



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 07:25 PM UTC

PDB ID : 3HSU / pdb_00003hsu
Title : Functional roles of the 6-s-cysteinyI, 8 alpha-N1-histidyl FAD in Glucoooligosaccharide Oxidase from Acremonium strictum
Authors : Liaw, S.-H.; Huang, C.-H.
Deposited on : 2009-06-10
Resolution : 1.69 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

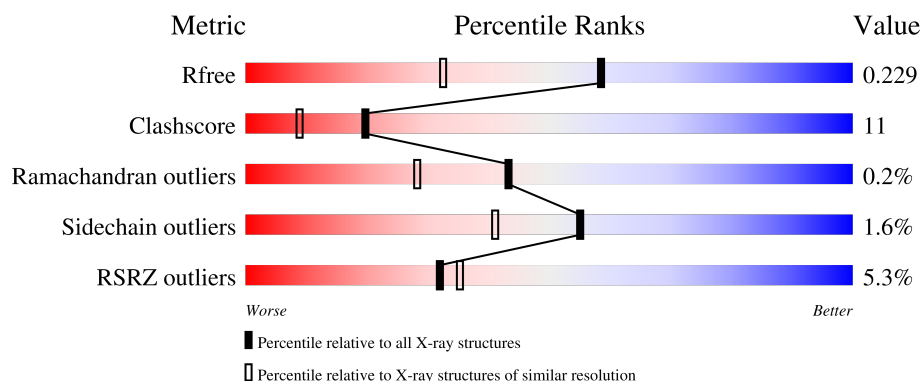
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.69 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	503	5% 75% 18% 6%
2	B	3	33% 67%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4254 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 Glucosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	475	Total	C	N	O	S	0	0	0
			3721	2362	623	727	9			

There are 30 discrepancies between the modelled and reference sequences:

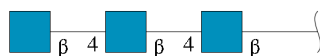
Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLU	-	expression tag	UNP Q6PW77
A	-4	ALA	-	expression tag	UNP Q6PW77
A	-3	GLU	-	expression tag	UNP Q6PW77
A	-2	ALA	-	expression tag	UNP Q6PW77
A	-1	GLU	-	expression tag	UNP Q6PW77
A	0	PHE	-	expression tag	UNP Q6PW77
A	130	ALA	CYS	engineered mutation	UNP Q6PW77
A	475	TYR	-	expression tag	UNP Q6PW77
A	476	LEU	-	expression tag	UNP Q6PW77
A	477	GLU	-	expression tag	UNP Q6PW77
A	478	GLN	-	expression tag	UNP Q6PW77
A	479	LYS	-	expression tag	UNP Q6PW77
A	480	LEU	-	expression tag	UNP Q6PW77
A	481	ILE	-	expression tag	UNP Q6PW77
A	482	SER	-	expression tag	UNP Q6PW77
A	483	GLU	-	expression tag	UNP Q6PW77
A	484	GLU	-	expression tag	UNP Q6PW77
A	485	ASP	-	expression tag	UNP Q6PW77
A	486	LEU	-	expression tag	UNP Q6PW77
A	487	ASN	-	expression tag	UNP Q6PW77
A	488	SER	-	expression tag	UNP Q6PW77
A	489	ALA	-	expression tag	UNP Q6PW77
A	490	VAL	-	expression tag	UNP Q6PW77
A	491	ASP	-	expression tag	UNP Q6PW77
A	492	HIS	-	expression tag	UNP Q6PW77
A	493	HIS	-	expression tag	UNP Q6PW77
A	494	HIS	-	expression tag	UNP Q6PW77

Continued on next page...

Continued from previous page...

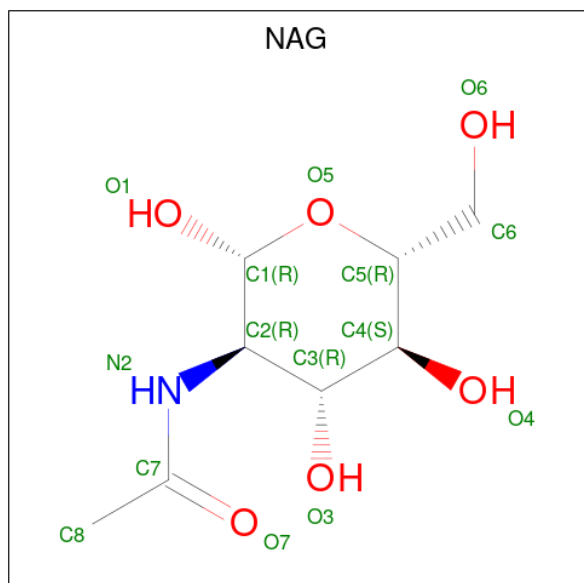
Chain	Residue	Modelled	Actual	Comment	Reference
A	495	HIS	-	expression tag	UNP Q6PW77
A	496	HIS	-	expression tag	UNP Q6PW77
A	497	HIS	-	expression tag	UNP Q6PW77

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	3	Total	C	N	O	0	0	0
			42	24	3	15			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: 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		

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Zn 1 1	0	0

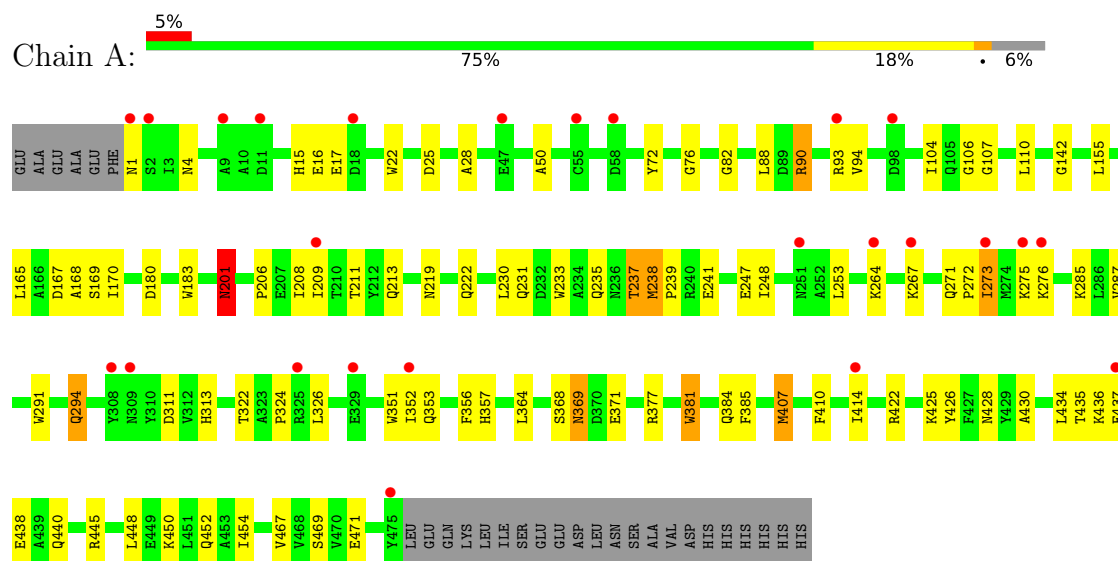
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	423	Total O 423 423	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: Glucoligosaccharide oxidase



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.48Å 97.57Å 98.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.88 – 1.69 30.88 – 1.69	Depositor EDS
% Data completeness (in resolution range)	93.8 (30.88-1.69) 94.3 (30.88-1.69)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 1.70Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.199 , 0.228 0.201 , 0.229	Depositor DCC
R_{free} test set	6306 reflections (10.12%)	wwPDB-VP
Wilson B-factor (Å ²)	20.9	Xtriage
Anisotropy	0.376	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 39.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.017 for -h,l,k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4254	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.01% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FAD, NAG, ZN

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	0.35	1/3817 (0.0%)	0.93	18/5192 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	407	MET	SD-CE	-6.13	1.64	1.79

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	201	ASN	N-CA-C	-9.39	97.87	110.55
1	A	237	THR	N-CA-C	7.08	122.35	112.93
1	A	82	GLY	N-CA-C	6.73	124.66	115.30
1	A	238	MET	CA-C-N	6.58	126.56	119.78
1	A	238	MET	C-N-CA	6.58	126.56	119.78
1	A	430	ALA	N-CA-C	6.57	120.01	110.28
1	A	110	LEU	N-CA-C	6.17	117.68	111.07
1	A	106	GLY	N-CA-C	6.04	121.10	114.40
1	A	381	TRP	N-CA-C	5.71	119.03	109.95
1	A	76	GLY	N-CA-C	-5.57	107.42	114.16
1	A	467	VAL	N-CA-C	5.50	119.74	112.76
1	A	357	HIS	N-CA-C	5.33	116.95	111.03
1	A	469	SER	N-CA-C	5.21	117.41	110.53
1	A	16	GLU	N-CA-C	-5.12	102.10	110.20
1	A	90	ARG	N-CA-C	-5.09	107.06	113.28
1	A	322	THR	N-CA-C	-5.09	101.46	109.50
1	A	356	PHE	CA-C-N	5.04	127.49	120.63
1	A	356	PHE	C-N-CA	5.04	127.49	120.63

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	3721	0	3493	84	0
2	B	42	0	37	0	0
3	A	14	0	13	0	0
4	A	53	0	29	1	0
5	A	1	0	0	0	0
6	A	423	0	0	5	0
All	All	4254	0	3572	85	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 11.

All (85) 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:206:PRO:HG2	1:A:209:ILE:HD11	1.41	1.00
1:A:230:LEU:HD23	1:A:273:ILE:HD11	1.44	0.99
1:A:248:ILE:CD1	1:A:253:LEU:HG	2.04	0.88
1:A:407:MET:HE3	1:A:407:MET:HA	1.54	0.88
1:A:231:GLN:HE22	1:A:326:LEU:H	1.23	0.84
1:A:368:SER:HB3	1:A:371:GLU:HG3	1.61	0.81
1:A:231:GLN:HE21	1:A:381:TRP:HE1	1.24	0.80
1:A:231:GLN:NE2	1:A:326:LEU:H	1.80	0.79
1:A:385:PHE:HB3	1:A:407:MET:HE2	1.64	0.79
1:A:230:LEU:CD2	1:A:273:ILE:HD11	2.12	0.78
1:A:407:MET:HE3	1:A:407:MET:CA	2.16	0.74
1:A:180:ASP:HB2	1:A:454:ILE:HD12	1.70	0.73
1:A:271:GLN:HG2	1:A:275:LYS:HE2	1.70	0.72
1:A:326:LEU:HD13	1:A:414:ILE:HD12	1.70	0.72
1:A:94:VAL:HG22	1:A:104:ILE:HD12	1.72	0.70
1:A:248:ILE:HD11	1:A:253:LEU:HG	1.74	0.69
1:A:94:VAL:HG13	1:A:104:ILE:CD1	2.23	0.68
1:A:271:GLN:HB3	1:A:272:PRO:HD3	1.75	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:TRP:CE3	1:A:273:ILE:HD12	2.29	0.67
1:A:1:ASN:HB3	1:A:4:ASN:HB2	1.78	0.66
1:A:369:ASN:HD21	1:A:377:ARG:H	1.46	0.64
1:A:233:TRP:CD2	1:A:273:ILE:HD12	2.33	0.63
1:A:28:ALA:O	1:A:313:HIS:HD2	1.83	0.61
1:A:352:ILE:CD1	1:A:385:PHE:HA	2.30	0.61
1:A:352:ILE:HD12	1:A:385:PHE:CD1	2.36	0.61
1:A:170:ILE:HD12	1:A:170:ILE:N	2.16	0.60
1:A:311:ASP:OD1	1:A:313:HIS:HE1	1.84	0.60
1:A:351:TRP:O	1:A:352:ILE:HD13	2.01	0.60
1:A:267:LYS:HD3	6:A:786:HOH:O	2.03	0.59
1:A:324:PRO:HB3	1:A:422:ARG:NH2	2.17	0.58
1:A:385:PHE:CD1	1:A:407:MET:HE1	2.39	0.58
1:A:385:PHE:CD1	1:A:407:MET:CE	2.85	0.58
1:A:264:LYS:O	1:A:267:LYS:HG2	2.04	0.58
1:A:385:PHE:HD1	1:A:407:MET:HE1	1.70	0.57
1:A:15:HIS:HE1	1:A:25:ASP:OD2	1.87	0.57
1:A:264:LYS:HA	1:A:267:LYS:HE3	1.87	0.56
1:A:276:LYS:HG3	6:A:730:HOH:O	2.05	0.56
1:A:169:SER:C	1:A:170:ILE:HD12	2.30	0.56
4:A:502:FAD:H9	4:A:502:FAD:O2'	2.06	0.55
1:A:364:LEU:C	1:A:364:LEU:HD23	2.32	0.55
1:A:93:ARG:HH11	1:A:93:ARG:HG2	1.71	0.55
1:A:352:ILE:HD12	1:A:385:PHE:HA	1.88	0.55
1:A:90:ARG:HB2	6:A:527:HOH:O	2.07	0.54
1:A:211:THR:OG1	1:A:287:VAL:HG13	2.07	0.54
1:A:385:PHE:CB	1:A:407:MET:HE2	2.37	0.54
1:A:435:THR:OG1	1:A:438:GLU:HG3	2.09	0.53
1:A:248:ILE:HD12	1:A:253:LEU:HG	1.89	0.53
1:A:208:ILE:C	1:A:209:ILE:HD12	2.35	0.52
1:A:15:HIS:HD2	6:A:803:HOH:O	1.94	0.50
1:A:88:LEU:O	1:A:107:GLY:HA3	2.12	0.50
1:A:219:ASN:OD1	1:A:222:GLN:HG3	2.12	0.49
1:A:426:TYR:CE2	1:A:428:ASN:HB2	2.47	0.49
1:A:450:LYS:O	1:A:454:ILE:HG12	2.12	0.49
1:A:385:PHE:CD1	1:A:407:MET:HE2	2.47	0.49
1:A:435:THR:HG1	1:A:438:GLU:HG3	1.79	0.47
1:A:209:ILE:HD12	1:A:209:ILE:N	2.29	0.47
1:A:436:LYS:HD3	1:A:471:GLU:HG2	1.96	0.47
1:A:237:THR:O	1:A:238:MET:C	2.57	0.47
1:A:238:MET:HA	1:A:239:PRO:HD3	1.78	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:GLN:HE22	1:A:326:LEU:N	2.03	0.46
1:A:264:LYS:HG3	6:A:672:HOH:O	2.14	0.46
1:A:369:ASN:ND2	1:A:377:ARG:H	2.13	0.46
1:A:369:ASN:HD22	1:A:369:ASN:HA	1.63	0.46
1:A:213:GLN:HB3	1:A:285:LYS:HB2	1.97	0.45
1:A:385:PHE:HD1	1:A:407:MET:CE	2.28	0.45
1:A:291:TRP:O	1:A:294:GLN:HG3	2.17	0.44
1:A:440:GLN:HE22	1:A:471:GLU:CD	2.25	0.44
1:A:50:ALA:HB2	1:A:170:ILE:HD11	1.98	0.44
1:A:425:LYS:HD2	1:A:434:LEU:HD11	2.00	0.44
1:A:271:GLN:O	1:A:275:LYS:HG3	2.18	0.44
1:A:167:ASP:O	1:A:168:ALA:HB3	2.19	0.42
1:A:253:LEU:HD23	1:A:253:LEU:C	2.43	0.42
1:A:435:THR:OG1	1:A:437:GLU:HG2	2.19	0.42
1:A:448:LEU:O	1:A:452:GLN:HG3	2.18	0.42
1:A:201:ASN:HD22	1:A:201:ASN:HA	1.59	0.42
1:A:183:TRP:CH2	1:A:450:LYS:HD3	2.54	0.42
1:A:17:GLU:HA	1:A:22:TRP:CD2	2.55	0.41
1:A:241:GLU:H	1:A:241:GLU:CD	2.28	0.41
1:A:407:MET:HE1	1:A:410:PHE:HB3	2.02	0.41
1:A:72:TYR:OH	1:A:384:GLN:NE2	2.51	0.41
1:A:351:TRP:CZ3	1:A:353:GLN:HG3	2.56	0.41
1:A:170:ILE:N	1:A:170:ILE:CD1	2.83	0.40
1:A:352:ILE:HD13	1:A:385:PHE:HA	2.03	0.40
1:A:142:GLY:HA2	1:A:155:LEU:CD2	2.51	0.40
1:A:165:LEU:HD12	1:A:169:SER:OG	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	473/503 (94%)	451 (95%)	21 (4%)	1 (0%)	43 28

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	445	ARG

5.3.2 Protein sidechains ⓘ

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	378/403 (94%)	372 (98%)	6 (2%)	55 41

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	201	ASN
1	A	235	GLN
1	A	247	GLU
1	A	273	ILE
1	A	294	GLN
1	A	369	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	HIS
1	A	100	ASN
1	A	201	ASN
1	A	231	GLN
1	A	294	GLN
1	A	296	ASN
1	A	309	ASN
1	A	313	HIS
1	A	369	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	384	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 ⓘ

3 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	B	1	1,2	14,14,15	0.50	0	17,19,21	0.74	1 (5%)
2	NAG	B	2	2	14,14,15	0.52	0	17,19,21	0.70	1 (5%)
2	NAG	B	3	2	14,14,15	0.59	0	17,19,21	0.65	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	1/6/23/26	0/1/1/1
2	NAG	B	3	2	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	NAG	C2-N2-C7	-2.27	119.86	122.90
2	B	2	NAG	C2-N2-C7	-2.13	120.04	122.90

There are no chirality outliers.

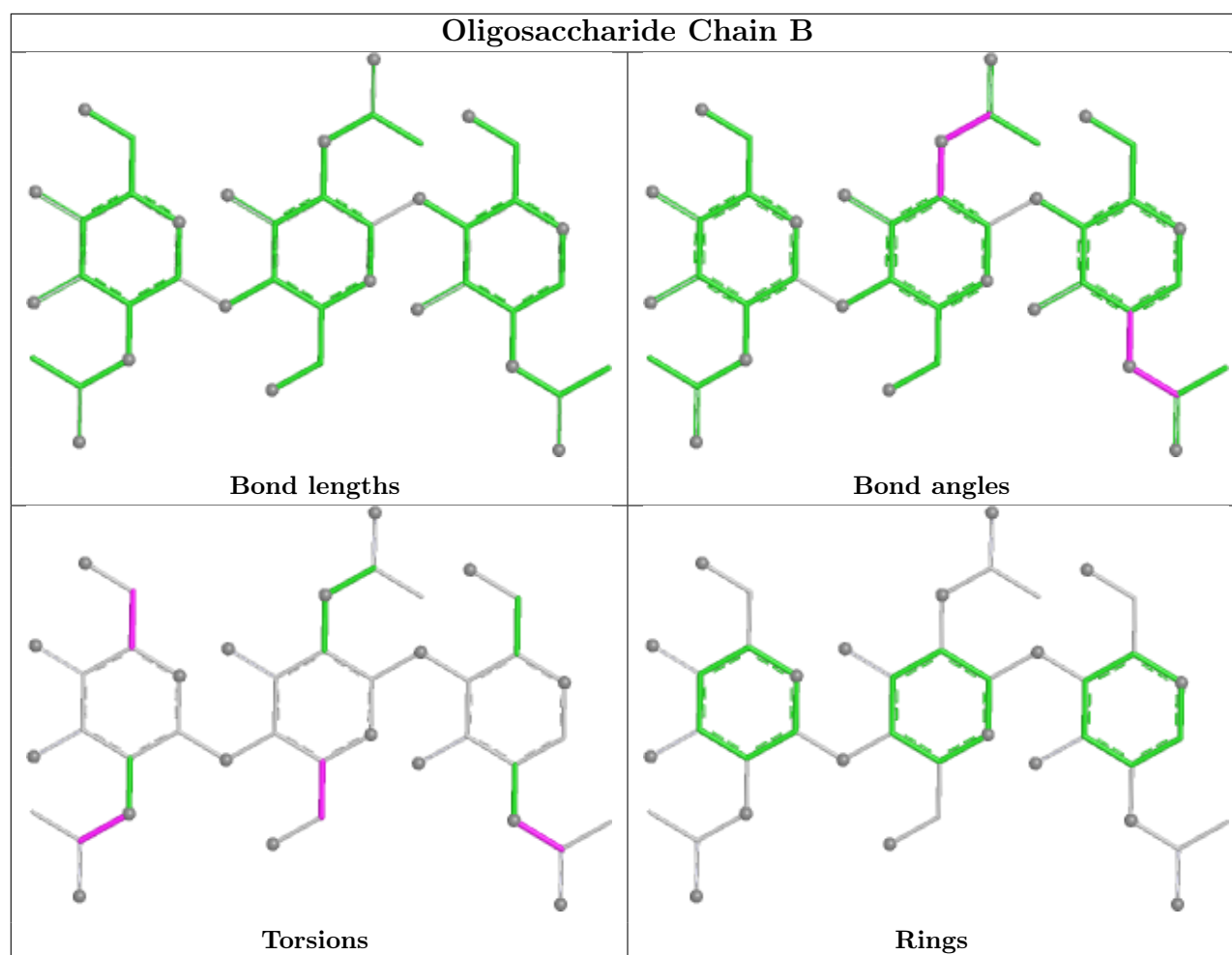
All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1	NAG	C8-C7-N2-C2
2	B	1	NAG	O7-C7-N2-C2
2	B	3	NAG	C8-C7-N2-C2
2	B	3	NAG	O7-C7-N2-C2
2	B	3	NAG	O5-C5-C6-O6
2	B	3	NAG	C4-C5-C6-O6
2	B	2	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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



5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	FAD	A	502	1	58,58,58	1.56	8 (13%)	85,89,89	1.43	10 (11%)
3	NAG	A	501	1	14,14,15	0.49	0	17,19,21	0.68	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	FAD	A	502	1	-	6/34/50/50	0/6/6/6
3	NAG	A	501	1	-	3/6/23/26	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	502	FAD	C4X-N5	5.04	1.41	1.30
4	A	502	FAD	C9-C8	4.26	1.45	1.39
4	A	502	FAD	C4A-N3A	3.88	1.41	1.34
4	A	502	FAD	C9A-N10	3.63	1.47	1.41
4	A	502	FAD	C9A-C5X	3.34	1.46	1.41
4	A	502	FAD	C10-N1	2.74	1.38	1.33
4	A	502	FAD	C5A-C4A	-2.32	1.35	1.39
4	A	502	FAD	C4'-C3'	2.02	1.57	1.53

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	502	FAD	O4B-C1B-N9A	5.51	118.68	108.09
4	A	502	FAD	O4B-C4B-C5B	4.37	123.34	109.33
4	A	502	FAD	C4X-C10-N10	3.50	121.49	116.48
4	A	502	FAD	C2B-C3B-C4B	-3.30	96.24	102.61
4	A	502	FAD	O4B-C4B-C3B	-3.08	99.04	105.15
4	A	502	FAD	C2B-C1B-N9A	2.69	120.00	113.30
4	A	502	FAD	C1B-N9A-C8A	2.65	132.98	127.09
4	A	502	FAD	C2'-C1'-N10	2.60	122.51	110.20
4	A	502	FAD	C9-C9A-N10	2.32	124.97	121.85
4	A	502	FAD	C5B-C4B-C3B	2.13	122.89	115.21

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	NAG	C8-C7-N2-C2
3	A	501	NAG	O7-C7-N2-C2
4	A	502	FAD	C2'-C1'-N10-C10
4	A	502	FAD	C3'-C4'-C5'-O5'
4	A	502	FAD	O4'-C4'-C5'-O5'
3	A	501	NAG	C3-C2-N2-C7

Continued on next page...

Continued from previous page...

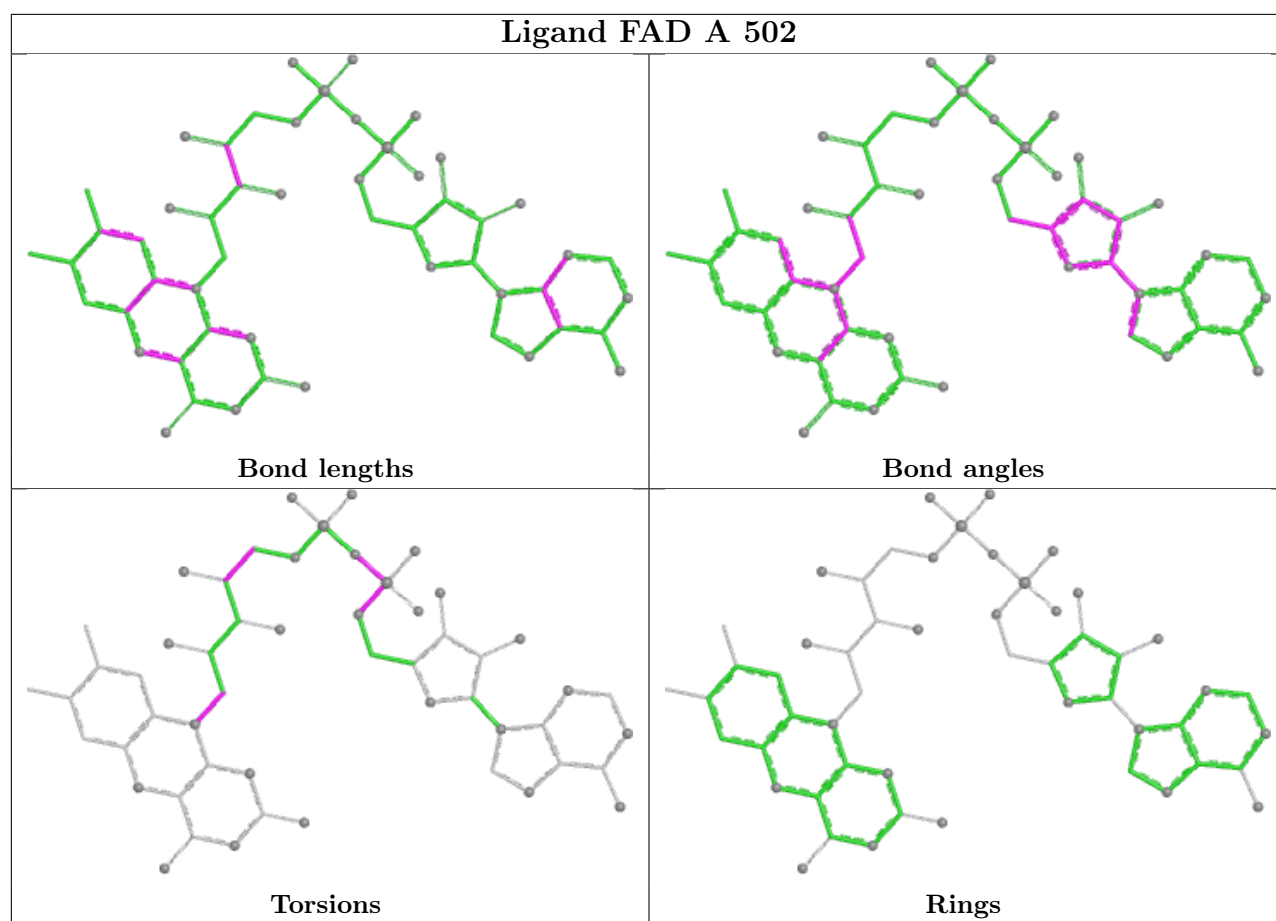
Mol	Chain	Res	Type	Atoms
4	A	502	FAD	P-O3P-PA-O1A
4	A	502	FAD	C5B-O5B-PA-O1A
4	A	502	FAD	P-O3P-PA-O2A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	502	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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th 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	475/503 (94%)	0.30	25 (5%) 32 35	14, 22, 34, 49	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	309	ASN	6.2
1	A	2	SER	5.9
1	A	475	TYR	5.8
1	A	18	ASP	5.7
1	A	1	ASN	5.3
1	A	47	GLU	3.4
1	A	273	ILE	3.1
1	A	325	ARG	2.9
1	A	275	LYS	2.8
1	A	276	LYS	2.7
1	A	414	ILE	2.7
1	A	437	GLU	2.6
1	A	267	LYS	2.5
1	A	58	ASP	2.4
1	A	329	GLU	2.4
1	A	308	TYR	2.4
1	A	251	ASN	2.3
1	A	352	ILE	2.2
1	A	264	LYS	2.2
1	A	9	ALA	2.2
1	A	55	CYS	2.1
1	A	209	ILE	2.1
1	A	93	ARG	2.1
1	A	98	ASP	2.0
1	A	11	ASP	2.0

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

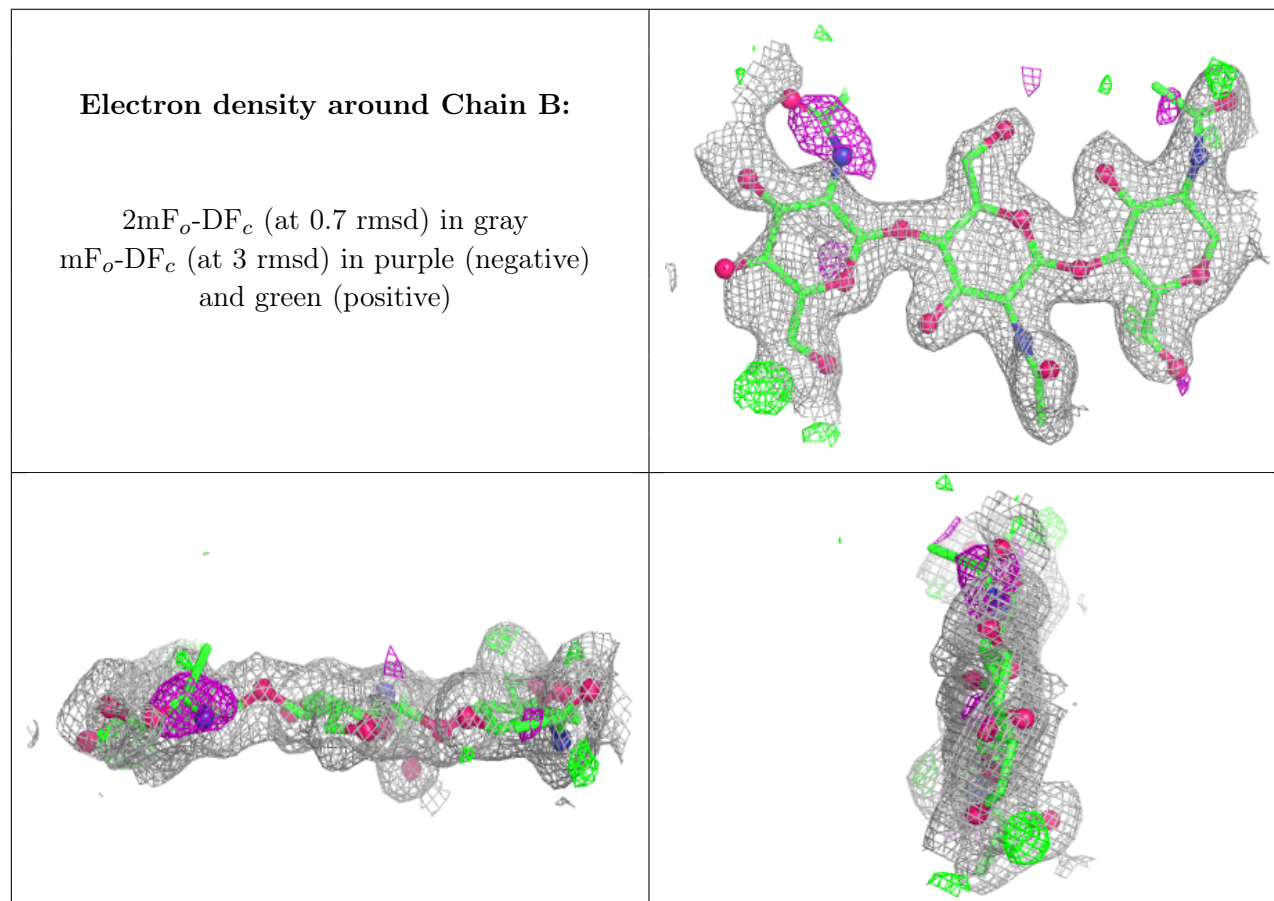
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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, 95th 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($\text{\AA}^2$)	Q<0.9
2	NAG	B	3	14/15	0.47	0.21	51,52,56,56	0
2	NAG	B	1	14/15	0.84	0.13	34,37,42,42	0
2	NAG	B	2	14/15	0.87	0.10	39,42,45,48	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.

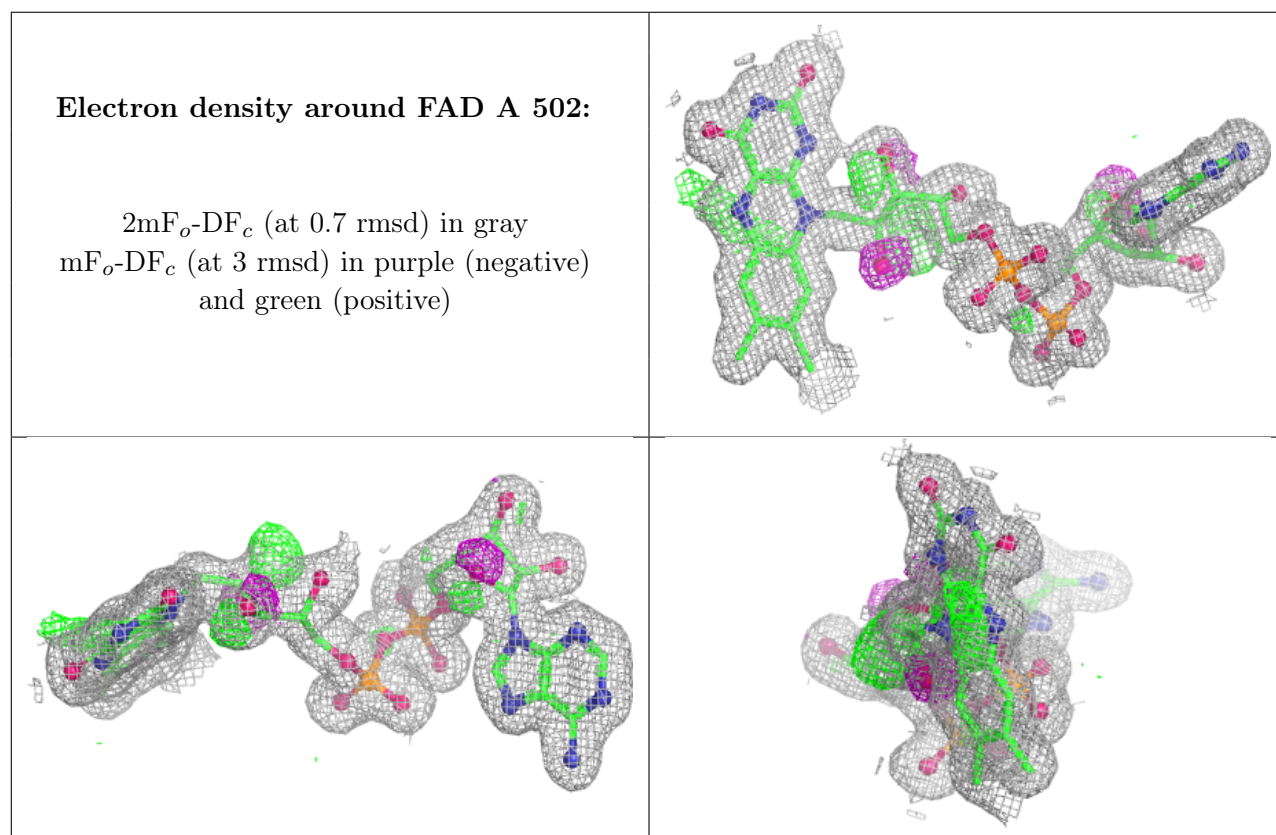


6.4 Ligands [i](#)

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, 95th 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
3	NAG	A	501	14/15	0.69	0.15	46,50,52,53	0
4	FAD	A	502	53/53	0.95	0.07	13,16,26,33	0
5	ZN	A	503	1/1	0.99	0.03	22,22,22,22	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.