



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:19 PM UTC

PDB ID : 3VMO / pdb_00003vmo
Title : Crystal structure of dextranase from Streptococcus mutans in complex with isomaltotriose
Authors : Suzuki, N.; Fujimoto, Z.; Kim, Y.M.; Momma, M.; Okuyama, M.; Mori, H.; Funane, K.; Kimura, A.
Deposited on : 2011-12-14
Resolution : 1.90 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

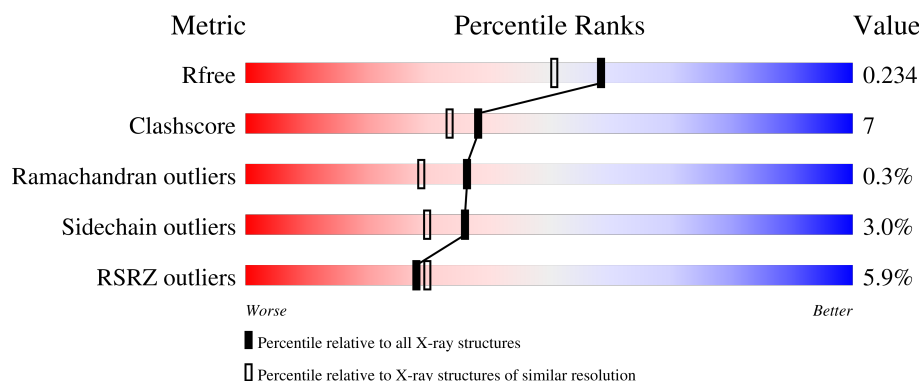
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
R_{free}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (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 $\leq 5\%$. 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	643	6% 84% 12% ..
2	B	4	100%
3	C	2	50% 50%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5333 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.

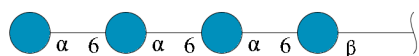
- Molecule 1 is a protein called Dextranase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	628	Total	C	N	O	S	0	0	0
			4985	3137	844	988	16			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	98	MET	-	expression tag	UNP F5BA50
A	99	ASP	-	expression tag	UNP F5BA50
A	733	LEU	-	expression tag	UNP F5BA50
A	734	GLU	-	expression tag	UNP F5BA50
A	735	HIS	-	expression tag	UNP F5BA50
A	736	HIS	-	expression tag	UNP F5BA50
A	737	HIS	-	expression tag	UNP F5BA50
A	738	HIS	-	expression tag	UNP F5BA50
A	739	HIS	-	expression tag	UNP F5BA50
A	740	HIS	-	expression tag	UNP F5BA50

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose-(1-6)-beta-D-glucopyranose.



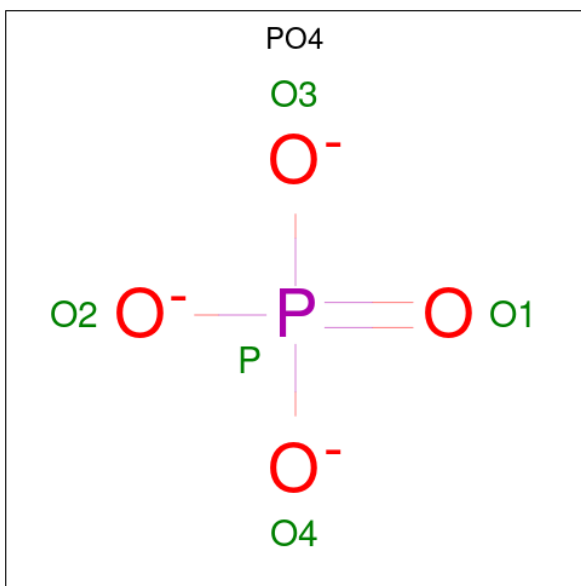
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	B	4	Total	C	O	0	0	0
			45	24	21			

- Molecule 3 is an oligosaccharide called alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	C	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		

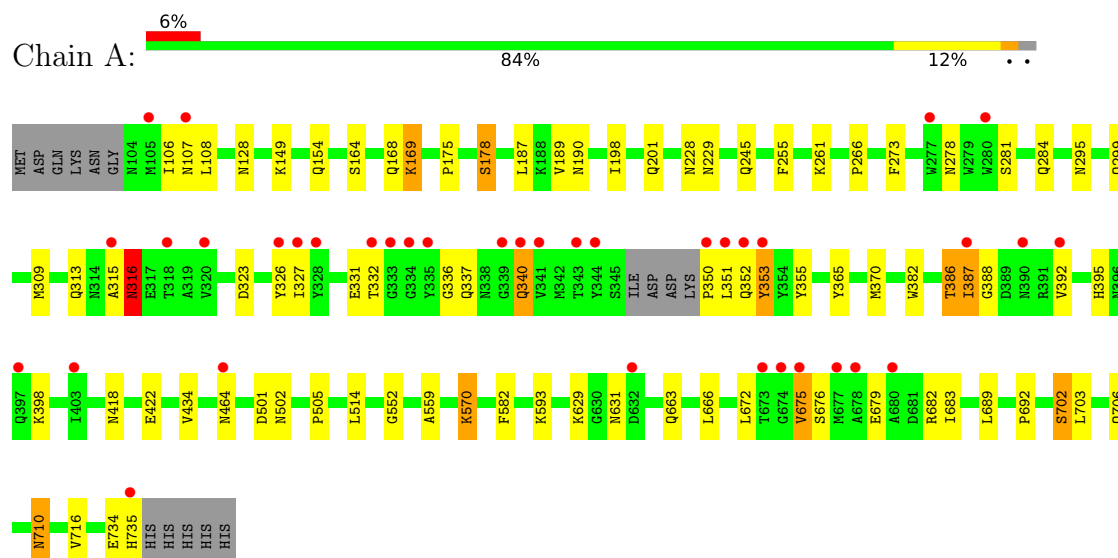
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	275	Total	O	0	0
			275	275		

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: Dextranase



- Molecule 2: alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose-(1-6)-beta-D-glucopyranose



- Molecule 3: alpha-D-glucopyranose-(1-6)-alpha-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.03Å 90.34Å 63.00Å 90.00° 100.33° 90.00°	Depositor
Resolution (Å)	29.22 – 1.90 29.22 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.22-1.90) 99.7 (29.22-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.03 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.187 , 0.237 0.186 , 0.234	Depositor DCC
R_{free} test set	2518 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	31.3	Xtriage
Anisotropy	0.094	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5333	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.93% 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: GLC, BGC, PO4

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	1.00	0/5091	0.97	3/6927 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	675	VAL	N-CA-C	6.69	118.21	109.58
1	A	266	PRO	CA-C-N	-5.05	117.83	122.28
1	A	266	PRO	C-N-CA	-5.05	117.83	122.28

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	4985	0	4804	68	0
2	B	45	0	39	1	0
3	C	23	0	21	0	0
4	A	5	0	0	0	0
5	A	275	0	0	10	0
All	All	5333	0	4864	68	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.

All (68) 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:710:ASN:HB3	1:A:716:VAL:HG21	1.47	0.93
1:A:734:GLU:O	1:A:735:HIS:CG	2.33	0.80
1:A:315:ALA:HB2	1:A:351:LEU:HA	1.65	0.77
1:A:422:GLU:OE1	5:A:1111:HOH:O	2.03	0.76
1:A:683:ILE:HD13	1:A:734:GLU:HG2	1.70	0.72
1:A:326:TYR:CE1	1:A:353:TYR:HD2	2.09	0.70
1:A:395:HIS:O	1:A:398:LYS:HG2	1.91	0.70
1:A:309:MET:HE3	5:A:1054:HOH:O	1.93	0.69
1:A:337:GLN:O	1:A:340:GLN:HB3	1.95	0.66
1:A:323:ASP:HA	1:A:326:TYR:HD2	1.61	0.66
1:A:323:ASP:HA	1:A:326:TYR:CD2	2.31	0.65
1:A:315:ALA:HB2	1:A:351:LEU:O	1.97	0.65
1:A:387:ILE:HD12	1:A:388:GLY:H	1.63	0.63
1:A:190:ASN:ND2	1:A:201:GLN:HG2	2.16	0.61
1:A:418:ASN:O	1:A:422:GLU:HG3	2.00	0.61
1:A:702:SER:OG	5:A:1233:HOH:O	2.16	0.60
1:A:386:THR:HG22	5:A:1119:HOH:O	2.02	0.59
1:A:245:GLN:HE22	1:A:552:GLY:HA2	1.68	0.57
1:A:559:ALA:HB1	2:B:1:BGC:H3	1.84	0.57
1:A:128:ASN:OD1	1:A:164:SER:OG	2.17	0.57
1:A:228:ASN:HB3	1:A:281:SER:O	2.04	0.57
1:A:710:ASN:HB3	1:A:716:VAL:CG2	2.31	0.56
1:A:734:GLU:O	1:A:735:HIS:CD2	2.59	0.56
1:A:370:MET:HE2	1:A:382:TRP:CD1	2.41	0.55
1:A:434:VAL:O	5:A:1200:HOH:O	2.18	0.55
1:A:689:LEU:HB2	1:A:703:LEU:HD11	1.90	0.54
1:A:706:GLN:OE1	5:A:1174:HOH:O	2.18	0.54
1:A:245:GLN:HG3	5:A:1100:HOH:O	2.06	0.54
1:A:315:ALA:HB2	1:A:351:LEU:CA	2.36	0.53
1:A:315:ALA:HB2	1:A:351:LEU:C	2.35	0.52
1:A:675:VAL:HG12	1:A:676:SER:O	2.09	0.52
1:A:326:TYR:HE1	1:A:353:TYR:HD2	1.57	0.49
1:A:710:ASN:C	1:A:710:ASN:HD22	2.20	0.49
1:A:353:TYR:CD1	1:A:353:TYR:N	2.80	0.49
1:A:350:PRO:C	1:A:351:LEU:HD22	2.39	0.48
1:A:593:LYS:HD2	5:A:1148:HOH:O	2.14	0.47
1:A:228:ASN:O	1:A:229:ASN:HB2	2.14	0.47
1:A:175:PRO:O	1:A:178:SER:OG	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:TYR:HH	1:A:353:TYR:HE2	1.60	0.45
1:A:332:THR:HA	1:A:336:GLY:O	2.15	0.45
1:A:570:LYS:HA	1:A:570:LYS:HD3	1.83	0.45
1:A:261:LYS:HD3	1:A:273:PHE:HB2	1.98	0.45
1:A:501:ASP:OD1	1:A:501:ASP:N	2.50	0.45
1:A:502:ASN:HB2	5:A:1137:HOH:O	2.17	0.45
1:A:108:LEU:HD22	1:A:189:VAL:HG21	1.98	0.45
1:A:313:GLN:HB2	1:A:355:TYR:HE2	1.82	0.44
1:A:316:ASN:HD22	1:A:316:ASN:N	2.15	0.44
1:A:198:ILE:HG21	1:A:201:GLN:HG3	1.99	0.44
1:A:168:GLN:O	1:A:169:LYS:C	2.61	0.44
1:A:365:TYR:CD1	1:A:365:TYR:C	2.96	0.43
1:A:672:LEU:HB3	1:A:675:VAL:HB	2.01	0.43
1:A:679:GLU:O	1:A:683:ILE:HG13	2.19	0.43
1:A:106:ILE:O	1:A:107:ASN:C	2.61	0.43
1:A:505:PRO:HG3	1:A:514:LEU:CD1	2.49	0.43
1:A:327:ILE:HG13	1:A:392:VAL:HB	2.01	0.42
1:A:663:GLN:HB3	1:A:666:LEU:HD21	2.02	0.42
1:A:278:ASN:OD1	1:A:278:ASN:C	2.62	0.42
1:A:582:PHE:HB2	1:A:692:PRO:HB3	2.01	0.42
1:A:370:MET:HE2	1:A:382:TRP:CG	2.55	0.42
1:A:629:LYS:HE3	1:A:629:LYS:HB2	1.72	0.42
1:A:190:ASN:ND2	1:A:201:GLN:OE1	2.48	0.41
1:A:295:ASN:O	1:A:299:GLN:HG3	2.20	0.41
1:A:332:THR:OG1	1:A:337:GLN:HA	2.21	0.41
1:A:387:ILE:H	1:A:387:ILE:HG13	1.54	0.41
1:A:149:LYS:NZ	5:A:1220:HOH:O	2.53	0.41
1:A:313:GLN:HG2	1:A:353:TYR:CE2	2.56	0.41
1:A:679:GLU:HG2	1:A:682:ARG:HD2	2.03	0.41
1:A:351:LEU:O	1:A:352:GLN:HG2	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	624/643 (97%)	602 (96%)	20 (3%)	2 (0%)	36	29

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	316	ASN
1	A	464	ASN

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	538/552 (98%)	522 (97%)	16 (3%)	36	30

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154	GLN
1	A	169	LYS
1	A	178	SER
1	A	187	LEU
1	A	255	PHE
1	A	284	GLN
1	A	316	ASN
1	A	331	GLU
1	A	340	GLN
1	A	353	TYR
1	A	386	THR
1	A	387	ILE
1	A	570	LYS
1	A	631	ASN
1	A	702	SER
1	A	710	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	ASN
1	A	168	GLN
1	A	190	ASN
1	A	201	GLN
1	A	245	GLN
1	A	269	ASN
1	A	284	GLN
1	A	299	GLN
1	A	338	ASN
1	A	396	ASN
1	A	602	GLN
1	A	607	ASN
1	A	619	ASN
1	A	710	ASN
1	A	735	HIS

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	BGC	B	1	2	12,12,12	0.64	0	17,17,17	0.81	0
2	GLC	B	2	2	11,11,12	0.65	0	15,15,17	1.25	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GLC	B	3	2	11,11,12	0.57	0	15,15,17	0.88	1 (6%)
2	GLC	B	4	2	11,11,12	0.59	0	15,15,17	1.32	3 (20%)
3	GLC	C	1	3	12,12,12	0.65	0	17,17,17	0.88	0
3	GLC	C	2	3	11,11,12	0.58	0	15,15,17	1.49	1 (6%)

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	BGC	B	1	2	-	0/2/22/22	0/1/1/1
2	GLC	B	2	2	-	0/2/19/22	0/1/1/1
2	GLC	B	3	2	-	0/2/19/22	0/1/1/1
2	GLC	B	4	2	-	1/2/19/22	0/1/1/1
3	GLC	C	1	3	-	0/2/22/22	0/1/1/1
3	GLC	C	2	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2	GLC	C1-O5-C5	4.38	118.06	112.19
2	B	2	GLC	C1-O5-C5	2.95	116.14	112.19
2	B	4	GLC	C2-C3-C4	2.53	115.32	110.86
2	B	3	GLC	C1-O5-C5	2.46	115.48	112.19
2	B	4	GLC	C3-C4-C5	2.37	114.52	110.23
2	B	4	GLC	O5-C5-C6	2.22	111.98	107.66

There are no chirality outliers.

All (1) torsion outliers are listed below:

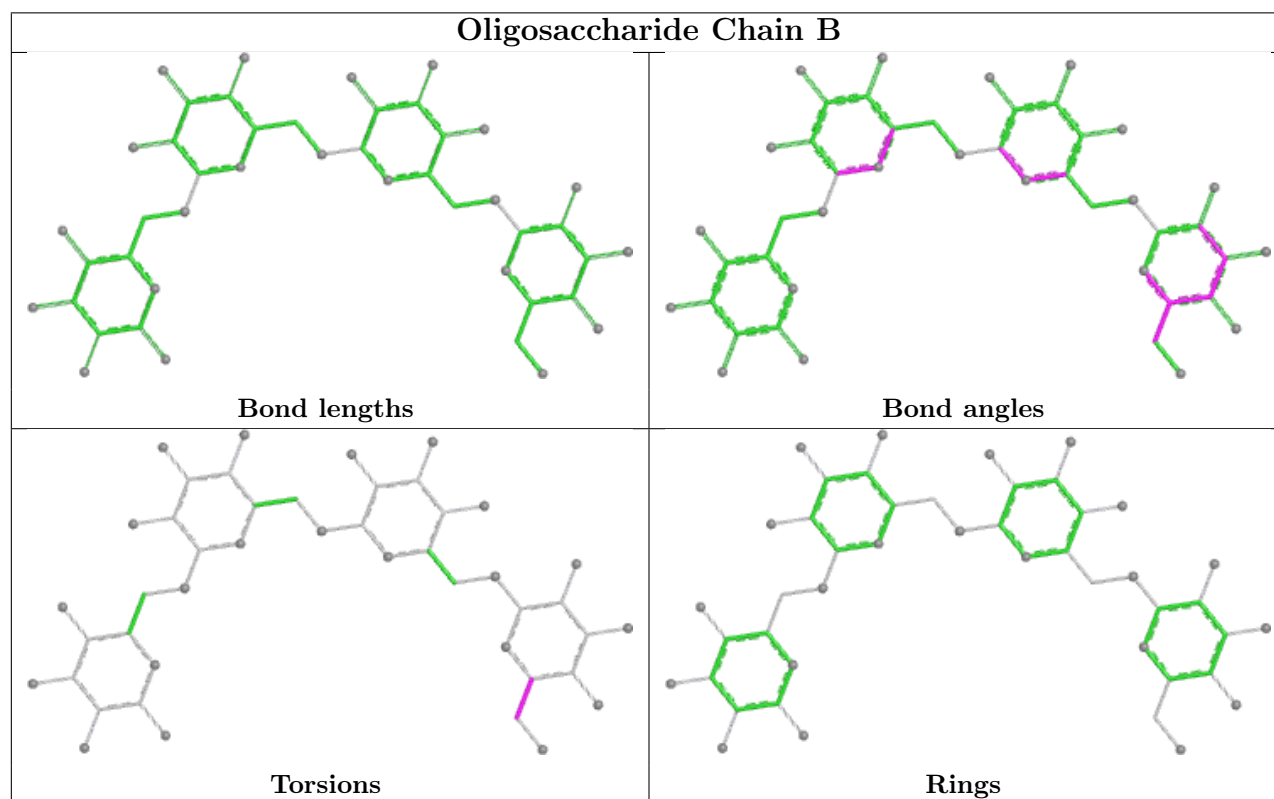
Mol	Chain	Res	Type	Atoms
2	B	4	GLC	C4-C5-C6-O6

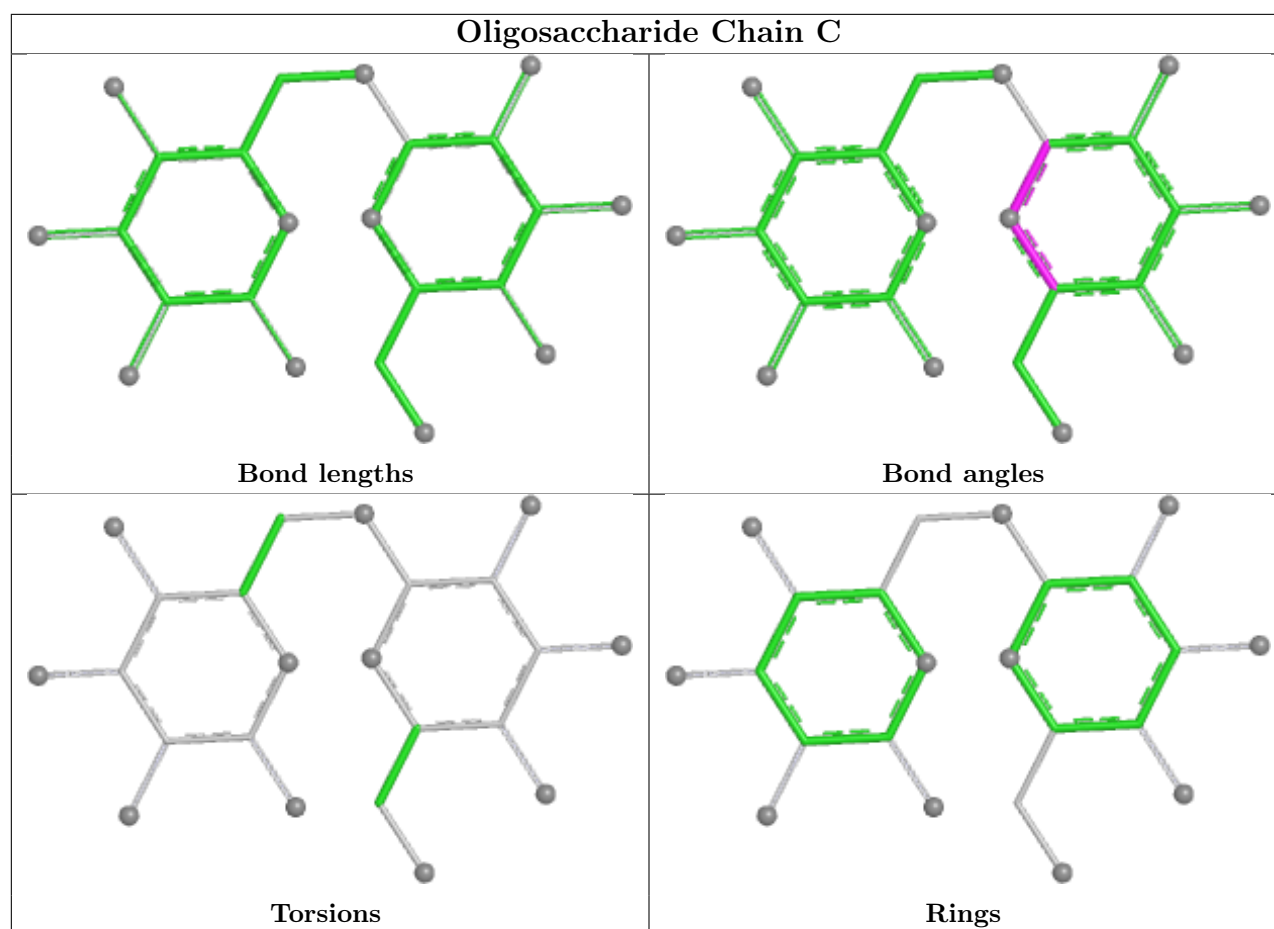
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	BGC	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](#)

1 ligand is 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	$\# Z > 2$
4	PO4	A	807	-	4,4,4	0.84	0	6,6,6	0.80	0

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

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

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	628/643 (97%)	0.23	37 (5%) 28 30	17, 32, 58, 66	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	351	LEU	5.8
1	A	350	PRO	4.7
1	A	353	TYR	4.1
1	A	339	GLY	3.6
1	A	107	ASN	3.6
1	A	341	VAL	3.4
1	A	344	TYR	3.3
1	A	352	GLN	3.3
1	A	343	THR	3.2
1	A	387	ILE	3.0
1	A	327	ILE	3.0
1	A	280	TRP	2.9
1	A	735	HIS	2.8
1	A	105	MET	2.8
1	A	673	THR	2.7
1	A	277	TRP	2.7
1	A	680	ALA	2.6
1	A	326	TYR	2.6
1	A	675	VAL	2.6
1	A	315	ALA	2.5
1	A	335	TYR	2.4
1	A	318	THR	2.4
1	A	320	VAL	2.4
1	A	328	TYR	2.3
1	A	677	MET	2.3
1	A	678	ALA	2.2
1	A	632	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	340	GLN	2.2
1	A	403	ILE	2.2
1	A	392	VAL	2.2
1	A	390	ASN	2.1
1	A	674	GLY	2.1
1	A	464	ASN	2.1
1	A	332	THR	2.1
1	A	333	GLY	2.1
1	A	334	GLY	2.1
1	A	397	GLN	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](#)

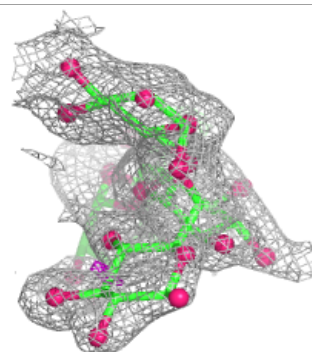
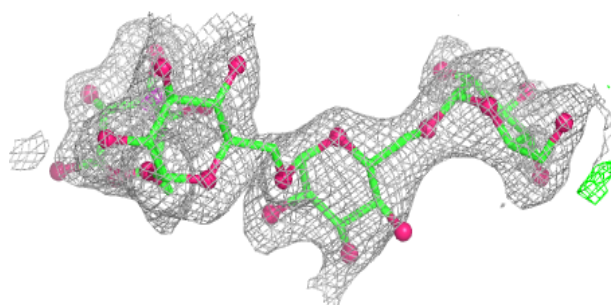
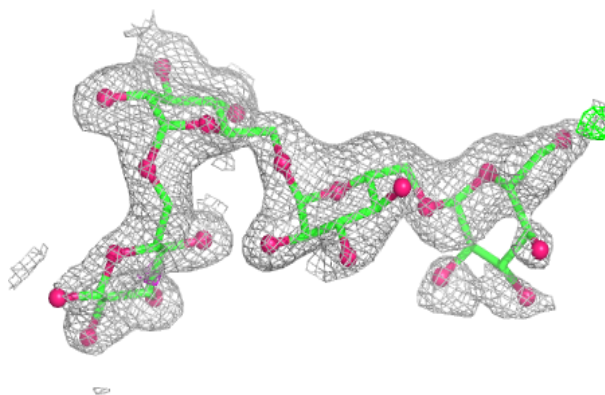
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

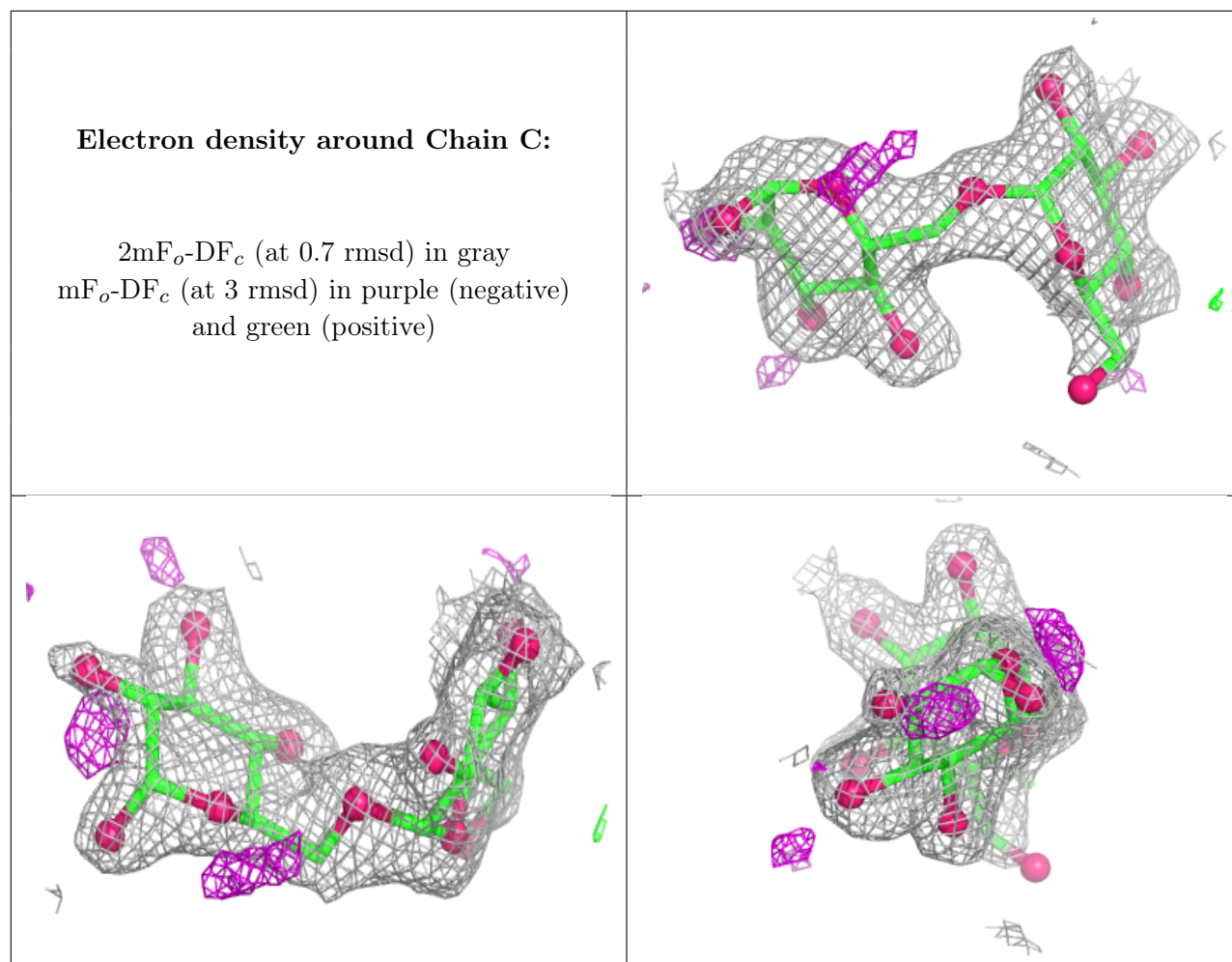
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GLC	B	4	11/12	0.67	0.14	63,65,66,67	0
2	GLC	B	3	11/12	0.83	0.11	53,57,60,62	0
2	BGC	B	1	12/12	0.85	0.11	46,51,54,56	0
3	GLC	C	2	11/12	0.87	0.10	38,43,48,53	0
3	GLC	C	1	12/12	0.89	0.08	39,43,45,47	0
2	GLC	B	2	11/12	0.91	0.07	43,45,49,51	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($\text{\AA}^2$)	Q<0.9
4	PO4	A	807	5/5	0.81	0.11	67,68,69,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.