



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:28 PM UTC

PDB ID : 3OJA / pdb_00003oja
Title : Crystal structure of LRIM1/APL1C complex
Authors : Baxter, R.H.G.; Deisenhofer, J.
Deposited on : 2010-08-20
Resolution : 2.70 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

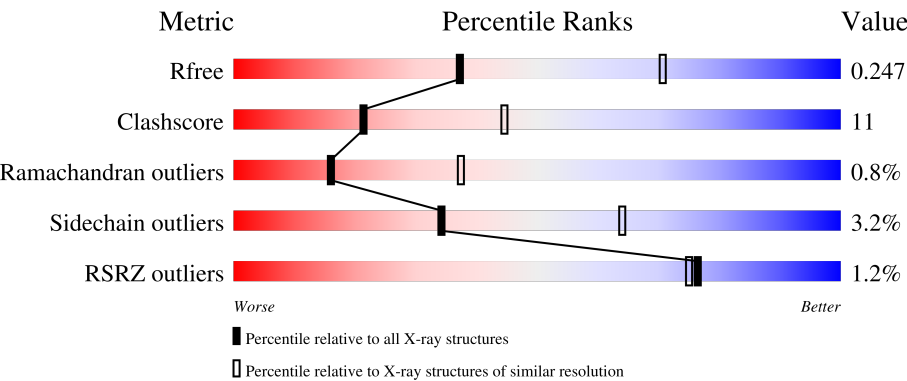
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	487	% 73%24%..
2	B	597	% 67%21%•11%
3	C	2	100%
3	D	2	100%
3	E	2	100%

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Mol	Chain	Length	Quality of chain
3	G	2	 50% 50%
4	F	6	 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
4	MAN	F	3	X	-	-	-
5	NAG	B	1017	X	-	-	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9028 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 Leucine-rich Immune Molecule 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	482	Total	C	N	O	S	0	0	0
			3837	2386	691	749	11			

- Molecule 2 is a protein called Anopheles Plasmodium-responsive Leucine-rich repeat protein 1.

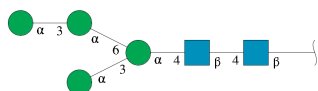
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	534	Total	C	N	O	S	0	0	0
			4366	2748	774	832	12			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



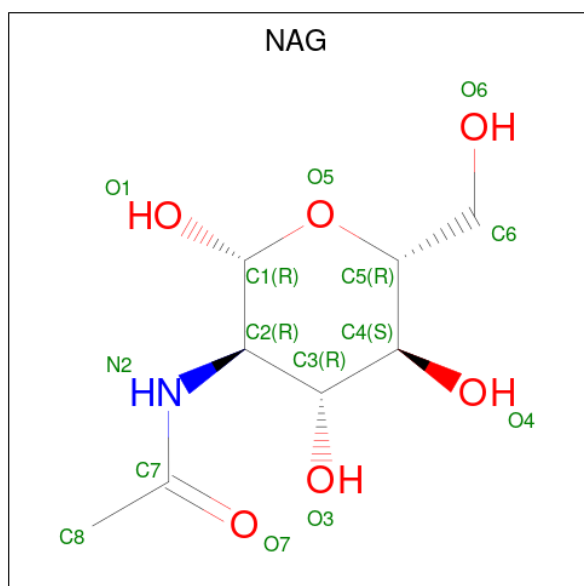
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	265	Total	O	0	0
			265	265		
6	B	348	Total	O	0	0
			348	348		

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:  100%

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  100%

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%

MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  50% 50%

MAG1
MAG2

- Molecule 4: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  50% 50%

MAG1
MAG2
MAN3
MAN4
MAN5
MAN6

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	109.89Å 110.89Å 168.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.56 – 2.70 45.56 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.4 (45.56-2.70) 99.4 (45.56-2.70)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.69Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.205 , 0.265 0.183 , 0.247	Depositor DCC
R_{free} test set	2881 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.012 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9028	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% 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, MAN

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	1.20	3/3884 (0.1%)	1.21	13/5238 (0.2%)
2	B	1.18	2/4441 (0.0%)	1.19	18/6019 (0.3%)
All	All	1.19	5/8325 (0.1%)	1.20	31/11257 (0.3%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	407	GLU	CA-C	5.53	1.60	1.52
1	A	405	HIS	CA-C	5.42	1.59	1.52
1	A	36	ILE	CA-CB	-5.39	1.48	1.54
2	B	658	GLU	CA-C	5.36	1.59	1.52
2	B	183	VAL	CA-C	5.25	1.59	1.52

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	120	GLY	CA-C-N	8.02	128.21	119.87
1	A	120	GLY	C-N-CA	8.02	128.21	119.87
2	B	582	GLU	N-CA-C	-7.65	104.86	112.97
2	B	384	VAL	N-CA-C	-7.43	105.88	112.12
2	B	425	GLN	CA-C-N	-7.10	113.00	120.03
2	B	425	GLN	C-N-CA	-7.10	113.00	120.03
2	B	707	LYS	N-CA-C	-6.64	105.25	113.15
2	B	183	VAL	N-CA-C	6.54	117.99	108.58
1	A	179	ASP	CB-CA-C	-6.38	99.58	110.24
1	A	357	GLN	N-CA-C	-6.21	104.06	111.69
2	B	698	ARG	N-CA-C	-5.91	104.92	111.36
1	A	470	ALA	N-CA-C	-5.82	106.02	113.23
1	A	391	LYS	N-CA-C	-5.71	105.14	111.36
2	B	530	ARG	N-CA-C	-5.67	105.08	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	424	GLY	N-CA-C	-5.64	105.81	112.64
1	A	147	ILE	N-CA-C	5.54	115.83	107.80
2	B	636	LYS	N-CA-C	-5.51	105.35	111.36
1	A	314	GLY	N-CA-C	-5.48	100.19	113.18
2	B	510	ILE	N-CA-C	5.43	117.84	111.05
2	B	289	ILE	N-CA-C	-5.39	99.39	107.37
2	B	484	TRP	N-CA-C	5.33	118.01	110.50
1	A	198	LEU	N-CA-C	-5.31	105.08	112.30
2	B	199	ASP	N-CA-C	-5.30	105.59	111.36
2	B	674	ILE	N-CA-C	-5.29	104.34	111.44
1	A	217	THR	N-CA-C	5.24	117.35	109.23
1	A	113	TYR	N-CA-C	-5.20	104.74	111.71
2	B	583	ALA	N-CA-C	-5.12	106.54	112.89
1	A	262	GLU	CB-CA-C	-5.05	102.64	109.16
1	A	478	LYS	N-CA-C	-5.01	105.48	112.45
2	B	534	TYR	N-CA-C	-5.00	105.73	111.14
2	B	658	GLU	N-CA-C	5.00	116.73	111.28

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	3837	0	3848	90	0
2	B	4366	0	4359	96	0
3	C	28	0	25	0	0
3	D	28	0	25	2	0
3	E	28	0	25	0	0
3	G	28	0	25	2	0
4	F	72	0	61	5	0
5	B	28	0	26	2	0
6	A	265	0	0	8	0
6	B	348	0	0	17	0
All	All	9028	0	8394	183	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 11.

All (183) 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:341:SER:HB3	6:B:942:HOH:O	1.66	0.93
2:B:140:GLN:HB2	2:B:141:PRO:HD3	1.57	0.85
1:A:248:LEU:HB2	1:A:269:ASN:OD1	1.84	0.77
1:A:200:TYR:CE2	1:A:362:GLU:HG3	2.23	0.74
2:B:540:VAL:HG23	6:B:968:HOH:O	1.90	0.71
1:A:303:GLU:HG3	1:A:317:CYS:SG	2.31	0.70
2:B:581:LEU:HD12	2:B:581:LEU:O	1.92	0.69
1:A:136:VAL:HG12	1:A:164:CYS:SG	2.32	0.69
1:A:179:ASP:O	1:A:203:ILE:HA	1.93	0.69
4:F:3:MAN:H2	4:F:6:MAN:H2	1.76	0.68
1:A:277:ARG:HB2	1:A:313:TYR:CE1	2.31	0.66
1:A:449:GLN:NE2	6:A:754:HOH:O	2.29	0.65
3:D:1:NAG:H61	3:D:2:NAG:C1	2.26	0.65
1:A:170:TYR:CD1	1:A:195:HIS:HB2	2.32	0.65
2:B:625:ASP:OD1	2:B:627:LEU:HB2	1.97	0.65
1:A:66:ASN:HB3	1:A:67:PRO:CD	2.27	0.64
1:A:434:LEU:HD13	2:B:634:LEU:HD11	1.79	0.64
2:B:157:TYR:CE1	2:B:186:LYS:HD3	2.32	0.64
1:A:206:VAL:HG23	1:A:225:LEU:HD21	1.81	0.61
2:B:182:ILE:HG22	2:B:182:ILE:O	2.01	0.60
2:B:161:ILE:CD1	2:B:194:PRO:HG3	2.32	0.59
2:B:185:PHE:CE1	2:B:190:MET:CE	2.85	0.59
1:A:480:ASN:OD1	2:B:680:LEU:HD13	2.02	0.59
1:A:119:VAL:HB	1:A:123:ILE:HG13	1.83	0.59
1:A:77:ALA:N	1:A:78:PRO:CD	2.66	0.58
2:B:145:CYS:O	2:B:146:ILE:HG12	2.03	0.58
1:A:308:PRO:C	1:A:310:LEU:H	2.11	0.58
2:B:358:ASN:OD1	2:B:358:ASN:C	2.47	0.57
1:A:366:LEU:C	1:A:366:LEU:HD23	2.29	0.57
1:A:508:LEU:HD11	2:B:707:LYS:O	2.03	0.57
2:B:185:PHE:CZ	2:B:190:MET:HE1	2.40	0.56
2:B:476:ASN:OD1	5:B:1017:NAG:O5	2.23	0.56
1:A:248:LEU:CB	1:A:269:ASN:OD1	2.53	0.56
2:B:185:PHE:CE1	2:B:190:MET:HE2	2.41	0.56
1:A:158:ARG:HH11	1:A:158:ARG:HG3	1.71	0.55
2:B:145:CYS:O	2:B:146:ILE:CG1	2.55	0.55
2:B:374:THR:HB	2:B:377:LEU:HD12	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:432:VAL:HG22	2:B:455:ASN:HB2	1.89	0.55
2:B:185:PHE:CD1	2:B:190:MET:HE2	2.43	0.54
2:B:511:ASP:N	6:B:816:HOH:O	2.18	0.54
2:B:217:ILE:HD11	2:B:233:MET:HE1	1.89	0.53
1:A:312:HIS:N	1:A:312:HIS:ND1	2.56	0.53
4:F:3:MAN:C2	4:F:6:MAN:H2	2.38	0.53
2:B:161:ILE:HD13	2:B:194:PRO:HG3	1.90	0.53
2:B:193:LEU:O	2:B:218:ASP:HB2	2.08	0.53
2:B:249:VAL:HG23	2:B:249:VAL:O	2.08	0.53
2:B:313:VAL:HG13	2:B:313:VAL:O	2.08	0.53
1:A:73:ALA:HB2	1:A:97:ASP:O	2.09	0.53
1:A:273:CYS:O	1:A:274:GLY:C	2.51	0.52
1:A:452:GLN:HA	2:B:652:THR:HG23	1.91	0.52
2:B:322:PHE:CE2	2:B:323:HIS:CE1	2.97	0.52
2:B:542:GLU:C	2:B:544:VAL:H	2.17	0.52
2:B:708:LYS:HG2	2:B:708:LYS:O	2.10	0.52
1:A:200:TYR:CZ	1:A:362:GLU:HG3	2.45	0.51
5:B:1007:NAG:O3	6:B:127:HOH:O	2.17	0.51
2:B:299:SER:O	2:B:301:GLN:HG3	2.11	0.51
1:A:249:VAL:O	1:A:250:LEU:HD23	2.10	0.51
2:B:152:TYR:HA	2:B:182:ILE:HG22	1.92	0.51
1:A:272:HIS:HA	1:A:319:GLU:O	2.10	0.51
2:B:202:ARG:HD3	2:B:224:TYR:HB3	1.93	0.51
1:A:146:ASN:HD22	1:A:146:ASN:N	2.09	0.50
2:B:536:ALA:O	6:B:968:HOH:O	2.19	0.50
1:A:408:LEU:HD13	2:B:609:LEU:CD2	2.41	0.50
1:A:248:LEU:HB2	1:A:269:ASN:CG	2.35	0.50
2:B:282:SER:HA	2:B:306:SER:O	2.12	0.49
2:B:362:THR:HG23	2:B:384:VAL:CG2	2.42	0.49
1:A:313:TYR:C	1:A:313:TYR:CD2	2.91	0.49
1:A:203:ILE:HG13	1:A:223:ASN:OD1	2.12	0.48
2:B:385:GLU:OE1	2:B:409:ARG:NH1	2.45	0.48
2:B:376:TRP:H	2:B:376:TRP:CD1	2.31	0.48
1:A:296:LYS:NZ	6:A:620:HOH:O	2.47	0.48
1:A:472:GLU:OE1	1:A:475:ARG:HD3	2.13	0.48
1:A:174:LYS:HB2	1:A:199:GLN:HG2	1.96	0.48
1:A:313:TYR:C	1:A:313:TYR:HD2	2.20	0.48
1:A:347:THR:N	6:A:731:HOH:O	2.46	0.48
1:A:261:LEU:O	1:A:285:ARG:NH2	2.46	0.48
1:A:307:VAL:O	1:A:310:LEU:HB2	2.14	0.48
1:A:265:ASP:O	1:A:266:LEU:HD23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:GLN:HA	1:A:53:GLN:OE1	2.13	0.47
1:A:140:ARG:HG3	6:A:674:HOH:O	2.14	0.47
1:A:308:PRO:C	1:A:310:LEU:N	2.69	0.47
1:A:365:ALA:O	1:A:368:GLU:HB2	2.14	0.47
1:A:308:PRO:O	1:A:310:LEU:N	2.47	0.47
1:A:66:ASN:HB3	1:A:67:PRO:HD2	1.97	0.47
2:B:510:ILE:CG2	6:B:816:HOH:O	2.63	0.47
1:A:249:VAL:HG11	1:A:324:PRO:HG2	1.96	0.47
2:B:526:PRO:O	2:B:529:ASP:HB3	2.14	0.47
1:A:215:LEU:HD23	1:A:238:VAL:CG1	2.44	0.47
1:A:500:ARG:HG3	6:A:635:HOH:O	2.15	0.47
1:A:179:ASP:OD2	2:B:543:LYS:HE2	2.14	0.47
2:B:272:ASN:HB2	6:B:57:HOH:O	2.15	0.46
2:B:289:ILE:HB	2:B:313:VAL:HG23	1.98	0.46
2:B:143:TYR:HA	6:B:751:HOH:O	2.15	0.46
2:B:581:LEU:N	6:B:860:HOH:O	2.48	0.46
2:B:706:ALA:C	2:B:708:LYS:H	2.24	0.46
1:A:405:HIS:CE1	2:B:606:LEU:HD21	2.51	0.46
1:A:165:ARG:HD2	1:A:185:GLU:O	2.15	0.46
1:A:405:HIS:ND1	2:B:606:LEU:HD11	2.29	0.46
2:B:140:GLN:HB2	2:B:141:PRO:CD	2.36	0.46
2:B:461:ASN:HB2	2:B:482:ASN:OD1	2.16	0.46
1:A:77:ALA:N	1:A:78:PRO:HD2	2.31	0.45
2:B:174:ASP:O	2:B:175:ILE:C	2.60	0.45
1:A:181:VAL:HG23	1:A:203:ILE:HD13	1.98	0.45
1:A:277:ARG:NH1	6:A:666:HOH:O	2.48	0.45
1:A:303:GLU:HG2	1:A:316:TYR:HA	1.99	0.45
1:A:160:LEU:CD1	1:A:160:LEU:N	2.80	0.45
1:A:181:VAL:HG21	1:A:198:LEU:HD13	1.99	0.45
1:A:115:GLN:OE1	3:D:1:NAG:O6	2.26	0.44
2:B:152:TYR:HA	2:B:182:ILE:CG2	2.46	0.44
2:B:428:PRO:HD2	6:B:95:HOH:O	2.17	0.44
2:B:208:ASN:OD1	2:B:208:ASN:C	2.60	0.44
6:B:738:HOH:O	4:F:6:MAN:C1	2.65	0.44
1:A:108:ASP:HA	1:A:127:HIS:HB2	1.98	0.44
1:A:372:THR:HG22	1:A:373:VAL:N	2.31	0.44
2:B:185:PHE:CE1	2:B:190:MET:HE1	2.52	0.44
3:G:2:NAG:H2	3:G:2:NAG:H61	2.00	0.44
2:B:387:ASP:OD1	2:B:389:SER:HB2	2.18	0.44
1:A:457:ARG:HA	1:A:457:ARG:HD2	1.69	0.43
4:F:2:NAG:H62	4:F:3:MAN:C1	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:ARG:HH11	1:A:158:ARG:CG	2.29	0.43
1:A:273:CYS:SG	1:A:319:GLU:N	2.91	0.43
1:A:112:ASN:HB2	1:A:131:ASN:OD1	2.17	0.43
2:B:490:ARG:HH22	2:B:522:GLU:CD	2.26	0.43
2:B:267:ARG:NH2	2:B:290:GLU:HG3	2.33	0.43
1:A:170:TYR:CD1	1:A:195:HIS:CB	3.00	0.43
1:A:229:GLY:O	1:A:230:PRO:C	2.60	0.43
1:A:285:ARG:NH2	1:A:289:VAL:HG21	2.33	0.43
2:B:494:ARG:HG2	6:B:934:HOH:O	2.19	0.43
2:B:508:CYS:HA	6:B:823:HOH:O	2.17	0.43
1:A:140:ARG:HD2	6:A:529:HOH:O	2.18	0.43
2:B:143:TYR:CD1	2:B:159:VAL:HG22	2.54	0.43
2:B:399:HIS:N	2:B:400:PRO:CD	2.81	0.43
1:A:168:VAL:HG11	1:A:171:LEU:HB2	2.01	0.43
1:A:244:ARG:HG2	1:A:245:ASN:N	2.33	0.43
2:B:179:ASN:HB2	2:B:203:GLN:NE2	2.33	0.43
2:B:202:ARG:NH1	2:B:224:TYR:CD1	2.87	0.43
1:A:55:ALA:O	1:A:56:TRP:C	2.62	0.42
1:A:72:SER:O	1:A:73:ALA:C	2.60	0.42
2:B:457:TYR:HA	2:B:478:THR:OG1	2.19	0.42
3:G:2:NAG:H2	3:G:2:NAG:C6	2.49	0.42
1:A:350:LEU:O	1:A:354:ARG:HG2	2.19	0.42
2:B:190:MET:O	2:B:214:ILE:HA	2.19	0.42
2:B:210:ASN:O	2:B:211:ASP:HB3	2.20	0.42
1:A:241:ILE:O	1:A:241:ILE:HG23	2.19	0.42
2:B:138:PRO:O	2:B:139:ARG:HB2	2.19	0.42
2:B:605:LEU:HD12	2:B:605:LEU:O	2.19	0.42
1:A:123:ILE:HD13	1:A:123:ILE:HA	1.82	0.42
1:A:219:ASP:OD1	1:A:219:ASP:C	2.62	0.42
2:B:157:TYR:CZ	2:B:186:LYS:HD3	2.54	0.42
2:B:423:TYR:HB3	2:B:446:ASN:HA	2.02	0.42
2:B:385:GLU:HB2	2:B:409:ARG:NH1	2.34	0.42
2:B:664:LYS:HD2	2:B:664:LYS:HA	1.76	0.41
1:A:266:LEU:HB2	1:A:316:TYR:CE2	2.55	0.41
1:A:321:LEU:HA	1:A:322:PRO:HD3	1.91	0.41
2:B:337:PRO:HD2	2:B:340:VAL:HG11	2.03	0.41
2:B:624:LYS:N	2:B:624:LYS:HD3	2.35	0.41
2:B:489:LEU:HD12	2:B:520:CYS:HB3	2.02	0.41
2:B:498:ARG:NH1	2:B:516:HIS:O	2.52	0.41
2:B:515:GLU:O	2:B:516:HIS:C	2.62	0.41
1:A:453:ASN:ND2	4:F:2:NAG:H81	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:622:LEU:HD22	6:B:956:HOH:O	2.19	0.41
2:B:581:LEU:C	2:B:583:ALA:H	2.28	0.41
1:A:114:VAL:HG12	1:A:115:GLN:N	2.35	0.41
2:B:218:ASP:O	2:B:220:TYR:N	2.54	0.41
2:B:498:ARG:HG2	2:B:501:VAL:O	2.21	0.41
1:A:477:LYS:HG3	2:B:676:LEU:CD1	2.51	0.41
1:A:375:ASP:OD1	1:A:377:VAL:HG12	2.21	0.40
1:A:508:LEU:HD23	1:A:508:LEU:O	2.21	0.40
2:B:174:ASP:O	2:B:176:THR:N	2.53	0.40
2:B:265:LEU:HA	2:B:266:PRO:HD3	1.90	0.40
2:B:285:ASN:HB3	2:B:309:ARG:NH1	2.36	0.40
2:B:523:SER:HB3	6:B:65:HOH:O	2.22	0.40
2:B:542:GLU:C	2:B:544:VAL:N	2.79	0.40
2:B:275:LYS:HD2	6:B:802:HOH:O	2.20	0.40
2:B:607:GLN:O	2:B:609:LEU:N	2.54	0.40
1:A:136:VAL:CG1	1:A:164:CYS:SG	3.07	0.40
1:A:156:MET:O	1:A:159:ASP:HB2	2.21	0.40
1:A:174:LYS:NZ	6:A:727:HOH:O	2.45	0.40
1:A:449:GLN:OE1	2:B:648:LYS:HE2	2.21	0.40
2:B:415:ASN:HB3	2:B:416:ARG:H	1.76	0.40
1:A:451:VAL:HG12	2:B:652:THR:HG21	2.03	0.40
2:B:540:VAL:N	6:B:968:HOH:O	2.54	0.40
2:B:607:GLN:C	2:B:609:LEU:N	2.78	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	478/487 (98%)	430 (90%)	46 (10%)	2 (0%)	30	54
2	B	528/597 (88%)	478 (90%)	44 (8%)	6 (1%)	11	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1006/1084 (93%)	908 (90%)	90 (9%)	8 (1%)	16	37

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	226	HIS
2	B	146	ILE
2	B	158	ASP
2	B	139	ARG
1	A	309	THR
2	B	213	GLN
2	B	282	SER
1	A	67	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	420/423 (99%)	401 (96%)	19 (4%)	24	52
2	B	495/550 (90%)	485 (98%)	10 (2%)	48	76
All	All	915/973 (94%)	886 (97%)	29 (3%)	34	64

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	LYS
1	A	109	LEU
1	A	137	SER
1	A	174	LYS
1	A	190	SER
1	A	296	LYS
1	A	298	THR
1	A	302	GLU
1	A	310	LEU
1	A	313	TYR

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Mol	Chain	Res	Type
1	A	333	LYS
1	A	341	SER
1	A	386	THR
1	A	396	GLU
1	A	399	SER
1	A	425	THR
1	A	438	VAL
1	A	453	ASN
1	A	499	VAL
2	B	151	GLN
2	B	158	ASP
2	B	277	THR
2	B	354	ARG
2	B	365	LYS
2	B	476	ASN
2	B	518	LEU
2	B	599	GLN
2	B	603	GLU
2	B	624	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	HIS
1	A	146	ASN
1	A	356	ASN
1	A	405	HIS
1	A	414	GLN
1	A	448	GLN
1	A	452	GLN
1	A	453	ASN
2	B	414	ASN
2	B	481	HIS
2	B	516	HIS
2	B	586	ASN
2	B	602	GLN
2	B	645	GLN
2	B	679	GLN
2	B	703	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 ⓘ

14 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$
3	NAG	C	1	3,1	14,14,15	0.75	0	17,19,21	1.66	4 (23%)
3	NAG	C	2	3	14,14,15	1.05	1 (7%)	17,19,21	1.92	6 (35%)
3	NAG	D	1	3,1	14,14,15	0.84	0	17,19,21	1.79	4 (23%)
3	NAG	D	2	3	14,14,15	0.92	0	17,19,21	3.45	7 (41%)
3	NAG	E	1	3,1	14,14,15	0.81	0	17,19,21	2.24	4 (23%)
3	NAG	E	2	3	14,14,15	0.99	1 (7%)	17,19,21	2.07	4 (23%)
4	NAG	F	1	2,4	14,14,15	1.34	1 (7%)	17,19,21	2.09	6 (35%)
4	NAG	F	2	4	14,14,15	1.14	2 (14%)	17,19,21	2.59	5 (29%)
4	MAN	F	3	4	11,11,12	1.25	2 (18%)	15,15,17	1.56	2 (13%)
4	MAN	F	4	4	11,11,12	1.26	2 (18%)	15,15,17	1.46	3 (20%)
4	MAN	F	5	4	11,11,12	1.21	0	15,15,17	2.07	5 (33%)
4	MAN	F	6	4	11,11,12	1.13	1 (9%)	15,15,17	1.77	4 (26%)
3	NAG	G	1	3,2	14,14,15	1.02	2 (14%)	17,19,21	1.88	4 (23%)
3	NAG	G	2	3	14,14,15	0.60	0	17,19,21	1.78	3 (17%)

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	C	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	NAG	D	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	NAG	E	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
4	NAG	F	1	2,4	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	1/6/23/26	0/1/1/1
4	MAN	F	3	4	1/1/4/5	2/2/19/22	0/1/1/1
4	MAN	F	4	4	-	0/2/19/22	0/1/1/1
4	MAN	F	5	4	-	1/2/19/22	0/1/1/1
4	MAN	F	6	4	-	1/2/19/22	0/1/1/1
3	NAG	G	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	1	NAG	O5-C1	-3.98	1.37	1.43
3	C	2	NAG	O5-C1	-3.48	1.37	1.43
4	F	3	MAN	O5-C1	-2.96	1.38	1.43
4	F	6	MAN	C2-C3	2.91	1.56	1.52
4	F	4	MAN	O5-C1	-2.89	1.38	1.43
3	E	2	NAG	C1-C2	2.47	1.55	1.52
4	F	3	MAN	O5-C5	-2.47	1.38	1.43
4	F	4	MAN	O2-C2	-2.40	1.38	1.43
3	G	1	NAG	C2-N2	-2.37	1.42	1.46
4	F	2	NAG	O5-C1	-2.33	1.39	1.43
3	G	1	NAG	O5-C1	-2.20	1.40	1.43
4	F	2	NAG	O7-C7	2.09	1.27	1.23

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	2	NAG	C1-O5-C5	10.75	126.60	112.19
4	F	2	NAG	C1-O5-C5	7.88	122.75	112.19
3	D	2	NAG	C2-N2-C7	-6.35	114.39	122.90
3	E	1	NAG	C1-O5-C5	6.30	120.63	112.19
3	G	1	NAG	C2-N2-C7	-5.51	115.51	122.90
3	E	2	NAG	C1-C2-N2	4.82	118.03	110.43
3	D	1	NAG	C1-O5-C5	4.67	118.45	112.19
4	F	3	MAN	O3-C3-C2	4.42	119.08	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	2	NAG	C1-O5-C5	4.20	117.81	112.19
4	F	5	MAN	C3-C4-C5	4.16	117.77	110.23
4	F	1	NAG	O6-C6-C5	-4.13	97.29	111.33
3	E	1	NAG	C2-N2-C7	-4.05	117.48	122.90
3	G	2	NAG	O5-C5-C6	4.01	115.47	107.66
4	F	2	NAG	C4-C3-C2	3.96	116.82	111.02
3	C	2	NAG	C1-O5-C5	3.74	117.20	112.19
4	F	5	MAN	C1-O5-C5	-3.57	107.40	112.19
3	D	2	NAG	C4-C3-C2	3.54	116.20	111.02
3	E	2	NAG	C4-C3-C2	3.53	116.19	111.02
4	F	1	NAG	C1-O5-C5	3.53	116.91	112.19
3	C	2	NAG	C2-N2-C7	-3.50	118.20	122.90
4	F	2	NAG	C6-C5-C4	-3.37	104.75	113.02
4	F	6	MAN	O5-C5-C6	3.28	114.04	107.66
4	F	1	NAG	C6-C5-C4	-3.21	105.13	113.02
3	E	2	NAG	C2-N2-C7	3.11	127.06	122.90
3	C	1	NAG	O7-C7-C8	-3.09	116.56	122.05
3	E	2	NAG	C3-C4-C5	3.05	115.75	110.23
4	F	5	MAN	O2-C2-C3	3.04	116.44	110.15
4	F	4	MAN	C2-C3-C4	3.03	116.19	110.86
3	C	1	NAG	C1-O5-C5	2.96	116.15	112.19
3	C	1	NAG	O7-C7-N2	2.91	127.13	121.98
3	D	1	NAG	O3-C3-C2	2.84	115.29	109.40
3	C	2	NAG	O4-C4-C5	2.82	116.27	109.32
3	D	2	NAG	C3-C4-C5	2.78	115.27	110.23
4	F	6	MAN	O2-C2-C3	2.77	115.89	110.15
4	F	6	MAN	C2-C3-C4	2.72	115.65	110.86
3	G	1	NAG	C1-O5-C5	2.69	115.80	112.19
4	F	1	NAG	C2-N2-C7	2.65	126.44	122.90
4	F	1	NAG	O5-C5-C4	2.63	117.22	110.83
3	D	2	NAG	O5-C5-C4	2.53	116.97	110.83
3	G	2	NAG	O5-C5-C4	-2.52	104.70	110.83
4	F	2	NAG	O6-C6-C5	-2.47	102.93	111.33
3	G	1	NAG	C1-C2-N2	-2.43	106.61	110.43
3	C	2	NAG	O5-C5-C6	-2.39	103.01	107.66
3	E	1	NAG	O7-C7-C8	-2.38	117.83	122.05
3	E	1	NAG	C1-C2-N2	2.34	114.13	110.43
4	F	4	MAN	O3-C3-C4	2.34	115.89	110.38
3	D	2	NAG	O5-C1-C2	2.31	114.87	111.29
3	C	2	NAG	O4-C4-C3	-2.29	104.97	110.38
3	G	1	NAG	O3-C3-C2	2.25	114.08	109.40
3	D	1	NAG	C2-N2-C7	-2.25	119.89	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	4	MAN	O5-C5-C6	2.24	112.02	107.66
4	F	3	MAN	O5-C5-C4	-2.21	105.46	110.83
4	F	6	MAN	O4-C4-C3	2.17	115.50	110.38
3	D	2	NAG	O3-C3-C4	-2.17	105.26	110.38
4	F	2	NAG	O4-C4-C3	-2.17	105.27	110.38
4	F	5	MAN	O6-C6-C5	-2.12	104.11	111.33
4	F	5	MAN	C2-C3-C4	2.10	114.55	110.86
4	F	1	NAG	O7-C7-N2	2.09	125.68	121.98
3	C	1	NAG	O4-C4-C5	-2.06	104.25	109.32
3	D	1	NAG	O5-C1-C2	2.04	114.44	111.29
3	C	2	NAG	O6-C6-C5	-2.03	104.43	111.33

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	F	3	MAN	C1

All (17) torsion outliers are listed below:

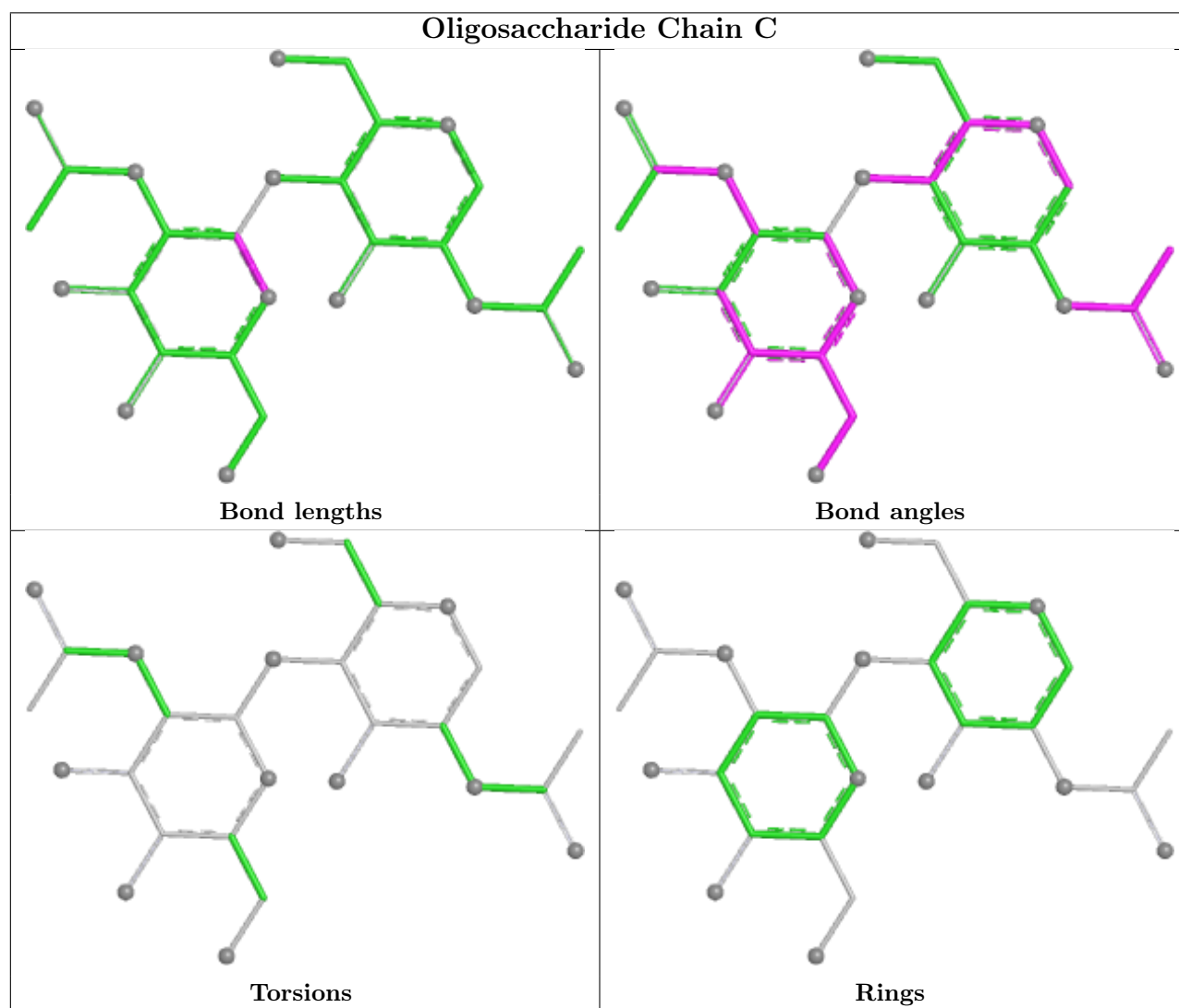
Mol	Chain	Res	Type	Atoms
3	E	1	NAG	C8-C7-N2-C2
3	E	1	NAG	O7-C7-N2-C2
3	E	2	NAG	C1-C2-N2-C7
4	F	1	NAG	C4-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6
4	F	3	MAN	C4-C5-C6-O6
4	F	1	NAG	O5-C5-C6-O6
3	D	1	NAG	C4-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
4	F	5	MAN	O5-C5-C6-O6
4	F	3	MAN	O5-C5-C6-O6
4	F	6	MAN	O5-C5-C6-O6
3	D	1	NAG	C8-C7-N2-C2
4	F	2	NAG	C4-C5-C6-O6
3	D	1	NAG	O7-C7-N2-C2
3	E	2	NAG	O7-C7-N2-C2

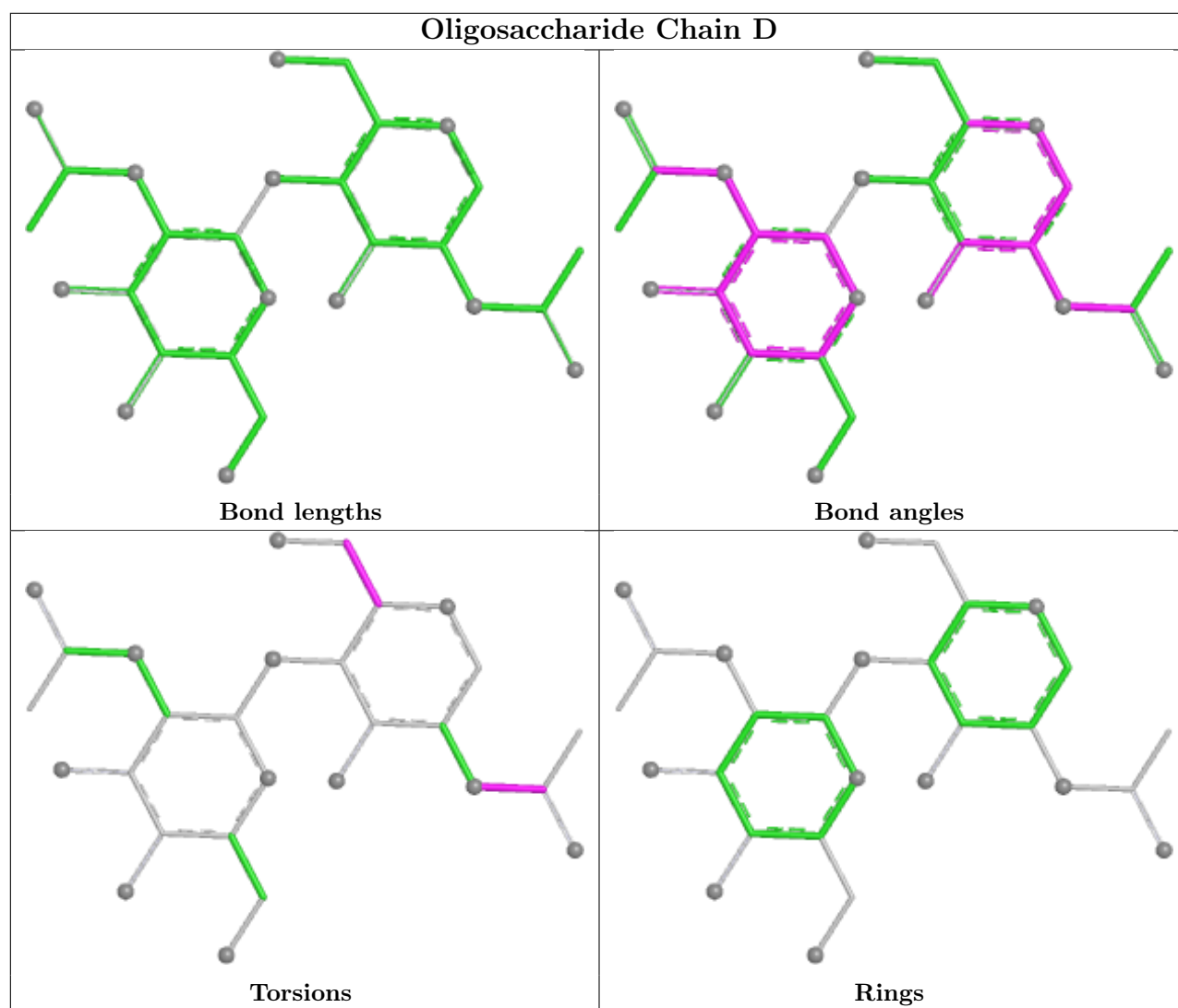
There are no ring outliers.

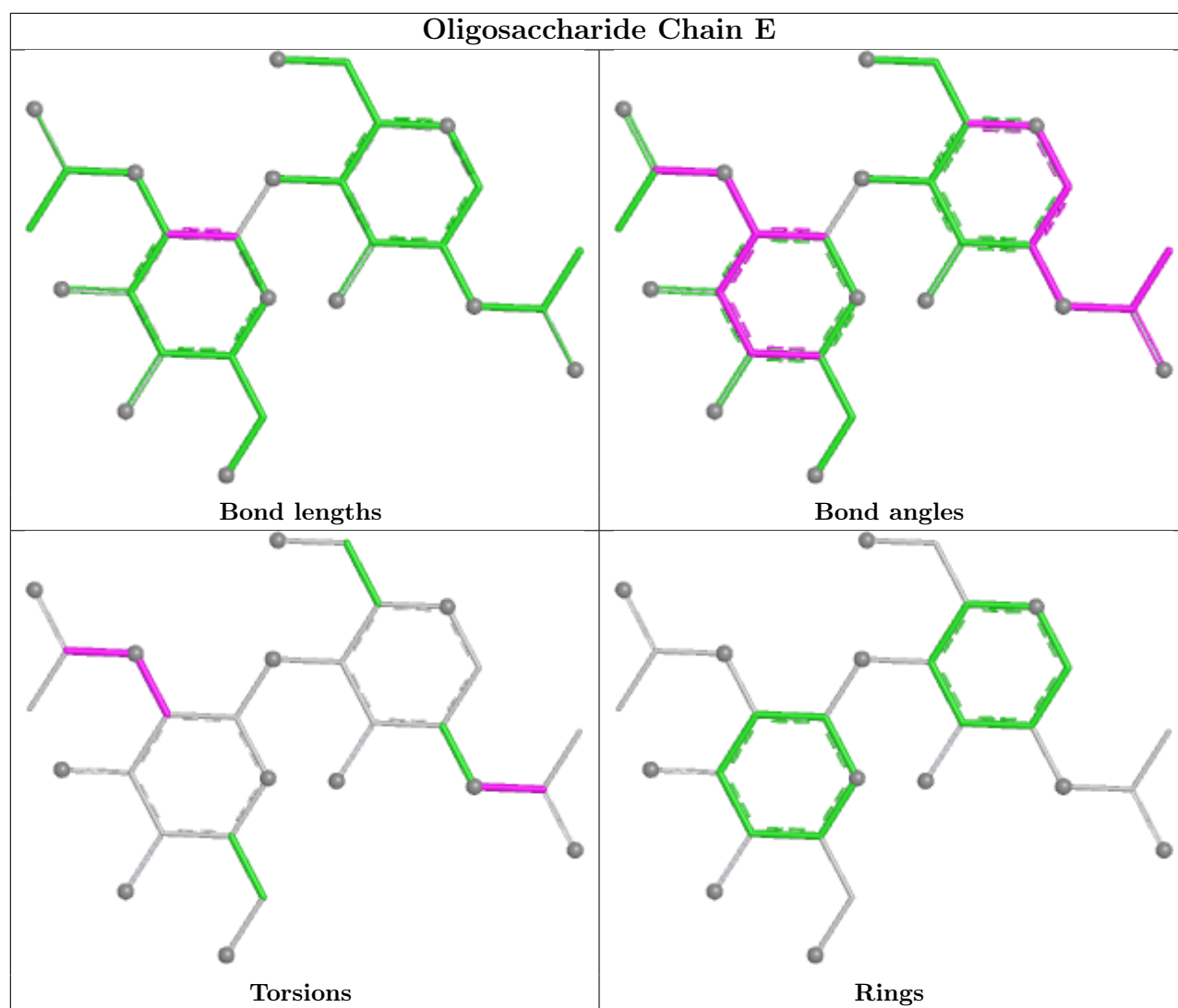
6 monomers are involved in 9 short contacts:

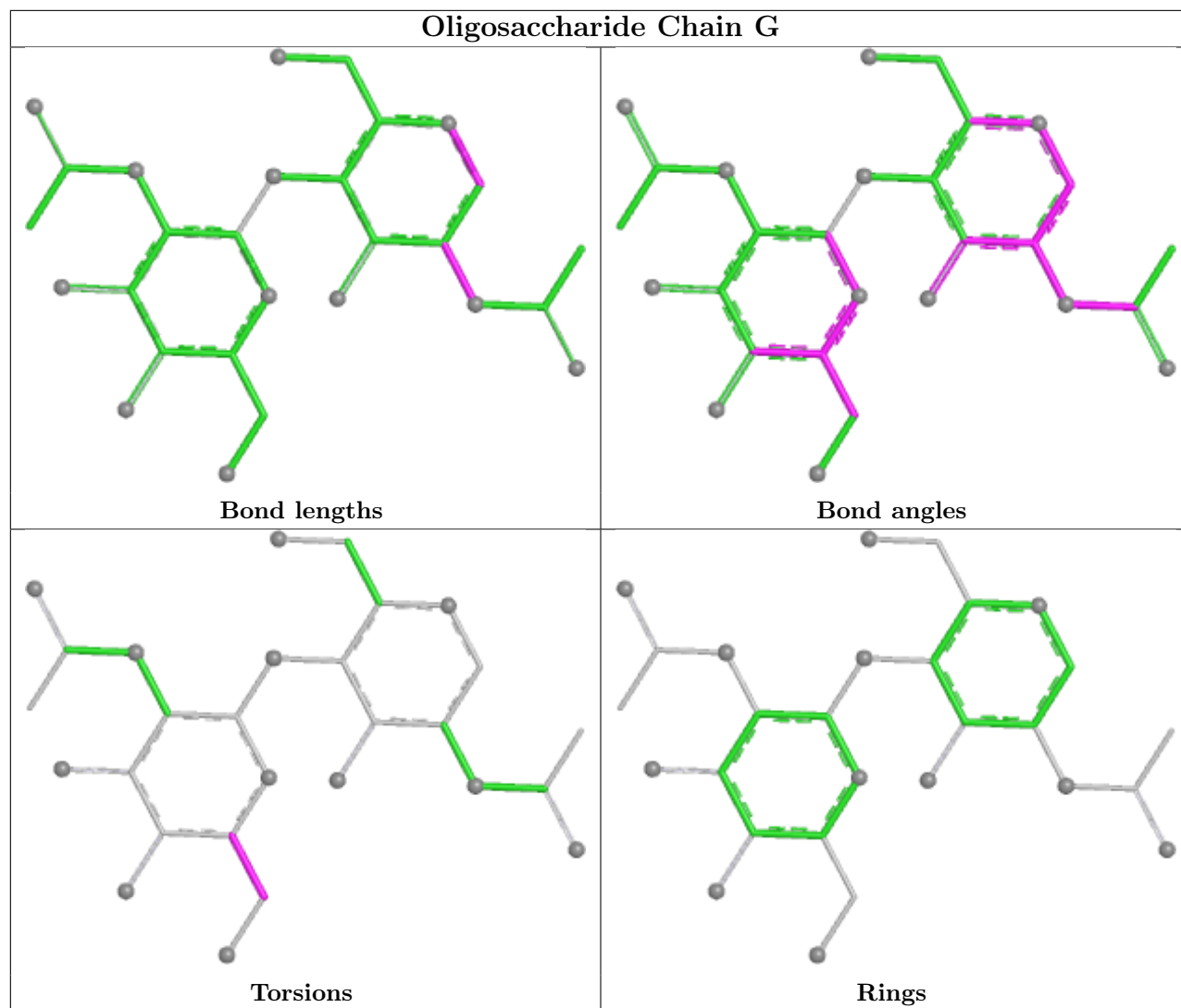
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	3	MAN	3	0
3	D	2	NAG	1	0
3	D	1	NAG	2	0
4	F	2	NAG	2	0
4	F	6	MAN	3	0
3	G	2	NAG	2	0

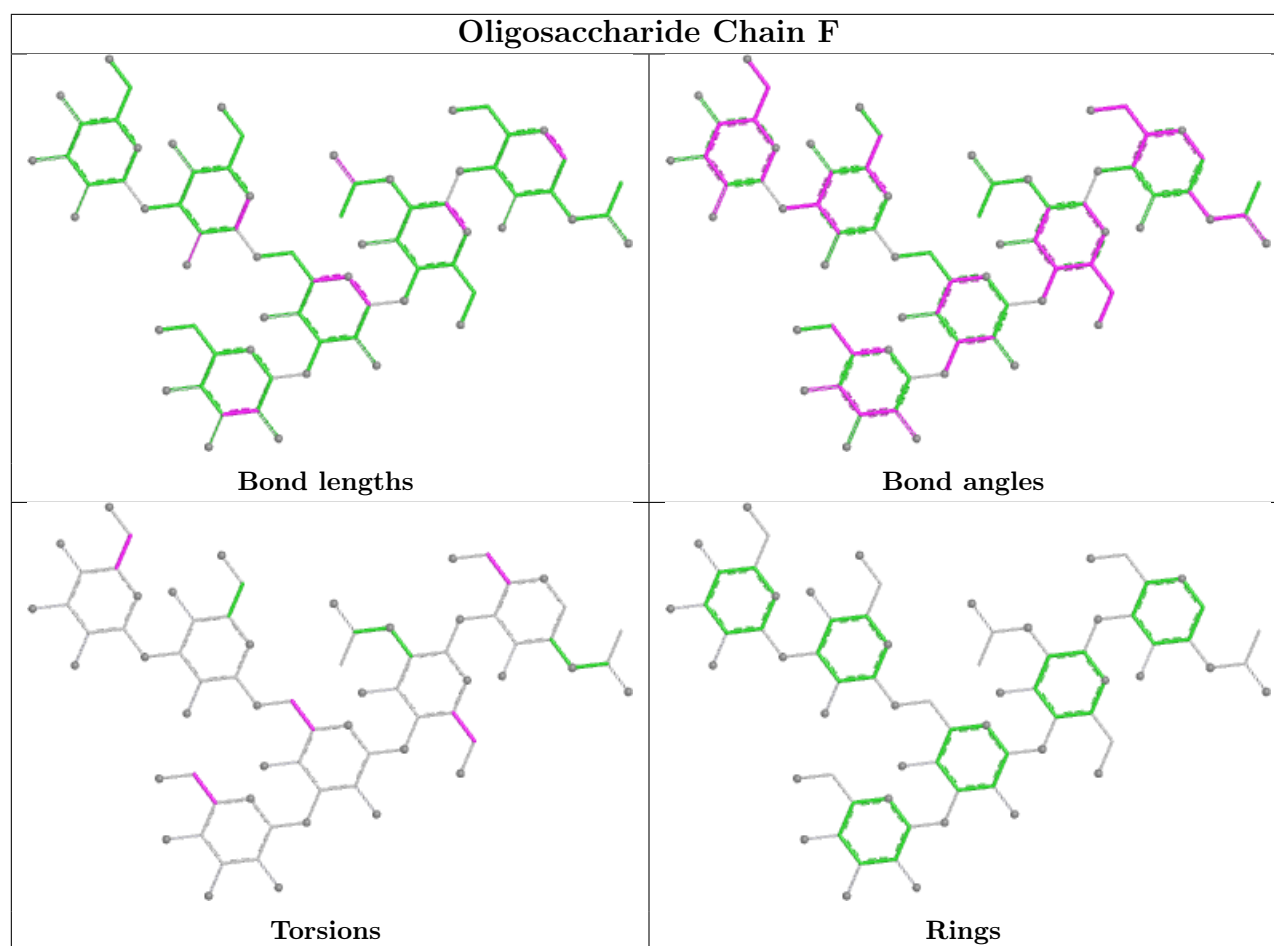
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

2 ligands 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	$\# Z > 2$
5	NAG	B	1017	2	14,14,15	0.86	0	17,19,21	2.33	8 (47%)
5	NAG	B	1007	2	14,14,15	1.11	1 (7%)	17,19,21	2.81	8 (47%)

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
5	NAG	B	1017	2	1/1/5/7	5/6/23/26	0/1/1/1
5	NAG	B	1007	2	-	1/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1007	NAG	O7-C7	2.66	1.29	1.23

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1007	NAG	C4-C3-C2	-7.22	100.43	111.02
5	B	1017	NAG	C1-O5-C5	6.37	120.72	112.19
5	B	1007	NAG	C2-N2-C7	-4.64	116.68	122.90
5	B	1007	NAG	C1-O5-C5	3.74	117.20	112.19
5	B	1007	NAG	O4-C4-C3	3.56	118.78	110.38
5	B	1007	NAG	O3-C3-C4	3.09	117.66	110.38
5	B	1017	NAG	C6-C5-C4	3.04	120.47	113.02
5	B	1017	NAG	O5-C5-C6	2.68	112.88	107.66
5	B	1017	NAG	O5-C5-C4	-2.61	104.47	110.83
5	B	1007	NAG	O5-C5-C6	2.41	112.34	107.66
5	B	1017	NAG	O7-C7-C8	-2.26	118.04	122.05
5	B	1017	NAG	O4-C4-C5	-2.22	103.85	109.32
5	B	1017	NAG	O3-C3-C2	2.11	113.78	109.40
5	B	1007	NAG	C3-C4-C5	-2.04	106.53	110.23
5	B	1017	NAG	C1-C2-N2	-2.04	107.22	110.43
5	B	1007	NAG	C8-C7-N2	-2.02	112.77	116.12

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	B	1017	NAG	C1

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1017	NAG	O5-C5-C6-O6
5	B	1017	NAG	C4-C5-C6-O6
5	B	1017	NAG	C3-C2-N2-C7
5	B	1017	NAG	C8-C7-N2-C2
5	B	1017	NAG	O7-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
5	B	1007	NAG	C8-C7-N2-C2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1017	NAG	1	0
5	B	1007	NAG	1	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 [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	482/487 (98%)	-0.47	7 (1%) 72 70	18, 36, 62, 97	0
2	B	534/597 (89%)	-0.62	5 (0%) 81 80	13, 31, 65, 87	0
All	All	1016/1084 (93%)	-0.55	12 (1%) 76 75	13, 34, 64, 97	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	148	SER	4.3
2	B	138	PRO	4.1
2	B	581	LEU	2.9
1	A	349	ARG	2.8
1	A	306	THR	2.4
1	A	347	THR	2.4
2	B	544	VAL	2.4
1	A	350	LEU	2.4
2	B	141	PRO	2.4
1	A	348	GLU	2.2
1	A	371	ARG	2.1
1	A	354	ARG	2.0

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

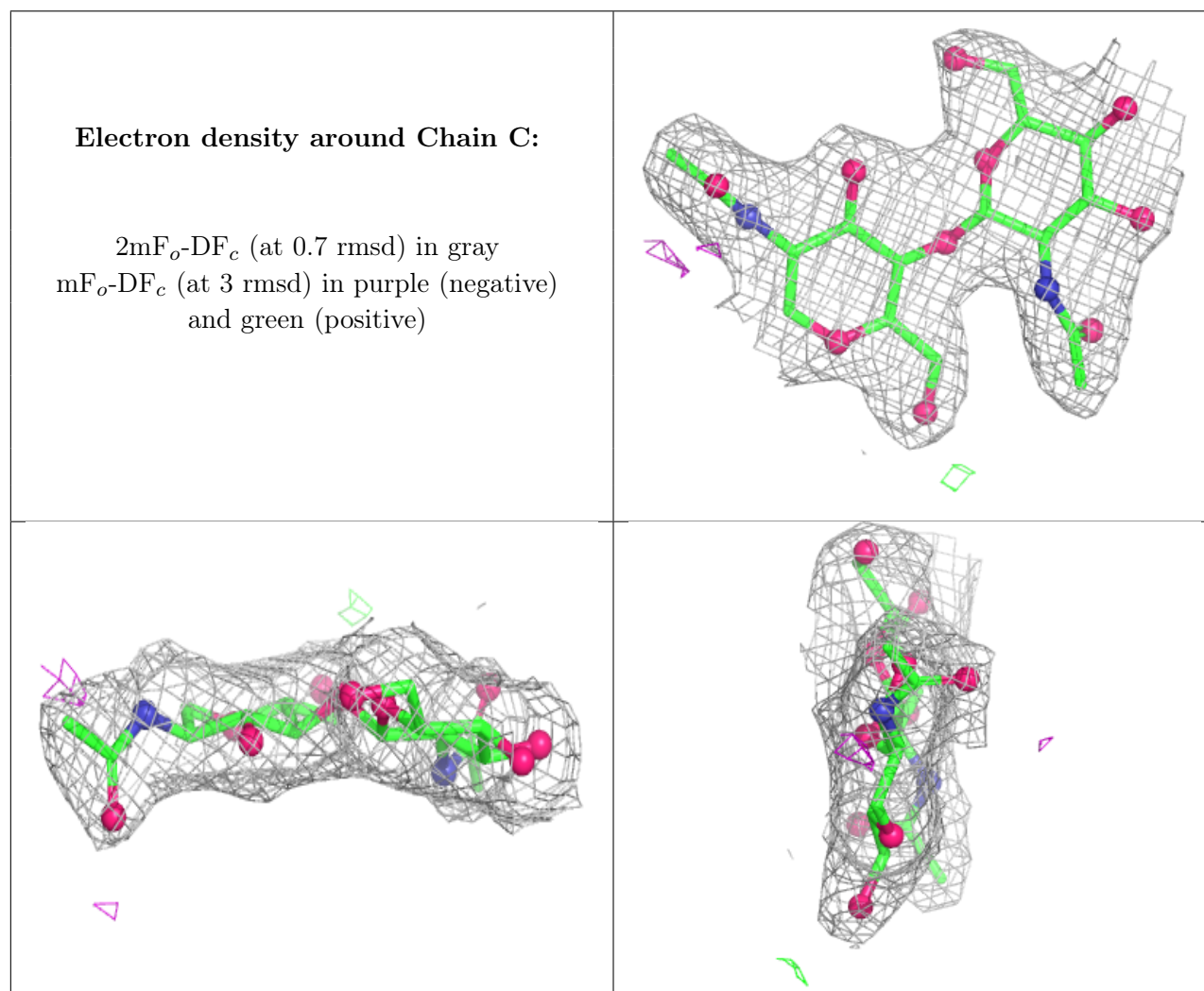
There are no non-standard protein/DNA/RNA residues in this entry.

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.

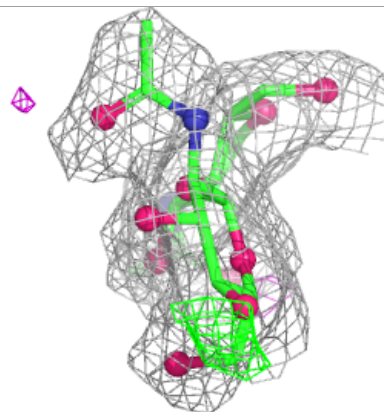
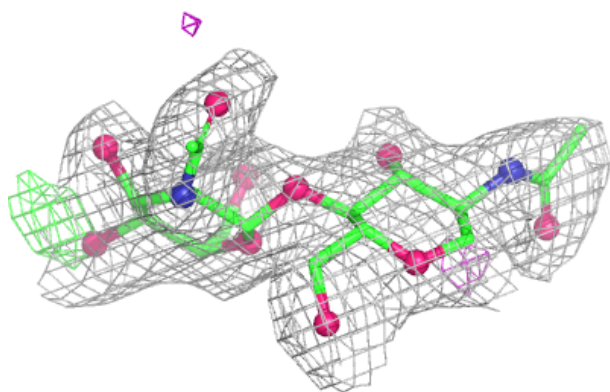
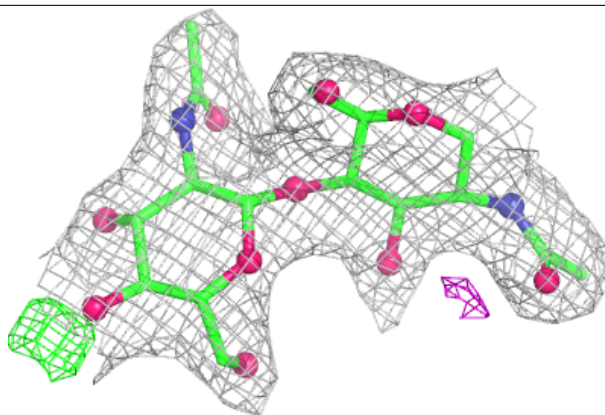
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	E	2	14/15	0.63	0.18	59,84,99,100	0
3	NAG	E	1	14/15	0.68	0.16	59,69,77,87	0
4	MAN	F	6	11/12	0.75	0.20	35,63,93,99	0
3	NAG	D	2	14/15	0.83	0.13	39,55,71,72	0
3	NAG	G	2	14/15	0.85	0.11	30,61,79,81	0
4	MAN	F	5	11/12	0.89	0.12	40,49,70,84	0
4	MAN	F	4	11/12	0.89	0.10	39,42,55,56	0
3	NAG	C	2	14/15	0.94	0.08	37,52,63,65	0
4	NAG	F	2	14/15	0.95	0.09	14,31,43,46	0
4	MAN	F	3	11/12	0.96	0.07	29,41,45,46	0
3	NAG	G	1	14/15	0.96	0.06	20,33,46,51	0
4	NAG	F	1	14/15	0.97	0.07	15,25,35,37	0
3	NAG	D	1	14/15	0.97	0.06	28,44,49,54	0
3	NAG	C	1	14/15	0.97	0.06	12,28,35,40	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



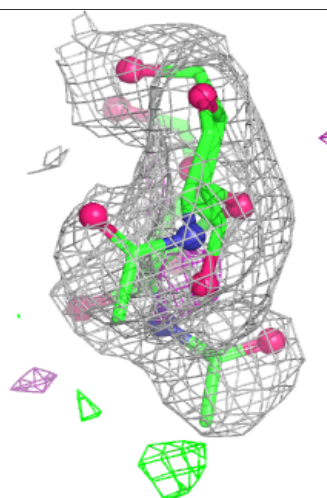
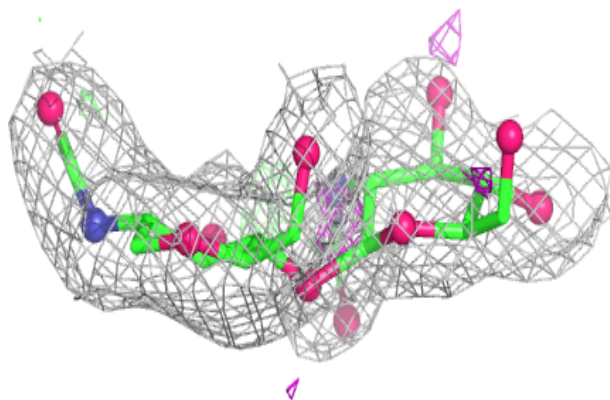
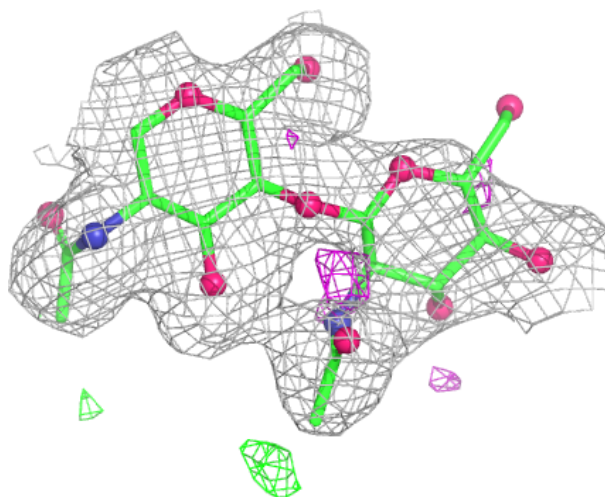
Electron density around Chain D:

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



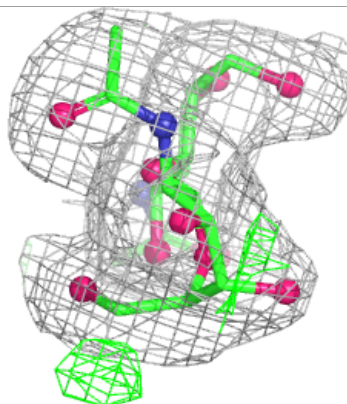
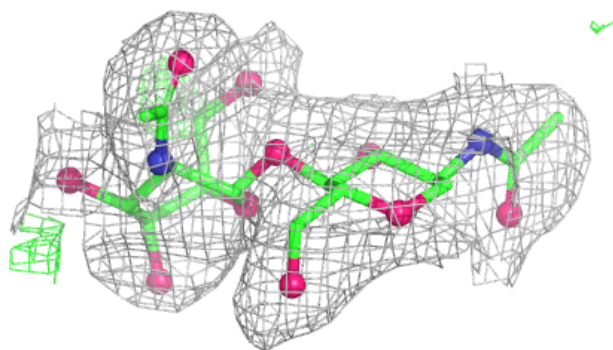
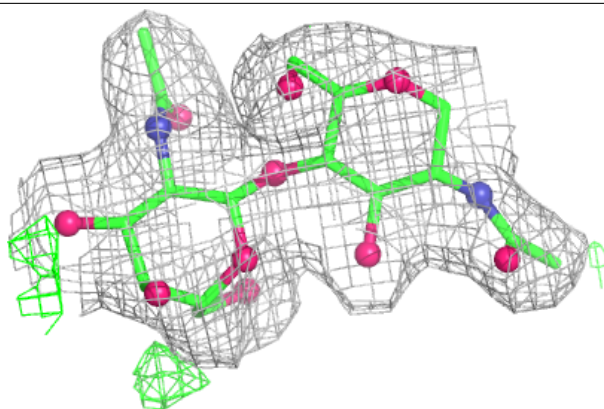
Electron density around Chain E:

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

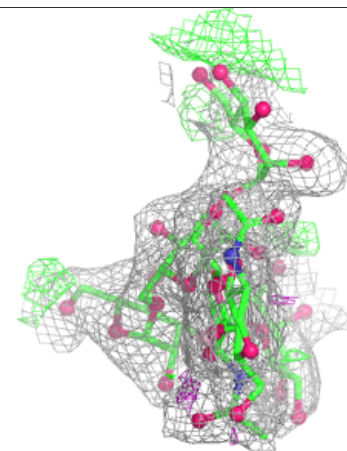
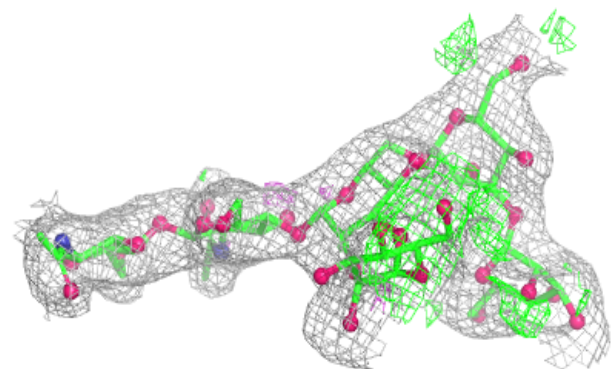
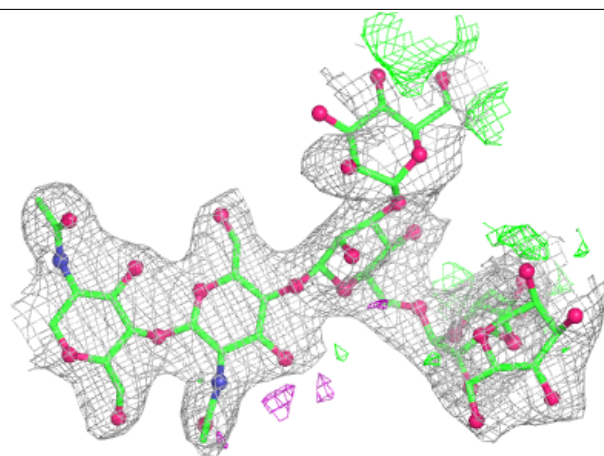


Electron density around Chain G:

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

**Electron density around Chain F:**

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



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
5	NAG	B	1017	14/15	0.73	0.16	47,62,80,93	0
5	NAG	B	1007	14/15	0.83	0.12	47,56,67,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.