



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:14 PM UTC

PDB ID : 2R68 / pdb_00002r68
Title : Complex Structure of Sucrose Phosphate Synthase (SPS)-S6P of *Halothermothrix orenii*
Authors : Sivaraman, J.; Chua, T.K.
Deposited on : 2007-09-05
Resolution : 2.40 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

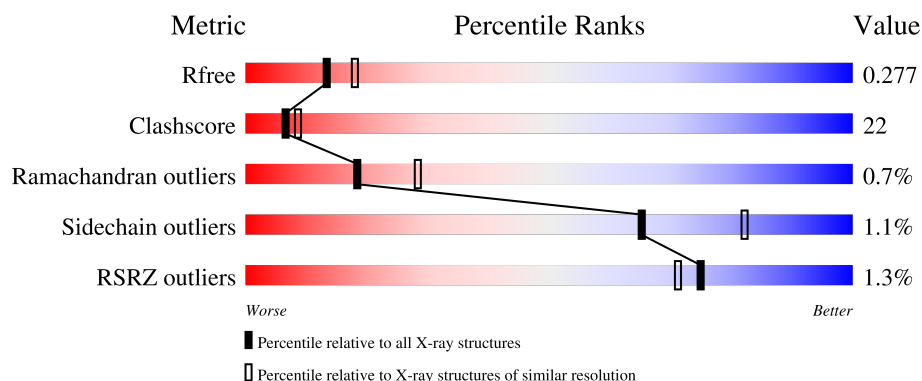
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	499	% 58% 31% • 9%
2	B	2	50% 50%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GLC	B	1	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3931 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.

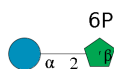
- Molecule 1 is a protein called Glycosyl transferase, group 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	456	Total	C	N	O	S	0	0	0
			3611	2300	609	693	9			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	SEE REMARK 999	UNP Q2ADF5
A	2	VAL	-	SEE REMARK 999	UNP Q2ADF5
A	3	GLU	-	SEE REMARK 999	UNP Q2ADF5

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	O	P	0	0	0
			27	12	14	1			

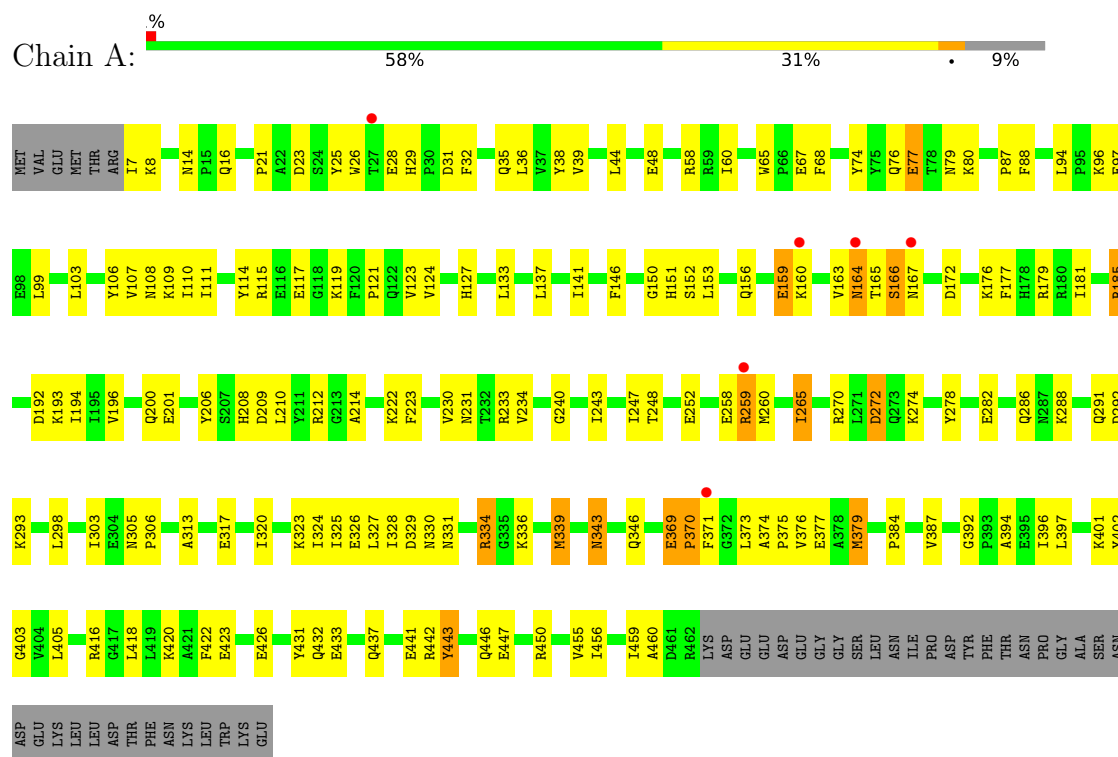
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	293	Total	O	0	0
			293	293		

3 Residue-property plots

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: Glycosyl transferase, group 1



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



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	155.40Å 48.19Å 75.01Å 90.00° 101.21° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40 20.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	92.3 (20.00-2.40) 97.6 (20.00-2.40)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.54 (at 2.27Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.209 , 0.268 0.222 , 0.277	Depositor DCC
R_{free} test set	2547 reflections (9.85%)	wwPDB-VP
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.549	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 84.4	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	0.93	EDS
Total number of atoms	3931	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.92% 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: GLC, F6P

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	0.47	2/3692 (0.1%)	0.97	18/4988 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	379	MET	SD-CE	-12.38	1.48	1.79
1	A	339	MET	SD-CE	-6.11	1.64	1.79

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	77	GLU	N-CA-C	7.29	119.86	111.11
1	A	334	ARG	N-CA-C	-6.74	100.46	110.23
1	A	166	SER	N-CA-C	-6.69	104.06	111.36
1	A	387	VAL	N-CA-C	6.23	119.23	108.95
1	A	443	TYR	N-CA-C	6.13	120.07	112.59
1	A	265	ILE	N-CA-C	-5.60	98.38	107.28
1	A	431	TYR	O-C-N	-5.55	116.24	122.12
1	A	292	ASP	N-CA-C	-5.54	106.02	112.89
1	A	442	ARG	N-CA-C	5.47	121.64	114.75
1	A	369	GLU	CA-C-N	5.27	126.43	119.84
1	A	369	GLU	C-N-CA	5.27	126.43	119.84
1	A	172	ASP	N-CA-C	-5.22	106.75	113.01
1	A	65	TRP	CA-C-N	5.17	124.84	119.56
1	A	65	TRP	C-N-CA	5.17	124.84	119.56
1	A	432	GLN	CA-C-N	-5.11	113.80	120.44
1	A	432	GLN	C-N-CA	-5.11	113.80	120.44
1	A	460	ALA	N-CA-C	-5.08	105.39	112.45
1	A	384	PRO	N-CA-C	-5.05	103.26	111.19

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	3611	0	3495	154	0
2	B	27	0	20	4	0
3	A	293	0	0	22	0
All	All	3931	0	3515	155	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 22.

All (155) 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:123:VAL:HG21	1:A:456:ILE:HG23	1.33	1.11
1:A:185:ARG:HB3	1:A:185:ARG:HH11	1.20	1.07
1:A:21:PRO:HG3	1:A:74:TYR:O	1.67	0.95
1:A:108:ASN:O	1:A:111:ILE:HG12	1.67	0.95
1:A:293:LYS:HD3	1:A:422:PHE:HB3	1.56	0.86
1:A:185:ARG:HB3	1:A:185:ARG:NH1	1.95	0.81
1:A:194:ILE:HD11	1:A:206:TYR:CE2	2.16	0.81
1:A:259:ARG:HH11	1:A:336:LYS:HD3	1.44	0.80
1:A:194:ILE:HG22	1:A:222:LYS:O	1.84	0.77
1:A:376:VAL:HA	1:A:379:MET:CE	2.14	0.77
1:A:230:VAL:HG12	1:A:443:TYR:O	1.87	0.74
1:A:375:PRO:C	1:A:379:MET:HE2	2.14	0.73
1:A:259:ARG:HD3	1:A:336:LYS:HD2	1.71	0.73
1:A:329:ASP:OD1	1:A:334:ARG:HD2	1.89	0.73
1:A:96:LYS:HE3	2:B:2:F6P:H61	1.71	0.72
1:A:185:ARG:HH11	1:A:185:ARG:CB	2.00	0.72
1:A:371:PHE:HA	1:A:392:GLY:HA3	1.71	0.72
1:A:29:HIS:CD2	1:A:31:ASP:H	2.06	0.72
1:A:298:LEU:HB2	1:A:339:MET:HG2	1.73	0.71
1:A:374:ALA:HB3	1:A:375:PRO:HD3	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:437:GLN:O	1:A:441:GLU:HG3	1.91	0.70
1:A:258:GLU:HG2	1:A:259:ARG:HE	1.57	0.69
1:A:373:LEU:O	1:A:377:GLU:HG3	1.91	0.69
1:A:252:GLU:HG2	1:A:260:MET:HE2	1.75	0.69
1:A:48:GLU:HG3	1:A:446:GLN:HE22	1.58	0.69
1:A:243:ILE:O	1:A:247:ILE:HG12	1.92	0.69
1:A:370:PRO:O	1:A:371:PHE:HB3	1.91	0.69
1:A:123:VAL:HG21	1:A:456:ILE:CG2	2.20	0.68
1:A:14:ASN:HD21	1:A:35:GLN:HE21	1.39	0.68
1:A:16:GLN:HG2	3:A:986:HOH:O	1.93	0.67
1:A:123:VAL:CG2	1:A:456:ILE:HG23	2.18	0.67
1:A:323:LYS:O	1:A:327:LEU:HD13	1.95	0.66
1:A:324:ILE:HG22	3:A:956:HOH:O	1.95	0.65
1:A:233:ARG:HG3	3:A:972:HOH:O	1.97	0.64
1:A:376:VAL:HA	1:A:379:MET:HE3	1.78	0.64
1:A:14:ASN:ND2	1:A:35:GLN:HE21	1.97	0.63
1:A:272:ASP:OD2	1:A:274:LYS:HB2	1.99	0.62
1:A:317:GLU:HG3	3:A:1200:HOH:O	1.99	0.61
1:A:32:PHE:HB2	3:A:1095:HOH:O	2.01	0.61
1:A:23:ASP:HB3	1:A:26:TRP:CE2	2.36	0.60
1:A:259:ARG:HD3	1:A:336:LYS:CD	2.30	0.60
1:A:103:LEU:HD12	1:A:133:LEU:HD23	1.83	0.60
1:A:248:THR:O	1:A:252:GLU:HG3	2.01	0.59
1:A:416:ARG:HD2	3:A:1028:HOH:O	2.00	0.59
1:A:288:LYS:HG2	3:A:1097:HOH:O	2.04	0.58
1:A:107:VAL:HG21	1:A:137:LEU:HB2	1.86	0.57
1:A:376:VAL:HA	1:A:379:MET:HE2	1.85	0.57
1:A:16:GLN:NE2	2:B:2:F6P:O4	2.36	0.57
1:A:164:ASN:C	1:A:166:SER:H	2.12	0.57
1:A:153:LEU:HB2	1:A:156:GLN:OE1	2.05	0.57
1:A:209:ASP:O	1:A:212:ARG:HG2	2.05	0.57
1:A:375:PRO:O	1:A:379:MET:HG3	2.05	0.57
1:A:32:PHE:HA	1:A:36:LEU:HD11	1.86	0.56
1:A:265:ILE:HD13	1:A:418:LEU:HD13	1.86	0.56
1:A:376:VAL:N	1:A:379:MET:HE2	2.20	0.56
1:A:185:ARG:NH1	1:A:214:ALA:HB2	2.21	0.56
1:A:288:LYS:HA	1:A:291:GLN:HG2	1.88	0.56
1:A:156:GLN:O	1:A:159:GLU:HB2	2.06	0.56
1:A:193:LYS:HG3	1:A:455:VAL:HG13	1.86	0.55
1:A:194:ILE:HG23	1:A:223:PHE:CD1	2.42	0.55
1:A:29:HIS:HD2	1:A:31:ASP:H	1.50	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:TYR:O	1:A:110:ILE:HG13	2.07	0.55
1:A:177:PHE:O	1:A:181:ILE:HG12	2.07	0.54
1:A:303:ILE:HD11	1:A:313:ALA:HB2	1.89	0.54
1:A:200:GLN:HG3	3:A:993:HOH:O	2.08	0.54
1:A:455:VAL:O	1:A:459:ILE:HG23	2.08	0.54
1:A:181:ILE:O	1:A:185:ARG:HG3	2.06	0.54
1:A:222:LYS:HE2	3:A:1027:HOH:O	2.06	0.54
1:A:67:GLU:OE1	1:A:67:GLU:N	2.37	0.53
1:A:77:GLU:OE1	1:A:77:GLU:N	2.34	0.53
1:A:96:LYS:HG3	1:A:97:GLU:OE1	2.09	0.53
1:A:44:LEU:HD13	1:A:233:ARG:HH21	1.74	0.53
1:A:313:ALA:HB1	1:A:317:GLU:HB2	1.90	0.53
1:A:233:ARG:HH11	1:A:233:ARG:HG2	1.74	0.53
1:A:339:MET:HE1	3:A:956:HOH:O	2.08	0.52
3:A:945:HOH:O	2:B:2:F6P:H62	2.09	0.52
1:A:60:ILE:HB	1:A:68:PHE:HB2	1.92	0.52
1:A:193:LYS:HE2	3:A:1130:HOH:O	2.09	0.52
1:A:124:VAL:O	1:A:146:PHE:HA	2.10	0.51
1:A:164:ASN:O	1:A:166:SER:N	2.43	0.51
1:A:176:LYS:N	1:A:176:LYS:HD2	2.26	0.50
1:A:233:ARG:HG2	1:A:233:ARG:NH1	2.27	0.50
1:A:150:GLY:C	1:A:152:SER:H	2.20	0.50
1:A:376:VAL:CA	1:A:379:MET:HE2	2.42	0.50
1:A:320:ILE:O	1:A:324:ILE:HG13	2.11	0.49
1:A:196:VAL:HB	1:A:201:GLU:HB3	1.95	0.49
1:A:179:ARG:HG3	3:A:1050:HOH:O	2.13	0.49
1:A:259:ARG:NH1	1:A:336:LYS:HD3	2.20	0.48
1:A:371:PHE:CA	1:A:392:GLY:HA3	2.41	0.48
1:A:394:ALA:HB3	3:A:1159:HOH:O	2.13	0.48
1:A:326:GLU:HG2	1:A:330:ASN:HD21	1.79	0.48
1:A:433:GLU:O	1:A:437:GLN:HG3	2.12	0.48
1:A:107:VAL:O	1:A:111:ILE:HG23	2.14	0.48
1:A:258:GLU:HG2	1:A:259:ARG:NE	2.25	0.47
1:A:44:LEU:HD13	1:A:233:ARG:NH2	2.29	0.47
1:A:14:ASN:HD22	1:A:39:VAL:HG21	1.80	0.47
1:A:58:ARG:NH2	1:A:94:LEU:N	2.63	0.47
1:A:115:ARG:HD3	3:A:1148:HOH:O	2.14	0.47
1:A:150:GLY:O	1:A:151:HIS:HB2	2.14	0.47
1:A:14:ASN:ND2	1:A:39:VAL:HG21	2.30	0.47
1:A:343:ASN:ND2	1:A:343:ASN:N	2.60	0.47
1:A:127:HIS:HB3	1:A:151:HIS:CD2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:LEU:HD13	1:A:403:GLY:HA3	1.97	0.46
1:A:231:ASN:OD1	1:A:234:VAL:HG23	2.15	0.46
1:A:293:LYS:HD3	1:A:422:PHE:CB	2.38	0.46
1:A:79:ASN:OD1	1:A:80:LYS:HD2	2.15	0.46
1:A:240:GLY:O	1:A:243:ILE:HG22	2.16	0.46
1:A:208:HIS:CE1	1:A:210:LEU:HD12	2.51	0.45
1:A:423:GLU:HA	3:A:978:HOH:O	2.16	0.45
1:A:194:ILE:HD11	1:A:206:TYR:HE2	1.78	0.45
1:A:450:ARG:HH11	1:A:450:ARG:HG3	1.80	0.45
1:A:58:ARG:HD3	1:A:88:PHE:CZ	2.52	0.44
1:A:193:LYS:HG2	3:A:1130:HOH:O	2.16	0.44
1:A:420:LYS:O	1:A:423:GLU:HG2	2.17	0.44
1:A:194:ILE:CD1	1:A:206:TYR:CE2	2.94	0.44
1:A:282:GLU:O	1:A:286:GLN:HG3	2.18	0.44
1:A:32:PHE:HA	1:A:36:LEU:CD1	2.47	0.44
1:A:87:PRO:O	1:A:109:LYS:HD2	2.16	0.44
1:A:117:GLU:HB3	1:A:119:LYS:HG2	1.99	0.44
1:A:447:GLU:HB2	3:A:1212:HOH:O	2.18	0.43
1:A:379:MET:HE1	1:A:396:ILE:CG2	2.48	0.43
1:A:97:GLU:OE1	1:A:97:GLU:N	2.46	0.43
1:A:76:GLN:NE2	1:A:76:GLN:C	2.77	0.43
1:A:99:LEU:O	1:A:103:LEU:HG	2.19	0.43
1:A:278:TYR:OH	1:A:327:LEU:HD11	2.18	0.43
1:A:326:GLU:HG2	1:A:330:ASN:ND2	2.34	0.43
1:A:325:ILE:HA	3:A:956:HOH:O	2.19	0.42
1:A:163:VAL:O	1:A:165:THR:N	2.49	0.42
1:A:379:MET:HE1	1:A:396:ILE:HG21	2.02	0.42
1:A:397:LEU:HD12	1:A:405:LEU:HD23	2.02	0.42
1:A:401:LYS:HD3	1:A:402:TYR:CE2	2.55	0.42
1:A:327:LEU:O	1:A:331:ASN:ND2	2.38	0.42
1:A:25:TYR:O	1:A:28:GLU:HB2	2.20	0.42
1:A:328:ILE:HD12	3:A:956:HOH:O	2.19	0.42
1:A:194:ILE:HD11	1:A:206:TYR:CZ	2.55	0.42
1:A:397:LEU:HD13	1:A:403:GLY:CA	2.50	0.42
1:A:38:TYR:CD2	1:A:38:TYR:C	2.98	0.41
1:A:114:TYR:CD1	1:A:121:PRO:HD3	2.54	0.41
1:A:298:LEU:O	1:A:339:MET:HA	2.20	0.41
1:A:343:ASN:N	1:A:343:ASN:HD22	2.16	0.41
1:A:7:ILE:HG23	1:A:8:LYS:N	2.35	0.41
1:A:16:GLN:HE22	2:B:2:F6P:C4	2.33	0.41
1:A:426:GLU:HG3	3:A:958:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:ASP:HB3	1:A:26:TRP:CD2	2.55	0.41
1:A:167:ASN:C	3:A:1118:HOH:O	2.63	0.41
1:A:160:LYS:HD3	1:A:160:LYS:HA	1.80	0.41
1:A:192:ASP:O	1:A:193:LYS:HG2	2.21	0.41
1:A:305:ASN:HA	1:A:306:PRO:HD2	1.93	0.40
1:A:114:TYR:HB3	1:A:119:LYS:O	2.21	0.40
1:A:137:LEU:O	1:A:141:ILE:HG13	2.21	0.40
1:A:369:GLU:HA	1:A:370:PRO:HD2	1.85	0.40
1:A:346:GLN:H	1:A:346:GLN:CD	2.30	0.40
1:A:164:ASN:C	1:A:166:SER:N	2.77	0.40
1:A:270:ARG:NH1	1:A:270:ARG:HG2	2.37	0.40
1:A:278:TYR:CE1	1:A:327:LEU:HD11	2.57	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	454/499 (91%)	423 (93%)	28 (6%)	3 (1%)	18 28

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	159	GLU
1	A	164	ASN
1	A	370	PRO

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	377/428 (88%)	373 (99%)	4 (1%)	65 82

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	185	ARG
1	A	259	ARG
1	A	272	ASP
1	A	343	ASN

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	14	ASN
1	A	16	GLN
1	A	29	HIS
1	A	76	GLN
1	A	112	ASN
1	A	127	HIS
1	A	291	GLN
1	A	295	ASN
1	A	315	GLN
1	A	330	ASN
1	A	343	ASN
1	A	432	GLN
1	A	446	GLN

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

2 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	2.23	5 (45%)	15,15,17	1.26	1 (6%)
2	F6P	B	2	2	15,16,16	2.87	8 (53%)	16,25,25	2.34	5 (31%)

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	1/1/4/5	2/2/19/22	0/1/1/1
2	F6P	B	2	2	-	5/9/28/28	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	F6P	P-O6	6.81	1.81	1.60
2	B	2	F6P	C4-C5	-5.08	1.40	1.53
2	B	1	GLC	O5-C1	4.13	1.50	1.43
2	B	2	F6P	C1-C2	3.46	1.60	1.52
2	B	2	F6P	O5-C2	-3.25	1.38	1.43
2	B	1	GLC	C4-C5	3.20	1.59	1.53
2	B	1	GLC	O5-C5	2.70	1.48	1.43
2	B	1	GLC	C4-C3	2.56	1.59	1.52
2	B	2	F6P	O3-C3	2.52	1.47	1.42
2	B	2	F6P	O2-C2	2.30	1.44	1.40
2	B	1	GLC	C2-C3	2.16	1.55	1.52
2	B	2	F6P	O1-C1	2.09	1.49	1.42
2	B	2	F6P	O5-C5	2.04	1.48	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	2	F6P	O3P-P-O6	5.17	120.14	106.67
2	B	2	F6P	O4-C4-C5	-3.88	99.93	111.08
2	B	2	F6P	O6-C6-C5	3.68	121.53	108.99
2	B	2	F6P	O2-C2-O5	-3.49	102.62	109.33
2	B	2	F6P	O5-C5-C6	2.67	115.77	109.50
2	B	1	GLC	C1-O5-C5	2.29	115.25	112.19

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	1	GLC	C1

All (7) torsion outliers are listed below:

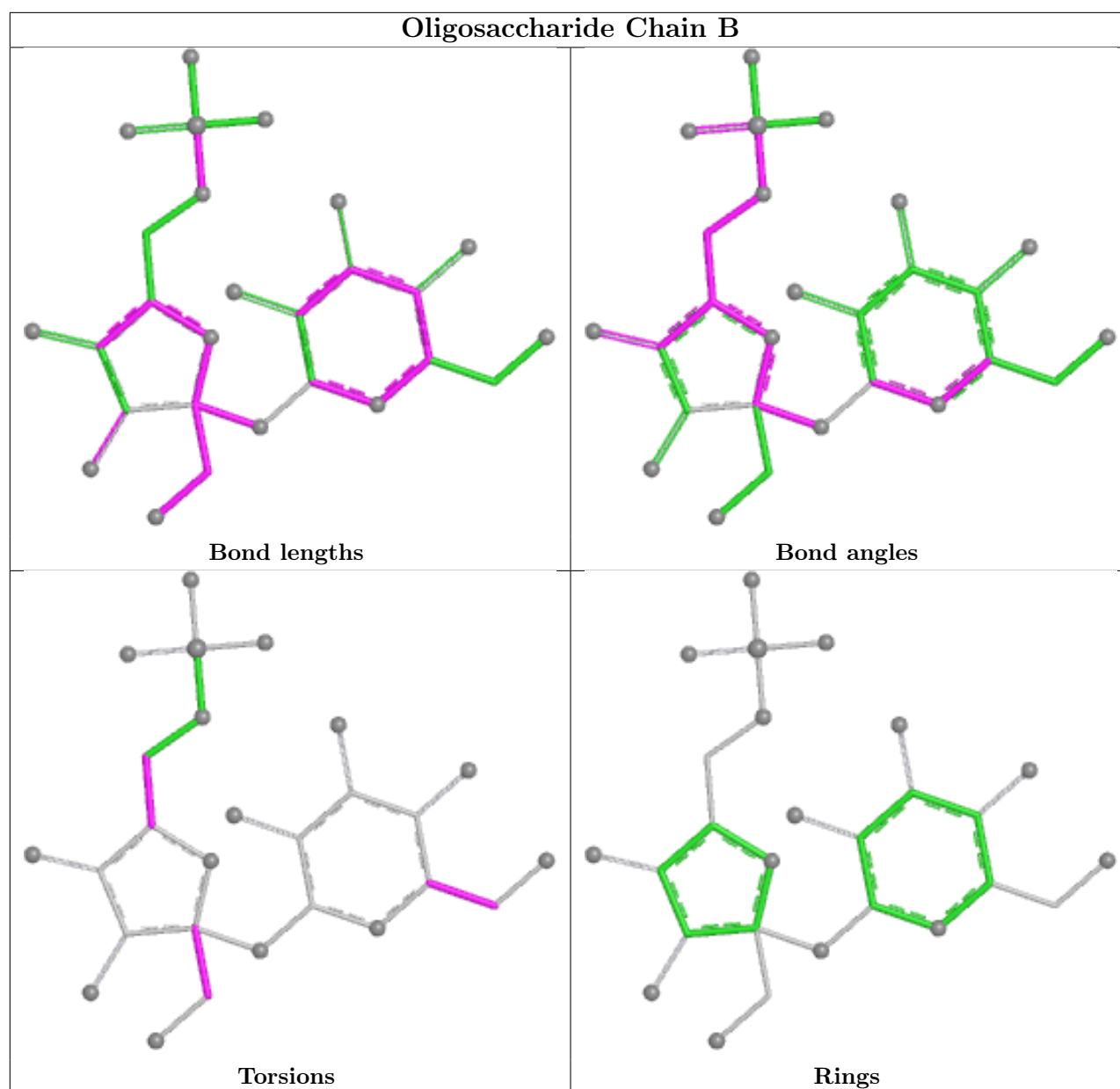
Mol	Chain	Res	Type	Atoms
2	B	2	F6P	O1-C1-C2-O2
2	B	2	F6P	O1-C1-C2-C3
2	B	2	F6P	O1-C1-C2-O5
2	B	1	GLC	O5-C5-C6-O6
2	B	2	F6P	C4-C5-C6-O6
2	B	1	GLC	C4-C5-C6-O6
2	B	2	F6P	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2	F6P	4	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](#)

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 [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	456/499 (91%)	-0.10	6 (1%) 75 71	16, 40, 70, 113	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	167	ASN	4.6
1	A	160	LYS	2.8
1	A	259	ARG	2.5
1	A	371	PHE	2.4
1	A	27	THR	2.2
1	A	164	ASN	2.0

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

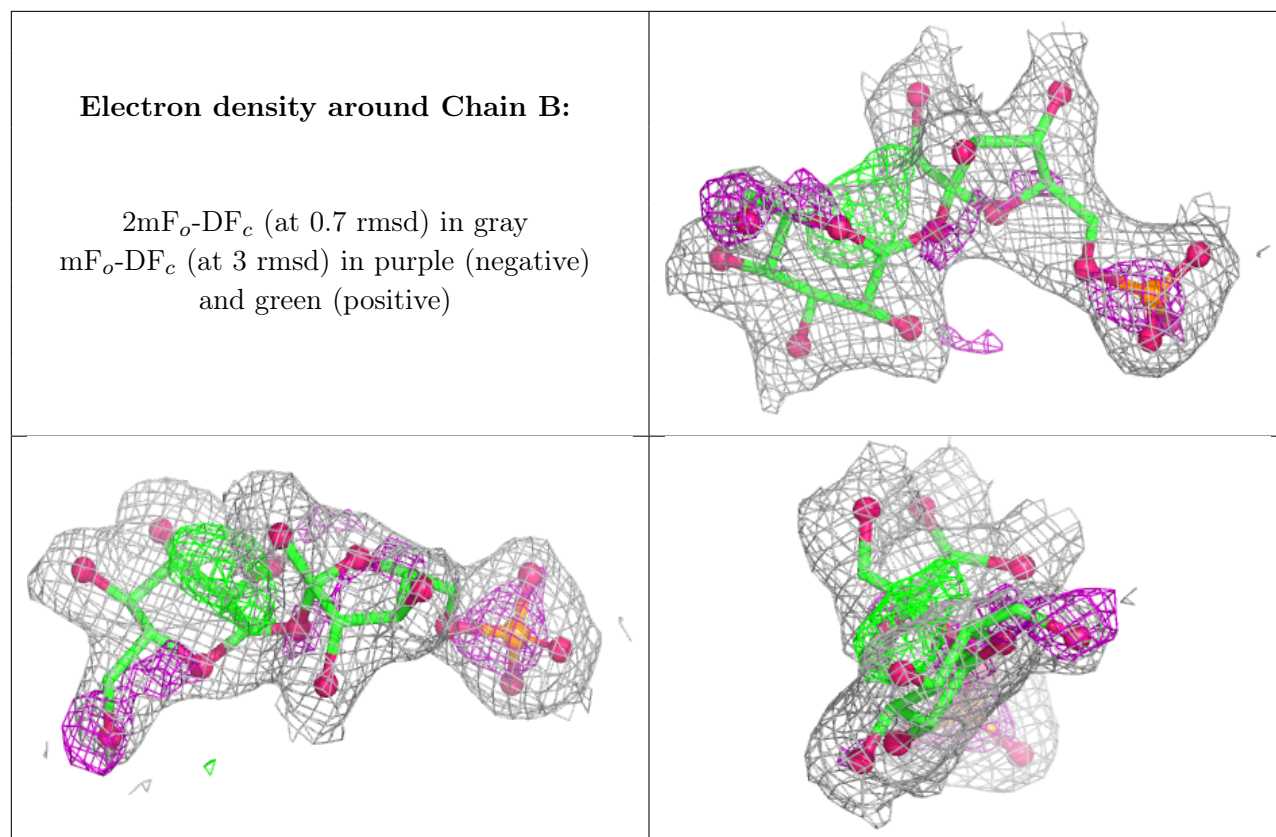
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [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	0.83	0.10	20,20,20,20	0
2	F6P	B	2	16/16	0.95	0.08	20,20,20,20	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.



6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.