



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 28, 2024 – 11:48 pm BST

PDB ID : 4A6O
Title : CpGH89CBM32-4, produced by Clostridium perfringens, in complex with glc NAc-alpha-1,4-galactose
Authors : Ficko-Blean, E.; Stuart, C.P.; Suits, M.D.; Cid, M.; Tessier, M.; Woods, R.J.; Boraston, A.B.
Deposited on : 2011-11-07
Resolution : 2.80 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36.2
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) : 2.36.2

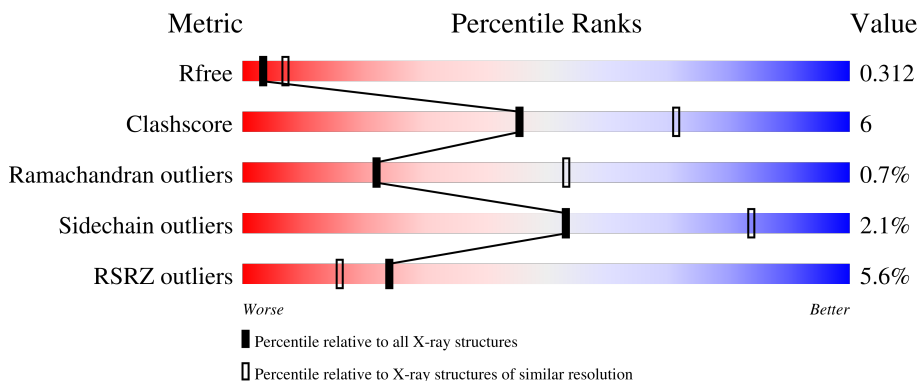
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	161	 7% 74% 16% 11%
1	B	161	 2% 74% 14% 11%
2	C	2	 100%
2	D	2	 50% 50%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2366 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 ALPHA-N-ACETYLGLUCOSAMINIDASE FAMILY PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	144	1097	678	186	229	4	0	0	0
1	B	144	1103	682	186	231	4	0	2	0

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1183	MET	-	expression tag	UNP Q0TST1
A	1184	GLY	-	expression tag	UNP Q0TST1
A	1185	SER	-	expression tag	UNP Q0TST1
A	1186	SER	-	expression tag	UNP Q0TST1
A	1187	HIS	-	expression tag	UNP Q0TST1
A	1188	HIS	-	expression tag	UNP Q0TST1
A	1189	HIS	-	expression tag	UNP Q0TST1
A	1190	HIS	-	expression tag	UNP Q0TST1
A	1191	HIS	-	expression tag	UNP Q0TST1
A	1192	HIS	-	expression tag	UNP Q0TST1
A	1193	SER	-	expression tag	UNP Q0TST1
A	1194	SER	-	expression tag	UNP Q0TST1
A	1195	GLY	-	expression tag	UNP Q0TST1
A	1196	LEU	-	expression tag	UNP Q0TST1
A	1197	VAL	-	expression tag	UNP Q0TST1
A	1198	PRO	-	expression tag	UNP Q0TST1
A	1199	ARG	-	expression tag	UNP Q0TST1
A	1200	GLY	-	expression tag	UNP Q0TST1
A	1201	SER	-	expression tag	UNP Q0TST1
A	1202	HIS	-	expression tag	UNP Q0TST1
A	1203	MET	-	expression tag	UNP Q0TST1
A	1204	ALA	-	expression tag	UNP Q0TST1
A	1205	SER	-	expression tag	UNP Q0TST1
B	1183	MET	-	expression tag	UNP Q0TST1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1184	GLY	-	expression tag	UNP Q0TST1
B	1185	SER	-	expression tag	UNP Q0TST1
B	1186	SER	-	expression tag	UNP Q0TST1
B	1187	HIS	-	expression tag	UNP Q0TST1
B	1188	HIS	-	expression tag	UNP Q0TST1
B	1189	HIS	-	expression tag	UNP Q0TST1
B	1190	HIS	-	expression tag	UNP Q0TST1
B	1191	HIS	-	expression tag	UNP Q0TST1
B	1192	HIS	-	expression tag	UNP Q0TST1
B	1193	SER	-	expression tag	UNP Q0TST1
B	1194	SER	-	expression tag	UNP Q0TST1
B	1195	GLY	-	expression tag	UNP Q0TST1
B	1196	LEU	-	expression tag	UNP Q0TST1
B	1197	VAL	-	expression tag	UNP Q0TST1
B	1198	PRO	-	expression tag	UNP Q0TST1
B	1199	ARG	-	expression tag	UNP Q0TST1
B	1200	GLY	-	expression tag	UNP Q0TST1
B	1201	SER	-	expression tag	UNP Q0TST1
B	1202	HIS	-	expression tag	UNP Q0TST1
B	1203	MET	-	expression tag	UNP Q0TST1
B	1204	ALA	-	expression tag	UNP Q0TST1
B	1205	SER	-	expression tag	UNP Q0TST1

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace	
2	C	2	Total	C	N	O	0	0	0
			26	14	1	11			
2	D	2	Total	C	N	O	0	0	0
			26	14	1	11			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Ca	0	0
			2	2		


- Molecule 4 is water.

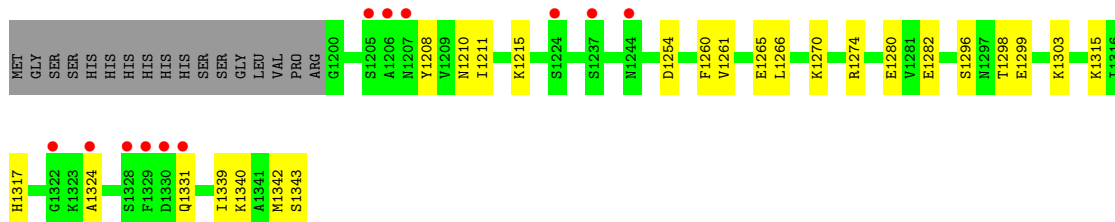
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	57	Total	O	0	0
			57	57		
4	B	54	Total	O	0	0
			54	54		

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.

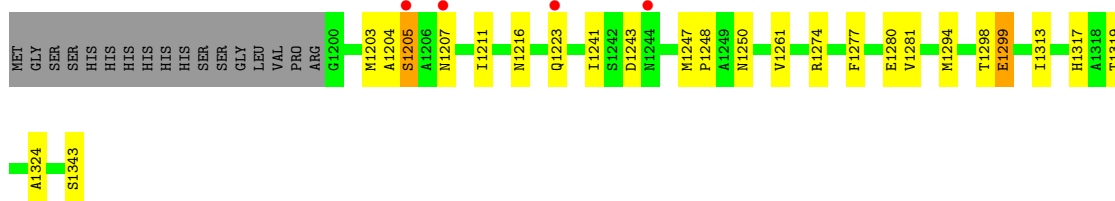
- Molecule 1: ALPHA-N-ACETYLGLUCOSAMINIDASE FAMILY PROTEIN

Chain A: 

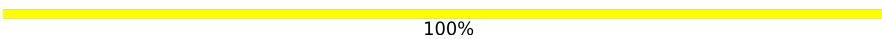


- Molecule 1: ALPHA-N-ACETYLGLUCOSAMINIDASE FAMILY PROTEIN

Chain B: 



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

Chain C: 



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

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	89.71Å 49.89Å 63.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80 19.91 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.3 (20.00-2.80) 97.7 (19.91-2.80)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.38 (at 2.79Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.285 , 0.318 0.282 , 0.312	Depositor DCC
R_{free} test set	336 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å ²)	21.4	Xtrriage
Anisotropy	0.326	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 23.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	2366	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 51.47 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.5837e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: CA, NDG, GAL

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	0.33	0/1116	0.51	0/1507
1	B	0.34	0/1128	0.52	0/1523
All	All	0.33	0/2244	0.52	0/3030

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1097	0	1040	15	0
1	B	1103	0	1049	13	0
2	C	26	0	23	0	0
2	D	26	0	23	1	0
3	A	1	0	0	0	0
3	B	2	0	0	0	0
4	A	57	0	0	0	0
4	B	54	0	0	1	0
All	All	2366	0	2135	28	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 6.

All (28) 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:1340:LYS:HB3	1:A:1342:MET:HE3	1.70	0.73
1:B:1281:VAL:HB	1:B:1313:ILE:HG21	1.75	0.68
1:B:1298:THR:O	1:B:1299:GLU:HB2	2.01	0.60
1:B:1223:GLN:HB3	1:B:1243:ASP:HA	1.85	0.59
1:B:1274:ARG:HB3	1:B:1324:ALA:HB3	1.86	0.57
1:B:1204:ALA:HA	1:B:1205:SER:HB2	1.87	0.56
1:A:1282:GLU:HB3	1:A:1315:LYS:HB2	1.88	0.55
1:A:1274:ARG:HB3	1:A:1324:ALA:HB3	1.88	0.55
1:A:1280:GLU:HB2	1:A:1317:HIS:HB2	1.88	0.54
1:B:1203:MET:HA	1:B:1204:ALA:HB2	1.93	0.51
1:B:1250:ASN:HB3	1:B:1319:THR:HG23	1.92	0.51
1:A:1265:GLU:HB2	1:A:1340:LYS:HB2	1.92	0.51
1:B:1211:ILE:HD11	1:B:1261:VAL:HG22	1.93	0.51
1:A:1260:PHE:O	1:A:1343:SER:HB3	2.12	0.49
1:A:1260:PHE:O	1:A:1343:SER:CB	2.61	0.48
1:B:1277:PHE:CE2	1:B:1294:MET:HG3	2.48	0.48
1:A:1340:LYS:HB3	1:A:1342:MET:CE	2.41	0.47
1:A:1210:ASN:HA	1:A:1342:MET:HE2	1.97	0.46
1:A:1211:ILE:HD11	1:A:1261:VAL:HG22	1.98	0.46
1:A:1270:LYS:HA	1:A:1303:LYS:HG3	1.98	0.45
1:A:1298:THR:O	1:A:1299:GLU:HB2	2.17	0.45
1:B:1247:MET:HA	1:B:1248:PRO:C	2.37	0.44
1:A:1266:LEU:HD12	1:A:1339:ILE:HG12	2.00	0.42
1:B:1241:ILE:HD13	2:D:1:GAL:O3	2.20	0.42
1:A:1215:LYS:HB3	1:A:1254:ASP:O	2.19	0.42
1:B:1317:HIS:HB3	4:B:2021:HOH:O	2.20	0.41
1:B:1261:VAL:HA	1:B:1343:SER:HB3	2.03	0.41
1:A:1208:TYR:HB3	1:A:1342:MET:HB3	2.03	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	142/161 (88%)	130 (92%)	12 (8%)	0	100	100
1	B	144/161 (89%)	134 (93%)	8 (6%)	2 (1%)	11	34
All	All	286/322 (89%)	264 (92%)	20 (7%)	2 (1%)	22	53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1205	SER
1	B	1299	GLU

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	120/135 (89%)	118 (98%)	2 (2%)	60	87
1	B	122/135 (90%)	119 (98%)	3 (2%)	47	80
All	All	242/270 (90%)	237 (98%)	5 (2%)	53	84

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1296	SER
1	A	1331	GLN
1	B	1207	ASN
1	B	1216	ASN
1	B	1280	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1207	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	GAL	C	1	2	12,12,12	0.80	0	17,17,17	0.94	1 (5%)
2	NDG	C	2	2	14,14,15	0.95	0	17,19,21	1.39	3 (17%)
2	GAL	D	1	2	12,12,12	0.82	0	17,17,17	1.13	2 (11%)
2	NDG	D	2	2	14,14,15	1.05	1 (7%)	17,19,21	1.06	2 (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
2	GAL	C	1	2	-	2/2/22/22	0/1/1/1
2	NDG	C	2	2	-	0/6/23/26	0/1/1/1
2	GAL	D	1	2	-	0/2/22/22	0/1/1/1
2	NDG	D	2	2	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	NDG	O5-C1	2.42	1.47	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	GAL	C3-C4-C5	-3.18	104.56	110.24
2	C	2	NDG	C6-C5-C4	-2.79	106.47	113.00
2	D	1	GAL	O5-C5-C4	2.39	114.04	109.69
2	D	2	NDG	C1-O5-C5	2.34	115.36	112.19
2	C	1	GAL	C3-C4-C5	-2.31	106.12	110.24
2	C	2	NDG	C1-O5-C5	2.24	115.22	112.19
2	C	2	NDG	C3-C4-C5	2.21	114.18	110.24
2	D	2	NDG	O5-C5-C6	2.10	110.50	107.20

There are no chirality outliers.

All (4) torsion outliers are listed below:

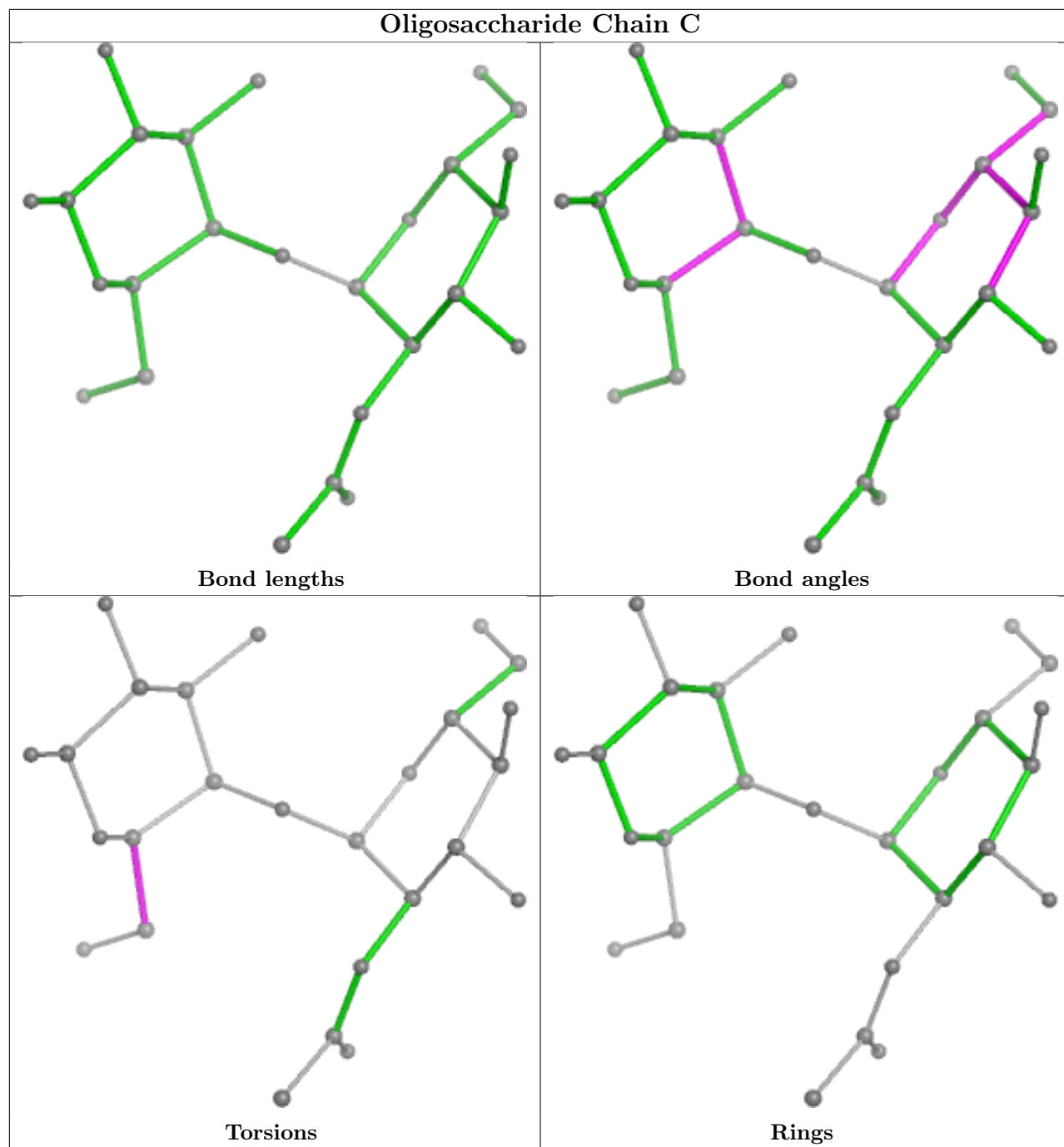
Mol	Chain	Res	Type	Atoms
2	C	1	GAL	C4-C5-C6-O6
2	C	1	GAL	O5-C5-C6-O6
2	D	2	NDG	C4-C5-C6-O6
2	D	2	NDG	O5-C5-C6-O6

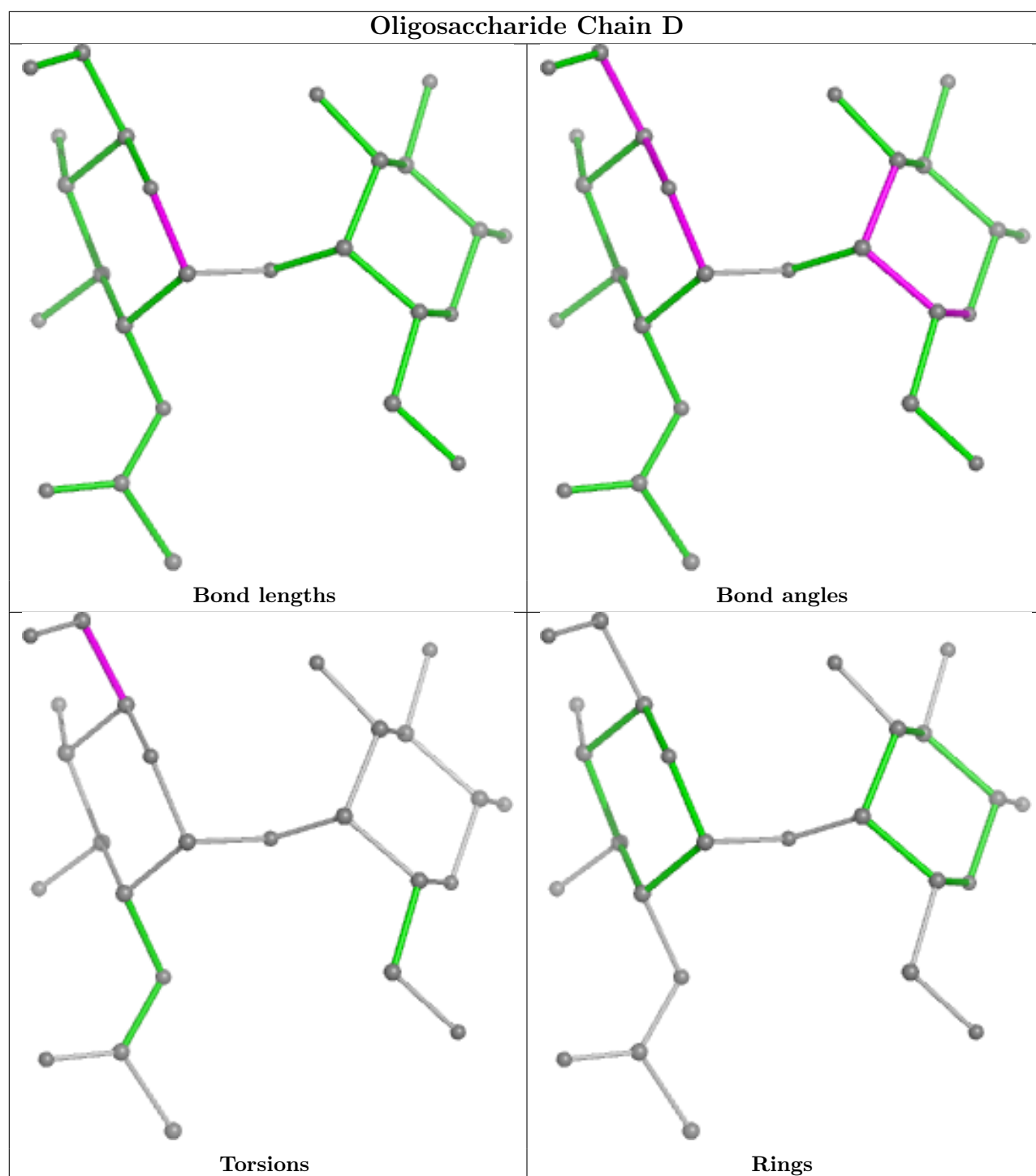
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	GAL	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 oligosaccharide.





5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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 [i](#)

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	144/161 (89%)	0.66	12 (8%) 11 6	16, 22, 33, 36	0
1	B	144/161 (89%)	0.40	4 (2%) 53 43	17, 19, 23, 24	0
All	All	288/322 (89%)	0.53	16 (5%) 24 16	16, 20, 30, 36	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1205	SER	4.7
1	B	1223	GLN	3.9
1	B	1207	ASN	3.6
1	A	1244	ASN	3.4
1	A	1328	SER	3.2
1	A	1329	PHE	2.9
1	A	1322	GLY	2.8
1	A	1207	ASN	2.7
1	A	1324	ALA	2.7
1	A	1206	ALA	2.4
1	A	1331	GLN	2.2
1	A	1224	SER	2.1
1	B	1205	SER	2.1
1	A	1330	ASP	2.1
1	A	1237	SER	2.0
1	B	1244	ASN	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

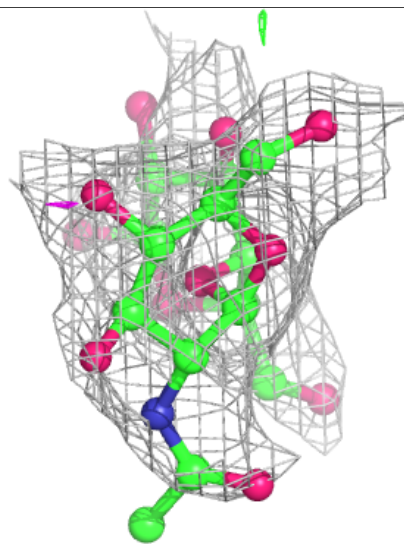
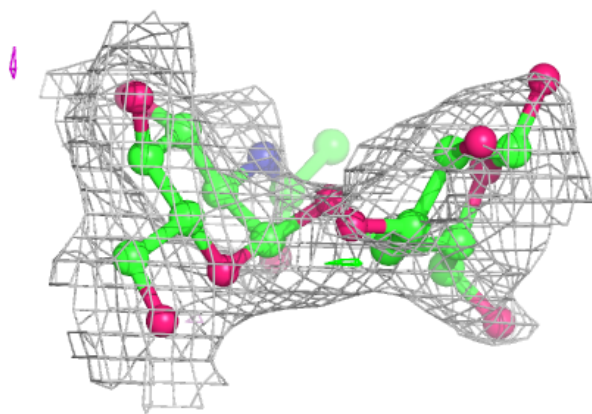
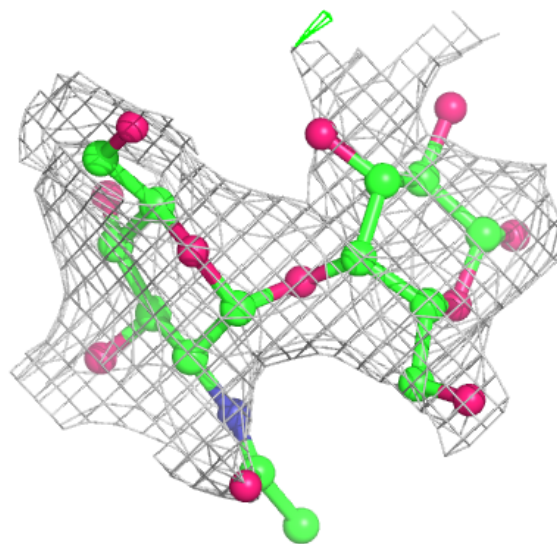
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

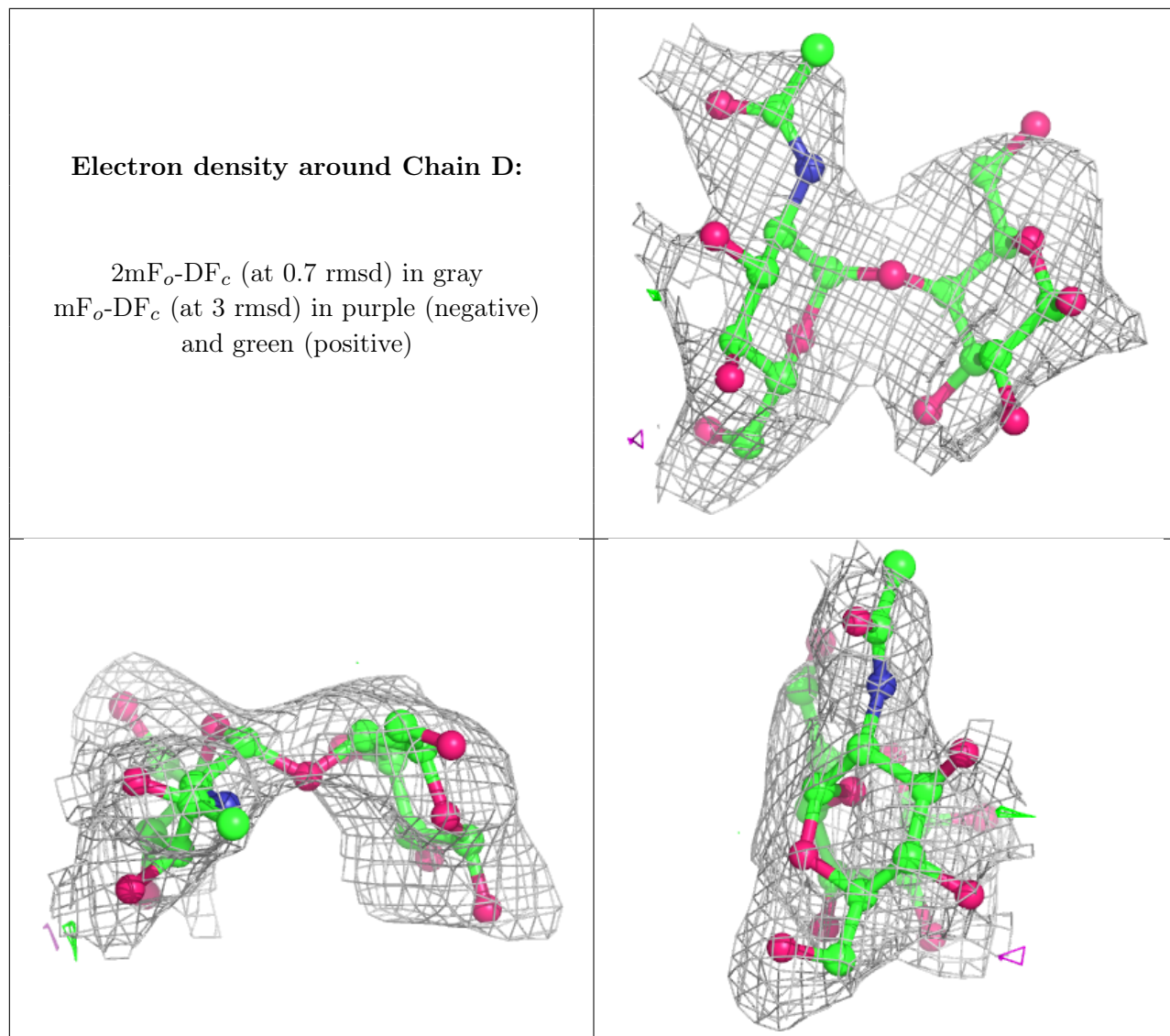
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NDG	C	2	14/15	0.51	0.39	63,66,73,75	0
2	GAL	D	1	12/12	0.75	0.30	27,33,37,41	0
2	NDG	D	2	14/15	0.75	0.28	27,31,38,38	0
2	GAL	C	1	12/12	0.80	0.30	63,68,78,87	0

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 C:

$2mF_o-DF_c$ (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	CA	A	2346	1/1	0.95	0.08	24,24,24,24	0
3	CA	B	2345	1/1	0.96	0.07	26,26,26,26	0
3	CA	B	2344	1/1	0.97	0.17	11,11,11,11	0

6.5 Other polymers [i](#)

There are no such residues in this entry.