



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:57 AM UTC

PDB ID : 4MMZ / pdb_00004mmz
Title : Integrin AlphaVBeta3 ectodomain bound to an antagonistic tenth domain of Fibronectin
Authors : van Agthoven, J.; Xiong, J.; Arnaout, M.A.
Deposited on : 2013-09-09
Resolution : 3.10 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

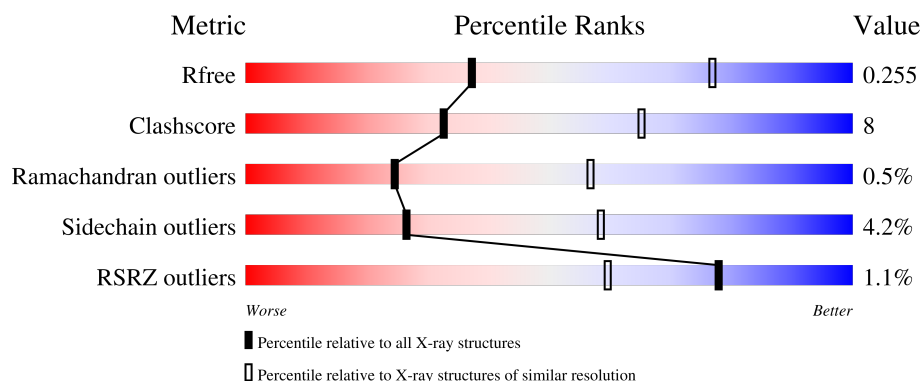
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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.



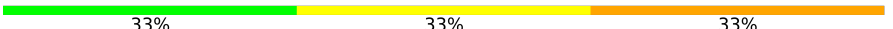
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	959	% 76% 19% • •
2	B	692	2% 76% 22% •
3	C	98	% 72% 18% • 7%
4	D	2	100%
4	F	2	50% 50%

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Mol	Chain	Length	Quality of chain
4	G	2	 50% 50%
4	H	2	 50% 50%
5	E	6	 50% 17% 33%
6	I	3	 33% 33% 33%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 13512 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 Integrin alpha-V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	920	Total	C	N	O	S	0	0	0
			7163	4535	1216	1377	35			

- Molecule 2 is a protein called Integrin beta-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	690	Total	C	N	O	S	0	0	0
			5294	3250	904	1070	70			

- Molecule 3 is a protein called Fibronectin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	91	Total	C	N	O	0	0	0
			690	439	112	139			

There are 10 discrepancies between the modelled and reference sequences:

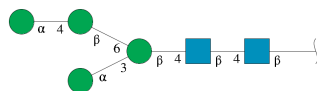
Chain	Residue	Modelled	Actual	Comment	Reference
C	1492	PRO	GLY	engineered mutation	UNP P02751
C	1496	TRP	SER	engineered mutation	UNP P02751
C	1497	ASN	PRO	engineered mutation	UNP P02751
C	1498	GLU	ALA	engineered mutation	UNP P02751
C	1499	GLY	SER	engineered mutation	UNP P02751
C	1510	GLY	-	expression tag	UNP P02751
C	1511	LYS	-	expression tag	UNP P02751
C	1512	LYS	-	expression tag	UNP P02751
C	1513	GLY	-	expression tag	UNP P02751
C	1514	LYS	-	expression tag	UNP P02751

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



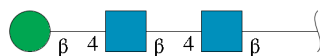
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-4)-beta-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-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
5	E	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 6 is an oligosaccharide called beta-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
6	I	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 8 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	5	Total	Mn	0	0
			5	5		
8	B	3	Total	Mn	0	0
			3	3		

- Molecule 9 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	Na	0	0
			1	1		

- Molecule 10 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			6	3	3		
10	C	1	Total	C	O	0	0
			6	3	3		

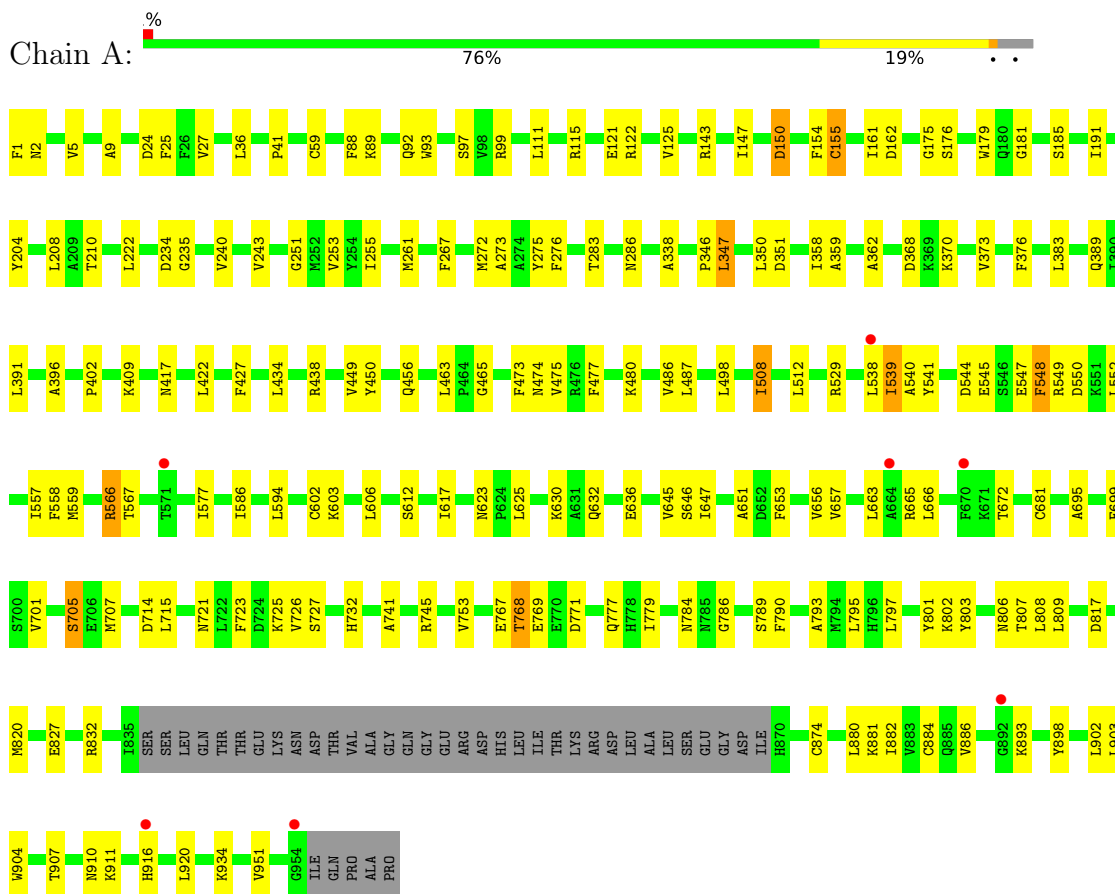
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	2	Total	O	0	0
			2	2		
11	B	1	Total	O	0	0
			1	1		
11	C	6	Total	O	0	0
			6	6		

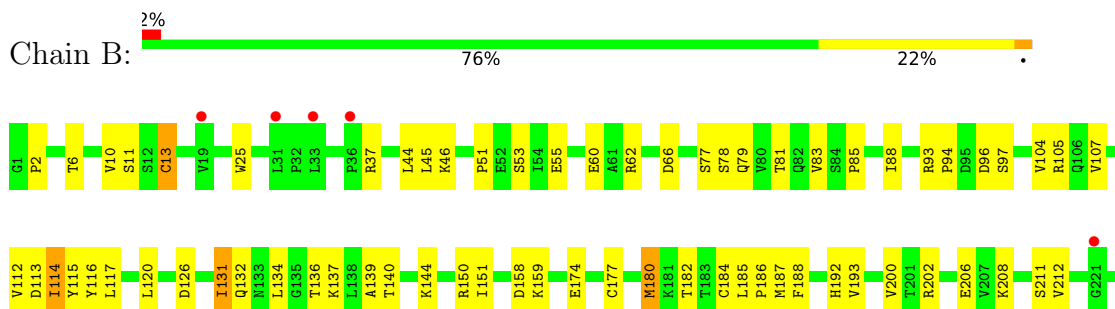
3 Residue-property plots

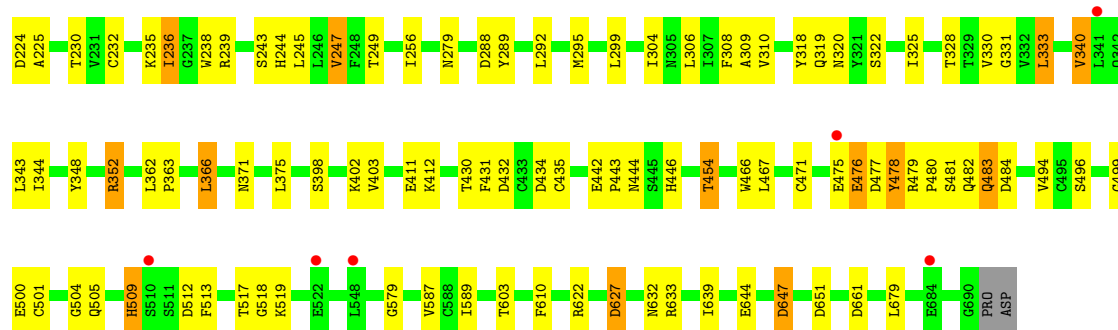
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Integrin alpha-V

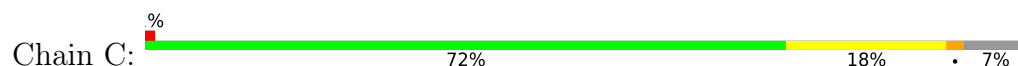


• Molecule 2: Integrin beta-3





• Molecule 3: Fibronectin



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



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



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

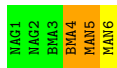


• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

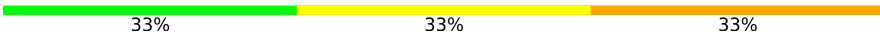


- Molecule 5: α -D-mannopyranose-(1-4)- β -D-mannopyranose-(1-6)-[α -D-mannopyranose-(1-3)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain E: 



- Molecule 6: β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain I: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	129.79Å 129.79Å 307.68Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.48 – 3.10 42.48 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.48-3.10) 99.8 (42.48-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 3.12Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.207 , 0.255 0.207 , 0.255	Depositor DCC
R_{free} test set	2707 reflections (4.03%)	wwPDB-VP
Wilson B-factor (Å ²)	94.8	Xtriage
Anisotropy	0.223	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 78.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13512	wwPDB-VP
Average B, all atoms (Å ²)	118.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.21% 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: MN, GOL, BMA, NAG, MAN, NA

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	0.12	0/7319	0.37	0/9922
2	B	0.14	0/5390	0.43	0/7289
3	C	0.15	0/708	0.47	0/974
All	All	0.13	0/13417	0.40	0/18185

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	2
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	539	ILE	Peptide
2	B	476	GLU	Peptide
2	B	632	ASN	Peptide

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	7163	0	6982	105	0
2	B	5294	0	5024	95	0
3	C	690	0	675	9	0
4	D	28	0	25	0	0
4	F	28	0	25	1	0
4	G	28	0	25	1	0
4	H	28	0	25	0	0
5	E	72	0	61	1	0
6	I	39	0	34	1	0
7	A	70	0	65	1	0
7	B	42	0	39	2	0
8	A	5	0	0	0	0
8	B	3	0	0	0	0
9	A	1	0	0	0	0
10	A	6	0	8	0	0
10	C	6	0	8	0	0
11	A	2	0	0	0	0
11	B	1	0	0	0	0
11	C	6	0	0	1	0
All	All	13512	0	12996	210	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 8.

All (210) 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)
2:B:114:ILE:HG22	2:B:245:LEU:HB2	1.64	0.77
2:B:366:LEU:HB3	2:B:403:VAL:HG12	1.66	0.76
1:A:99:ARG:HD2	1:A:162:ASP:HA	1.69	0.73
1:A:450:TYR:HB2	1:A:474:ASN:HB2	1.71	0.72
1:A:9:ALA:HB3	1:A:434:LEU:HB3	1.71	0.71
1:A:725:LYS:HG3	1:A:726:VAL:HG13	1.75	0.69
2:B:239:ARG:O	2:B:244:HIS:NE2	2.26	0.69
1:A:741:ALA:H	1:A:786:GLY:HA3	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:753:VAL:HB	1:A:951:VAL:HG12	1.75	0.68
2:B:499:GLY:HA2	2:B:509:HIS:H	1.57	0.68
2:B:174:GLU:HA	2:B:186:PRO:HG3	1.76	0.68
2:B:478:TYR:O	2:B:480:PRO:HD3	1.94	0.68
2:B:115:TYR:HH	2:B:192:HIS:HD1	1.39	0.67
2:B:442:GLU:OE1	2:B:446:HIS:NE2	2.29	0.65
1:A:240:VAL:HG22	1:A:255:ILE:HG12	1.79	0.64
1:A:438:ARG:HH21	1:A:577:ILE:HB	1.62	0.64
2:B:139:ALA:HB2	2:B:200:VAL:HG11	1.77	0.63
2:B:403:VAL:HG11	2:B:431:PHE:HE1	1.63	0.63
2:B:331:GLY:HA3	2:B:343:LEU:HD11	1.81	0.62
2:B:482:GLN:HG2	2:B:504:GLY:HA2	1.81	0.62
1:A:487:LEU:HD11	1:A:529:ARG:HH11	1.65	0.62
1:A:251:GLY:HA3	1:A:276:PHE:HB3	1.81	0.61
1:A:24:ASP:OD1	1:A:25:PHE:N	2.34	0.61
2:B:308:PHE:HB2	2:B:330:VAL:HG12	1.84	0.60
2:B:319:GLN:HG2	2:B:330:VAL:HG21	1.83	0.59
2:B:480:PRO:HB2	2:B:482:GLN:HG3	1.84	0.59
1:A:827:GLU:OE2	1:A:832:ARG:NH2	2.36	0.59
2:B:112:VAL:HG22	2:B:243:SER:HB3	1.85	0.58
2:B:288:ASP:OD1	2:B:289:TYR:N	2.36	0.58
2:B:647:ASP:HA	7:B:703:NAG:H3	1.86	0.58
2:B:60:GLU:HB3	2:B:62:ARG:HG3	1.85	0.57
2:B:151:ILE:HD11	2:B:200:VAL:HA	1.86	0.57
1:A:150:ASP:OD1	1:A:150:ASP:N	2.32	0.57
2:B:467:LEU:HD23	2:B:505:GLN:HB2	1.86	0.57
2:B:113:ASP:HB3	2:B:150:ARG:HB2	1.86	0.56
1:A:36:LEU:HB2	1:A:59:CYS:HB2	1.86	0.56
1:A:24:ASP:HA	1:A:409:LYS:HG2	1.87	0.56
1:A:645:VAL:HG22	1:A:715:LEU:HD22	1.89	0.55
1:A:806:ASN:HB2	1:A:907:THR:HG22	1.87	0.55
2:B:466:TRP:HB3	2:B:471:CYS:HB3	1.89	0.55
1:A:376:PHE:HB3	1:A:383:LEU:HD11	1.88	0.55
1:A:904:TRP:CD1	1:A:907:THR:HG23	2.42	0.55
4:F:1:NAG:H83	4:F:1:NAG:H3	1.88	0.55
1:A:630:LYS:NZ	1:A:632:GLN:OE1	2.37	0.55
1:A:181:GLY:HA3	1:A:222:LEU:HB3	1.89	0.55
1:A:753:VAL:HG11	1:A:903:LEU:HD22	1.89	0.55
2:B:105:ARG:HD2	2:B:107:VAL:HG22	1.88	0.55
7:A:1002:NAG:H83	7:A:1002:NAG:H3	1.89	0.55
1:A:802:LYS:HG2	1:A:807:THR:HA	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:I:2:NAG:H3	6:I:2:NAG:H83	1.90	0.54
2:B:150:ARG:HE	2:B:239:ARG:HH21	1.54	0.54
1:A:234:ASP:OD1	1:A:235:GLY:N	2.41	0.54
1:A:474:ASN:HA	1:A:539:ILE:HG22	1.90	0.53
2:B:236:ILE:HD11	2:B:238:TRP:CE2	2.43	0.53
2:B:120:LEU:HD12	2:B:188:PHE:HZ	1.73	0.53
1:A:1:PHE:HA	1:A:389:GLN:HB2	1.90	0.53
1:A:795:LEU:HB3	1:A:884:CYS:HB2	1.91	0.53
1:A:768:THR:HB	1:A:771:ASP:H	1.74	0.53
2:B:432:ASP:OD1	2:B:432:ASP:N	2.42	0.52
3:C:1445:ARG:HB2	3:C:1492:PRO:HB3	1.91	0.52
1:A:210:THR:HG23	1:A:261:MET:HE3	1.92	0.52
2:B:83:VAL:HG22	2:B:104:VAL:HG12	1.92	0.52
2:B:134:LEU:HD12	2:B:137:LYS:HD2	1.92	0.52
1:A:449:VAL:HG21	1:A:557:ILE:HD13	1.92	0.51
1:A:779:ILE:HD12	1:A:898:TYR:HD2	1.75	0.51
1:A:417:ASN:HA	1:A:486:VAL:HB	1.92	0.51
1:A:803:TYR:HB2	1:A:808:LEU:HD11	1.93	0.51
1:A:548:PHE:HB2	1:A:550:ASP:H	1.75	0.51
1:A:769:GLU:HG3	1:A:902:LEU:HD11	1.92	0.51
3:C:1486:THR:HG22	3:C:1504:SER:HB2	1.93	0.51
1:A:41:PRO:HB3	1:A:93:TRP:HA	1.93	0.51
2:B:159:LYS:NZ	2:B:224:ASP:OD2	2.43	0.51
1:A:508:ILE:HG23	2:B:475:GLU:HG3	1.92	0.51
2:B:77:SER:OG	2:B:78:SER:N	2.43	0.50
1:A:603:LYS:HG2	1:A:723:PHE:HB2	1.93	0.50
1:A:784:ASN:HB2	1:A:790:PHE:HE2	1.76	0.50
2:B:93:ARG:HB2	2:B:94:PRO:HD2	1.93	0.50
1:A:797:LEU:HD23	1:A:882:ILE:HD12	1.93	0.50
1:A:273:ALA:HA	2:B:256:ILE:HD12	1.93	0.50
1:A:779:ILE:HD12	1:A:898:TYR:CD2	2.47	0.50
2:B:116:TYR:CZ	2:B:131:ILE:HD11	2.47	0.50
1:A:155:CYS:HB2	1:A:176:SER:OG	2.11	0.49
2:B:295:MET:O	2:B:299:LEU:HB2	2.12	0.49
2:B:481:SER:O	2:B:483:GLN:NE2	2.44	0.49
1:A:705:SER:HB3	1:A:707:MET:H	1.77	0.49
2:B:116:TYR:HA	2:B:247:VAL:HG13	1.94	0.49
2:B:232:CYS:O	2:B:235:LYS:N	2.42	0.49
3:C:1421:ARG:NH2	3:C:1438:ASP:OD1	2.46	0.49
2:B:375:LEU:HD13	2:B:633:ARG:HD2	1.95	0.49
2:B:306:LEU:HB3	2:B:328:THR:HG22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:PHE:O	1:A:175:GLY:HA3	2.12	0.49
2:B:249:THR:HG22	2:B:309:ALA:HB3	1.95	0.49
2:B:512:ASP:OD1	2:B:513:PHE:N	2.44	0.49
1:A:663:LEU:HB2	1:A:695:ALA:HA	1.93	0.49
1:A:2:ASN:OD1	1:A:2:ASN:N	2.45	0.48
2:B:442:GLU:HB3	2:B:446:HIS:CD2	2.48	0.48
2:B:476:GLU:O	2:B:477:ASP:HB2	2.11	0.48
1:A:820:MET:HE2	1:A:886:VAL:HG22	1.95	0.48
3:C:1423:LEU:HD22	3:C:1503:ILE:HG22	1.95	0.48
1:A:777:GLN:HG2	1:A:779:ILE:HD11	1.96	0.48
1:A:93:TRP:CD1	1:A:111:LEU:HD12	2.48	0.48
3:C:1417:SER:HA	3:C:1441:ALA:HB3	1.95	0.48
1:A:347:LEU:HD23	1:A:422:LEU:HD13	1.96	0.48
2:B:494:VAL:CG1	2:B:501:CYS:HB2	2.44	0.47
1:A:463:LEU:HD23	1:A:465:GLY:H	1.80	0.47
2:B:292:LEU:HD22	2:B:325:ILE:HD11	1.96	0.47
3:C:1420:PRO:HA	3:C:1440:PRO:HG3	1.95	0.47
1:A:368:ASP:HB2	1:A:370:LYS:HE3	1.95	0.47
1:A:456:GLN:HB3	1:A:545:GLU:HG2	1.95	0.47
2:B:10:VAL:HG11	2:B:37:ARG:HD3	1.97	0.47
2:B:627:ASP:OD1	2:B:627:ASP:N	2.31	0.47
2:B:639:ILE:HG12	2:B:679:LEU:HB2	1.96	0.47
2:B:126:ASP:OD1	2:B:126:ASP:N	2.46	0.47
1:A:801:TYR:HB2	1:A:880:LEU:HB2	1.96	0.47
2:B:114:ILE:HG13	2:B:151:ILE:HG22	1.97	0.47
2:B:66:ASP:HB3	2:B:85:PRO:HB3	1.96	0.46
2:B:362:LEU:HD12	2:B:363:PRO:HD2	1.96	0.46
1:A:602:CYS:HA	1:A:636:GLU:OE1	2.14	0.46
2:B:333:LEU:HD21	2:B:340:VAL:HG13	1.97	0.46
2:B:140:THR:O	2:B:144:LYS:NZ	2.49	0.46
5:E:4:BMA:H4	5:E:5:MAN:H2	1.57	0.46
2:B:10:VAL:HG11	2:B:37:ARG:HH11	1.81	0.46
1:A:97:SER:HB3	1:A:161:ILE:HG12	1.98	0.46
2:B:202:ARG:NH1	2:B:206:GLU:OE2	2.49	0.46
2:B:230:THR:HG23	2:B:304:ILE:HG13	1.98	0.45
1:A:606:LEU:HB2	1:A:727:SER:HB3	1.98	0.45
2:B:97:SER:HB3	2:B:402:LYS:HG3	1.98	0.45
2:B:158:ASP:HB3	2:B:187:MET:HE1	1.98	0.45
1:A:566:ARG:HB3	1:A:567:THR:H	1.66	0.45
1:A:612:SER:OG	1:A:732:HIS:NE2	2.46	0.45
1:A:647:ILE:HB	1:A:651:ALA:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:177:CYS:SG	2:B:184:CYS:N	2.90	0.45
2:B:375:LEU:HB2	2:B:633:ARG:HD2	1.99	0.45
2:B:13:CYS:SG	2:B:25:TRP:CD1	3.09	0.45
2:B:579:GLY:HA2	2:B:589:ILE:HG12	1.97	0.45
1:A:473:PHE:O	1:A:540:ALA:HB3	2.16	0.45
2:B:444:ASN:HA	2:B:454:THR:HA	1.98	0.45
1:A:347:LEU:HD21	1:A:359:ALA:HB2	1.99	0.45
1:A:784:ASN:HD21	1:A:789:SER:HA	1.82	0.45
2:B:117:LEU:HD11	2:B:225:ALA:HB1	1.98	0.45
2:B:185:LEU:H	2:B:185:LEU:HD23	1.82	0.45
3:C:1497:ASN:ND2	11:C:1701:HOH:O	2.32	0.45
1:A:817:ASP:HB2	1:A:898:TYR:HE1	1.82	0.44
1:A:185:SER:HB3	1:A:208:LEU:HB2	1.99	0.44
2:B:2:PRO:O	2:B:6:THR:HB	2.17	0.44
3:C:1446:TYR:HD1	3:C:1466:PRO:HA	1.81	0.44
1:A:396:ALA:O	1:A:402:PRO:HG3	2.18	0.44
1:A:893:LYS:HD2	1:A:893:LYS:HA	1.75	0.44
1:A:745:ARG:HE	2:B:603:THR:HG21	1.83	0.44
1:A:646:SER:OG	1:A:714:ASP:HB2	2.18	0.44
1:A:617:ILE:HD11	1:A:625:LEU:HD23	2.00	0.44
1:A:88:PHE:CZ	1:A:122:ARG:HG2	2.53	0.43
1:A:623:ASN:OD1	1:A:623:ASN:N	2.49	0.43
2:B:96:ASP:OD1	2:B:97:SER:N	2.41	0.43
1:A:473:PHE:CZ	1:A:540:ALA:HB1	2.53	0.43
2:B:622:ARG:NH1	2:B:661:ASP:OD2	2.30	0.43
4:G:1:NAG:O3	4:G:2:NAG:O7	2.35	0.43
2:B:51:PRO:HD2	2:B:53:SER:HB3	2.00	0.43
2:B:371:ASN:HB2	2:B:398:SER:OG	2.18	0.43
1:A:338:ALA:HB1	1:A:362:ALA:HB1	2.01	0.43
1:A:286:ASN:OD1	1:A:286:ASN:N	2.50	0.43
1:A:653:PHE:HB2	1:A:699:PHE:CE2	2.54	0.43
2:B:499:GLY:O	2:B:500:GLU:HG3	2.19	0.43
2:B:55:GLU:HG2	2:B:435:CYS:HB3	2.01	0.43
2:B:310:VAL:HG11	2:B:318:TYR:CD2	2.53	0.43
1:A:272:MET:HE1	2:B:320:ASN:HD22	1.84	0.43
1:A:351:ASP:OD1	1:A:351:ASP:N	2.47	0.43
1:A:512:LEU:HB2	1:A:541:TYR:CE2	2.54	0.43
1:A:809:LEU:HG	1:A:920:LEU:HD13	2.01	0.43
2:B:245:LEU:HD11	2:B:348:TYR:HD1	1.83	0.42
1:A:175:GLY:HA2	1:A:179:TRP:CD1	2.54	0.42
2:B:132:GLN:HB3	2:B:208:LYS:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:11:SER:HB2	2:B:519:LYS:HE3	2.02	0.42
1:A:806:ASN:HB2	1:A:907:THR:CG2	2.49	0.42
2:B:319:GLN:O	2:B:322:SER:OG	2.36	0.42
1:A:253:VAL:HB	1:A:267:PHE:HB2	2.01	0.42
1:A:666:LEU:HD13	1:A:681:CYS:HB3	2.02	0.42
2:B:247:VAL:HG21	2:B:344:ILE:HD11	2.02	0.42
1:A:548:PHE:O	1:A:549:ARG:HB3	2.20	0.42
1:A:910:ASN:OD1	1:A:911:LYS:N	2.49	0.42
2:B:299:LEU:HD12	2:B:299:LEU:HA	1.92	0.42
1:A:125:VAL:HG11	1:A:143:ARG:HB2	2.02	0.41
2:B:136:THR:HG22	2:B:200:VAL:HG23	2.02	0.41
2:B:647:ASP:HA	7:B:703:NAG:C3	2.50	0.41
1:A:2:ASN:ND2	1:A:350:LEU:O	2.52	0.41
1:A:89:LYS:HG3	1:A:92:GLN:CD	2.45	0.41
2:B:132:GLN:CB	2:B:208:LYS:HD2	2.51	0.41
1:A:657:VAL:HB	1:A:663:LEU:HD11	2.01	0.41
1:A:191:ILE:HA	1:A:204:TYR:CE1	2.55	0.41
2:B:245:LEU:HD11	2:B:348:TYR:CD1	2.56	0.41
2:B:187:MET:HE3	2:B:187:MET:HB2	1.87	0.41
1:A:797:LEU:HB3	1:A:882:ILE:HB	2.02	0.41
3:C:1453:GLU:HB3	3:C:1454:THR:H	1.76	0.41
1:A:115:ARG:HA	1:A:121:GLU:O	2.20	0.41
1:A:480:LYS:HB3	1:A:480:LYS:HE2	1.88	0.41
1:A:498:LEU:HB2	1:A:558:PHE:HB3	2.03	0.41
1:A:721:ASN:O	1:A:725:LYS:HE2	2.21	0.41
1:A:767:GLU:O	1:A:767:GLU:HG2	2.21	0.41
1:A:666:LEU:HD23	1:A:666:LEU:HA	1.73	0.41
2:B:180:MET:HB2	2:B:182:THR:HG22	2.02	0.41
1:A:346:PRO:HA	1:A:358:ILE:HG13	2.03	0.40
1:A:477:PHE:HB2	1:A:559:MET:SD	2.62	0.40
2:B:517:THR:OG1	2:B:518:GLY:N	2.53	0.40
2:B:79:GLN:O	2:B:81:THR:HG22	2.20	0.40
1:A:88:PHE:CE2	1:A:122:ARG:HG2	2.56	0.40
1:A:373:VAL:HB	1:A:391:LEU:HB2	2.03	0.40
1:A:450:TYR:O	1:A:474:ASN:N	2.44	0.40
2:B:352:ARG:HD2	2:B:352:ARG:HA	1.77	0.40
1:A:793:ALA:HB3	1:A:886:VAL:HB	2.03	0.40
2:B:192:HIS:O	2:B:279:ASN:HB3	2.22	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	916/959 (96%)	856 (93%)	56 (6%)	4 (0%)	30	61
2	B	688/692 (99%)	613 (89%)	72 (10%)	3 (0%)	30	61
3	C	89/98 (91%)	75 (84%)	12 (14%)	2 (2%)	5	24
All	All	1693/1749 (97%)	1544 (91%)	140 (8%)	9 (0%)	24	57

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	1453	GLU
1	A	665	ARG
1	A	566	ARG
1	A	705	SER
3	C	1458	SER
1	A	552	LEU
2	B	412	LYS
2	B	644	GLU
2	B	443	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	780/813 (96%)	754 (97%)	26 (3%)	33	63
2	B	612/614 (100%)	580 (95%)	32 (5%)	21	51
3	C	77/82 (94%)	74 (96%)	3 (4%)	28	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1469/1509 (97%)	1408 (96%)	61 (4%)	26 58

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	VAL
1	A	27	VAL
1	A	147	ILE
1	A	150	ASP
1	A	155	CYS
1	A	243	VAL
1	A	275	TYR
1	A	283	THR
1	A	347	LEU
1	A	427	PHE
1	A	475	VAL
1	A	508	ILE
1	A	538	LEU
1	A	544	ASP
1	A	547	GLU
1	A	548	PHE
1	A	586	ILE
1	A	594	LEU
1	A	656	VAL
1	A	672	THR
1	A	701	VAL
1	A	768	THR
1	A	874	CYS
1	A	881	LYS
1	A	916	HIS
1	A	934	LYS
2	B	13	CYS
2	B	44	LEU
2	B	45	LEU
2	B	46	LYS
2	B	88	ILE
2	B	114	ILE
2	B	131	ILE
2	B	180	MET
2	B	193	VAL
2	B	211	SER
2	B	212	VAL

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Mol	Chain	Res	Type
2	B	236	ILE
2	B	247	VAL
2	B	333	LEU
2	B	340	VAL
2	B	352	ARG
2	B	366	LEU
2	B	411	GLU
2	B	430	THR
2	B	434	ASP
2	B	454	THR
2	B	478	TYR
2	B	479	ARG
2	B	483	GLN
2	B	484	ASP
2	B	496	SER
2	B	509	HIS
2	B	587	VAL
2	B	610	PHE
2	B	627	ASP
2	B	647	ASP
2	B	651	ASP
3	C	1460	VAL
3	C	1477	LEU
3	C	1497	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	716	GLN
1	A	718	GLN
1	A	784	ASN
2	B	303	ASN
2	B	339	ASN
2	B	428	GLN
2	B	483	GLN
2	B	632	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 ⓘ

17 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
4	NAG	D	1	4,1	14,14,15	0.33	0	17,19,21	0.40	0
4	NAG	D	2	4	14,14,15	0.25	0	17,19,21	0.42	0
5	NAG	E	1	5,1	14,14,15	0.31	0	17,19,21	0.43	0
5	NAG	E	2	5	14,14,15	0.22	0	17,19,21	0.45	0
5	BMA	E	3	5	11,11,12	0.69	0	15,15,17	0.81	0
5	BMA	E	4	5	11,11,12	1.20	1 (9%)	15,15,17	1.04	0
5	MAN	E	5	5	11,11,12	0.99	1 (9%)	15,15,17	0.90	1 (6%)
5	MAN	E	6	5	11,11,12	0.69	0	15,15,17	0.95	2 (13%)
4	NAG	F	1	4,1	14,14,15	0.50	0	17,19,21	1.36	2 (11%)
4	NAG	F	2	4	14,14,15	0.28	0	17,19,21	0.42	0
4	NAG	G	1	4,1	14,14,15	0.35	0	17,19,21	0.67	0
4	NAG	G	2	4	14,14,15	0.66	0	17,19,21	0.91	1 (5%)
4	NAG	H	1	4,2	14,14,15	0.30	0	17,19,21	0.48	0
4	NAG	H	2	4	14,14,15	0.84	2 (14%)	17,19,21	0.86	1 (5%)
6	NAG	I	1	6,2	14,14,15	0.24	0	17,19,21	0.48	0
6	NAG	I	2	6	14,14,15	0.66	1 (7%)	17,19,21	1.45	3 (17%)
6	BMA	I	3	6	11,11,12	0.81	0	15,15,17	1.06	1 (6%)

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
4	NAG	D	1	4,1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
5	NAG	E	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	E	2	5	-	0/6/23/26	0/1/1/1
5	BMA	E	3	5	-	1/2/19/22	0/1/1/1
5	BMA	E	4	5	-	1/2/19/22	0/1/1/1
5	MAN	E	5	5	-	0/2/19/22	0/1/1/1
5	MAN	E	6	5	-	0/2/19/22	0/1/1/1
4	NAG	F	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	NAG	G	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	G	2	4	-	0/6/23/26	0/1/1/1
4	NAG	H	1	4,2	-	2/6/23/26	0/1/1/1
4	NAG	H	2	4	-	4/6/23/26	0/1/1/1
6	NAG	I	1	6,2	-	2/6/23/26	0/1/1/1
6	NAG	I	2	6	-	4/6/23/26	0/1/1/1
6	BMA	I	3	6	-	1/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	5	MAN	O5-C1	-2.32	1.39	1.43
5	E	4	BMA	C4-C5	2.30	1.57	1.53
4	H	2	NAG	O5-C1	2.29	1.47	1.43
6	I	2	NAG	C1-C2	2.20	1.55	1.52
4	H	2	NAG	C1-C2	2.02	1.55	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	1	NAG	C2-N2-C7	4.59	129.05	122.90
6	I	2	NAG	C2-N2-C7	4.48	128.91	122.90
4	G	2	NAG	C1-O5-C5	3.52	116.90	112.19
4	H	2	NAG	C1-O5-C5	3.24	116.53	112.19
6	I	3	BMA	C1-O5-C5	2.97	116.17	112.19
5	E	6	MAN	C1-O5-C5	2.22	115.16	112.19
5	E	6	MAN	O2-C2-C3	-2.19	105.62	110.15
5	E	5	MAN	O2-C2-C3	-2.18	105.64	110.15
4	F	1	NAG	C1-C2-N2	2.13	113.78	110.43
6	I	2	NAG	C1-O5-C5	2.10	115.00	112.19
6	I	2	NAG	C1-C2-N2	2.06	113.67	110.43

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	2	NAG	C4-C5-C6-O6
4	H	2	NAG	O5-C5-C6-O6
4	F	1	NAG	C8-C7-N2-C2
4	F	1	NAG	O7-C7-N2-C2
4	F	2	NAG	C8-C7-N2-C2
4	F	2	NAG	O7-C7-N2-C2
4	H	2	NAG	C8-C7-N2-C2
4	H	2	NAG	O7-C7-N2-C2
6	I	2	NAG	C8-C7-N2-C2
6	I	2	NAG	O7-C7-N2-C2
6	I	1	NAG	O5-C5-C6-O6
6	I	1	NAG	C4-C5-C6-O6
4	D	1	NAG	O5-C5-C6-O6
5	E	1	NAG	C4-C5-C6-O6
4	D	2	NAG	O5-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6
4	H	1	NAG	O5-C5-C6-O6
5	E	3	BMA	O5-C5-C6-O6
6	I	3	BMA	O5-C5-C6-O6
5	E	1	NAG	O5-C5-C6-O6
5	E	4	BMA	C4-C5-C6-O6
4	F	1	NAG	C1-C2-N2-C7
4	H	1	NAG	C1-C2-N2-C7
6	I	2	NAG	C1-C2-N2-C7
4	F	1	NAG	C3-C2-N2-C7
6	I	2	NAG	C3-C2-N2-C7
4	D	1	NAG	C4-C5-C6-O6

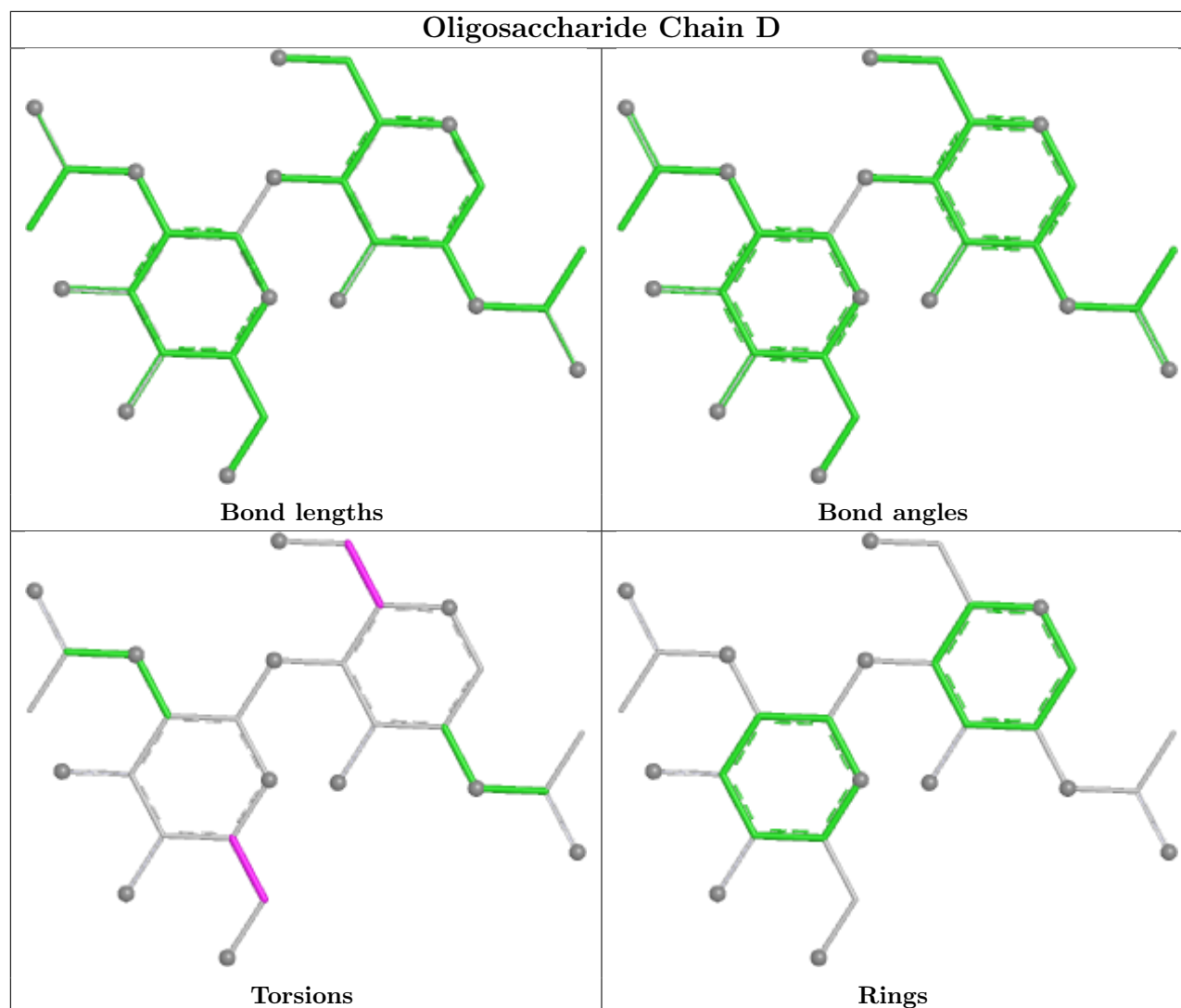
There are no ring outliers.

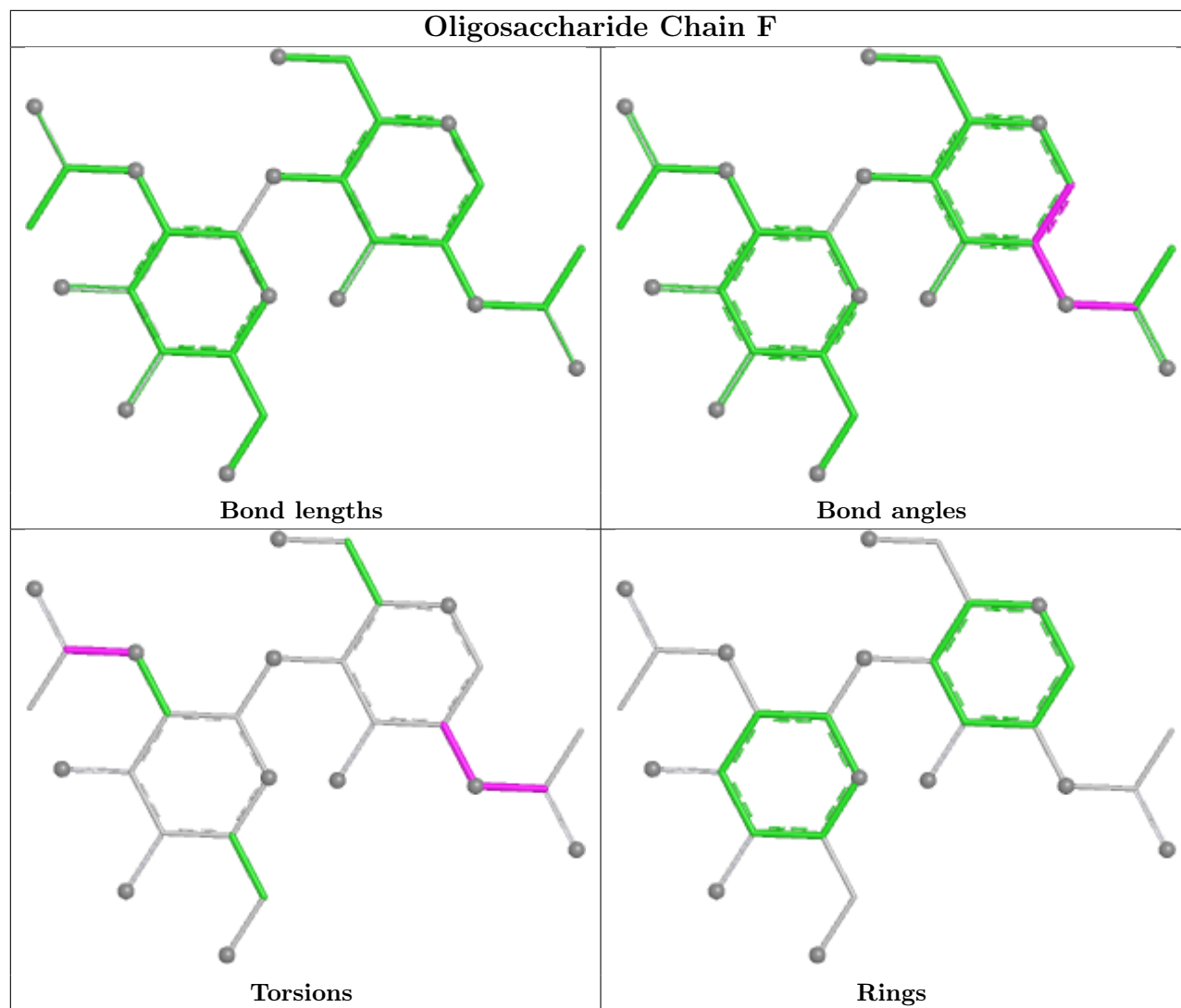
6 monomers are involved in 4 short contacts:

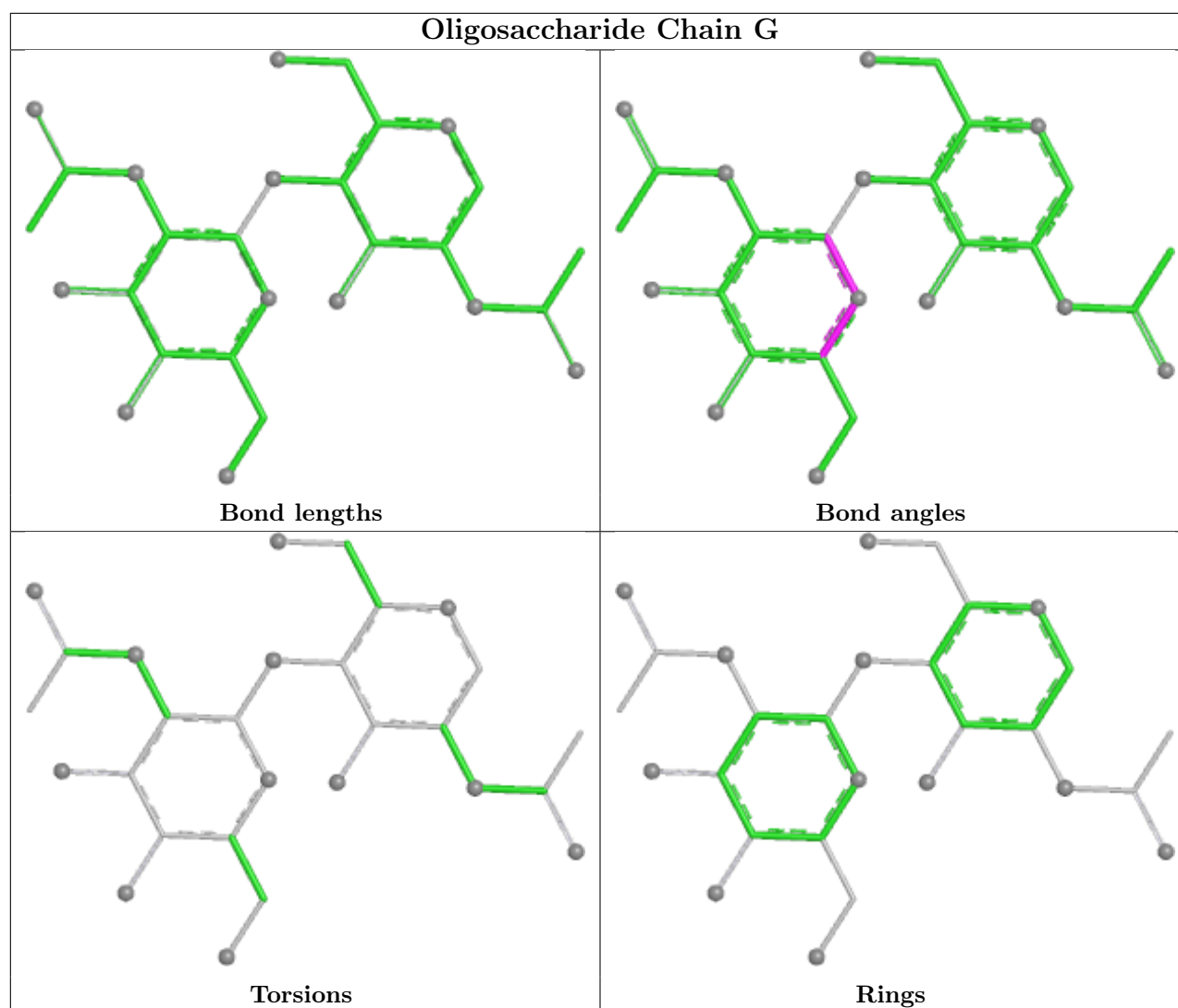
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	2	NAG	1	0
4	G	1	NAG	1	0
5	E	5	MAN	1	0
6	I	2	NAG	1	0
5	E	4	BMA	1	0
4	F	1	NAG	1	0

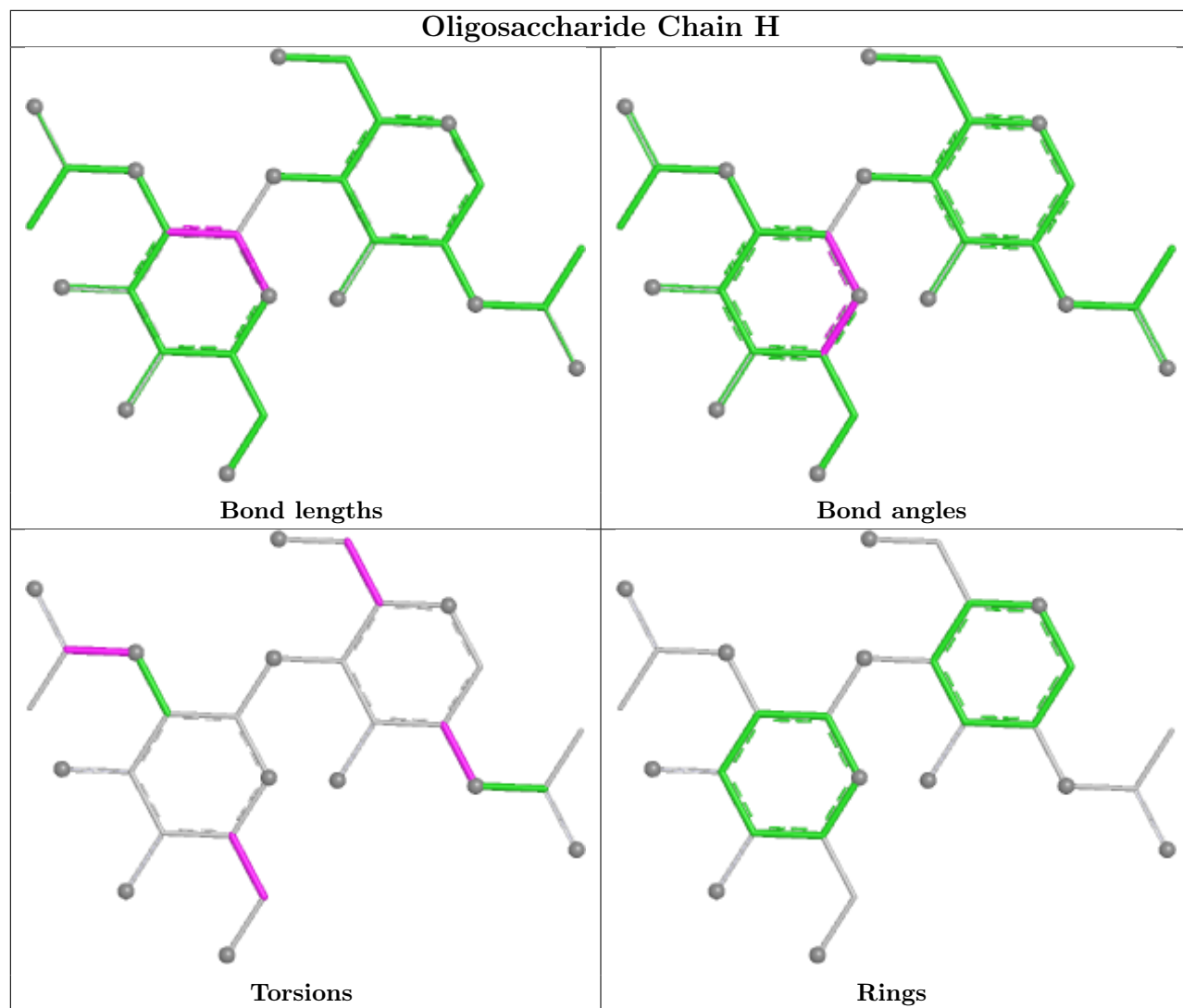
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for oligosaccharide.

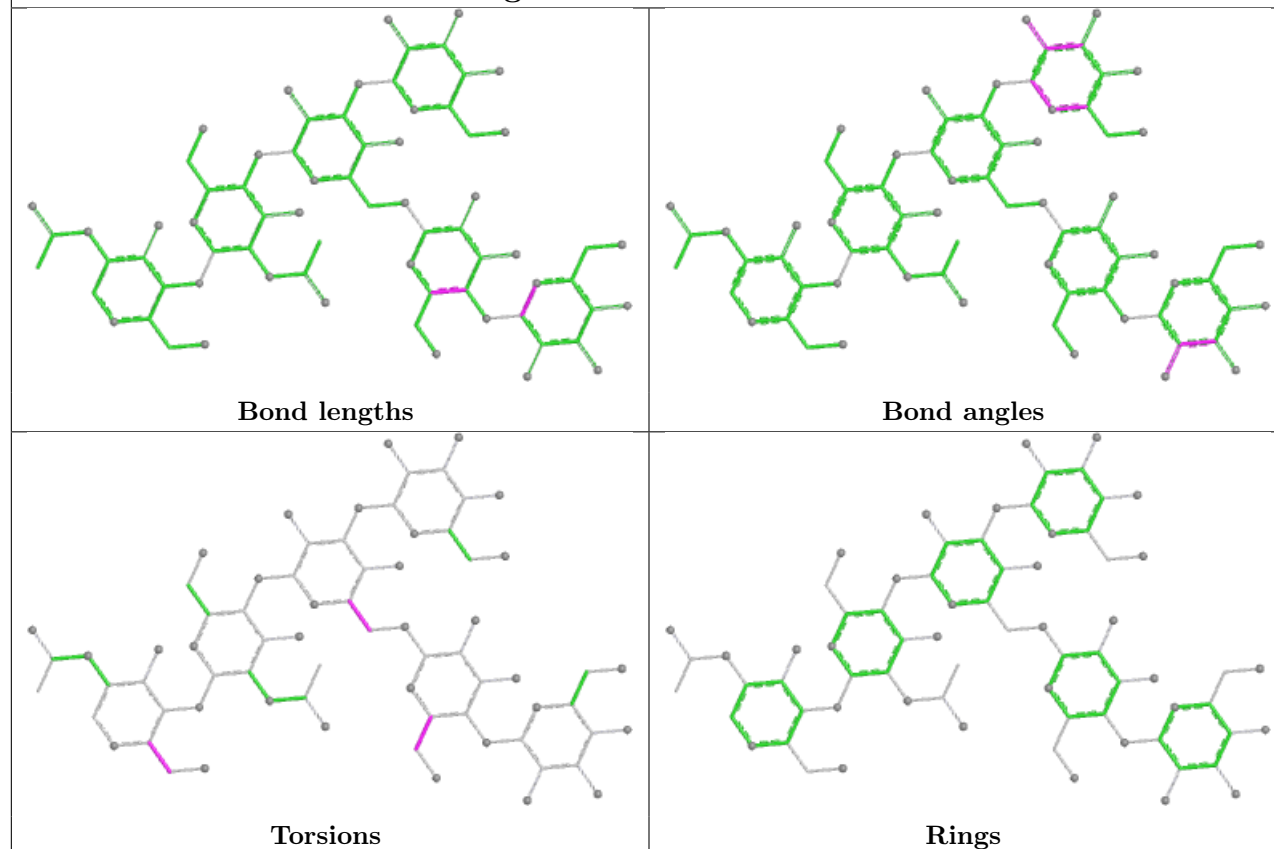




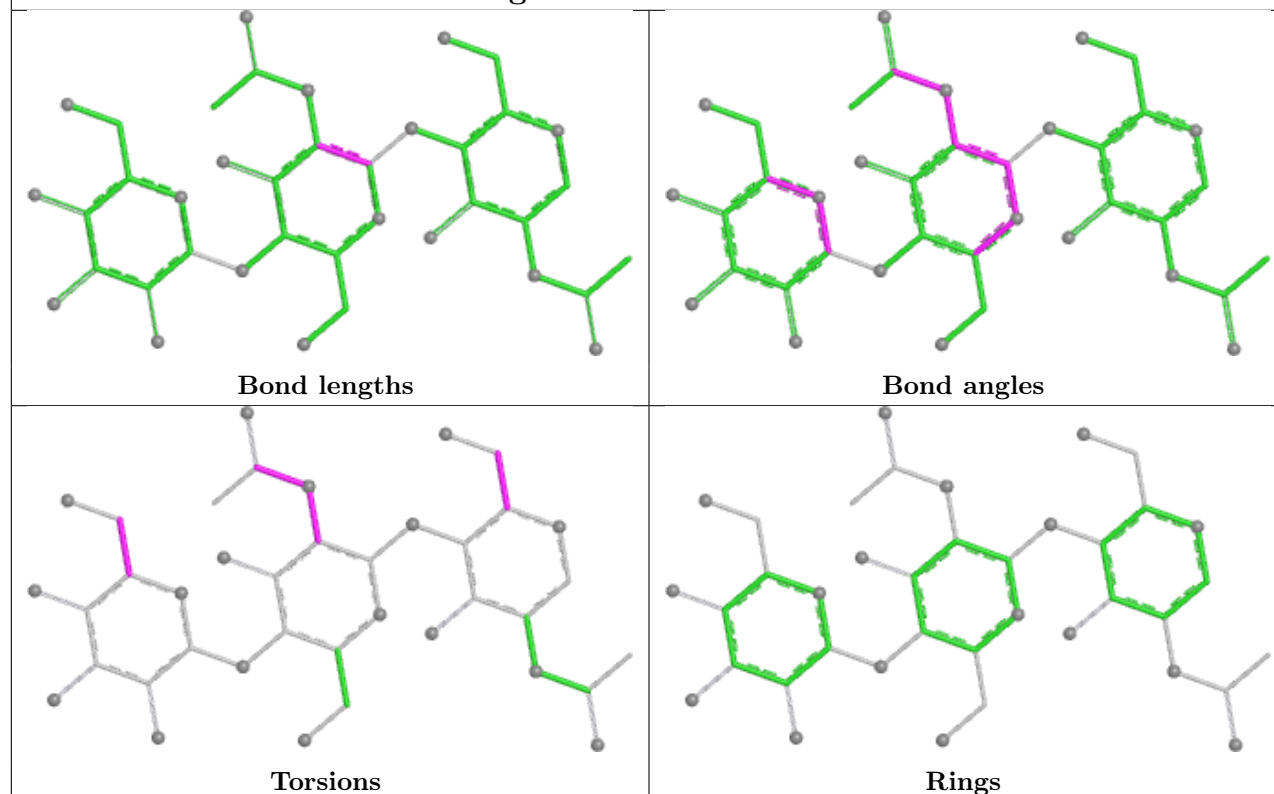




Oligosaccharide Chain E



Oligosaccharide Chain I



5.6 Ligand geometry

Of 19 ligands modelled in this entry, 9 are monoatomic - leaving 10 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
7	NAG	A	1004	1	14,14,15	0.24	0	17,19,21	0.46	0
7	NAG	A	1001	1	14,14,15	0.81	1 (7%)	17,19,21	1.31	1 (5%)
7	NAG	A	1002	1	14,14,15	0.45	0	17,19,21	1.33	2 (11%)
7	NAG	B	701	2	14,14,15	0.62	0	17,19,21	0.85	1 (5%)
7	NAG	A	1005	1	14,14,15	0.24	0	17,19,21	0.48	0
10	GOL	C	1601	-	5,5,5	0.94	0	5,5,5	1.13	1 (20%)
7	NAG	B	703	2	14,14,15	0.42	0	17,19,21	0.58	0
7	NAG	B	702	2	14,14,15	0.28	0	17,19,21	0.45	0
7	NAG	A	1003	1	14,14,15	0.24	0	17,19,21	0.49	0
10	GOL	A	1012	-	5,5,5	0.94	0	5,5,5	1.12	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
7	NAG	A	1004	1	-	1/6/23/26	0/1/1/1
7	NAG	A	1001	1	-	1/6/23/26	0/1/1/1
7	NAG	A	1002	1	-	6/6/23/26	0/1/1/1
7	NAG	B	701	2	-	0/6/23/26	0/1/1/1
7	NAG	A	1005	1	-	3/6/23/26	0/1/1/1
10	GOL	C	1601	-	-	1/4/4/4	-
7	NAG	B	703	2	-	0/6/23/26	0/1/1/1
7	NAG	B	702	2	-	2/6/23/26	0/1/1/1
7	NAG	A	1003	1	-	2/6/23/26	0/1/1/1
10	GOL	A	1012	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1001	NAG	O5-C1	2.88	1.48	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1001	NAG	C1-O5-C5	5.14	119.07	112.19
7	A	1002	NAG	C2-N2-C7	4.58	129.04	122.90
7	B	701	NAG	C1-O5-C5	3.26	116.55	112.19
7	A	1002	NAG	C1-C2-N2	2.22	113.93	110.43
10	C	1601	GOL	C3-C2-C1	-2.01	104.42	111.80

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	1012	GOL	O1-C1-C2-C3
7	A	1003	NAG	O5-C5-C6-O6
7	A	1002	NAG	C8-C7-N2-C2
7	A	1002	NAG	O7-C7-N2-C2
7	A	1005	NAG	C8-C7-N2-C2
7	A	1005	NAG	O7-C7-N2-C2
7	A	1002	NAG	O5-C5-C6-O6
7	B	702	NAG	O5-C5-C6-O6
7	A	1005	NAG	O5-C5-C6-O6
10	A	1012	GOL	O1-C1-C2-O2
7	A	1001	NAG	C4-C5-C6-O6
7	A	1002	NAG	C4-C5-C6-O6
7	A	1003	NAG	C4-C5-C6-O6
10	C	1601	GOL	O1-C1-C2-O2
7	B	702	NAG	C4-C5-C6-O6
7	A	1002	NAG	C1-C2-N2-C7
7	A	1004	NAG	C1-C2-N2-C7
7	A	1002	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1002	NAG	1	0
7	B	703	NAG	2	0

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	920/959 (95%)	-0.17	7 (0%) 82 65	59, 98, 163, 209	0
2	B	690/692 (99%)	0.07	11 (1%) 70 49	64, 116, 218, 283	2 (0%)
3	C	91/98 (92%)	0.38	1 (1%) 78 59	81, 162, 228, 289	0
All	All	1701/1749 (97%)	-0.04	19 (1%) 78 59	59, 108, 200, 289	2 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	510	SER	4.2
2	B	221	GLY	3.0
3	C	1425	VAL	3.0
1	A	664	ALA	2.8
2	B	341	LEU	2.7
1	A	538	LEU	2.7
1	A	670	PHE	2.5
1	A	892	GLY	2.2
1	A	954	GLY	2.2
2	B	522	GLU	2.2
2	B	31	LEU	2.2
2	B	684	GLU	2.2
2	B	36	PRO	2.2
2	B	19	VAL	2.1
1	A	571	THR	2.1
2	B	475	GLU	2.1
2	B	33	LEU	2.0
1	A	916	HIS	2.0
2	B	548	LEU	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](#)

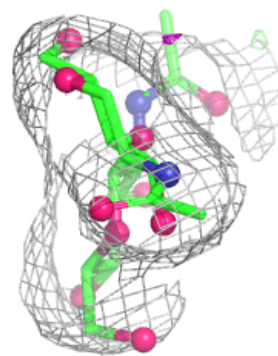
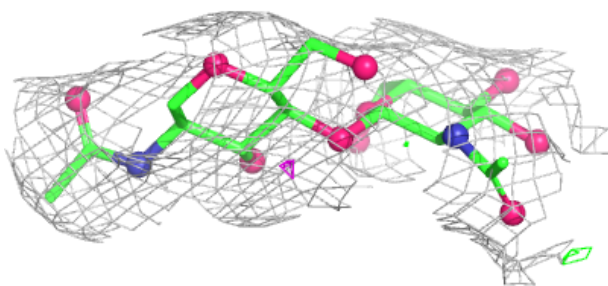
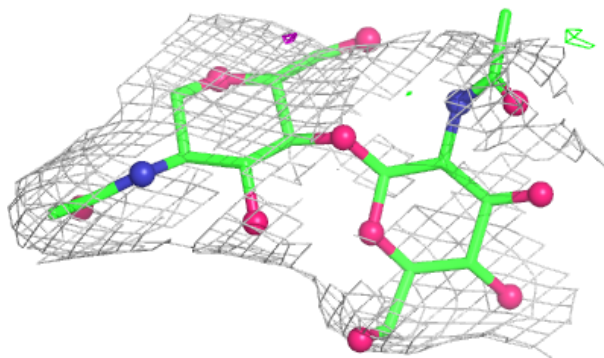
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	G	2	14/15	0.45	0.11	118,159,178,180	0
5	MAN	E	6	11/12	0.60	0.10	132,147,158,160	0
4	NAG	H	2	14/15	0.65	0.09	156,164,169,172	0
4	NAG	F	1	14/15	0.66	0.12	127,140,154,159	0
4	NAG	F	2	14/15	0.76	0.11	125,151,163,176	0
5	MAN	E	5	11/12	0.77	0.10	148,158,166,168	0
4	NAG	G	1	14/15	0.78	0.11	86,128,146,166	0
4	NAG	D	2	14/15	0.79	0.10	119,135,151,162	0
6	BMA	I	3	11/12	0.79	0.10	112,144,157,163	0
6	NAG	I	2	14/15	0.82	0.14	132,144,154,155	0
5	BMA	E	4	11/12	0.83	0.11	128,139,148,152	0
4	NAG	H	1	14/15	0.89	0.09	101,126,147,150	0
5	BMA	E	3	11/12	0.90	0.07	108,121,135,143	0
6	NAG	I	1	14/15	0.92	0.12	119,130,136,139	0
4	NAG	D	1	14/15	0.94	0.09	78,105,126,133	0
5	NAG	E	2	14/15	0.96	0.08	70,91,102,121	0
5	NAG	E	1	14/15	0.96	0.07	66,78,118,120	0

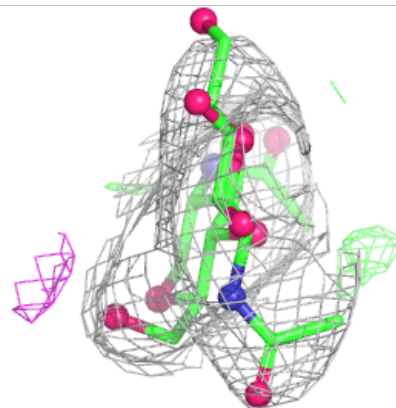
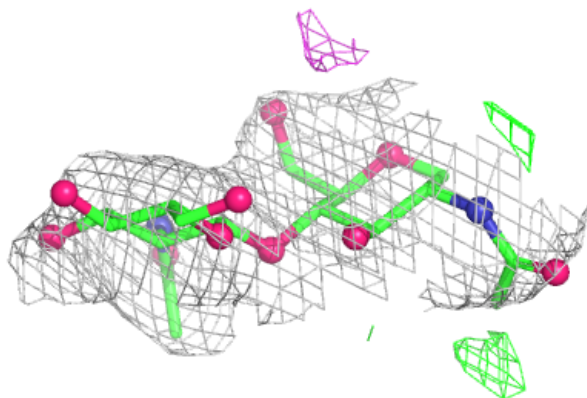
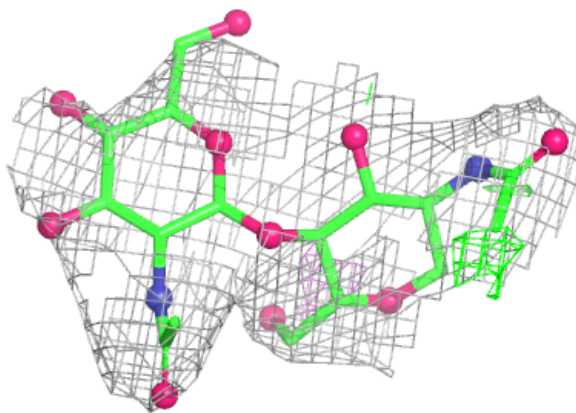
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

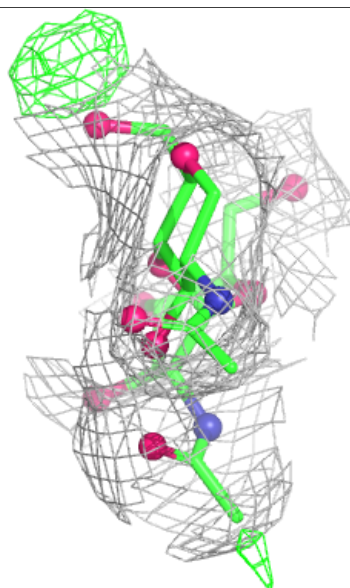
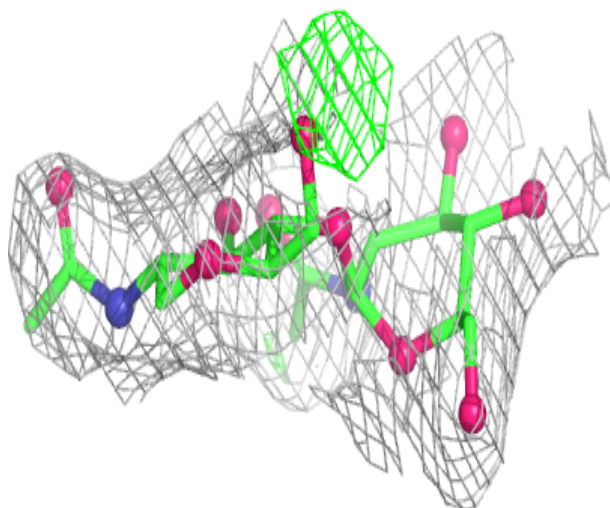
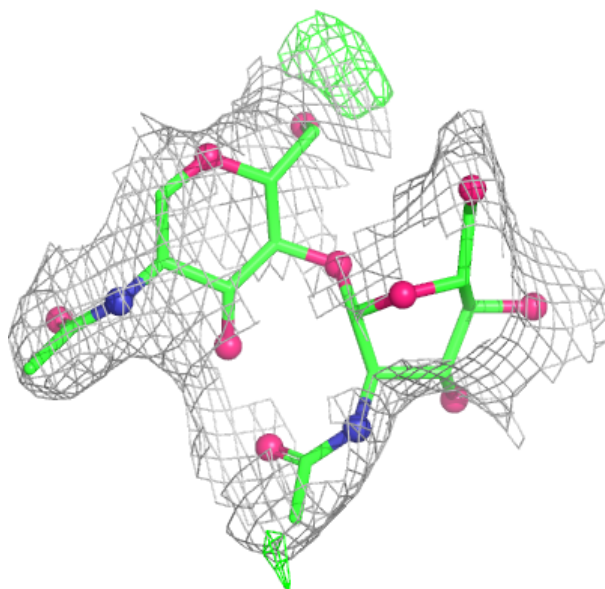
**Electron density around Chain F:**

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



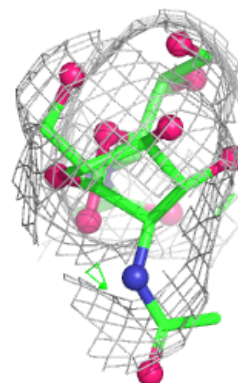
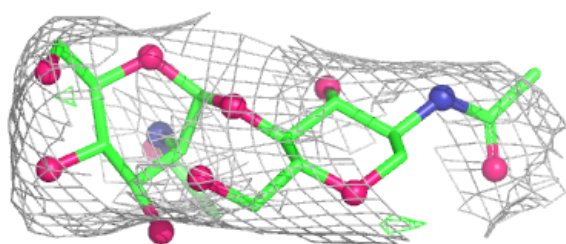
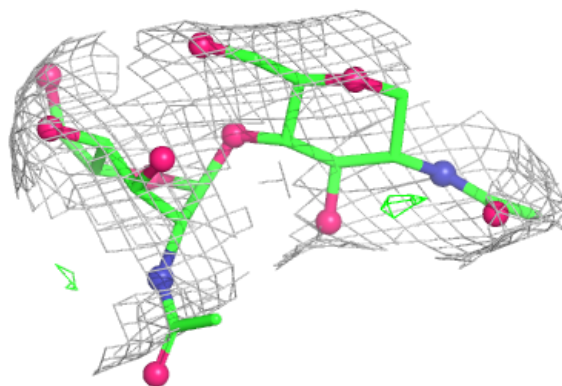
Electron density around Chain G:

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



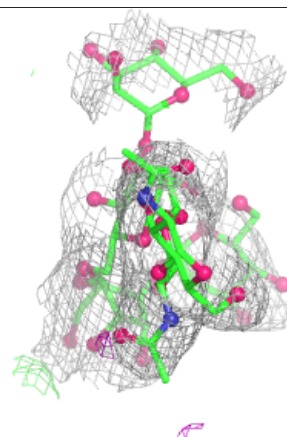
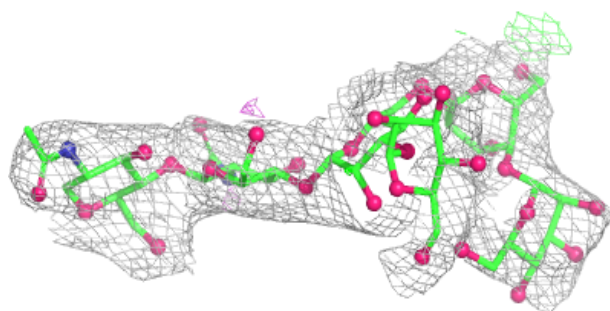
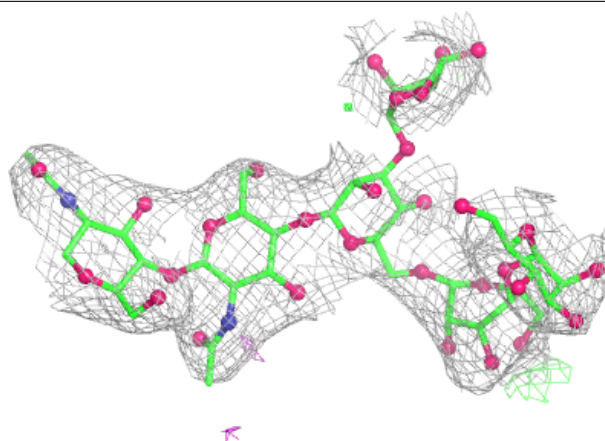
Electron density around Chain H:

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

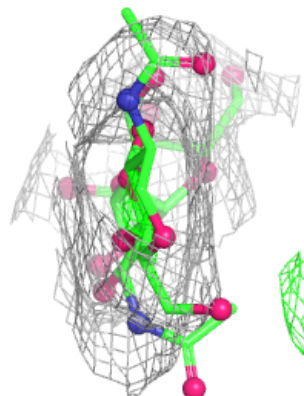
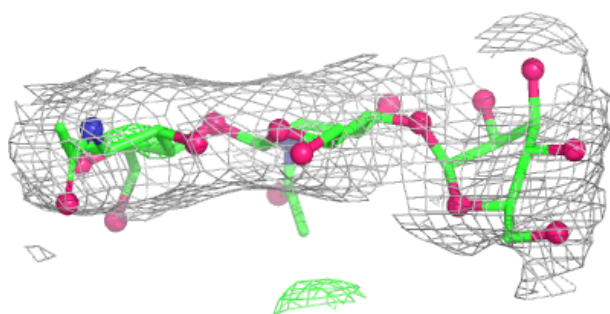
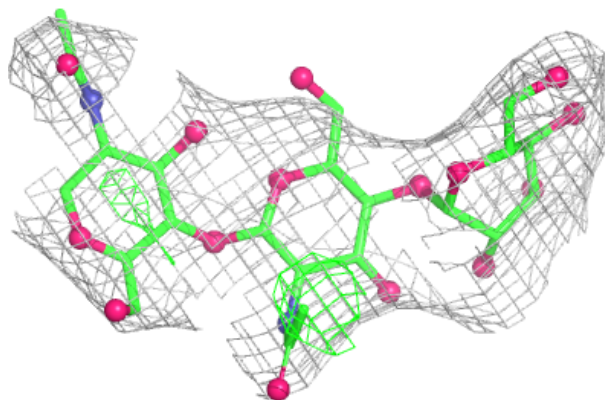


Electron density around Chain E:

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

**Electron density around Chain I:**

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



6.4 Ligands

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
7	NAG	B	703	14/15	0.59	0.14	125,147,162,165	0
7	NAG	A	1003	14/15	0.60	0.10	148,166,178,179	0
10	GOL	A	1012	6/6	0.64	0.14	131,140,144,149	0
10	GOL	C	1601	6/6	0.69	0.16	128,136,147,150	0
7	NAG	A	1002	14/15	0.70	0.09	120,142,150,157	0
7	NAG	A	1004	14/15	0.73	0.11	117,138,147,147	0
7	NAG	B	701	14/15	0.76	0.10	131,162,179,185	0
7	NAG	A	1005	14/15	0.78	0.11	103,124,144,150	0
7	NAG	B	702	14/15	0.83	0.14	137,149,165,170	0
7	NAG	A	1001	14/15	0.90	0.10	96,117,130,137	0
9	NA	A	1011	1/1	0.96	0.08	111,111,111,111	0
8	MN	B	705	1/1	0.98	0.07	111,111,111,111	0
8	MN	A	1006	1/1	0.98	0.04	115,115,115,115	0
8	MN	A	1007	1/1	0.98	0.06	159,159,159,159	0
8	MN	A	1010	1/1	0.98	0.04	131,131,131,131	0
8	MN	B	706	1/1	0.99	0.04	95,95,95,95	0
8	MN	A	1008	1/1	0.99	0.03	119,119,119,119	0
8	MN	B	704	1/1	0.99	0.12	143,143,143,143	0
8	MN	A	1009	1/1	0.99	0.03	153,153,153,153	0

6.5 Other polymers

There are no such residues in this entry.