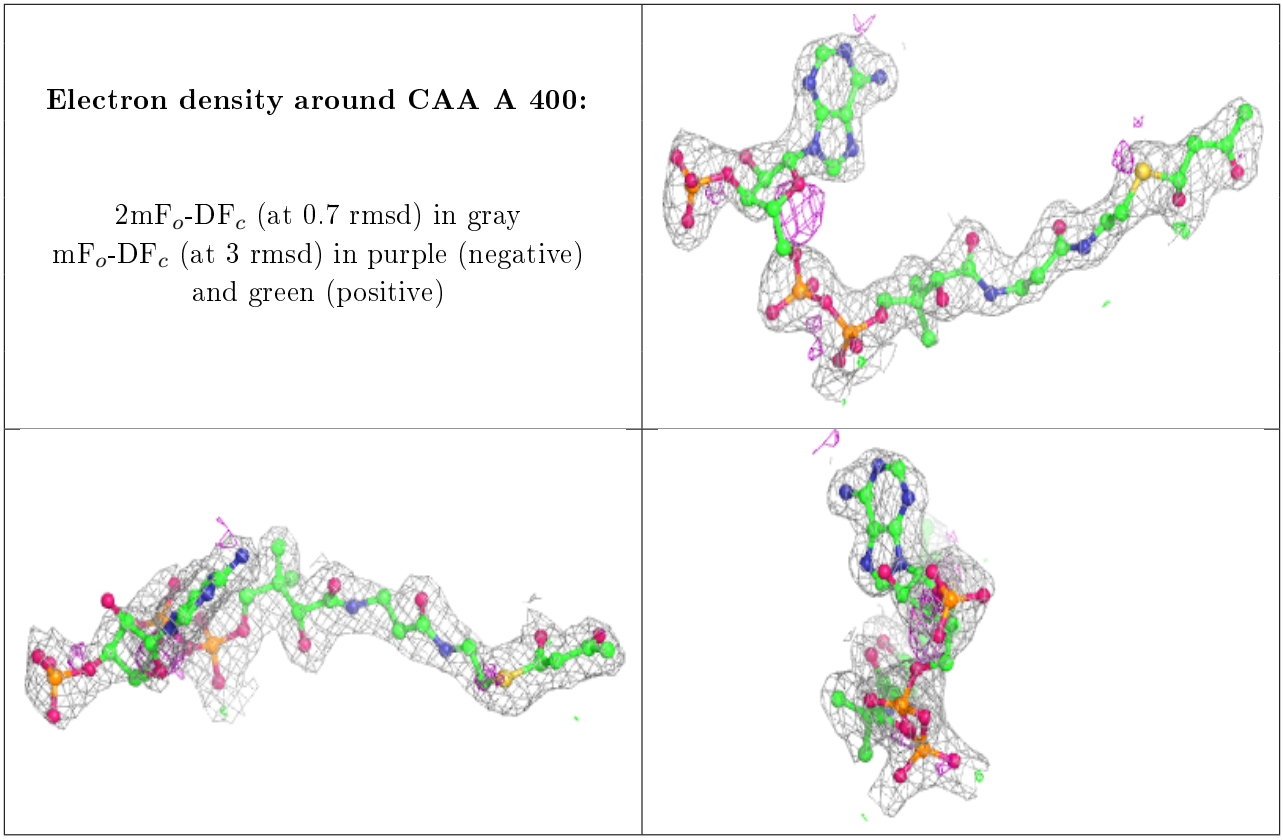
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	FAD	A	399	53/53	0.97	0.09	14,22,31,33	0
3	FAD	B	799	53/53	0.98	0.07	9,17,23,24	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.

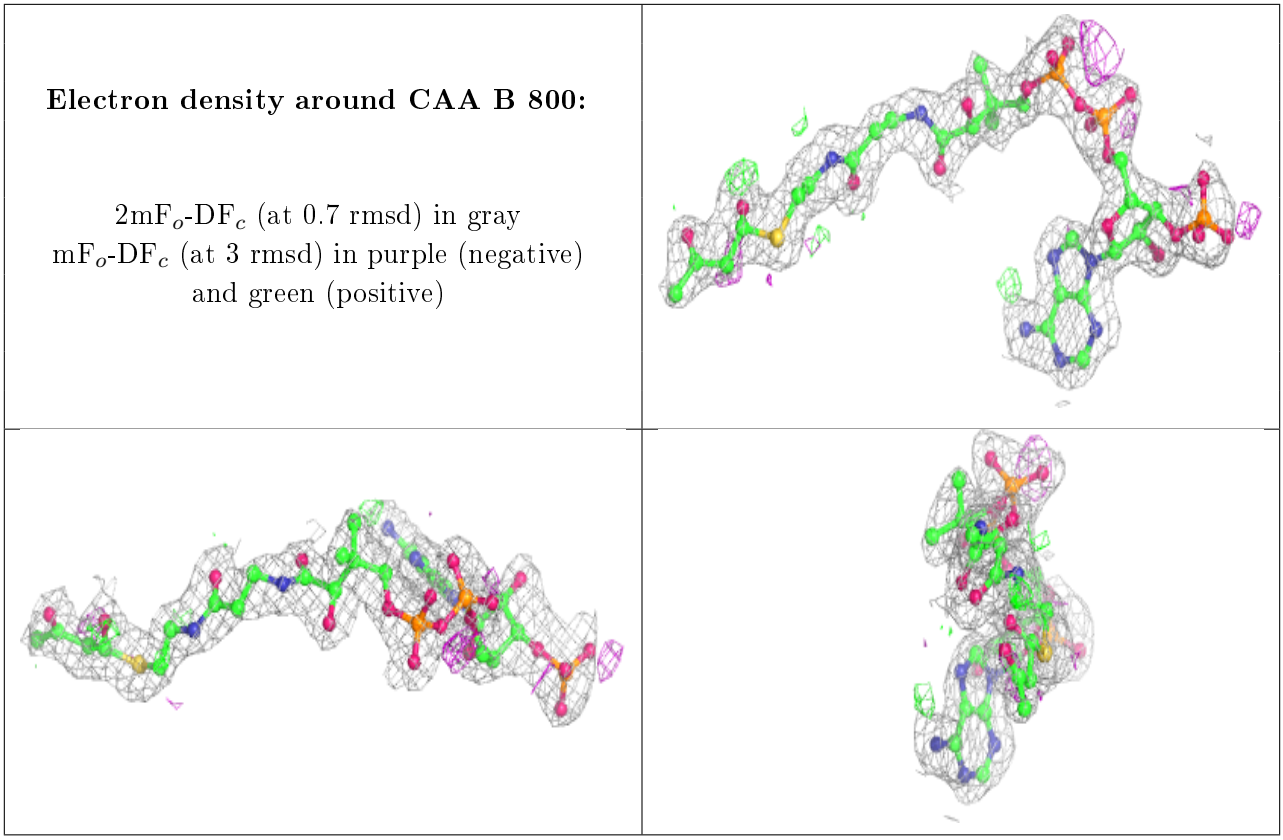
Electron density around CAA A 400:

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



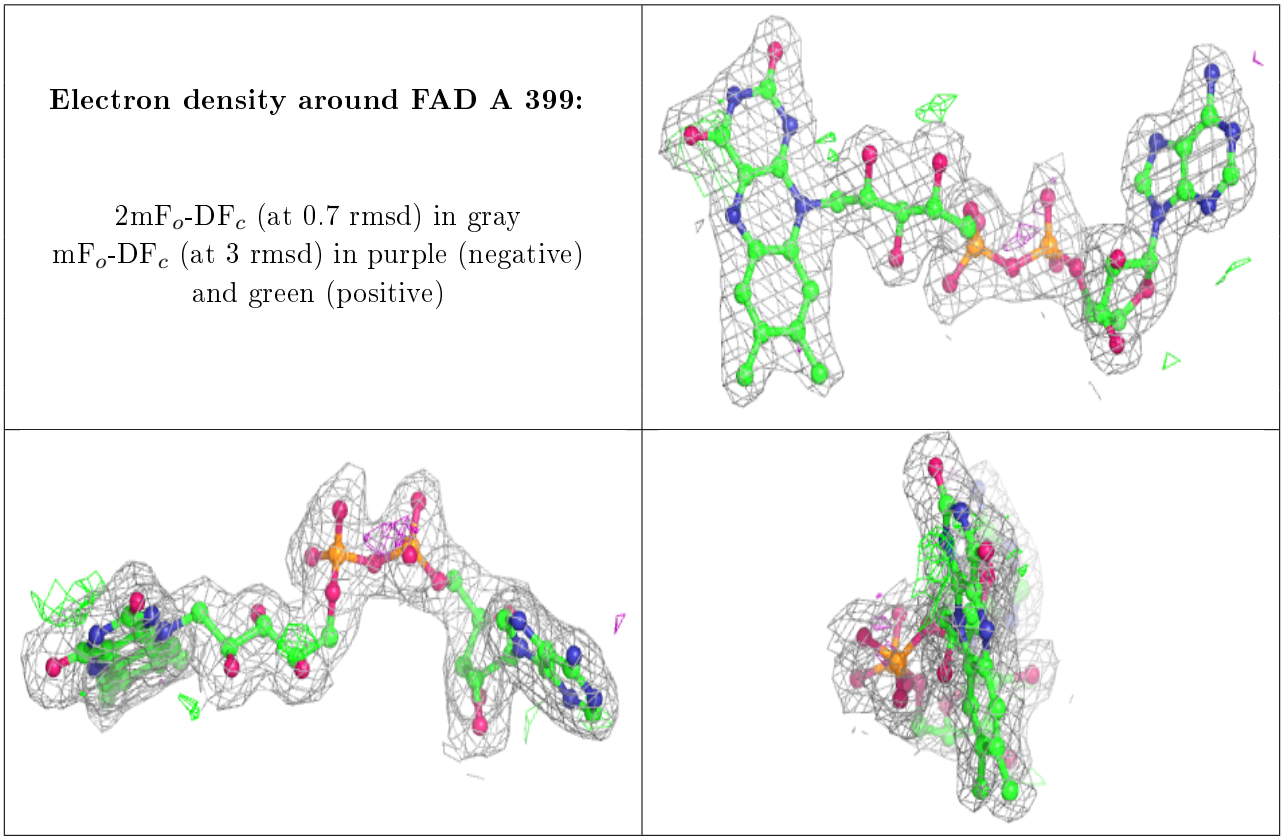
Electron density around CAA B 800:

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



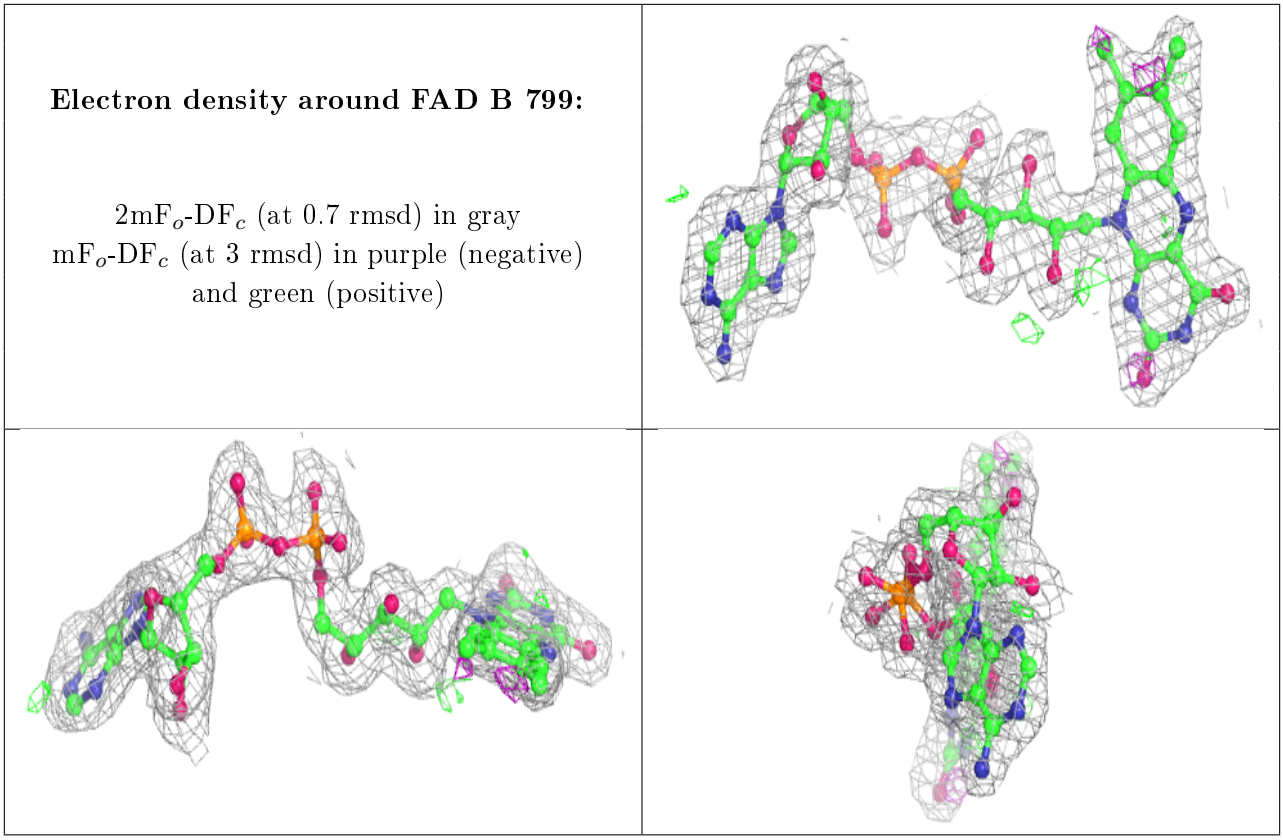
Electron density around FAD A 399:

$2mF_o$-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 799:

$2mF_o$-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.