



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:55 AM UTC

PDB ID : 3LRM / pdb_00003lrm
Title : Structure of alfa-galactosidase from Saccharomyces cerevisiae with raffinose
Authors : Fernandez-Leiro, R.; Pereira-Rodriguez, A.; Cerdan, M.E.; Becerra, M.; Sanz-Aparicio, J.
Deposited on : 2010-02-11
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

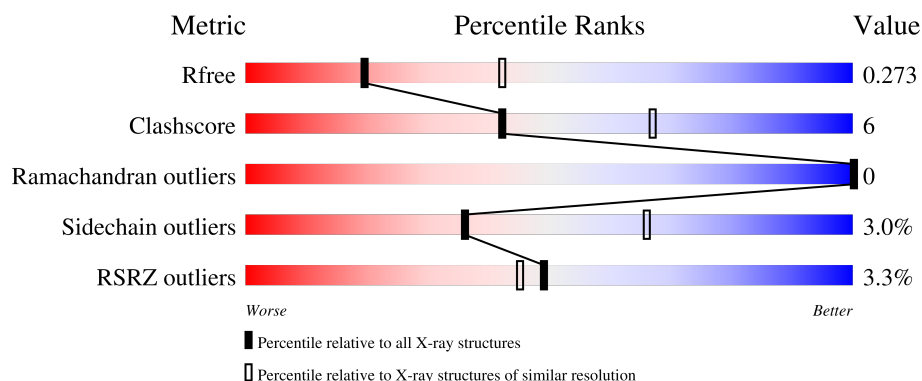
1 Overall quality at a glance

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.



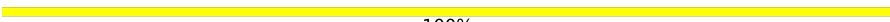
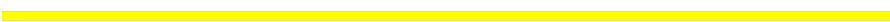
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	479	 3% 82% 12% • 6%
1	B	479	 4% 81% 13% • 6%
1	C	479	 2% 82% 12% 6%
1	D	479	 3% 83% 11% 6%
2	E	2	 100%

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Mol	Chain	Length	Quality of chain
2	G	2	 100%
2	I	2	 100%
3	F	2	 50% 50%
3	H	2	 100%
3	J	2	 100%
4	K	3	 33% 67%
4	L	3	 33% 67%
4	M	3	 67% 33%
4	N	3	 67% 33%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	E	1	X	-	-	-
2	NAG	G	1	X	-	-	-
2	NAG	I	1	X	-	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15512 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 Alpha-galactosidase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	0	0	0
			3515	2203	596	695	21			
1	B	452	Total	C	N	O	S	0	0	0
			3515	2203	596	695	21			
1	C	452	Total	C	N	O	S	0	0	0
			3515	2203	596	695	21			
1	D	452	Total	C	N	O	S	0	0	0
			3515	2203	596	695	21			

There are 40 discrepancies between the modelled and reference sequences:

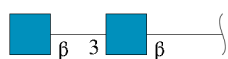
Chain	Residue	Modelled	Actual	Comment	Reference
A	149	ALA	ASP	engineered mutation	UNP P04824
A	181	VAL	ILE	engineered mutation	UNP P04824
A	472	ASP	-	expression tag	UNP P04824
A	473	TYR	-	expression tag	UNP P04824
A	474	LYS	-	expression tag	UNP P04824
A	475	ASP	-	expression tag	UNP P04824
A	476	ASP	-	expression tag	UNP P04824
A	477	ASP	-	expression tag	UNP P04824
A	478	ASP	-	expression tag	UNP P04824
A	479	LYS	-	expression tag	UNP P04824
B	149	ALA	ASP	engineered mutation	UNP P04824
B	181	VAL	ILE	engineered mutation	UNP P04824
B	472	ASP	-	expression tag	UNP P04824
B	473	TYR	-	expression tag	UNP P04824
B	474	LYS	-	expression tag	UNP P04824
B	475	ASP	-	expression tag	UNP P04824
B	476	ASP	-	expression tag	UNP P04824
B	477	ASP	-	expression tag	UNP P04824
B	478	ASP	-	expression tag	UNP P04824
B	479	LYS	-	expression tag	UNP P04824
C	149	ALA	ASP	engineered mutation	UNP P04824

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Chain	Residue	Modelled	Actual	Comment	Reference
C	181	VAL	ILE	engineered mutation	UNP P04824
C	472	ASP	-	expression tag	UNP P04824
C	473	TYR	-	expression tag	UNP P04824
C	474	LYS	-	expression tag	UNP P04824
C	475	ASP	-	expression tag	UNP P04824
C	476	ASP	-	expression tag	UNP P04824
C	477	ASP	-	expression tag	UNP P04824
C	478	ASP	-	expression tag	UNP P04824
C	479	LYS	-	expression tag	UNP P04824
D	149	ALA	ASP	engineered mutation	UNP P04824
D	181	VAL	ILE	engineered mutation	UNP P04824
D	472	ASP	-	expression tag	UNP P04824
D	473	TYR	-	expression tag	UNP P04824
D	474	LYS	-	expression tag	UNP P04824
D	475	ASP	-	expression tag	UNP P04824
D	476	ASP	-	expression tag	UNP P04824
D	477	ASP	-	expression tag	UNP P04824
D	478	ASP	-	expression tag	UNP P04824
D	479	LYS	-	expression tag	UNP P04824

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



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

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



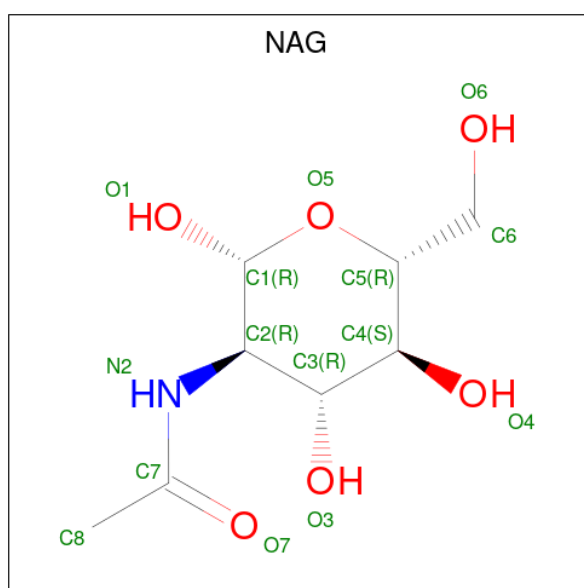
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	J	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called beta-D-fructofuranose-(2-1)-[alpha-D-galactopyranoside-(1-6)]alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	K	3	Total	C	O	0	0	0
			34	18	16			
4	L	3	Total	C	O	0	0	0
			34	18	16			
4	M	3	Total	C	O	0	0	0
			34	18	16			
4	N	3	Total	C	O	0	0	0
			34	18	16			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

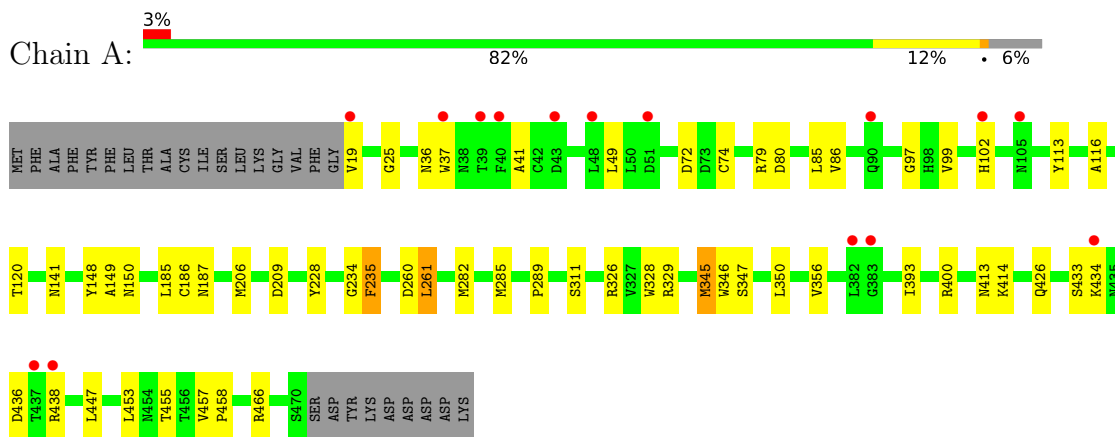
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	286	Total	O	0	0
			286	286		
6	B	235	Total	O	0	0
			235	235		
6	C	264	Total	O	0	0
			264	264		
6	D	237	Total	O	0	0
			237	237		

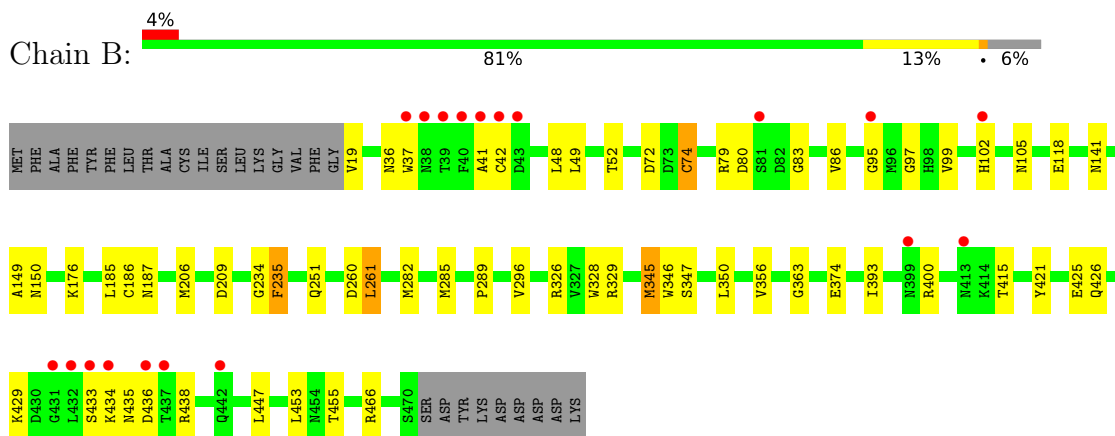
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

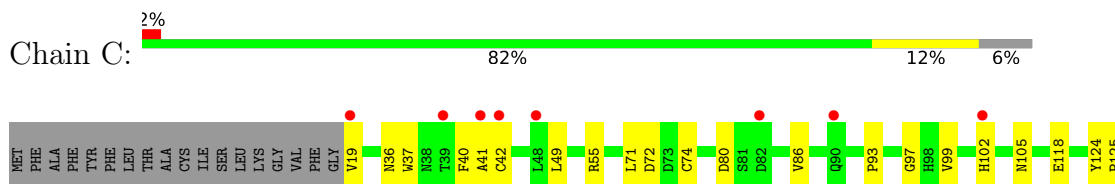
- Molecule 1: Alpha-galactosidase 1

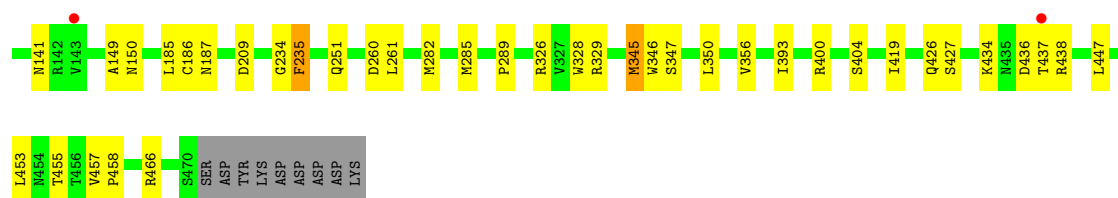


- Molecule 1: Alpha-galactosidase 1

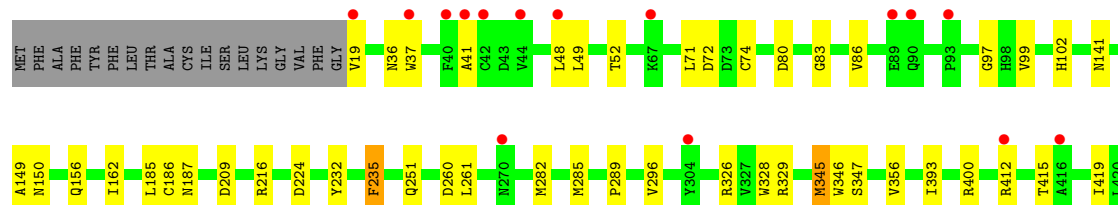
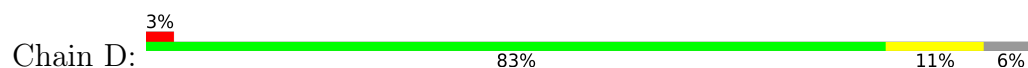


- Molecule 1: Alpha-galactosidase 1





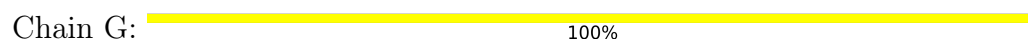
- Molecule 1: Alpha-galactosidase 1



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



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



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



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





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

Chain H:  100%



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

Chain J:  100%



- Molecule 4: beta-D-fructofuranose-(2-1)-[alpha-D-galactopyranose-(1-6)]alpha-D-glucopyranose

Chain K:  33% 67%



- Molecule 4: beta-D-fructofuranose-(2-1)-[alpha-D-galactopyranose-(1-6)]alpha-D-glucopyranose

Chain L:  33% 67%



- Molecule 4: beta-D-fructofuranose-(2-1)-[alpha-D-galactopyranose-(1-6)]alpha-D-glucopyranose

Chain M:  67% 33%



- Molecule 4: beta-D-fructofuranose-(2-1)-[alpha-D-galactopyranose-(1-6)]alpha-D-glucopyranose

Chain N:  67% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	111.17Å 129.53Å 136.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	94.05 – 2.70 94.05 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (94.05-2.70) 100.0 (94.05-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.91 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.241 , 0.284 0.237 , 0.273	Depositor DCC
R_{free} test set	2781 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	44.0	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	15512	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.40% 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: GLA, NAG, FRU, GLC

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	0.45	0/3602	0.76	0/4891
1	B	0.46	0/3602	0.76	0/4891
1	C	0.44	0/3602	0.75	0/4891
1	D	0.45	0/3602	0.76	0/4891
All	All	0.45	0/14408	0.76	0/19564

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 [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3515	0	3283	45	2
1	B	3515	0	3283	49	2
1	C	3515	0	3283	43	0
1	D	3515	0	3284	43	0
2	E	28	0	25	0	0
2	G	28	0	25	0	0
2	I	28	0	25	0	0
3	F	28	0	25	0	0
3	H	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	J	28	0	25	0	0
4	K	34	0	30	1	0
4	L	34	0	30	0	0
4	M	34	0	30	1	0
4	N	34	0	30	0	0
5	A	28	0	26	0	0
5	B	28	0	26	0	0
5	C	42	0	39	1	0
5	D	28	0	26	0	0
6	A	286	0	0	14	0
6	B	235	0	0	21	0
6	C	264	0	0	10	0
6	D	237	0	0	8	0
All	All	15512	0	13520	177	2

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 6.

All (177) 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:79:ARG:HA	6:A:1534:HOH:O	1.31	1.26
1:B:435:ASN:HB2	6:B:537:HOH:O	1.47	1.12
1:C:42:CYS:HB3	6:C:1121:HOH:O	1.58	1.01
1:A:438:ARG:CZ	6:A:1610:HOH:O	2.20	0.88
1:A:85:LEU:HA	6:A:1534:HOH:O	1.72	0.87
1:D:421:TYR:HA	1:D:438:ARG:HH21	1.40	0.84
1:B:421:TYR:CD1	1:B:438:ARG:NH2	2.48	0.81
1:B:79:ARG:HB3	6:B:1368:HOH:O	1.80	0.81
1:B:425:GLU:HG2	6:B:1162:HOH:O	1.81	0.79
1:C:436:ASP:OD1	1:C:438:ARG:HG2	1.85	0.75
1:B:118:GLU:HG3	6:B:1470:HOH:O	1.90	0.70
1:D:421:TYR:HA	1:D:438:ARG:NH2	2.09	0.68
1:B:95:GLY:HA3	6:B:534:HOH:O	1.96	0.66
1:C:40:PHE:HA	6:C:1555:HOH:O	1.94	0.66
1:C:436:ASP:OD1	1:C:438:ARG:CG	2.44	0.65
1:D:436:ASP:OD1	1:D:438:ARG:HG3	1.97	0.64
1:D:48:LEU:HA	6:D:518:HOH:O	1.97	0.63
1:D:436:ASP:OD1	1:D:438:ARG:CG	2.48	0.61
1:B:74:CYS:HB3	6:B:1037:HOH:O	2.01	0.61
1:B:326:ARG:HD2	6:B:1321:HOH:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:ASP:OD1	1:A:438:ARG:HG3	2.00	0.60
1:D:436:ASP:CG	1:D:438:ARG:HB2	2.27	0.60
1:A:36:ASN:HD21	1:A:72:ASP:H	1.49	0.60
1:B:49:LEU:HD23	1:B:99:VAL:HG11	1.84	0.60
1:C:93:PRO:HG2	6:C:1010:HOH:O	2.01	0.60
1:B:435:ASN:CB	6:B:537:HOH:O	2.26	0.58
1:B:36:ASN:HD21	1:B:72:ASP:H	1.50	0.58
1:A:49:LEU:HD23	1:A:99:VAL:HG11	1.86	0.58
1:B:97:GLY:H	1:B:141:ASN:HD22	1.50	0.57
1:C:49:LEU:HD23	1:C:99:VAL:HG11	1.85	0.57
1:A:80:ASP:HB3	1:A:86:VAL:CG2	2.35	0.57
1:C:97:GLY:H	1:C:141:ASN:HD22	1.51	0.57
1:A:413:ASN:ND2	6:A:1292:HOH:O	2.38	0.57
1:B:80:ASP:HB3	1:B:86:VAL:CG2	2.34	0.57
1:A:436:ASP:CG	1:A:438:ARG:HB2	2.30	0.56
1:C:36:ASN:HD21	1:C:72:ASP:H	1.52	0.56
1:D:49:LEU:HD23	1:D:99:VAL:HG11	1.85	0.56
1:C:80:ASP:HB3	1:C:86:VAL:CG2	2.35	0.56
1:B:415:THR:HB	6:B:1079:HOH:O	2.06	0.56
1:D:80:ASP:HB3	1:D:86:VAL:CG2	2.36	0.56
1:C:209:ASP:HB2	1:C:235:PHE:HB2	1.87	0.55
1:D:36:ASN:HD21	1:D:72:ASP:H	1.53	0.55
1:D:436:ASP:OD2	1:D:438:ARG:HD3	2.05	0.55
1:D:393:ILE:HD13	1:D:453:LEU:HD13	1.89	0.55
1:B:42:CYS:HB3	6:B:1037:HOH:O	2.05	0.55
1:A:426:GLN:NE2	1:A:434:LYS:HD2	2.21	0.55
1:D:426:GLN:NE2	1:D:434:LYS:HD2	2.22	0.55
1:A:436:ASP:OD1	1:A:438:ARG:HB2	2.07	0.54
1:B:83:GLY:C	6:B:1368:HOH:O	2.51	0.54
1:B:105:ASN:ND2	6:B:555:HOH:O	2.39	0.54
1:B:421:TYR:CE1	1:B:438:ARG:NH2	2.67	0.54
1:A:97:GLY:H	1:A:141:ASN:HD22	1.56	0.54
1:B:150:ASN:HB2	1:B:187:ASN:HA	1.90	0.54
1:D:97:GLY:H	1:D:141:ASN:HD22	1.55	0.54
1:A:436:ASP:OD1	1:A:438:ARG:CG	2.56	0.54
1:C:437:THR:HG23	6:C:1086:HOH:O	2.06	0.53
1:D:209:ASP:HB2	1:D:235:PHE:HB2	1.90	0.53
1:D:285:MET:HE1	1:D:346:TRP:CB	2.38	0.53
1:D:436:ASP:OD1	1:D:438:ARG:HB2	2.09	0.53
1:A:209:ASP:HB2	1:A:235:PHE:HB2	1.89	0.53
6:A:1587:HOH:O	1:D:156:GLN:HG2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:436:ASP:OD1	1:D:438:ARG:CB	2.56	0.53
1:D:345:MET:HE1	1:D:347:SER:HB2	1.90	0.53
1:D:419:ILE:HA	6:D:1508:HOH:O	2.07	0.53
1:C:436:ASP:CG	1:C:438:ARG:HB2	2.33	0.52
1:B:429:LYS:CD	6:B:1286:HOH:O	2.57	0.52
1:C:393:ILE:HD13	1:C:453:LEU:HD13	1.91	0.52
1:B:209:ASP:HB2	1:B:235:PHE:HB2	1.91	0.52
1:A:150:ASN:HB2	1:A:187:ASN:HA	1.91	0.52
1:C:150:ASN:HB2	1:C:187:ASN:HA	1.92	0.52
1:C:426:GLN:NE2	1:C:434:LYS:HD2	2.24	0.52
1:D:285:MET:HE1	1:D:346:TRP:HB2	1.91	0.52
1:A:436:ASP:OD1	1:A:438:ARG:CB	2.58	0.51
5:C:4001:NAG:H3	6:C:1156:HOH:O	2.09	0.51
1:B:285:MET:HE1	1:B:346:TRP:CB	2.41	0.51
1:D:150:ASN:HB2	1:D:187:ASN:HA	1.92	0.51
1:D:415:THR:HG22	6:D:1244:HOH:O	2.10	0.51
1:B:176:LYS:HD2	6:B:1499:HOH:O	2.10	0.51
1:C:436:ASP:OD1	1:C:438:ARG:CB	2.58	0.51
1:A:393:ILE:HD13	1:A:453:LEU:HD13	1.93	0.51
1:A:149:ALA:HA	1:A:186:CYS:HB3	1.93	0.51
1:A:285:MET:HE1	1:A:346:TRP:CB	2.41	0.51
1:B:282:MET:HE1	1:B:285:MET:HE1	1.92	0.51
1:C:37:TRP:HZ2	4:M:2:FRU:H3	1.77	0.50
1:C:404:SER:HB3	6:C:1032:HOH:O	2.10	0.50
1:C:285:MET:HE1	1:C:346:TRP:CB	2.41	0.50
1:D:149:ALA:HA	1:D:186:CYS:HB3	1.93	0.50
1:B:426:GLN:NE2	1:B:434:LYS:HD2	2.27	0.50
1:C:149:ALA:HA	1:C:186:CYS:HB3	1.92	0.50
1:B:328:TRP:CE2	1:B:345:MET:HB2	2.47	0.49
1:A:345:MET:HE1	1:A:347:SER:HB2	1.93	0.49
1:C:328:TRP:CE2	1:C:345:MET:HB2	2.48	0.49
1:A:85:LEU:CA	6:A:1534:HOH:O	2.46	0.49
1:C:282:MET:HE1	1:C:285:MET:HE1	1.94	0.49
1:A:282:MET:HE1	1:A:285:MET:HE1	1.94	0.49
1:B:285:MET:HE1	1:B:346:TRP:HB2	1.95	0.48
1:B:149:ALA:HA	1:B:186:CYS:HB3	1.94	0.48
1:D:282:MET:HE1	1:D:285:MET:HE1	1.96	0.48
1:A:285:MET:HE1	1:A:346:TRP:HB2	1.96	0.48
1:A:426:GLN:HE22	1:A:434:LYS:HD2	1.78	0.48
1:C:285:MET:HE1	1:C:346:TRP:HB2	1.96	0.48
1:B:393:ILE:HD13	1:B:453:LEU:HD13	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:345:MET:HE1	1:B:347:SER:HB2	1.97	0.47
1:B:429:LYS:HD3	6:B:1286:HOH:O	2.13	0.47
1:A:438:ARG:NH2	6:A:1610:HOH:O	2.38	0.47
1:B:282:MET:HE1	1:B:285:MET:CE	2.43	0.47
1:C:326:ARG:HD3	1:C:329:ARG:HB2	1.96	0.47
1:C:436:ASP:OD1	1:C:438:ARG:HB2	2.14	0.47
1:D:37:TRP:CE3	1:D:41:ALA:HA	2.50	0.47
1:D:282:MET:HE1	1:D:285:MET:CE	2.44	0.47
1:B:80:ASP:N	6:B:1368:HOH:O	2.48	0.47
1:A:326:ARG:HD3	1:A:329:ARG:HB2	1.95	0.47
1:B:326:ARG:HD3	1:B:329:ARG:HB2	1.96	0.46
1:C:37:TRP:CE3	1:C:41:ALA:HA	2.51	0.46
1:C:345:MET:HE1	1:C:347:SER:HB2	1.96	0.46
1:A:438:ARG:NE	6:A:1610:HOH:O	2.40	0.46
1:C:419:ILE:O	1:C:438:ARG:NH2	2.49	0.46
1:A:328:TRP:CE2	1:A:345:MET:HB2	2.51	0.45
1:A:86:VAL:N	6:A:1534:HOH:O	2.48	0.45
1:A:260:ASP:HA	1:A:289:PRO:HD2	1.99	0.45
1:C:234:GLY:HA2	1:D:251:GLN:HE22	1.82	0.45
1:C:328:TRP:CZ2	1:C:345:MET:HB2	2.52	0.45
1:D:326:ARG:HD3	1:D:329:ARG:HB2	1.99	0.45
1:C:260:ASP:HA	1:C:289:PRO:HD2	1.99	0.45
1:B:328:TRP:CZ2	1:B:345:MET:HB2	2.52	0.45
1:D:260:ASP:HA	1:D:289:PRO:HD2	1.98	0.45
1:D:412:ARG:HB2	6:D:1104:HOH:O	2.17	0.45
1:A:282:MET:HE1	1:A:285:MET:CE	2.47	0.44
1:C:105:ASN:ND2	6:C:1308:HOH:O	2.50	0.44
1:A:37:TRP:HZ2	4:K:2:FRU:H3	1.82	0.44
1:A:350:LEU:HD13	1:A:466:ARG:CZ	2.48	0.44
1:B:37:TRP:CE3	1:B:41:ALA:HA	2.52	0.44
1:B:374:GLU:HB2	6:B:1223:HOH:O	2.17	0.44
1:B:234:GLY:HA2	1:C:251:GLN:HE22	1.81	0.44
1:A:206:MET:SD	1:A:261:LEU:HD22	2.58	0.44
1:C:118:GLU:HG3	6:C:1256:HOH:O	2.18	0.44
1:C:55:ARG:HD3	6:C:1173:HOH:O	2.17	0.44
1:C:282:MET:HE1	1:C:285:MET:CE	2.48	0.44
1:B:206:MET:SD	1:B:261:LEU:HD22	2.58	0.43
1:C:350:LEU:HD13	1:C:466:ARG:CZ	2.47	0.43
1:A:37:TRP:CE3	1:A:41:ALA:HA	2.53	0.43
1:B:363:GLY:HA3	6:B:1080:HOH:O	2.17	0.43
1:B:260:ASP:HA	1:B:289:PRO:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:426:GLN:HE22	1:C:434:LYS:HD2	1.83	0.43
1:D:224:ASP:HB2	6:D:495:HOH:O	2.19	0.43
1:B:426:GLN:HE22	1:B:434:LYS:HD2	1.83	0.42
1:D:83:GLY:HA3	6:D:1671:HOH:O	2.18	0.42
1:A:25:GLY:HA2	6:A:1083:HOH:O	2.18	0.42
1:D:216:ARG:NH2	6:D:496:HOH:O	2.52	0.42
1:C:80:ASP:HB3	1:C:86:VAL:HG21	2.02	0.42
1:B:429:LYS:HD2	6:B:1286:HOH:O	2.19	0.42
1:C:427:SER:HB2	6:C:1140:HOH:O	2.20	0.42
1:B:433:SER:HB3	6:B:1193:HOH:O	2.19	0.42
1:D:426:GLN:HE22	1:D:434:LYS:HD2	1.82	0.42
1:A:438:ARG:CZ	6:A:1167:HOH:O	2.67	0.41
1:A:328:TRP:CZ2	1:A:345:MET:HB2	2.55	0.41
1:A:414:LYS:NZ	6:A:1469:HOH:O	2.53	0.41
1:B:350:LEU:HD13	1:B:466:ARG:CZ	2.50	0.41
1:A:116:ALA:HB2	1:A:148:TYR:CE2	2.56	0.41
1:A:234:GLY:HA2	1:B:251:GLN:HE22	1.85	0.41
1:B:48:LEU:HA	6:B:1051:HOH:O	2.21	0.41
1:D:52:THR:HG23	1:D:296:VAL:HG22	2.02	0.41
1:B:52:THR:HG23	1:B:296:VAL:CG2	2.51	0.41
1:B:436:ASP:C	1:B:438:ARG:N	2.77	0.41
1:C:36:ASN:HD21	1:C:71:LEU:HA	1.86	0.41
1:C:457:VAL:HA	1:C:458:PRO:HD3	1.96	0.41
1:D:52:THR:HG23	1:D:296:VAL:CG2	2.51	0.41
1:D:328:TRP:CE2	1:D:345:MET:HB2	2.55	0.41
1:C:124:TYR:HB3	1:C:125:PRO:HD2	2.03	0.41
1:D:80:ASP:HB3	1:D:86:VAL:HG21	2.03	0.41
1:A:86:VAL:HA	6:A:1215:HOH:O	2.20	0.40
1:A:228:TYR:CE1	1:D:232:TYR:HB2	2.57	0.40
1:A:113:TYR:HE1	1:A:120:THR:HB	1.86	0.40
6:A:1587:HOH:O	1:D:162:ILE:HD11	2.20	0.40
1:D:36:ASN:HD21	1:D:71:LEU:HA	1.86	0.40
1:D:412:ARG:CB	6:D:1104:HOH:O	2.68	0.40
1:A:457:VAL:HA	1:A:458:PRO:HD3	1.98	0.40

All (2) 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:434:LYS:CG	1:B:438:ARG:NH1[2_454]	1.84	0.36
1:A:433:SER:CB	1:B:436:ASP:OD1[2_454]	2.11	0.09

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	450/479 (94%)	430 (96%)	20 (4%)	0	100	100
1	B	450/479 (94%)	430 (96%)	20 (4%)	0	100	100
1	C	450/479 (94%)	429 (95%)	21 (5%)	0	100	100
1	D	450/479 (94%)	429 (95%)	21 (5%)	0	100	100
All	All	1800/1916 (94%)	1718 (95%)	82 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	375/398 (94%)	363 (97%)	12 (3%)	34	64
1	B	375/398 (94%)	364 (97%)	11 (3%)	37	67
1	C	375/398 (94%)	364 (97%)	11 (3%)	37	67
1	D	375/398 (94%)	364 (97%)	11 (3%)	37	67
All	All	1500/1592 (94%)	1455 (97%)	45 (3%)	36	66

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	VAL
1	A	74	CYS

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Mol	Chain	Res	Type
1	A	102	HIS
1	A	185	LEU
1	A	235	PHE
1	A	261	LEU
1	A	311	SER
1	A	345	MET
1	A	356	VAL
1	A	400	ARG
1	A	447	LEU
1	A	455	THR
1	B	19	VAL
1	B	74	CYS
1	B	102	HIS
1	B	185	LEU
1	B	235	PHE
1	B	261	LEU
1	B	345	MET
1	B	356	VAL
1	B	400	ARG
1	B	447	LEU
1	B	455	THR
1	C	19	VAL
1	C	74	CYS
1	C	102	HIS
1	C	185	LEU
1	C	235	PHE
1	C	261	LEU
1	C	345	MET
1	C	356	VAL
1	C	400	ARG
1	C	447	LEU
1	C	455	THR
1	D	19	VAL
1	D	74	CYS
1	D	102	HIS
1	D	185	LEU
1	D	235	PHE
1	D	261	LEU
1	D	345	MET
1	D	356	VAL
1	D	400	ARG
1	D	447	LEU

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Mol	Chain	Res	Type
1	D	455	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
1	A	136	GLN
1	A	141	ASN
1	A	251	GLN
1	A	355	GLN
1	A	413	ASN
1	A	426	GLN
1	B	36	ASN
1	B	105	ASN
1	B	136	GLN
1	B	141	ASN
1	B	156	GLN
1	B	251	GLN
1	B	355	GLN
1	B	426	GLN
1	C	36	ASN
1	C	136	GLN
1	C	141	ASN
1	C	187	ASN
1	C	251	GLN
1	C	263	ASN
1	C	355	GLN
1	C	370	ASN
1	C	426	GLN
1	D	36	ASN
1	D	136	GLN
1	D	141	ASN
1	D	156	GLN
1	D	187	ASN
1	D	251	GLN
1	D	263	ASN
1	D	355	GLN
1	D	426	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 ⓘ

24 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	E	1	1,2	14,14,15	0.85	1 (7%)	17,19,21	1.16	3 (17%)
2	NAG	E	2	2	14,14,15	0.49	0	17,19,21	0.97	1 (5%)
3	NAG	F	1	1,3	14,14,15	0.43	0	17,19,21	1.26	2 (11%)
3	NAG	F	2	3	14,14,15	0.57	0	17,19,21	0.88	0
2	NAG	G	1	1,2	14,14,15	0.84	0	17,19,21	1.47	4 (23%)
2	NAG	G	2	2	14,14,15	0.55	0	17,19,21	1.12	1 (5%)
3	NAG	H	1	1,3	14,14,15	0.47	0	17,19,21	1.43	3 (17%)
3	NAG	H	2	3	14,14,15	0.55	0	17,19,21	1.26	2 (11%)
2	NAG	I	1	1,2	14,14,15	0.67	0	17,19,21	0.93	1 (5%)
2	NAG	I	2	2	14,14,15	0.46	0	17,19,21	1.12	1 (5%)
3	NAG	J	1	1,3	14,14,15	0.45	0	17,19,21	1.37	3 (17%)
3	NAG	J	2	3	14,14,15	0.54	0	17,19,21	1.36	1 (5%)
4	GLC	K	1	4	11,11,12	0.58	0	15,15,17	1.17	1 (6%)
4	FRU	K	2	4	11,12,12	0.69	0	10,18,18	0.91	0
4	GLA	K	3	4	11,11,12	0.44	0	15,15,17	0.52	0
4	GLC	L	1	4	11,11,12	0.54	0	15,15,17	1.35	1 (6%)
4	FRU	L	2	4	11,12,12	0.69	0	10,18,18	0.95	0
4	GLA	L	3	4	11,11,12	0.54	0	15,15,17	0.90	1 (6%)
4	GLC	M	1	4	11,11,12	0.62	0	15,15,17	0.95	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	FRU	M	2	4	11,12,12	0.70	0	10,18,18	0.81	0
4	GLA	M	3	4	11,11,12	0.39	0	15,15,17	0.66	0
4	GLC	N	1	4	11,11,12	0.58	0	15,15,17	1.21	1 (6%)
4	FRU	N	2	4	11,12,12	0.67	0	10,18,18	0.84	0
4	GLA	N	3	4	11,11,12	0.42	0	15,15,17	0.57	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	E	1	1,2	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
2	NAG	G	1	1,2	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	2/6/23/26	0/1/1/1
3	NAG	H	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
2	NAG	I	1	1,2	1/1/5/7	2/6/23/26	0/1/1/1
2	NAG	I	2	2	-	2/6/23/26	0/1/1/1
3	NAG	J	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1
4	GLC	K	1	4	-	0/2/19/22	0/1/1/1
4	FRU	K	2	4	-	2/5/24/24	0/1/1/1
4	GLA	K	3	4	-	1/2/19/22	0/1/1/1
4	GLC	L	1	4	-	0/2/19/22	0/1/1/1
4	FRU	L	2	4	-	1/5/24/24	0/1/1/1
4	GLA	L	3	4	-	2/2/19/22	0/1/1/1
4	GLC	M	1	4	-	2/2/19/22	0/1/1/1
4	FRU	M	2	4	-	1/5/24/24	0/1/1/1
4	GLA	M	3	4	-	2/2/19/22	0/1/1/1
4	GLC	N	1	4	-	2/2/19/22	0/1/1/1
4	FRU	N	2	4	-	2/5/24/24	0/1/1/1
4	GLA	N	3	4	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	NAG	C1-C2	2.04	1.55	1.52

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	2	NAG	C1-O5-C5	4.65	118.42	112.19
4	L	1	GLC	C1-O5-C5	4.34	118.00	112.19
4	K	1	GLC	C1-O5-C5	3.60	117.00	112.19
2	G	2	NAG	C1-O5-C5	3.23	116.51	112.19
4	N	1	GLC	C1-O5-C5	3.12	116.36	112.19
3	H	2	NAG	C4-C3-C2	3.11	115.58	111.02
3	H	1	NAG	C4-C3-C2	3.02	115.44	111.02
2	G	1	NAG	C1-O5-C5	-3.02	108.14	112.19
3	J	1	NAG	O5-C1-C2	-3.01	106.64	111.29
3	J	1	NAG	C4-C3-C2	2.93	115.31	111.02
2	I	2	NAG	C1-O5-C5	2.86	116.02	112.19
2	G	1	NAG	O5-C5-C4	-2.72	104.20	110.83
2	E	1	NAG	C4-C3-C2	2.59	114.82	111.02
2	E	2	NAG	C1-O5-C5	2.48	115.51	112.19
3	F	1	NAG	C4-C3-C2	2.45	114.61	111.02
3	H	1	NAG	C3-C4-C5	2.42	114.62	110.23
3	F	1	NAG	C1-O5-C5	2.42	115.43	112.19
2	G	1	NAG	O5-C1-C2	-2.38	107.61	111.29
2	E	1	NAG	C1-C2-N2	2.32	114.09	110.43
4	L	3	GLA	C1-O5-C5	2.29	115.25	112.19
3	J	1	NAG	C1-O5-C5	2.26	115.21	112.19
2	G	1	NAG	C6-C5-C4	2.23	118.50	113.02
2	I	1	NAG	C4-C3-C2	2.06	114.04	111.02
3	H	2	NAG	C1-C2-N2	-2.06	107.19	110.43
3	H	1	NAG	O5-C1-C2	-2.05	108.11	111.29
2	E	1	NAG	O5-C1-C2	-2.04	108.14	111.29

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	E	1	NAG	C1
2	G	1	NAG	C1
2	I	1	NAG	C1

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	N	2	FRU	O5-C5-C6-O6

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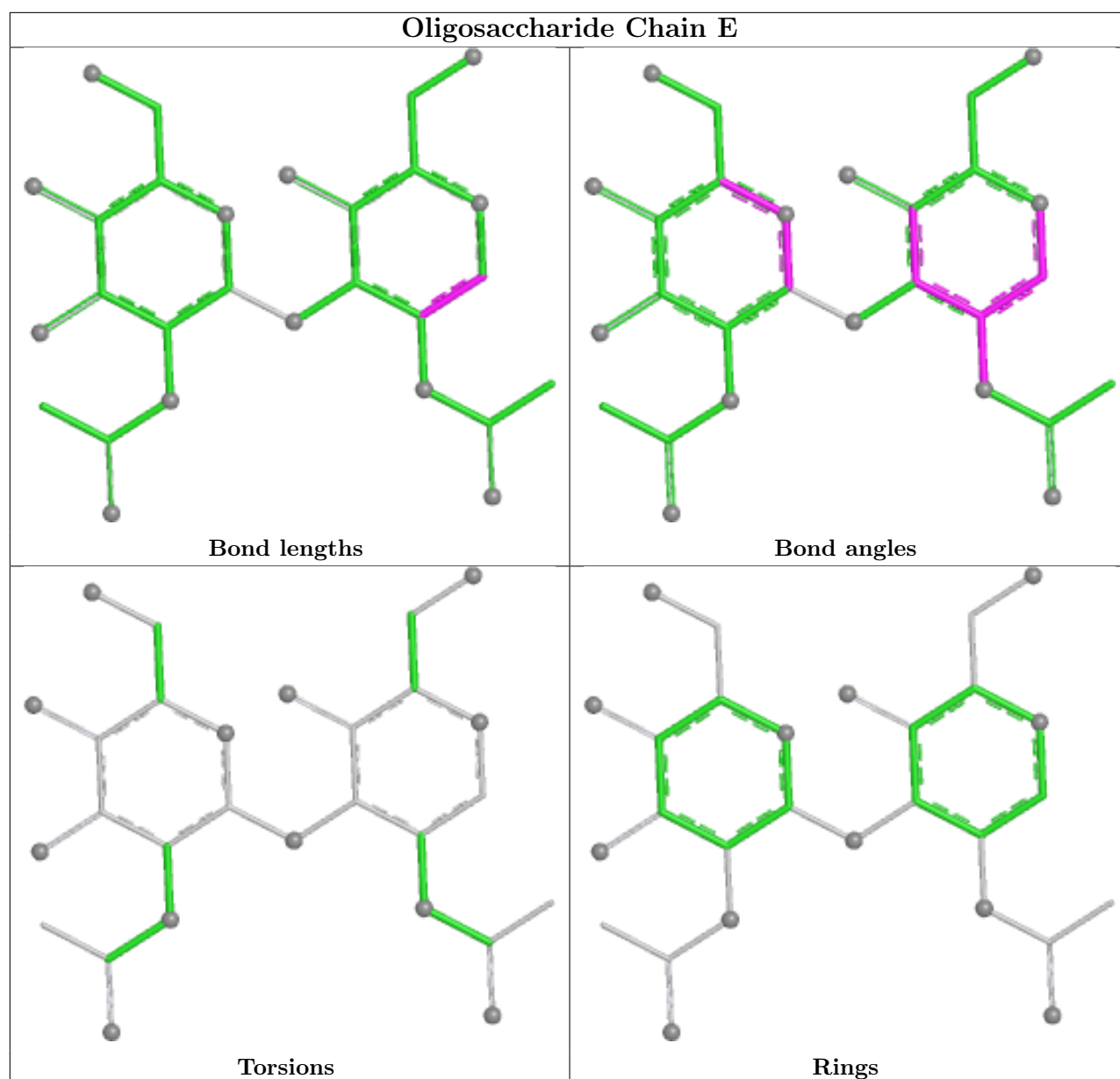
Mol	Chain	Res	Type	Atoms
4	K	2	FRU	C4-C5-C6-O6
4	N	2	FRU	C4-C5-C6-O6
4	K	2	FRU	O5-C5-C6-O6
2	G	2	NAG	O5-C5-C6-O6
2	I	2	NAG	O5-C5-C6-O6
2	G	2	NAG	C4-C5-C6-O6
2	I	2	NAG	C4-C5-C6-O6
4	L	3	GLA	C4-C5-C6-O6
4	N	1	GLC	O5-C5-C6-O6
4	M	3	GLA	C4-C5-C6-O6
4	M	1	GLC	O5-C5-C6-O6
4	L	3	GLA	O5-C5-C6-O6
4	M	3	GLA	O5-C5-C6-O6
2	I	1	NAG	C4-C5-C6-O6
3	J	1	NAG	C4-C5-C6-O6
2	I	1	NAG	O5-C5-C6-O6
4	K	3	GLA	C4-C5-C6-O6
4	N	1	GLC	C4-C5-C6-O6
3	H	2	NAG	C4-C5-C6-O6
4	M	1	GLC	C4-C5-C6-O6
4	M	2	FRU	O1-C1-C2-O2
3	H	2	NAG	O5-C5-C6-O6
3	H	1	NAG	O5-C5-C6-O6
3	J	1	NAG	O5-C5-C6-O6
4	L	2	FRU	O1-C1-C2-C3

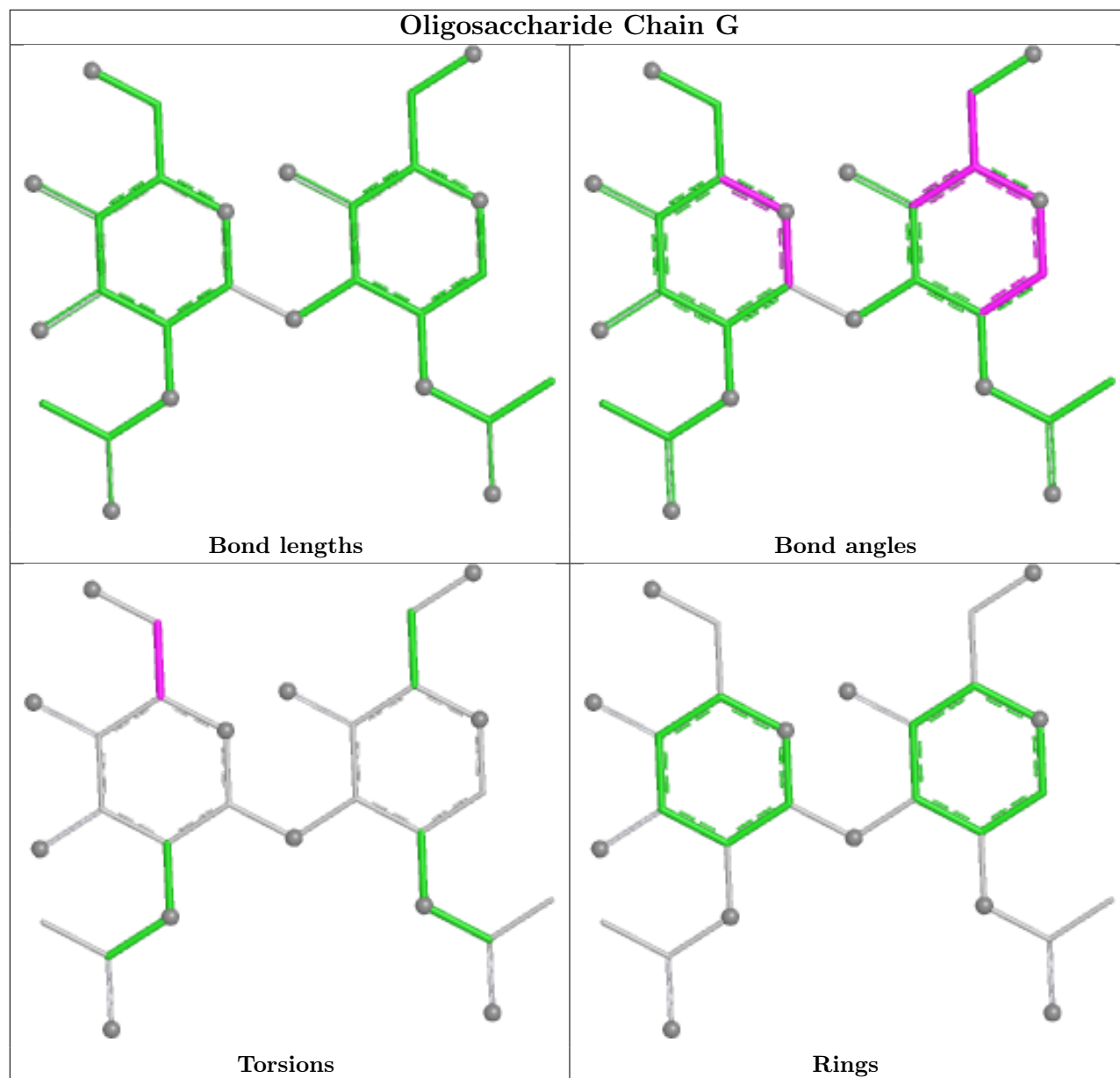
There are no ring outliers.

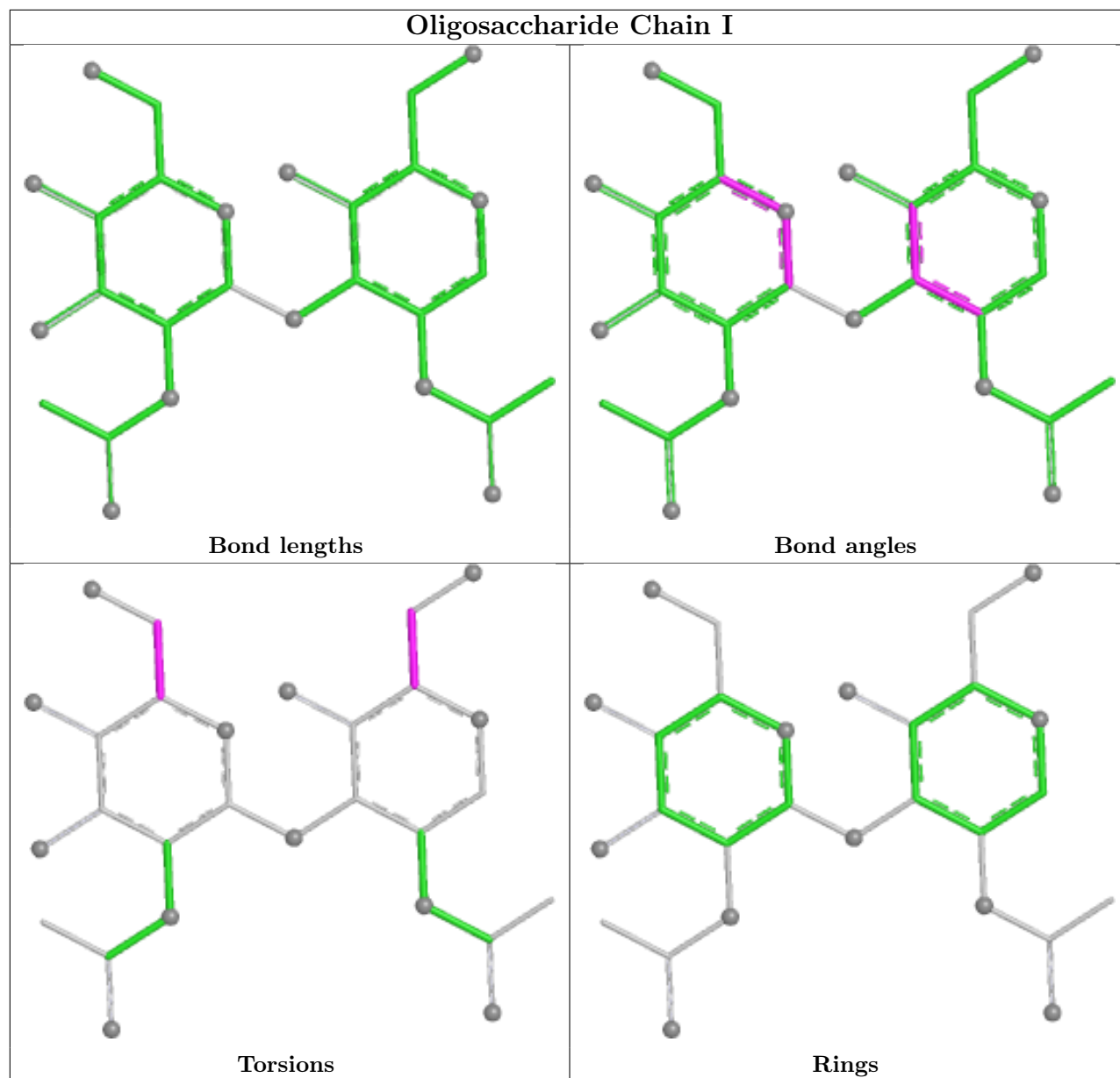
2 monomers are involved in 2 short contacts:

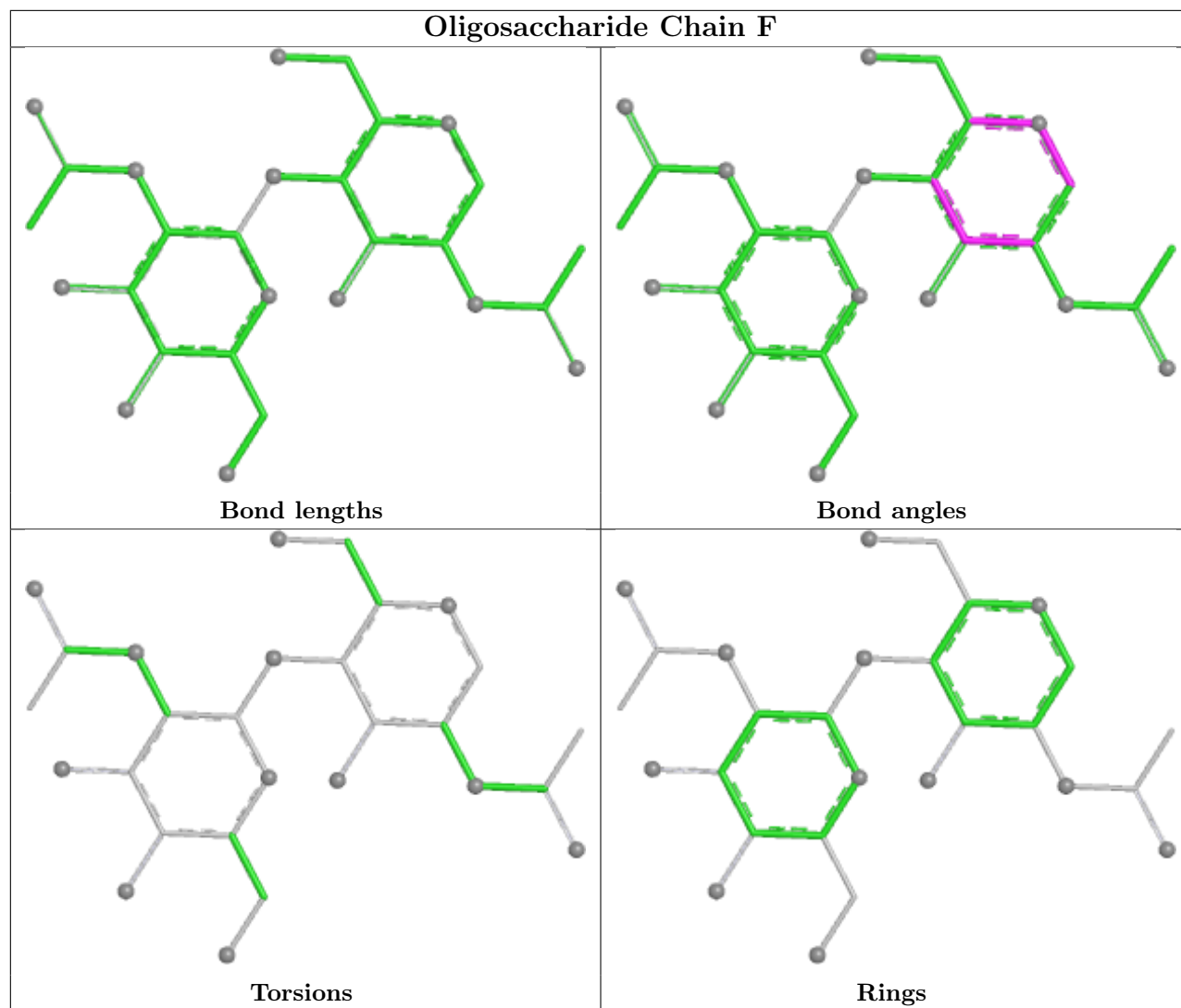
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	M	2	FRU	1	0
4	K	2	FRU	1	0

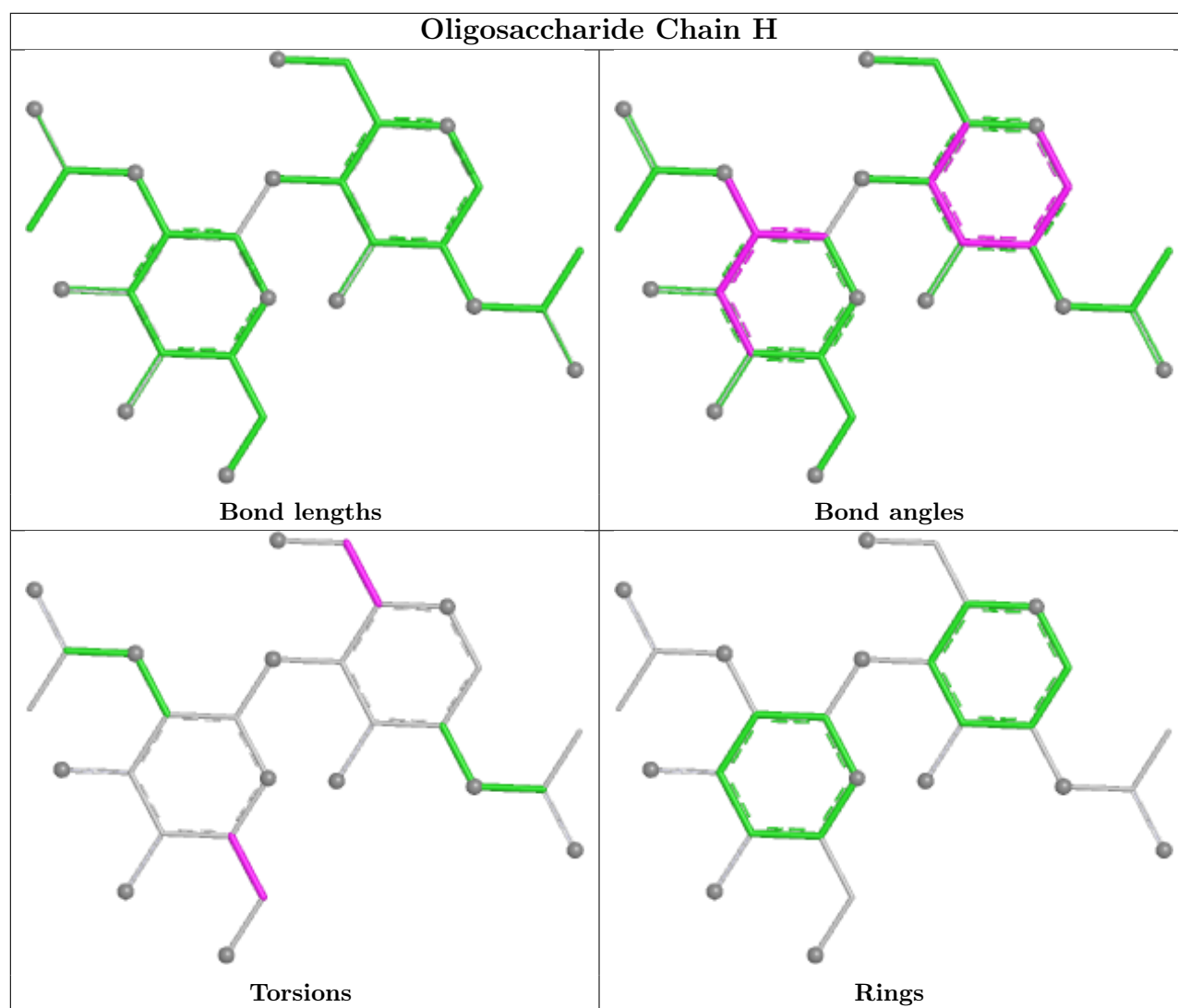
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

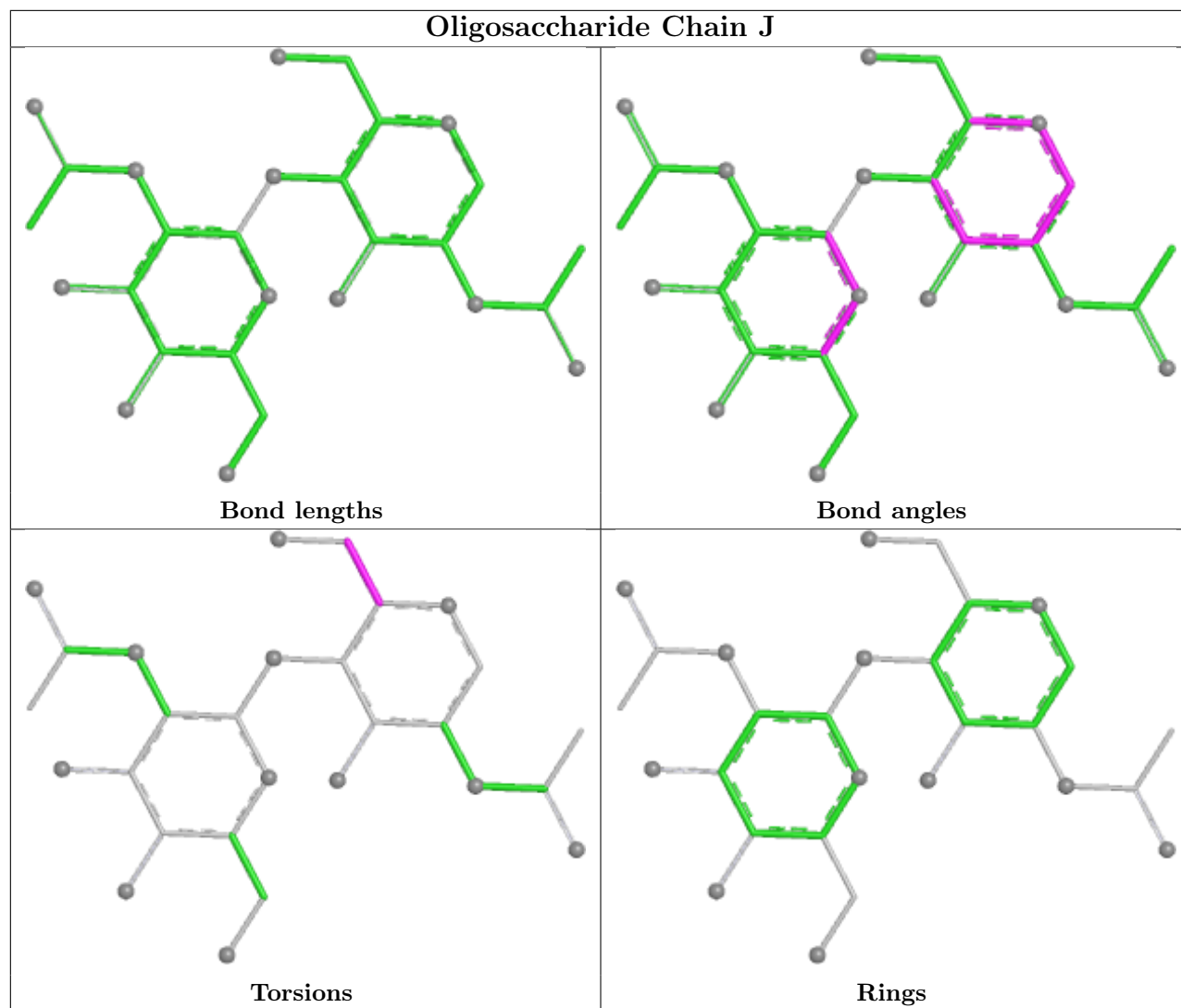


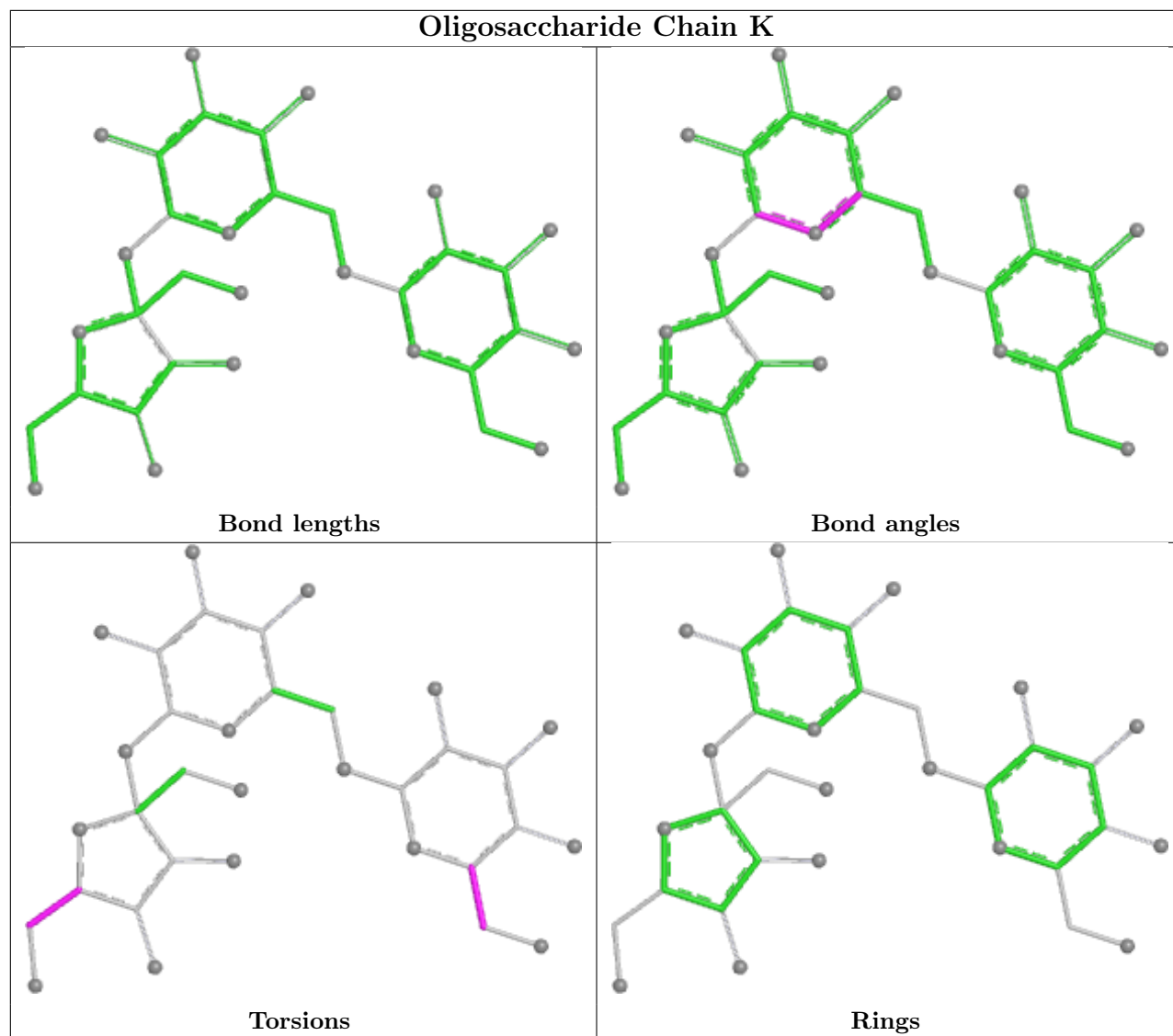


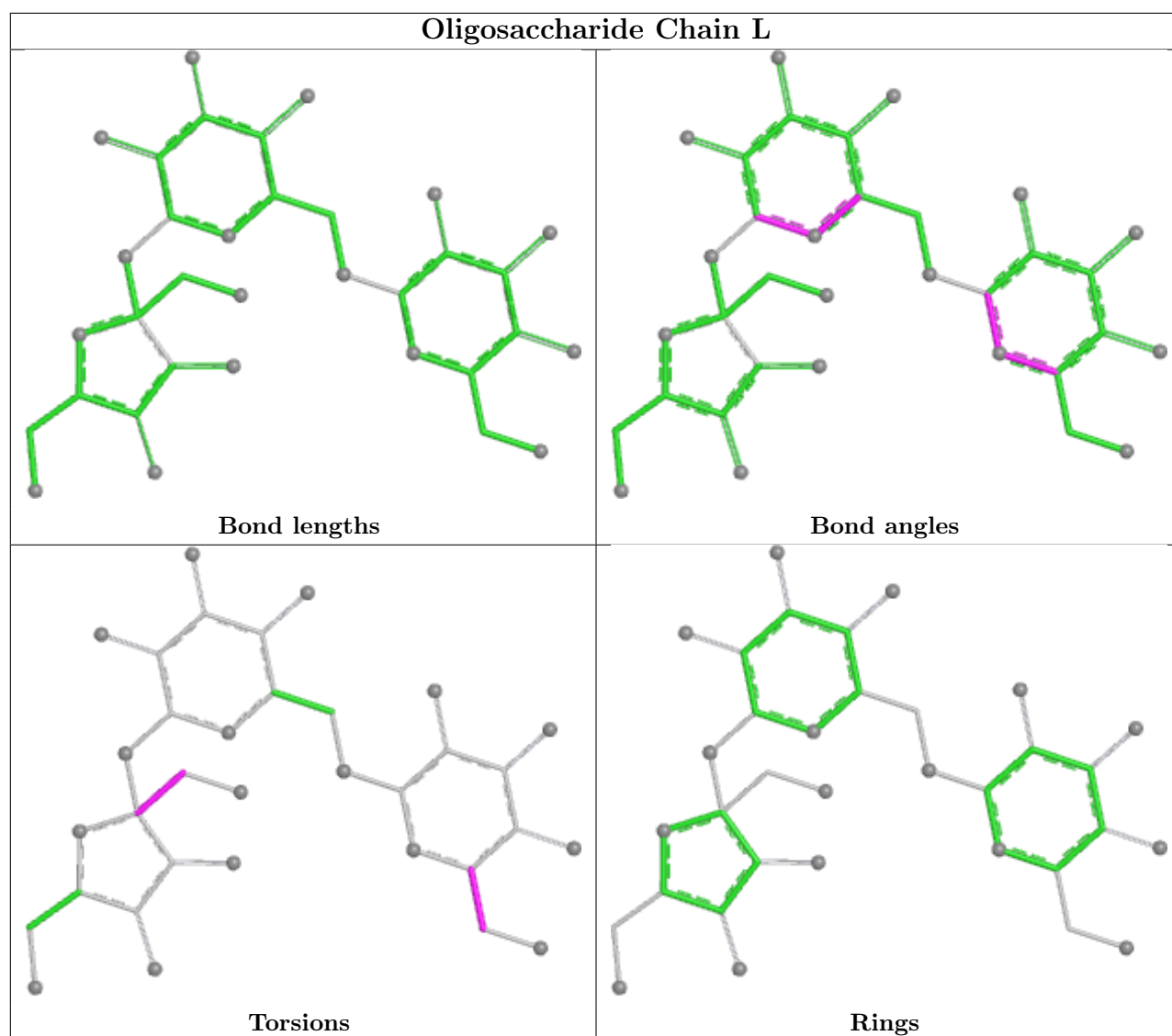


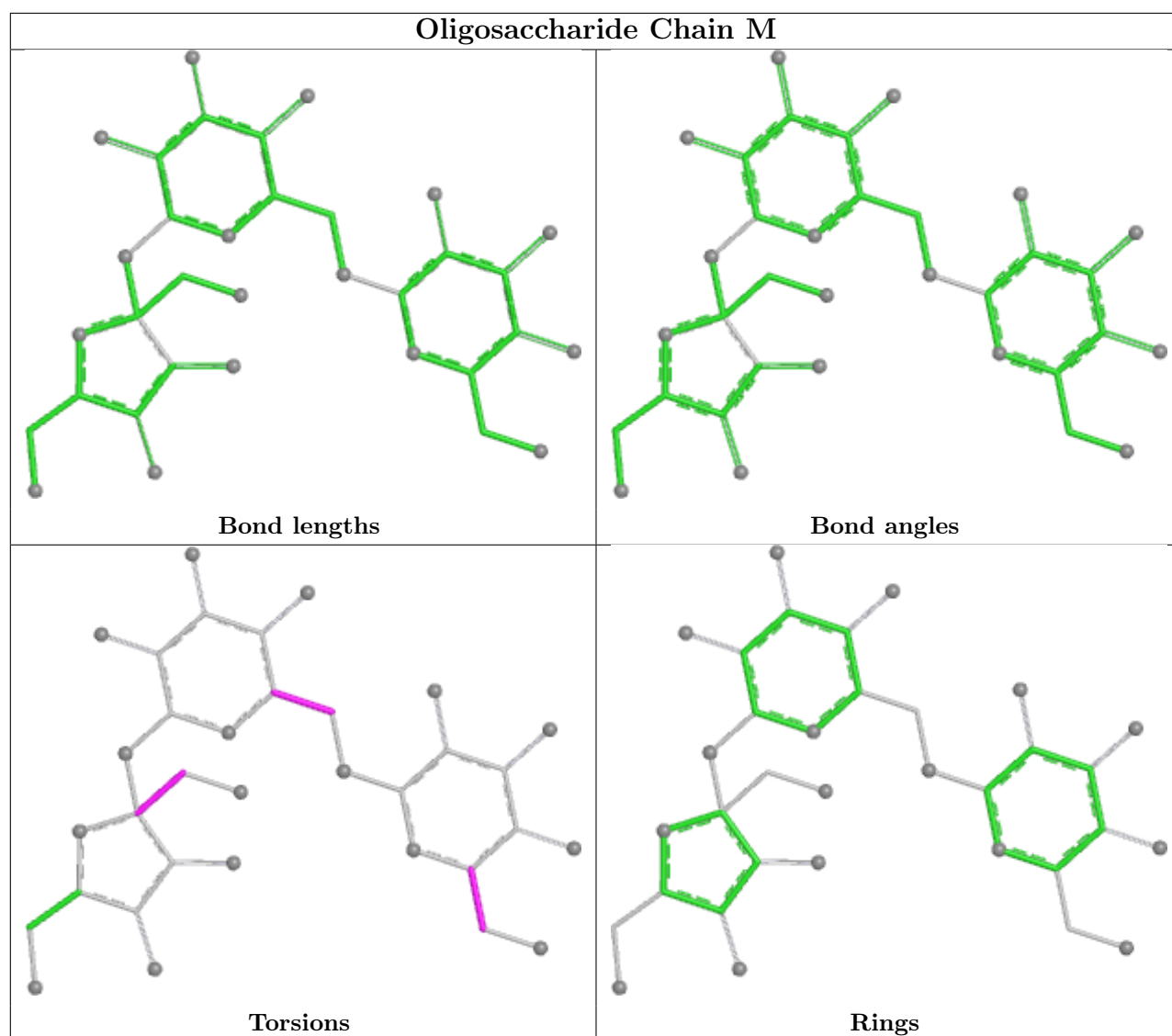


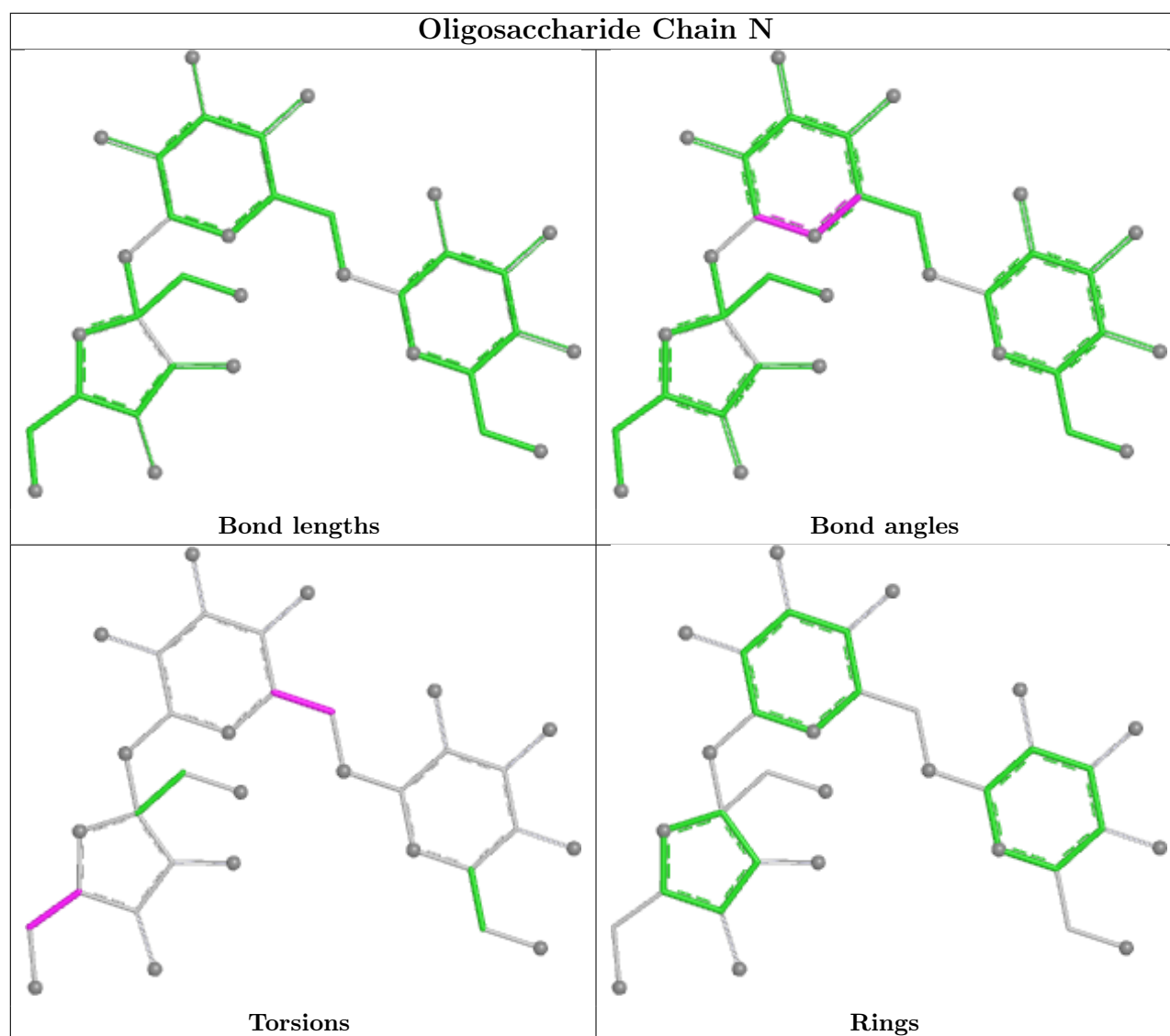












5.6 Ligand geometry [i](#)

9 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	C	2001	1	14,14,15	0.44	0	17,19,21	1.23	1 (5%)
5	NAG	D	4001	1	14,14,15	0.47	0	17,19,21	0.74	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	C	4001	1	14,14,15	0.47	0	17,19,21	0.67	0
5	NAG	B	2001	1	14,14,15	0.43	0	17,19,21	2.23	4 (23%)
5	NAG	A	4001	1	14,14,15	0.56	0	17,19,21	1.24	1 (5%)
5	NAG	C	5001	1	14,14,15	0.45	0	17,19,21	0.98	1 (5%)
5	NAG	D	2001	1	14,14,15	0.60	0	17,19,21	1.16	1 (5%)
5	NAG	B	4001	1	14,14,15	0.54	0	17,19,21	1.11	1 (5%)
5	NAG	A	2001	1	14,14,15	0.44	0	17,19,21	0.70	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
5	NAG	C	2001	1	-	0/6/23/26	0/1/1/1
5	NAG	D	4001	1	-	0/6/23/26	0/1/1/1
5	NAG	C	4001	1	-	0/6/23/26	0/1/1/1
5	NAG	B	2001	1	-	2/6/23/26	0/1/1/1
5	NAG	A	4001	1	-	2/6/23/26	0/1/1/1
5	NAG	C	5001	1	-	2/6/23/26	0/1/1/1
5	NAG	D	2001	1	-	2/6/23/26	0/1/1/1
5	NAG	B	4001	1	-	2/6/23/26	0/1/1/1
5	NAG	A	2001	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	2001	NAG	C1-O5-C5	6.90	121.44	112.19
5	C	2001	NAG	C1-O5-C5	3.67	117.11	112.19
5	B	2001	NAG	C3-C4-C5	3.30	116.21	110.23
5	B	4001	NAG	C1-O5-C5	2.90	116.07	112.19
5	A	4001	NAG	C1-O5-C5	2.79	115.92	112.19
5	D	2001	NAG	C2-N2-C7	2.43	126.16	122.90
5	C	5001	NAG	C1-O5-C5	2.20	115.14	112.19
5	B	2001	NAG	O5-C5-C4	2.13	116.00	110.83
5	D	4001	NAG	C1-O5-C5	2.11	115.01	112.19
5	B	2001	NAG	O7-C7-N2	2.05	125.60	121.98

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	2001	NAG	O5-C5-C6-O6
5	A	4001	NAG	O5-C5-C6-O6
5	A	4001	NAG	C4-C5-C6-O6
5	C	5001	NAG	O5-C5-C6-O6
5	B	2001	NAG	C4-C5-C6-O6
5	D	2001	NAG	O5-C5-C6-O6
5	D	2001	NAG	C4-C5-C6-O6
5	A	2001	NAG	O5-C5-C6-O6
5	B	4001	NAG	C4-C5-C6-O6
5	B	4001	NAG	O5-C5-C6-O6
5	C	5001	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	4001	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

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	452/479 (94%)	0.37	15 (3%) 49 45	33, 40, 45, 48	0
1	B	452/479 (94%)	0.50	19 (4%) 40 37	32, 40, 45, 48	0
1	C	452/479 (94%)	0.30	10 (2%) 62 59	33, 40, 45, 48	0
1	D	452/479 (94%)	0.43	16 (3%) 47 43	33, 40, 45, 48	0
All	All	1808/1916 (94%)	0.40	60 (3%) 49 45	32, 40, 45, 48	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	41	ALA	4.1
1	D	41	ALA	3.9
1	C	42	CYS	3.6
1	A	382	LEU	3.5
1	A	434	LYS	3.3
1	B	42	CYS	3.3
1	B	37	TRP	3.3
1	D	19	VAL	3.2
1	B	432	LEU	3.2
1	D	37	TRP	3.2
1	B	434	LYS	3.1
1	C	437	THR	3.1
1	A	39	THR	3.0
1	A	37	TRP	3.0
1	A	102	HIS	2.9
1	B	437	THR	2.9
1	B	399	ASN	2.9
1	A	383	GLY	2.9
1	B	95	GLY	2.9
1	D	48	LEU	2.7
1	A	90	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	90	GLN	2.7
1	B	39	THR	2.6
1	A	48	LEU	2.6
1	C	48	LEU	2.6
1	A	105	ASN	2.6
1	D	40	PHE	2.6
1	C	19	VAL	2.6
1	A	43	ASP	2.5
1	B	433	SER	2.5
1	B	431	GLY	2.5
1	D	470	SER	2.5
1	B	436	ASP	2.5
1	B	41	ALA	2.5
1	A	40	PHE	2.4
1	A	51	ASP	2.4
1	D	270	ASN	2.4
1	B	442	GLN	2.4
1	A	438	ARG	2.3
1	D	416	ALA	2.3
1	C	39	THR	2.3
1	D	93	PRO	2.3
1	B	38	ASN	2.2
1	D	412	ARG	2.2
1	D	90	GLN	2.2
1	C	102	HIS	2.2
1	C	82	ASP	2.2
1	D	44	VAL	2.2
1	B	413	ASN	2.1
1	B	43	ASP	2.1
1	B	102	HIS	2.1
1	C	143	VAL	2.1
1	B	40	PHE	2.1
1	A	437	THR	2.1
1	D	67	LYS	2.1
1	D	304	TYR	2.1
1	D	42	CYS	2.1
1	A	19	VAL	2.1
1	B	81	SER	2.0
1	D	89	GLU	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](#)

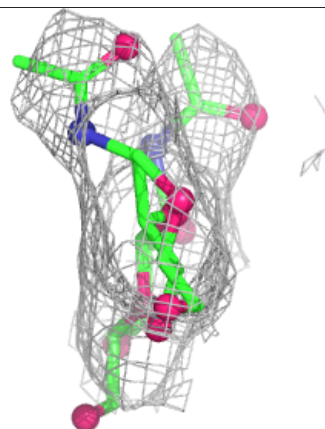
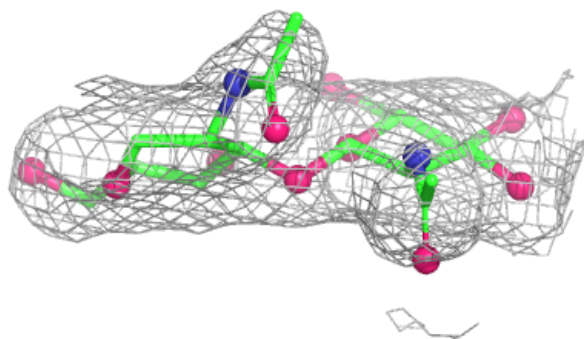
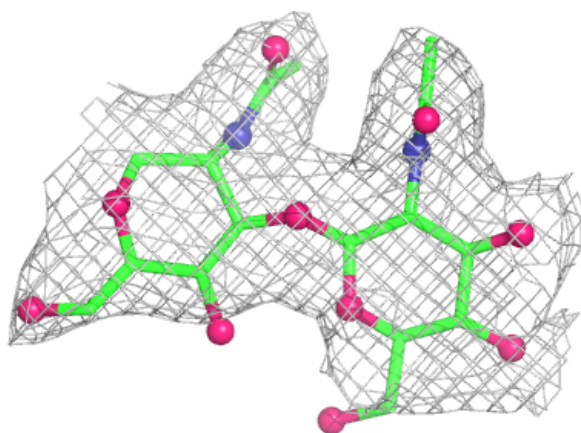
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	H	2	14/15	0.46	0.17	70,73,74,74	0
4	GLA	L	3	11/12	0.62	0.19	81,82,82,83	0
4	FRU	M	2	12/12	0.68	0.19	87,88,89,89	0
4	FRU	K	2	12/12	0.69	0.15	76,77,78,78	0
4	FRU	N	2	12/12	0.71	0.20	100,101,102,102	0
2	NAG	G	2	14/15	0.74	0.12	60,61,64,64	0
4	GLA	N	3	11/12	0.74	0.18	96,97,97,97	0
3	NAG	F	2	14/15	0.76	0.12	68,70,71,71	0
4	GLA	K	3	11/12	0.79	0.14	74,75,75,75	0
4	FRU	L	2	12/12	0.79	0.14	82,83,83,83	0
3	NAG	J	2	14/15	0.80	0.12	63,64,67,67	0
4	GLC	L	1	11/12	0.81	0.14	82,82,82,82	0
4	GLA	M	3	11/12	0.82	0.14	79,80,80,81	0
2	NAG	E	1	14/15	0.82	0.14	48,51,53,53	0
2	NAG	G	1	14/15	0.82	0.10	50,53,57,57	0
2	NAG	I	1	14/15	0.83	0.13	50,53,57,58	0
4	GLC	M	1	11/12	0.83	0.16	83,85,86,86	0
2	NAG	E	2	14/15	0.83	0.12	56,57,59,61	0
4	GLC	N	1	11/12	0.84	0.17	97,98,99,99	0
3	NAG	H	1	14/15	0.85	0.11	54,57,61,66	0
4	GLC	K	1	11/12	0.86	0.13	75,75,76,76	0
2	NAG	I	2	14/15	0.86	0.09	57,57,58,58	0
3	NAG	J	1	14/15	0.88	0.11	55,58,60,61	0
3	NAG	F	1	14/15	0.90	0.10	55,57,61,64	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.

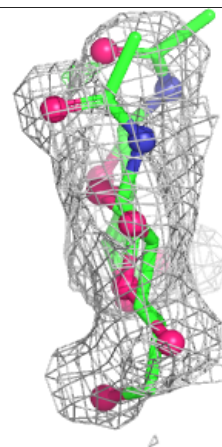
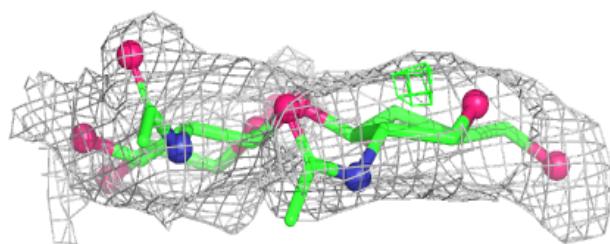
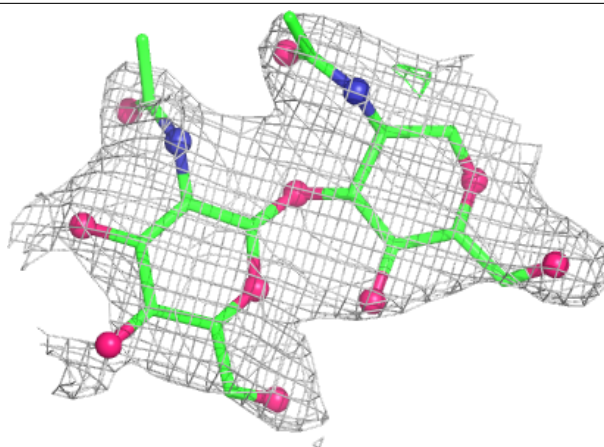
Electron density around Chain E:

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



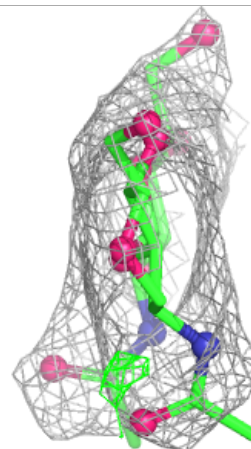
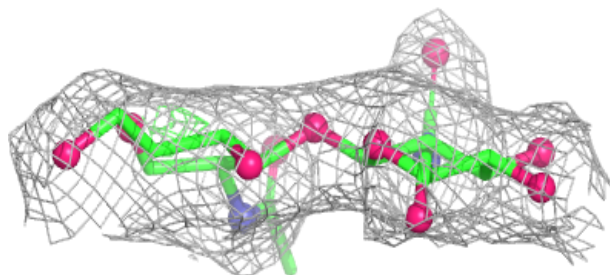
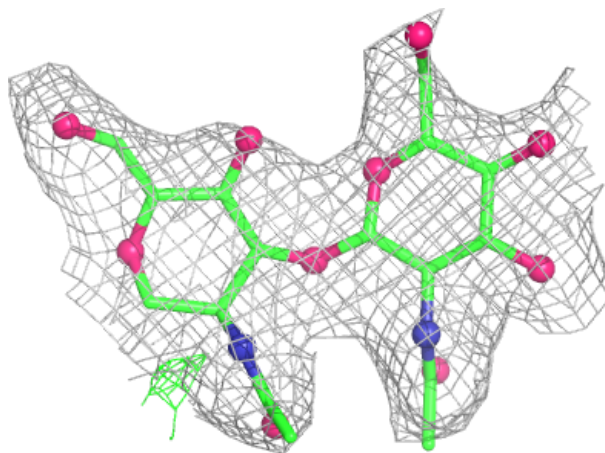
Electron density around Chain G:

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



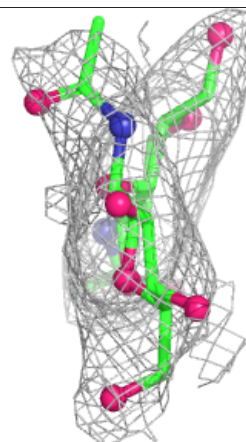
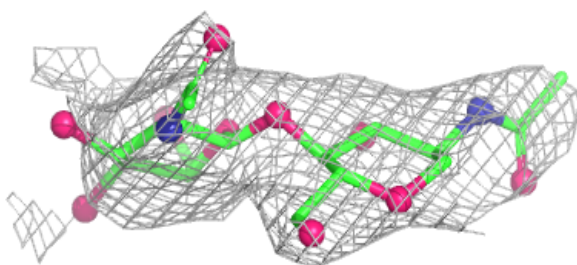
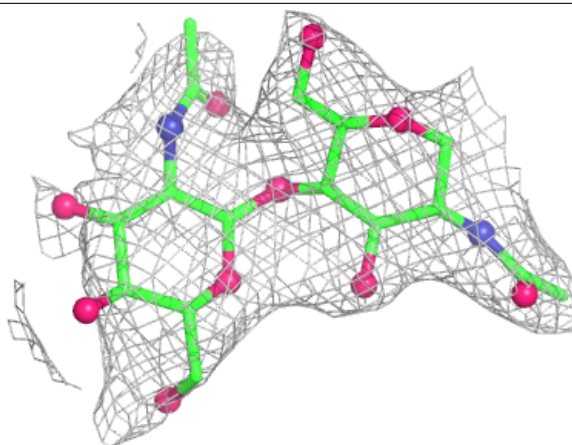
Electron density around Chain I:

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



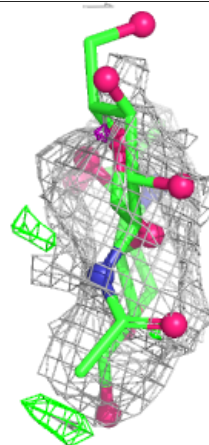
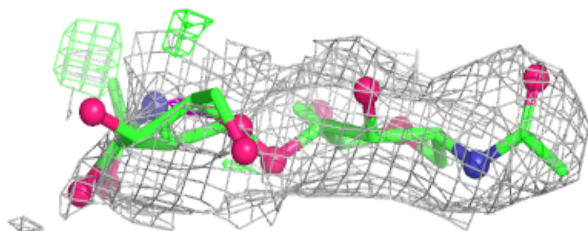
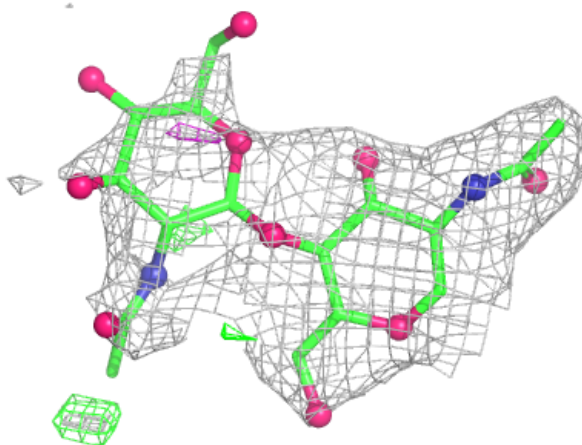
Electron density around Chain F:

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



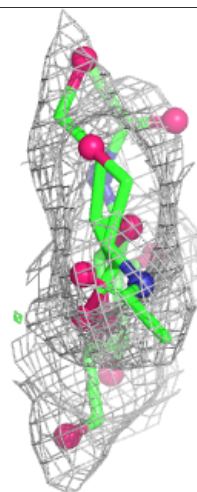
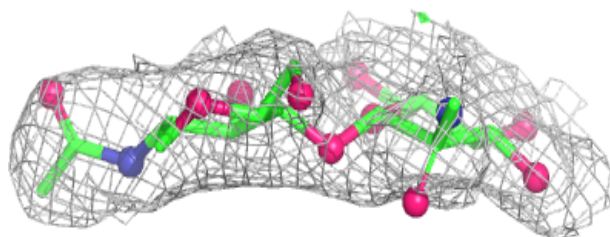
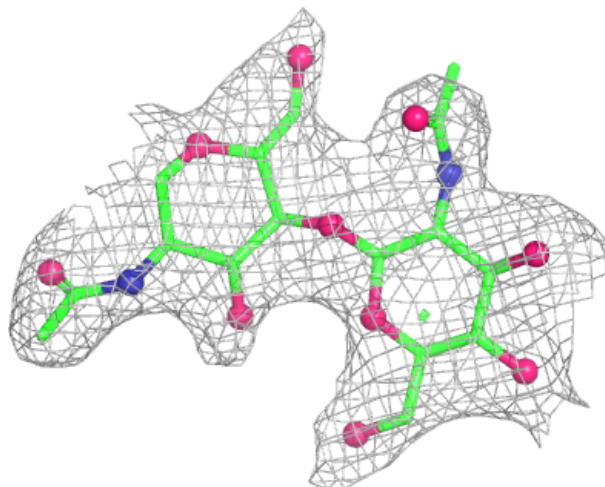
Electron density around Chain H:

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



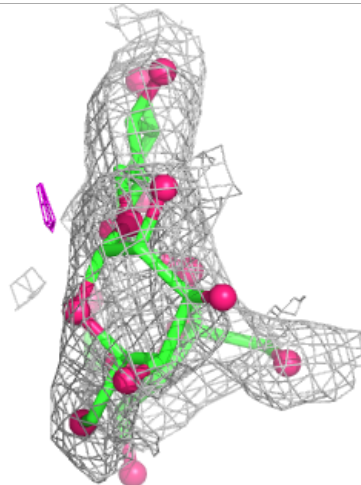
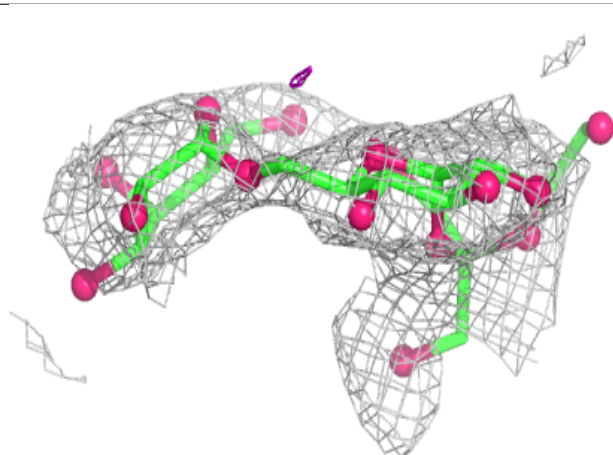
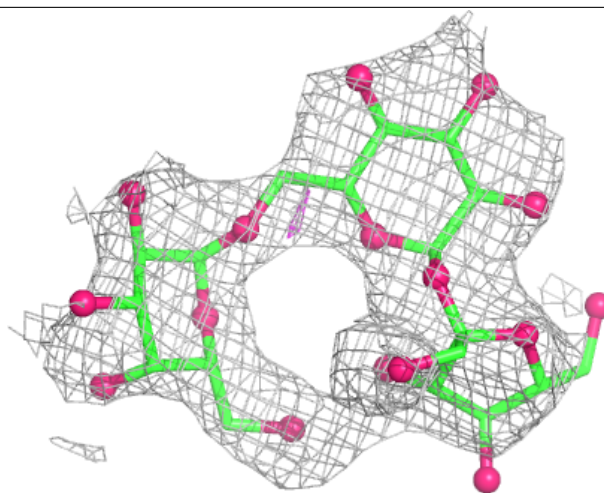
Electron density around Chain J:

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



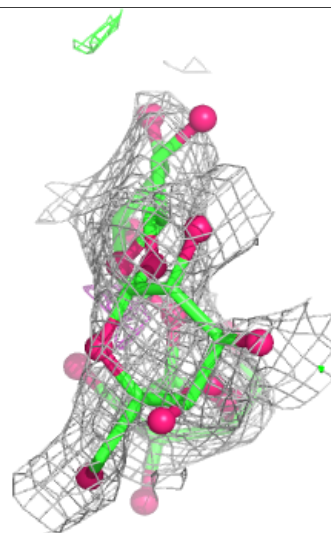
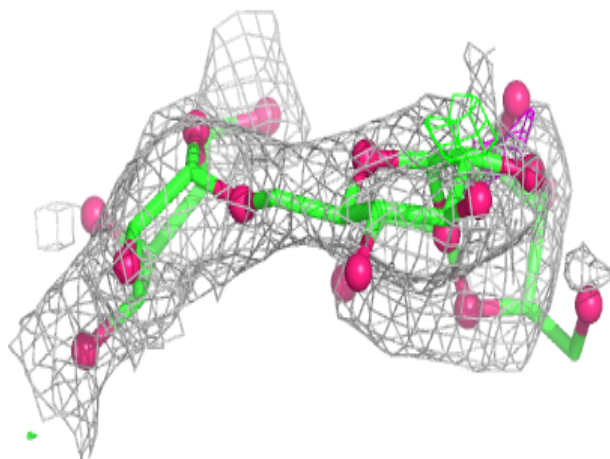
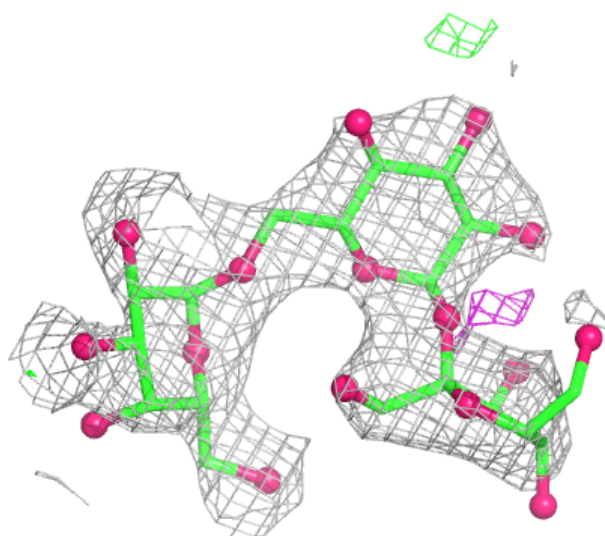
Electron density around Chain K:

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



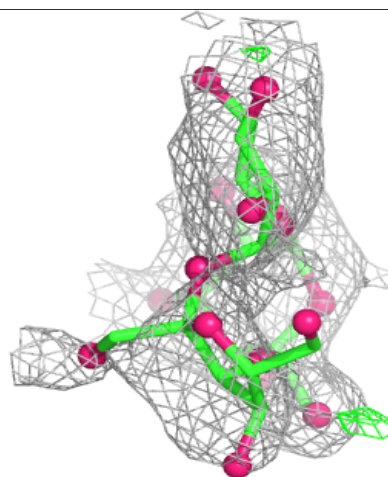
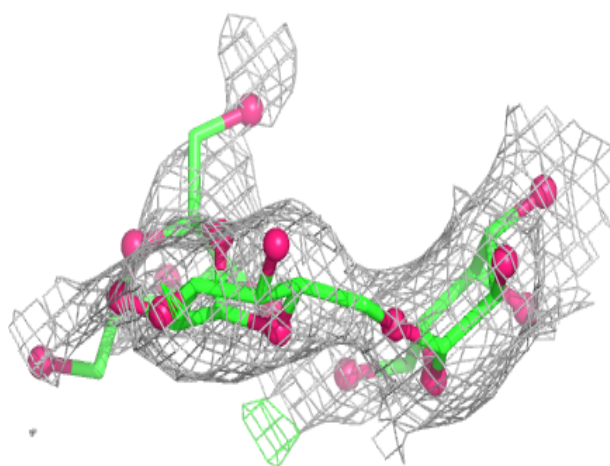
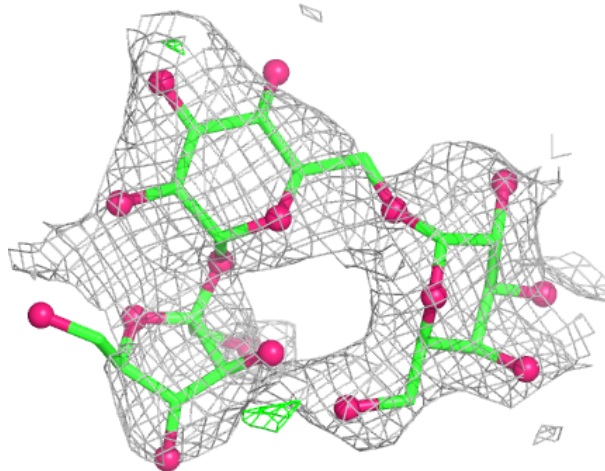
Electron density around Chain L:

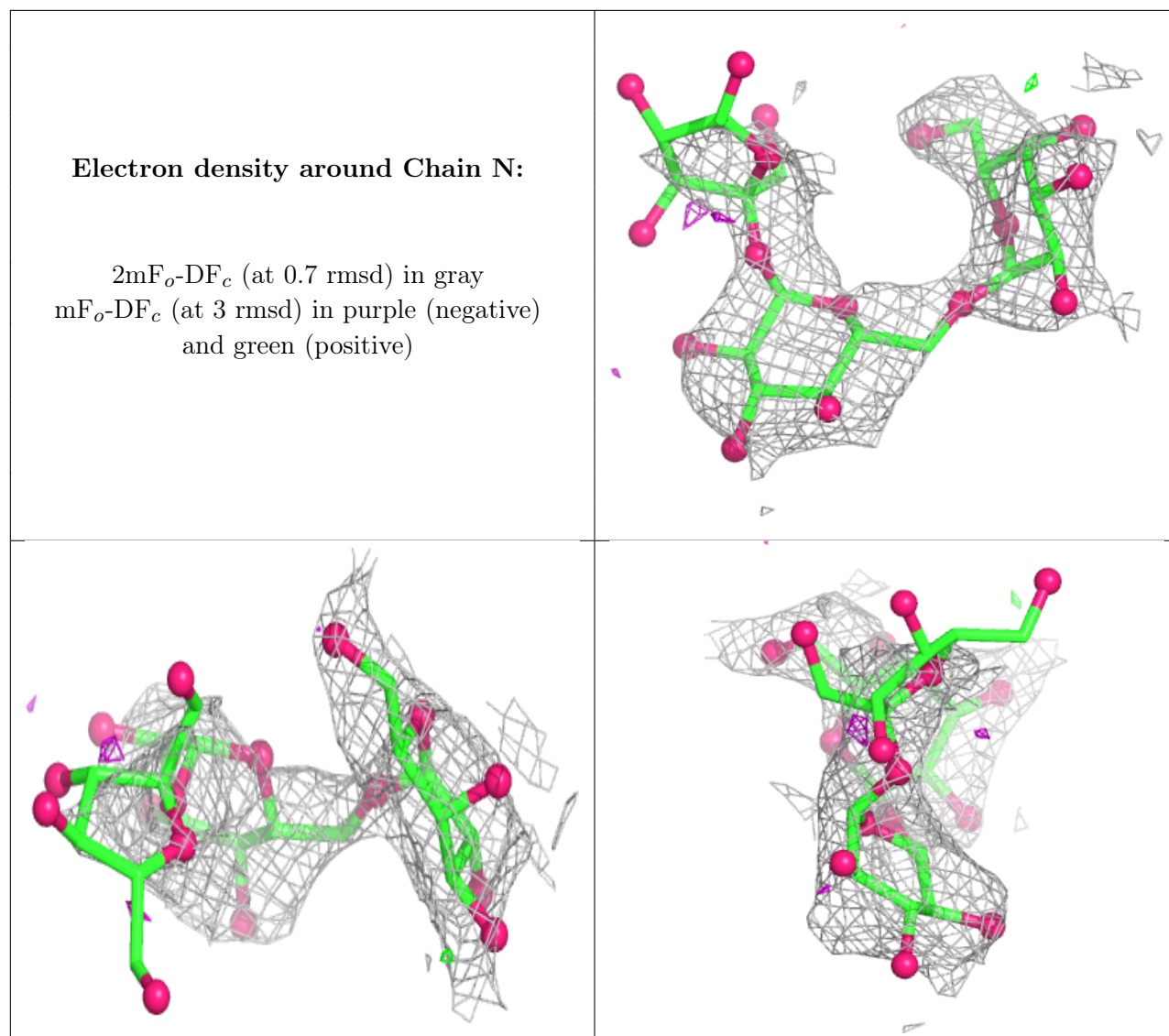
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain M:

$2mF_o-DF_c$ (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(Å ²)	Q<0.9
5	NAG	C	4001	14/15	0.75	0.12	53,55,56,57	0
5	NAG	B	4001	14/15	0.78	0.12	52,55,57,57	0
5	NAG	D	4001	14/15	0.79	0.12	53,56,57,57	0
5	NAG	B	2001	14/15	0.85	0.10	49,51,52,53	0
5	NAG	A	4001	14/15	0.85	0.12	50,52,52,53	0
5	NAG	A	2001	14/15	0.88	0.10	46,48,49,49	0
5	NAG	C	5001	14/15	0.88	0.11	51,53,54,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	NAG	D	2001	14/15	0.88	0.10	47,49,51,51	0
5	NAG	C	2001	14/15	0.88	0.09	45,47,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.