



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:56 PM UTC

PDB ID : 3LEM / pdb_00003lem
Title : Crystal structure of fructosyltransferase (D191A) from *A. japonicus* in complex with Nystose
Authors : Chuankhayan, P.; Chen, C.J.; Chiang, C.M.
Deposited on : 2010-01-15
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 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

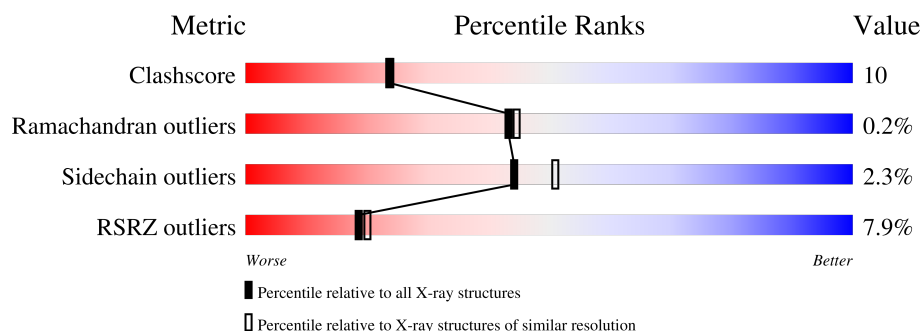
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (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 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	634	8% 75% 21% .
2	B	4	50% 50%

2 Entry composition [i](#)

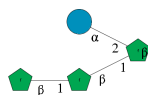
There are 3 unique types of molecules in this entry. The entry contains 5147 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Fructosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	634	Total	C	N	O	S	0	0	0
			4883	3091	824	965	3			

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



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

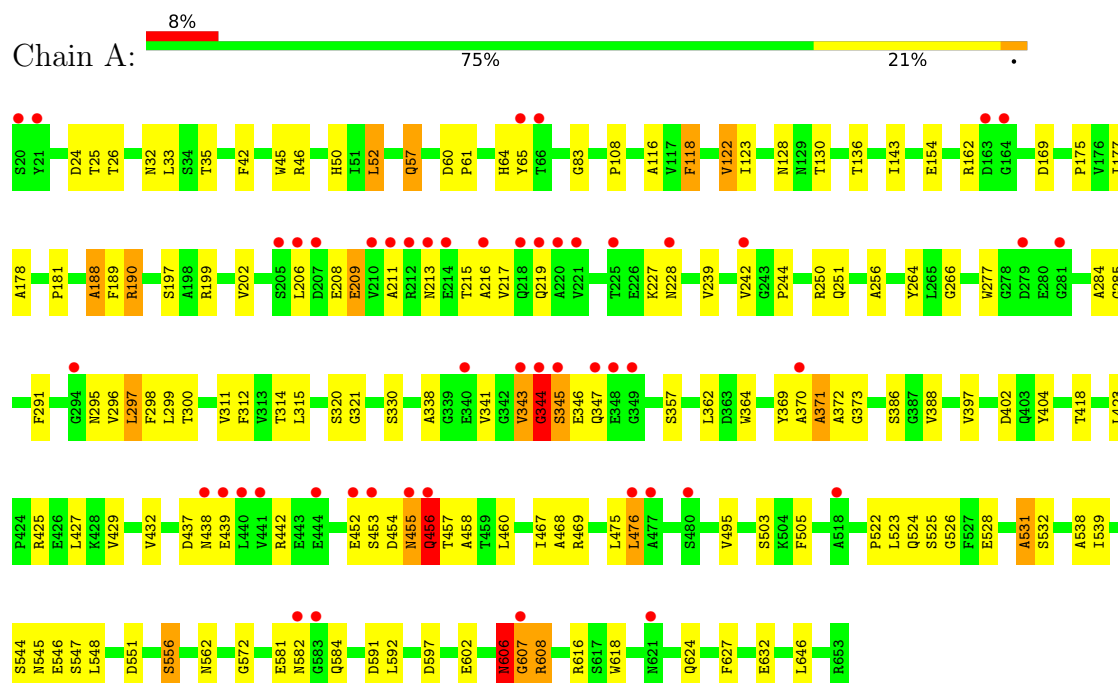
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	219	Total	O	0	0
			219	219		

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: Fructosyltransferase



• Molecule 2: beta-D-fructofuranose-(2-1)-beta-D-fructofuranose-(2-1)-beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	98.68Å 110.73Å 66.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.10 30.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.1 (30.00-2.10) 96.1 (30.00-2.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.68 (at 1.93Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.214 , 0.252 0.228 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	30.8	Xtriage
Anisotropy	0.492	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 38.3	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	0.95	EDS
Total number of atoms	5147	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% 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: FRU, GLC

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	0.64	19/5014 (0.4%)	1.03	37/6858 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	608	ARG	C-N	10.02	1.46	1.33
1	A	505	PHE	C-N	8.79	1.44	1.33
1	A	455	ASN	C-N	8.64	1.44	1.33
1	A	189	PHE	C-N	8.54	1.44	1.33
1	A	188	ALA	C-N	-8.48	1.22	1.33
1	A	544	SER	C-N	8.19	1.46	1.33
1	A	547	SER	C-N	-8.19	1.21	1.33
1	A	404	TYR	C-N	8.03	1.44	1.33
1	A	402	ASP	C-N	-6.99	1.23	1.33
1	A	370	ALA	C-N	-6.60	1.24	1.33
1	A	503	SER	C-N	-6.41	1.25	1.33
1	A	438	ASN	C-N	-6.00	1.25	1.33
1	A	607	GLY	C-N	-5.88	1.24	1.33
1	A	118	PHE	C-N	5.76	1.41	1.33
1	A	344	GLY	C-N	5.60	1.41	1.33
1	A	25	THR	C-N	-5.59	1.25	1.33
1	A	24	ASP	C-N	-5.43	1.24	1.33
1	A	606	ASN	C-N	5.22	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	190	ARG	C-N	5.05	1.44	1.33

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	344	GLY	CA-C-N	-9.00	107.41	122.89
1	A	344	GLY	C-N-CA	-9.00	107.41	122.89
1	A	369	TYR	O-C-N	-8.49	114.80	123.29
1	A	122	VAL	N-CA-C	7.46	119.35	108.53
1	A	26	THR	N-CA-C	-7.15	104.43	113.72
1	A	357	SER	N-CA-C	-7.04	105.22	113.88
1	A	123	ILE	N-CA-C	-6.81	100.81	107.55
1	A	531	ALA	N-CA-C	6.69	120.37	109.59
1	A	188	ALA	CA-C-N	-6.59	113.08	123.23
1	A	188	ALA	C-N-CA	-6.59	113.08	123.23
1	A	343	VAL	O-C-N	-6.35	116.00	122.54
1	A	548	LEU	N-CA-C	-6.16	99.23	109.46
1	A	532	SER	O-C-N	-6.12	114.83	122.73
1	A	362	LEU	N-CA-C	-5.97	104.70	112.23
1	A	345	SER	CB-CA-C	-5.96	109.69	116.54
1	A	370	ALA	CA-C-N	-5.88	112.31	121.02
1	A	370	ALA	C-N-CA	-5.88	112.31	121.02
1	A	476	LEU	N-CA-C	5.87	118.39	110.88
1	A	321	GLY	N-CA-C	-5.80	103.73	112.89
1	A	456	GLN	O-C-N	-5.75	114.66	122.19
1	A	627	PHE	N-CA-C	-5.71	102.03	110.48
1	A	42	PHE	N-CA-C	5.58	117.81	111.11
1	A	581	GLU	CA-C-N	-5.57	115.56	123.03
1	A	581	GLU	C-N-CA	-5.57	115.56	123.03
1	A	371	ALA	O-C-N	-5.55	115.63	123.01
1	A	227	LYS	N-CA-C	5.51	118.00	111.33
1	A	618	TRP	N-CA-C	5.38	119.84	112.68
1	A	528	GLU	N-CA-C	-5.37	100.15	108.90
1	A	83	GLY	N-CA-C	5.31	118.22	111.85
1	A	469	ARG	N-CA-C	5.25	117.69	111.33
1	A	299	LEU	N-CA-C	5.25	118.62	110.17
1	A	556	SER	N-CA-C	5.22	116.91	108.41
1	A	177	ILE	N-CA-C	-5.16	98.63	106.42
1	A	46	ARG	N-CA-C	5.13	117.05	109.50
1	A	592	LEU	N-CA-C	5.11	118.44	110.32
1	A	495	VAL	N-CA-C	5.05	113.49	107.73
1	A	64	HIS	O-C-N	-5.01	117.09	123.01

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	344	GLY	Mainchain

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	4883	0	4610	97	0
2	B	45	0	41	3	0
3	A	219	0	0	1	0
All	All	5147	0	4651	97	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 10.

All (97) 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:295:ASN:HD21	1:A:373:GLY:H	1.16	0.91
1:A:61:PRO:O	1:A:372:ALA:HB2	1.78	0.83
1:A:591:ASP:H	1:A:606:ASN:HD21	1.20	0.83
1:A:33:LEU:H	1:A:562:ASN:HD21	1.29	0.81
1:A:61:PRO:O	1:A:372:ALA:CB	2.29	0.80
1:A:606:ASN:HD22	1:A:606:ASN:N	1.82	0.77
1:A:454:ASP:HB2	1:A:456:GLN:NE2	2.03	0.73
1:A:295:ASN:ND2	1:A:373:GLY:H	1.86	0.73
1:A:591:ASP:H	1:A:606:ASN:ND2	1.85	0.73
1:A:606:ASN:HD22	1:A:606:ASN:H	1.40	0.67
1:A:213:ASN:ND2	1:A:216:ALA:H	1.93	0.67
1:A:50:HIS:ND1	1:A:597:ASP:OD2	2.25	0.67
1:A:439:GLU:H	1:A:439:GLU:CD	2.03	0.66
1:A:202:VAL:O	1:A:206:LEU:HG	1.96	0.65
1:A:545:ASN:O	1:A:546:GLU:C	2.37	0.65
1:A:162:ARG:HG3	1:A:169:ASP:OD2	1.96	0.65
1:A:60:ASP:OD2	2:B:4:FRU:H11	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:ALA:HA	1:A:219:GLN:OE1	1.97	0.64
1:A:454:ASP:CB	1:A:456:GLN:NE2	2.64	0.61
1:A:523:LEU:C	1:A:523:LEU:HD23	2.25	0.61
1:A:453:SER:HB2	1:A:458:ALA:HB2	1.83	0.60
1:A:475:LEU:HD22	1:A:646:LEU:HD22	1.84	0.60
1:A:33:LEU:H	1:A:562:ASN:ND2	1.97	0.60
1:A:556:SER:HB2	1:A:616:ARG:O	2.02	0.59
1:A:454:ASP:HB2	1:A:456:GLN:HE21	1.66	0.59
1:A:297:LEU:HD12	1:A:297:LEU:N	2.17	0.58
1:A:591:ASP:N	1:A:606:ASN:HD21	1.97	0.58
1:A:454:ASP:OD2	1:A:456:GLN:NE2	2.37	0.58
1:A:523:LEU:HD23	1:A:524:GLN:N	2.19	0.57
1:A:454:ASP:CB	1:A:456:GLN:HE21	2.18	0.57
1:A:531:ALA:O	1:A:624:GLN:HB2	2.05	0.57
1:A:320:SER:HA	1:A:330:SER:OG	2.05	0.57
1:A:295:ASN:HB2	1:A:314:THR:OG1	2.05	0.56
1:A:386:SER:OG	1:A:388:VAL:HG23	2.06	0.56
1:A:154:GLU:OE2	1:A:190:ARG:HD3	2.05	0.55
1:A:344:GLY:O	1:A:345:SER:C	2.49	0.54
1:A:582:ASN:C	1:A:584:GLN:N	2.62	0.54
1:A:454:ASP:HB2	1:A:456:GLN:HG3	1.90	0.53
1:A:60:ASP:CG	2:B:4:FRU:H11	2.34	0.53
1:A:343:VAL:O	1:A:345:SER:N	2.41	0.53
1:A:315:LEU:N	1:A:315:LEU:HD23	2.24	0.52
1:A:582:ASN:C	1:A:584:GLN:H	2.17	0.52
1:A:244:PRO:HB2	1:A:291:PHE:CD1	2.44	0.52
1:A:57:GLN:HB2	1:A:418:THR:HB	1.92	0.52
1:A:452:GLU:O	1:A:458:ALA:HB1	2.09	0.52
1:A:311:VAL:HG21	1:A:341:VAL:HG23	1.93	0.51
1:A:456:GLN:NE2	1:A:457:THR:H	2.08	0.51
1:A:251:GLN:OE1	1:A:256:ALA:HA	2.10	0.51
1:A:295:ASN:HD21	1:A:373:GLY:N	1.96	0.51
1:A:277:TRP:HB3	1:A:284:ALA:HB3	1.93	0.51
1:A:296:VAL:C	1:A:297:LEU:HD12	2.37	0.50
1:A:297:LEU:N	1:A:297:LEU:CD1	2.76	0.49
1:A:454:ASP:CG	1:A:456:GLN:NE2	2.70	0.49
1:A:175:PRO:HG2	1:A:178:ALA:HB2	1.94	0.48
1:A:213:ASN:HD21	1:A:216:ALA:HB2	1.78	0.48
1:A:239:VAL:HB	1:A:242:VAL:HB	1.95	0.47
1:A:454:ASP:HB2	1:A:456:GLN:CG	2.44	0.47
1:A:606:ASN:N	1:A:606:ASN:ND2	2.54	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:606:ASN:C	1:A:608:ARG:H	2.22	0.47
1:A:45:TRP:CE2	1:A:616:ARG:HB3	2.50	0.47
1:A:118:PHE:HB2	1:A:136:THR:HB	1.97	0.47
1:A:206:LEU:CB	1:A:211:ALA:HB2	2.44	0.47
1:A:364:TRP:CE3	1:A:572:GLY:HA2	2.50	0.46
1:A:371:ALA:HB2	1:A:397:VAL:HG22	1.98	0.46
1:A:453:SER:HB2	1:A:458:ALA:CB	2.45	0.46
1:A:454:ASP:O	1:A:455:ASN:HB2	2.16	0.46
1:A:199:ARG:HH12	1:A:217:VAL:HG11	1.80	0.46
1:A:52:LEU:HD12	1:A:52:LEU:N	2.32	0.46
1:A:454:ASP:HB2	1:A:456:GLN:CD	2.41	0.46
1:A:432:VAL:HB	1:A:460:LEU:HB2	1.98	0.45
1:A:437:ASP:OD2	1:A:442:ARG:NH2	2.33	0.45
1:A:284:ALA:O	1:A:285:GLY:C	2.60	0.45
1:A:423:LEU:O	1:A:425:ARG:HG3	2.17	0.45
1:A:538:ALA:HB3	1:A:551:ASP:HB3	1.99	0.45
1:A:522:PRO:HB2	1:A:632:GLU:HG3	1.99	0.45
1:A:312:PHE:CE1	1:A:338:ALA:HB2	2.51	0.45
1:A:143:ILE:O	2:B:3:FRU:H61	2.17	0.44
1:A:65:TYR:HB3	1:A:122:VAL:HB	2.00	0.44
1:A:606:ASN:C	1:A:608:ARG:N	2.75	0.44
1:A:50:HIS:NE2	1:A:602:GLU:OE2	2.50	0.44
1:A:453:SER:CB	1:A:458:ALA:HB2	2.46	0.44
1:A:32:ASN:ND2	1:A:35:THR:HG23	2.33	0.44
1:A:300:THR:O	1:A:429:VAL:HB	2.17	0.44
1:A:250:ARG:O	1:A:251:GLN:C	2.62	0.43
1:A:523:LEU:HD21	1:A:525:SER:OG	2.19	0.43
1:A:197:SER:HB2	1:A:298:PHE:CZ	2.55	0.42
1:A:199:ARG:HH11	1:A:199:ARG:HG3	1.85	0.42
1:A:108:PRO:HB3	1:A:116:ALA:HA	2.01	0.42
1:A:454:ASP:C	1:A:456:GLN:H	2.27	0.42
1:A:526:GLY:HA3	1:A:539:ILE:O	2.20	0.42
1:A:213:ASN:HD22	1:A:215:THR:HB	1.84	0.41
1:A:128:ASN:O	1:A:130:THR:HG23	2.20	0.41
1:A:467:ILE:O	1:A:468:ALA:C	2.64	0.41
1:A:264:TYR:CZ	1:A:266:GLY:HA2	2.56	0.41
1:A:199:ARG:NH1	1:A:217:VAL:HG11	2.36	0.40
1:A:208:GLU:HG3	1:A:209:GLU:OE1	2.22	0.40
1:A:188:ALA:HB2	3:A:736:HOH:O	2.21	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	632/634 (100%)	600 (95%)	31 (5%)	1 (0%)	43	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	607	GLY

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	516/516 (100%)	504 (98%)	12 (2%)	44	51

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	LEU
1	A	57	GLN
1	A	181	PRO
1	A	209	GLU
1	A	228	ASN
1	A	297	LEU
1	A	346	GLU
1	A	347	GLN
1	A	427	LEU
1	A	456	GLN

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Mol	Chain	Res	Type
1	A	476	LEU
1	A	606	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	39	ASN
1	A	156	GLN
1	A	213	ASN
1	A	295	ASN
1	A	434	ASN
1	A	456	GLN
1	A	562	ASN
1	A	586	GLN
1	A	606	ASN
1	A	639	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 ⓘ

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	GLC	B	1	2	11,11,12	2.01	4 (36%)	15,15,17	1.01	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FRU	B	2	2	11,12,12	2.01	3 (27%)	10,18,18	1.80	1 (10%)
2	FRU	B	3	2	11,11,12	1.16	2 (18%)	15,15,18	3.38	4 (26%)
2	FRU	B	4	2	11,11,12	1.15	1 (9%)	15,15,18	1.10	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	GLC	B	1	2	-	0/2/19/22	0/1/1/1
2	FRU	B	2	2	-	2/5/24/24	0/1/1/1
2	FRU	B	3	2	-	4/4/20/24	0/1/1/1
2	FRU	B	4	2	-	0/4/20/24	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	FRU	O2-C2	5.07	1.49	1.40
2	B	1	GLC	O5-C1	3.18	1.49	1.43
2	B	1	GLC	C1-C2	3.15	1.59	1.52
2	B	1	GLC	O5-C5	3.00	1.49	1.43
2	B	2	FRU	C1-C2	2.47	1.58	1.52
2	B	4	FRU	C4-C3	2.45	1.60	1.53
2	B	1	GLC	C2-C3	2.43	1.56	1.52
2	B	3	FRU	O1-C1	2.39	1.52	1.42
2	B	2	FRU	O5-C5	2.09	1.48	1.43
2	B	3	FRU	C4-C5	2.04	1.58	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3	FRU	O1-C1-C2	9.85	144.86	111.33
2	B	3	FRU	O6-C6-C5	7.08	135.45	111.33
2	B	2	FRU	O2-C2-O5	4.20	117.40	109.33
2	B	3	FRU	C6-C5-C4	-3.54	106.74	115.10
2	B	3	FRU	C1-C2-C3	-2.69	108.74	115.10
2	B	4	FRU	C6-C5-C4	-2.57	109.04	115.10
2	B	1	GLC	C1-C2-C3	-2.38	106.18	109.64

There are no chirality outliers.

All (6) torsion outliers are listed below:

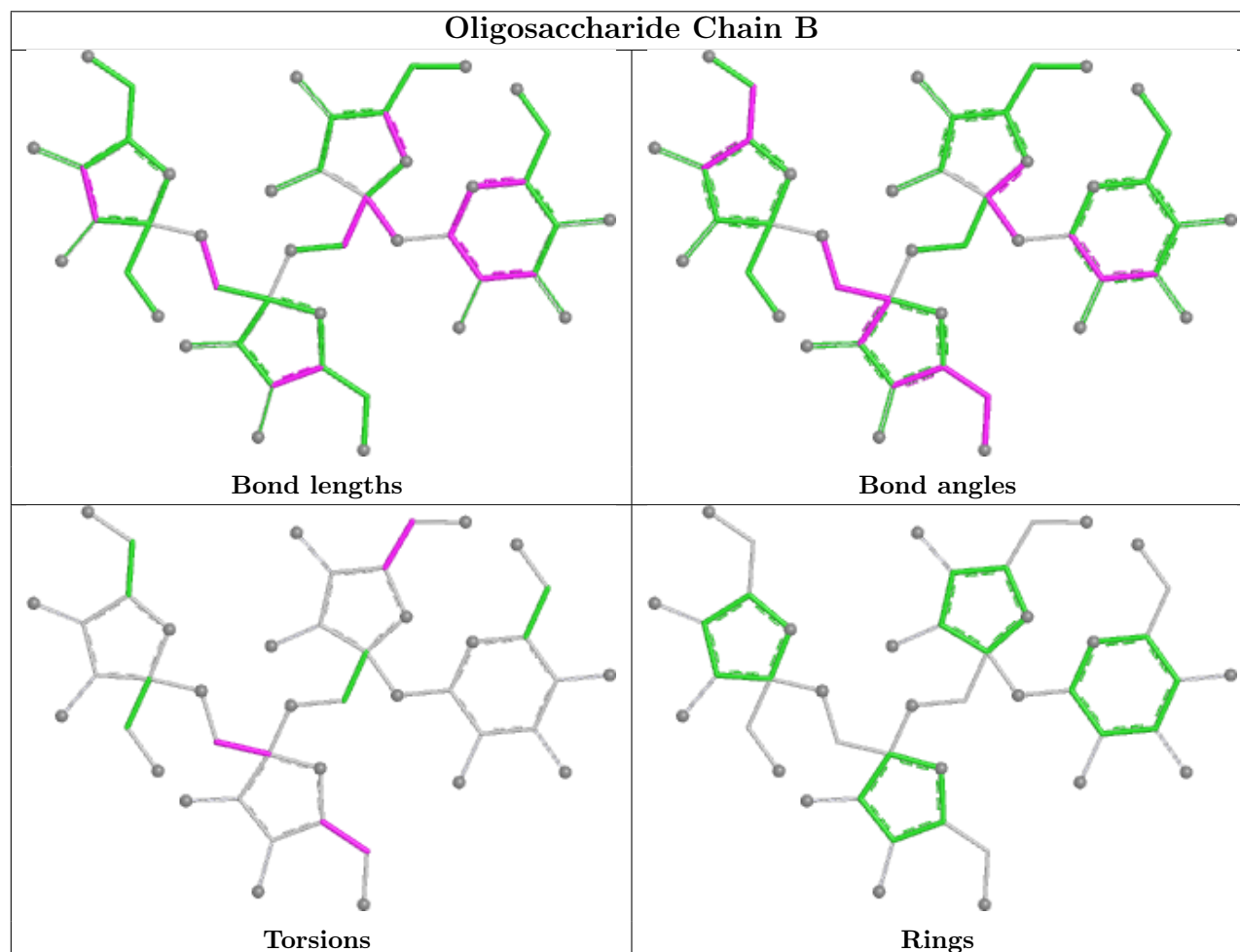
Mol	Chain	Res	Type	Atoms
2	B	3	FRU	O1-C1-C2-C3
2	B	2	FRU	O5-C5-C6-O6
2	B	3	FRU	O1-C1-C2-O5
2	B	2	FRU	C4-C5-C6-O6
2	B	3	FRU	O5-C5-C6-O6
2	B	3	FRU	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	4	FRU	2	0
2	B	3	FRU	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

There are no ligands in this entry.

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	634/634 (100%)	0.52	50 (7%)	18 20	20, 36, 66, 97	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	345	SER	7.0
1	A	206	LEU	6.6
1	A	210	VAL	5.4
1	A	164	GLY	4.9
1	A	211	ALA	4.5
1	A	476	LEU	4.1
1	A	21	TYR	3.9
1	A	455	ASN	3.6
1	A	20	SER	3.6
1	A	294	GLY	3.4
1	A	607	GLY	3.1
1	A	348	GLU	3.0
1	A	440	LEU	3.0
1	A	228	ASN	3.0
1	A	207	ASP	2.9
1	A	66	THR	2.8
1	A	347	GLN	2.8
1	A	349	GLY	2.7
1	A	281	GLY	2.7
1	A	456	GLN	2.7
1	A	163	ASP	2.7
1	A	212	ARG	2.6
1	A	480	SER	2.6
1	A	221	VAL	2.5
1	A	220	ALA	2.5
1	A	205	SER	2.5
1	A	344	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	370	ALA	2.5
1	A	453	SER	2.5
1	A	242	VAL	2.4
1	A	343	VAL	2.4
1	A	213	ASN	2.4
1	A	214	GLU	2.4
1	A	219	GLN	2.4
1	A	452	GLU	2.4
1	A	218	GLN	2.3
1	A	621	ASN	2.3
1	A	225	THR	2.3
1	A	216	ALA	2.3
1	A	65	TYR	2.3
1	A	279	ASP	2.2
1	A	444	GLU	2.2
1	A	583	GLY	2.2
1	A	518	ALA	2.2
1	A	439	GLU	2.2
1	A	477	ALA	2.2
1	A	441	VAL	2.1
1	A	438	ASN	2.1
1	A	340	GLU	2.1
1	A	582	ASN	2.1

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

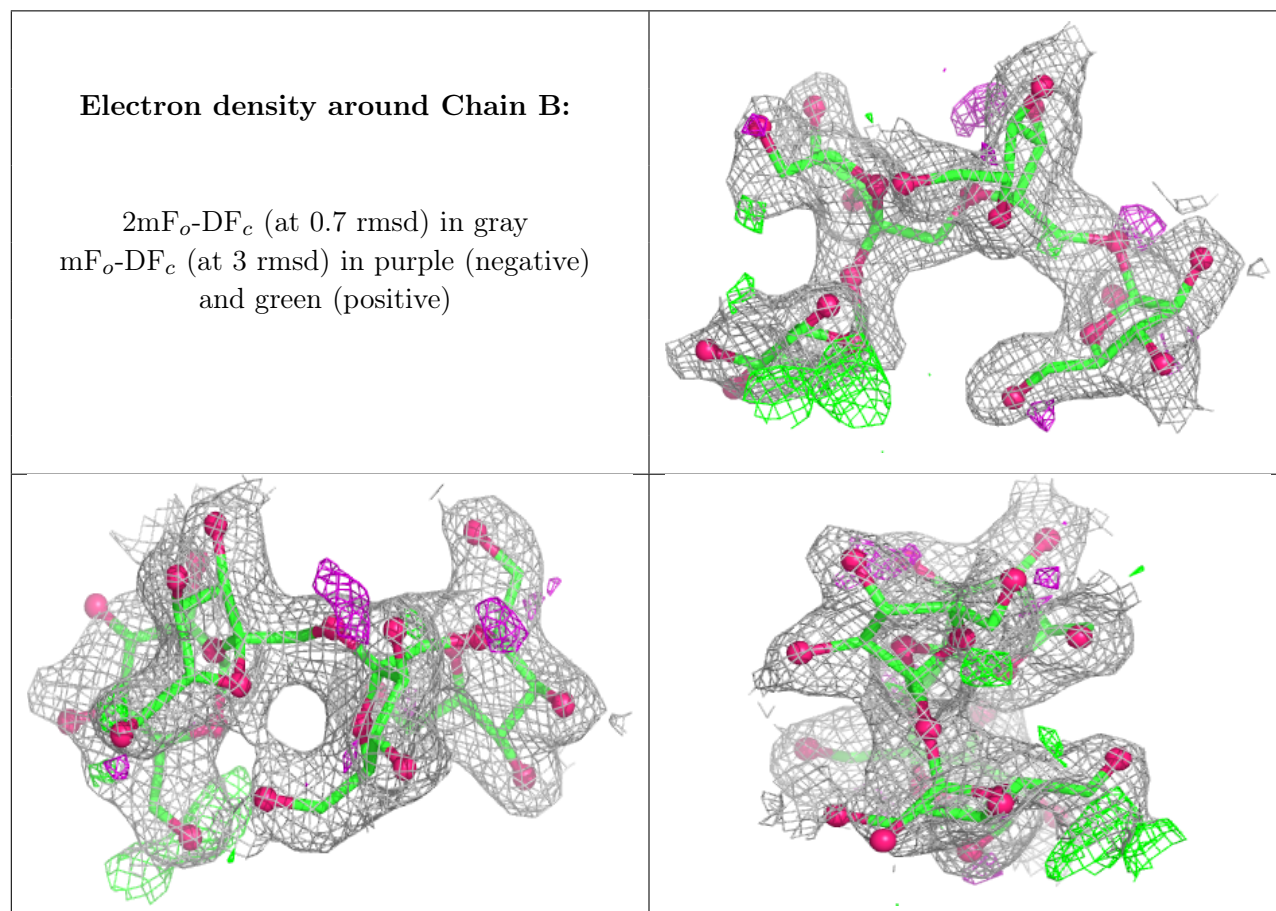
There are no non-standard protein/DNA/RNA residues in this entry.

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	GLC	B	1	11/12	0.57	0.19	58,61,62,63	0
2	FRU	B	3	11/12	0.80	0.14	33,36,40,47	0
2	FRU	B	2	12/12	0.83	0.11	38,47,50,53	0
2	FRU	B	4	11/12	0.89	0.10	34,37,38,40	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.