



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:14 AM UTC

PDB ID : 1HG8 / pdb_00001hg8
Title : Endopolygalacturonase from the phytopathogenic fungus *Fusarium moniliforme*
Authors : Federici, L.; Caprari, C.; Mattei, B.; Savino, C.; De Lorenzo, G.; Cervone, F.; Tsernoglou, D.
Deposited on : 2000-12-13
Resolution : 1.73 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

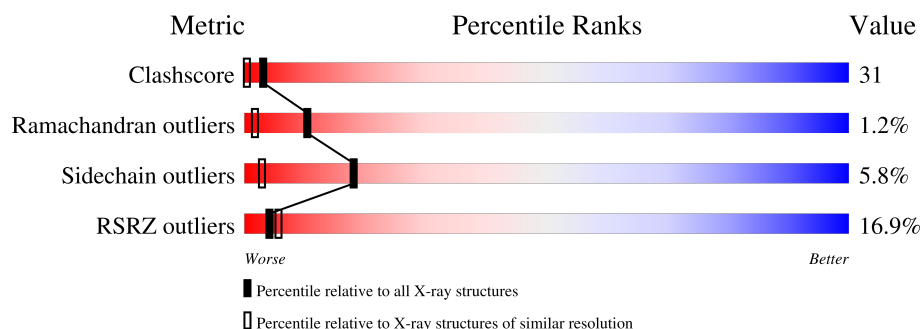
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.73 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	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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	349	
2	B	2	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2908 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 ENDOPOLY GALACTURONASE.

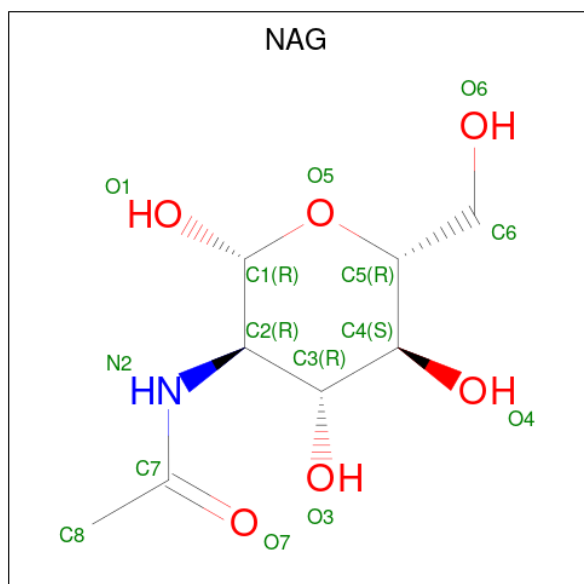
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	349	2540	1553	440	536	11	0	0	0

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	2	28	16	2	10	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

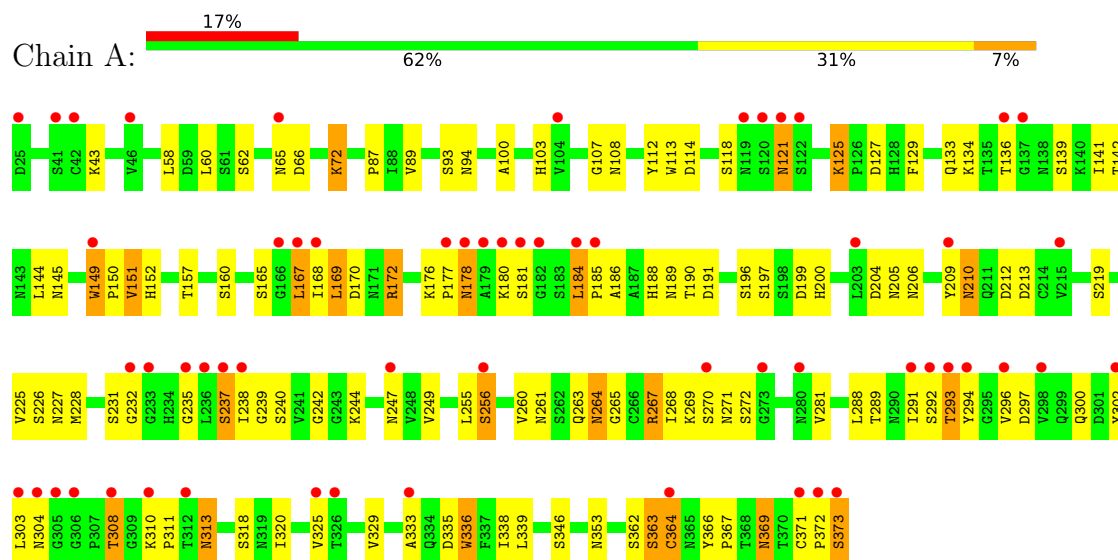
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	326	Total	O	0	0
			326	326		

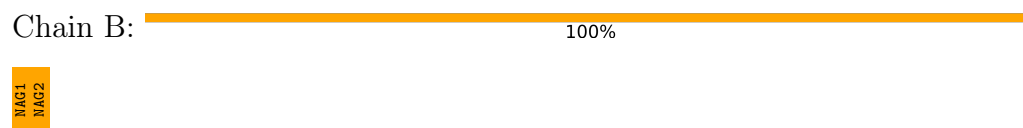
3 Residue-property plots [i](#)

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: ENDOPOLY GALACTURONASE



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-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	58.26Å 61.59Å 98.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.90 – 1.73 17.90 – 1.73	Depositor EDS
% Data completeness (in resolution range)	99.4 (17.90-1.73) 99.1 (17.90-1.73)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.14 (at 1.73Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.173 , 0.203 0.250 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	14.4	Xtriage
Anisotropy	0.618	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.54 , 72.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	2908	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.42% 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: NAG

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	0.88	4/2583 (0.2%)	1.49	8/3517 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	149	TRP	NE1-CE2	10.44	1.49	1.37
1	A	113	TRP	NE1-CE2	10.40	1.48	1.37
1	A	336	TRP	NE1-CE2	10.31	1.48	1.37
1	A	121	ASN	CB-CG	9.99	1.77	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	121	ASN	N-CA-CB	-8.21	99.23	110.56
1	A	121	ASN	CA-CB-CG	-6.46	106.14	112.60
1	A	114	ASP	CA-C-N	6.04	133.43	121.53
1	A	114	ASP	C-N-CA	6.04	133.43	121.53
1	A	267	ARG	CD-NE-CZ	-5.08	117.29	124.40
1	A	172	ARG	CD-NE-CZ	-5.05	117.33	124.40
1	A	363	SER	CA-C-N	-5.03	113.05	121.75
1	A	363	SER	C-N-CA	-5.03	113.05	121.75

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	2540	0	2417	155	0
2	B	28	0	25	4	0
3	A	14	0	12	2	0
4	A	326	0	0	5	0
All	All	2908	0	2454	156	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 31.

All (156) 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:121:ASN:CB	1:A:121:ASN:CG	1.77	1.58
1:A:94:ASN:HD21	2:B:1:NAG:C1	1.17	1.55
1:A:65:ASN:HD21	3:A:1374:NAG:C1	1.27	1.42
1:A:65:ASN:ND2	3:A:1374:NAG:C1	2.09	1.16
1:A:338:ILE:HB	1:A:364:CYS:HB3	1.04	1.03
1:A:308:THR:HG22	1:A:310:LYS:H	1.26	1.00
1:A:141:ILE:HG12	4:A:2108:HOH:O	1.61	0.99
1:A:338:ILE:CB	1:A:364:CYS:HB3	1.96	0.96
1:A:338:ILE:HB	1:A:364:CYS:CB	1.95	0.95
1:A:369:ASN:HD22	1:A:369:ASN:H	1.18	0.91
1:A:336:TRP:CE2	1:A:372:PRO:HG2	2.08	0.89
1:A:178:ASN:ND2	1:A:180:LYS:H	1.70	0.89
1:A:292:SER:C	1:A:333:ALA:HB2	1.99	0.88
1:A:178:ASN:C	1:A:178:ASN:HD22	1.82	0.85
1:A:325:VAL:H	1:A:353:ASN:HD22	1.24	0.85
1:A:210:ASN:H	1:A:210:ASN:HD22	1.28	0.82
1:A:144:LEU:HB2	1:A:167:LEU:HD22	1.61	0.81
1:A:244:LYS:H	1:A:247:ASN:HD21	1.29	0.79
1:A:178:ASN:ND2	1:A:181:SER:H	1.81	0.79
1:A:292:SER:O	1:A:333:ALA:HB2	1.83	0.78
1:A:366:TYR:CG	1:A:367:PRO:HA	2.17	0.78
1:A:178:ASN:HD21	1:A:181:SER:N	1.85	0.75
1:A:369:ASN:HD22	1:A:369:ASN:N	1.84	0.74
1:A:206:ASN:HB2	1:A:228:MET:SD	2.27	0.74
1:A:170:ASP:OD1	1:A:172:ARG:HD3	1.89	0.73
1:A:308:THR:CG2	1:A:310:LYS:H	2.01	0.72
1:A:178:ASN:HD21	1:A:181:SER:H	1.38	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:HIS:CE1	1:A:145:ASN:H	2.07	0.71
1:A:325:VAL:H	1:A:353:ASN:ND2	1.88	0.71
1:A:308:THR:HG21	4:A:2268:HOH:O	1.90	0.70
1:A:121:ASN:CG	1:A:121:ASN:CA	2.63	0.69
1:A:151:VAL:O	1:A:190:THR:HA	1.93	0.69
1:A:325:VAL:HB	1:A:353:ASN:HD22	1.59	0.68
1:A:311:PRO:HG3	1:A:339:LEU:HG	1.75	0.68
1:A:178:ASN:ND2	1:A:178:ASN:C	2.51	0.67
1:A:255:LEU:O	1:A:256:SER:C	2.37	0.67
1:A:121:ASN:CB	1:A:121:ASN:ND2	2.57	0.67
1:A:293:THR:C	1:A:333:ALA:HB1	2.20	0.66
1:A:313:ASN:C	1:A:313:ASN:HD22	2.04	0.66
1:A:325:VAL:HB	1:A:353:ASN:ND2	2.11	0.64
1:A:346:SER:HA	1:A:366:TYR:OH	1.98	0.64
2:B:1:NAG:C4	2:B:2:NAG:C1	2.75	0.64
1:A:94:ASN:HD21	2:B:1:NAG:C2	2.07	0.64
1:A:292:SER:OG	1:A:293:THR:HG22	1.97	0.64
1:A:270:SER:OG	1:A:300:GLN:HA	1.98	0.63
1:A:366:TYR:HA	1:A:367:PRO:C	2.24	0.63
1:A:210:ASN:HD22	1:A:210:ASN:N	1.86	0.63
1:A:112:TYR:HB3	1:A:125:LYS:HB3	1.81	0.63
1:A:235:GLY:HA3	1:A:264:ASN:O	1.98	0.62
1:A:177:PRO:HB3	1:A:184:LEU:O	2.00	0.61
1:A:303:LEU:O	1:A:304:ASN:HB2	2.00	0.61
1:A:313:ASN:ND2	1:A:313:ASN:H	1.99	0.61
1:A:133:GLN:HA	1:A:157:THR:O	2.02	0.60
1:A:366:TYR:CD1	1:A:367:PRO:HA	2.36	0.60
1:A:240:SER:N	1:A:269:LYS:HE2	2.17	0.59
1:A:210:ASN:H	1:A:210:ASN:ND2	1.99	0.59
1:A:325:VAL:N	1:A:353:ASN:HD22	1.97	0.58
1:A:336:TRP:CD2	1:A:372:PRO:HG2	2.38	0.57
1:A:291:ILE:HG21	1:A:294:TYR:O	2.05	0.57
1:A:336:TRP:CZ2	1:A:372:PRO:HG2	2.40	0.57
1:A:308:THR:HG23	1:A:310:LYS:HE2	1.86	0.56
1:A:167:LEU:HB2	1:A:206:ASN:OD1	2.05	0.56
1:A:292:SER:OG	1:A:293:THR:CG2	2.53	0.56
1:A:372:PRO:O	1:A:373:SER:HB2	2.05	0.56
1:A:176:LYS:HE3	4:A:2189:HOH:O	2.05	0.56
1:A:293:THR:O	1:A:333:ALA:HB1	2.06	0.56
1:A:371:CYS:HB3	1:A:372:PRO:HD2	1.88	0.56
1:A:185:PRO:O	1:A:186:ALA:C	2.48	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:THR:HA	1:A:165:SER:O	2.06	0.55
1:A:369:ASN:H	1:A:369:ASN:ND2	1.95	0.55
1:A:43:LYS:NZ	1:A:65:ASN:O	2.33	0.55
1:A:281:VAL:HB	1:A:320:ILE:HD12	1.89	0.55
1:A:210:ASN:N	1:A:210:ASN:ND2	2.50	0.55
1:A:242:GLY:O	1:A:271:ASN:ND2	2.30	0.54
1:A:87:PRO:HG2	1:A:129:PHE:HD1	1.72	0.54
1:A:296:VAL:HG11	1:A:336:TRP:CZ3	2.42	0.54
1:A:237:SER:HA	1:A:267:ARG:O	2.08	0.54
1:A:308:THR:HG22	1:A:310:LYS:N	2.10	0.54
1:A:172:ARG:HD2	1:A:209:TYR:CG	2.43	0.54
1:A:260:VAL:HG12	1:A:289:THR:HB	1.91	0.53
1:A:118:SER:H	1:A:189:ASN:HD22	1.56	0.53
1:A:169:LEU:HD23	1:A:169:LEU:N	2.23	0.52
1:A:219:SER:HA	1:A:249:VAL:HG22	1.91	0.52
1:A:313:ASN:ND2	1:A:313:ASN:N	2.56	0.52
1:A:172:ARG:HD2	1:A:209:TYR:CD2	2.45	0.52
1:A:363:SER:C	1:A:364:CYS:SG	2.92	0.52
1:A:263:GLN:HA	1:A:292:SER:OG	2.09	0.52
1:A:244:LYS:N	1:A:247:ASN:HD21	2.05	0.51
1:A:72:LYS:HG2	1:A:100:ALA:HB3	1.94	0.50
1:A:264:ASN:HA	1:A:294:TYR:O	2.12	0.50
1:A:364:CYS:N	1:A:371:CYS:SG	2.85	0.50
1:A:371:CYS:C	1:A:373:SER:N	2.70	0.50
1:A:144:LEU:H	1:A:167:LEU:HD22	1.76	0.50
1:A:325:VAL:CB	1:A:353:ASN:HD22	2.24	0.49
1:A:371:CYS:C	1:A:373:SER:H	2.19	0.49
1:A:313:ASN:C	1:A:313:ASN:ND2	2.70	0.49
1:A:60:LEU:HB2	1:A:89:VAL:O	2.11	0.49
1:A:205:ASN:H	1:A:227:ASN:HB2	1.77	0.49
1:A:199:ASP:OD2	1:A:200:HIS:HD2	1.96	0.48
1:A:263:GLN:HG3	1:A:293:THR:CG2	2.42	0.48
1:A:225:VAL:CG1	1:A:228:MET:HG3	2.44	0.48
1:A:209:TYR:CD1	1:A:209:TYR:N	2.81	0.48
1:A:281:VAL:HB	1:A:320:ILE:CD1	2.43	0.48
1:A:366:TYR:CD2	1:A:367:PRO:HA	2.49	0.48
1:A:267:ARG:HA	1:A:297:ASP:O	2.14	0.47
1:A:160:SER:HA	1:A:199:ASP:O	2.14	0.47
1:A:210:ASN:ND2	1:A:210:ASN:C	2.73	0.47
1:A:144:LEU:H	1:A:167:LEU:CD2	2.28	0.47
1:A:244:LYS:H	1:A:247:ASN:ND2	2.07	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:VAL:O	1:A:261:ASN:C	2.58	0.47
1:A:313:ASN:HD22	1:A:313:ASN:H	1.63	0.47
1:A:313:ASN:HD22	1:A:313:ASN:N	2.12	0.47
1:A:94:ASN:CG	2:B:1:NAG:C1	2.80	0.46
1:A:240:SER:HA	1:A:269:LYS:HG3	1.97	0.46
1:A:144:LEU:HB2	1:A:167:LEU:CD2	2.39	0.46
1:A:188:HIS:O	1:A:189:ASN:HB2	2.16	0.46
1:A:263:GLN:HG3	1:A:293:THR:HG21	1.98	0.46
1:A:225:VAL:HG12	1:A:228:MET:HG3	1.97	0.45
1:A:133:GLN:O	1:A:134:LYS:HB2	2.16	0.45
1:A:212:ASP:OD1	1:A:213:ASP:N	2.38	0.45
1:A:265:GLY:HA3	1:A:288:LEU:HD22	1.98	0.45
1:A:239:GLY:CA	1:A:240:SER:C	2.90	0.45
1:A:152:HIS:HD2	1:A:191:ASP:HB2	1.81	0.45
1:A:294:TYR:HB3	1:A:297:ASP:HB2	1.98	0.44
1:A:149:TRP:NE1	1:A:151:VAL:O	2.51	0.44
1:A:238:ILE:HB	1:A:268:ILE:HG12	1.99	0.44
1:A:204:ASP:HA	1:A:226:SER:O	2.18	0.44
1:A:231:SER:HA	1:A:260:VAL:O	2.17	0.44
1:A:72:LYS:HB3	1:A:72:LYS:HE2	1.62	0.43
1:A:127:ASP:O	1:A:152:HIS:HB2	2.17	0.43
1:A:139:SER:HB2	4:A:2178:HOH:O	2.18	0.43
1:A:165:SER:HA	1:A:204:ASP:O	2.18	0.43
1:A:335:ASP:HB2	1:A:362:SER:OG	2.19	0.43
1:A:308:THR:HG23	1:A:310:LYS:CE	2.48	0.43
1:A:318:SER:HA	1:A:346:SER:O	2.18	0.43
1:A:196:SER:O	1:A:197:SER:C	2.61	0.43
1:A:168:ILE:C	1:A:169:LEU:HD23	2.44	0.43
1:A:293:THR:OG1	1:A:294:TYR:N	2.52	0.43
1:A:255:LEU:O	1:A:256:SER:O	2.37	0.42
1:A:157:THR:HA	1:A:196:SER:O	2.19	0.42
1:A:291:ILE:HB	1:A:329:VAL:HG12	2.01	0.42
1:A:372:PRO:O	1:A:373:SER:CB	2.67	0.42
1:A:100:ALA:O	1:A:103:HIS:HD2	2.03	0.42
1:A:270:SER:OG	1:A:300:GLN:CA	2.66	0.42
1:A:308:THR:HG23	1:A:310:LYS:HZ3	1.84	0.41
1:A:62:SER:HB2	4:A:2047:HOH:O	2.20	0.41
1:A:103:HIS:HE1	1:A:145:ASN:H	1.63	0.41
1:A:232:GLY:HA2	1:A:261:ASN:O	2.21	0.41
1:A:149:TRP:CD1	1:A:151:VAL:O	2.74	0.41
1:A:210:ASN:HD22	1:A:210:ASN:C	2.26	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:SER:HA	1:A:136:THR:O	2.20	0.41
1:A:107:GLY:O	1:A:108:ASN:HB3	2.20	0.41
1:A:238:ILE:N	1:A:267:ARG:O	2.49	0.41
1:A:65:ASN:O	1:A:66:ASP:HB2	2.22	0.40
1:A:172:ARG:HD2	1:A:209:TYR:CB	2.52	0.40
1:A:178:ASN:ND2	1:A:180:LYS:N	2.53	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	347/349 (99%)	317 (91%)	26 (8%)	4 (1%)	10 2

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	PRO
1	A	256	SER
1	A	58	LEU
1	A	151	VAL

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	292/292 (100%)	275 (94%)	17 (6%)	18 3

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	LYS
1	A	125	LYS
1	A	167	LEU
1	A	169	LEU
1	A	178	ASN
1	A	184	LEU
1	A	210	ASN
1	A	237	SER
1	A	264	ASN
1	A	272	SER
1	A	293	THR
1	A	302	TYR
1	A	308	THR
1	A	313	ASN
1	A	364	CYS
1	A	369	ASN
1	A	373	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	65	ASN
1	A	94	ASN
1	A	103	HIS
1	A	133	GLN
1	A	147	GLN
1	A	152	HIS
1	A	178	ASN
1	A	189	ASN
1	A	200	HIS
1	A	205	ASN
1	A	210	ASN
1	A	227	ASN
1	A	247	ASN
1	A	313	ASN
1	A	319	ASN

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Mol	Chain	Res	Type
1	A	353	ASN
1	A	369	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 ⓘ

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	NAG	B	1	1,2	14,14,15	1.68	2 (14%)	17,19,21	1.87	5 (29%)
2	NAG	B	2	2	14,14,15	2.12	3 (21%)	17,19,21	3.13	2 (11%)

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	NAG	B	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	NAG	O5-C1	-5.78	1.34	1.43
2	B	1	NAG	O5-C1	-4.47	1.36	1.43
2	B	1	NAG	O7-C7	-3.89	1.14	1.23
2	B	2	NAG	O7-C7	-3.81	1.14	1.23
2	B	2	NAG	C1-C2	-3.11	1.48	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAG	C1-O5-C5	11.81	128.02	112.19
2	B	2	NAG	C3-C4-C5	4.16	117.78	110.23
2	B	1	NAG	C2-N2-C7	3.04	126.98	122.90
2	B	1	NAG	O4-C4-C3	-2.97	103.37	110.38
2	B	1	NAG	C3-C4-C5	2.96	115.60	110.23
2	B	1	NAG	C1-O5-C5	2.83	115.98	112.19
2	B	1	NAG	C4-C3-C2	-2.75	106.99	111.02

There are no chirality outliers.

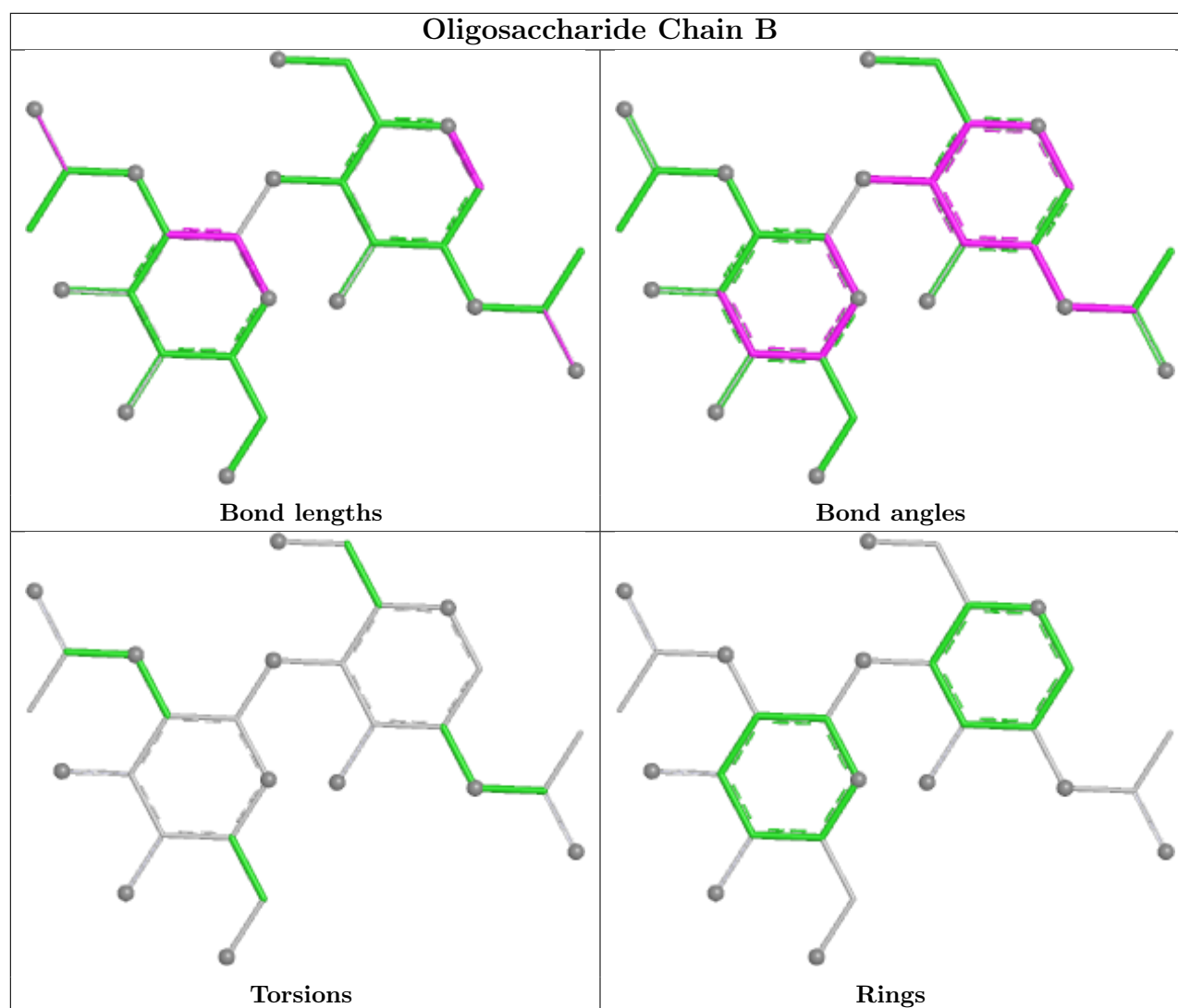
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	NAG	4	0
2	B	2	NAG	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	$\# Z > 2$
3	NAG	A	1374	-	14,14,15	1.32	1 (7%)	17,19,21	2.46	4 (23%)

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
3	NAG	A	1374	-	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1374	NAG	O7-C7	-3.89	1.14	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1374	NAG	C1-O5-C5	7.91	122.78	112.19
3	A	1374	NAG	O5-C1-C2	-4.37	104.52	111.29
3	A	1374	NAG	C3-C4-C5	2.60	114.94	110.23
3	A	1374	NAG	C4-C3-C2	-2.24	107.73	111.02

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1374	NAG	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	349/349 (100%)	1.12	59 (16%) 4 5	11, 15, 28, 46	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	373	SER	9.3
1	A	237	SER	7.3
1	A	121	ASN	6.0
1	A	371	CYS	5.5
1	A	372	PRO	5.1
1	A	178	ASN	5.0
1	A	238	ILE	4.7
1	A	364	CYS	4.4
1	A	333	ALA	4.4
1	A	305	GLY	4.4
1	A	308	THR	4.2
1	A	185	PRO	4.1
1	A	179	ALA	4.1
1	A	293	THR	3.8
1	A	235	GLY	3.7
1	A	137	GLY	3.6
1	A	184	LEU	3.4
1	A	306	GLY	3.4
1	A	215	VAL	3.4
1	A	298	VAL	3.2
1	A	303	LEU	3.2
1	A	182	GLY	3.1
1	A	325	VAL	3.1
1	A	310	LYS	3.1
1	A	304	ASN	3.1
1	A	41	SER	3.1
1	A	233	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	302	TYR	3.0
1	A	120	SER	2.9
1	A	149	TRP	2.8
1	A	119	ASN	2.8
1	A	291	ILE	2.8
1	A	203	LEU	2.6
1	A	181	SER	2.6
1	A	167	LEU	2.6
1	A	209	TYR	2.6
1	A	326	THR	2.6
1	A	42	CYS	2.6
1	A	65	ASN	2.6
1	A	177	PRO	2.6
1	A	273	GLY	2.5
1	A	180	LYS	2.5
1	A	312	THR	2.5
1	A	236	LEU	2.4
1	A	136	THR	2.4
1	A	232	GLY	2.4
1	A	256	SER	2.4
1	A	168	ILE	2.3
1	A	46	VAL	2.3
1	A	270	SER	2.3
1	A	166	GLY	2.3
1	A	104	VAL	2.3
1	A	294	TYR	2.2
1	A	122	SER	2.2
1	A	296	VAL	2.1
1	A	292	SER	2.1
1	A	280	ASN	2.1
1	A	247	ASN	2.0
1	A	25	ASP	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.

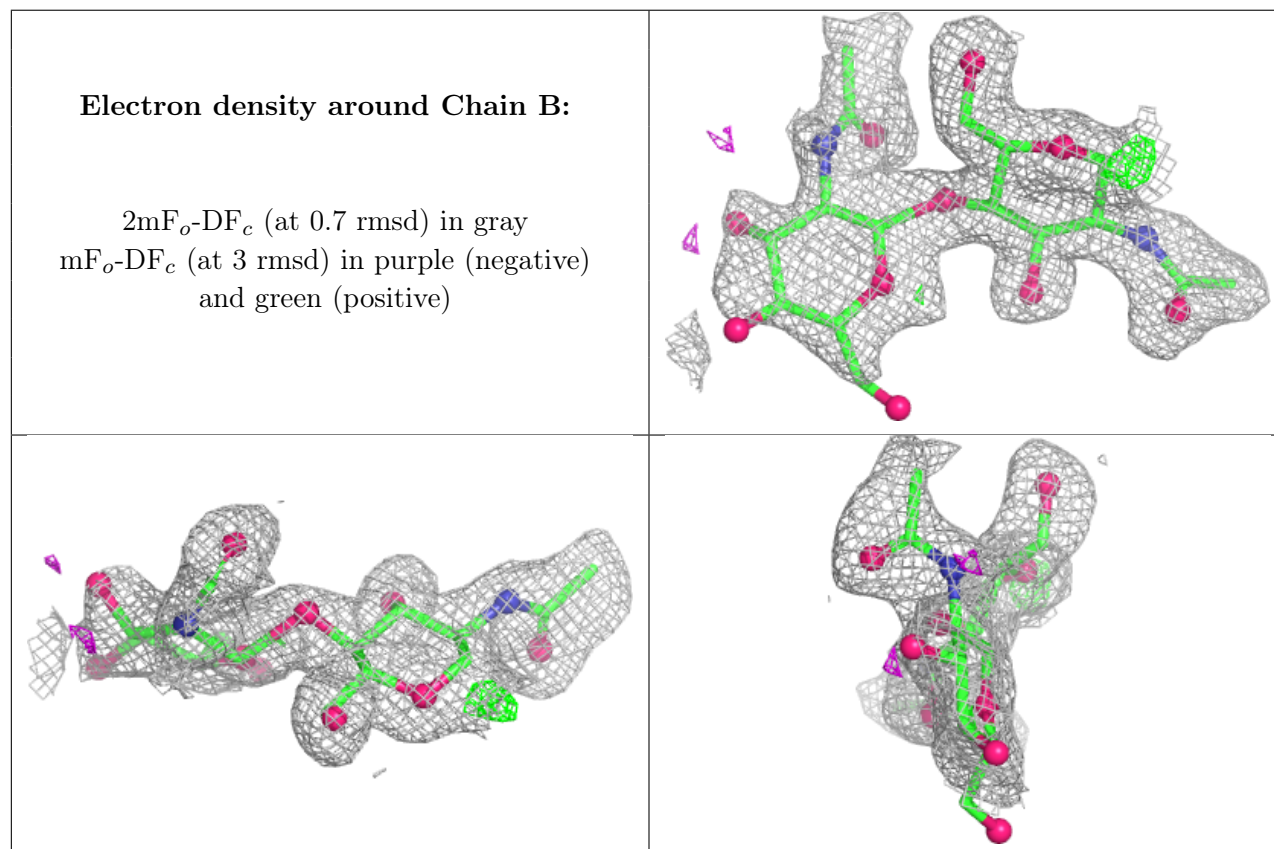
6.3 Carbohydrates [i](#)

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	NAG	B	2	14/15	0.64	0.19	46,49,50,50	0
2	NAG	B	1	14/15	0.85	0.11	23,26,28,29	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](#)

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
3	NAG	A	1374	14/15	0.58	0.22	51,51,51,51	0

6.5 Other polymers ⓘ

There are no such residues in this entry.