Full wwPDB X-ray Structure Validation Report (i)

Nov 1, 2021 – 02:45 PM EDT

PDB ID	:	2Z1S
Title	:	Beta-glucosidase B from paenibacillus polymyxa complexed with cellotetraose
Authors	:	Isorna, P.; Sanz-Aparicio, J.
Deposited on	:	2007-05-12
Resolution	:	2.46 Å(reported)

The following versions of software and data (see references (i)) 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	:	2.23.2
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)	:	2.23.2
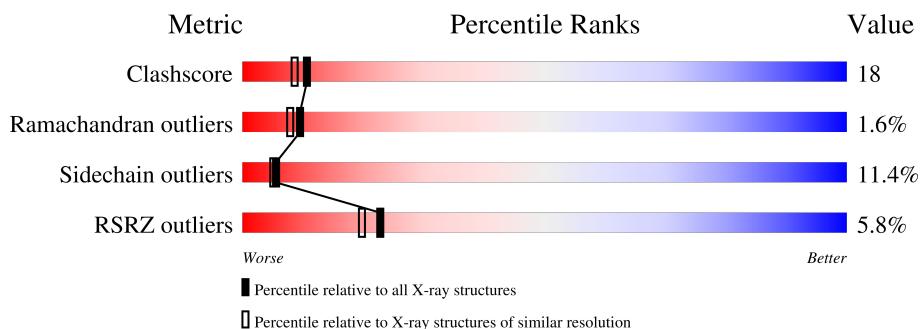
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION
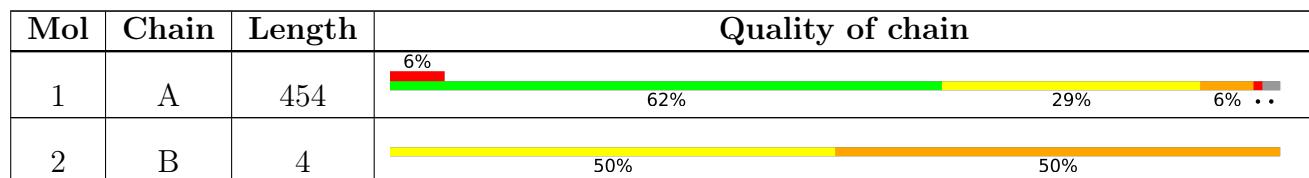
The reported resolution of this entry is 2.46 Å.

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	Percentile Ranks	Value
Clashscore		18
Ramachandran outliers		1.6%
Sidechain outliers		11.4%
RSRZ outliers		5.8%

Worse   *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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 <=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	454	6% — 62% / 29% / 6% ··
2	B	4	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	BGC	B	1	-	-	-	X
2	BGC	B	2	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BGC	B	4	-	-	X	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3793 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 Beta-glucosidase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	445	Total 3625	C 2327	N 612	O 666	S 20	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	expression tag	UNP P22505
A	-4	HIS	-	expression tag	UNP P22505
A	-3	HIS	-	expression tag	UNP P22505
A	-2	HIS	-	expression tag	UNP P22505
A	-1	HIS	-	expression tag	UNP P22505
A	0	HIS	-	expression tag	UNP P22505
A	1	HIS	-	expression tag	UNP P22505
A	376	GLN	HIS	engineered mutation	UNP P22505
A	377	ARG	GLY	engineered mutation	UNP P22505

- Molecule 2 is an oligosaccharide called beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1 -4)-beta-D-glucopyranose-(1-4)-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	B	4	Total 45	C 24	O 21	0	0	0
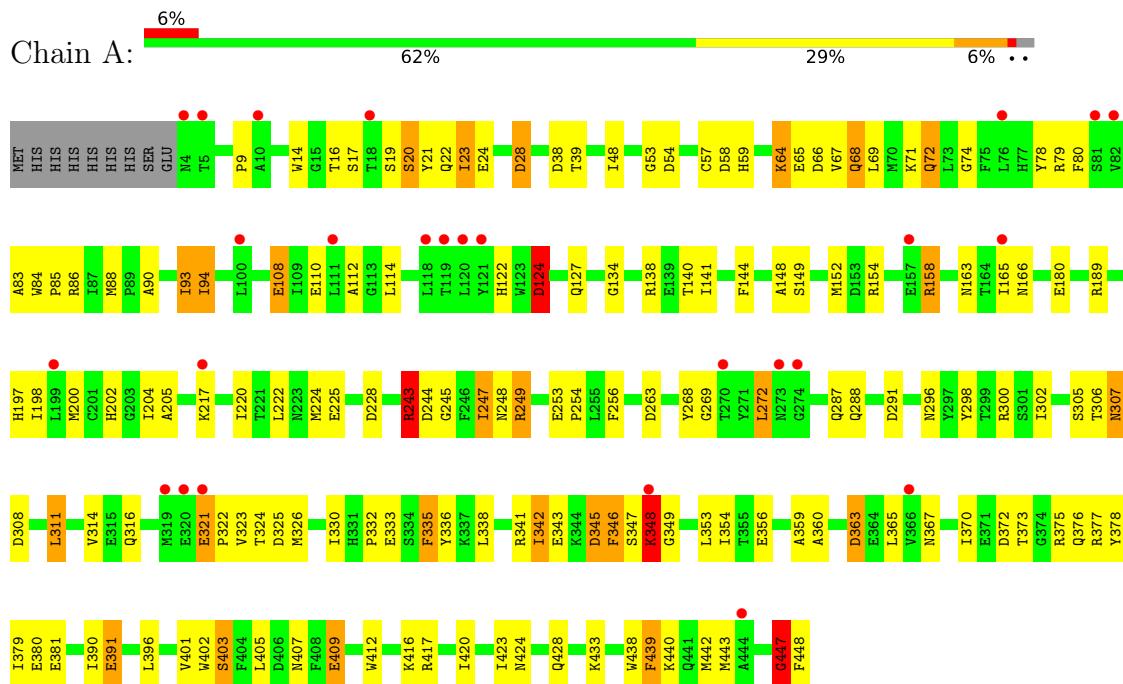
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	123	Total 123	O 123	0	0

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: Beta-glucosidase B

• Molecule 2: beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1-4)-beta-D-glucopyranose-(1-4)-beta-D-glucopyranose

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	71.32Å 75.28Å 88.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.08 – 2.46 26.08 – 2.46	Depositor EDS
% Data completeness (in resolution range)	99.2 (26.08-2.46) 99.4 (26.08-2.46)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	2.34 (at 2.44Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.215 , 0.272 0.220 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	40.4	Xtriage
Anisotropy	0.529	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 45.2	EDS
L-test for twinning[2]	$< \lvert L \rvert > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	3793	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.59% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< \lvert L \rvert >$, $< L^2 >$ 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: BGC

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	0.86	1/3736 (0.0%)	0.97	15/5066 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	349	GLY	N-CA	6.04	1.55	1.46

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	228	ASP	CB-CG-OD2	7.92	125.43	118.30
1	A	325	ASP	CB-CG-OD2	7.44	124.99	118.30
1	A	349	GLY	N-CA-C	7.19	131.08	113.10
1	A	244	ASP	CB-CG-OD2	7.13	124.72	118.30
1	A	308	ASP	CB-CG-OD2	6.66	124.30	118.30
1	A	363	ASP	CB-CG-OD2	6.09	123.78	118.30
1	A	124	ASP	CB-CG-OD2	5.99	123.69	118.30
1	A	311	LEU	CA-CB-CG	5.99	129.07	115.30
1	A	58	ASP	CB-CG-OD2	5.95	123.66	118.30
1	A	28	ASP	CB-CG-OD2	5.74	123.47	118.30
1	A	243	ARG	NE-CZ-NH1	-5.64	117.48	120.30
1	A	372	ASP	CB-CG-OD2	5.45	123.20	118.30
1	A	249	ARG	NE-CZ-NH1	5.33	122.96	120.30
1	A	447	GLY	N-CA-C	5.19	126.06	113.10
1	A	291	ASP	CB-CG-OD2	5.15	122.93	118.30

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	3625	0	3423	131	0
2	B	45	0	37	11	0
3	A	123	0	0	6	0
All	All	3793	0	3460	131	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 18.

All (131) 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:409:GLU:OE2	2:B:4:BGC:H6C1	1.45	1.16
1:A:409:GLU:OE2	2:B:4:BGC:C6	1.96	1.13
1:A:93:ILE:HD12	1:A:93:ILE:H	0.93	1.05
1:A:93:ILE:HD13	1:A:94:ILE:N	1.70	1.05
1:A:373:THR:O	1:A:377:ARG:HG3	1.58	1.03
1:A:93:ILE:HD13	1:A:94:ILE:H	1.21	1.01
1:A:321:GLU:HB3	1:A:322:PRO:HD3	1.43	0.99
1:A:93:ILE:H	1:A:93:ILE:CD1	1.75	0.99
1:A:354:ILE:HD12	1:A:396:LEU:HD11	1.46	0.97
1:A:93:ILE:HD12	1:A:93:ILE:N	1.70	0.97
1:A:321:GLU:HB3	1:A:322:PRO:CD	2.06	0.84
1:A:409:GLU:OE2	2:B:4:BGC:O6	1.96	0.83
1:A:409:GLU:CD	2:B:4:BGC:H6C1	1.98	0.83
1:A:93:ILE:CD1	1:A:94:ILE:H	1.93	0.82
1:A:48:ILE:HD12	1:A:412:TRP:HA	1.60	0.81
1:A:110:GLU:OE2	1:A:158:ARG:HD2	1.84	0.77
1:A:390:ILE:O	1:A:391:GLU:HB3	1.86	0.75
1:A:84:TRP:HE1	1:A:88:MET:CE	1.99	0.74
1:A:243:ARG:CZ	1:A:247:ILE:HD11	2.19	0.72
1:A:93:ILE:CD1	1:A:93:ILE:N	2.41	0.72
1:A:256:PHE:CD1	1:A:346:PHE:HB3	2.23	0.72
1:A:59:HIS:HD2	1:A:66:ASP:OD2	1.72	0.72
1:A:243:ARG:HH12	2:B:2:BGC:H2	1.55	0.71
1:A:93:ILE:CD1	1:A:94:ILE:N	2.50	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:GLU:O	1:A:323:VAL:HG13	1.91	0.71
1:A:110:GLU:OE2	1:A:158:ARG:CD	2.41	0.68
1:A:324:THR:HG23	1:A:330:ILE:HD11	1.76	0.68
1:A:180:GLU:OE1	2:B:2:BGC:H6C1	1.93	0.68
1:A:16:THR:HG22	1:A:401:VAL:HG13	1.76	0.67
1:A:84:TRP:HE1	1:A:88:MET:HE2	1.59	0.67
1:A:22:GLN:O	1:A:407:ASN:HB2	1.96	0.66
1:A:243:ARG:NH1	1:A:247:ILE:HD11	2.10	0.65
1:A:249:ARG:NH2	1:A:263:ASP:OD1	2.30	0.65
1:A:447:GLY:O	1:A:448:PHE:C	2.34	0.65
1:A:373:THR:HG22	1:A:377:ARG:NE	2.12	0.64
1:A:67:VAL:HG21	1:A:108:GLU:HB3	1.79	0.63
1:A:222:LEU:HD12	1:A:224:MET:CE	2.29	0.62
1:A:79:ARG:NH1	1:A:356:GLU:OE1	2.31	0.62
1:A:16:THR:HG22	1:A:401:VAL:CG1	2.31	0.60
1:A:253:GLU:HB3	1:A:254:PRO:HD3	1.81	0.60
1:A:324:THR:CG2	1:A:330:ILE:HD11	2.31	0.60
1:A:245:GLY:HA2	1:A:249:ARG:HB2	1.86	0.58
1:A:359:ALA:O	1:A:375:ARG:HD3	2.04	0.57
1:A:122:HIS:HD2	3:A:508:HOH:O	1.88	0.56
1:A:124:ASP:OD1	1:A:124:ASP:N	2.34	0.56
1:A:69:LEU:O	1:A:69:LEU:HD23	2.05	0.56
1:A:373:THR:HG22	1:A:377:ARG:HE	1.70	0.56
1:A:72:GLN:NE2	3:A:608:HOH:O	2.39	0.55
1:A:71:LYS:HD3	1:A:112:ALA:O	2.07	0.55
1:A:222:LEU:HD12	1:A:224:MET:HE1	1.89	0.55
1:A:202:HIS:HE1	1:A:288:GLN:O	1.90	0.55
1:A:14:TRP:HB3	1:A:443:MET:CE	2.37	0.55
1:A:373:THR:CG2	1:A:377:ARG:HE	2.20	0.54
1:A:316:GLN:OE1	2:B:2:BGC:O2	2.25	0.54
1:A:141:ILE:HG23	1:A:204:ILE:HG13	1.89	0.54
1:A:378:TYR:CD1	1:A:378:TYR:C	2.81	0.54
1:A:84:TRP:HE1	1:A:88:MET:HE3	1.72	0.53
1:A:74:GLY:O	1:A:443:MET:HE1	2.08	0.53
1:A:202:HIS:HB2	1:A:220:ILE:HD12	1.90	0.53
1:A:268:TYR:HB2	1:A:272:LEU:HD22	1.91	0.53
1:A:341:ARG:HD3	3:A:601:HOH:O	2.09	0.53
1:A:14:TRP:CB	1:A:443:MET:CE	2.88	0.52
1:A:326:MET:HE3	1:A:412:TRP:CD1	2.44	0.52
1:A:197:HIS:HA	1:A:200:MET:HE2	1.92	0.51
1:A:166:ASN:HD21	1:A:296:ASN:HD21	1.57	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:ILE:HG21	1:A:439:PHE:HE1	1.76	0.50
1:A:14:TRP:CB	1:A:443:MET:HE2	2.41	0.50
1:A:84:TRP:HB3	1:A:85:PRO:HD3	1.93	0.50
1:A:380:GLU:HG3	1:A:438:TRP:CZ2	2.46	0.50
1:A:14:TRP:HB2	1:A:443:MET:HE2	1.94	0.50
1:A:335:PHE:HZ	1:A:354:ILE:HG12	1.77	0.49
1:A:356:GLU:HB3	1:A:402:TRP:HB2	1.93	0.49
1:A:403:SER:OG	1:A:407:ASN:ND2	2.46	0.49
1:A:249:ARG:O	1:A:253:GLU:HB2	2.13	0.49
1:A:141:ILE:CG2	1:A:204:ILE:HG13	2.42	0.49
1:A:354:ILE:HD12	1:A:396:LEU:CD1	2.31	0.48
1:A:39:THR:OG1	1:A:127:GLN:NE2	2.46	0.48
1:A:298:TYR:CE2	2:B:4:BGC:H3	2.49	0.48
1:A:330:ILE:HD13	1:A:330:ILE:N	2.28	0.48
1:A:342:ILE:O	1:A:345:ASP:O	2.32	0.47
1:A:59:HIS:CD2	1:A:66:ASP:OD2	2.61	0.47
1:A:141:ILE:CD1	1:A:200:MET:HE3	2.45	0.47
1:A:405:LEU:HD22	1:A:423:ILE:HD11	1.96	0.47
1:A:428:GLN:NE2	3:A:553:HOH:O	2.46	0.47
1:A:225:GLU:H	1:A:248:ASN:HD21	1.62	0.47
1:A:88:MET:HA	1:A:93:ILE:HD11	1.97	0.46
1:A:287:GLN:O	1:A:287:GLN:HG2	2.14	0.46
1:A:20:SER:O	1:A:24:GLU:HB2	2.16	0.46
1:A:222:LEU:HD12	1:A:224:MET:HE2	1.98	0.46
1:A:28:ASP:N	1:A:28:ASP:OD1	2.45	0.46
1:A:321:GLU:O	1:A:322:PRO:C	2.52	0.46
1:A:84:TRP:N	1:A:85:PRO:CD	2.79	0.46
1:A:360:ALA:HA	1:A:417:ARG:O	2.16	0.45
1:A:409:GLU:CD	2:B:4:BGC:C6	2.68	0.45
1:A:20:SER:HB2	1:A:83:ALA:HB2	1.98	0.44
1:A:243:ARG:NH1	2:B:2:BGC:H2	2.29	0.44
1:A:412:TRP:HB3	1:A:416:LYS:HG2	2.00	0.44
1:A:416:LYS:HA	1:A:416:LYS:HD3	1.82	0.44
1:A:110:GLU:OE2	1:A:158:ARG:HD3	2.16	0.44
1:A:332:PRO:HG3	1:A:381:GLU:HB3	2.00	0.44
1:A:84:TRP:NE1	1:A:88:MET:HE2	2.29	0.44
1:A:21:TYR:CZ	1:A:53:GLY:HA3	2.52	0.44
1:A:180:GLU:OE2	2:B:2:BGC:O6	2.26	0.44
1:A:249:ARG:HH22	1:A:263:ASP:CG	2.20	0.44
1:A:256:PHE:CE1	1:A:346:PHE:HB3	2.52	0.44
1:A:165:ILE:HG23	1:A:198:ILE:HD11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:ASP:OD2	1:A:375:ARG:NH2	2.51	0.43
1:A:78:TYR:CE2	1:A:80:PHE:HB3	2.54	0.43
1:A:154:ARG:O	1:A:154:ARG:HD2	2.19	0.43
1:A:202:HIS:CB	1:A:220:ILE:HD12	2.47	0.43
1:A:268:TYR:CE1	1:A:311:LEU:HD11	2.54	0.43
1:A:307:ASN:HD22	1:A:307:ASN:HA	1.60	0.43
1:A:300:ARG:CZ	1:A:302:ILE:HD11	2.49	0.42
1:A:38:ASP:OD2	3:A:557:HOH:O	2.21	0.42
1:A:144:PHE:HE2	1:A:205:ALA:HB2	1.84	0.42
1:A:90:ALA:O	1:A:93:ILE:HG13	2.20	0.42
1:A:324:THR:C	1:A:326:MET:H	2.22	0.42
1:A:341:ARG:CD	3:A:601:HOH:O	2.66	0.41
1:A:148:ALA:O	1:A:152:MET:HG3	2.20	0.41
1:A:198:ILE:O	1:A:198:ILE:HG13	2.20	0.41
1:A:370:ILE:HB	1:A:433:LYS:HB3	2.02	0.41
1:A:19:SER:O	1:A:23:ILE:CD1	2.67	0.41
1:A:224:MET:HB2	1:A:338:LEU:HD21	2.02	0.41
1:A:424:ASN:O	1:A:428:GLN:N	2.52	0.41
1:A:141:ILE:HD13	1:A:200:MET:HE3	2.03	0.41
1:A:222:LEU:HB2	1:A:224:MET:HE2	2.03	0.41
1:A:224:MET:HA	1:A:248:ASN:ND2	2.36	0.41
1:A:333:GLU:O	1:A:336:TYR:HB3	2.20	0.41
1:A:64:LYS:HE2	1:A:68:GLN:NE2	2.37	0.40
1:A:347:SER:O	1:A:348:LYS:C	2.60	0.40
1:A:134:GLY:O	1:A:140:THR:OG1	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	443/454 (98%)	408 (92%)	28 (6%)	7 (2%)	9	8

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	321	GLU
1	A	348	LYS
1	A	9	PRO
1	A	346	PHE
1	A	94	ILE
1	A	447	GLY
1	A	269	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	377/386 (98%)	334 (89%)	43 (11%)	5	5

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	SER
1	A	20	SER
1	A	23	ILE
1	A	54	ASP
1	A	57	CYS
1	A	64	LYS
1	A	65	GLU
1	A	68	GLN
1	A	72	GLN
1	A	86	ARG
1	A	93	ILE
1	A	108	GLU
1	A	114	LEU
1	A	124	ASP
1	A	138	ARG
1	A	149	SER
1	A	158	ARG
1	A	163	ASN

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Mol	Chain	Res	Type
1	A	189	ARG
1	A	217	LYS
1	A	243	ARG
1	A	247	ILE
1	A	272	LEU
1	A	305	SER
1	A	306	THR
1	A	307	ASN
1	A	314	VAL
1	A	335	PHE
1	A	342	ILE
1	A	343	GLU
1	A	345	ASP
1	A	348	LYS
1	A	353	LEU
1	A	365	LEU
1	A	367	ASN
1	A	376	GLN
1	A	391	GLU
1	A	403	SER
1	A	409	GLU
1	A	420	ILE
1	A	439	PHE
1	A	440	LYS
1	A	442	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	HIS
1	A	62	HIS
1	A	68	GLN
1	A	77	HIS
1	A	95	ASN
1	A	122	HIS
1	A	127	GLN
1	A	166	ASN
1	A	202	HIS
1	A	207	ASN
1	A	209	HIS
1	A	248	ASN
1	A	287	GLN

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Mol	Chain	Res	Type
1	A	288	GLN
1	A	307	ASN
1	A	313	GLN
1	A	331	HIS
1	A	369	GLN
1	A	441	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 ⓘ

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	BGC	B	1	2	12,12,12	1.44	1 (8%)	17,17,17	3.28	10 (58%)
2	BGC	B	2	2	11,11,12	0.97	0	15,15,17	3.97	8 (53%)
2	BGC	B	3	2	11,11,12	1.54	1 (9%)	15,15,17	4.08	10 (66%)
2	BGC	B	4	2	11,11,12	1.13	0	15,15,17	4.26	11 (73%)

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	BGC	O1-C1	2.81	1.48	1.39
2	B	3	BGC	C4-C5	2.38	1.58	1.53

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3	BGC	C1-O5-C5	9.05	124.45	112.19
2	B	4	BGC	C1-O5-C5	8.79	124.11	112.19
2	B	2	BGC	O5-C1-C2	8.19	123.41	110.77
2	B	2	BGC	C1-C2-C3	7.43	118.79	109.67
2	B	4	BGC	O5-C1-C2	7.18	121.86	110.77
2	B	4	BGC	C3-C4-C5	6.71	122.21	110.24
2	B	3	BGC	C1-C2-C3	6.54	117.71	109.67
2	B	1	BGC	O5-C5-C4	6.21	120.96	109.69
2	B	3	BGC	O5-C1-C2	6.17	120.30	110.77
2	B	2	BGC	O5-C5-C4	5.72	124.73	110.83
2	B	1	BGC	C1-O5-C5	5.10	123.29	113.66
2	B	2	BGC	O5-C5-C6	4.95	114.96	107.20
2	B	1	BGC	C1-C2-C3	4.94	120.57	110.31
2	B	3	BGC	C3-C4-C5	4.90	118.98	110.24
2	B	3	BGC	C2-C3-C4	4.64	118.93	110.89
2	B	1	BGC	C3-C4-C5	4.61	118.46	110.24
2	B	2	BGC	C3-C4-C5	4.39	118.07	110.24
2	B	4	BGC	O2-C2-C3	4.38	118.91	110.14
2	B	4	BGC	O4-C4-C3	4.28	120.25	110.35
2	B	1	BGC	O1-C1-C2	4.14	120.68	109.03
2	B	1	BGC	O5-C1-C2	4.04	117.49	110.28
2	B	4	BGC	C1-C2-C3	3.54	114.01	109.67
2	B	4	BGC	C2-C3-C4	3.39	116.75	110.89
2	B	2	BGC	O6-C6-C5	-3.31	99.93	111.29
2	B	4	BGC	O5-C5-C6	3.29	112.36	107.20
2	B	3	BGC	O4-C4-C5	3.27	117.41	109.30
2	B	1	BGC	O3-C3-C2	3.16	117.67	110.35
2	B	1	BGC	C4-C3-C2	3.10	116.24	110.82
2	B	4	BGC	O3-C3-C2	2.90	115.55	109.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1	BGC	O3-C3-C4	2.78	116.78	110.35
2	B	4	BGC	O2-C2-C1	-2.61	103.81	109.15
2	B	3	BGC	C6-C5-C4	2.54	118.96	113.00
2	B	2	BGC	O3-C3-C4	2.53	116.19	110.35
2	B	1	BGC	O6-C6-C5	-2.50	102.72	111.29
2	B	4	BGC	C6-C5-C4	2.47	118.79	113.00
2	B	3	BGC	O5-C5-C4	2.45	116.78	110.83
2	B	3	BGC	O3-C3-C4	2.42	115.95	110.35
2	B	2	BGC	O4-C4-C3	2.41	115.93	110.35
2	B	3	BGC	O2-C2-C3	2.09	114.32	110.14

There are no chirality outliers.

All (4) torsion outliers are listed below:
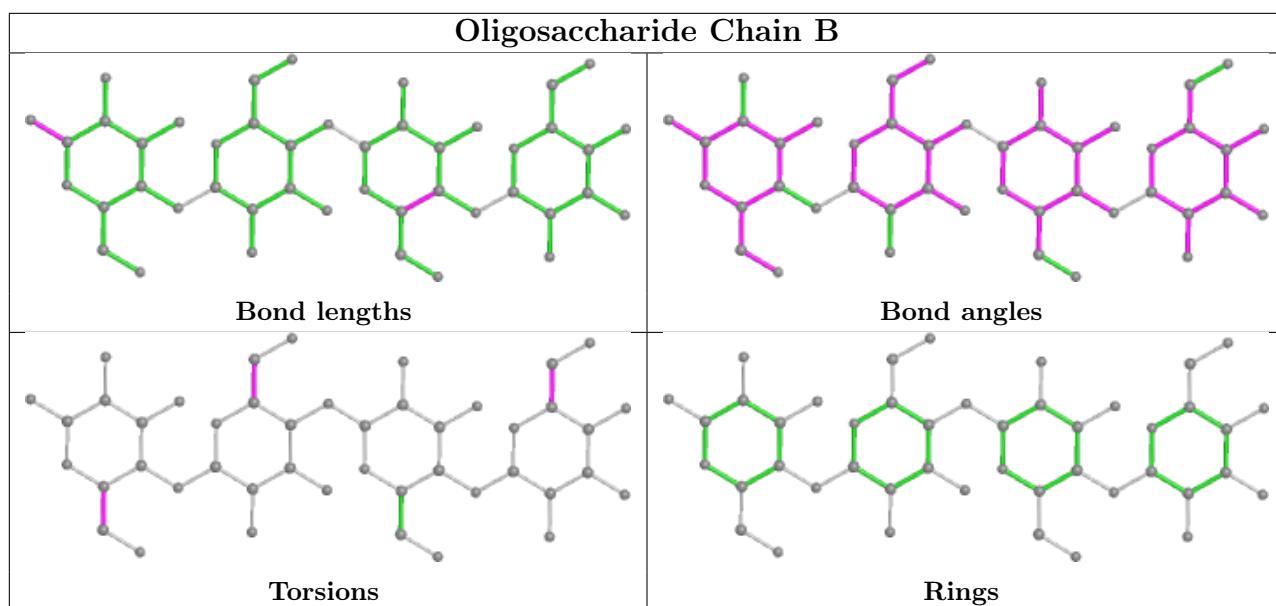
Mol	Chain	Res	Type	Atoms
2	B	4	BGC	O5-C5-C6-O6
2	B	2	BGC	C4-C5-C6-O6
2	B	4	BGC	C4-C5-C6-O6
2	B	1	BGC	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2	BGC	5	0
2	B	4	BGC	6	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.

Oligosaccharide Chain B

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	445/454 (98%)	0.39	26 (5%)	23	20	31, 47, 63, 80	0

All (26) RSRZ outliers are listed below:

| Mol	Chain	Res	Type	RSRZ
1	A	4	ASN	6.5
1	A	366	VAL	4.7
1	A	444	ALA	4.0
1	A	82	VAL	4.0
1	A	120	LEU	3.9
1	A	118	LEU	3.4
1	A	319	MET	3.3
1	A	321	GLU	3.2
1	A	10	ALA	3.1
1	A	119	THR	3.1
1	A	274	GLY	3.1
1	A	121	TYR	3.1
1	A	111	LEU	3.1
1	A	320	GLU	3.1
1	A	157	GLU	2.9
1	A	165	ILE	2.6
1	A	273	ASN	2.5
1	A	199	LEU	2.4
1	A	5	THR	2.4
1	A	76	LEU	2.4
1	A	81	SER	2.4
1	A	100	LEU	2.2
1	A	348	LYS	2.1
1	A	270	THR	2.1
1	A	18	THR	2.1
1	A	217	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ
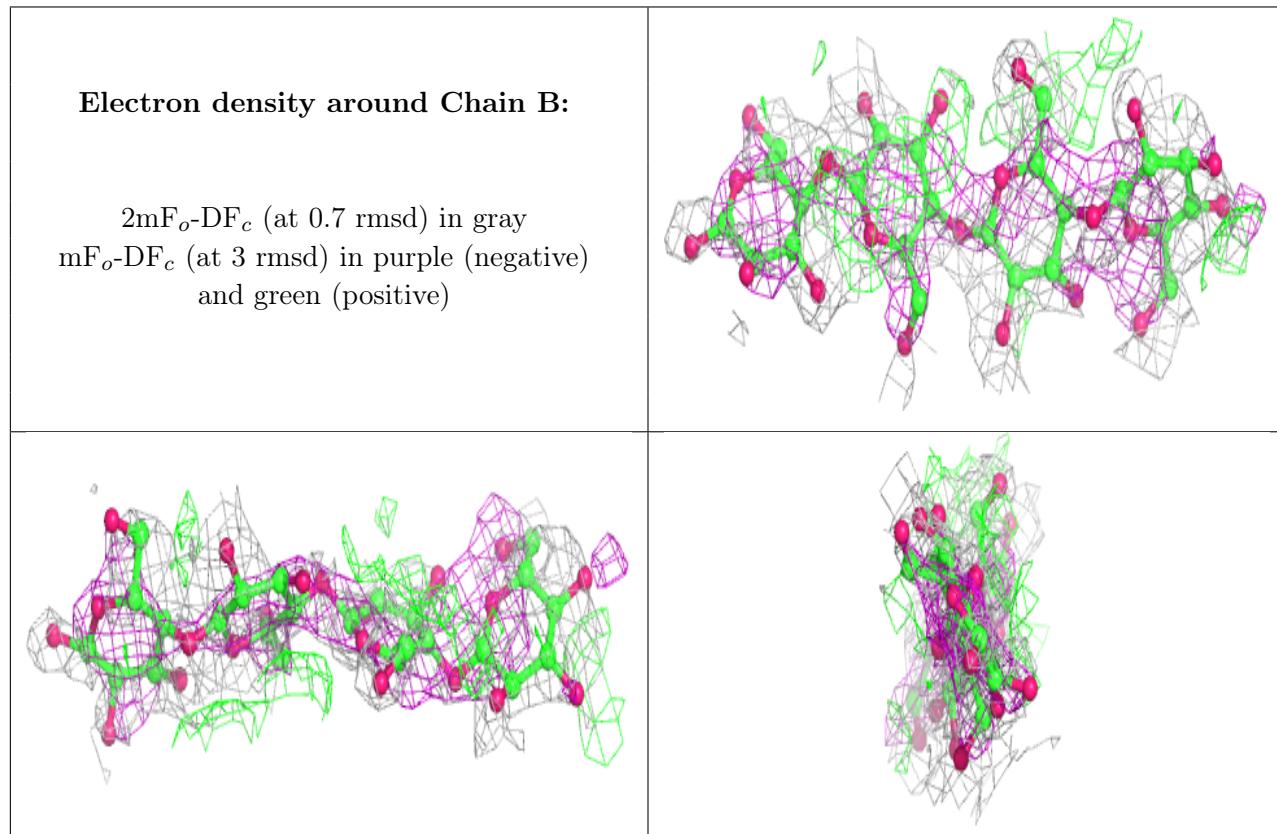
There are no non-standard protein/DNA/RNA residues in this entry.

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	BGC	B	2	11/12	0.50	0.56	56,57,63,65	0
2	BGC	B	1	12/12	0.59	0.45	47,54,55,56	0
2	BGC	B	4	11/12	0.62	0.38	46,48,51,56	0
2	BGC	B	3	11/12	0.65	0.40	47,54,58,60	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:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative) and green (positive)

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.