



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:08 PM UTC

PDB ID : 6YA0 / pdb_00006ya0
Title : Crystal structure of TSWV glycoprotein N ectodomain (Trypsin treated)
Authors : Dessau, M.; Bahat, Y.
Deposited on : 2020-03-11
Resolution : 2.86 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

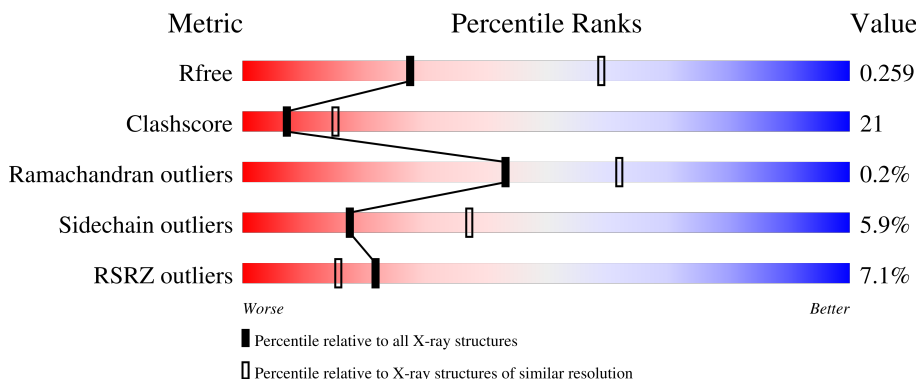
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.86 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	288	 3% 43% 22% 34%
1	B	288	 3% 45% 18% 34%
1	C	288	 7% 37% 22% 40%
2	D	2	 100%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4400 atoms, of which 4 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 Glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	190	Total	C	N	O	S	0	0	0
			1467	925	240	294	8			
1	B	189	Total	C	N	O	S	0	0	0
			1460	920	239	293	8			
1	C	174	Total	C	N	O	S	0	0	0
			1337	842	221	266	8			

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



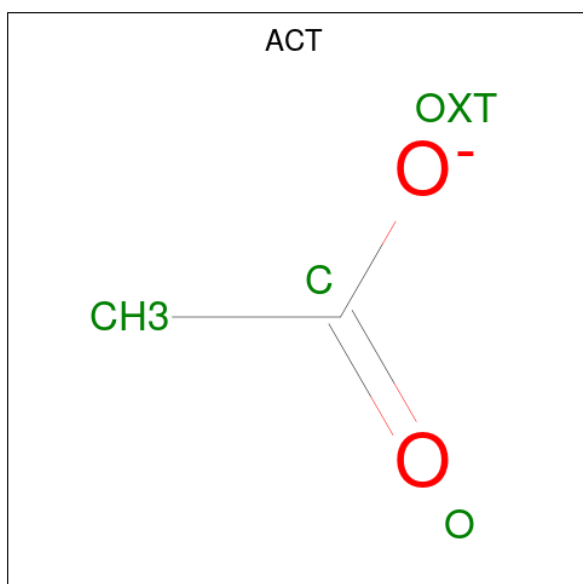
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	2	Total	C	N	O	25	0	0
			25	14	1	10			

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



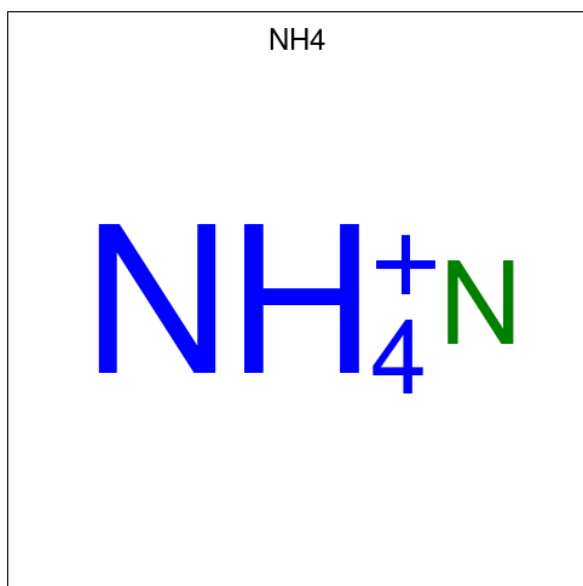
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	14	0
			14	8	1	5		
3	A	1	Total	C	N	O	14	0
			14	8	1	5		
3	B	1	Total	C	N	O	14	0
			14	8	1	5		
3	B	1	Total	C	N	O	14	0
			14	8	1	5		
3	C	1	Total	C	N	O	14	0
			14	8	1	5		

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is AMMONIUM ION (CCD ID: NH4) (formula: H₄N).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	H	N	0	0
			5	4	1		

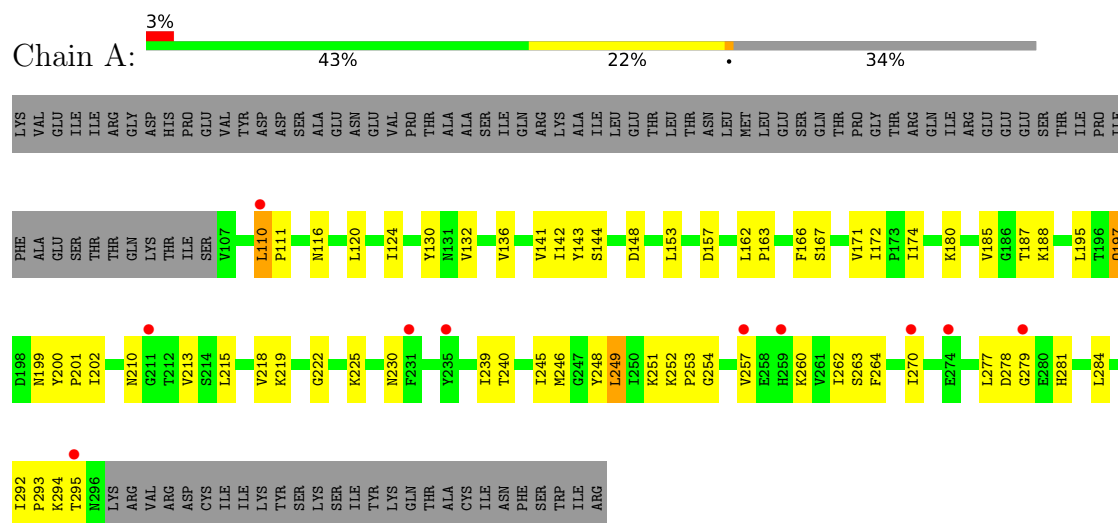
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	10	Total	O	0	0
			10	10		
6	B	14	Total	O	0	0
			14	14		
6	C	8	Total	O	0	0
			8	8		

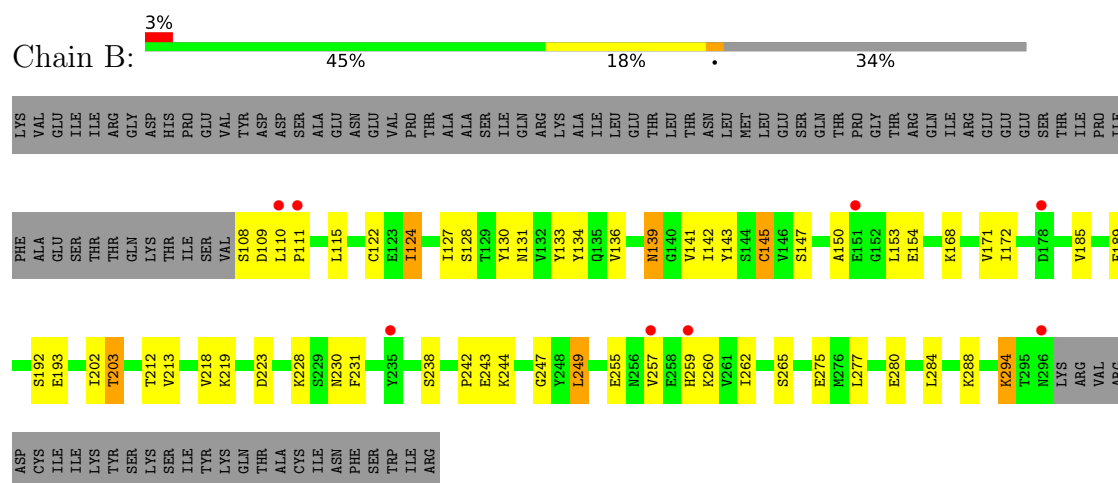
3 Residue-property plots

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.

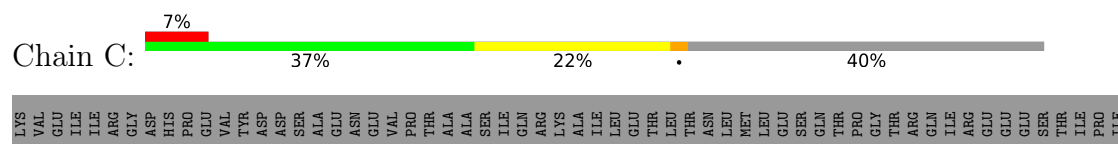
• Molecule 1: Glycoprotein

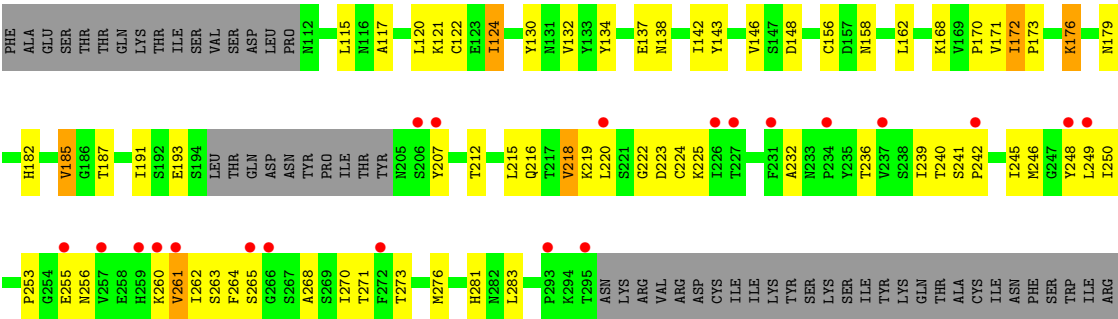


• Molecule 1: Glycoprotein

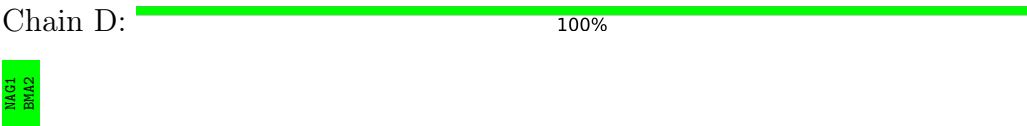


• Molecule 1: Glycoprotein





● Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.82Å 74.85Å 81.28Å 90.00° 103.27° 90.00°	Depositor
Resolution (Å)	49.91 – 2.86 49.91 – 2.86	Depositor EDS
% Data completeness (in resolution range)	75.9 (49.91-2.86) 75.9 (49.91-2.86)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.217 , 0.261 0.217 , 0.259	Depositor DCC
R_{free} test set	1425 reflections (7.60%)	wwPDB-VP
Wilson B-factor (Å ²)	77.7	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 87.2	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	0.92	EDS
Total number of atoms	4400	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.28% 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: NAG, ACT, BMA, NH4

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	0.27	0/1495	0.44	0/2025
1	B	0.26	0/1488	0.46	0/2015
1	C	0.23	0/1360	0.41	0/1835
All	All	0.25	0/4343	0.44	0/5875

There are no bond length outliers.

There are no bond angle outliers.

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	1467	0	1454	54	1
1	B	1460	0	1445	49	1
1	C	1337	0	1332	74	0
2	D	25	0	22	0	0
3	A	28	0	26	0	0
3	B	28	0	26	0	0
3	C	14	0	13	0	0
4	B	4	0	3	0	0
5	C	1	4	0	0	0
6	A	10	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	14	0	0	1	0
6	C	8	0	0	0	0
All	All	4396	4	4321	175	1

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 21.

All (175) 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:C:249:LEU:HD21	1:C:261:VAL:HA	1.14	1.07
1:B:257:VAL:HG22	1:B:260:LYS:HB3	1.44	0.95
1:B:110:LEU:HG	1:B:143:TYR:HD2	1.32	0.93
1:A:171:VAL:HG22	1:A:218:VAL:HG22	1.52	0.91
1:B:249:LEU:HD11	1:B:257:VAL:HG13	1.52	0.91
1:C:249:LEU:HD11	1:C:261:VAL:HB	1.52	0.89
1:C:222:GLY:HA3	1:C:246:MET:HE1	1.56	0.86
1:B:257:VAL:HG22	1:B:260:LYS:CB	2.07	0.84
1:C:249:LEU:CD2	1:C:261:VAL:HA	2.04	0.83
1:C:171:VAL:HG12	1:C:218:VAL:HG22	1.61	0.81
1:A:202:ILE:HD13	1:A:213:VAL:HG23	1.62	0.80
1:A:199:ASN:HB3	1:A:210:ASN:O	1.82	0.80
1:B:171:VAL:HG13	1:B:218:VAL:HB	1.64	0.77
1:C:171:VAL:HG11	1:C:218:VAL:CG1	2.15	0.77
1:C:171:VAL:HG11	1:C:218:VAL:HG13	1.68	0.73
1:B:122:CYS:HB3	1:B:136:VAL:HG12	1.71	0.73
1:C:239:ILE:HG22	1:C:264:PHE:CE1	2.25	0.72
1:A:144:SER:HB2	1:A:202:ILE:HG12	1.73	0.70
1:B:249:LEU:HD12	1:B:260:LYS:HG3	1.74	0.69
1:C:185:VAL:HG22	1:C:249:LEU:HD12	1.76	0.68
1:C:250:ILE:HD13	1:C:276:MET:SD	2.35	0.67
1:C:182:HIS:HB3	1:C:253:PRO:HB3	1.77	0.66
1:B:154:GLU:H	1:B:154:GLU:CD	2.04	0.64
1:C:137:GLU:HB2	1:C:142:ILE:HD13	1.80	0.63
1:B:277:LEU:O	1:B:294:LYS:HA	1.97	0.63
1:C:249:LEU:HD21	1:C:261:VAL:CA	2.09	0.62
1:C:124:ILE:HG13	1:C:158:ASN:HB2	1.82	0.62
1:A:279:GLY:N	1:A:294:LYS:HB2	2.14	0.62
1:B:115:LEU:N	1:B:115:LEU:HD22	2.15	0.62
1:C:187:THR:HB	1:C:215:LEU:HD11	1.82	0.62
1:C:273:THR:HB	1:C:276:MET:HB3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:225:LYS:HG2	1:C:240:THR:O	2.00	0.61
1:C:249:LEU:HD11	1:C:261:VAL:CB	2.30	0.59
1:C:122:CYS:HB3	1:C:156:CYS:HA	1.84	0.59
1:A:257:VAL:HG22	1:A:260:LYS:HB2	1.85	0.59
1:A:293:PRO:HB2	1:A:295:THR:CG2	2.33	0.59
1:C:171:VAL:HG12	1:C:218:VAL:CG2	2.33	0.58
1:B:145:CYS:HA	1:B:202:ILE:HG13	1.86	0.58
1:A:153:LEU:HB2	1:A:162:LEU:HD11	1.86	0.58
1:C:171:VAL:CG1	1:C:218:VAL:HG13	2.33	0.58
1:C:171:VAL:HG13	1:C:219:LYS:O	2.04	0.58
1:C:250:ILE:HG23	1:C:281:HIS:HD2	1.69	0.58
1:C:130:TYR:OH	1:C:185:VAL:HG13	2.03	0.58
1:B:108:SER:OG	1:B:109:ASP:N	2.37	0.58
1:C:193:GLU:OE1	1:C:193:GLU:N	2.37	0.58
1:B:171:VAL:CG1	1:B:218:VAL:HB	2.33	0.57
1:C:232:ALA:CB	1:C:236:THR:HB	2.34	0.57
1:A:130:TYR:HB2	1:A:188:LYS:HD2	1.85	0.57
1:B:110:LEU:HG	1:B:143:TYR:CD2	2.24	0.57
1:A:110:LEU:N	1:A:111:PRO:HD2	2.19	0.57
1:C:264:PHE:O	1:C:264:PHE:CG	2.57	0.56
1:C:120:LEU:HD13	1:C:138:ASN:HB2	1.86	0.56
1:C:124:ILE:HA	1:C:134:TYR:HA	1.86	0.56
1:A:195:LEU:HD12	1:A:195:LEU:H	1.71	0.56
1:B:249:LEU:HD12	1:B:260:LYS:CG	2.34	0.56
1:B:257:VAL:HG13	1:B:257:VAL:O	2.05	0.56
1:B:249:LEU:HD11	1:B:257:VAL:CG1	2.33	0.56
1:C:225:LYS:HG2	1:C:240:THR:C	2.31	0.55
1:A:249:LEU:HD11	1:A:257:VAL:HG11	1.87	0.55
1:C:262:ILE:H	1:C:262:ILE:HD12	1.70	0.55
1:C:191:ILE:HD11	1:C:207:TYR:CE2	2.42	0.54
1:B:122:CYS:CB	1:B:136:VAL:HG12	2.37	0.54
1:C:171:VAL:CG1	1:C:218:VAL:HG22	2.34	0.54
1:A:200:TYR:CE1	1:A:202:ILE:HD11	2.43	0.54
1:A:225:LYS:HB3	1:A:240:THR:HB	1.90	0.54
1:A:130:TYR:HB3	6:A:501:HOH:O	2.07	0.54
1:A:171:VAL:HG22	1:A:218:VAL:CG2	2.33	0.53
1:A:252:LYS:O	1:A:254:GLY:N	2.42	0.53
1:A:171:VAL:HG23	1:A:219:LYS:O	2.08	0.53
1:C:172:ILE:HG13	1:C:173:PRO:HD2	1.89	0.53
1:A:245:ILE:HD11	1:A:263:SER:HB2	1.91	0.53
1:A:279:GLY:CA	1:A:294:LYS:HB2	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:ILE:HD13	1:A:180:LYS:HA	1.91	0.52
1:B:124:ILE:HD13	1:B:127:ILE:HG23	1.90	0.52
1:C:240:THR:HG22	1:C:241:SER:N	2.25	0.52
1:B:128:SER:HB3	1:B:189:PHE:CE2	2.44	0.52
1:B:249:LEU:HD23	1:B:284:LEU:HD12	1.91	0.51
1:A:257:VAL:CG2	1:A:260:LYS:HB2	2.39	0.51
1:B:133:TYR:CE2	1:B:213:VAL:HG11	2.45	0.51
1:B:228:LYS:NZ	6:B:704:HOH:O	2.44	0.51
1:C:239:ILE:HG22	1:C:264:PHE:CZ	2.46	0.51
1:B:171:VAL:HG11	1:B:218:VAL:HG21	1.91	0.51
1:B:260:LYS:HG3	1:B:260:LYS:O	2.11	0.51
1:C:264:PHE:HB2	1:C:268:ALA:HB2	1.92	0.51
1:A:222:GLY:HA3	1:A:246:MET:HE1	1.92	0.51
1:C:245:ILE:HD11	1:C:263:SER:HB2	1.92	0.51
1:A:116:ASN:O	1:A:120:LEU:HG	2.12	0.50
1:B:150:ALA:HA	1:B:153:LEU:HD12	1.93	0.50
1:C:232:ALA:HB1	1:C:236:THR:HB	1.92	0.50
1:B:109:ASP:C	1:B:111:PRO:HD2	2.37	0.50
1:C:245:ILE:HD12	1:C:265:SER:HB3	1.94	0.50
1:C:162:LEU:HD23	1:C:162:LEU:H	1.77	0.49
1:B:141:VAL:HB	1:B:143:TYR:CE1	2.47	0.49
1:A:142:ILE:HD12	1:A:142:ILE:H	1.78	0.49
1:A:249:LEU:HD11	1:A:257:VAL:CG1	2.42	0.49
1:B:110:LEU:N	1:B:111:PRO:HD2	2.27	0.49
1:B:230:ASN:OD1	1:B:230:ASN:N	2.44	0.49
1:A:277:LEU:HA	1:A:292:ILE:HD13	1.95	0.49
1:B:247:GLY:HA2	1:B:262:ILE:O	2.13	0.49
1:C:185:VAL:HG13	1:C:185:VAL:O	2.12	0.48
1:B:111:PRO:O	1:B:115:LEU:HD21	2.14	0.48
1:A:262:ILE:HD12	1:A:262:ILE:N	2.28	0.48
1:A:262:ILE:HD12	1:A:262:ILE:H	1.78	0.47
1:C:225:LYS:HG3	1:C:240:THR:HB	1.96	0.47
1:C:223:ASP:O	1:C:242:PRO:HD2	2.14	0.47
1:A:167:SER:O	6:A:501:HOH:O	2.20	0.47
1:A:171:VAL:CG2	1:A:219:LYS:O	2.63	0.47
1:C:148:ASP:OD1	1:C:168:LYS:HE3	2.15	0.47
1:A:225:LYS:O	1:A:239:ILE:HA	2.14	0.47
1:B:130:TYR:OH	1:B:185:VAL:HG23	2.15	0.47
1:A:278:ASP:OD1	1:A:281:HIS:ND1	2.45	0.46
1:C:236:THR:HA	1:C:270:ILE:O	2.15	0.46
1:A:163:PRO:HG2	1:A:166:PHE:CE1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:171:VAL:HG11	1:C:218:VAL:HG11	1.96	0.46
1:A:293:PRO:HB2	1:A:295:THR:HG23	1.97	0.46
1:C:225:LYS:CG	1:C:240:THR:HB	2.45	0.46
1:B:124:ILE:HA	1:B:134:TYR:CB	2.45	0.46
1:C:171:VAL:HG12	1:C:172:ILE:N	2.30	0.46
1:B:128:SER:HB3	1:B:189:PHE:CD2	2.52	0.45
1:A:144:SER:CB	1:A:202:ILE:HG12	2.46	0.45
1:A:110:LEU:N	1:A:111:PRO:CD	2.80	0.45
1:A:248:TYR:CE1	1:A:270:ILE:HG21	2.51	0.45
1:C:171:VAL:HG22	1:C:220:LEU:HD23	1.98	0.45
1:A:197:GLN:HE21	1:A:197:GLN:HB2	1.67	0.45
1:C:171:VAL:CG1	1:C:218:VAL:CG2	2.94	0.45
1:C:255:GLU:HG3	1:C:256:ASN:H	1.82	0.44
1:C:130:TYR:HH	1:C:185:VAL:HG13	1.81	0.44
1:A:187:THR:HB	1:A:215:LEU:HD11	1.98	0.44
1:C:250:ILE:HG23	1:C:281:HIS:CD2	2.51	0.44
1:B:192:SER:O	1:B:212:THR:HG22	2.18	0.44
1:C:124:ILE:C	1:C:124:ILE:HD12	2.43	0.44
1:A:171:VAL:HG23	1:A:219:LYS:C	2.42	0.44
1:C:232:ALA:HB3	1:C:236:THR:HB	2.00	0.44
1:C:236:THR:HG23	1:C:270:ILE:O	2.18	0.43
1:C:176:LYS:HB3	1:C:179:ASN:ND2	2.34	0.43
1:C:264:PHE:O	1:C:264:PHE:CD1	2.71	0.43
1:B:139:ASN:N	1:B:139:ASN:OD1	2.51	0.43
1:C:248:TYR:O	1:C:249:LEU:HD23	2.17	0.43
1:B:131:ASN:HB2	1:B:147:SER:O	2.19	0.43
1:C:162:LEU:H	1:C:162:LEU:CD2	2.32	0.43
1:A:201:PRO:HA	1:A:210:ASN:HA	2.01	0.43
1:A:293:PRO:C	1:A:295:THR:HG23	2.43	0.43
1:B:231:PHE:HB3	1:C:215:LEU:HB2	2.00	0.43
1:A:172:ILE:HD11	1:A:219:LYS:HE3	2.00	0.42
1:A:251:LYS:HD3	1:A:284:LEU:HD11	2.01	0.42
1:C:172:ILE:HG13	1:C:173:PRO:CD	2.48	0.42
1:C:249:LEU:HD23	1:C:249:LEU:HA	1.62	0.42
1:C:249:LEU:HD23	1:C:262:ILE:HD12	2.01	0.42
1:A:174:ILE:HG12	1:A:219:LYS:HB3	2.00	0.42
1:C:120:LEU:CD1	1:C:138:ASN:HB2	2.49	0.42
1:C:191:ILE:HD11	1:C:207:TYR:HE2	1.84	0.42
1:B:145:CYS:HB3	1:B:203:THR:HB	2.02	0.41
1:A:136:VAL:HG22	1:A:143:TYR:HB2	2.02	0.41
1:B:185:VAL:HG23	1:B:185:VAL:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:249:LEU:CD2	1:C:260:LYS:O	2.69	0.41
1:B:142:ILE:HD12	1:B:142:ILE:N	2.35	0.41
1:C:115:LEU:C	1:C:117:ALA:H	2.28	0.41
1:A:292:ILE:HD12	1:A:292:ILE:C	2.46	0.41
1:B:124:ILE:HA	1:B:134:TYR:HA	2.02	0.41
1:B:172:ILE:HD11	1:B:219:LYS:HE3	2.02	0.41
1:B:265:SER:HB3	1:C:143:TYR:CE2	2.55	0.41
1:A:148:ASP:O	1:A:166:PHE:HB2	2.20	0.41
1:B:244:LYS:HE2	1:B:244:LYS:HB2	1.87	0.41
1:C:255:GLU:OE2	1:C:255:GLU:HA	2.21	0.41
1:A:230:ASN:O	1:A:230:ASN:ND2	2.53	0.41
1:A:124:ILE:HD11	1:A:153:LEU:HB3	2.02	0.41
1:A:185:VAL:HG22	1:A:219:LYS:HA	2.03	0.41
1:A:239:ILE:HD12	1:A:264:PHE:CE2	2.55	0.41
1:C:170:PRO:C	1:C:171:VAL:HG23	2.45	0.41
1:C:283:LEU:C	1:C:283:LEU:HD13	2.45	0.41
1:A:252:LYS:O	1:A:252:LYS:HG2	2.20	0.41
1:B:171:VAL:CG1	1:B:218:VAL:CB	2.99	0.40
1:B:110:LEU:N	1:B:111:PRO:CD	2.84	0.40
1:B:223:ASP:O	1:B:242:PRO:HD2	2.21	0.40
1:C:132:VAL:O	1:C:146:VAL:HA	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:ASP:OD2	1:B:288:LYS:NZ[2_545]	2.18	0.02

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	188/288 (65%)	175 (93%)	12 (6%)	1 (0%)	24	42
1	B	187/288 (65%)	176 (94%)	11 (6%)	0	100	100
1	C	170/288 (59%)	158 (93%)	12 (7%)	0	100	100
All	All	545/864 (63%)	509 (93%)	35 (6%)	1 (0%)	43	62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	253	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	174/264 (66%)	169 (97%)	5 (3%)	37	61
1	B	173/264 (66%)	159 (92%)	14 (8%)	11	23
1	C	158/264 (60%)	147 (93%)	11 (7%)	14	29
All	All	505/792 (64%)	475 (94%)	30 (6%)	18	37

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	110	LEU
1	A	132	VAL
1	A	141	VAL
1	A	197	GLN
1	A	249	LEU
1	B	124	ILE
1	B	139	ASN
1	B	145	CYS
1	B	168	LYS
1	B	193	GLU
1	B	203	THR
1	B	238	SER

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Mol	Chain	Res	Type
1	B	243	GLU
1	B	249	LEU
1	B	255	GLU
1	B	259	HIS
1	B	275	GLU
1	B	280	GLU
1	B	294	LYS
1	C	121	LYS
1	C	124	ILE
1	C	172	ILE
1	C	176	LYS
1	C	185	VAL
1	C	212	THR
1	C	216	GLN
1	C	218	VAL
1	C	224	CYS
1	C	261	VAL
1	C	271	THR

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	113	ASN
1	A	138	ASN
1	A	182	HIS
1	A	197	GLN
1	A	216	GLN
1	B	113	ASN
1	B	135	GLN
1	B	138	ASN
1	B	216	GLN
1	C	135	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	NAG	D	1	1,2	14,14,15	0.34	0	17,19,21	0.50	0
2	BMA	D	2	2	11,11,12	0.51	0	15,15,17	0.77	0

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	D	1	1,2	-	2/6/23/26	0/1/1/1
2	BMA	D	2	2	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

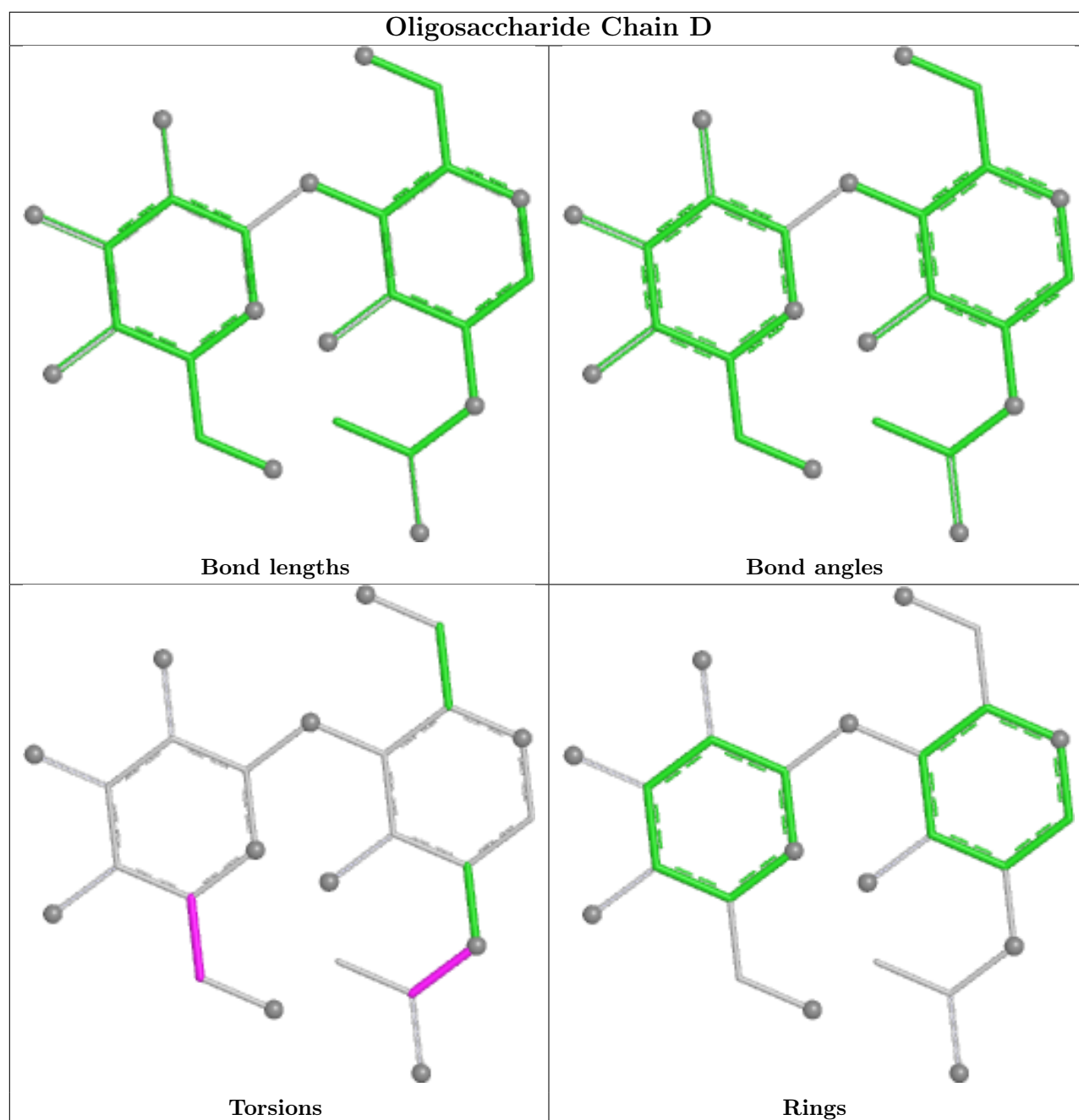
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
2	D	2	BMA	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

Of 7 ligands modelled in this entry, 1 is modelled with single atom - leaving 6 for Mogul analysis.

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	B	602	1	14,14,15	0.96	2 (14%)	17,19,21	0.73	0
4	ACT	B	601	-	3,3,3	1.40	1 (33%)	3,3,3	1.48	0
3	NAG	C	403	1	14,14,15	0.49	0	17,19,21	0.66	1 (5%)
3	NAG	A	401	1	14,14,15	0.50	0	17,19,21	0.40	0
3	NAG	B	603	1	14,14,15	0.34	0	17,19,21	0.57	0
3	NAG	A	402	1	14,14,15	0.51	0	17,19,21	0.54	0

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	B	602	1	-	3/6/23/26	0/1/1/1
3	NAG	C	403	1	-	2/6/23/26	0/1/1/1
3	NAG	A	401	1	-	3/6/23/26	0/1/1/1
3	NAG	B	603	1	-	0/6/23/26	0/1/1/1
3	NAG	A	402	1	-	2/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	602	NAG	C1-C2	2.34	1.55	1.52
3	B	602	NAG	O5-C1	-2.26	1.39	1.43
4	B	601	ACT	CH3-C	2.03	1.57	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	403	NAG	C1-O5-C5	2.24	115.19	112.19

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	NAG	O5-C5-C6-O6
3	A	402	NAG	C4-C5-C6-O6
3	A	401	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
3	A	401	NAG	O7-C7-N2-C2
3	B	602	NAG	C3-C2-N2-C7
3	B	602	NAG	C4-C5-C6-O6
3	C	403	NAG	C1-C2-N2-C7
3	B	602	NAG	O5-C5-C6-O6
3	A	401	NAG	C3-C2-N2-C7
3	C	403	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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	190/288 (65%)	0.44	10 (5%) 32 24	39, 79, 147, 190	0
1	B	189/288 (65%)	0.17	8 (4%) 40 32	30, 64, 113, 147	0
1	C	174/288 (60%)	0.84	21 (12%) 8 6	45, 117, 209, 236	0
All	All	553/864 (64%)	0.47	39 (7%) 22 16	30, 80, 181, 236	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	257	VAL	3.7
1	C	226	ILE	3.6
1	A	211	GLY	3.6
1	C	255	GLU	3.3
1	C	295	THR	3.3
1	B	111	PRO	3.1
1	B	110	LEU	3.0
1	C	265	SER	2.9
1	B	259	HIS	2.9
1	B	151	GLU	2.8
1	A	110	LEU	2.8
1	C	293	PRO	2.6
1	C	206	SER	2.6
1	A	257	VAL	2.6
1	B	235	TYR	2.6
1	C	207	TYR	2.5
1	A	295	THR	2.5
1	C	227	THR	2.5
1	C	242	PRO	2.4
1	C	231	PHE	2.4
1	C	260	LYS	2.4
1	A	231	PHE	2.3
1	A	270	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	257	VAL	2.3
1	A	274	GLU	2.2
1	C	266	GLY	2.2
1	C	220	LEU	2.2
1	C	234	PRO	2.2
1	C	261	VAL	2.2
1	A	279	GLY	2.1
1	C	272	PHE	2.1
1	A	235	TYR	2.1
1	C	237	VAL	2.1
1	C	248	TYR	2.1
1	B	296	ASN	2.0
1	C	249	LEU	2.0
1	A	259	HIS	2.0
1	C	259	HIS	2.0
1	B	178	ASP	2.0

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

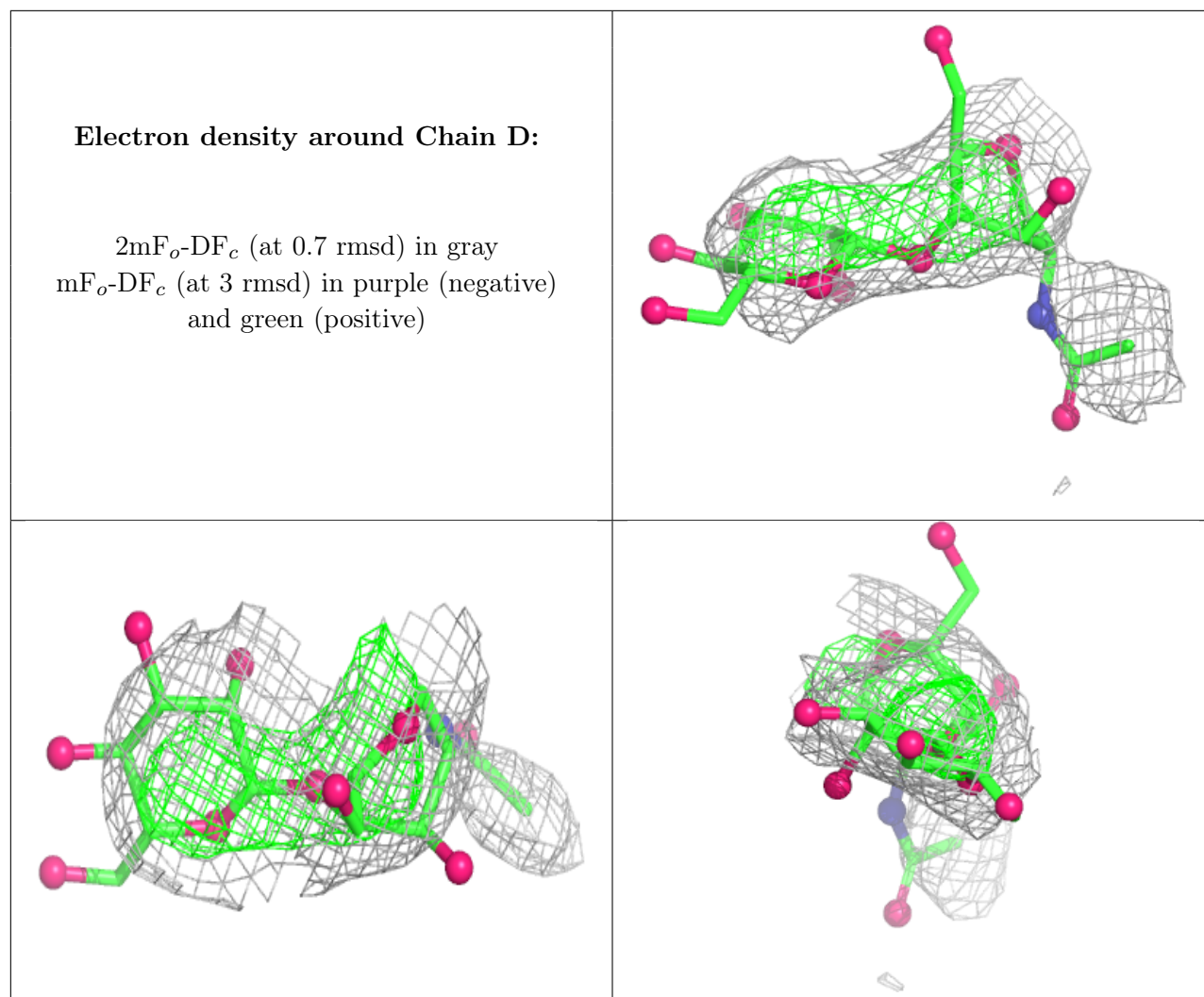
There are no non-standard protein/DNA/RNA residues in this entry.

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(Å ²)	Q<0.9
2	NAG	D	1	14/15	-	-	61,74,84,90	14
2	BMA	D	2	11/12	-	-	67,73,79,81	11

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 ⓘ

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
3	NAG	A	401	14/15	-	-	76,80,85,86	14
3	NAG	A	402	14/15	-	-	51,55,59,66	14
3	NAG	B	602	14/15	-	-	72,82,87,95	14
3	NAG	B	603	14/15	-	-	50,57,60,63	14
3	NAG	C	403	14/15	-	-	45,52,56,62	14
4	ACT	B	601	4/4	0.97	0.10	61,72,77,78	0
5	NH4	C	404	1/1	0.97	0.10	39,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.