wwPDB X-ray Structure Validation Summary Report (i)

Dec 20, 2023 – 10:28 AM EST

PDB ID	:	1B5Q
Title	:	A 30 ANGSTROM U-SHAPED CATALYTIC TUNNEL IN THE CRYSTAL STRUCTURE OF POLYAMINE OXIDASE
Authors	:	Binda, C.; Coda, A.; Angelini, R.; Federico, R.; Ascenzi, P.; Mattevi, A.
Deposited on	:	1999-01-07
Resolution	:	1.90 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:

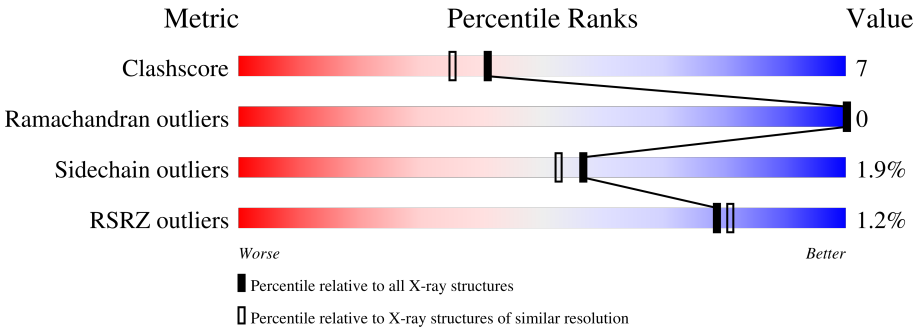
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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))
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 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	472	78% 17%
1	B	472	84% 13%
1	C	472	84% 14%
2	D	2	100%
2	E	2	100%
3	F	5	100%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12059 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.

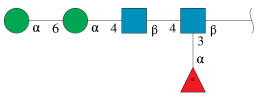
- Molecule 1 is a protein called PROTEIN (POLYAMINE OXIDASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	459	Total	C	N	O	S	60	0	0
			3684	2353	621	696	14			
1	B	462	Total	C	N	O	S	53	0	0
			3715	2374	627	700	14			
1	C	462	Total	C	N	O	S	44	0	0
			3715	2374	627	700	14			

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

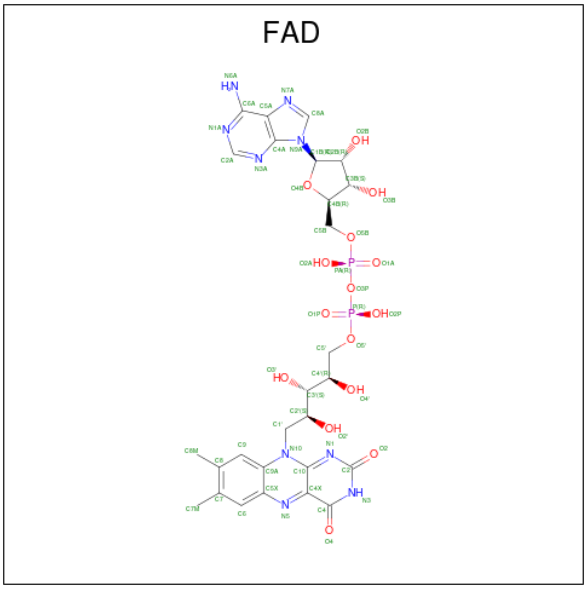
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-D-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose.



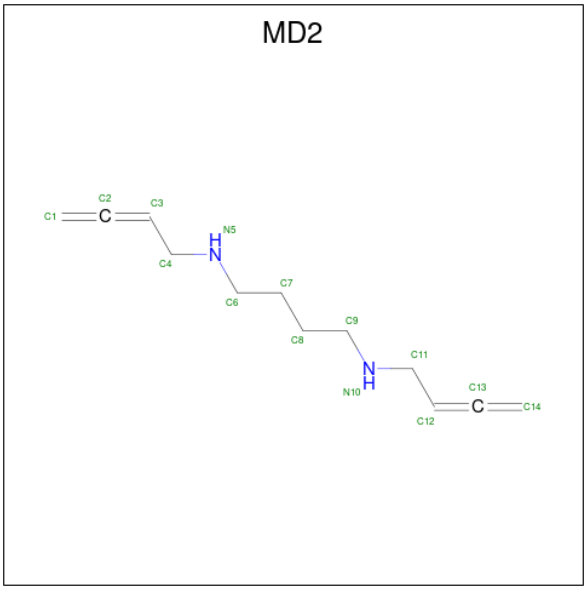
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	5	Total	C	N	O	0	0	0
			60	34	2	24			

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

- Molecule 5 is N,N'-BIS(2,3-BUTADIENYL)-1,4-BUTANE-DIAMINE (three-letter code: MD2) (formula: $C_{12}H_{20}N_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N 14 12 2	0	0
5	B	1	Total C N 14 12 2	0	0
5	C	1	Total C N 14 12 2	0	0

- Molecule 6 is water.

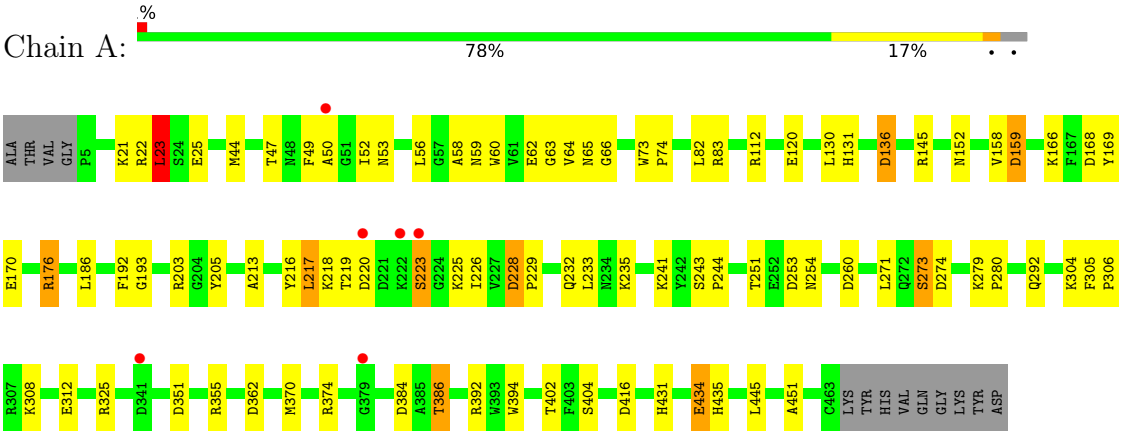
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	195	Total O 195 195	0	0
6	B	207	Total O 207 207	0	0
6	C	226	Total O 226 226	0	0

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.

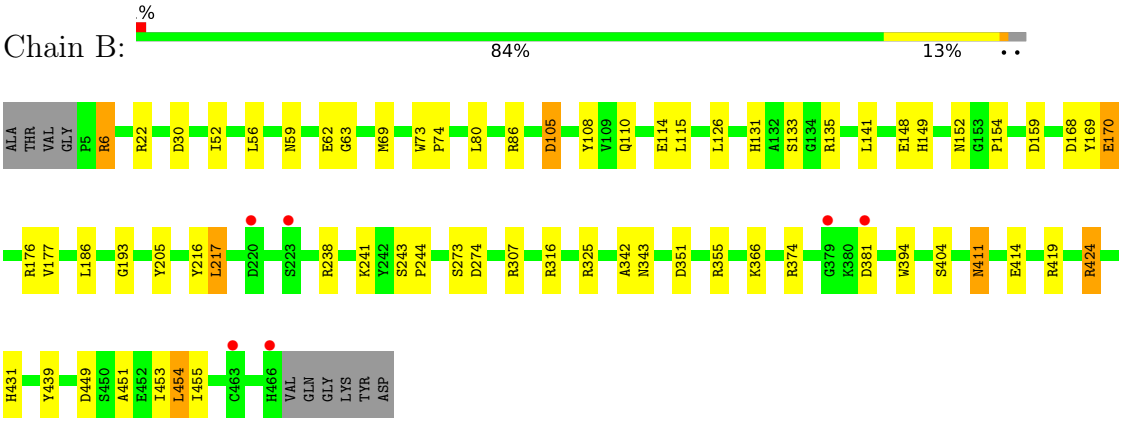
• Molecule 1: PROTEIN (POLYAMINE OXIDASE)

Chain A:



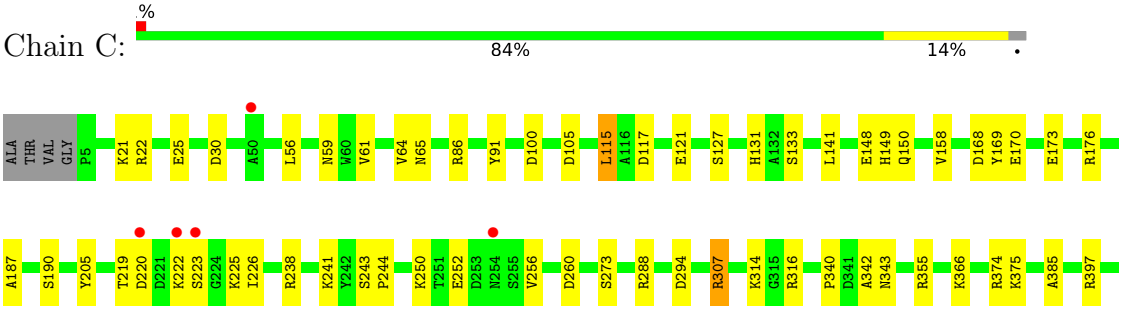
• Molecule 1: PROTEIN (POLYAMINE OXIDASE)

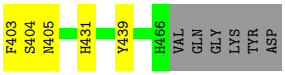
Chain B:



• Molecule 1: PROTEIN (POLYAMINE OXIDASE)

Chain C:





• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:

• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:

• Molecule 3: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-D-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α, β, γ	184.60Å 184.60Å 281.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.90 20.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	96.0 (50.00-1.90) 96.0 (20.00-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.95 (at 1.90Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.193 , (Not available) 0.182 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	19.3	Xtriage
Anisotropy	0.117	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 71.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	12059	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.60% 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: MD2, FCA, MAN, FAD, NAG

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	0.63	0/3775	1.33	35/5116 (0.7%)
1	B	0.64	0/3808	1.31	22/5160 (0.4%)
1	C	0.64	0/3808	1.31	21/5160 (0.4%)
All	All	0.64	0/11391	1.32	78/15436 (0.5%)

There are no bond length outliers.

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	307	ARG	NE-CZ-NH1	-18.26	111.17	120.30
1	A	355	ARG	NE-CZ-NH2	-15.39	112.61	120.30
1	C	307	ARG	NE-CZ-NH2	14.42	127.51	120.30
1	C	115	LEU	CB-CG-CD1	-12.25	90.18	111.00
1	B	135	ARG	NE-CZ-NH1	-11.46	114.57	120.30

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	3684	0	3585	58	0
1	B	3715	0	3614	53	0
1	C	3715	0	3614	35	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	28	0	26	3	0
2	E	28	0	26	4	0
3	F	60	0	52	5	0
4	A	53	0	31	2	0
4	B	53	0	31	0	0
4	C	53	0	31	0	0
5	A	14	0	20	4	0
5	B	14	0	20	5	0
5	C	14	0	20	6	0
6	A	195	0	0	7	0
6	B	207	0	0	2	0
6	C	226	0	0	3	0
All	All	12059	0	11070	153	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 7.

The worst 5 of 153 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:192:PHE:O	6:A:794:HOH:O	1.60	1.19
1:B:69:MET:HE3	1:B:73:TRP:HB3	1.17	1.15
1:B:69:MET:CE	1:B:74:PRO:HD3	1.80	1.10
1:B:69:MET:HE2	1:B:74:PRO:HD3	1.10	1.08
1:B:69:MET:CE	1:B:73:TRP:HB3	1.88	1.02

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	457/472 (97%)	438 (96%)	19 (4%)	0	100	100
1	B	460/472 (98%)	442 (96%)	18 (4%)	0	100	100
1	C	460/472 (98%)	442 (96%)	18 (4%)	0	100	100
All	All	1377/1416 (97%)	1322 (96%)	55 (4%)	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	394/404 (98%)	387 (98%)	7 (2%)	59	55
1	B	397/404 (98%)	389 (98%)	8 (2%)	55	51
1	C	397/404 (98%)	390 (98%)	7 (2%)	59	55
All	All	1188/1212 (98%)	1166 (98%)	22 (2%)	57	53

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	454	LEU
1	C	115	LEU
1	C	105	ASP
1	C	127	SER
1	A	434	GLU

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	411	ASN
1	B	431	HIS
1	C	431	HIS
1	C	131	HIS
1	C	360	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)

9 monosaccharides 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	NAG	D	1	1,2	14,14,15	1.72	2 (14%)	17,19,21	3.29	10 (58%)
2	NAG	D	2	2	14,14,15	1.45	2 (14%)	17,19,21	2.17	6 (35%)
2	NAG	E	1	1,2	14,14,15	1.94	4 (28%)	17,19,21	3.07	12 (70%)
2	NAG	E	2	1,2	14,14,15	1.25	1 (7%)	17,19,21	3.33	6 (35%)
3	NAG	F	1	1,3	14,14,15	1.77	4 (28%)	17,19,21	4.31	12 (70%)
3	NAG	F	2	3	14,14,15	1.55	3 (21%)	17,19,21	3.10	5 (29%)
3	MAN	F	3	3	11,11,12	0.83	0	15,15,17	2.17	4 (26%)
3	MAN	F	4	3	11,11,12	0.77	0	15,15,17	1.75	4 (26%)
3	FCA	F	5	3	10,10,11	1.60	1 (10%)	14,14,16	2.17	7 (50%)

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	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	NAG	E	1	1,2	-	2/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	2	1,2	-	2/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	2/6/23/26	0/1/1/1
3	MAN	F	3	3	-	0/2/19/22	0/1/1/1
3	MAN	F	4	3	-	2/2/19/22	0/1/1/1
3	FCA	F	5	3	-	-	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	NAG	O5-C5	4.66	1.52	1.43
2	D	1	NAG	O5-C5	4.53	1.52	1.43
3	F	5	FCA	C2-C3	-3.50	1.47	1.52
3	F	2	NAG	O5-C5	3.45	1.50	1.43
2	D	2	NAG	C1-C2	-3.39	1.47	1.52

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	F	2	NAG	O5-C5-C6	-9.45	92.39	107.20
3	F	1	NAG	C8-C7-N2	-8.29	102.06	116.10
2	E	2	NAG	O6-C6-C5	8.09	139.05	111.29
2	E	2	NAG	O5-C5-C6	-7.66	95.19	107.20
3	F	1	NAG	C1-O5-C5	7.20	121.95	112.19

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	2	NAG	C4-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
2	E	1	NAG	C4-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6

There are no ring outliers.

9 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	4	MAN	2	0

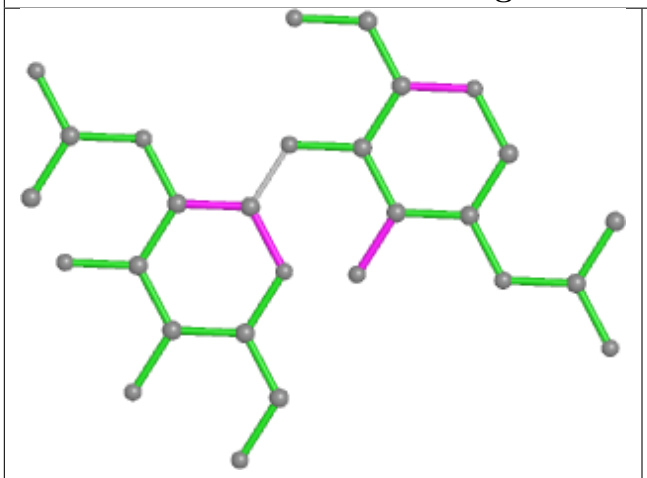
Continued on next page...

Continued from previous page...

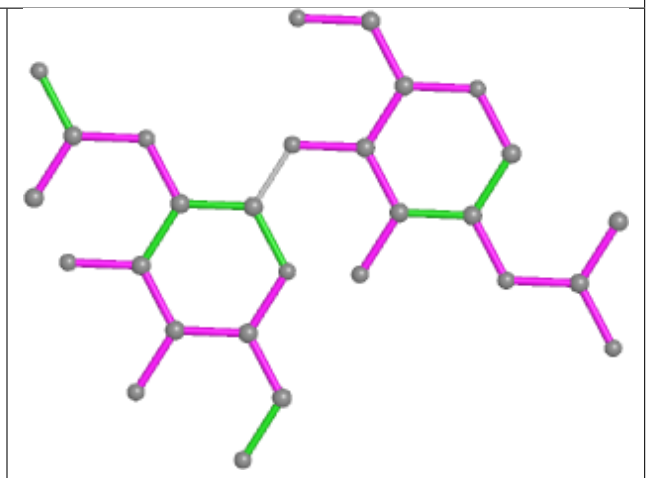
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	2	NAG	4	0
3	F	2	NAG	1	0
3	F	1	NAG	3	0
3	F	3	MAN	2	0
3	F	5	FCA	2	0
2	D	2	NAG	3	0
2	D	1	NAG	3	0
2	E	1	NAG	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

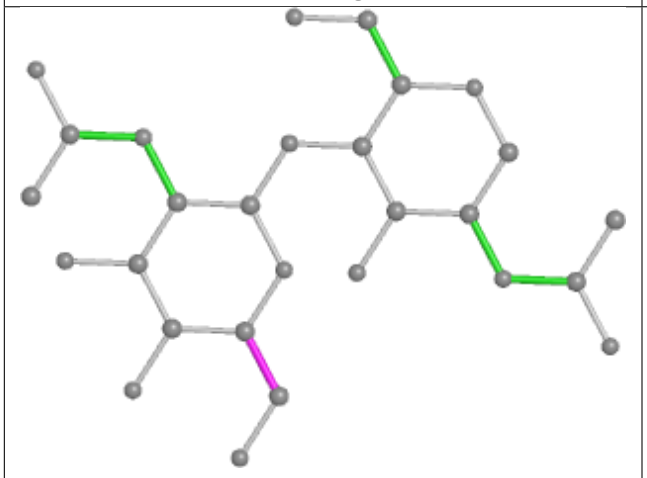
Oligosaccharide Chain D



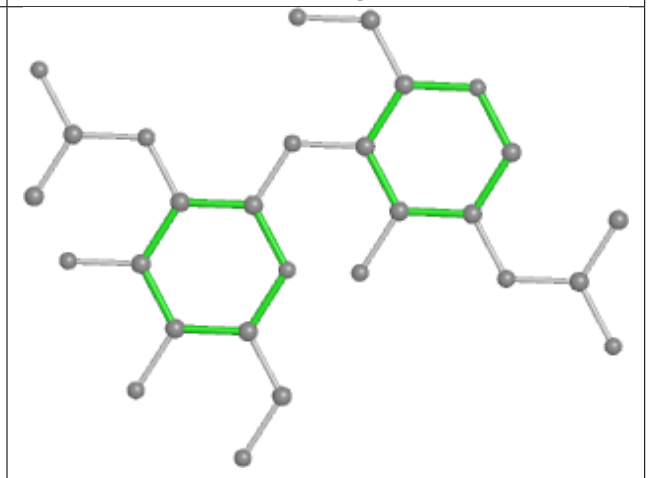
Bond lengths



Bond angles

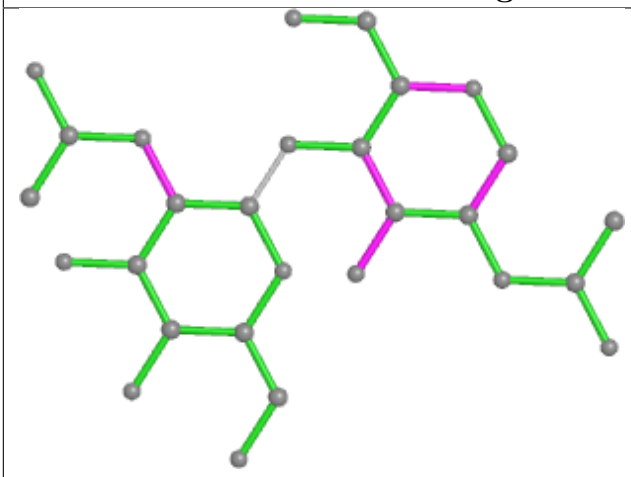


Torsions

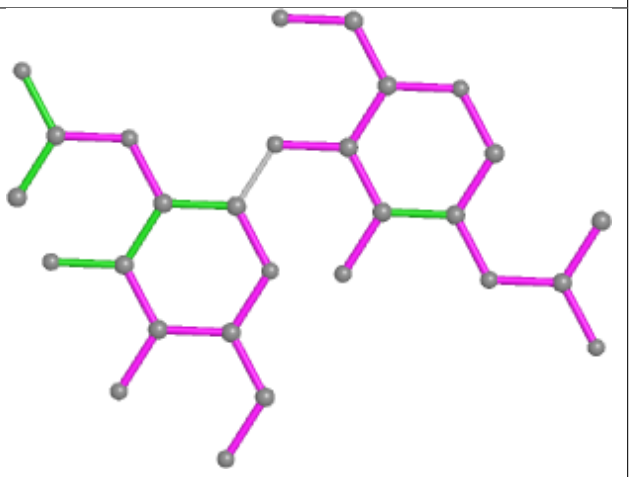


Rings

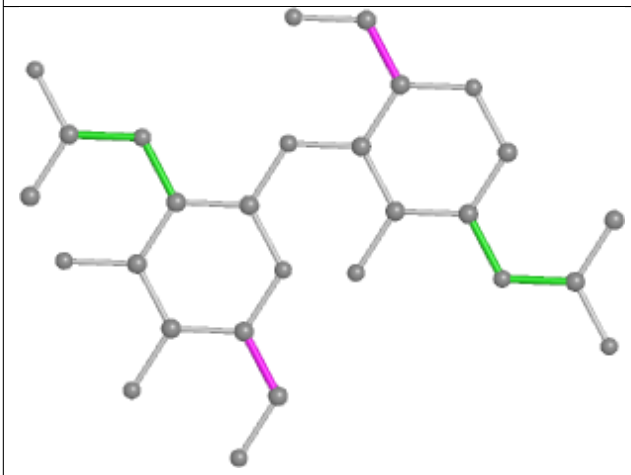
Oligosaccharide Chain E



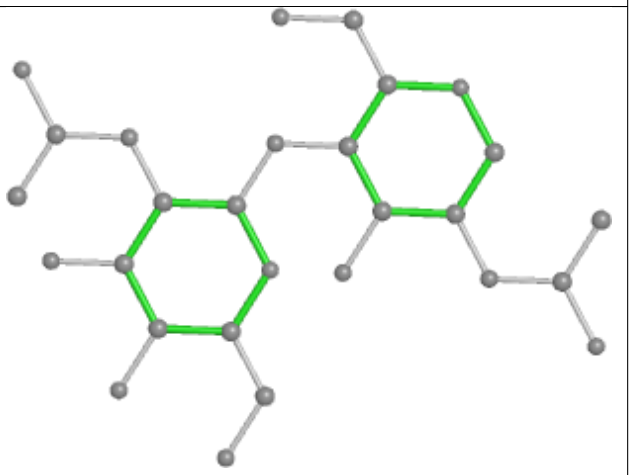
Bond lengths



Bond angles

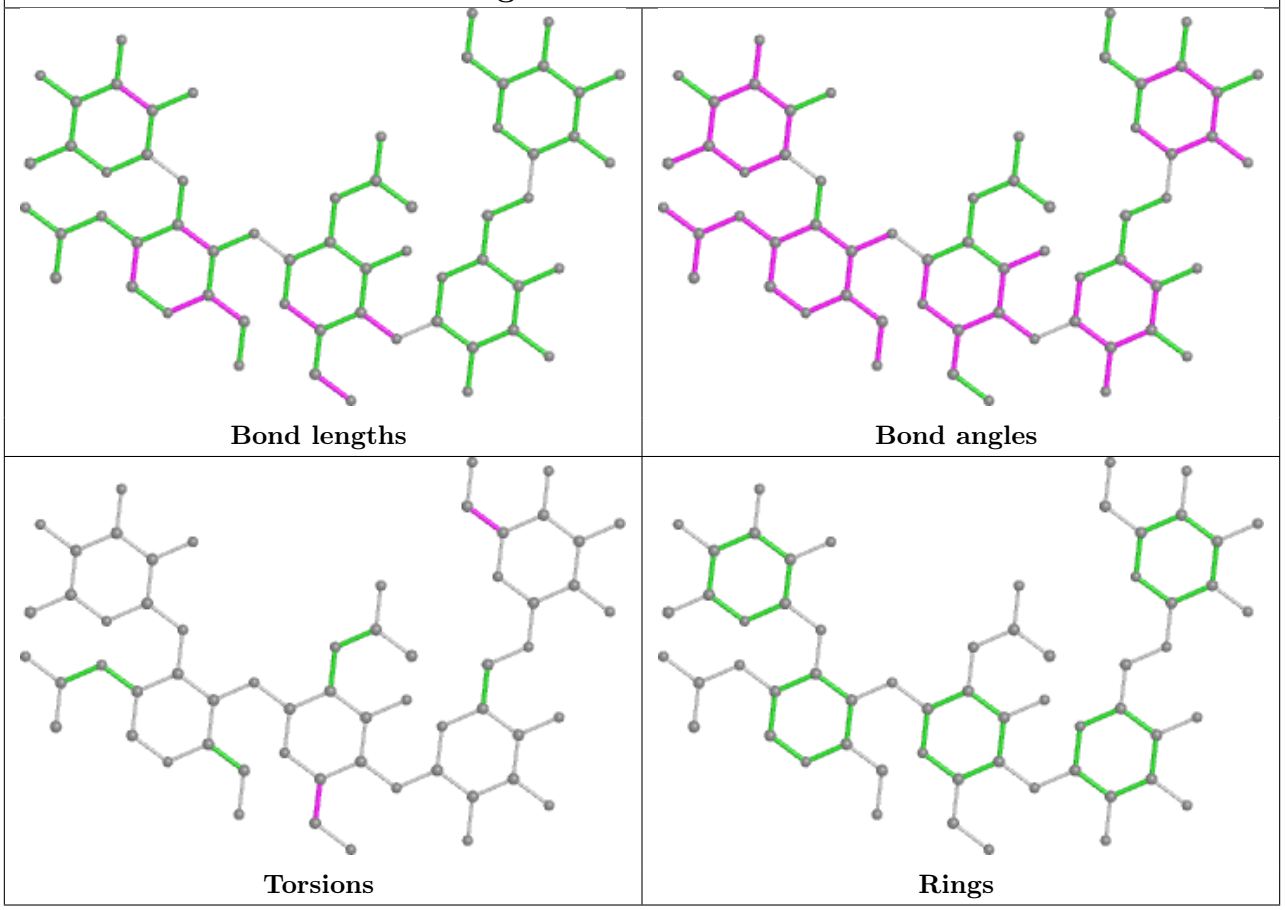


Torsions



Rings

Oligosaccharide Chain F



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	$\#\|Z\| > 2$
5	MD2	A	590	-	11,13,13	0.86	0	10,12,12	4.40	4 (40%)
4	FAD	A	579	-	53,58,58	0.97	3 (5%)	68,89,89	1.41	13 (19%)
4	FAD	B	579	-	53,58,58	0.85	1 (1%)	68,89,89	1.38	10 (14%)
5	MD2	B	590	-	11,13,13	0.93	0	10,12,12	3.19	3 (30%)
5	MD2	C	590	-	11,13,13	0.98	1 (9%)	10,12,12	6.37	4 (40%)
4	FAD	C	579	-	53,58,58	1.13	5 (9%)	68,89,89	1.28	8 (11%)

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
5	MD2	A	590	-	-	8/9/11/11	-
4	FAD	A	579	-	-	2/30/50/50	0/6/6/6
4	FAD	B	579	-	-	1/30/50/50	0/6/6/6
5	MD2	B	590	-	-	6/9/11/11	-
5	MD2	C	590	-	-	7/9/11/11	-
4	FAD	C	579	-	-	3/30/50/50	0/6/6/6

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	579	FAD	C4X-N5	3.50	1.37	1.30
4	A	579	FAD	C4X-N5	2.81	1.36	1.30
4	B	579	FAD	C4X-N5	2.78	1.36	1.30
4	A	579	FAD	C1'-C2'	2.51	1.56	1.52
5	C	590	MD2	C13-C12	2.29	1.34	1.29

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	C	590	MD2	C4-C3-C2	15.47	135.90	124.21
5	C	590	MD2	C11-C12-C13	-11.06	115.85	124.21
5	B	590	MD2	C11-C12-C13	-8.16	118.04	124.21
5	A	590	MD2	C11-C12-C13	-8.11	118.08	124.21
5	A	590	MD2	C4-C3-C2	-7.79	118.32	124.21

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	579	FAD	C5B-O5B-PA-O1A
5	A	590	MD2	N10-C11-C12-C13
5	B	590	MD2	N10-C11-C12-C13
5	C	590	MD2	N10-C11-C12-C13
5	B	590	MD2	N5-C6-C7-C8

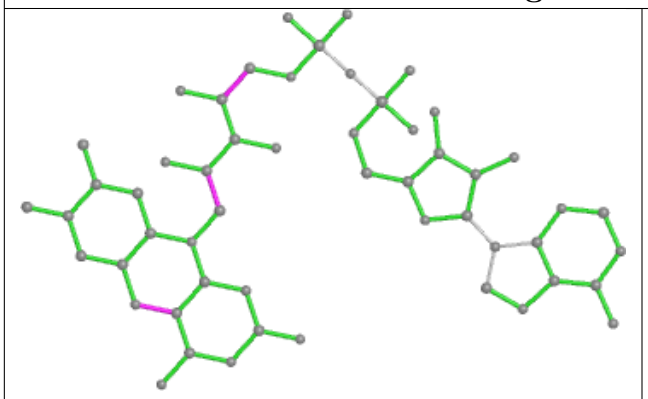
There are no ring outliers.

4 monomers are involved in 17 short contacts:

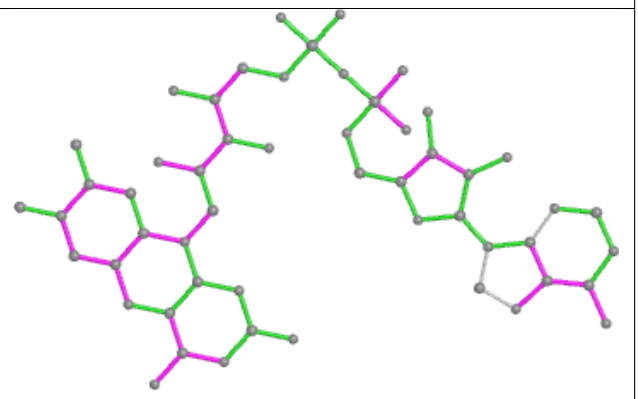
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	590	MD2	4	0
4	A	579	FAD	2	0
5	B	590	MD2	5	0
5	C	590	MD2	6	0

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.

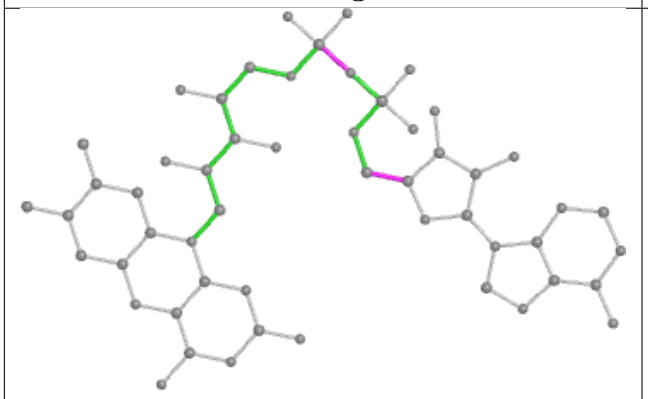
Ligand FAD A 579



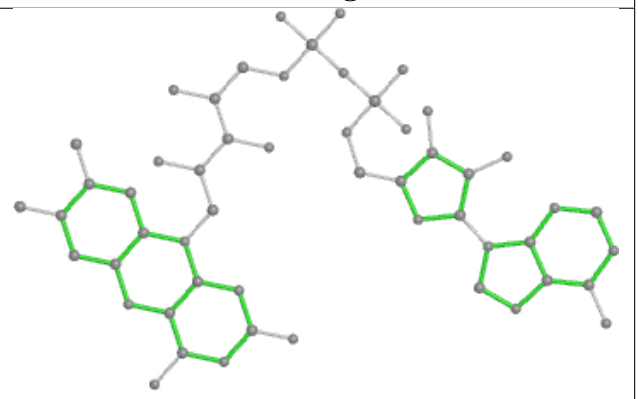
Bond lengths



Bond angles

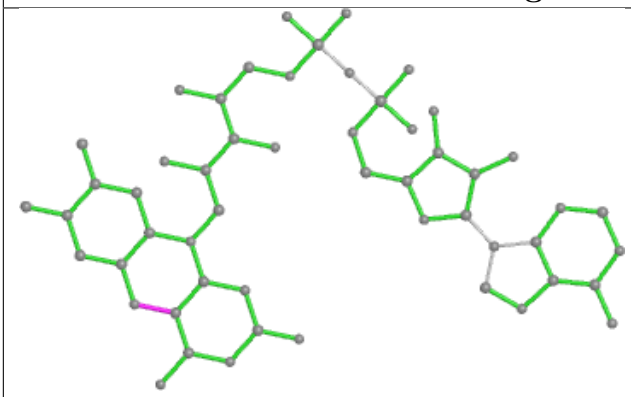


Torsions

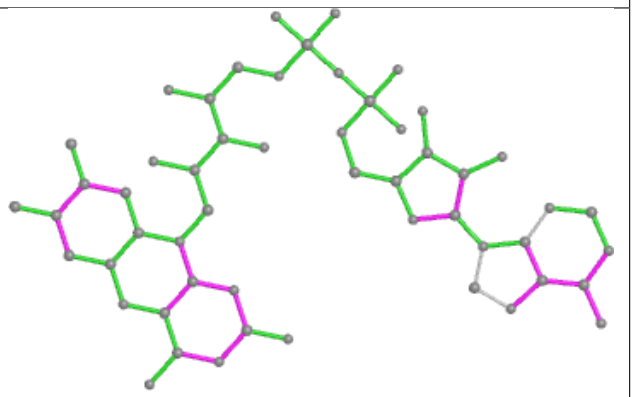


Rings

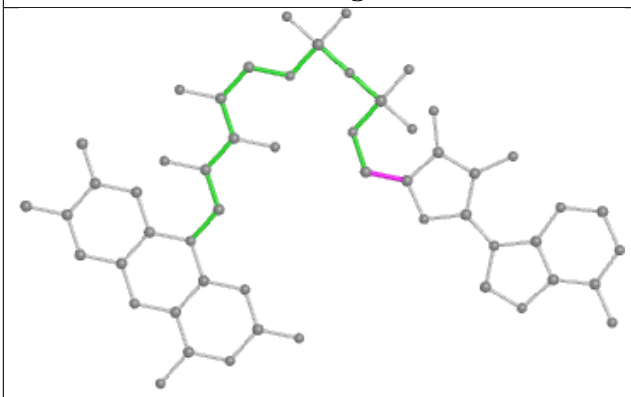
Ligand FAD B 579



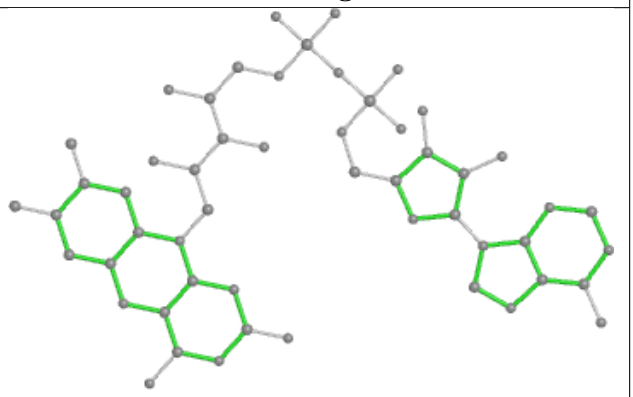
Bond lengths



Bond angles

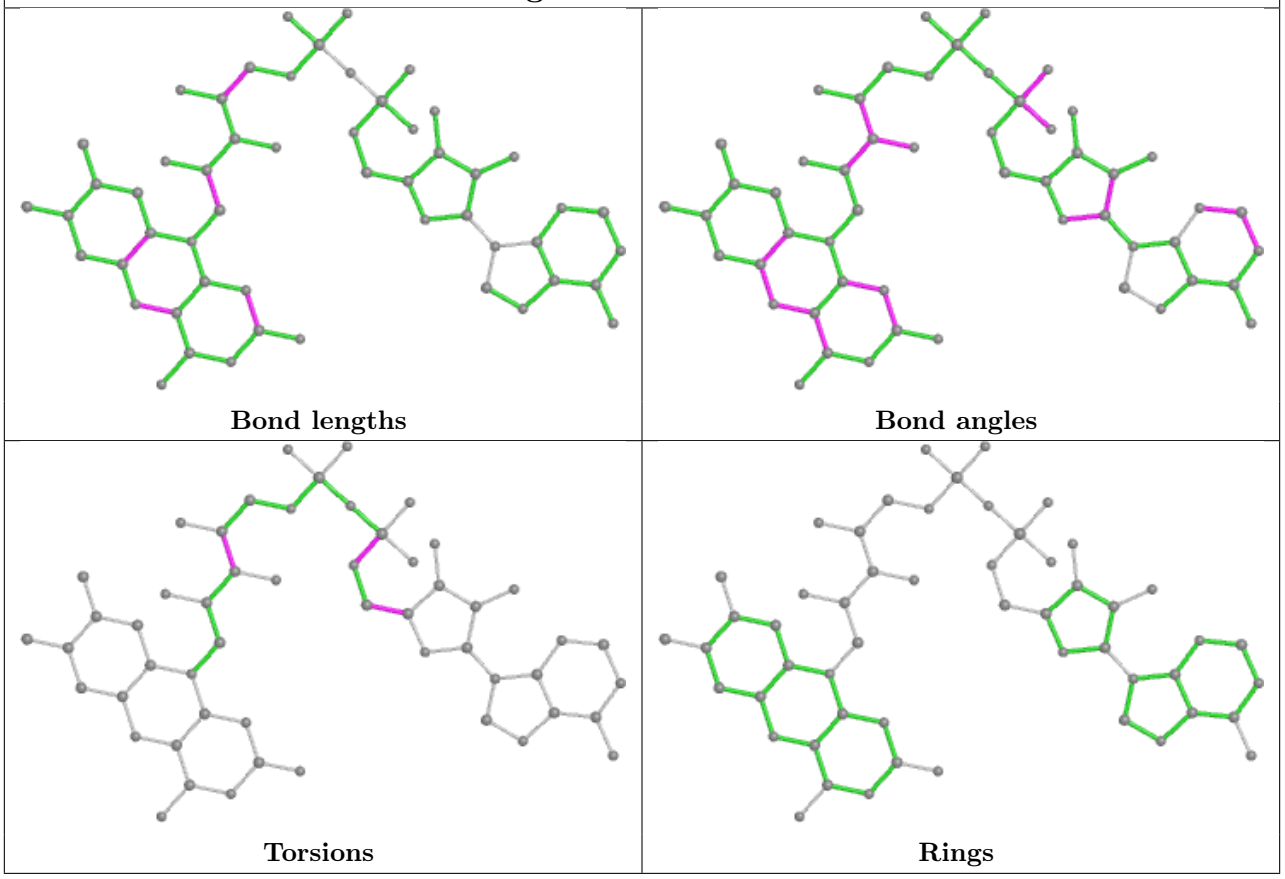


Torsions



Rings

Ligand FAD C 579



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	459/472 (97%)	-0.32	6 (1%)	77	79	6, 15, 38, 69	20 (4%)
1	B	462/472 (97%)	-0.41	6 (1%)	77	79	4, 13, 36, 70	18 (3%)
1	C	462/472 (97%)	-0.41	5 (1%)	80	82	5, 12, 36, 57	15 (3%)
All	All	1383/1416 (97%)	-0.38	17 (1%)	79	81	4, 13, 37, 70	53 (3%)

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	223	SER	3.5
1	A	379	GLY	3.4
1	A	50	ALA	3.4
1	A	341	ASP	2.9
1	B	463	CYS	2.7

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

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	NAG	D	1	14/15	0.75	0.17	17,35,71,100	0
3	MAN	F	3	11/12	0.75	0.25	24,36,53,55	0
3	NAG	F	2	14/15	0.79	0.22	3,12,39,74	0

Continued on next page...

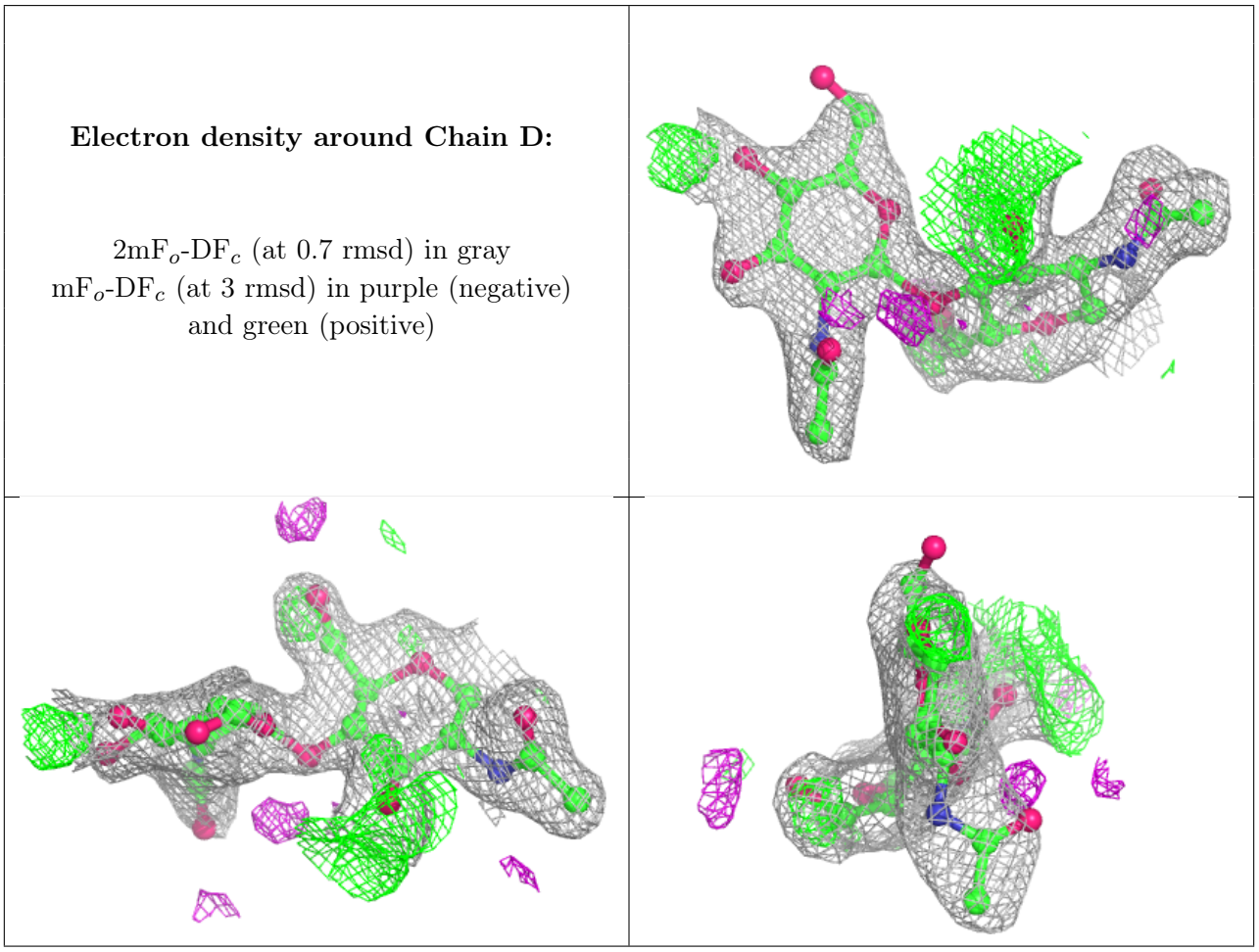
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	E	1	14/15	0.87	0.15	9,24,38,100	0
3	NAG	F	1	14/15	0.89	0.15	1,12,24,57	0
3	FCA	F	5	10/11	0.89	0.20	9,34,42,75	0
3	MAN	F	4	11/12	0.90	0.29	30,40,63,96	0
2	NAG	E	2	14/15	0.90	0.28	14,46,98,100	0
2	NAG	D	2	14/15	0.91	0.33	26,53,100,100	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

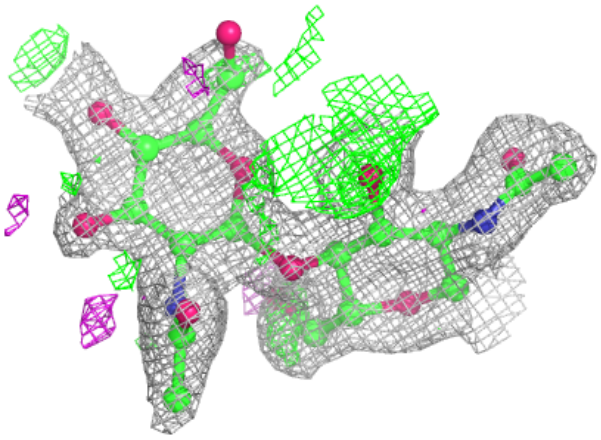
Electron density around Chain D:

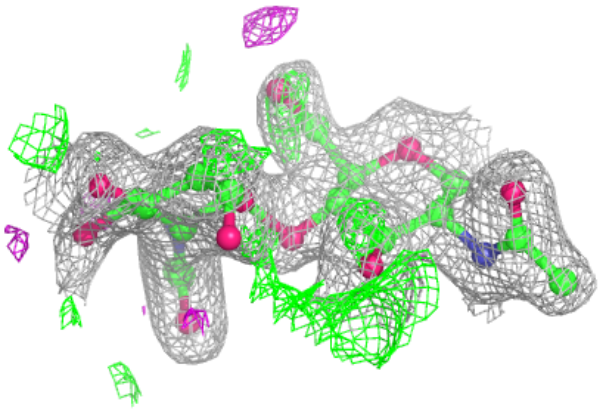
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

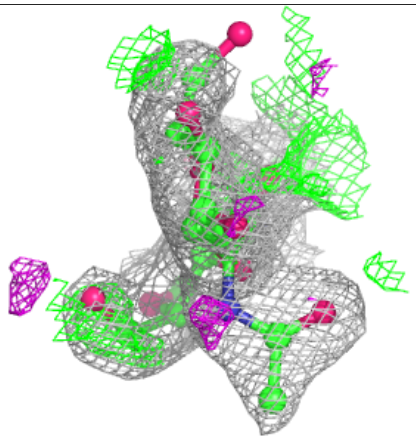


Electron density around Chain E:

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

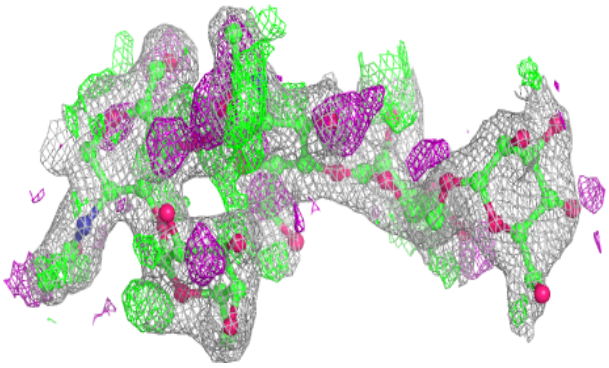


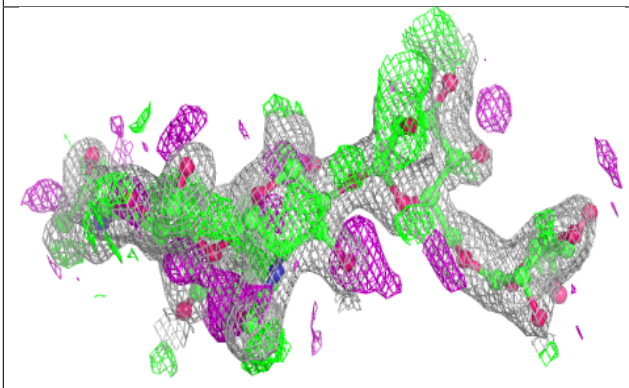


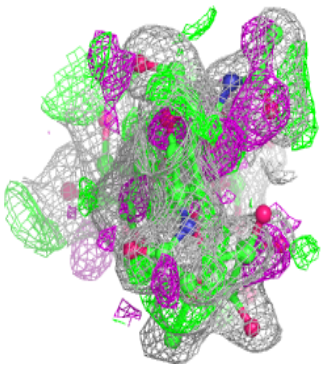


Electron density around Chain F:

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







6.4 Ligands (i)

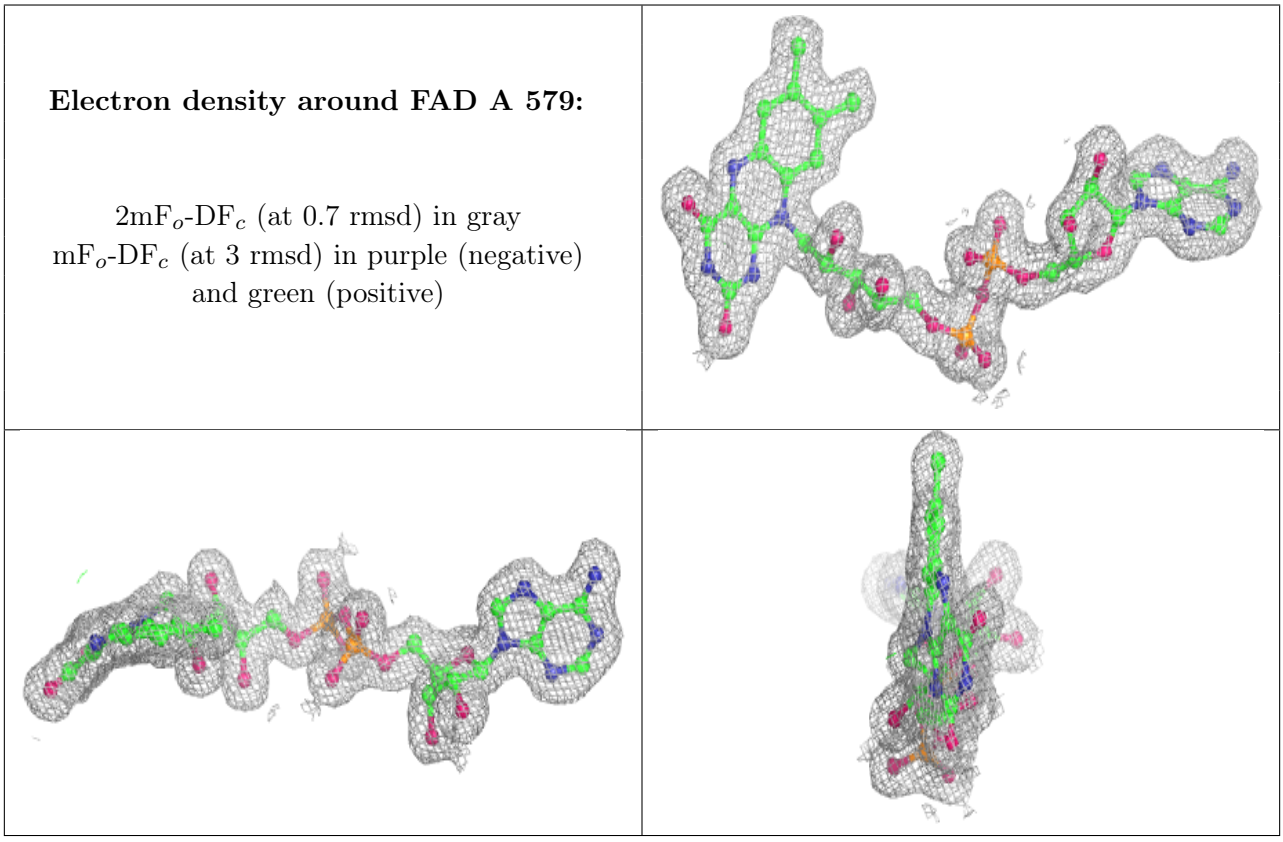
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	MD2	C	590	14/14	0.91	0.14	19,30,38,46	0
5	MD2	B	590	14/14	0.93	0.16	13,33,55,55	0
5	MD2	A	590	14/14	0.93	0.14	19,32,39,41	0
4	FAD	A	579	53/53	0.98	0.07	3,9,13,16	0
4	FAD	B	579	53/53	0.98	0.07	1,6,9,10	0
4	FAD	C	579	53/53	0.98	0.07	3,7,12,12	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.

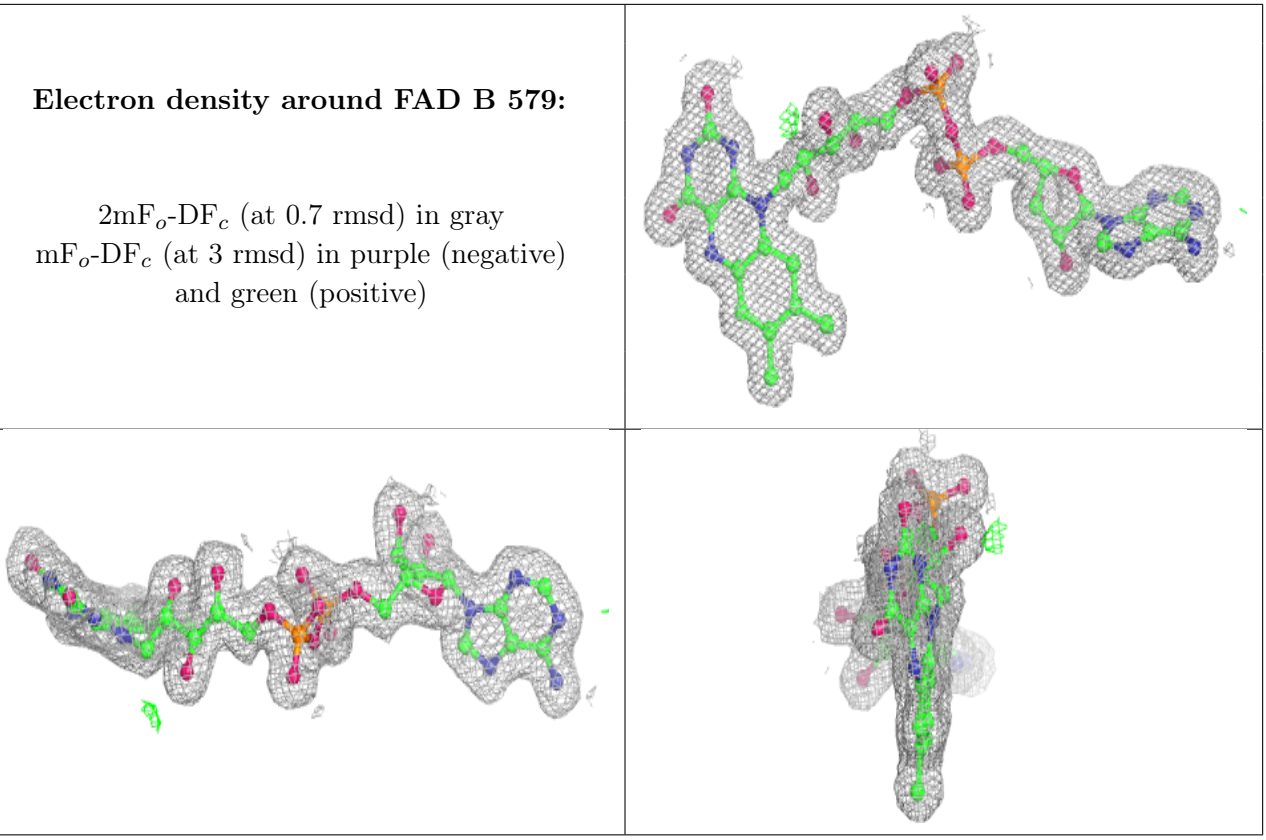
Electron density around FAD A 579:

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



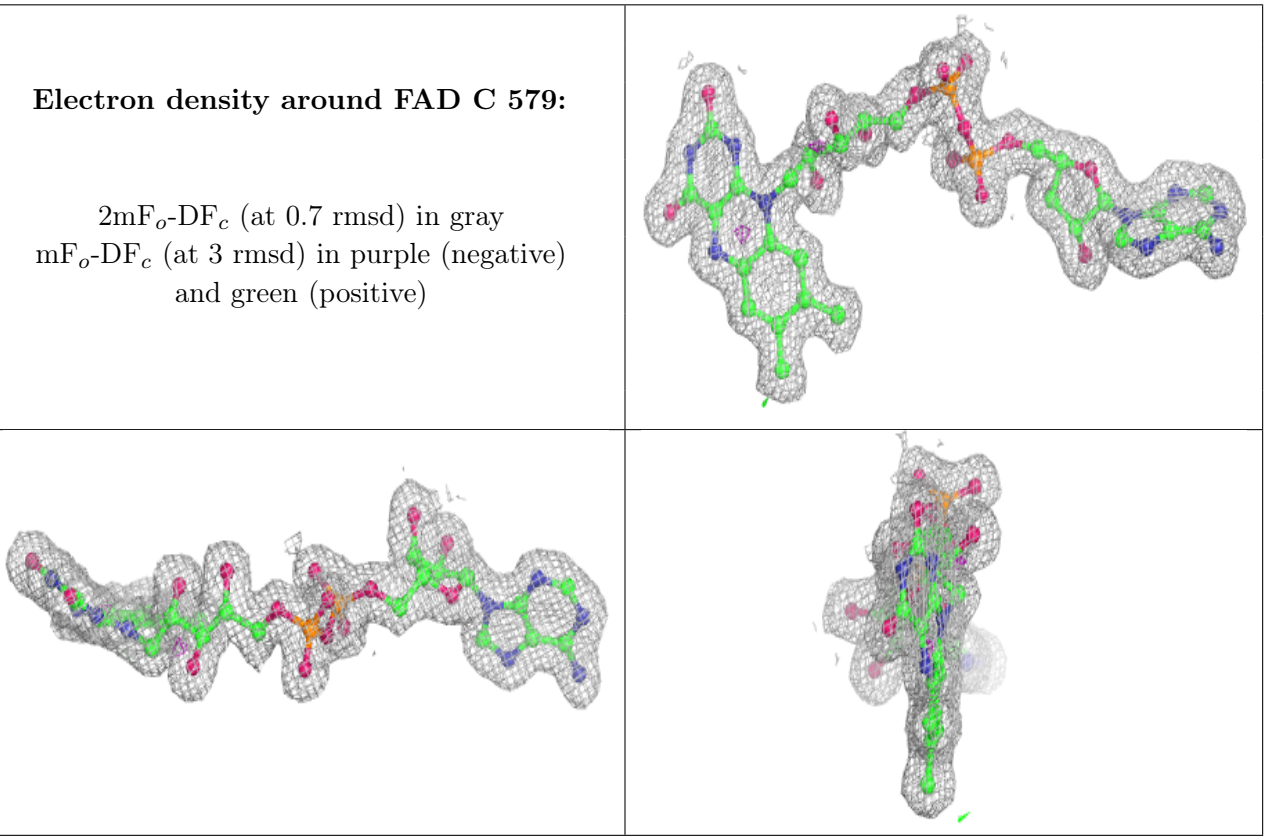
Electron density around FAD B 579:

$2mF_o$-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 C 579:

$2mF_o$-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.