wwPDB X-ray Structure Validation Summary Report (i)

Aug 28, 2023 – 09:50 AM EDT

PDB ID	:	3K4N
Title	:	Pyranose 2-oxidase F454A/S455A/Y456A mutant
Authors	:	Divne, C.; Tan, T.C.
Deposited on	:	2009-10-05
Resolution	:	2.75 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

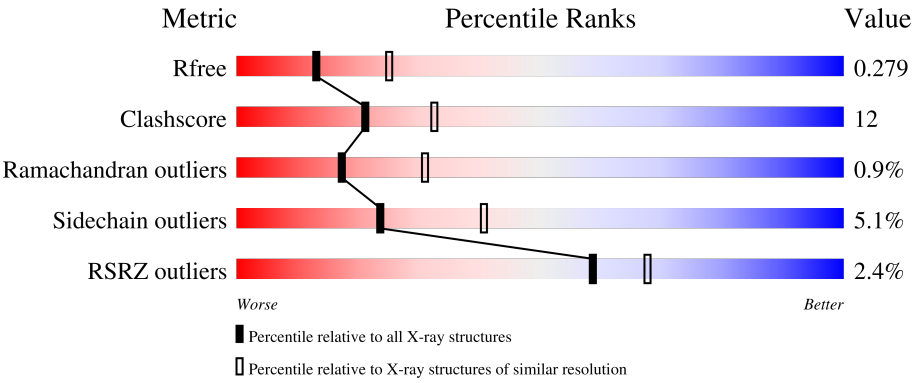
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	623	2%, 70%, 20%, ·, 8%
1	B	623	2%, 66%, 23%, ·, 8%

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
2	FAD	A	801	X	-	-	-
2	FAD	B	801	X	-	-	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9263 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.

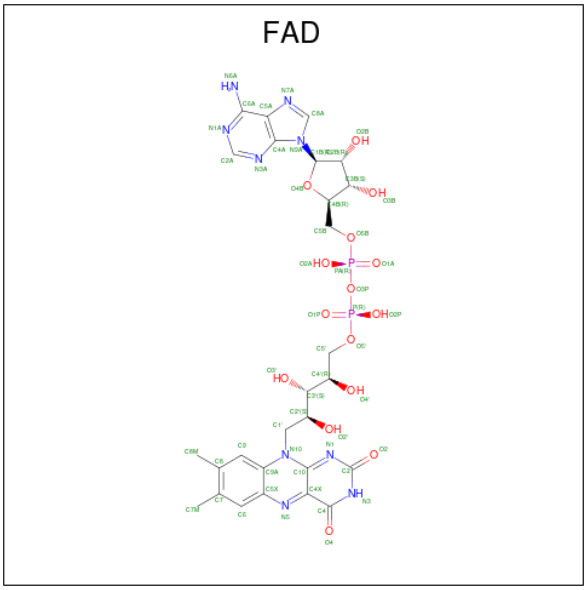
- Molecule 1 is a protein called Pyranose 2-oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	573	Total	C	N	O	S	0	0	0
			4504	2841	774	865	24			
1	B	573	Total	C	N	O	S	0	0	0
			4504	2841	774	865	24			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	454	ALA	PHE	engineered mutation	UNP Q7ZA32
A	455	ALA	SER	engineered mutation	UNP Q7ZA32
A	456	ALA	TYR	engineered mutation	UNP Q7ZA32
B	454	ALA	PHE	engineered mutation	UNP Q7ZA32
B	455	ALA	SER	engineered mutation	UNP Q7ZA32
B	456	ALA	TYR	engineered mutation	UNP Q7ZA32

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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 water.

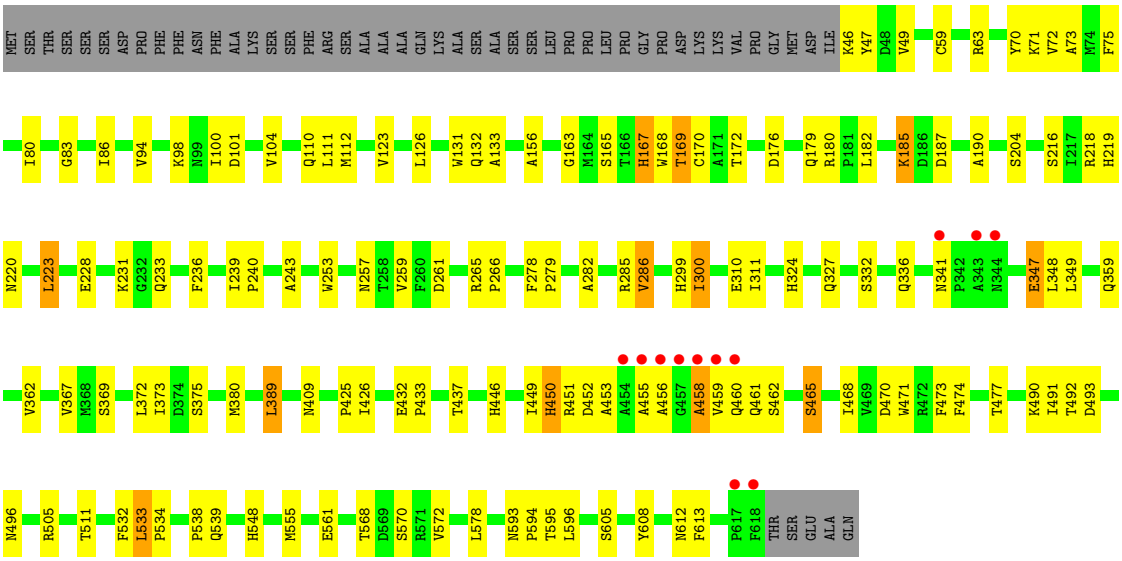
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	94	Total	O	0	0
			94	94		
3	B	55	Total	O	0	0
			55	55		

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.

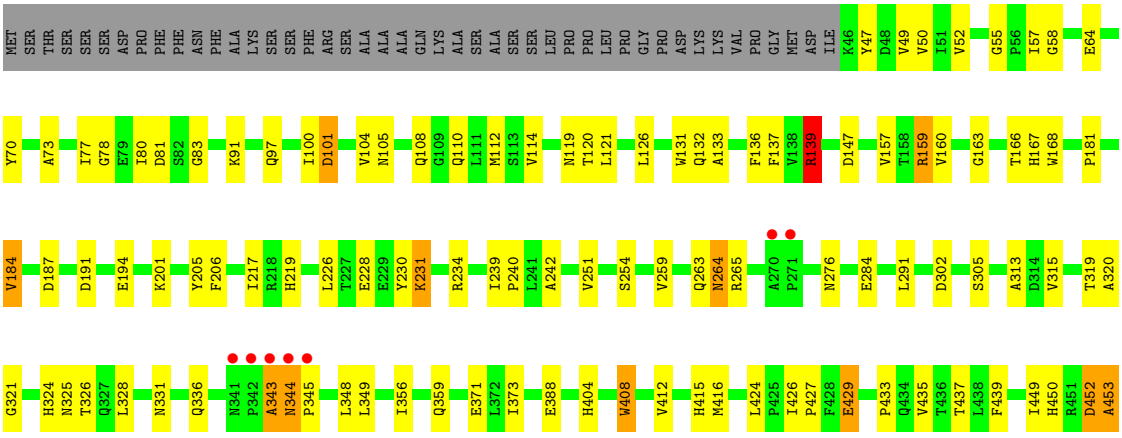
• Molecule 1: Pyranose 2-oxidase

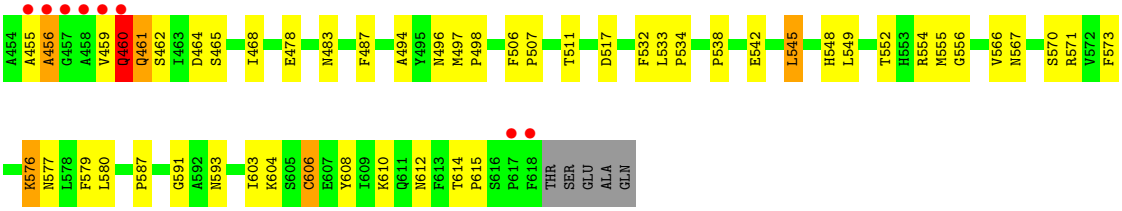
Chain A:



• Molecule 1: Pyranose 2-oxidase

Chain B:




A454 A455 A456 G457 A458 V459 Q460 Q461 S462 I463 D464 S465 I468 E478 N483 F487 A494 Y495 N496 M497 P498 F506 P507 T511 D517 F532 L533 P534 P538 E542 L545 H548 L549 T552 H553 R554 M555 G556 V566 N567 S570 R571 V572 F573
K576 N577 L578 F579 L580 P587 G591 A592 N593 I603 K604 S605 C606 E607 Y608 I609 K610 Q611 N612 F613 T614 P615 S616 P617 F618 THR SER GLU ALA GLN

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	101.58Å 101.58Å 250.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.75 29.97 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.00-2.75) 99.8 (29.97-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.19	Depositor
$< I/\sigma(I) >$ [1]	2.77 (at 2.76Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.191 , 0.274 0.200 , 0.279	Depositor DCC
R_{free} test set	1931 reflections (5.54%)	wwPDB-VP
Wilson B-factor (Å^2)	25.8	Xtriage
Anisotropy	0.004	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 42.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	9263	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.70% 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: 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	0.85	3/4618 (0.1%)	0.84	1/6280 (0.0%)
1	B	0.86	5/4618 (0.1%)	0.85	5/6280 (0.1%)
All	All	0.86	8/9236 (0.1%)	0.85	6/12560 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	228	GLU	CG-CD	8.15	1.64	1.51
1	B	429	GLU	CG-CD	5.49	1.60	1.51
1	A	59	CYS	CB-SG	-5.49	1.72	1.81
1	B	108	GLN	CG-CD	5.41	1.63	1.51
1	A	347	GLU	CB-CG	5.36	1.62	1.52

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	139	ARG	NE-CZ-NH2	-5.99	117.30	120.30
1	B	147	ASP	CB-CG-OD1	5.96	123.66	118.30
1	B	159	ARG	NE-CZ-NH1	5.75	123.17	120.30
1	B	517	ASP	CB-CG-OD1	5.62	123.36	118.30
1	A	452	ASP	CB-CG-OD1	5.45	123.20	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	460	GLN	Peptide

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	4504	0	4356	105	0
1	B	4504	0	4356	120	0
2	A	53	0	27	9	0
2	B	53	0	28	8	0
3	A	94	0	0	1	0
3	B	55	0	0	2	0
All	All	9263	0	8767	215	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 12.

The worst 5 of 215 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:167:HIS:NE2	2:B:801:FAD:HM82	1.21	1.47
1:A:167:HIS:NE2	2:A:801:FAD:HM82	1.04	1.35
1:A:167:HIS:CE1	2:A:801:FAD:HM82	1.63	1.32
1:A:456:ALA:CB	1:A:461:GLN:HE21	1.70	1.04
1:A:167:HIS:NE2	2:A:801:FAD:C8	2.27	0.96

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	571/623 (92%)	533 (93%)	35 (6%)	3 (0%)	29	47
1	B	571/623 (92%)	517 (90%)	47 (8%)	7 (1%)	13	23
All	All	1142/1246 (92%)	1050 (92%)	82 (7%)	10 (1%)	17	31

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	231	LYS
1	B	453	ALA
1	A	231	LYS
1	A	453	ALA
1	A	458	ALA

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	498/539 (92%)	470 (94%)	28 (6%)	21	36
1	B	498/539 (92%)	475 (95%)	23 (5%)	27	46
All	All	996/1078 (92%)	945 (95%)	51 (5%)	24	41

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	112	MET

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Mol	Chain	Res	Type
1	B	326	THR
1	B	576	LYS
1	B	139	ARG
1	B	184	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	108	GLN
1	B	263	GLN
1	B	461	GLN
1	B	276	ASN
1	B	324	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	$\#\|Z\|>2$
2	FAD	A	801	1	53,58,58	1.33	7 (13%)	68,89,89	2.10	16 (23%)
2	FAD	B	801	1	53,58,58	1.42	9 (16%)	68,89,89	1.95	18 (26%)

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
2	FAD	A	801	1	1/1/9/9	12/30/50/50	0/6/6/6
2	FAD	B	801	1	2/2/9/9	5/30/50/50	0/6/6/6

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	FAD	C8M-C8	-4.63	1.41	1.51
2	B	801	FAD	C2A-N3A	3.54	1.37	1.32
2	A	801	FAD	C2A-N3A	3.37	1.37	1.32
2	A	801	FAD	C2A-N1A	3.04	1.39	1.33
2	B	801	FAD	C2A-N1A	2.89	1.39	1.33

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	801	FAD	O3B-C3B-C4B	7.05	131.43	111.05
2	A	801	FAD	N3A-C2A-N1A	-6.20	118.99	128.68
2	B	801	FAD	N3A-C2A-N1A	-5.47	120.13	128.68
2	A	801	FAD	O2B-C2B-C1B	5.40	130.81	110.85
2	B	801	FAD	O3B-C3B-C4B	5.13	125.88	111.05

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	801	FAD	C4B
2	B	801	FAD	C4B
2	B	801	FAD	C1B

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	FAD	C5B-O5B-PA-O1A

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Mol	Chain	Res	Type	Atoms
2	A	801	FAD	C5B-O5B-PA-O3P
2	A	801	FAD	PA-O3P-P-O5'
2	A	801	FAD	C3B-C4B-C5B-O5B
2	A	801	FAD	O3'-C3'-C4'-C5'

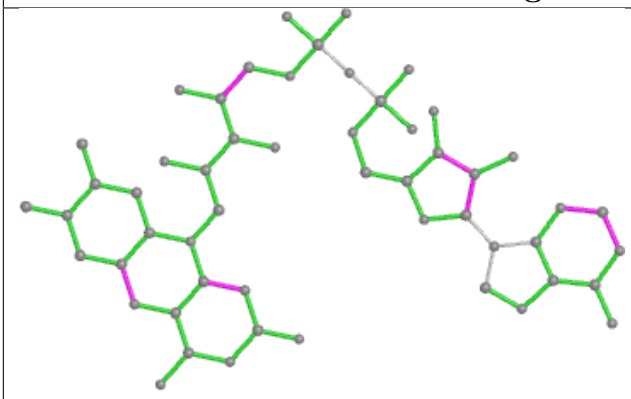
There are no ring outliers.

2 monomers are involved in 17 short contacts:

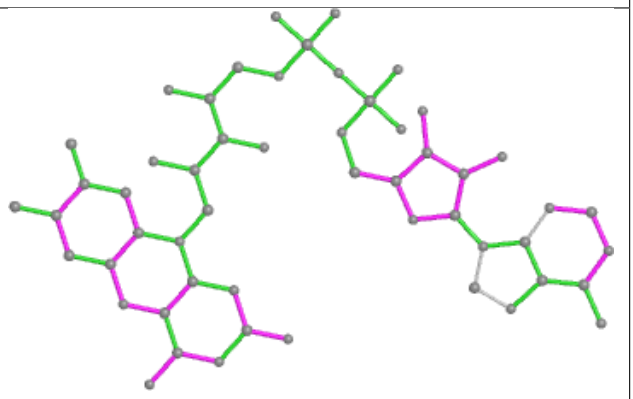
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	FAD	9	0
2	B	801	FAD	8	0

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.

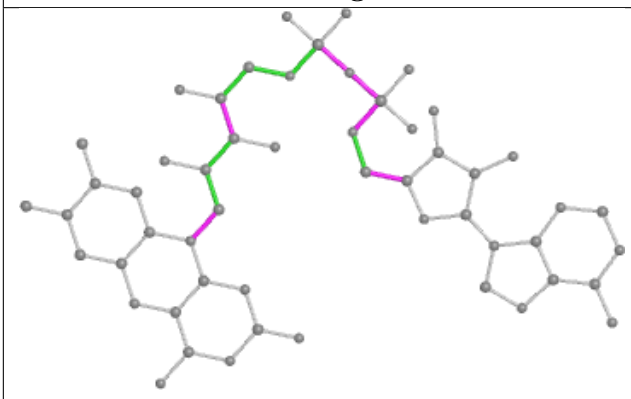
Ligand FAD A 801



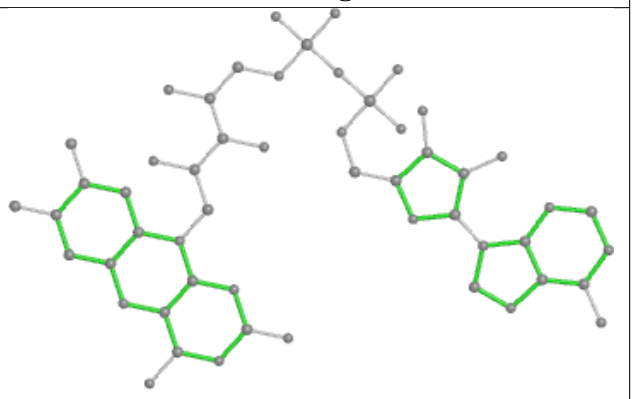
Bond lengths



Bond angles

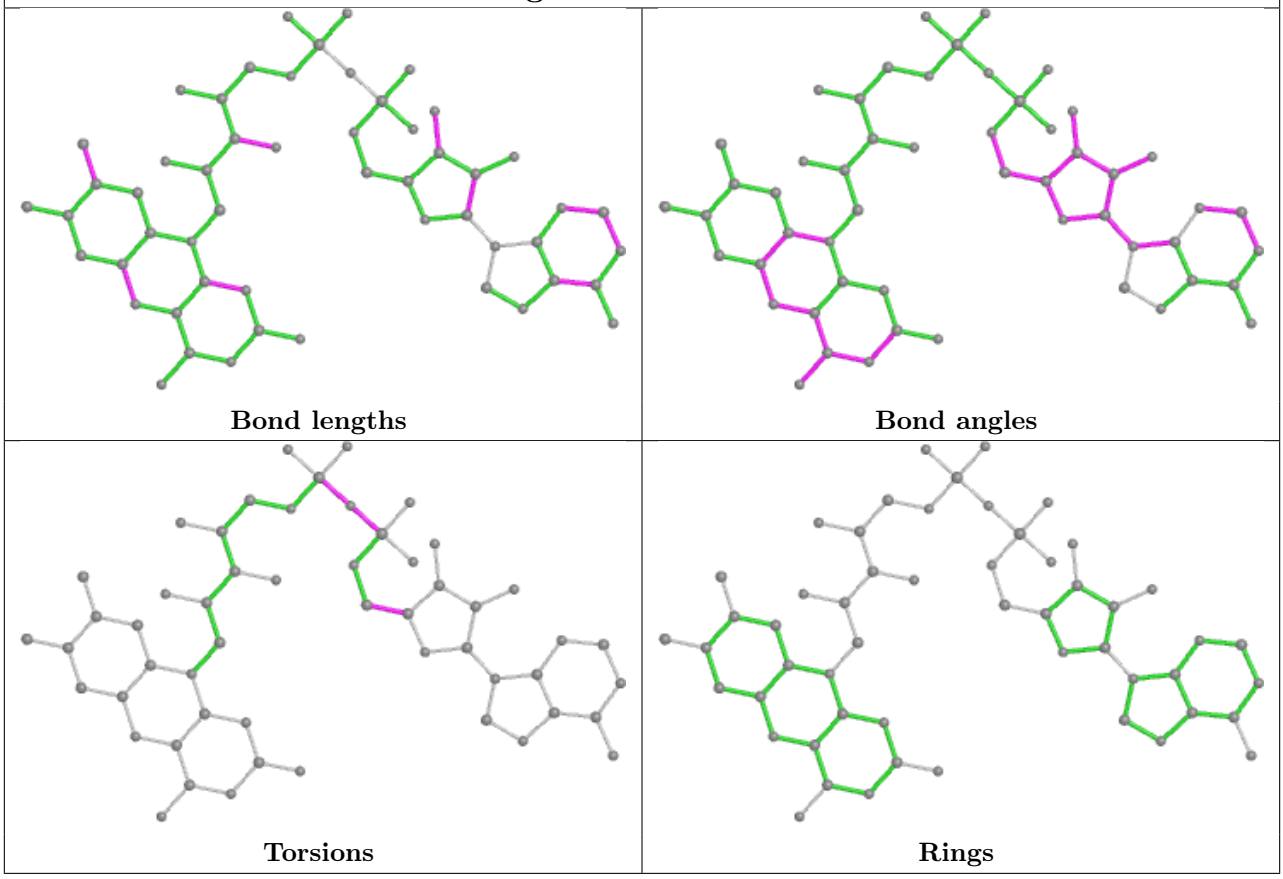


Torsions



Rings

Ligand FAD B 801



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^{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	573/623 (91%)	-0.25	12 (2%)	63	72	17, 24, 33, 51	0
1	B	573/623 (91%)	-0.19	15 (2%)	56	65	17, 25, 37, 49	0
All	All	1146/1246 (91%)	-0.22	27 (2%)	59	68	17, 25, 36, 51	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	458	ALA	5.1
1	B	456	ALA	5.1
1	B	459	VAL	5.0
1	A	459	VAL	4.5
1	B	618	PHE	4.4

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 monosaccharides in this entry.

6.4 Ligands

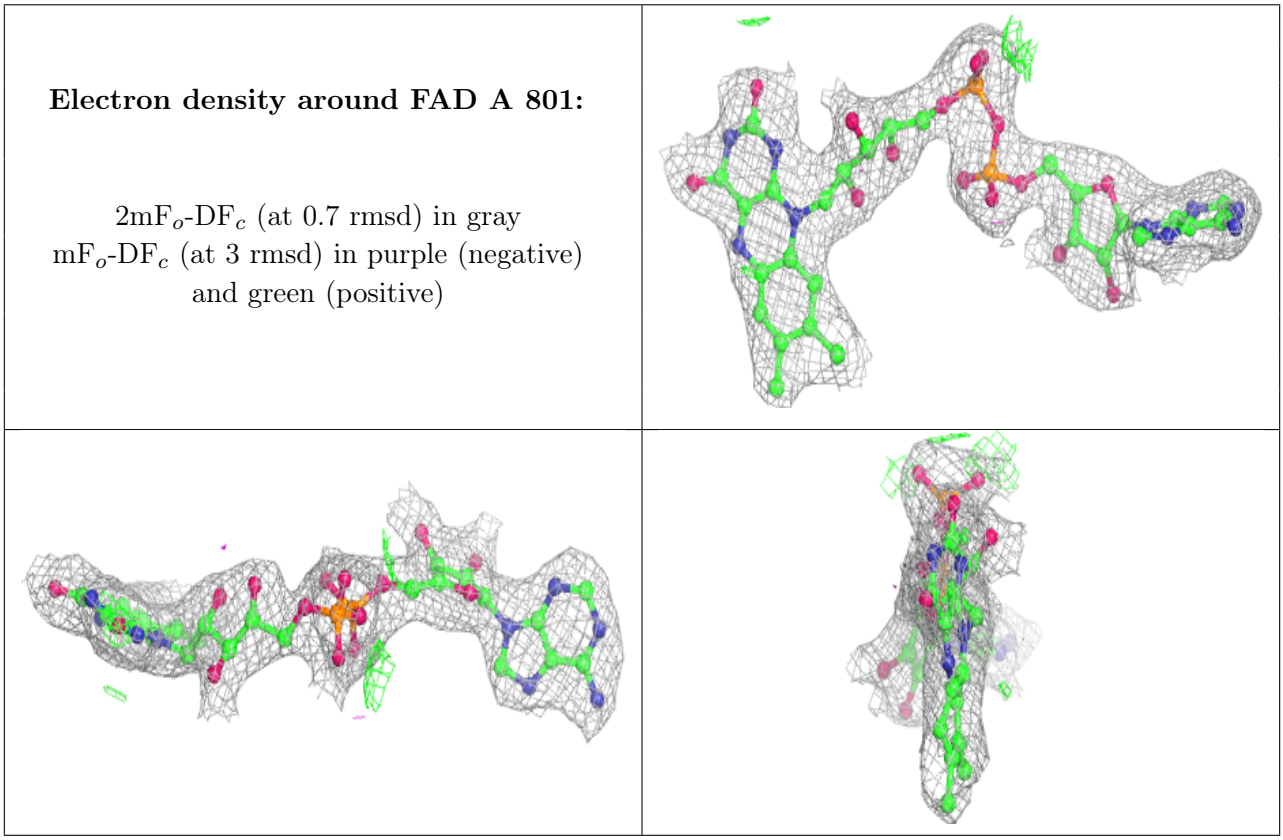
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	FAD	A	801	53/53	0.97	0.12	20,25,30,33	0
2	FAD	B	801	53/53	0.97	0.12	16,27,34,35	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.

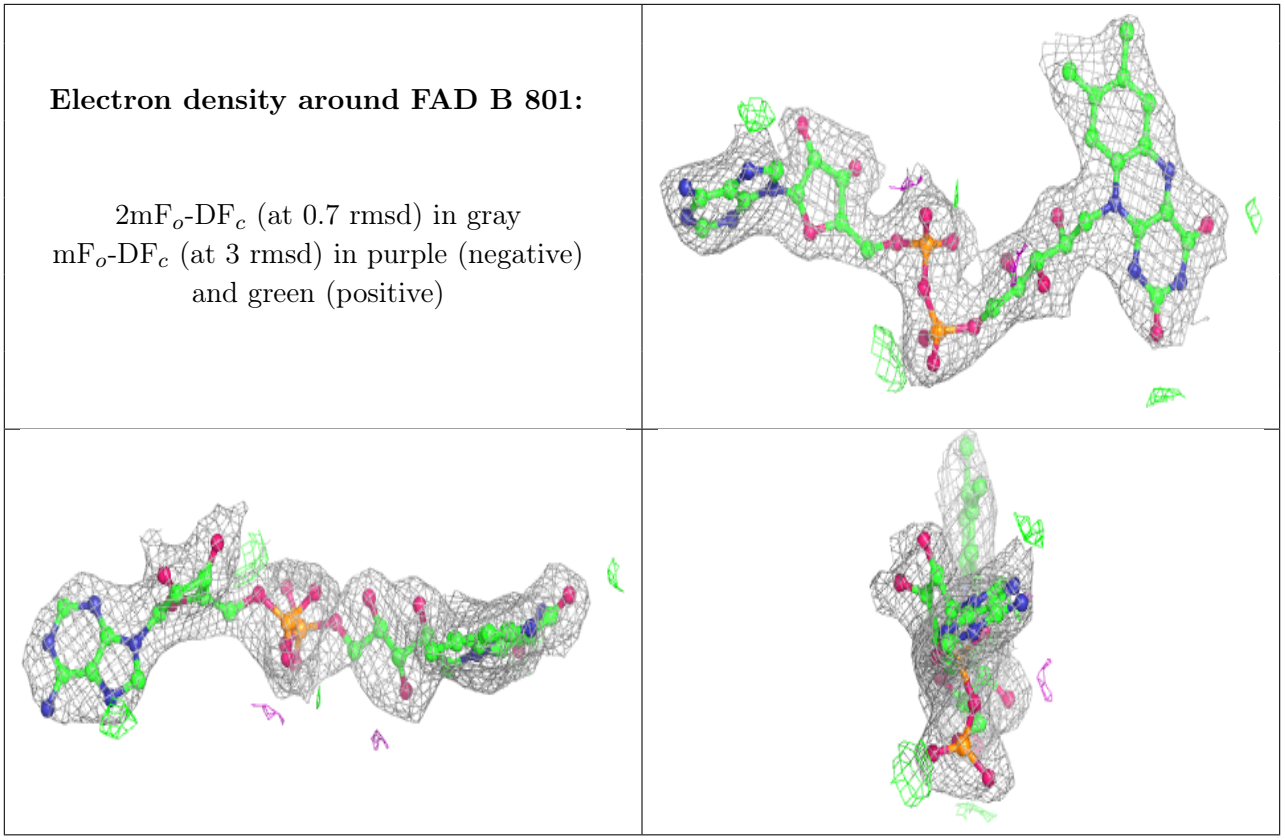
Electron density around FAD A 801:

$2mF_o$-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 801:

$2mF_o$-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.