



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:25 PM UTC

PDB ID : 4A2E / pdb_00004a2e
Title : Crystal Structure of a Corioloropsis gallica Laccase at 1.7 Å Resolution pH 5.5
Authors : De La Mora, E.; Valderrama, B.; Horjales, E.; Rudino-Pinera, E.
Deposited on : 2011-09-26
Resolution : 1.80 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
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

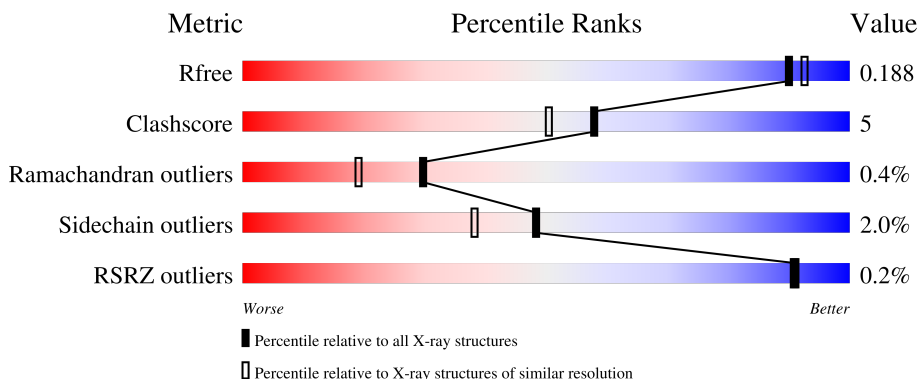
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


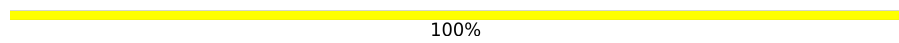
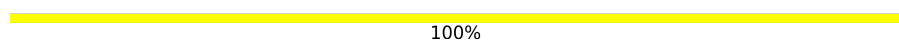
The reported resolution of this entry is 1.80 Å.

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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	496	 86% 12%
2	B	2	 100%
2	C	2	 100%

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 4466 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 LACCASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	496	3800	2411	640	740	9	0	10	0

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	ASP	TYR	conflict	UNP Q1W6B1
A	151	ASN	GLN	conflict	UNP Q1W6B1
A	178	LYS	ARG	conflict	UNP Q1W6B1
A	182	PRO	ALA	conflict	UNP Q1W6B1
A	183	VAL	ILE	conflict	UNP Q1W6B1
A	229	TYR	HIS	conflict	UNP Q1W6B1
A	256	LEU	ILE	conflict	UNP Q1W6B1
A	287	THR	ASN	conflict	UNP Q1W6B1
A	288	GLN	THR	conflict	UNP Q1W6B1
A	294	THR	VAL	conflict	UNP Q1W6B1
A	314	THR	ALA	conflict	UNP Q1W6B1
A	329	LYS	GLU	conflict	UNP Q1W6B1
A	356	ASN	ARG	conflict	UNP Q1W6B1
A	358	THR	SER	conflict	UNP Q1W6B1
A	423	VAL	ALA	conflict	UNP Q1W6B1

- 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
			Total	C	N	O			
2	B	2	28	16	2	10	0	0	0

Continued on next page...

Continued from previous page...

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

- Molecule 3 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	Cu	0	0
			4	4		


- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	606	Total	O	0	0
			606	606		

3 Residue-property plots [i](#)

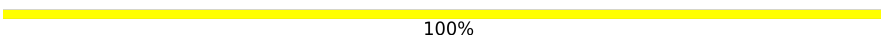
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: LACCASE

Chain A:  86% 12%

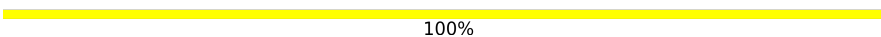


- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:  100%



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

Chain C:  100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.38Å 86.13Å 152.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.63 – 1.80 25.63 – 1.80	Depositor EDS
% Data completeness (in resolution range)	96.6 (25.63-1.80) 96.6 (25.63-1.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.88 (at 1.80Å)	Xtrriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.154 , 0.187 0.154 , 0.188	Depositor DCC
R_{free} test set	3389 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	16.4	Xtrriage
Anisotropy	0.110	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4466	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.33% 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 [i](#)

5.1 Standard geometry [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.71	25/3925 (0.6%)	1.29	12/5398 (0.2%)

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	464	PRO	CA-CB	11.31	1.68	1.53
1	A	489	ILE	CA-CB	8.70	1.58	1.54
1	A	230	THR	CA-CB	7.72	1.63	1.53
1	A	103	VAL	CA-CB	7.38	1.63	1.55
1	A	517	GLN	C-OXT	7.37	1.38	1.23
1	A	92	HIS	N-CA	7.07	1.54	1.46
1	A	508	THR	N-CA	6.65	1.54	1.46
1	A	41	PHE	N-CA	5.76	1.53	1.46
1	A	338	THR	CA-CB	5.71	1.62	1.54
1	A	425	ALA	CA-CB	5.70	1.61	1.53
1	A	347	ASN	CG-OD1	5.70	1.34	1.23
1	A	24	GLY	N-CA	5.63	1.52	1.44
1	A	180	GLY	C-O	5.58	1.29	1.23
1	A	351	GLY	N-CA	5.57	1.51	1.44
1	A	198	ALA	CA-CB	5.53	1.62	1.53
1	A	166	VAL	C-O	5.38	1.29	1.24
1	A	130	HIS	CA-C	-5.37	1.46	1.52
1	A	221	VAL	CB-CG1	-5.27	1.35	1.52
1	A	226	ASP	CA-C	5.27	1.59	1.52
1	A	126	THR	C-O	5.16	1.30	1.24
1	A	230	THR	C-O	5.10	1.30	1.24
1	A	188	ALA	C-O	5.10	1.30	1.23
1	A	427	VAL	CA-CB	5.07	1.61	1.54
1	A	91	GLN	CD-OE1	5.05	1.33	1.23
1	A	135	THR	N-CA	5.01	1.51	1.46

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	125	GLY	N-CA-C	-6.25	102.29	110.29
1	A	83	SER	CA-CB-OG	-6.25	98.60	111.10
1	A	237	SER	CA-CB-OG	-5.79	99.53	111.10
1	A	238	LEU	CA-C-N	-5.75	115.37	122.84
1	A	238	LEU	C-N-CA	-5.75	115.37	122.84
1	A	462	ASP	CA-C-N	-5.54	116.01	122.00
1	A	462	ASP	C-N-CA	-5.54	116.01	122.00
1	A	99	GLY	CA-C-N	-5.41	113.99	119.83
1	A	99	GLY	C-N-CA	-5.41	113.99	119.83
1	A	485	MET	CG-SD-CE	-5.35	89.14	100.90
1	A	208	ILE	N-CA-C	-5.14	100.91	108.11
1	A	201	LEU	N-CA-C	5.05	118.92	112.87

There are no chirality outliers.

There are no planarity outliers.

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	3800	0	3601	34	0
2	B	28	0	25	0	0
2	C	28	0	25	0	0
3	A	4	0	0	0	0
4	A	606	0	0	6	0
All	All	4466	0	3651	34	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 5.

All (34) 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:418[B]:HIS:HE1	1:A:470:HIS:CE1	1.36	1.41
1:A:418[B]:HIS:CE1	1:A:470:HIS:CE1	2.09	1.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:329:LYS:H	1:A:329:LYS:HE2	1.13	1.08
1:A:418[B]:HIS:CE1	1:A:470:HIS:NE2	2.32	0.97
1:A:418[B]:HIS:HE1	1:A:470:HIS:HE1	1.09	0.89
1:A:199:ALA:HB2	4:A:2317:HOH:O	1.79	0.82
1:A:329:LYS:HE2	1:A:329:LYS:N	1.97	0.78
1:A:422:HIS:HE1	1:A:487:GLU:OE1	1.71	0.73
1:A:22:ALA:HB2	1:A:163:ASP:OD2	1.89	0.72
1:A:276:ASN:HD21	1:A:300:ARG:HE	1.38	0.71
1:A:418[B]:HIS:CE1	1:A:472:HIS:CD2	2.83	0.67
1:A:284:ASN:H	1:A:284:ASN:HD22	1.45	0.65
1:A:329:LYS:H	1:A:329:LYS:CE	2.03	0.62
1:A:276:ASN:ND2	1:A:300:ARG:HE	1.97	0.61
1:A:418[B]:HIS:NE2	1:A:470:HIS:NE2	2.48	0.60
1:A:422:HIS:CE1	1:A:487:GLU:OE1	2.54	0.60
1:A:251:HIS:HE1	4:A:2426:HOH:O	1.92	0.52
1:A:214:LYS:HE2	4:A:2257:HOH:O	2.09	0.52
1:A:33:ASN:ND2	1:A:74:THR:H	2.09	0.51
1:A:135:THR:HA	1:A:474:ASP:OD2	2.09	0.50
1:A:242:GLU:HB3	1:A:265:SER:HB2	1.94	0.49
1:A:199:ALA:CB	4:A:2317:HOH:O	2.47	0.48
1:A:33:ASN:HD22	1:A:74:THR:H	1.62	0.47
1:A:413:PHE:HB2	1:A:414:PRO:HA	1.94	0.47
1:A:418[B]:HIS:ND1	1:A:472:HIS:CD2	2.82	0.47
1:A:436:ASN:HD21	1:A:439:ASN:ND2	2.13	0.47
1:A:92:HIS:HD2	4:A:2147:HOH:O	1.99	0.46
1:A:227:PRO:HA	1:A:284:ASN:HD21	1.82	0.45
1:A:294:THR:CG2	4:A:2301:HOH:O	2.66	0.43
1:A:87:HIS:CD2	1:A:87:HIS:C	2.97	0.43
1:A:418[B]:HIS:ND1	1:A:472:HIS:HD2	2.16	0.43
1:A:418[B]:HIS:HB3	1:A:445:VAL:HG22	2.01	0.43
1:A:91:GLN:HE22	1:A:118:PHE:CB	2.33	0.41
1:A:208:ILE:HD13	1:A:279:ILE:CD1	2.51	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	504/496 (102%)	487 (97%)	15 (3%)	2 (0%)	30 19

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	226	ASP
1	A	79	LEU

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	411/401 (102%)	403 (98%)	8 (2%)	50 41

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	208	ILE
1	A	282	LEU
1	A	284	ASN
1	A	329	LYS
1	A	407	THR
1	A	439	ASN
1	A	468	PHE
1	A	481	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	91	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	92	HIS
1	A	251	HIS
1	A	269	ASN
1	A	272	GLN
1	A	276	ASN
1	A	284	ASN
1	A	318	ASN
1	A	356	ASN
1	A	380	GLN
1	A	422	HIS
1	A	439	ASN

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](#)

4 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	1.71	2 (14%)	17,19,21	1.56	4 (23%)
2	NAG	B	2	2	14,14,15	1.57	2 (14%)	17,19,21	1.61	5 (29%)
2	NAG	C	1	1,2	14,14,15	1.71	2 (14%)	17,19,21	2.17	6 (35%)
2	NAG	C	2	2	14,14,15	1.20	0	17,19,21	1.25	3 (17%)

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	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NAG	C1-C2	5.10	1.59	1.52
2	C	1	NAG	C1-C2	5.03	1.59	1.52
2	B	1	NAG	C4-C5	2.98	1.59	1.53
2	B	2	NAG	C3-C2	2.90	1.58	1.52
2	B	2	NAG	O4-C4	2.48	1.49	1.43
2	C	1	NAG	C2-N2	2.40	1.50	1.46

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	NAG	C2-N2-C7	-4.13	117.36	122.90
2	C	1	NAG	O5-C1-C2	-3.93	105.22	111.29
2	C	1	NAG	O7-C7-N2	3.86	128.80	121.98
2	C	2	NAG	O6-C6-C5	-3.12	100.70	111.33
2	B	1	NAG	O5-C1-C2	-3.06	106.56	111.29
2	B	1	NAG	O5-C5-C6	2.91	113.33	107.66
2	C	1	NAG	O7-C7-C8	-2.84	116.99	122.05
2	B	2	NAG	O7-C7-N2	2.77	126.88	121.98
2	B	1	NAG	O4-C4-C5	-2.42	103.37	109.32
2	B	2	NAG	O6-C6-C5	-2.24	103.72	111.33
2	C	2	NAG	O3-C3-C2	-2.23	104.77	109.40
2	B	1	NAG	O7-C7-C8	-2.18	118.17	122.05
2	C	2	NAG	C1-O5-C5	2.13	115.04	112.19
2	C	1	NAG	O5-C5-C4	-2.05	105.84	110.83
2	B	2	NAG	C8-C7-N2	-2.04	112.74	116.12
2	B	2	NAG	O3-C3-C2	-2.03	105.18	109.40
2	B	2	NAG	C3-C4-C5	-2.01	106.58	110.23
2	C	1	NAG	O4-C4-C3	-2.01	105.64	110.38

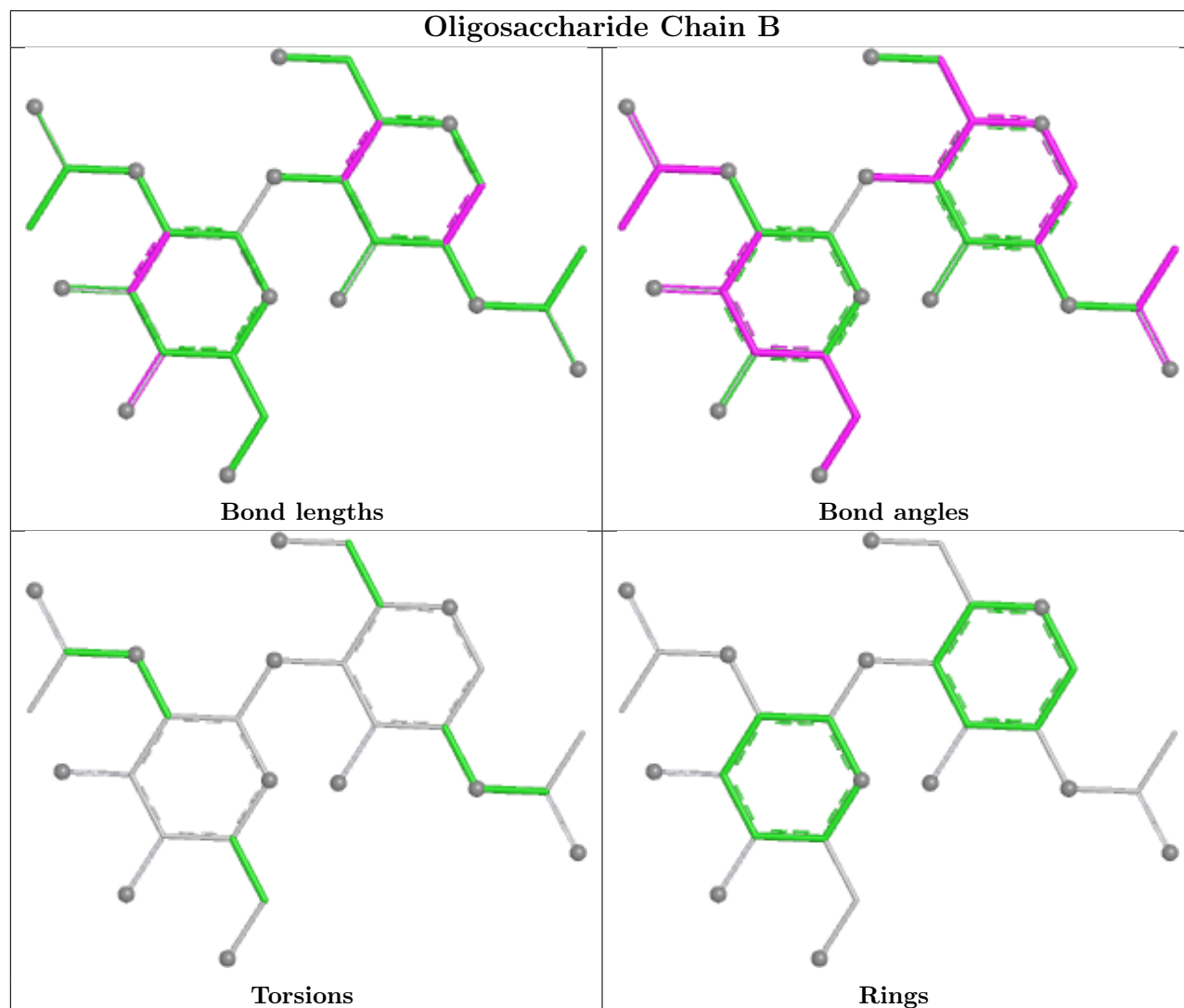
There are no chirality outliers.

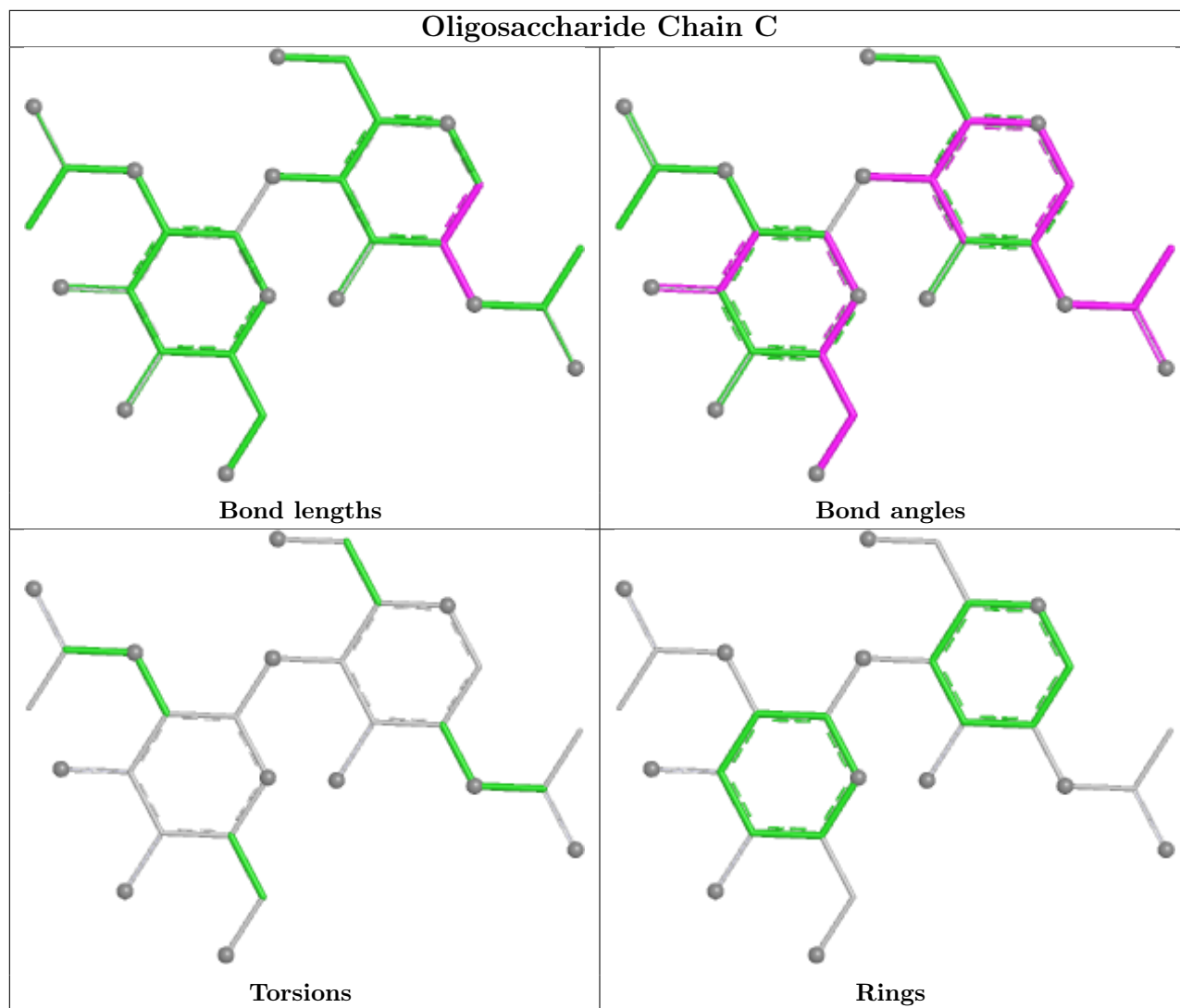
There are no torsion outliers.

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 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	496/496 (100%)	-0.83	1 (0%) 91 91	5, 13, 22, 34	10 (2%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	198	ALA	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](#)

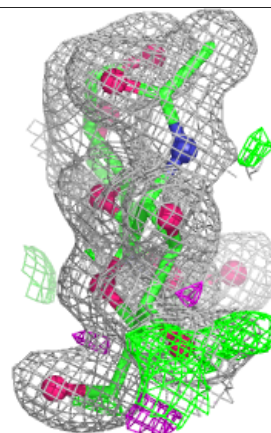
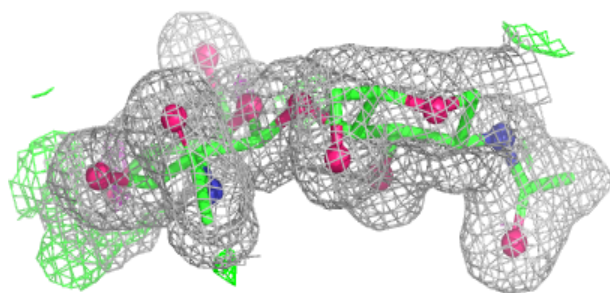
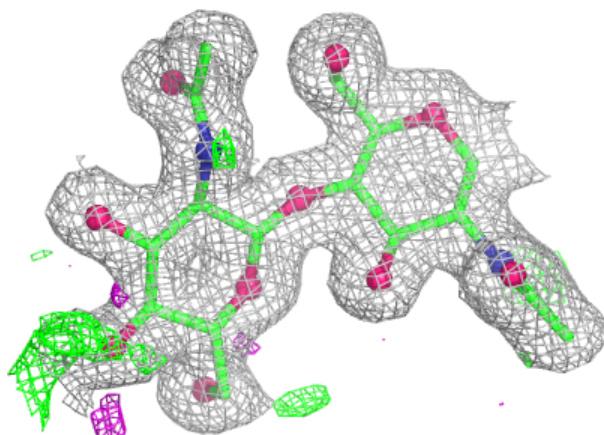
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

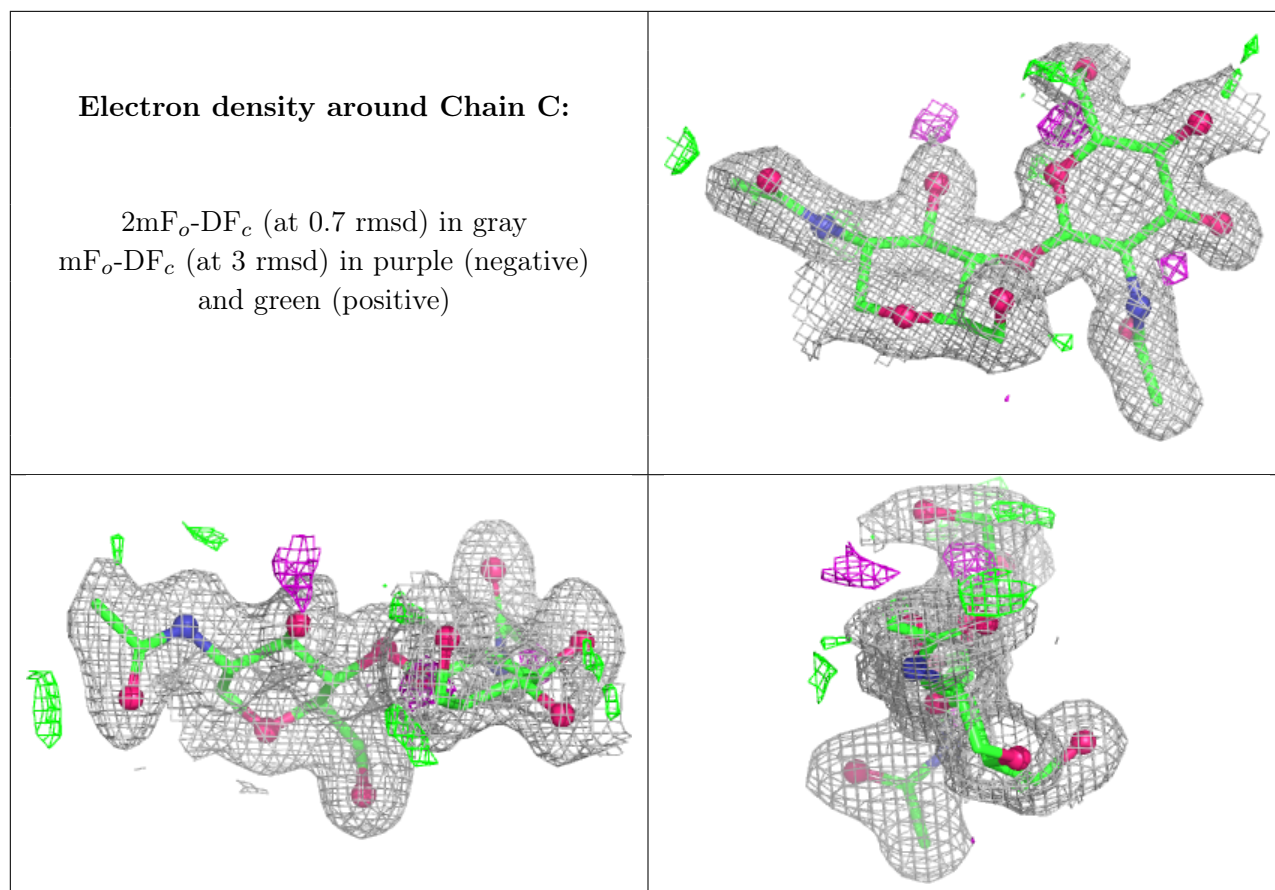
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	C	2	14/15	0.91	0.09	16,27,31,37	0
2	NAG	B	2	14/15	0.94	0.07	10,17,26,27	0
2	NAG	C	1	14/15	0.96	0.07	12,17,26,28	0
2	NAG	B	1	14/15	0.97	0.05	12,15,19,20	0

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 B:

$2mF_o-DF_c$ (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, 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(\AA^2)	Q<0.9
3	CU	A	1520	1/1	0.99	0.02	17,17,17,17	1
3	CU	A	1519	1/1	1.00	0.01	12,12,12,12	1
3	CU	A	1518	1/1	1.00	0.01	14,14,14,14	1
3	CU	A	1521	1/1	1.00	0.02	12,12,12,12	1

6.5 Other polymers [i](#)

There are no such residues in this entry.