



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 03:32 PM BST

PDB ID : 4RGA
Title : Phage 1358 receptor binding protein in complex with the trisaccharide GlcNAc-Galf-GlcOMe
Authors : Spinelli, S.; McCabe, O.; Farenc, C.; Tremblay, D.; Blangy, S.; Oscarson, S.; Moineau, S.; Cambillau, C.
Deposited on : 2014-09-29
Resolution : 2.10 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 following versions of software and data (see [references ⓘ](#)) 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	:	2.13.1
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)	:	2.13.1

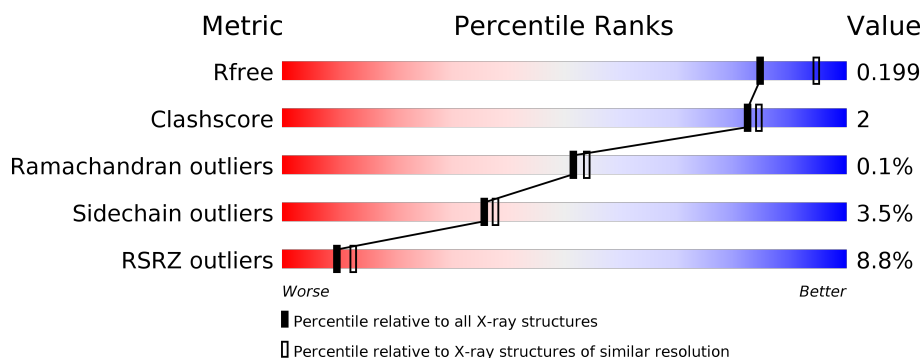
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 on 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	393	<div> <div>9%</div> <div> <div></div> <div>91%</div> <div>8% ..</div> </div> </div>
1	B	393	<div> <div>8%</div> <div> <div></div> <div>90%</div> <div>9% ..</div> </div> </div>
2	C	3	<div> <div></div> <div>100%</div> </div>
2	D	3	<div> <div>33%</div> <div>67%</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6995 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.

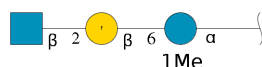
- Molecule 1 is a protein called Phage 1358 receptor binding protein (ORF20).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	1	0
			3039	1908	526	596	9			
1	B	390	Total	C	N	O	S	0	1	0
			3039	1908	526	596	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP D3W0F1
B	1	GLY	-	expression tag	UNP D3W0F1

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-beta-D-galactofuranose-(1-6)-methyl alpha-D-glucopyranoside.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			38	21	1	16			
2	D	3	Total	C	N	O	0	0	0
			38	21	1	16			

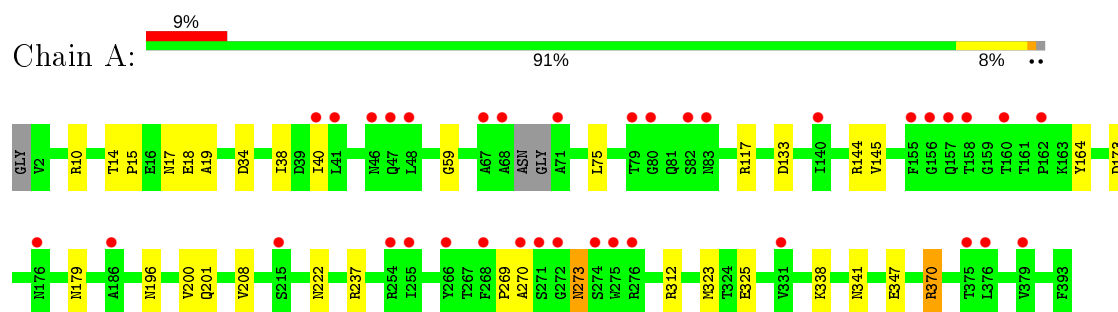
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	423	Total	O	0	0
			423	423		
3	B	418	Total	O	0	0
			418	418		

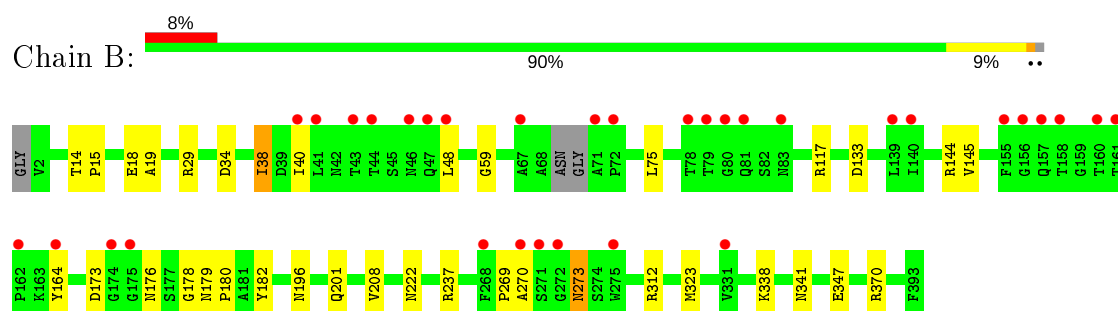
3 Residue-property plots [i](#)

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.

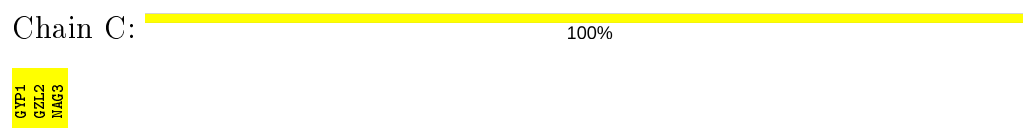
- Molecule 1: Phage 1358 receptor binding protein (ORF20)



- Molecule 1: Phage 1358 receptor binding protein (ORF20)



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-beta-D-galactofuranose-(1-6)-methyl alpha-D-glucopyranoside



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-beta-D-galactofuranose-(1-6)-methyl alpha-D-glucopyranoside



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	166.37Å 166.37Å 166.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.00 – 2.10 48.03 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.00-2.10) 100.0 (48.03-2.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.23 (at 2.10Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.180 , 0.192 0.184 , 0.199	Depositor DCC
R_{free} test set	4462 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	35.3	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 75.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.034 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6995	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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: GZL, NAG, GYP

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	0.51	0/3105	0.69	0/4230
1	B	0.50	0/3105	0.69	0/4230
All	All	0.50	0/6210	0.69	0/8460

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 [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	3039	0	2905	16	0
1	B	3039	0	2905	14	0
2	C	38	0	33	0	0
2	D	38	0	33	0	0
3	A	423	0	0	0	0
3	B	418	0	0	0	0
All	All	6995	0	5876	30	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 2.

All (30) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:196:ASN:H	1:B:201:GLN:HE22	1.20	0.88
1:A:196:ASN:H	1:A:201:GLN:HE22	1.22	0.83
1:A:133:ASP:OD1	1:A:338:LYS:NZ	2.22	0.72
1:A:237:ARG:NH2	1:A:341:ASN:HD21	1.94	0.65
1:B:133:ASP:OD1	1:B:338:LYS:NZ	2.33	0.62
1:A:200:VAL:HG22	1:A:347:GLU:HG2	1.85	0.58
1:B:29:ARG:HH12	1:B:176:ASN:ND2	2.05	0.54
1:A:40:ILE:HD12	1:A:164:TYR:HE2	1.73	0.54
1:B:176:ASN:O	1:B:180:PRO:HA	2.09	0.53
1:B:237:ARG:NH2	1:B:341:ASN:HD21	2.06	0.53
1:B:40:ILE:HD12	1:B:164:TYR:HE2	1.73	0.53
1:B:269:PRO:HA	1:B:273:ASN:HD21	1.80	0.47
1:B:312[B]:ARG:HH12	1:B:347:GLU:CD	2.18	0.47
1:A:19:ALA:O	1:A:59:GLY:HA3	2.15	0.47
1:B:19:ALA:O	1:B:59:GLY:HA3	2.15	0.47
1:A:269:PRO:HA	1:A:273:ASN:HD21	1.80	0.46
1:A:196:ASN:N	1:A:201:GLN:HE22	2.02	0.46
1:A:14:THR:H	1:A:17:ASN:HD22	1.64	0.46
1:A:237:ARG:HH22	1:A:341:ASN:HD21	1.60	0.45
1:A:14:THR:HB	1:A:15:PRO:HD2	1.98	0.45
1:B:208:VAL:HG22	1:B:222:ASN:HD22	1.82	0.45
1:B:270:ALA:H	1:B:273:ASN:HD21	1.65	0.44
1:A:208:VAL:HG22	1:A:222:ASN:HD22	1.82	0.44
1:A:312[A]:ARG:NH2	1:A:347:GLU:OE1	2.36	0.43
1:A:144:ARG:HH11	1:A:144:ARG:HG2	1.83	0.43
1:A:270:ALA:H	1:A:273:ASN:HD21	1.66	0.43
1:B:14:THR:HB	1:B:15:PRO:HD2	2.02	0.41
1:B:38:ILE:HD11	1:B:48:LEU:HD11	2.02	0.41
1:B:179:ASN:HD22	1:B:182:TYR:HB2	1.86	0.40
1:A:325:GLU:OE2	1:A:370:ARG:HD3	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	387/393 (98%)	375 (97%)	12 (3%)	0	100	100
1	B	387/393 (98%)	376 (97%)	10 (3%)	1 (0%)	41	41
All	All	774/786 (98%)	751 (97%)	22 (3%)	1 (0%)	51	54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	178	GLY

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	328/332 (99%)	316 (96%)	12 (4%)	34	35
1	B	328/332 (99%)	317 (97%)	11 (3%)	37	39
All	All	656/664 (99%)	633 (96%)	23 (4%)	36	38

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ARG
1	A	18	GLU
1	A	34	ASP
1	A	38	ILE
1	A	75	LEU
1	A	117	ARG
1	A	145	VAL
1	A	173	ASP
1	A	179	ASN
1	A	273	ASN
1	A	323	MET
1	A	370	ARG

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Mol	Chain	Res	Type
1	B	18	GLU
1	B	34	ASP
1	B	38	ILE
1	B	75	LEU
1	B	117	ARG
1	B	144	ARG
1	B	145	VAL
1	B	173	ASP
1	B	273	ASN
1	B	323	MET
1	B	370	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	ASN
1	A	83	ASN
1	A	157	GLN
1	A	179	ASN
1	A	196	ASN
1	A	201	GLN
1	A	222	ASN
1	A	273	ASN
1	A	341	ASN
1	B	81	GLN
1	B	83	ASN
1	B	157	GLN
1	B	176	ASN
1	B	179	ASN
1	B	196	ASN
1	B	201	GLN
1	B	222	ASN
1	B	273	ASN
1	B	341	ASN
1	B	371	ASN

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 ⓘ

6 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	GYP	C	1	2	13,13,13	0.66	0	18,18,18	2.13	6 (33%)
2	GZL	C	2	2	11,11,12	0.37	0	14,15,17	1.33	2 (14%)
2	NAG	C	3	2	14,14,15	0.70	0	17,19,21	1.26	2 (11%)
2	GYP	D	1	2	13,13,13	0.75	0	18,18,18	1.67	4 (22%)
2	GZL	D	2	2	11,11,12	0.37	0	14,15,17	1.03	0
2	NAG	D	3	2	14,14,15	0.66	0	17,19,21	1.08	1 (5%)

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	GYP	C	1	2	-	2/4/24/24	0/1/1/1
2	GZL	C	2	2	-	4/6/19/22	0/1/1/1
2	NAG	C	3	2	-	0/6/23/26	0/1/1/1
2	GYP	D	1	2	-	2/4/24/24	0/1/1/1
2	GZL	D	2	2	-	4/6/19/22	0/1/1/1
2	NAG	D	3	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	GYP	O1-C1-C2	5.37	114.45	108.15
2	C	3	NAG	C1-C2-N2	-3.99	103.67	110.49
2	D	1	GYP	O1-C1-C2	3.72	112.50	108.15
2	C	1	GYP	C3-C4-C5	-3.51	103.98	110.24
2	D	3	NAG	C1-C2-N2	-3.04	105.29	110.49
2	D	1	GYP	O6-C6-C5	2.67	120.47	111.29
2	C	1	GYP	O5-C1-C2	2.50	115.64	110.35
2	C	1	GYP	C7-O1-C1	-2.46	109.48	113.27
2	D	1	GYP	C3-C4-C5	-2.34	106.06	110.24
2	C	1	GYP	O2-C2-C3	2.21	115.45	110.35
2	C	2	GZL	C5-C4-C3	-2.07	113.09	115.86
2	C	3	NAG	O4-C4-C5	2.07	114.44	109.30
2	C	2	GZL	O4-C4-C3	2.05	107.26	103.59
2	C	1	GYP	C1-O5-C5	2.05	117.72	113.69
2	D	1	GYP	C1-O5-C5	2.05	117.71	113.69

There are no chirality outliers.

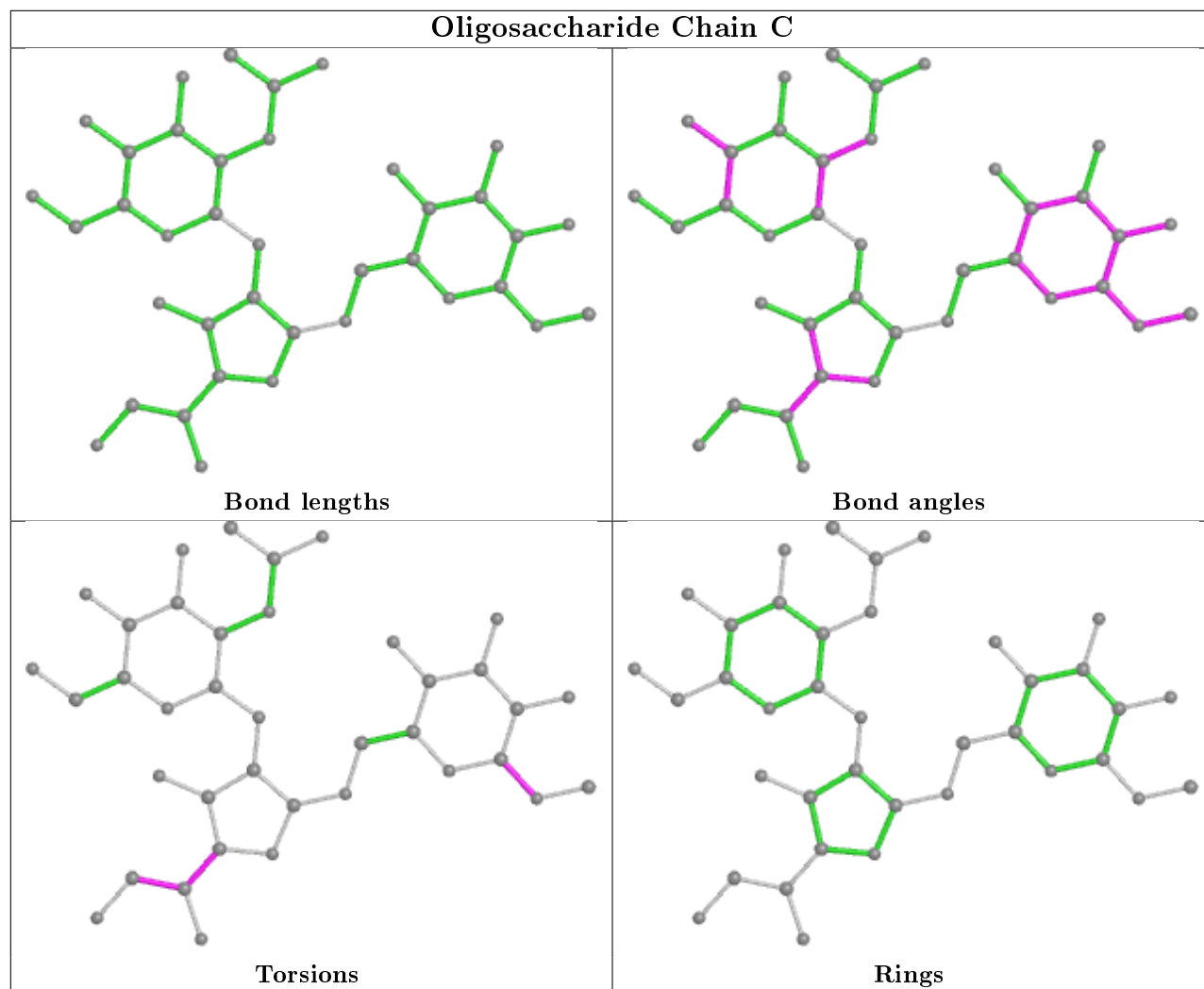
All (12) torsion outliers are listed below:

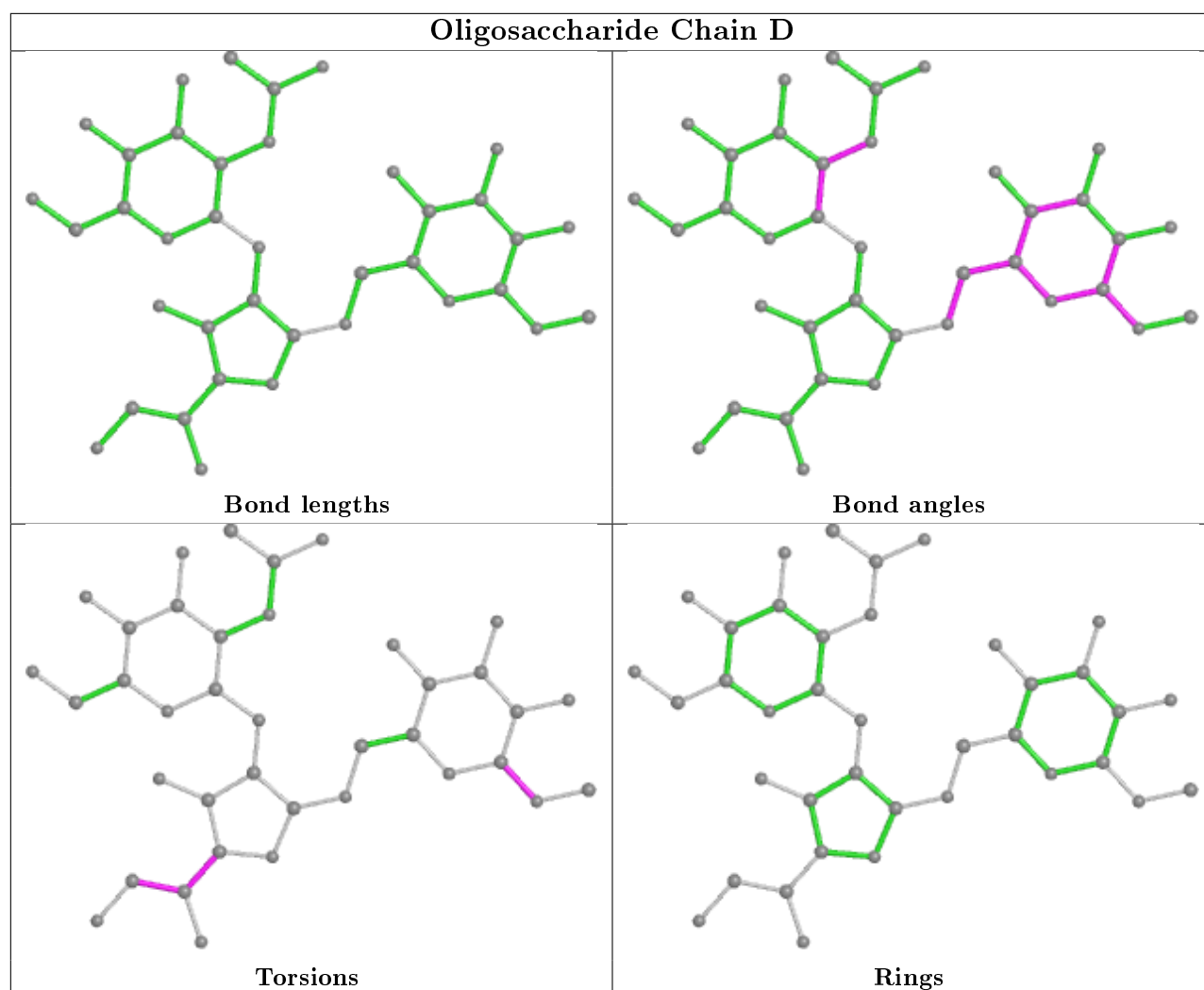
Mol	Chain	Res	Type	Atoms
2	D	1	GYP	C2-C1-O1-C7
2	D	2	GZL	C4-C5-C6-O6
2	D	2	GZL	O5-C5-C6-O6
2	C	1	GYP	C2-C1-O1-C7
2	D	1	GYP	O5-C1-O1-C7
2	C	1	GYP	O5-C1-O1-C7
2	C	2	GZL	C4-C5-C6-O6
2	C	2	GZL	O4-C4-C5-O5
2	D	2	GZL	O4-C4-C5-O5
2	C	2	GZL	O5-C5-C6-O6
2	C	2	GZL	O4-C4-C5-C6
2	D	2	GZL	O4-C4-C5-C6

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](#)

There are no ligands in this entry.

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	390/393 (99%)	0.21	36 (9%) 9 11	23, 40, 90, 132	0
1	B	390/393 (99%)	0.15	33 (8%) 10 13	23, 40, 85, 115	0
All	All	780/786 (99%)	0.18	69 (8%) 10 12	23, 40, 88, 132	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	275	TRP	7.7
1	B	275	TRP	5.7
1	A	67	ALA	5.5
1	B	41	LEU	5.1
1	B	140	ILE	4.9
1	B	174	GLY	4.7
1	B	67	ALA	4.4
1	B	71	ALA	4.3
1	B	270	ALA	4.3
1	A	268	PHE	4.2
1	B	271	SER	4.2
1	A	140	ILE	4.2
1	B	157	GLN	4.2
1	A	271	SER	4.2
1	B	175	GLY	4.1
1	A	156	GLY	4.1
1	B	160	THR	4.0
1	A	160	THR	4.0
1	A	157	GLN	3.8
1	B	48	LEU	3.7
1	B	79	THR	3.6
1	B	155	PHE	3.6
1	A	71	ALA	3.6
1	B	161	THR	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	83	ASN	3.5
1	A	176	ASN	3.5
1	B	268	PHE	3.5
1	A	155	PHE	3.5
1	B	40	ILE	3.4
1	A	158	THR	3.4
1	A	80	GLY	3.4
1	B	47	GLN	3.4
1	A	46	ASN	3.4
1	A	41	LEU	3.3
1	B	158	THR	3.2
1	B	331	VAL	3.2
1	A	266	TYR	3.1
1	A	79	THR	3.1
1	B	46	ASN	3.1
1	B	80	GLY	3.1
1	A	276	ARG	3.0
1	A	272	GLY	2.8
1	B	83	ASN	2.8
1	A	379	VAL	2.7
1	B	44	THR	2.7
1	A	40	ILE	2.6
1	B	162	PRO	2.5
1	B	156	GLY	2.5
1	A	47	GLN	2.4
1	A	82	SER	2.4
1	A	331	VAL	2.4
1	A	68	ALA	2.4
1	A	375	THR	2.4
1	A	186	ALA	2.4
1	B	72	PRO	2.4
1	A	215	SER	2.3
1	B	78	THR	2.3
1	A	162	PRO	2.3
1	A	376	LEU	2.3
1	B	139	LEU	2.3
1	A	270	ALA	2.3
1	A	274	SER	2.2
1	B	272	GLY	2.2
1	A	48	LEU	2.1
1	B	164	TYR	2.1
1	B	43	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	81	GLN	2.1
1	A	254	ARG	2.0
1	A	255	ILE	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](#)

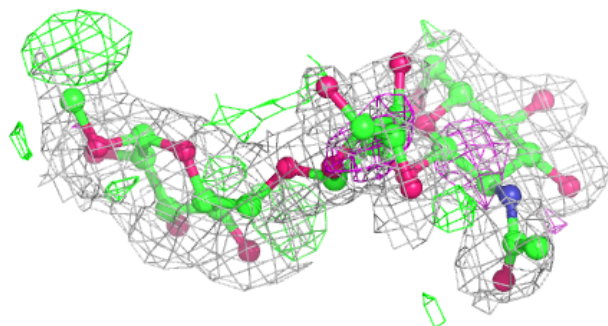
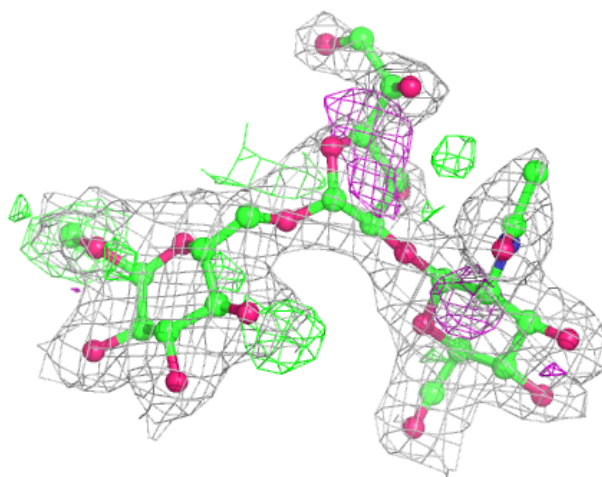
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

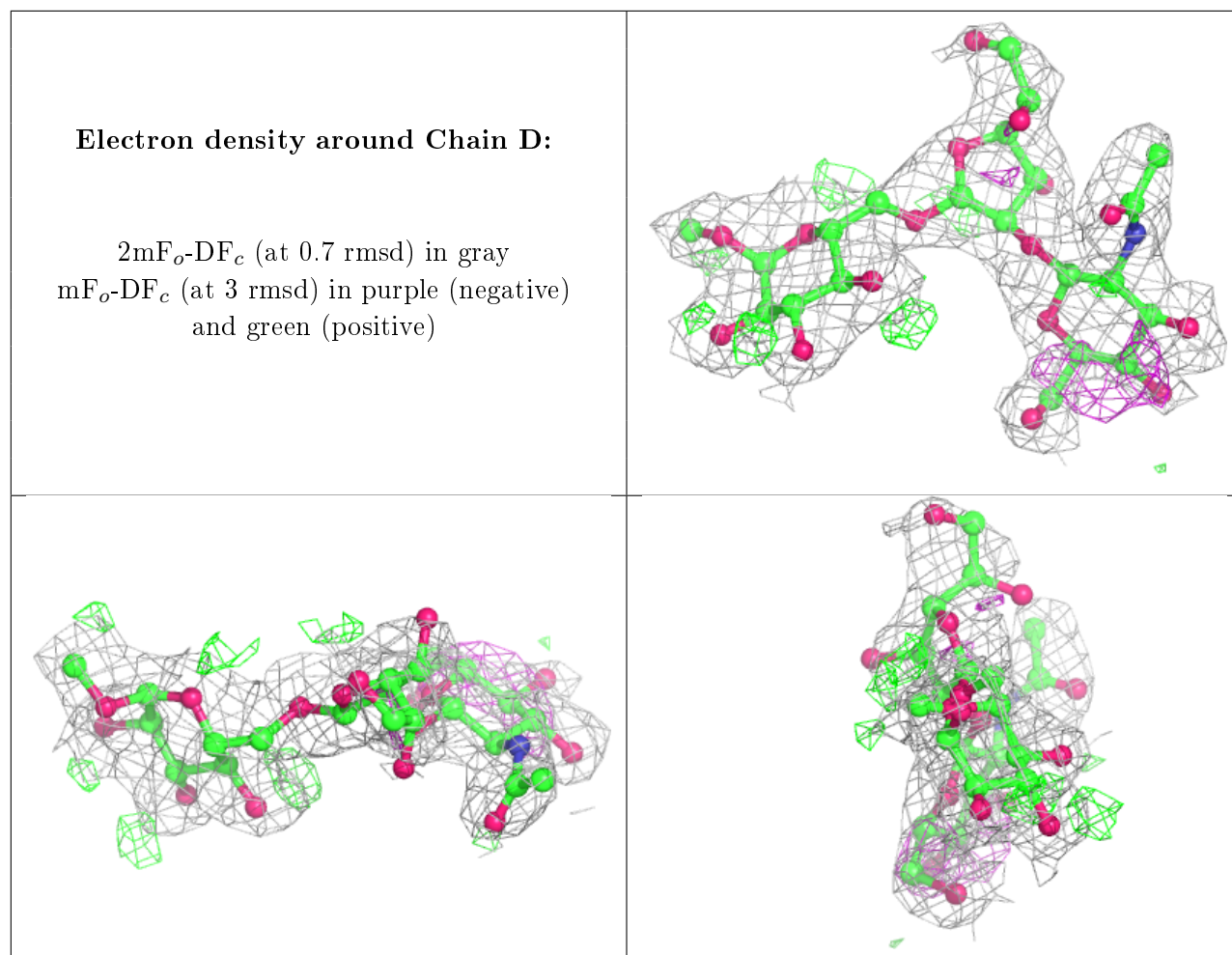
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GZL	C	2	11/12	0.79	0.39	65,71,76,77	0
2	GZL	D	2	11/12	0.86	0.27	66,76,83,83	0
2	NAG	D	3	14/15	0.87	0.25	39,58,61,62	0
2	NAG	C	3	14/15	0.88	0.20	41,55,61,61	0
2	GYP	C	1	13/13	0.88	0.12	33,48,60,66	0
2	GYP	D	1	13/13	0.93	0.12	39,52,63,67	0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.