



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:01 PM UTC

PDB ID : 4ADF / pdb_00004adf
Title : CRYSTAL STRUCTURE OF THE HUMAN COLONY-STIMULATING FACTOR 1 (hCSF-1) CYTOKINE IN COMPLEX WITH THE VIRAL RECEPTOR BARF1
Authors : Elegheert, J.; Bracke, N.; Savvides, S.N.
Deposited on : 2011-12-23
Resolution : 4.40 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

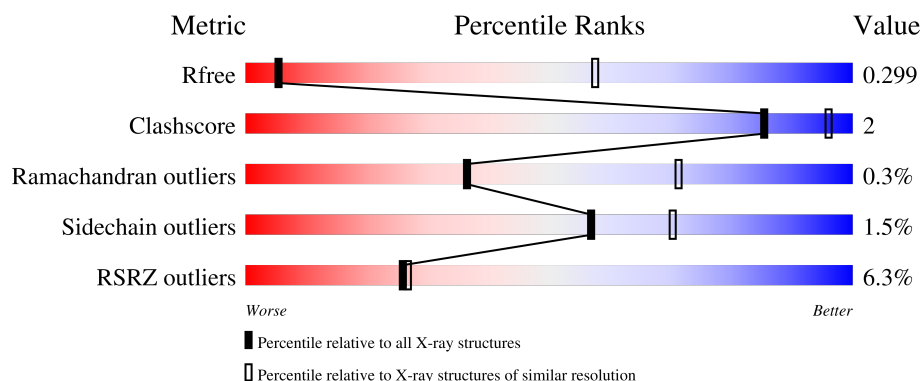
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.40 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.



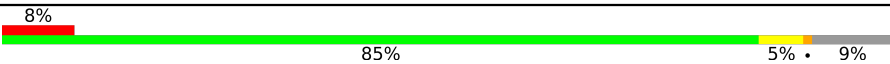
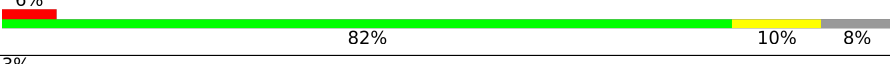
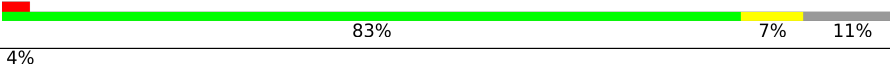
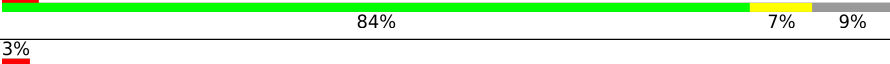
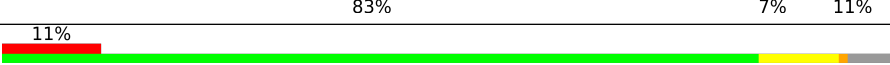
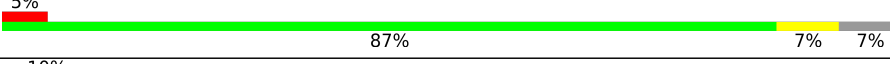
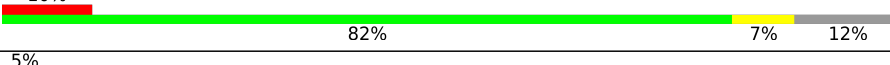
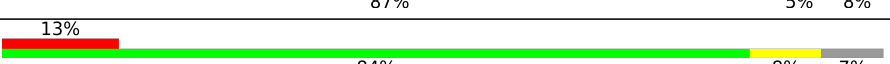
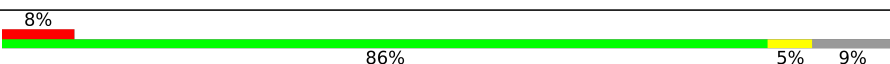
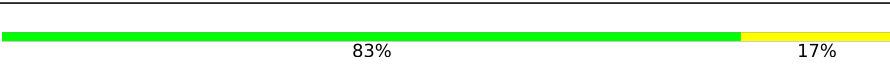
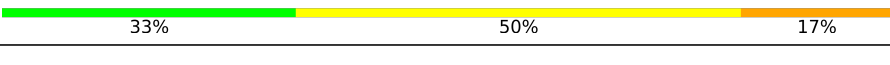
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1088 (4.90-3.90)
Clashscore	190562	1135 (4.90-3.90)
Ramachandran outliers	187476	1026 (4.90-3.90)
Sidechain outliers	187428	1010 (4.90-3.90)
RSRZ outliers	180081	1084 (4.90-3.90)

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	208	5% 87% 10%
1	B	208	6% 87% 9%
1	C	208	6% 84% 11%
1	D	208	4% 87% 10%
1	E	208	5% 85% 10%

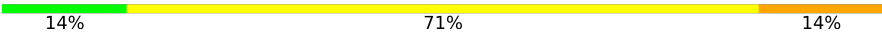
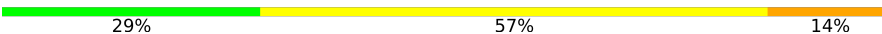
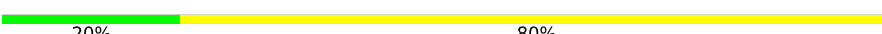
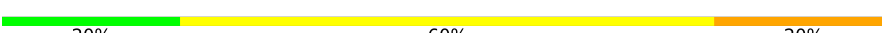
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Mol	Chain	Length	Quality of chain
1	F	208	
1	M	208	
1	N	208	
1	O	208	
1	P	208	
1	Q	208	
1	R	208	
2	G	153	
2	H	153	
2	I	153	
2	J	153	
2	K	153	
2	L	153	
2	S	153	
2	T	153	
2	U	153	
2	V	153	
2	W	153	
2	X	153	
3	Y	6	
3	e	6	
3	f	6	
3	h	6	
4	Z	7	
4	a	7	

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Mol	Chain	Length	Quality of chain
4	i	7	
4	j	7	
5	b	5	
5	c	5	
5	d	5	
5	g	5	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 32413 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 SECRETED PROTEIN BARF1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	0	0	0
			1494	965	255	267	7			
1	B	189	Total	C	N	O	S	0	0	0
			1498	967	255	269	7			
1	C	186	Total	C	N	O	S	0	0	0
			1481	956	253	265	7			
1	D	187	Total	C	N	O	S	0	0	0
			1487	960	253	267	7			
1	E	187	Total	C	N	O	S	0	0	0
			1485	959	253	266	7			
1	F	189	Total	C	N	O	S	0	0	0
			1495	965	255	268	7			
1	M	191	Total	C	N	O	S	0	0	0
			1507	973	257	270	7			
1	N	191	Total	C	N	O	S	0	0	0
			1517	978	259	273	7			
1	O	186	Total	C	N	O	S	0	0	0
			1476	954	250	265	7			
1	P	189	Total	C	N	O	S	0	0	0
			1502	970	256	269	7			
1	Q	185	Total	C	N	O	S	0	0	0
			1481	958	252	264	7			
1	R	186	Total	C	N	O	S	0	0	0
			1483	958	252	266	7			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	222	LYS	-	expression tag	UNP P0CW72
A	223	HIS	-	expression tag	UNP P0CW72
A	224	HIS	-	expression tag	UNP P0CW72
A	225	HIS	-	expression tag	UNP P0CW72
A	226	HIS	-	expression tag	UNP P0CW72

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Chain	Residue	Modelled	Actual	Comment	Reference
A	227	HIS	-	expression tag	UNP P0CW72
A	228	HIS	-	expression tag	UNP P0CW72
A	169	SER	THR	engineered mutation	UNP P0CW72
B	222	LYS	-	expression tag	UNP P0CW72
B	223	HIS	-	expression tag	UNP P0CW72
B	224	HIS	-	expression tag	UNP P0CW72
B	225	HIS	-	expression tag	UNP P0CW72
B	226	HIS	-	expression tag	UNP P0CW72
B	227	HIS	-	expression tag	UNP P0CW72
B	228	HIS	-	expression tag	UNP P0CW72
B	169	SER	THR	engineered mutation	UNP P0CW72
C	222	LYS	-	expression tag	UNP P0CW72
C	223	HIS	-	expression tag	UNP P0CW72
C	224	HIS	-	expression tag	UNP P0CW72
C	225	HIS	-	expression tag	UNP P0CW72
C	226	HIS	-	expression tag	UNP P0CW72
C	227	HIS	-	expression tag	UNP P0CW72
C	228	HIS	-	expression tag	UNP P0CW72
C	169	SER	THR	engineered mutation	UNP P0CW72
D	222	LYS	-	expression tag	UNP P0CW72
D	223	HIS	-	expression tag	UNP P0CW72
D	224	HIS	-	expression tag	UNP P0CW72
D	225	HIS	-	expression tag	UNP P0CW72
D	226	HIS	-	expression tag	UNP P0CW72
D	227	HIS	-	expression tag	UNP P0CW72
D	228	HIS	-	expression tag	UNP P0CW72
D	169	SER	THR	engineered mutation	UNP P0CW72
E	222	LYS	-	expression tag	UNP P0CW72
E	223	HIS	-	expression tag	UNP P0CW72
E	224	HIS	-	expression tag	UNP P0CW72
E	225	HIS	-	expression tag	UNP P0CW72
E	226	HIS	-	expression tag	UNP P0CW72
E	227	HIS	-	expression tag	UNP P0CW72
E	228	HIS	-	expression tag	UNP P0CW72
E	169	SER	THR	engineered mutation	UNP P0CW72
F	222	LYS	-	expression tag	UNP P0CW72
F	223	HIS	-	expression tag	UNP P0CW72
F	224	HIS	-	expression tag	UNP P0CW72
F	225	HIS	-	expression tag	UNP P0CW72
F	226	HIS	-	expression tag	UNP P0CW72
F	227	HIS	-	expression tag	UNP P0CW72
F	228	HIS	-	expression tag	UNP P0CW72

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Chain	Residue	Modelled	Actual	Comment	Reference
F	169	SER	THR	engineered mutation	UNP P0CW72
M	222	LYS	-	expression tag	UNP P0CW72
M	223	HIS	-	expression tag	UNP P0CW72
M	224	HIS	-	expression tag	UNP P0CW72
M	225	HIS	-	expression tag	UNP P0CW72
M	226	HIS	-	expression tag	UNP P0CW72
M	227	HIS	-	expression tag	UNP P0CW72
M	228	HIS	-	expression tag	UNP P0CW72
M	169	SER	THR	engineered mutation	UNP P0CW72
N	222	LYS	-	expression tag	UNP P0CW72
N	223	HIS	-	expression tag	UNP P0CW72
N	224	HIS	-	expression tag	UNP P0CW72
N	225	HIS	-	expression tag	UNP P0CW72
N	226	HIS	-	expression tag	UNP P0CW72
N	227	HIS	-	expression tag	UNP P0CW72
N	228	HIS	-	expression tag	UNP P0CW72
N	169	SER	THR	engineered mutation	UNP P0CW72
O	222	LYS	-	expression tag	UNP P0CW72
O	223	HIS	-	expression tag	UNP P0CW72
O	224	HIS	-	expression tag	UNP P0CW72
O	225	HIS	-	expression tag	UNP P0CW72
O	226	HIS	-	expression tag	UNP P0CW72
O	227	HIS	-	expression tag	UNP P0CW72
O	228	HIS	-	expression tag	UNP P0CW72
O	169	SER	THR	engineered mutation	UNP P0CW72
P	222	LYS	-	expression tag	UNP P0CW72
P	223	HIS	-	expression tag	UNP P0CW72
P	224	HIS	-	expression tag	UNP P0CW72
P	225	HIS	-	expression tag	UNP P0CW72
P	226	HIS	-	expression tag	UNP P0CW72
P	227	HIS	-	expression tag	UNP P0CW72
P	228	HIS	-	expression tag	UNP P0CW72
P	169	SER	THR	engineered mutation	UNP P0CW72
Q	222	LYS	-	expression tag	UNP P0CW72
Q	223	HIS	-	expression tag	UNP P0CW72
Q	224	HIS	-	expression tag	UNP P0CW72
Q	225	HIS	-	expression tag	UNP P0CW72
Q	226	HIS	-	expression tag	UNP P0CW72
Q	227	HIS	-	expression tag	UNP P0CW72
Q	228	HIS	-	expression tag	UNP P0CW72
Q	169	SER	THR	engineered mutation	UNP P0CW72
R	222	LYS	-	expression tag	UNP P0CW72

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Chain	Residue	Modelled	Actual	Comment	Reference
R	223	HIS	-	expression tag	UNP P0CW72
R	224	HIS	-	expression tag	UNP P0CW72
R	225	HIS	-	expression tag	UNP P0CW72
R	226	HIS	-	expression tag	UNP P0CW72
R	227	HIS	-	expression tag	UNP P0CW72
R	228	HIS	-	expression tag	UNP P0CW72
R	169	SER	THR	engineered mutation	UNP P0CW72

- Molecule 2 is a protein called MACROPHAGE COLONY-STIMULATING FACTOR 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	145	Total	C	N	O	S	0	0	0
			1161	729	193	228	11			
2	H	142	Total	C	N	O	S	0	0	0
			1145	722	192	220	11			
2	I	137	Total	C	N	O	S	0	0	0
			1097	690	182	214	11			
2	J	142	Total	C	N	O	S	0	0	0
			1149	723	192	223	11			
2	K	143	Total	C	N	O	S	0	0	0
			1157	726	193	227	11			
2	L	135	Total	C	N	O	S	0	0	0
			1089	686	183	209	11			
2	S	144	Total	C	N	O	S	0	0	0
			1157	726	190	230	11			
2	T	142	Total	C	N	O	S	0	0	0
			1148	723	191	223	11			
2	U	144	Total	C	N	O	S	0	0	0
			1159	727	194	227	11			
2	V	141	Total	C	N	O	S	0	0	0
			1140	719	192	218	11			
2	W	142	Total	C	N	O	S	0	0	0
			1128	710	188	219	11			
2	X	139	Total	C	N	O	S	0	0	0
			1113	702	183	217	11			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-3	GLY	-	expression tag	UNP P09603
G	-2	SER	-	expression tag	UNP P09603
G	-1	HIS	-	expression tag	UNP P09603

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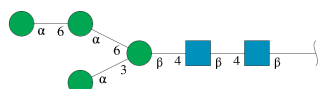
Chain	Residue	Modelled	Actual	Comment	Reference
G	0	MET	-	expression tag	UNP P09603
H	-3	GLY	-	expression tag	UNP P09603
H	-2	SER	-	expression tag	UNP P09603
H	-1	HIS	-	expression tag	UNP P09603
H	0	MET	-	expression tag	UNP P09603
I	-3	GLY	-	expression tag	UNP P09603
I	-2	SER	-	expression tag	UNP P09603
I	-1	HIS	-	expression tag	UNP P09603
I	0	MET	-	expression tag	UNP P09603
J	-3	GLY	-	expression tag	UNP P09603
J	-2	SER	-	expression tag	UNP P09603
J	-1	HIS	-	expression tag	UNP P09603
J	0	MET	-	expression tag	UNP P09603
K	-3	GLY	-	expression tag	UNP P09603
K	-2	SER	-	expression tag	UNP P09603
K	-1	HIS	-	expression tag	UNP P09603
K	0	MET	-	expression tag	UNP P09603
L	-3	GLY	-	expression tag	UNP P09603
L	-2	SER	-	expression tag	UNP P09603
L	-1	HIS	-	expression tag	UNP P09603
L	0	MET	-	expression tag	UNP P09603
S	-3	GLY	-	expression tag	UNP P09603
S	-2	SER	-	expression tag	UNP P09603
S	-1	HIS	-	expression tag	UNP P09603
S	0	MET	-	expression tag	UNP P09603
T	-3	GLY	-	expression tag	UNP P09603
T	-2	SER	-	expression tag	UNP P09603
T	-1	HIS	-	expression tag	UNP P09603
T	0	MET	-	expression tag	UNP P09603
U	-3	GLY	-	expression tag	UNP P09603
U	-2	SER	-	expression tag	UNP P09603
U	-1	HIS	-	expression tag	UNP P09603
U	0	MET	-	expression tag	UNP P09603
V	-3	GLY	-	expression tag	UNP P09603
V	-2	SER	-	expression tag	UNP P09603
V	-1	HIS	-	expression tag	UNP P09603
V	0	MET	-	expression tag	UNP P09603
W	-3	GLY	-	expression tag	UNP P09603
W	-2	SER	-	expression tag	UNP P09603
W	-1	HIS	-	expression tag	UNP P09603
W	0	MET	-	expression tag	UNP P09603
X	-3	GLY	-	expression tag	UNP P09603

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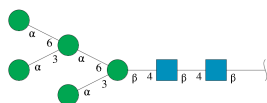
Chain	Residue	Modelled	Actual	Comment	Reference
X	-2	SER	-	expression tag	UNP P09603
X	-1	HIS	-	expression tag	UNP P09603
X	0	MET	-	expression tag	UNP P09603

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-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
3	Y	6	Total	C	N	O	0	0	0
			72	40	2	30			
3	e	6	Total	C	N	O	0	0	0
			72	40	2	30			
3	f	6	Total	C	N	O	0	0	0
			72	40	2	30			
3	h	6	Total	C	N	O	0	0	0
			72	40	2	30			

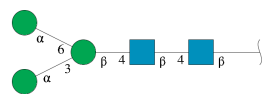
- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	Z	7	Total	C	N	O	0	0	0
			83	46	2	35			
4	a	7	Total	C	N	O	0	0	0
			83	46	2	35			
4	i	7	Total	C	N	O	0	0	0
			83	46	2	35			
4	j	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-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.

ose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a
cetamido-2-deoxy-beta-D-glucopyranose.

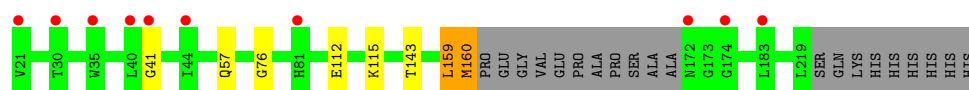
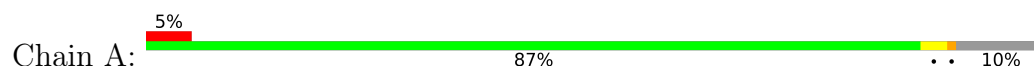


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	b	5	Total	C	N	O	0	0	0
			61	34	2	25			
5	c	5	Total	C	N	O	0	0	0
			61	34	2	25			
5	d	5	Total	C	N	O	0	0	0
			61	34	2	25			
5	g	5	Total	C	N	O	0	0	0
			61	34	2	25			

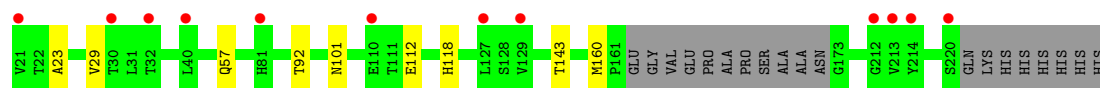
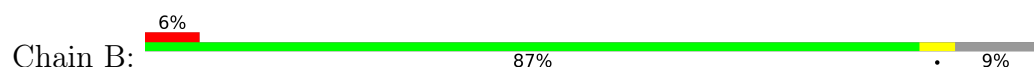
3 Residue-property plots [i](#)

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.

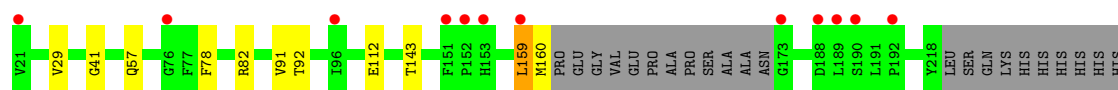
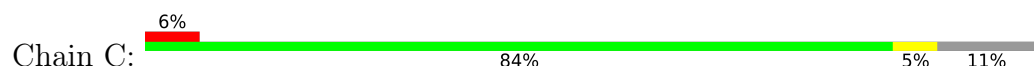
- Molecule 1: SECRETED PROTEIN BARF1



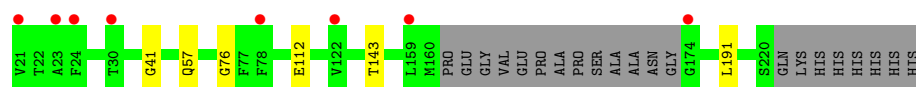
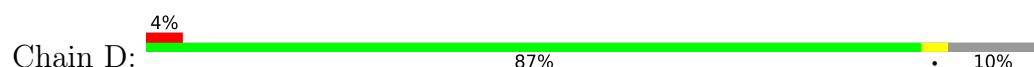
- Molecule 1: SECRETED PROTEIN BARF1



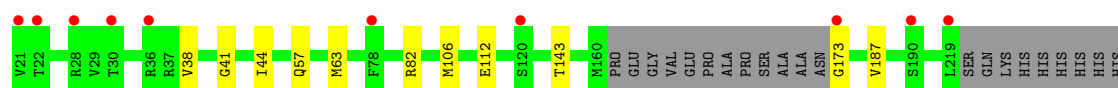
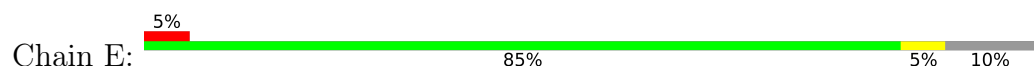
- Molecule 1: SECRETED PROTEIN BARF1



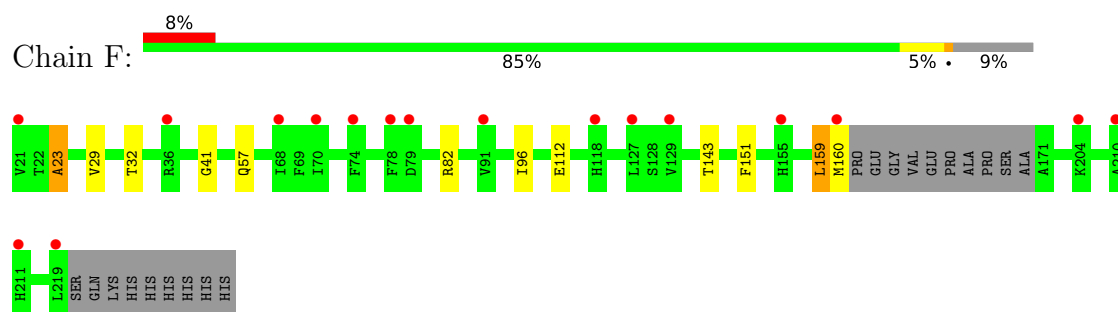
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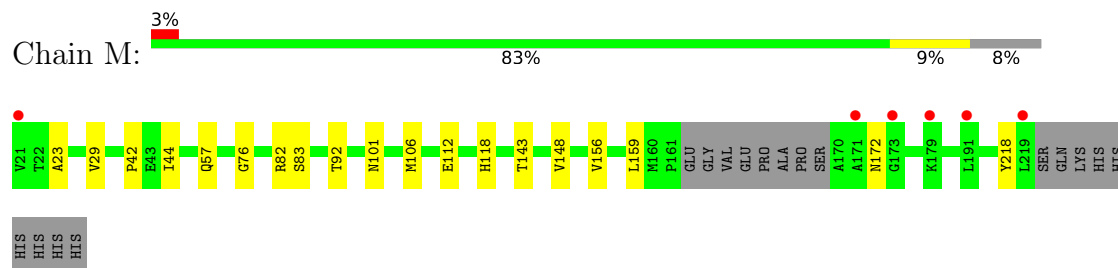
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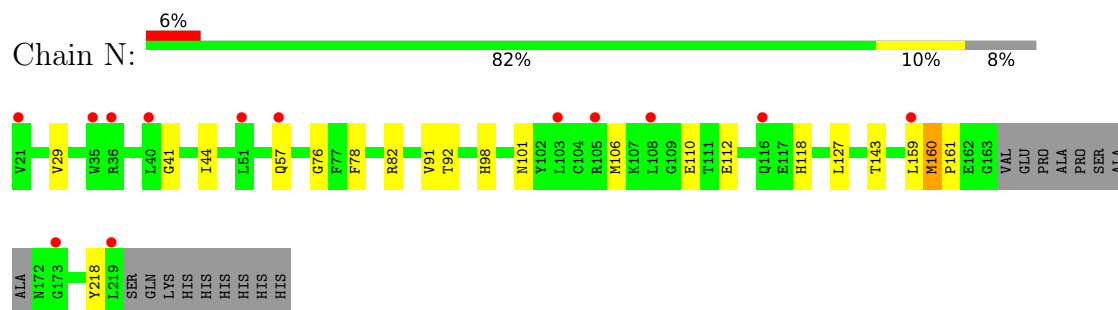
- Molecule 1: SECRETED PROTEIN BARF1



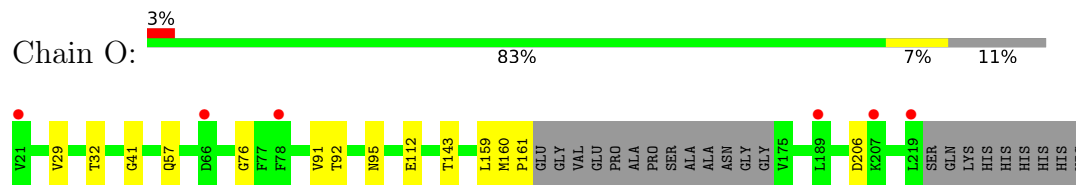
- Molecule 1: SECRETED PROTEIN BARF1



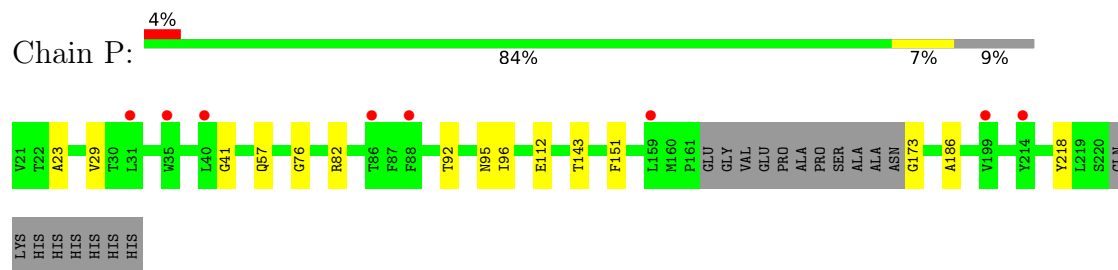
- Molecule 1: SECRETED PROTEIN BARF1



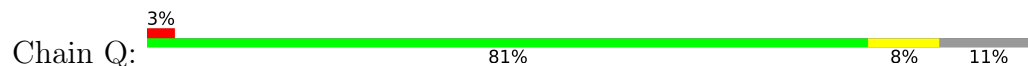
- Molecule 1: SECRETED PROTEIN BARF1

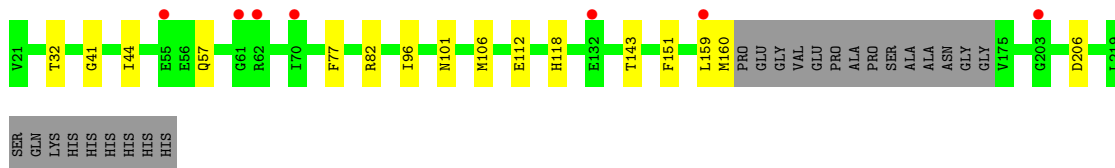


- Molecule 1: SECRETED PROTEIN BARF1

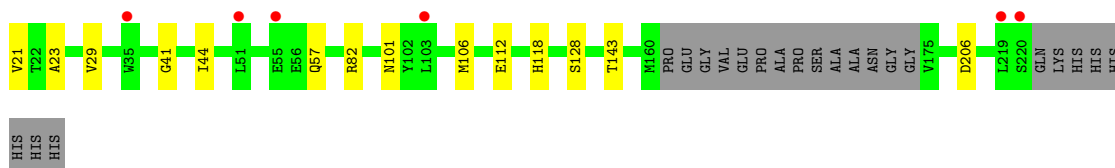
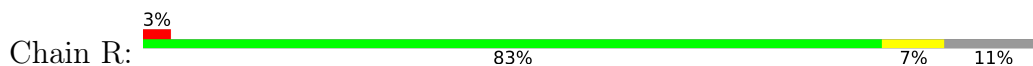


- Molecule 1: SECRETED PROTEIN BARF1

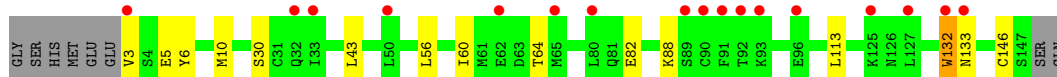
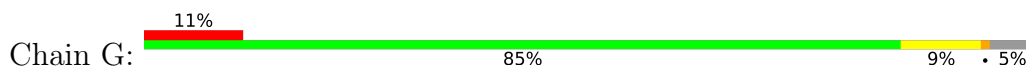




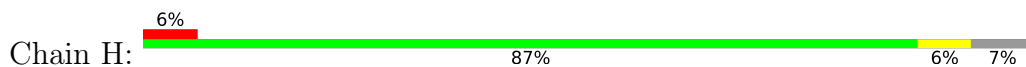
• Molecule 1: SECRETED PROTEIN BARF1



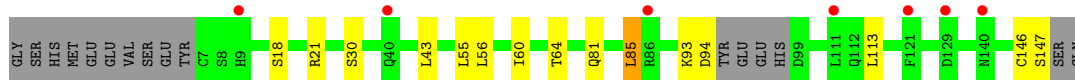
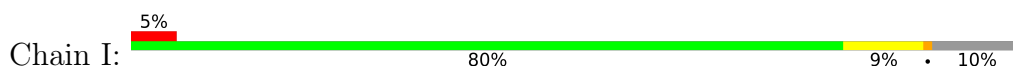
• Molecule 2: MACROPHAGE COLONY-STIMULATING FACTOR 1



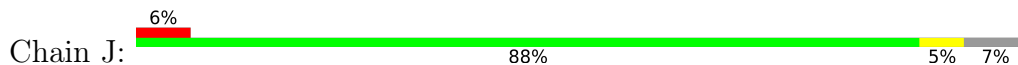
• Molecule 2: MACROPHAGE COLONY-STIMULATING FACTOR 1



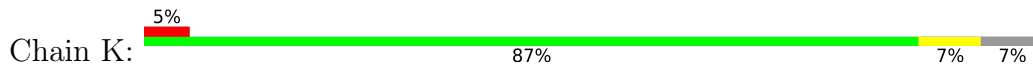
• Molecule 2: MACROPHAGE COLONY-STIMULATING FACTOR 1



• Molecule 2: MACROPHAGE COLONY-STIMULATING FACTOR 1

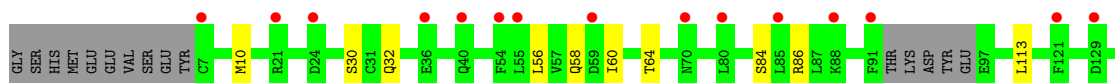
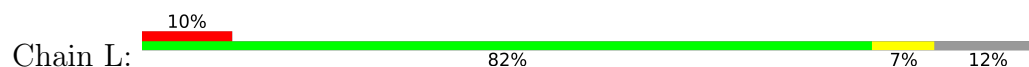


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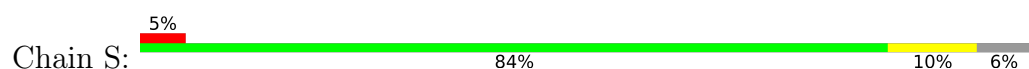




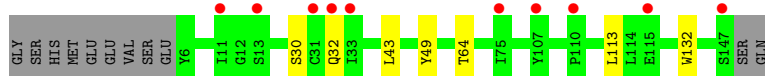
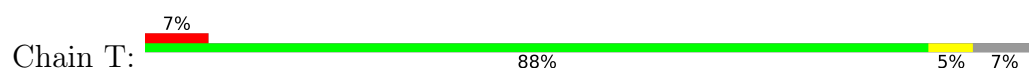
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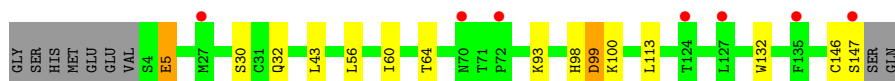
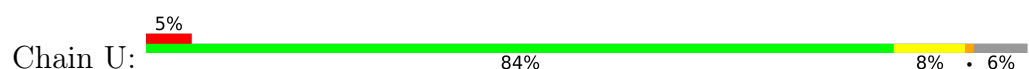
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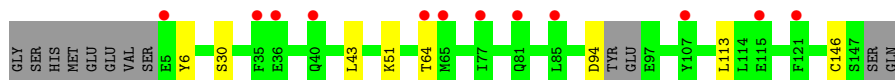
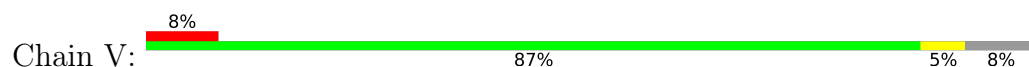
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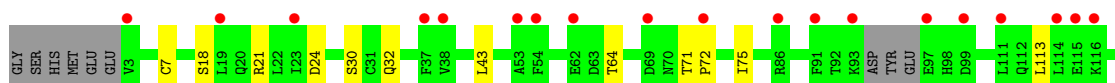
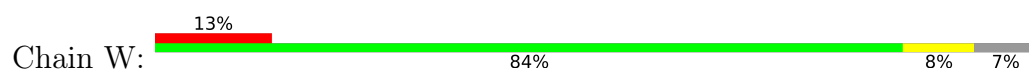
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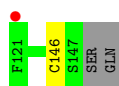


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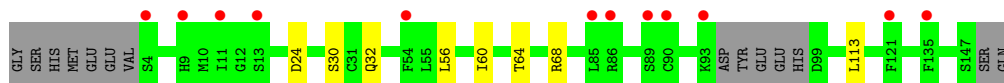
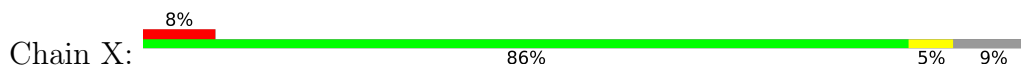


• Molecule 2: MACROPHAGE COLONY-STIMULATING FACTOR 1

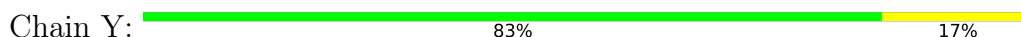




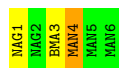
- Molecule 2: MACROPHAGE COLONY-STIMULATING FACTOR 1



- Molecule 3: alpha-D-mannopyranose-(1-6)-alpha-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



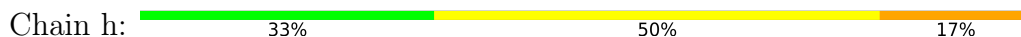
- Molecule 3: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



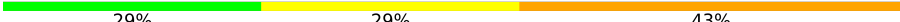
- Molecule 3: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

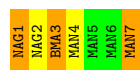


- Molecule 3: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



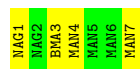
- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z:  29% 29% 43%

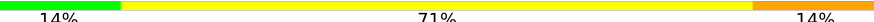


- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a:  43% 57%

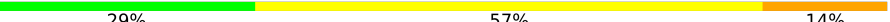


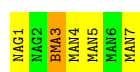
- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain i:  14% 71% 14%



- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-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

Chain j:  29% 57% 14%

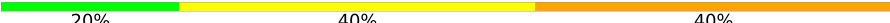


- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain b:  40% 60%



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

Chain c:  20% 40% 40%

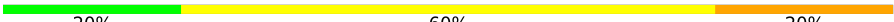


- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d:  20% 80%

MAG1	MAG2	BMA3	MAN4	MAN5
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- Molecule 5: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain g:  20% 60% 20%

MAG1	MAG2	BMA3	MAN4	MAN5
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4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	218.44Å 218.44Å 331.17Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	75.85 – 4.40 75.85 – 4.40	Depositor EDS
% Data completeness (in resolution range)	99.1 (75.85-4.40) 99.2 (75.85-4.40)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.16 (at 4.46Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.238 , 0.276 0.275 , 0.299	Depositor DCC
R_{free} test set	2874 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	165.8	Xtriage
Anisotropy	0.413	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 240.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.036 for -h,-k,l	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	32413	wwPDB-VP
Average B, all atoms (Å ²)	216.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.75% 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: MAN, NAG, BMA

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	0.39	0/1537	0.81	2/2090 (0.1%)
1	B	0.39	0/1542	0.76	1/2099 (0.0%)
1	C	0.40	0/1524	0.78	1/2072 (0.0%)
1	D	0.38	0/1530	0.78	2/2082 (0.1%)
1	E	0.39	0/1528	0.73	0/2079
1	F	0.44	1/1538 (0.1%)	0.81	4/2093 (0.2%)
1	M	0.44	0/1551	0.84	2/2112 (0.1%)
1	N	0.41	0/1561	0.78	0/2123
1	O	0.40	0/1520	0.80	2/2073 (0.1%)
1	P	0.41	0/1546	0.75	0/2103
1	Q	0.39	0/1524	0.76	1/2073 (0.0%)
1	R	0.41	0/1526	0.77	0/2077
2	G	0.44	0/1179	0.89	2/1591 (0.1%)
2	H	0.44	0/1164	0.88	2/1568 (0.1%)
2	I	0.42	0/1113	0.83	0/1500
2	J	0.40	0/1168	0.79	0/1574
2	K	0.40	0/1176	0.79	0/1586
2	L	0.43	0/1106	0.82	0/1490
2	S	0.43	0/1176	0.87	0/1589
2	T	0.45	0/1166	0.85	1/1570 (0.1%)
2	U	0.45	0/1178	0.97	5/1589 (0.3%)
2	V	0.39	0/1158	0.84	1/1558 (0.1%)
2	W	0.45	0/1145	0.91	1/1546 (0.1%)
2	X	0.43	0/1130	0.86	0/1523
All	All	0.42	1/32286 (0.0%)	0.82	27/43760 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	23	ALA	CA-CB	-5.12	1.45	1.53

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	159	LEU	N-CA-C	10.34	125.07	109.25
2	U	99	ASP	N-CA-C	9.10	123.42	110.23
2	U	93	LYS	N-CA-C	8.07	121.32	110.35
1	O	159	LEU	N-CA-C	7.89	121.33	109.25
1	A	159	LEU	N-CA-C	7.87	121.29	109.25
2	V	6	TYR	N-CA-C	7.85	119.61	108.54
1	M	172	ASN	N-CA-C	7.74	120.10	109.11
2	W	7	CYS	N-CA-C	7.17	120.14	111.82
1	D	191	LEU	CA-C-N	-7.10	113.00	120.03
1	D	191	LEU	C-N-CA	-7.10	113.00	120.03
1	A	160	MET	CA-CB-CG	7.09	128.28	114.10
1	B	160	MET	N-CA-C	6.81	121.86	107.91
2	U	98	HIS	CA-C-N	6.56	130.02	120.71
2	U	98	HIS	C-N-CA	6.56	130.02	120.71
2	H	132	TRP	N-CA-C	6.34	118.27	111.36
1	M	159	LEU	N-CA-C	-6.04	100.01	109.25
2	G	132	TRP	N-CA-C	5.97	117.86	111.36
2	H	138	ASN	N-CA-C	5.79	117.65	108.67
1	F	23	ALA	N-CA-C	5.74	117.83	108.76
1	F	159	LEU	CA-C-N	5.64	131.86	121.70
1	F	159	LEU	C-N-CA	5.64	131.86	121.70
2	T	132	TRP	N-CA-C	5.57	117.44	111.36
1	F	32	THR	N-CA-C	5.51	118.21	109.50
2	U	5	GLU	N-CA-C	5.50	118.43	109.24
1	Q	32	THR	N-CA-C	5.32	117.90	109.50
1	O	32	THR	N-CA-C	5.31	117.75	109.52
2	G	10	MET	N-CA-C	-5.03	105.71	111.14

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	1494	0	1464	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1498	0	1463	4	0
1	C	1481	0	1451	6	0
1	D	1487	0	1453	1	0
1	E	1485	0	1451	4	0
1	F	1495	0	1458	5	0
1	M	1507	0	1470	10	0
1	N	1517	0	1484	15	0
1	O	1476	0	1430	7	0
1	P	1502	0	1474	9	0
1	Q	1481	0	1456	8	0
1	R	1483	0	1450	7	0
2	G	1161	0	1115	9	0
2	H	1145	0	1112	4	0
2	I	1097	0	1062	9	0
2	J	1149	0	1111	4	0
2	K	1157	0	1110	8	0
2	L	1089	0	1053	5	0
2	S	1157	0	1095	11	0
2	T	1148	0	1117	3	0
2	U	1159	0	1111	7	0
2	V	1140	0	1111	3	0
2	W	1128	0	1078	8	0
2	X	1113	0	1074	5	0
3	Y	72	0	61	0	0
3	e	72	0	61	1	0
3	f	72	0	61	1	0
3	h	72	0	61	1	0
4	Z	83	0	70	2	0
4	a	83	0	70	0	0
4	i	83	0	70	1	0
4	j	83	0	70	1	0
5	b	61	0	52	0	0
5	c	61	0	52	2	0
5	d	61	0	52	0	0
5	g	61	0	52	1	0
All	All	32413	0	31385	139	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 2.

All (139) 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:J:10:MET:SD	2:J:86:ARG:NH1	2.64	0.71
1:A:159:LEU:O	1:A:160:MET:HG2	1.96	0.65
2:I:55:LEU:HD22	2:I:93:LYS:HD2	1.81	0.63
1:F:159:LEU:O	1:F:160:MET:HG2	1.99	0.62
1:F:23:ALA:CB	1:F:29:VAL:HG21	2.29	0.61
2:U:5:GLU:HB2	2:U:132:TRP:CZ3	2.36	0.61
1:N:160:MET:HB3	1:N:161:PRO:HA	1.82	0.60
2:X:64:THR:HG21	2:X:113:LEU:HD21	1.82	0.60
2:S:64:THR:HG21	2:S:113:LEU:HD21	1.84	0.59
2:U:64:THR:HG21	2:U:113:LEU:HD21	1.85	0.59
2:G:88:LYS:HE2	2:S:78:VAL:HG21	1.84	0.59
2:I:64:THR:HG21	2:I:113:LEU:HD21	1.84	0.58
2:L:10:MET:SD	2:L:86:ARG:NH1	2.78	0.57
2:W:24:ASP:OD1	2:X:68:ARG:NH1	2.38	0.56
1:B:23:ALA:HB3	1:B:29:VAL:HG21	1.89	0.55
1:M:23:ALA:CB	1:M:29:VAL:HG21	2.37	0.55
2:S:5:GLU:HB2	2:S:132:TRP:CZ3	2.41	0.55
2:W:64:THR:HG21	2:W:113:LEU:HD21	1.88	0.54
1:C:159:LEU:C	1:C:160:MET:HG2	2.32	0.54
4:j:3:BMA:O6	4:j:3:BMA:O4	2.24	0.54
1:C:29:VAL:HG12	1:C:91:VAL:CG2	2.37	0.54
1:F:82:ARG:NH2	2:L:32:GLN:OE1	2.41	0.54
2:K:58:GLN:NE2	2:K:84:SER:OG	2.41	0.54
2:J:64:THR:HG21	2:J:113:LEU:HD21	1.90	0.54
2:V:64:THR:HG21	2:V:113:LEU:HD21	1.90	0.54
2:K:64:THR:HG21	2:K:113:LEU:HD21	1.89	0.54
3:e:3:BMA:H62	3:e:4:MAN:H5	1.90	0.53
1:P:23:ALA:CB	1:P:29:VAL:HG21	2.37	0.53
2:K:5:GLU:HB2	2:K:132:TRP:CZ3	2.43	0.53
1:F:23:ALA:HB1	1:F:29:VAL:HG21	1.90	0.53
1:P:82:ARG:NH2	2:U:32:GLN:OE1	2.42	0.53
2:G:64:THR:HG21	2:G:113:LEU:HD21	1.91	0.52
1:O:29:VAL:HG12	1:O:91:VAL:CG1	2.39	0.52
1:N:29:VAL:HG12	1:N:91:VAL:CG2	2.38	0.52
1:B:23:ALA:CB	1:B:29:VAL:HG21	2.39	0.51
1:R:23:ALA:CB	1:R:29:VAL:HG21	2.40	0.51
2:I:93:LYS:O	2:I:94:ASP:CB	2.59	0.51
2:T:64:THR:HG21	2:T:113:LEU:HD21	1.91	0.51
1:R:82:ARG:NH2	2:W:32:GLN:OE1	2.45	0.50
1:P:173:GLY:N	1:P:186:ALA:O	2.44	0.50
1:P:23:ALA:HB3	1:P:29:VAL:HG21	1.93	0.50
2:I:146:CYS:O	2:I:147:SER:HB3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:64:THR:HG21	2:L:113:LEU:HD21	1.95	0.48
2:S:18:SER:HA	2:S:21:ARG:NH1	2.29	0.48
1:N:159:LEU:O	1:N:160:MET:HB2	2.14	0.48
2:J:58:GLN:OE1	2:J:84:SER:OG	2.32	0.47
2:S:56:LEU:HD23	2:S:60:ILE:HG13	1.96	0.47
1:C:82:ARG:NH2	2:J:32:GLN:OE1	2.47	0.47
2:H:64:THR:HG21	2:H:113:LEU:HD21	1.95	0.47
2:G:5:GLU:O	2:G:6:TYR:HB2	2.14	0.47
2:W:71:THR:OG1	2:X:24:ASP:HB3	2.14	0.47
4:Z:1:NAG:O3	4:Z:2:NAG:O5	2.25	0.47
1:M:23:ALA:HB3	1:M:29:VAL:HG21	1.96	0.47
1:M:76:GLY:HA2	1:N:92:THR:HG21	1.97	0.46
1:O:92:THR:HG21	1:P:76:GLY:HA2	1.98	0.46
2:S:5:GLU:HB2	2:S:132:TRP:CE3	2.51	0.46
2:U:99:ASP:OD1	2:U:100:LYS:N	2.49	0.46
1:O:95:ASN:ND2	5:g:1:NAG:O7	2.48	0.46
2:G:56:LEU:HD23	2:G:60:ILE:HG13	1.97	0.46
1:Q:101:ASN:OD1	1:Q:118:HIS:ND1	2.49	0.46
2:H:43:LEU:HD23	2:H:49:TYR:HA	1.98	0.45
1:N:98:HIS:NE2	3:f:1:NAG:H61	2.32	0.45
2:X:56:LEU:HD23	2:X:60:ILE:HG13	1.98	0.45
2:G:56:LEU:CD2	2:G:60:ILE:HD11	2.47	0.45
1:R:23:ALA:HB3	1:R:29:VAL:HG21	1.98	0.45
1:Q:77:PHE:CG	4:i:1:NAG:H61	2.51	0.45
2:I:56:LEU:HD23	2:I:60:ILE:HG13	1.99	0.45
2:S:56:LEU:CD2	2:S:60:ILE:HD11	2.47	0.45
1:Q:44:ILE:HG21	1:Q:106:MET:HB3	1.98	0.45
2:V:51:LYS:NZ	2:V:94:ASP:OD2	2.39	0.44
2:G:82:GLU:CD	2:S:86:ARG:HD2	2.43	0.44
2:L:58:GLN:OE1	2:L:84:SER:OG	2.35	0.44
2:W:71:THR:OG1	2:W:72:PRO:HD2	2.17	0.44
2:S:58:GLN:CG	2:S:59:ASP:N	2.81	0.44
2:W:43:LEU:HD13	2:W:146:CYS:SG	2.57	0.44
1:N:101:ASN:OD1	1:N:118:HIS:ND1	2.50	0.44
1:A:76:GLY:HA2	1:B:92:THR:HG21	1.99	0.44
2:S:58:GLN:HG3	2:S:59:ASP:N	2.32	0.44
1:N:78:PHE:CE2	1:N:91:VAL:HG12	2.52	0.44
1:B:101:ASN:OD1	1:B:118:HIS:ND1	2.51	0.44
1:E:173:GLY:N	1:E:187:VAL:HG22	2.33	0.44
1:N:44:ILE:HG21	1:N:106:MET:HB3	1.99	0.44
1:N:159:LEU:O	1:N:160:MET:CB	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:132:TRP:CZ3	2:G:133:ASN:HB2	2.53	0.43
1:Q:44:ILE:CG2	1:Q:106:MET:HB3	2.47	0.43
1:P:95:ASN:HD22	3:h:1:NAG:C7	2.30	0.43
1:A:115:LYS:NZ	1:N:110:GLU:OE1	2.51	0.43
1:R:101:ASN:OD1	1:R:118:HIS:ND1	2.52	0.43
2:G:43:LEU:HD13	2:G:146:CYS:SG	2.58	0.43
1:N:218:TYR:OH	1:R:206:ASP:OD2	2.34	0.43
2:U:56:LEU:HD23	2:U:60:ILE:HG13	1.99	0.43
4:Z:3:BMA:O2	4:Z:7:MAN:H2	2.19	0.43
1:P:218:TYR:OH	1:Q:206:ASP:OD2	2.36	0.43
1:Q:159:LEU:O	1:Q:160:MET:CB	2.66	0.43
2:W:18:SER:HA	2:W:21:ARG:NH1	2.34	0.43
2:H:18:SER:O	2:H:21:ARG:HG2	2.19	0.42
1:M:92:THR:HG21	1:N:76:GLY:HA2	2.00	0.42
1:M:218:TYR:OH	1:O:206:ASP:OD2	2.33	0.42
1:E:38:VAL:HG12	2:K:29:THR:HA	2.01	0.42
1:E:44:ILE:HG21	1:E:106:MET:HB3	2.02	0.42
5:c:3:BMA:O2	5:c:4:MAN:C1	2.67	0.42
2:I:18:SER:HA	2:I:21:ARG:NH1	2.34	0.42
1:F:96:ILE:HD12	1:F:151:PHE:CG	2.54	0.42
2:I:56:LEU:CD2	2:I:60:ILE:HD11	2.49	0.42
2:K:60:ILE:O	2:K:64:THR:N	2.49	0.42
2:U:56:LEU:CD2	2:U:60:ILE:HD11	2.50	0.42
2:K:58:GLN:CD	2:K:84:SER:OG	2.63	0.42
1:Q:82:ARG:NH2	2:X:32:GLN:OE1	2.52	0.42
1:O:91:VAL:O	1:O:91:VAL:HG13	2.19	0.42
1:M:42:PRO:HG3	1:M:82:ARG:CZ	2.50	0.41
2:G:64:THR:CG2	2:G:113:LEU:HD21	2.50	0.41
2:V:43:LEU:HD13	2:V:146:CYS:SG	2.59	0.41
1:C:91:VAL:HG23	1:C:91:VAL:O	2.21	0.41
1:M:101:ASN:OD1	1:M:118:HIS:ND1	2.53	0.41
5:c:2:NAG:H3	5:c:2:NAG:H83	2.02	0.41
2:T:43:LEU:HD23	2:T:49:TYR:HA	2.02	0.41
1:N:82:ARG:NH2	2:T:32:GLN:OE1	2.54	0.41
2:I:81:GLN:O	2:I:85:LEU:HD13	2.21	0.41
2:K:5:GLU:HB2	2:K:132:TRP:CE3	2.55	0.41
2:S:43:LEU:HD13	2:S:146:CYS:SG	2.61	0.41
2:H:64:THR:CG2	2:H:113:LEU:HD21	2.50	0.41
1:M:44:ILE:HG21	1:M:106:MET:HB3	2.02	0.41
1:M:148:VAL:CG2	1:M:156:VAL:HG22	2.51	0.41
1:P:96:ILE:HD12	1:P:151:PHE:CG	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:96:ILE:HD12	1:Q:151:PHE:CG	2.56	0.41
2:U:43:LEU:HD13	2:U:146:CYS:SG	2.61	0.41
1:E:63:MET:HE1	1:E:82:ARG:HB3	2.03	0.41
2:I:43:LEU:HD13	2:I:146:CYS:SG	2.61	0.41
1:M:82:ARG:HG2	1:M:83:SER:N	2.36	0.41
1:N:91:VAL:O	1:N:91:VAL:HG23	2.21	0.41
1:R:44:ILE:HG21	1:R:106:MET:HB3	2.03	0.40
2:L:56:LEU:HD23	2:L:60:ILE:HG13	2.02	0.40
1:N:127:LEU:O	1:R:128:SER:HA	2.21	0.40
1:O:76:GLY:HA2	1:P:92:THR:HG21	2.03	0.40
2:W:71:THR:OG1	2:W:72:PRO:CD	2.70	0.40
2:K:56:LEU:HD23	2:K:60:ILE:HG13	2.02	0.40
1:O:160:MET:HB3	1:O:161:PRO:HA	2.03	0.40
1:C:78:PHE:CE2	1:C:91:VAL:HG12	2.56	0.40
1:C:92:THR:HG21	1:D:76:GLY:HA2	2.03	0.40

There are no symmetry-related clashes.

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	184/208 (88%)	177 (96%)	6 (3%)	1 (0%)	24	62
1	B	185/208 (89%)	178 (96%)	7 (4%)	0	100	100
1	C	182/208 (88%)	175 (96%)	6 (3%)	1 (0%)	24	62
1	D	183/208 (88%)	176 (96%)	6 (3%)	1 (0%)	24	62
1	E	183/208 (88%)	176 (96%)	6 (3%)	1 (0%)	24	62
1	F	185/208 (89%)	177 (96%)	7 (4%)	1 (0%)	24	62
1	M	187/208 (90%)	178 (95%)	9 (5%)	0	100	100
1	N	187/208 (90%)	179 (96%)	6 (3%)	2 (1%)	11	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	182/208 (88%)	176 (97%)	5 (3%)	1 (0%)	24	62
1	P	185/208 (89%)	178 (96%)	6 (3%)	1 (0%)	24	62
1	Q	181/208 (87%)	174 (96%)	6 (3%)	1 (1%)	21	58
1	R	182/208 (88%)	175 (96%)	6 (3%)	1 (0%)	24	62
2	G	143/153 (94%)	139 (97%)	4 (3%)	0	100	100
2	H	140/153 (92%)	136 (97%)	4 (3%)	0	100	100
2	I	133/153 (87%)	130 (98%)	3 (2%)	0	100	100
2	J	140/153 (92%)	136 (97%)	4 (3%)	0	100	100
2	K	141/153 (92%)	139 (99%)	2 (1%)	0	100	100
2	L	131/153 (86%)	128 (98%)	3 (2%)	0	100	100
2	S	142/153 (93%)	138 (97%)	4 (3%)	0	100	100
2	T	140/153 (92%)	136 (97%)	4 (3%)	0	100	100
2	U	142/153 (93%)	138 (97%)	4 (3%)	0	100	100
2	V	137/153 (90%)	133 (97%)	4 (3%)	0	100	100
2	W	138/153 (90%)	134 (97%)	4 (3%)	0	100	100
2	X	135/153 (88%)	130 (96%)	5 (4%)	0	100	100
All	All	3868/4332 (89%)	3736 (97%)	121 (3%)	11 (0%)	36	71

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	N	160	MET
1	A	41	GLY
1	C	41	GLY
1	D	41	GLY
1	E	41	GLY
1	F	41	GLY
1	N	41	GLY
1	O	41	GLY
1	P	41	GLY
1	Q	41	GLY
1	R	41	GLY

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	166/183 (91%)	163 (98%)	3 (2%)	51	67
1	B	167/183 (91%)	164 (98%)	3 (2%)	51	67
1	C	165/183 (90%)	162 (98%)	3 (2%)	51	67
1	D	166/183 (91%)	163 (98%)	3 (2%)	51	67
1	E	165/183 (90%)	162 (98%)	3 (2%)	51	67
1	F	165/183 (90%)	162 (98%)	3 (2%)	51	67
1	M	166/183 (91%)	163 (98%)	3 (2%)	51	67
1	N	169/183 (92%)	166 (98%)	3 (2%)	51	67
1	O	164/183 (90%)	161 (98%)	3 (2%)	51	67
1	P	168/183 (92%)	165 (98%)	3 (2%)	51	67
1	Q	166/183 (91%)	163 (98%)	3 (2%)	51	67
1	R	166/183 (91%)	162 (98%)	4 (2%)	43	63
2	G	133/145 (92%)	131 (98%)	2 (2%)	57	70
2	H	131/145 (90%)	130 (99%)	1 (1%)	73	77
2	I	127/145 (88%)	125 (98%)	2 (2%)	55	69
2	J	132/145 (91%)	131 (99%)	1 (1%)	73	77
2	K	133/145 (92%)	132 (99%)	1 (1%)	73	77
2	L	125/145 (86%)	124 (99%)	1 (1%)	73	77
2	S	132/145 (91%)	131 (99%)	1 (1%)	73	77
2	T	132/145 (91%)	131 (99%)	1 (1%)	73	77
2	U	133/145 (92%)	131 (98%)	2 (2%)	57	70
2	V	131/145 (90%)	130 (99%)	1 (1%)	73	77
2	W	128/145 (88%)	126 (98%)	2 (2%)	55	69
2	X	128/145 (88%)	127 (99%)	1 (1%)	73	77
All	All	3558/3936 (90%)	3505 (98%)	53 (2%)	57	70

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	112	GLU
1	A	143	THR
1	B	57	GLN
1	B	112	GLU
1	B	143	THR
1	C	57	GLN
1	C	112	GLU
1	C	143	THR
1	D	57	GLN
1	D	112	GLU
1	D	143	THR
1	E	57	GLN
1	E	112	GLU
1	E	143	THR
1	F	57	GLN
1	F	112	GLU
1	F	143	THR
2	G	3	VAL
2	G	30	SER
2	H	30	SER
2	I	30	SER
2	I	85	LEU
2	J	30	SER
2	K	30	SER
2	L	30	SER
1	M	57	GLN
1	M	112	GLU
1	M	143	THR
1	N	57	GLN
1	N	112	GLU
1	N	143	THR
1	O	57	GLN
1	O	112	GLU
1	O	143	THR
1	P	57	GLN
1	P	112	GLU
1	P	143	THR
1	Q	57	GLN
1	Q	112	GLU
1	Q	143	THR
1	R	21	VAL
1	R	57	GLN

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Mol	Chain	Res	Type
1	R	112	GLU
1	R	143	THR
2	S	30	SER
2	T	30	SER
2	U	30	SER
2	U	147	SER
2	V	30	SER
2	W	30	SER
2	W	75	ILE
2	X	30	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (67) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	GLN
1	A	149	ASN
1	B	57	GLN
1	B	81	HIS
1	B	116	GLN
1	B	149	ASN
1	B	196	HIS
1	B	205	ASN
1	C	205	ASN
1	D	57	GLN
1	D	81	HIS
1	D	116	GLN
1	D	149	ASN
1	D	196	HIS
1	D	205	ASN
1	E	57	GLN
1	E	149	ASN
1	E	196	HIS
1	E	205	ASN
1	F	116	GLN
1	F	149	ASN
1	F	205	ASN
2	G	42	GLN
2	G	73	ASN
2	H	79	GLN
2	I	42	GLN
2	I	119	ASN
2	J	81	GLN

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Mol	Chain	Res	Type
2	J	119	ASN
2	K	79	GLN
2	K	98	HIS
2	L	42	GLN
2	L	81	GLN
1	M	57	GLN
1	M	81	HIS
1	M	149	ASN
1	M	196	HIS
1	M	205	ASN
1	N	64	HIS
1	N	65	HIS
1	N	116	GLN
1	N	149	ASN
1	N	196	HIS
1	N	205	ASN
1	O	81	HIS
1	O	116	GLN
1	O	205	ASN
1	P	57	GLN
1	P	81	HIS
1	P	116	GLN
1	P	196	HIS
1	Q	81	HIS
1	Q	149	ASN
1	Q	205	ASN
1	R	57	GLN
1	R	116	GLN
1	R	205	ASN
2	S	81	GLN
2	S	119	ASN
2	U	81	GLN
2	U	119	ASN
2	V	42	GLN
2	W	70	ASN
2	W	79	GLN
2	W	119	ASN
2	X	42	GLN
2	X	81	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 ⓘ

72 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	Y	1	3,1	14,14,15	0.53	0	17,19,21	1.02	1 (5%)
3	NAG	Y	2	3	14,14,15	0.54	0	17,19,21	0.63	0
3	BMA	Y	3	3	11,11,12	0.66	0	15,15,17	0.82	0
3	MAN	Y	4	3	11,11,12	0.56	0	15,15,17	0.79	0
3	MAN	Y	5	3	11,11,12	0.59	0	15,15,17	0.88	0
3	MAN	Y	6	3	11,11,12	0.60	0	15,15,17	0.59	0
4	NAG	Z	1	4,1	14,14,15	0.60	0	17,19,21	1.27	3 (17%)
4	NAG	Z	2	4	14,14,15	0.54	0	17,19,21	0.91	0
4	BMA	Z	3	4	11,11,12	0.60	0	15,15,17	2.03	3 (20%)
4	MAN	Z	4	4	11,11,12	0.53	0	15,15,17	1.50	2 (13%)
4	MAN	Z	5	4	11,11,12	0.58	0	15,15,17	0.54	0
4	MAN	Z	6	4	11,11,12	0.59	0	15,15,17	0.84	0
4	MAN	Z	7	4	11,11,12	0.64	0	15,15,17	1.27	3 (20%)
4	NAG	a	1	4,1	14,14,15	0.53	0	17,19,21	1.58	2 (11%)
4	NAG	a	2	4	14,14,15	0.55	0	17,19,21	0.96	0
4	BMA	a	3	4	11,11,12	0.56	0	15,15,17	1.73	2 (13%)
4	MAN	a	4	4	11,11,12	0.58	0	15,15,17	1.18	2 (13%)
4	MAN	a	5	4	11,11,12	0.59	0	15,15,17	0.64	0
4	MAN	a	6	4	11,11,12	0.55	0	15,15,17	0.66	0
4	MAN	a	7	4	11,11,12	0.63	0	15,15,17	0.74	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	b	1	5,1	14,14,15	0.61	0	17,19,21	1.78	4 (23%)
5	NAG	b	2	5	14,14,15	0.60	0	17,19,21	0.98	1 (5%)
5	BMA	b	3	5	11,11,12	0.57	0	15,15,17	1.41	2 (13%)
5	MAN	b	4	5	11,11,12	0.62	0	15,15,17	0.79	0
5	MAN	b	5	5	11,11,12	0.52	0	15,15,17	0.66	0
5	NAG	c	1	5,1	14,14,15	0.67	0	17,19,21	1.06	1 (5%)
5	NAG	c	2	5	14,14,15	0.61	0	17,19,21	0.94	0
5	BMA	c	3	5	11,11,12	0.69	0	15,15,17	1.66	3 (20%)
5	MAN	c	4	5	11,11,12	0.49	0	15,15,17	1.16	1 (6%)
5	MAN	c	5	5	11,11,12	0.57	0	15,15,17	0.78	0
5	NAG	d	1	5,1	14,14,15	0.58	0	17,19,21	1.42	3 (17%)
5	NAG	d	2	5	14,14,15	0.55	0	17,19,21	0.88	1 (5%)
5	BMA	d	3	5	11,11,12	0.76	0	15,15,17	1.33	1 (6%)
5	MAN	d	4	5	11,11,12	0.53	0	15,15,17	1.01	1 (6%)
5	MAN	d	5	5	11,11,12	0.58	0	15,15,17	0.69	0
3	NAG	e	1	3,1	14,14,15	0.56	0	17,19,21	1.02	1 (5%)
3	NAG	e	2	3	14,14,15	0.53	0	17,19,21	0.64	0
3	BMA	e	3	3	11,11,12	0.70	0	15,15,17	0.80	0
3	MAN	e	4	3	11,11,12	0.54	0	15,15,17	1.21	2 (13%)
3	MAN	e	5	3	11,11,12	0.67	0	15,15,17	0.64	0
3	MAN	e	6	3	11,11,12	0.58	0	15,15,17	0.71	0
3	NAG	f	1	3,1	14,14,15	0.60	0	17,19,21	1.40	3 (17%)
3	NAG	f	2	3	14,14,15	0.58	0	17,19,21	0.72	0
3	BMA	f	3	3	11,11,12	0.70	0	15,15,17	1.51	3 (20%)
3	MAN	f	4	3	11,11,12	0.49	0	15,15,17	1.39	2 (13%)
3	MAN	f	5	3	11,11,12	0.50	0	15,15,17	1.20	1 (6%)
3	MAN	f	6	3	11,11,12	0.49	0	15,15,17	0.89	0
5	NAG	g	1	5,1	14,14,15	0.61	0	17,19,21	0.99	1 (5%)
5	NAG	g	2	5	14,14,15	0.54	0	17,19,21	0.78	0
5	BMA	g	3	5	11,11,12	0.58	0	15,15,17	1.50	3 (20%)
5	MAN	g	4	5	11,11,12	0.56	0	15,15,17	0.92	1 (6%)
5	MAN	g	5	5	11,11,12	0.55	0	15,15,17	0.96	1 (6%)
3	NAG	h	1	3,1	14,14,15	0.56	0	17,19,21	1.11	1 (5%)
3	NAG	h	2	3	14,14,15	0.59	0	17,19,21	1.12	1 (5%)
3	BMA	h	3	3	11,11,12	0.80	0	15,15,17	1.10	1 (6%)
3	MAN	h	4	3	11,11,12	0.60	0	15,15,17	0.63	0
3	MAN	h	5	3	11,11,12	0.64	0	15,15,17	0.55	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MAN	h	6	3	11,11,12	0.65	0	15,15,17	0.89	1 (6%)
4	NAG	i	1	4,1	14,14,15	0.54	0	17,19,21	1.27	3 (17%)
4	NAG	i	2	4	14,14,15	0.51	0	17,19,21	0.66	0
4	BMA	i	3	4	11,11,12	0.75	0	15,15,17	1.15	1 (6%)
4	MAN	i	4	4	11,11,12	0.59	0	15,15,17	1.49	2 (13%)
4	MAN	i	5	4	11,11,12	0.59	0	15,15,17	0.75	1 (6%)
4	MAN	i	6	4	11,11,12	0.50	0	15,15,17	1.22	2 (13%)
4	MAN	i	7	4	11,11,12	0.60	0	15,15,17	1.00	1 (6%)
4	NAG	j	1	4,1	14,14,15	0.52	0	17,19,21	1.28	1 (5%)
4	NAG	j	2	4	14,14,15	0.59	0	17,19,21	0.78	0
4	BMA	j	3	4	11,11,12	0.68	0	15,15,17	1.59	5 (33%)
4	MAN	j	4	4	11,11,12	0.61	0	15,15,17	1.01	1 (6%)
4	MAN	j	5	4	11,11,12	0.57	0	15,15,17	0.89	1 (6%)
4	MAN	j	6	4	11,11,12	0.64	0	15,15,17	0.76	0
4	MAN	j	7	4	11,11,12	0.47	0	15,15,17	1.98	3 (20%)

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	Y	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	Y	2	3	-	2/6/23/26	0/1/1/1
3	BMA	Y	3	3	-	1/2/19/22	0/1/1/1
3	MAN	Y	4	3	-	2/2/19/22	0/1/1/1
3	MAN	Y	5	3	-	2/2/19/22	0/1/1/1
3	MAN	Y	6	3	-	0/2/19/22	0/1/1/1
4	NAG	Z	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	Z	2	4	-	0/6/23/26	0/1/1/1
4	BMA	Z	3	4	-	1/2/19/22	0/1/1/1
4	MAN	Z	4	4	-	2/2/19/22	0/1/1/1
4	MAN	Z	5	4	-	2/2/19/22	0/1/1/1
4	MAN	Z	6	4	-	0/2/19/22	0/1/1/1
4	MAN	Z	7	4	-	0/2/19/22	0/1/1/1
4	NAG	a	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	a	2	4	-	3/6/23/26	0/1/1/1
4	BMA	a	3	4	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MAN	a	4	4	-	0/2/19/22	0/1/1/1
4	MAN	a	5	4	-	0/2/19/22	0/1/1/1
4	MAN	a	6	4	-	0/2/19/22	0/1/1/1
4	MAN	a	7	4	-	2/2/19/22	0/1/1/1
5	NAG	b	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	b	2	5	-	2/6/23/26	0/1/1/1
5	BMA	b	3	5	-	0/2/19/22	0/1/1/1
5	MAN	b	4	5	-	2/2/19/22	0/1/1/1
5	MAN	b	5	5	-	0/2/19/22	0/1/1/1
5	NAG	c	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	c	2	5	-	5/6/23/26	0/1/1/1
5	BMA	c	3	5	-	2/2/19/22	0/1/1/1
5	MAN	c	4	5	-	1/2/19/22	0/1/1/1
5	MAN	c	5	5	-	2/2/19/22	0/1/1/1
5	NAG	d	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	d	2	5	-	0/6/23/26	0/1/1/1
5	BMA	d	3	5	-	1/2/19/22	0/1/1/1
5	MAN	d	4	5	-	1/2/19/22	0/1/1/1
5	MAN	d	5	5	-	0/2/19/22	0/1/1/1
3	NAG	e	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	e	2	3	-	0/6/23/26	0/1/1/1
3	BMA	e	3	3	-	1/2/19/22	0/1/1/1
3	MAN	e	4	3	-	1/2/19/22	0/1/1/1
3	MAN	e	5	3	-	2/2/19/22	0/1/1/1
3	MAN	e	6	3	-	0/2/19/22	0/1/1/1
3	NAG	f	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	f	2	3	-	2/6/23/26	0/1/1/1
3	BMA	f	3	3	-	1/2/19/22	0/1/1/1
3	MAN	f	4	3	-	1/2/19/22	0/1/1/1
3	MAN	f	5	3	-	2/2/19/22	0/1/1/1
3	MAN	f	6	3	-	0/2/19/22	0/1/1/1
5	NAG	g	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	g	2	5	-	3/6/23/26	0/1/1/1
5	BMA	g	3	5	-	2/2/19/22	0/1/1/1
5	MAN	g	4	5	-	1/2/19/22	0/1/1/1
5	MAN	g	5	5	-	2/2/19/22	0/1/1/1
3	NAG	h	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	h	2	3	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BMA	h	3	3	-	2/2/19/22	0/1/1/1
3	MAN	h	4	3	-	0/2/19/22	0/1/1/1
3	MAN	h	5	3	-	0/2/19/22	0/1/1/1
3	MAN	h	6	3	-	2/2/19/22	0/1/1/1
4	NAG	i	1	4,1	-	3/6/23/26	0/1/1/1
4	NAG	i	2	4	-	1/6/23/26	0/1/1/1
4	BMA	i	3	4	-	2/2/19/22	0/1/1/1
4	MAN	i	4	4	-	1/2/19/22	0/1/1/1
4	MAN	i	5	4	-	0/2/19/22	0/1/1/1
4	MAN	i	6	4	-	1/2/19/22	0/1/1/1
4	MAN	i	7	4	-	0/2/19/22	0/1/1/1
4	NAG	j	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	j	2	4	-	2/6/23/26	0/1/1/1
4	BMA	j	3	4	-	2/2/19/22	0/1/1/1
4	MAN	j	4	4	-	2/2/19/22	0/1/1/1
4	MAN	j	5	4	-	0/2/19/22	0/1/1/1
4	MAN	j	6	4	-	2/2/19/22	0/1/1/1
4	MAN	j	7	4	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (80) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	j	7	MAN	C1-O5-C5	6.46	120.84	112.19
4	Z	3	BMA	O3-C3-C2	6.46	123.23	110.05
4	a	3	BMA	C1-O5-C5	4.71	118.50	112.19
3	f	4	MAN	C1-O5-C5	4.36	118.02	112.19
5	d	3	BMA	O2-C2-C1	4.16	118.76	109.22
5	b	1	NAG	O5-C1-C2	-4.15	104.86	111.29
5	c	3	BMA	O3-C3-C2	4.08	118.39	110.05
4	Z	4	MAN	C1-O5-C5	3.92	117.44	112.19
4	a	1	NAG	O5-C1-C2	-3.77	105.46	111.29
4	Z	4	MAN	C1-C2-C3	3.76	115.12	109.64
5	b	3	BMA	C1-C2-C3	3.68	115.00	109.64
3	f	5	MAN	C1-O5-C5	3.60	117.01	112.19
4	a	1	NAG	C1-O5-C5	3.59	116.99	112.19
4	a	3	BMA	C1-C2-C3	3.59	114.86	109.64
4	i	6	MAN	C1-O5-C5	3.40	116.74	112.19
5	c	4	MAN	C1-O5-C5	3.38	116.71	112.19
5	d	1	NAG	C1-O5-C5	3.35	116.68	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	b	1	NAG	C1-O5-C5	3.35	116.67	112.19
3	h	3	BMA	O2-C2-C1	3.34	116.87	109.22
5	g	3	BMA	C1-C2-C3	3.26	114.39	109.64
3	f	3	BMA	C1-O5-C5	3.18	116.45	112.19
4	j	1	NAG	O5-C1-C2	-3.16	106.41	111.29
5	c	3	BMA	C1-O5-C5	3.14	116.39	112.19
4	i	4	MAN	C1-O5-C5	3.09	116.33	112.19
4	j	3	BMA	C1-C2-C3	3.09	114.14	109.64
3	h	2	NAG	C1-O5-C5	3.06	116.28	112.19
3	e	4	MAN	C1-C2-C3	3.06	114.09	109.64
5	d	4	MAN	C1-O5-C5	2.95	116.13	112.19
5	b	1	NAG	C1-C2-N2	2.94	115.06	110.43
4	Z	3	BMA	C1-O5-C5	2.93	116.11	112.19
5	g	5	MAN	C1-O5-C5	2.93	116.11	112.19
5	c	1	NAG	O5-C1-C2	-2.92	106.78	111.29
3	f	3	BMA	O3-C3-C4	2.83	117.06	110.38
5	b	3	BMA	C1-O5-C5	2.80	115.93	112.19
3	Y	1	NAG	C1-O5-C5	2.78	115.92	112.19
4	i	4	MAN	O3-C3-C2	2.75	115.67	110.05
4	i	7	MAN	C1-C2-C3	2.75	113.65	109.64
3	e	4	MAN	C1-O5-C5	2.73	115.85	112.19
4	j	7	MAN	C1-C2-C3	2.70	113.57	109.64
5	g	3	BMA	O3-C3-C4	2.68	116.70	110.38
3	f	1	NAG	O5-C1-C2	-2.68	107.14	111.29
4	a	4	MAN	O3-C3-C4	2.64	116.59	110.38
4	i	1	NAG	O5-C1-C2	-2.63	107.23	111.29
5	g	4	MAN	C1-O5-C5	2.62	115.70	112.19
3	h	6	MAN	C1-C2-C3	2.59	113.42	109.64
4	i	3	BMA	C1-O5-C5	-2.59	108.72	112.19
4	j	3	BMA	C3-C4-C5	-2.57	105.58	110.23
4	j	4	MAN	O3-C3-C2	2.56	115.27	110.05
5	d	1	NAG	C6-C5-C4	-2.54	106.77	113.02
4	Z	7	MAN	O5-C1-C2	-2.52	104.77	110.79
3	f	3	BMA	O5-C5-C6	-2.51	102.77	107.66
4	Z	1	NAG	C3-C4-C5	-2.51	105.69	110.23
4	Z	1	NAG	O5-C1-C2	-2.45	107.50	111.29
5	g	3	BMA	O3-C3-C2	-2.43	105.09	110.05
5	c	3	BMA	C1-C2-C3	2.43	113.18	109.64
4	j	5	MAN	C1-C2-C3	2.41	113.15	109.64
3	f	4	MAN	C1-C2-C3	2.39	113.13	109.64
5	d	1	NAG	O5-C1-C2	-2.39	107.59	111.29
3	f	1	NAG	C1-O5-C5	2.37	115.36	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	h	1	NAG	O5-C1-C2	-2.37	107.63	111.29
4	i	1	NAG	C6-C5-C4	-2.35	107.26	113.02
4	i	1	NAG	C4-C3-C2	2.35	114.45	111.02
3	e	1	NAG	O5-C5-C6	2.33	112.20	107.66
5	g	1	NAG	C1-O5-C5	2.33	115.31	112.19
5	d	2	NAG	C1-O5-C5	2.25	115.20	112.19
4	i	6	MAN	C2-C3-C4	-2.24	106.92	110.86
4	Z	7	MAN	C1-C2-C3	2.19	112.84	109.64
4	j	3	BMA	O5-C5-C6	2.19	111.92	107.66
4	j	3	BMA	O4-C4-C3	2.17	115.50	110.38
5	b	2	NAG	C1-O5-C5	2.15	115.06	112.19
4	a	4	MAN	O5-C1-C2	-2.15	105.67	110.79
5	b	1	NAG	C6-C5-C4	-2.14	107.77	113.02
3	f	1	NAG	C6-C5-C4	-2.13	107.79	113.02
4	j	7	MAN	C6-C5-C4	-2.11	107.83	113.02
4	i	5	MAN	C1-C2-C3	2.10	112.71	109.64
4	Z	7	MAN	C1-O5-C5	-2.07	109.42	112.19
4	Z	1	NAG	C1-O5-C5	2.06	114.94	112.19
4	a	7	MAN	C1-C2-C3	2.04	112.61	109.64
4	j	3	BMA	C2-C3-C4	-2.01	107.32	110.86
4	Z	3	BMA	O6-C6-C5	2.00	118.14	111.33

There are no chirality outliers.

All (96) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	e	1	NAG	C1-C2-N2-C7
4	Z	1	NAG	C1-C2-N2-C7
4	a	2	NAG	C3-C2-N2-C7
4	i	1	NAG	C1-C2-N2-C7
4	i	1	NAG	C8-C7-N2-C2
4	i	1	NAG	O7-C7-N2-C2
4	j	1	NAG	C1-C2-N2-C7
5	b	1	NAG	C1-C2-N2-C7
5	c	2	NAG	C8-C7-N2-C2
5	c	2	NAG	O7-C7-N2-C2
4	j	3	BMA	C4-C5-C6-O6
5	c	3	BMA	C4-C5-C6-O6
4	Z	4	MAN	O5-C5-C6-O6
5	c	3	BMA	O5-C5-C6-O6
4	a	7	MAN	O5-C5-C6-O6
4	j	3	BMA	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	a	3	BMA	O5-C5-C6-O6
3	f	1	NAG	O5-C5-C6-O6
4	a	7	MAN	C4-C5-C6-O6
5	g	2	NAG	C4-C5-C6-O6
3	Y	2	NAG	O5-C5-C6-O6
4	Z	5	MAN	O5-C5-C6-O6
3	f	5	MAN	C4-C5-C6-O6
4	Z	4	MAN	C4-C5-C6-O6
3	Y	4	MAN	O5-C5-C6-O6
5	g	2	NAG	O5-C5-C6-O6
3	h	3	BMA	O5-C5-C6-O6
3	h	3	BMA	C4-C5-C6-O6
4	a	3	BMA	C4-C5-C6-O6
3	f	2	NAG	O5-C5-C6-O6
3	f	5	MAN	O5-C5-C6-O6
4	a	2	NAG	O5-C5-C6-O6
4	j	7	MAN	O5-C5-C6-O6
3	Y	4	MAN	C4-C5-C6-O6
3	f	2	NAG	C4-C5-C6-O6
5	b	4	MAN	C4-C5-C6-O6
5	b	2	NAG	O5-C5-C6-O6
5	c	5	MAN	O5-C5-C6-O6
4	a	2	NAG	C4-C5-C6-O6
4	Z	5	MAN	C4-C5-C6-O6
4	j	2	NAG	O5-C5-C6-O6
5	b	4	MAN	O5-C5-C6-O6
3	h	6	MAN	C4-C5-C6-O6
5	c	5	MAN	C4-C5-C6-O6
4	j	1	NAG	O5-C5-C6-O6
3	h	1	NAG	C8-C7-N2-C2
5	g	4	MAN	O5-C5-C6-O6
3	h	6	MAN	O5-C5-C6-O6
3	Y	1	NAG	C4-C5-C6-O6
5	g	1	NAG	C4-C5-C6-O6
4	i	2	NAG	O5-C5-C6-O6
3	f	1	NAG	C4-C5-C6-O6
3	h	2	NAG	C4-C5-C6-O6
3	h	1	NAG	O5-C5-C6-O6
4	a	1	NAG	O5-C5-C6-O6
3	h	1	NAG	O7-C7-N2-C2
3	Y	2	NAG	C4-C5-C6-O6
5	g	5	MAN	C4-C5-C6-O6

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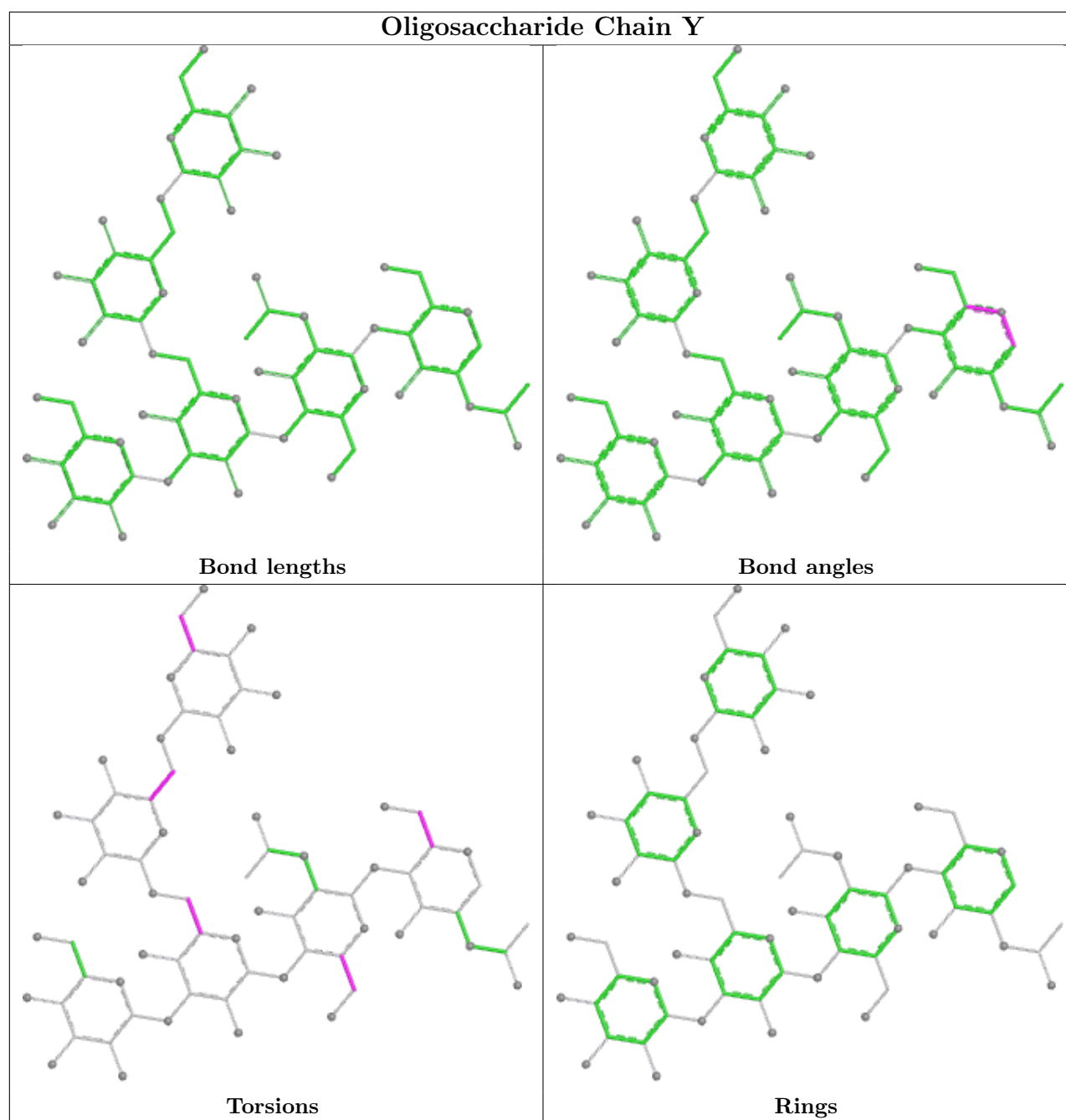
Mol	Chain	Res	Type	Atoms
3	f	3	BMA	O5-C5-C6-O6
3	h	2	NAG	O5-C5-C6-O6
3	e	4	MAN	O5-C5-C6-O6
4	j	4	MAN	C4-C5-C6-O6
4	j	6	MAN	C4-C5-C6-O6
3	Y	3	BMA	O5-C5-C6-O6
4	Z	3	BMA	O5-C5-C6-O6
5	c	2	NAG	C3-C2-N2-C7
5	g	1	NAG	O5-C5-C6-O6
3	e	3	BMA	O5-C5-C6-O6
5	d	3	BMA	O5-C5-C6-O6
5	c	2	NAG	C4-C5-C6-O6
4	i	3	BMA	O5-C5-C6-O6
4	j	6	MAN	O5-C5-C6-O6
5	g	5	MAN	O5-C5-C6-O6
3	Y	1	NAG	O5-C5-C6-O6
4	j	7	MAN	C4-C5-C6-O6
3	e	5	MAN	C4-C5-C6-O6
4	j	4	MAN	O5-C5-C6-O6
5	c	2	NAG	O5-C5-C6-O6
3	e	5	MAN	O5-C5-C6-O6
3	Y	5	MAN	O5-C5-C6-O6
5	b	2	NAG	C4-C5-C6-O6
4	i	6	MAN	C4-C5-C6-O6
4	j	2	NAG	C4-C5-C6-O6
5	c	1	NAG	C4-C5-C6-O6
3	Y	5	MAN	C4-C5-C6-O6
5	c	1	NAG	C3-C2-N2-C7
5	g	3	BMA	C4-C5-C6-O6
5	g	3	BMA	O5-C5-C6-O6
3	f	4	MAN	C4-C5-C6-O6
3	e	1	NAG	C8-C7-N2-C2
3	e	1	NAG	O7-C7-N2-C2
4	i	4	MAN	O5-C5-C6-O6
5	d	4	MAN	C4-C5-C6-O6
4	i	3	BMA	C4-C5-C6-O6
5	g	2	NAG	C8-C7-N2-C2
5	c	4	MAN	O5-C5-C6-O6

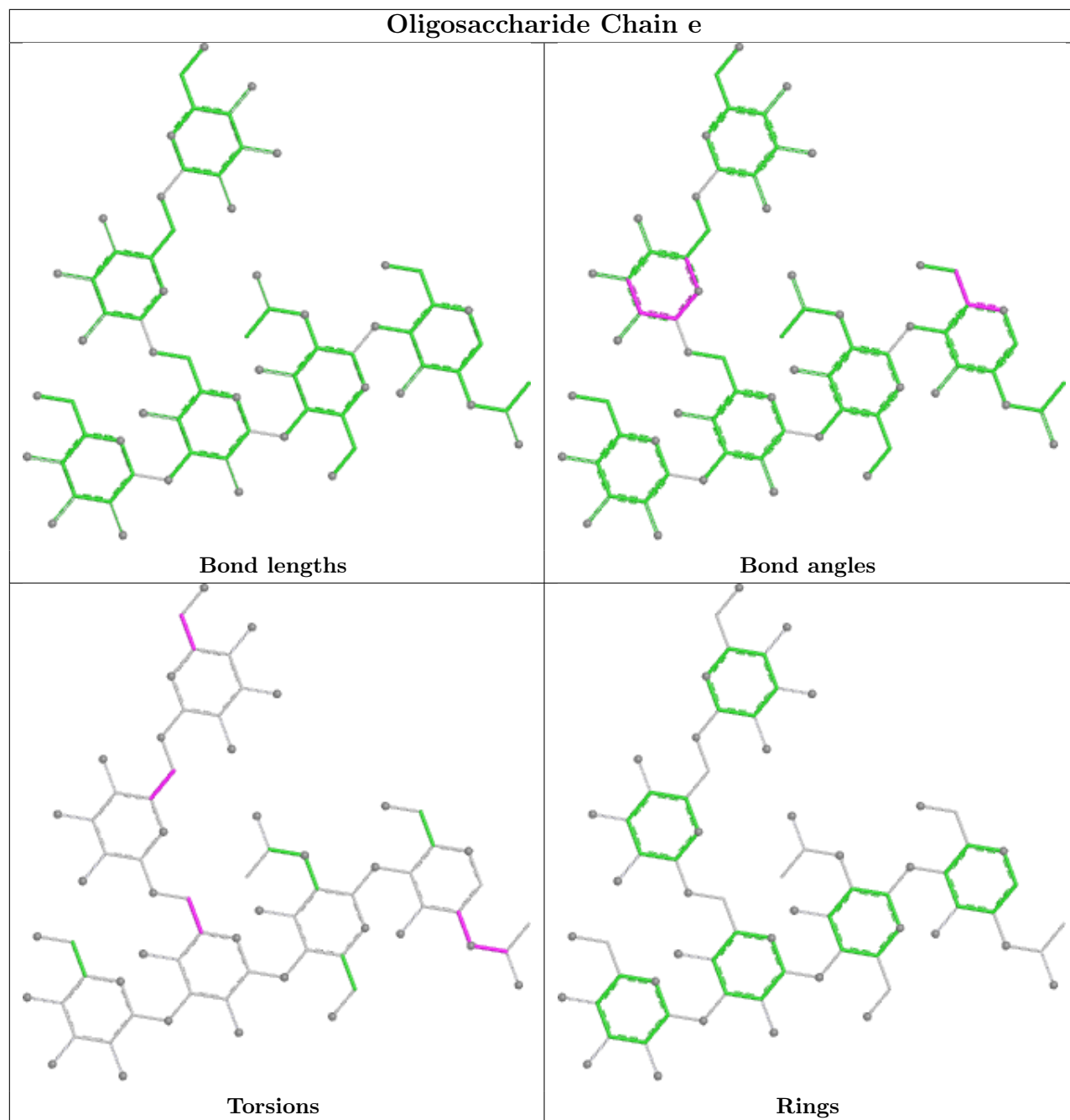
There are no ring outliers.

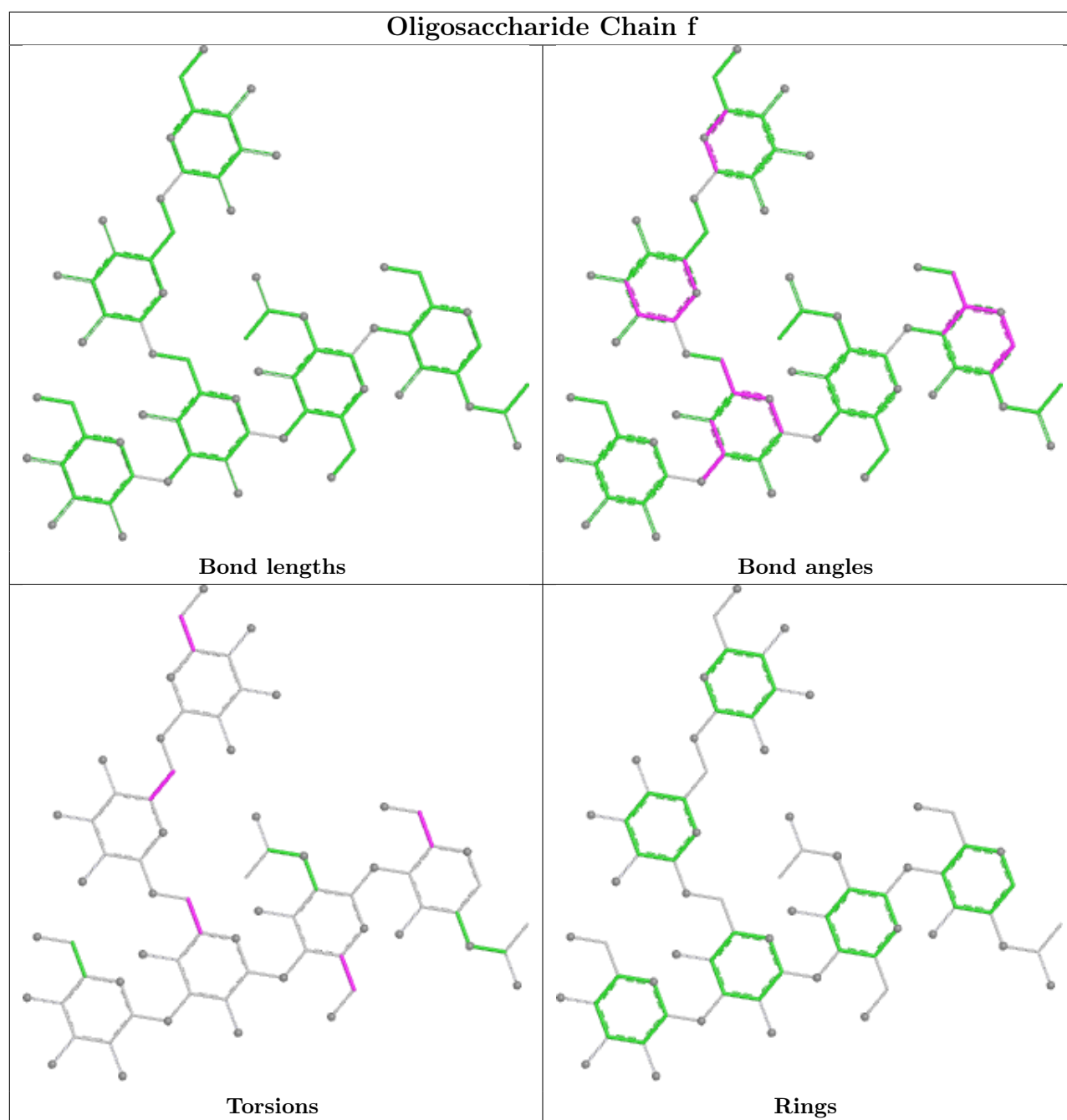
14 monomers are involved in 10 short contacts:

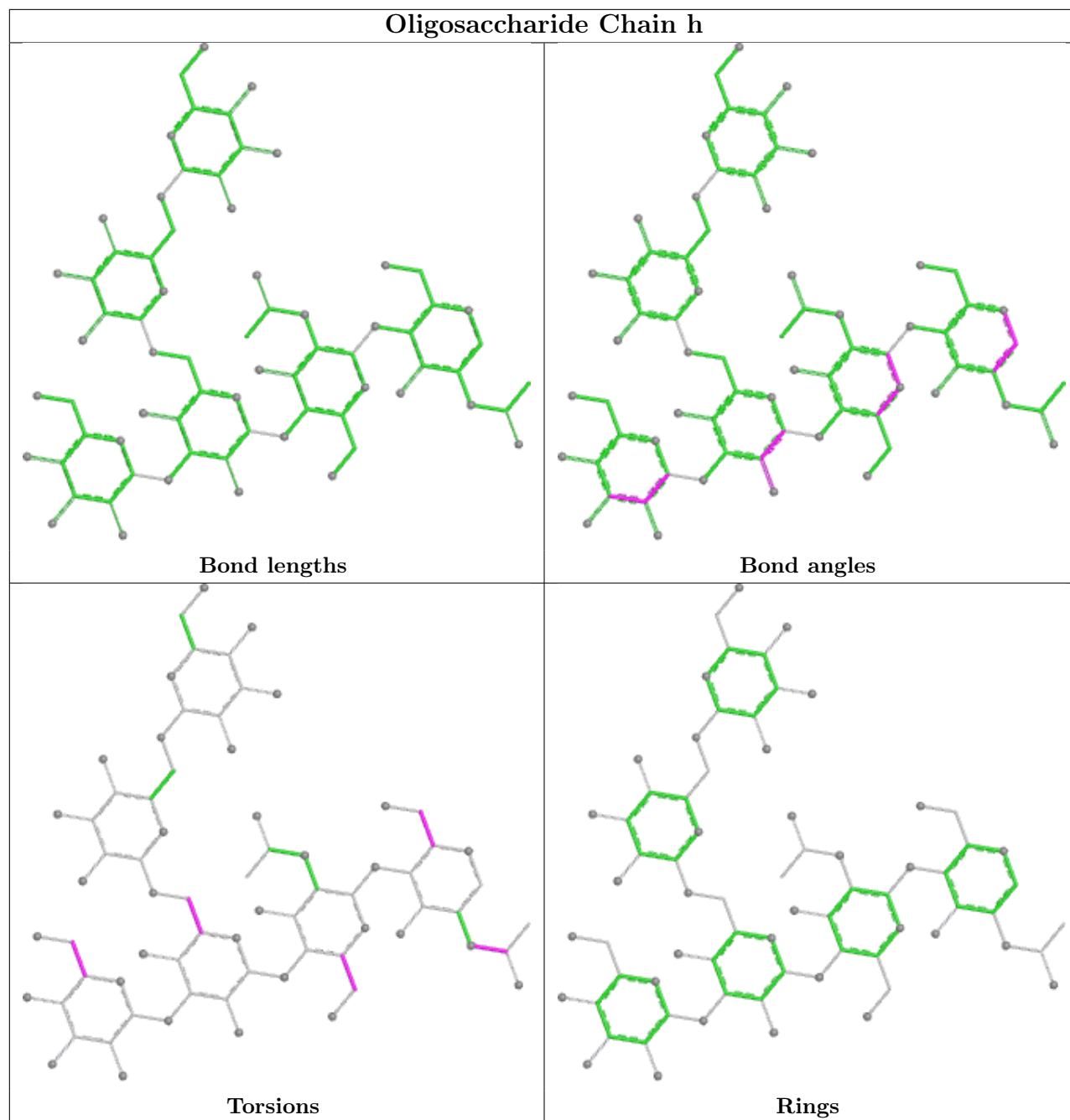
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	c	3	BMA	1	0
5	c	2	NAG	1	0
5	g	1	NAG	1	0
4	j	3	BMA	1	0
5	c	4	MAN	1	0
4	Z	1	NAG	1	0
3	h	1	NAG	1	0
3	e	4	MAN	1	0
3	e	3	BMA	1	0
4	i	1	NAG	1	0
4	Z	2	NAG	1	0
4	Z	3	BMA	1	0
3	f	1	NAG	1	0
4	Z	7	MAN	1	0

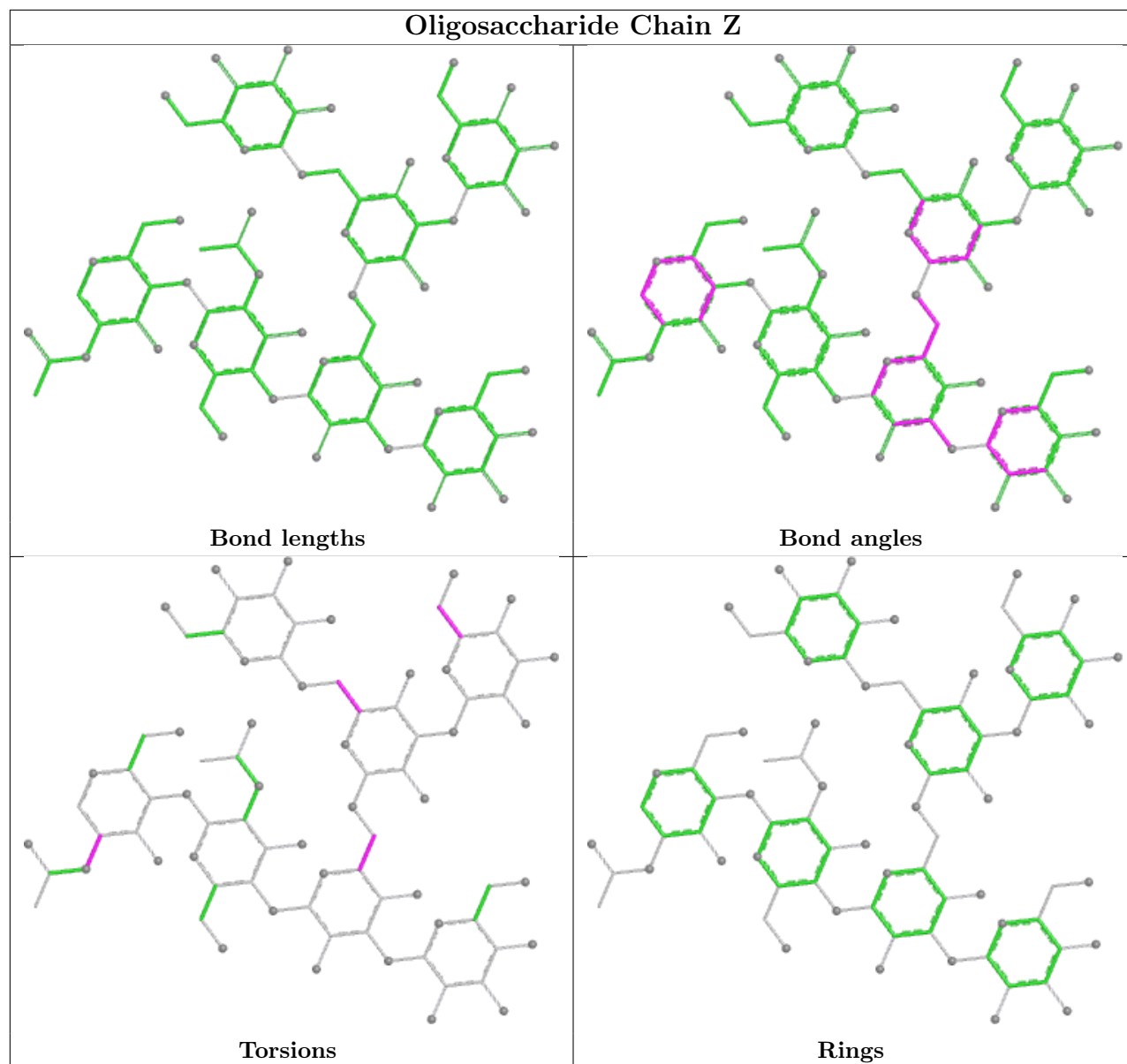
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

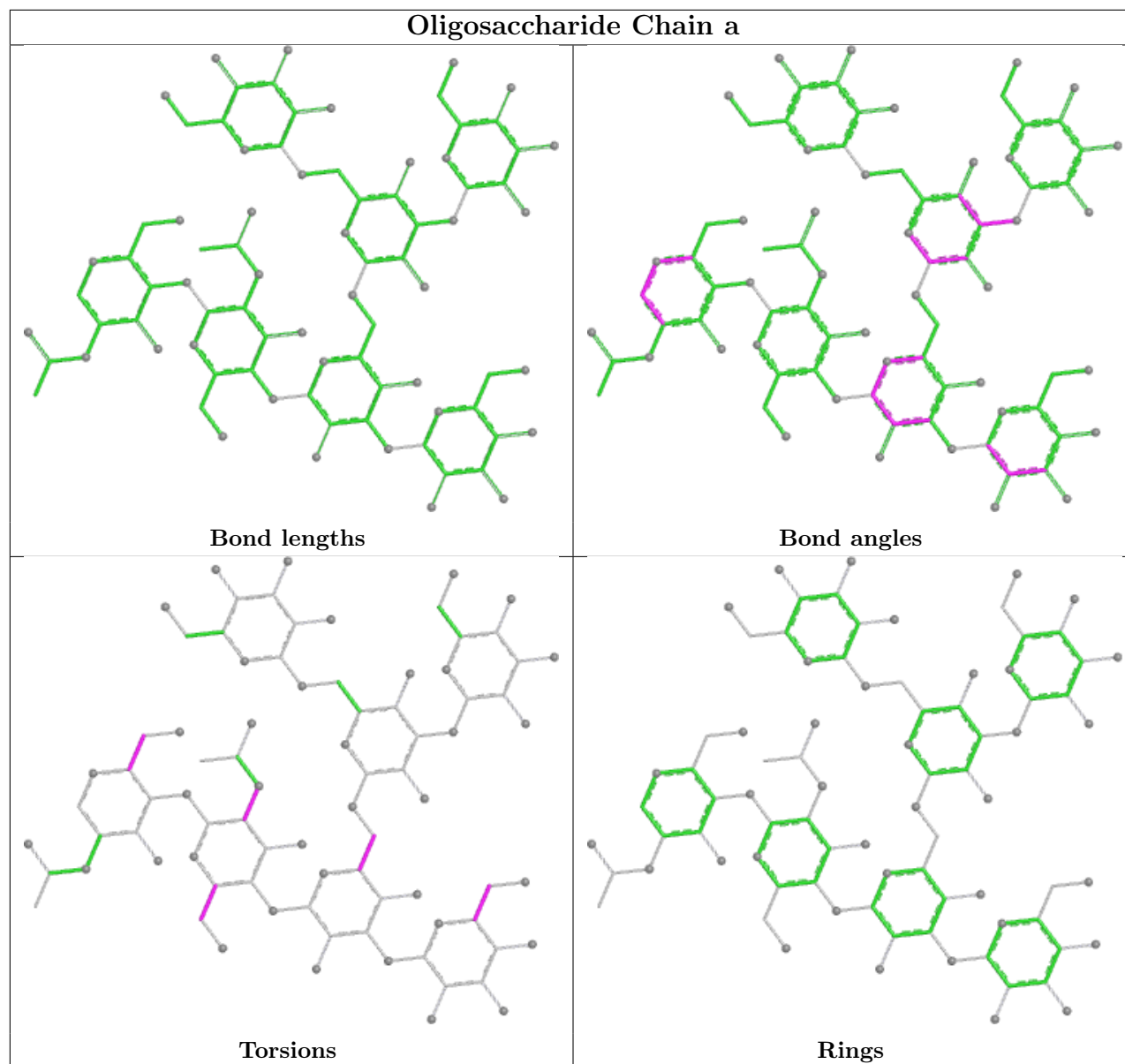


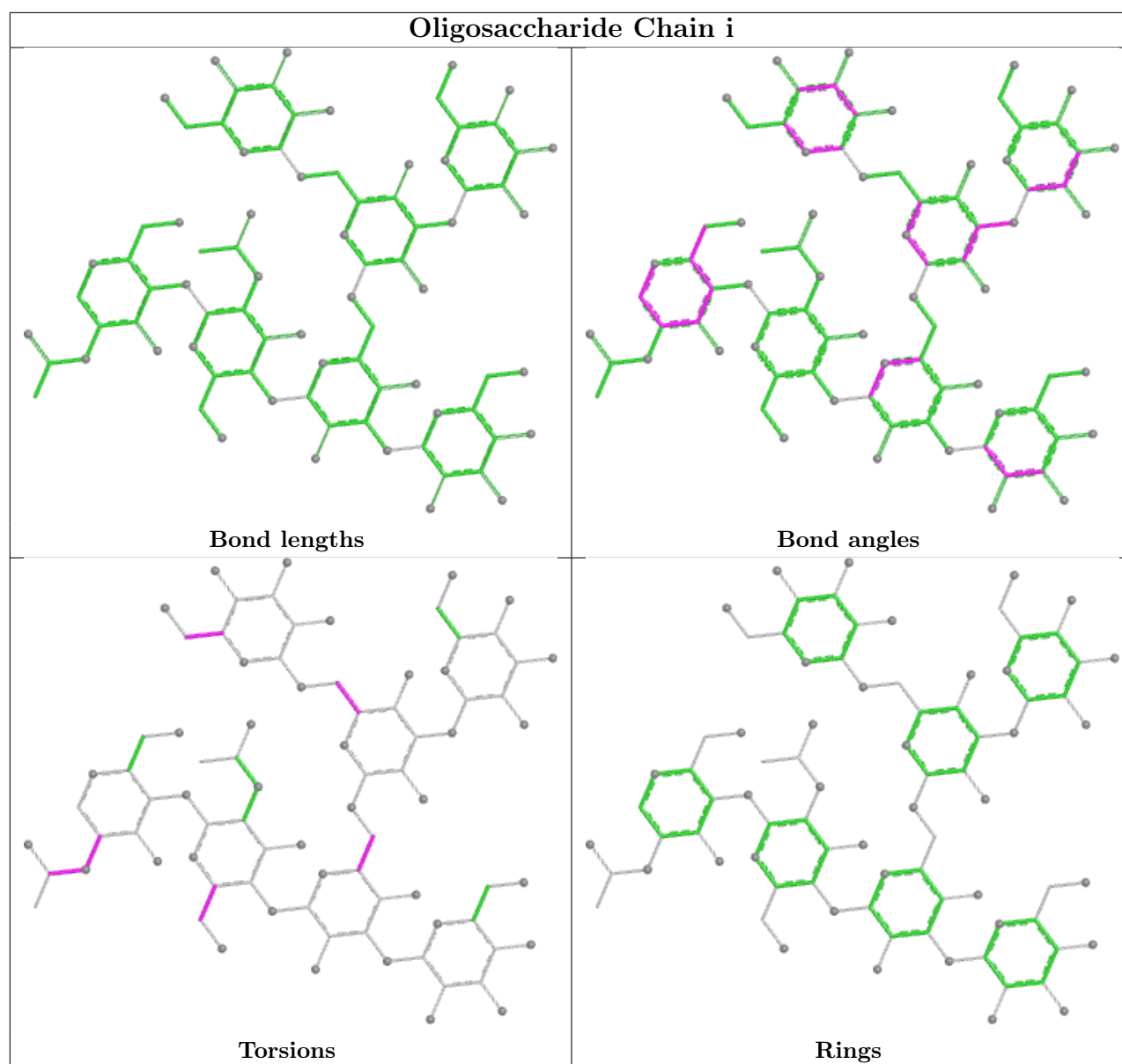


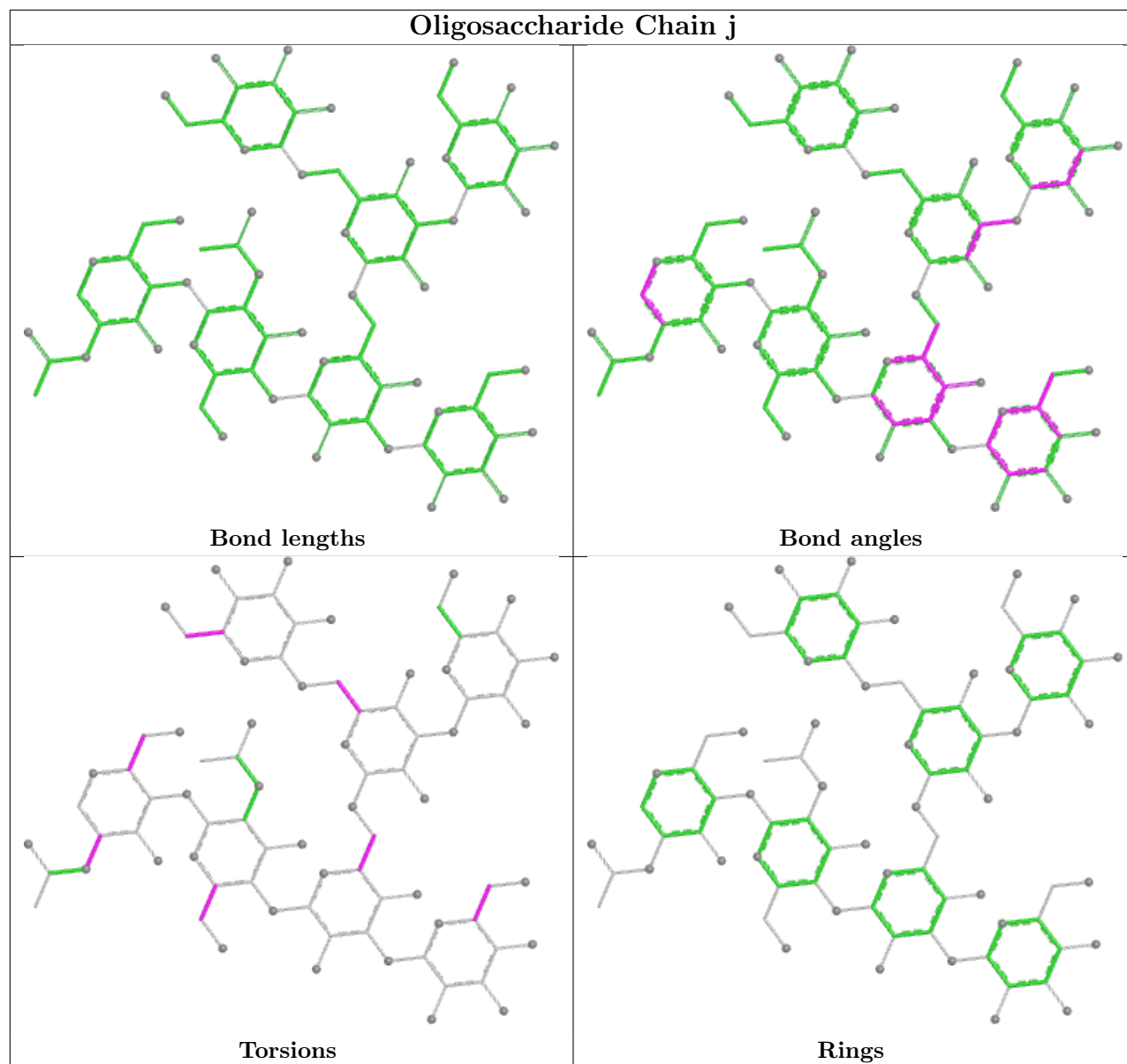


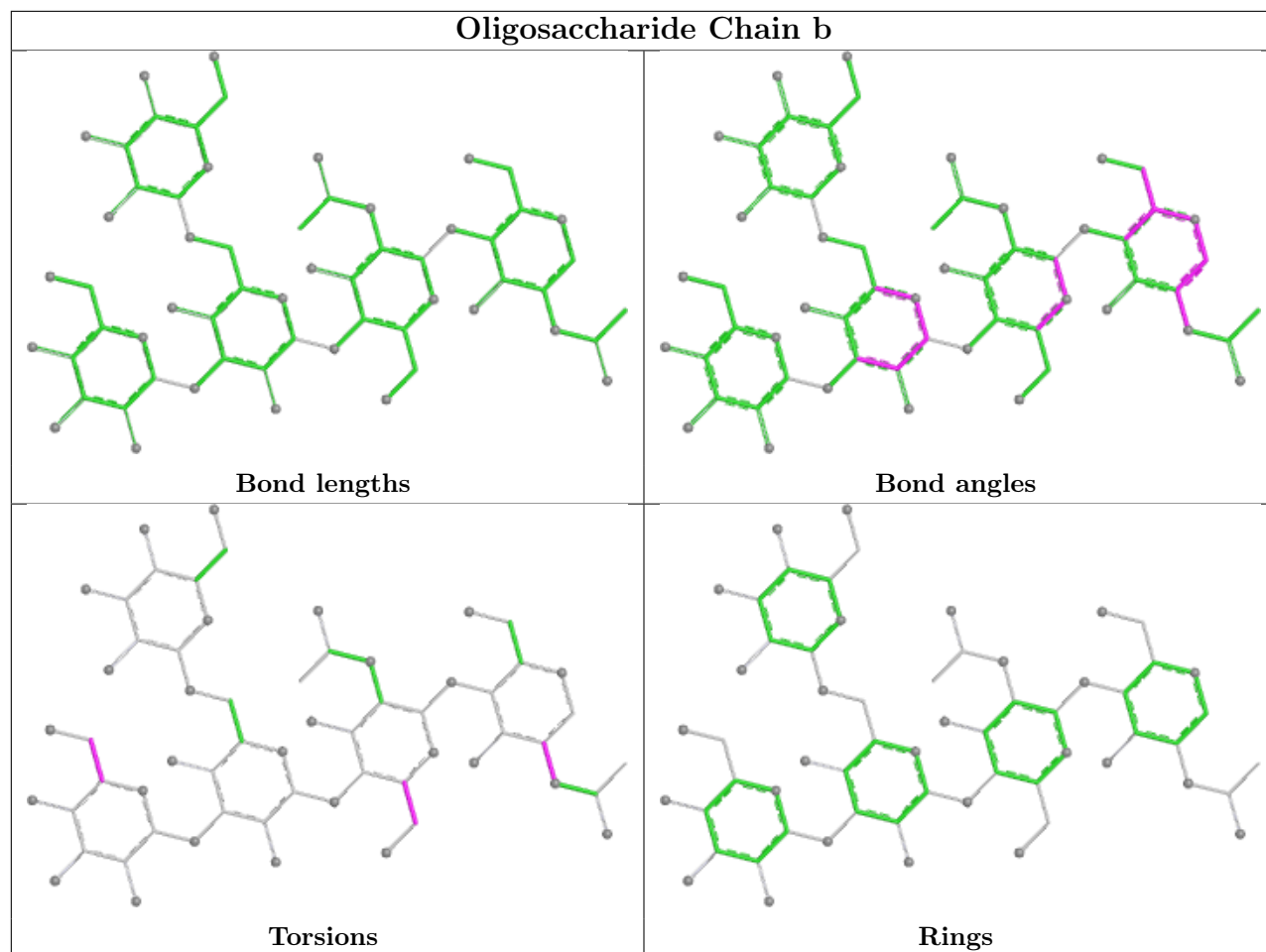


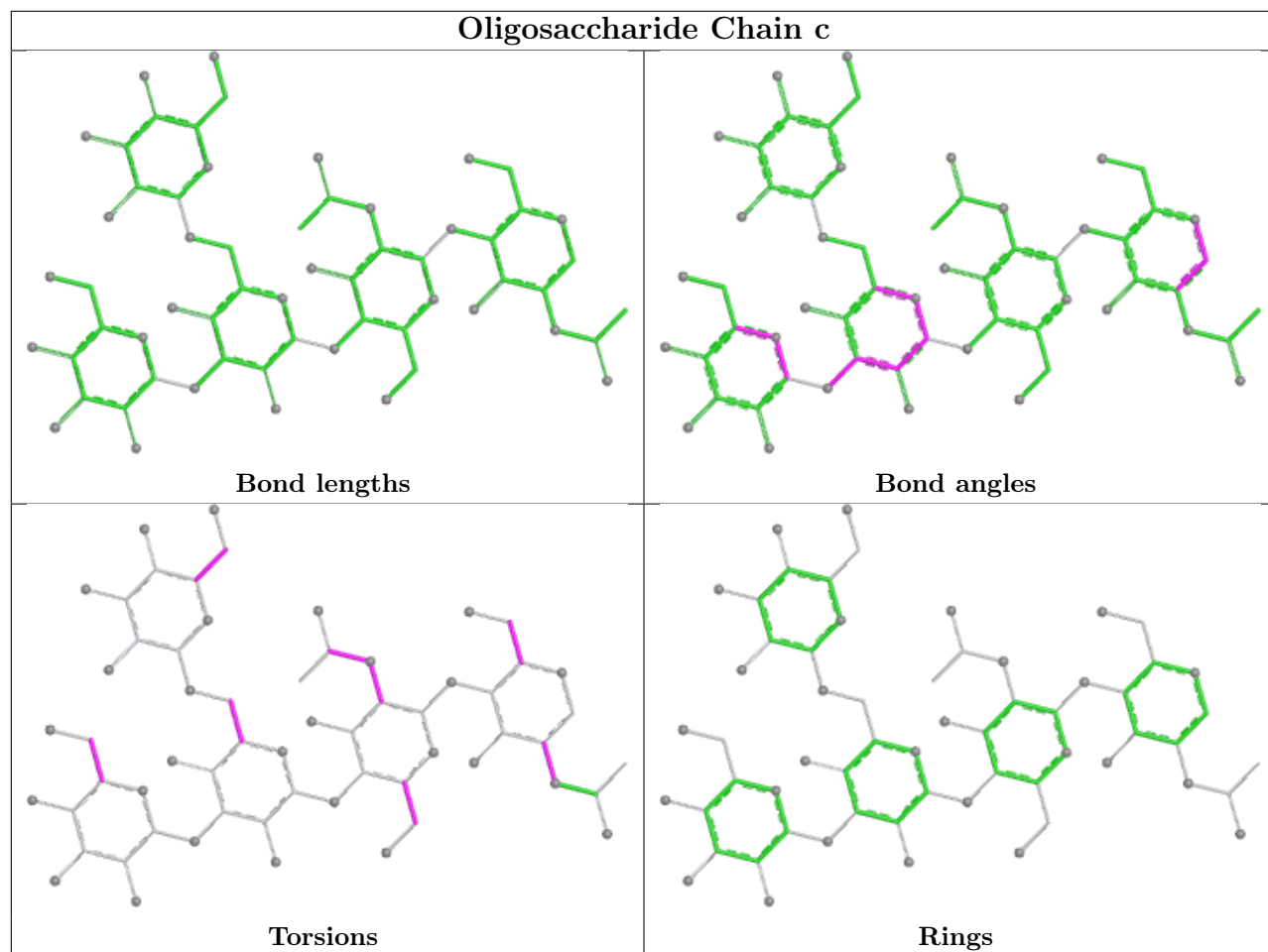


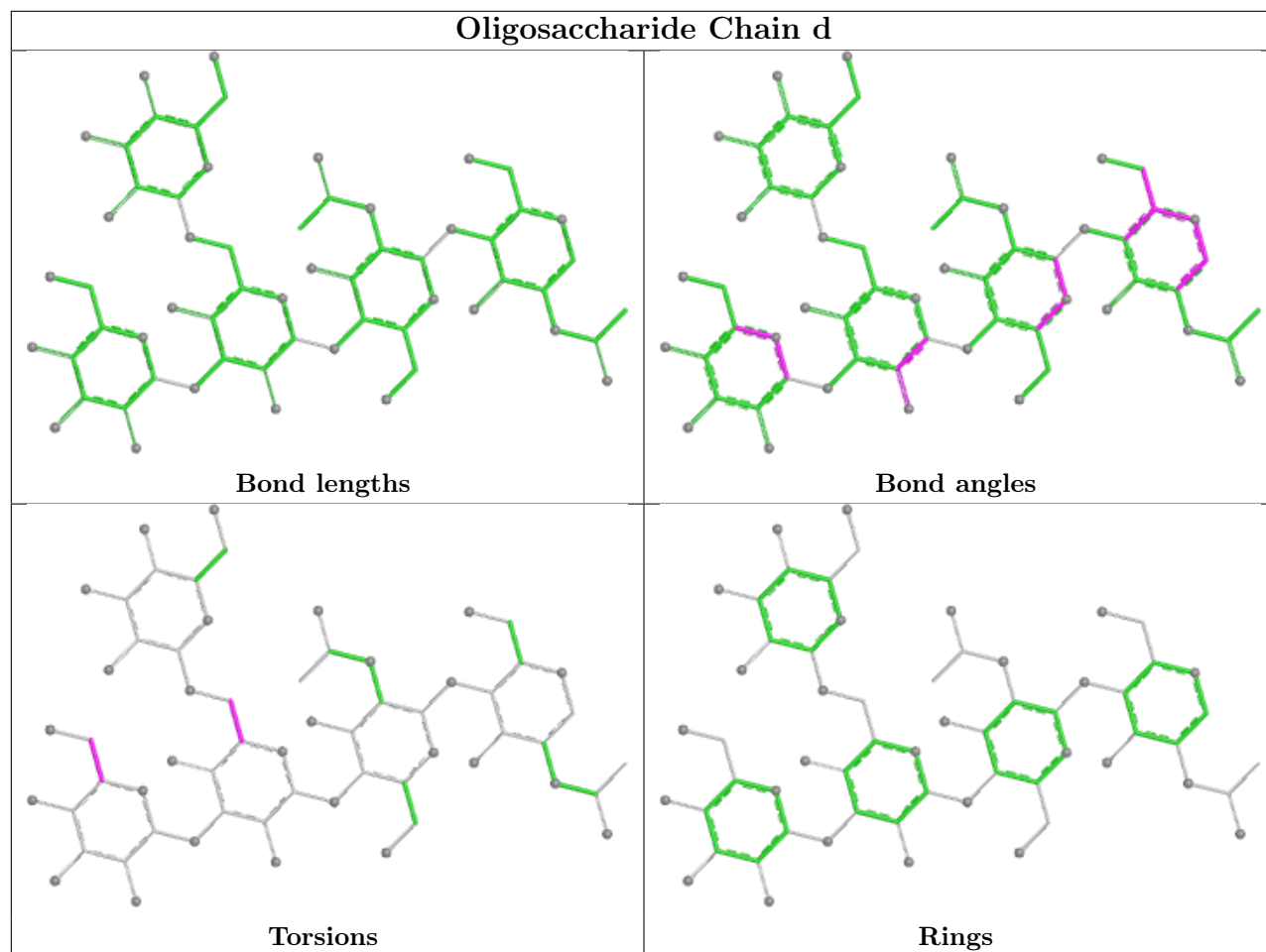


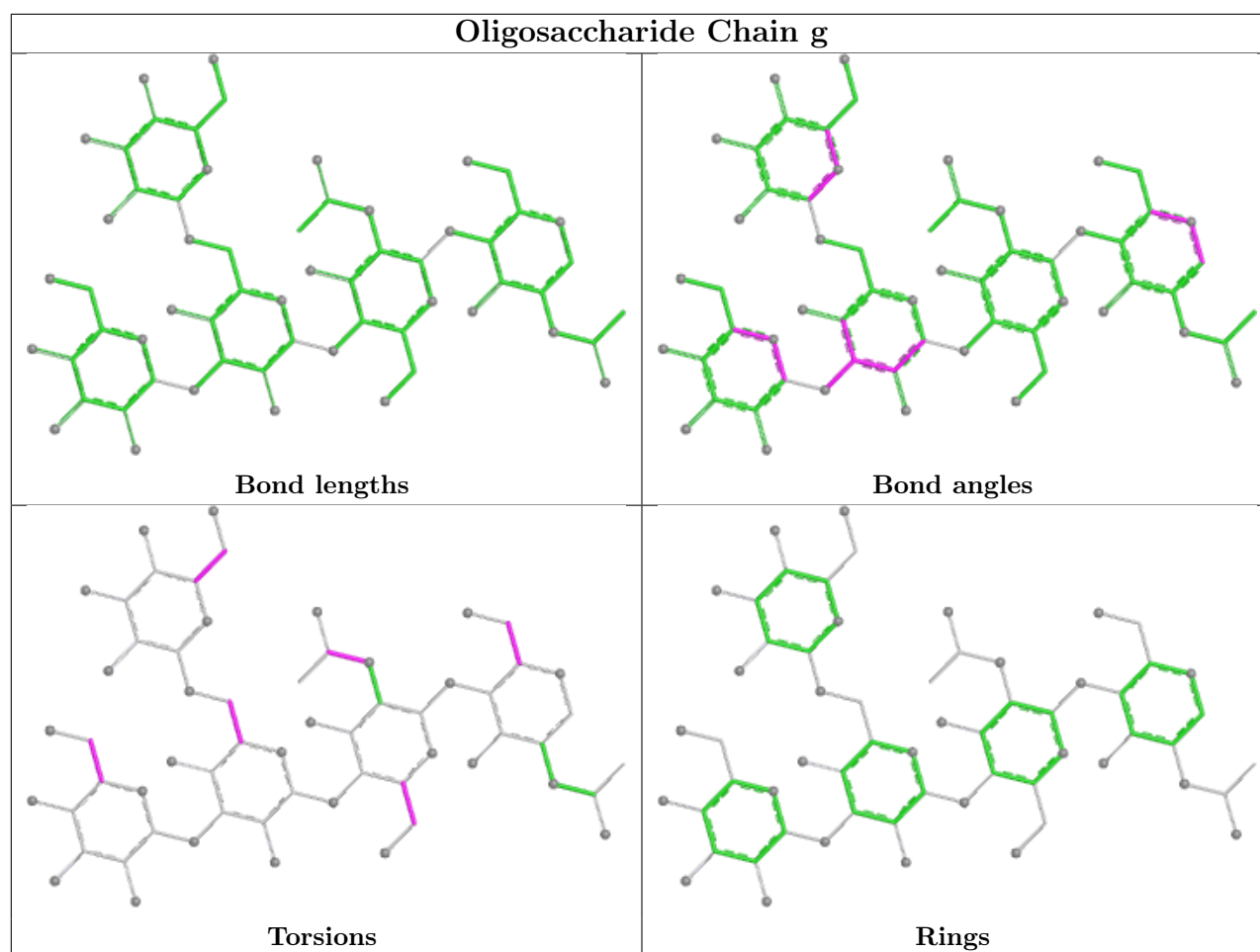












5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	188/208 (90%)	0.33	10 (5%) 32 30	143, 190, 239, 281	0
1	B	189/208 (90%)	0.50	12 (6%) 26 27	146, 194, 242, 283	0
1	C	186/208 (89%)	0.53	12 (6%) 25 25	157, 209, 248, 289	0
1	D	187/208 (89%)	0.39	8 (4%) 40 35	150, 202, 238, 288	0
1	E	187/208 (89%)	0.60	10 (5%) 32 30	167, 212, 249, 290	0
1	F	189/208 (90%)	0.58	17 (8%) 15 18	145, 205, 246, 291	0
1	M	191/208 (91%)	0.25	6 (3%) 51 40	143, 193, 248, 317	0
1	N	191/208 (91%)	0.40	13 (6%) 23 24	142, 189, 242, 289	0
1	O	186/208 (89%)	0.30	6 (3%) 50 40	132, 196, 237, 280	0
1	P	189/208 (90%)	0.45	8 (4%) 40 35	153, 193, 245, 281	0
1	Q	185/208 (88%)	0.41	7 (3%) 44 37	146, 199, 240, 280	0
1	R	186/208 (89%)	0.22	6 (3%) 50 40	135, 192, 238, 285	0
2	G	145/153 (94%)	0.89	17 (11%) 9 13	140, 215, 266, 338	0
2	H	142/153 (92%)	0.68	9 (6%) 26 27	155, 230, 283, 323	0
2	I	137/153 (89%)	0.57	7 (5%) 33 31	178, 246, 290, 316	0
2	J	142/153 (92%)	0.54	9 (6%) 26 27	184, 250, 298, 334	0
2	K	143/153 (93%)	0.65	7 (4%) 35 32	179, 248, 296, 336	0
2	L	135/153 (88%)	1.04	15 (11%) 10 15	187, 248, 301, 350	0
2	S	144/153 (94%)	0.46	8 (5%) 30 29	161, 225, 278, 327	0
2	T	142/153 (92%)	0.47	10 (7%) 22 24	164, 240, 292, 331	0
2	U	144/153 (94%)	0.52	7 (4%) 35 32	176, 243, 299, 325	0
2	V	141/153 (92%)	0.56	12 (8%) 16 20	166, 237, 280, 324	0
2	W	142/153 (92%)	0.72	20 (14%) 6 11	169, 235, 288, 321	0
2	X	139/153 (90%)	0.77	12 (8%) 16 19	159, 228, 282, 314	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
All	All	3950/4332 (91%)	0.52	248 (6%)	26	27	132, 210, 279, 350	0

All (248) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	X	85	LEU	4.6
2	S	31	CYS	4.5
1	F	78	PHE	4.5
2	T	32	GLN	4.4
2	S	32	GLN	4.4
2	S	107	TYR	4.3
1	N	103	LEU	4.3
2	K	121	PHE	4.3
1	R	220	SER	4.2
2	L	70	ASN	4.1
2	W	121	PHE	4.1
2	W	114	LEU	3.9
2	W	99	ASP	3.9
2	H	135	PHE	3.9
2	V	36	GLU	3.8
1	F	74	PHE	3.8
1	B	129	VAL	3.8
2	W	37	PHE	3.8
2	U	135	PHE	3.7
2	G	3	VAL	3.7
1	M	219	LEU	3.6
1	A	172	ASN	3.6
1	C	151	PHE	3.6
1	O	219	LEU	3.5
2	T	31	CYS	3.4
2	W	54	PHE	3.3
2	L	85	LEU	3.3
2	X	121	PHE	3.3
2	U	124	THR	3.3
2	I	140	ASN	3.3
2	W	93	LYS	3.2
1	O	21	VAL	3.2
1	P	214	TYR	3.2
1	A	183	LEU	3.2
1	Q	132	GLU	3.2
1	O	78	PHE	3.1
2	H	11	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
2	U	147	SER	3.1
1	R	55	GLU	3.1
2	G	132	TRP	3.1
1	A	40	LEU	3.1
1	B	21	VAL	3.1
2	V	107	TYR	3.0
1	B	40	LEU	3.0
2	K	21	ARG	3.0
2	V	121	PHE	3.0
2	I	9	HIS	3.0
2	U	72	PRO	3.0
2	J	69	ASP	3.0
1	A	35	TRP	3.0
1	P	40	LEU	3.0
2	X	4	SER	3.0
1	P	35	TRP	2.9
2	W	19	LEU	2.9
1	C	173	GLY	2.9
2	X	11	ILE	2.9
2	X	54	PHE	2.9
2	L	21	ARG	2.9
2	V	77	ILE	2.9
1	A	41	GLY	2.9
2	G	96	GLU	2.9
2	J	121	PHE	2.9
2	K	36	GLU	2.8
2	X	135	PHE	2.8
2	K	100	LYS	2.8
1	P	31	LEU	2.8
1	F	68	ILE	2.8
1	R	35	TRP	2.8
1	Q	159	LEU	2.8
1	C	21	VAL	2.8
1	Q	62	ARG	2.8
1	P	86	THR	2.8
1	D	23	ALA	2.8
1	A	44	ILE	2.8
2	X	9	HIS	2.8
1	F	219	LEU	2.8
1	E	21	VAL	2.7
2	X	90	CYS	2.7
1	N	116	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
2	L	40	GLN	2.7
1	B	213	VAL	2.7
2	L	59	ASP	2.7
1	F	210	ALA	2.7
1	B	214	TYR	2.7
2	T	75	ILE	2.7
1	N	40	LEU	2.7
1	E	36	ARG	2.7
2	V	5	GLU	2.7
2	U	127	LEU	2.7
2	L	129	ASP	2.7
2	V	65	MET	2.7
1	D	21	VAL	2.6
1	N	108	LEU	2.6
1	E	120	SER	2.6
2	W	3	VAL	2.6
1	E	78	PHE	2.6
2	G	127	LEU	2.6
2	U	27	MET	2.6
2	G	93	LYS	2.6
1	R	51	LEU	2.6
1	B	220	SER	2.6
2	X	93	LYS	2.6
1	C	189	LEU	2.6
1	B	30	THR	2.6
2	W	69	ASP	2.6
1	O	189	LEU	2.6
2	L	88	LYS	2.5
1	D	78	PHE	2.5
1	B	32	THR	2.5
2	S	33	ILE	2.5
2	I	121	PHE	2.5
1	B	212	GLY	2.5
2	G	32	GLN	2.5
2	W	62	GLU	2.5
1	F	79	ASP	2.5
1	B	127	LEU	2.5
2	G	90	CYS	2.5
2	W	72	PRO	2.5
1	F	204	LYS	2.5
2	G	89	SER	2.5
2	T	147	SER	2.5

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Mol	Chain	Res	Type	RSRZ
2	X	89	SER	2.5
2	G	91	PHE	2.5
2	L	121	PHE	2.5
1	N	159	LEU	2.4
1	P	159	LEU	2.4
1	N	57	GLN	2.4
1	F	127	LEU	2.4
2	X	86	ARG	2.4
2	S	80	LEU	2.4
1	F	211	HIS	2.4
1	F	91	VAL	2.4
2	W	53	ALA	2.4
2	T	33	ILE	2.4
1	Q	55	GLU	2.4
2	W	97	GLU	2.4
2	W	115	GLU	2.4
1	R	219	LEU	2.4
2	J	105	THR	2.4
1	F	129	VAL	2.4
1	D	159	LEU	2.4
2	H	36	GLU	2.4
1	Q	61	GLY	2.4
1	Q	203	GLY	2.4
1	Q	70	ILE	2.4
1	N	105	ARG	2.4
2	I	86	ARG	2.4
2	L	55	LEU	2.4
2	H	83	LEU	2.3
2	H	85	LEU	2.3
1	C	192	PRO	2.3
1	E	22	THR	2.3
2	L	24	ASP	2.3
1	E	173	GLY	2.3
2	G	33	ILE	2.3
2	J	97	GLU	2.3
1	F	21	VAL	2.3
2	I	111	LEU	2.3
1	E	190	SER	2.3
2	J	6	TYR	2.3
2	T	107	TYR	2.3
1	C	159	LEU	2.3
1	M	21	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	N	21	VAL	2.3
1	O	66	ASP	2.3
1	E	30	THR	2.2
1	A	174	GLY	2.2
2	L	80	LEU	2.2
2	W	38	VAL	2.2
1	N	36	ARG	2.2
1	N	35	TRP	2.2
1	M	179	LYS	2.2
1	N	51	LEU	2.2
2	T	110	PRO	2.2
2	G	65	MET	2.2
2	V	40	GLN	2.2
2	G	50	LEU	2.2
2	G	133	ASN	2.2
2	V	64	THR	2.2
2	L	54	PHE	2.2
2	G	62	GLU	2.2
2	K	122	ASN	2.2
1	C	153	HIS	2.2
1	B	110	GLU	2.2
2	V	115	GLU	2.2
1	D	174	GLY	2.2
1	E	28	ARG	2.2
2	H	98	HIS	2.2
2	T	13	SER	2.2
2	V	81	GLN	2.2
1	P	199	VAL	2.2
1	C	152	PRO	2.2
1	F	70	ILE	2.2
1	O	207	LYS	2.2
1	C	190	SER	2.2
1	F	155	HIS	2.2
2	S	35	PHE	2.1
2	G	80	LEU	2.1
2	H	111	LEU	2.1
2	U	70	ASN	2.1
2	W	23	ILE	2.1
2	W	111	LEU	2.1
1	A	81	HIS	2.1
2	H	69	ASP	2.1
2	J	72	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
2	J	131	ASP	2.1
2	S	110	PRO	2.1
2	G	125	LYS	2.1
1	D	122	VAL	2.1
1	F	36	ARG	2.1
1	N	173	GLY	2.1
2	L	36	GLU	2.1
2	H	121	PHE	2.1
1	D	30	THR	2.1
2	I	40	GLN	2.1
2	J	147	SER	2.1
2	K	13	SER	2.1
1	N	219	LEU	2.1
1	P	88	PHE	2.1
2	T	11	ILE	2.1
1	A	30	THR	2.1
1	M	173	GLY	2.1
1	C	188	ASP	2.1
2	W	86	ARG	2.1
2	V	35	PHE	2.1
1	F	160	MET	2.1
1	B	81	HIS	2.1
1	R	103	LEU	2.1
1	D	24	PHE	2.1
2	L	91	PHE	2.1
2	V	85	LEU	2.0
2	W	116	LYS	2.0
1	C	76	GLY	2.0
2	L	7	CYS	2.0
2	J	132	TRP	2.0
2	T	115	GLU	2.0
1	C	96	ILE	2.0
2	S	121	PHE	2.0
1	A	21	VAL	2.0
1	M	191	LEU	2.0
1	M	171	ALA	2.0
1	F	118	HIS	2.0
2	I	129	ASP	2.0
1	E	219	LEU	2.0
2	G	92	THR	2.0
2	K	141	ASN	2.0
2	X	13	SER	2.0

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Mol	Chain	Res	Type	RSRZ
2	W	91	PHE	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
3	MAN	Y	6	11/12	0.29	0.17	179,283,319,340	0
3	MAN	Y	4	11/12	0.38	0.17	215,291,309,312	0
4	MAN	Z	7	11/12	0.46	0.15	186,234,277,304	0
4	MAN	Z	5	11/12	0.51	0.10	219,268,297,306	0
4	MAN	Z	4	11/12	0.56	0.12	270,298,320,337	0
3	MAN	Y	5	11/12	0.68	0.15	172,278,292,311	0
3	NAG	e	1	14/15	-	-	142,190,244,278	0
3	NAG	e	2	14/15	-	-	157,188,237,248	0
3	BMA	e	3	11/12	-	-	199,229,289,318	0
3	MAN	e	4	11/12	-	-	242,274,322,327	0
3	MAN	e	5	11/12	-	-	229,267,300,324	0
3	MAN	e	6	11/12	-	-	159,266,328,347	0
3	NAG	f	1	14/15	-	-	101,187,221,223	0
3	NAG	f	2	14/15	-	-	113,159,214,279	0
3	BMA	f	3	11/12	-	-	122,186,227,233	0
3	MAN	f	4	11/12	-	-	222,259,293,368	0
3	MAN	f	5	11/12	-	-	165,285,305,311	0
3	MAN	f	6	11/12	-	-	183,247,291,293	0
3	NAG	h	1	14/15	-	-	129,218,239,239	0
3	NAG	h	2	14/15	-	-	109,185,229,268	0
3	BMA	h	3	11/12	-	-	189,230,277,279	0
3	MAN	h	4	11/12	-	-	235,283,301,320	0
3	MAN	h	5	11/12	-	-	294,320,348,349	0
3	MAN	h	6	11/12	-	-	214,290,327,327	0
4	MAN	Z	6	11/12	0.76	0.11	227,270,316,333	0
3	BMA	Y	3	11/12	0.76	0.12	196,227,268,279	0
4	BMA	Z	3	11/12	0.93	0.06	176,222,235,279	0

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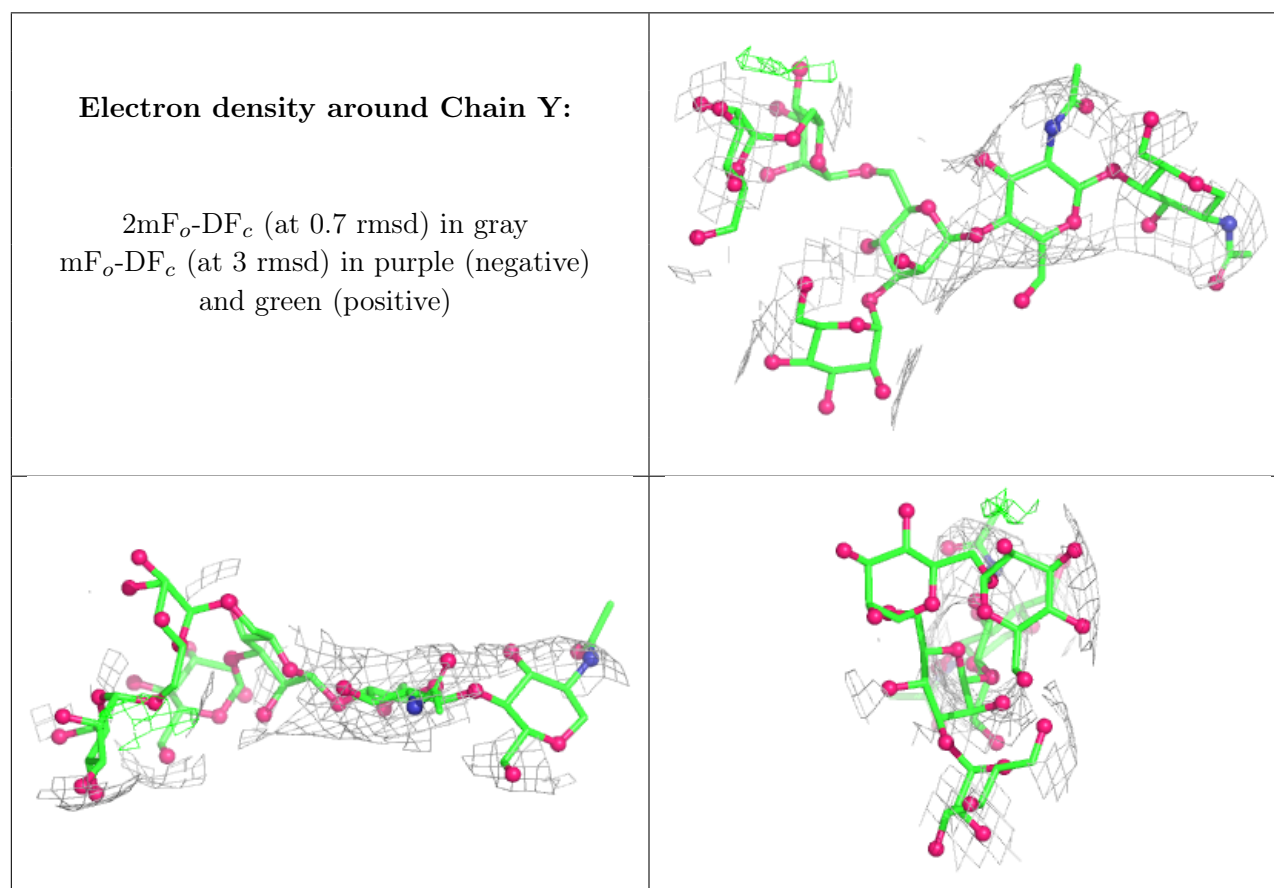
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	Y	2	14/15	0.94	0.24	111,181,227,233	0
3	NAG	Y	1	14/15	0.94	0.21	158,184,245,246	0
4	NAG	Z	1	14/15	0.95	0.10	158,192,224,246	0
4	NAG	Z	2	14/15	0.96	0.11	145,197,251,263	0
4	NAG	a	1	14/15	-	-	223,276,318,345	0
4	NAG	a	2	14/15	-	-	182,258,282,287	0
4	BMA	a	3	11/12	-	-	208,249,289,300	0
4	MAN	a	4	11/12	-	-	292,310,342,361	0
4	MAN	a	5	11/12	-	-	240,308,366,376	0
4	MAN	a	6	11/12	-	-	217,289,309,314	0
4	MAN	a	7	11/12	-	-	178,249,271,281	0
4	NAG	i	1	14/15	-	-	172,210,247,251	0
4	NAG	i	2	14/15	-	-	148,181,242,292	0
4	BMA	i	3	11/12	-	-	175,205,224,271	0
4	MAN	i	4	11/12	-	-	268,299,347,351	0
4	MAN	i	5	11/12	-	-	189,286,305,313	0
4	MAN	i	6	11/12	-	-	254,324,359,371	0
4	MAN	i	7	11/12	-	-	200,242,264,268	0
4	NAG	j	1	14/15	-	-	154,190,260,269	0
4	NAG	j	2	14/15	-	-	171,184,232,241	0
4	BMA	j	3	11/12	-	-	155,209,248,250	0
4	MAN	j	4	11/12	-	-	256,287,316,320	0
4	MAN	j	5	11/12	-	-	233,279,298,326	0
4	MAN	j	6	11/12	-	-	248,304,355,371	0
4	MAN	j	7	11/12	-	-	216,284,323,332	0
5	NAG	b	1	14/15	-	-	202,246,270,275	0
5	NAG	b	2	14/15	-	-	152,204,221,276	0
5	BMA	b	3	11/12	-	-	191,228,274,332	0
5	MAN	b	4	11/12	-	-	204,256,281,283	0
5	MAN	b	5	11/12	-	-	186,281,322,333	0
5	NAG	c	1	14/15	-	-	185,254,298,308	0
5	NAG	c	2	14/15	-	-	206,257,279,286	0
5	BMA	c	3	11/12	-	-	239,257,278,284	0
5	MAN	c	4	11/12	-	-	222,282,306,313	0
5	MAN	c	5	11/12	-	-	184,249,291,304	0
5	NAG	d	1	14/15	-	-	194,268,287,303	0
5	NAG	d	2	14/15	-	-	154,216,246,271	0
5	BMA	d	3	11/12	-	-	197,221,242,300	0
5	MAN	d	4	11/12	-	-	223,300,324,344	0
5	MAN	d	5	11/12	-	-	229,290,322,341	0
5	NAG	g	1	14/15	-	-	164,202,282,318	0
5	NAG	g	2	14/15	-	-	147,178,203,238	0

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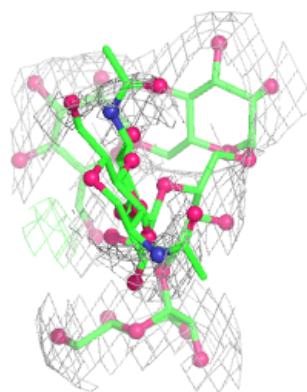
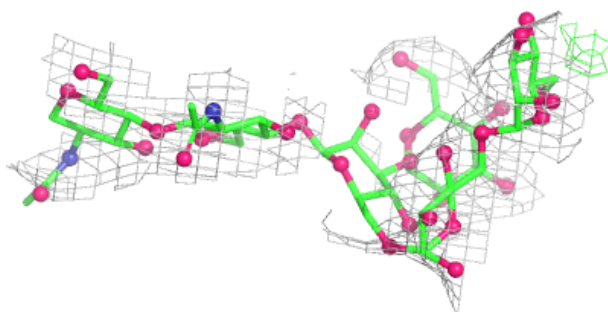
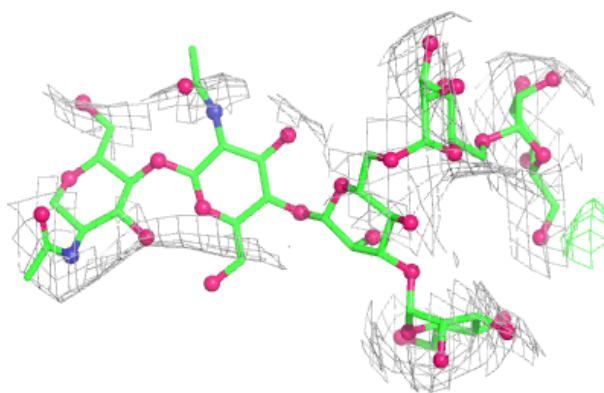
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	BMA	g	3	11/12	-	-	202,211,256,269	0
5	MAN	g	4	11/12	-	-	213,249,288,290	0
5	MAN	g	5	11/12	-	-	172,240,270,283	0

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.

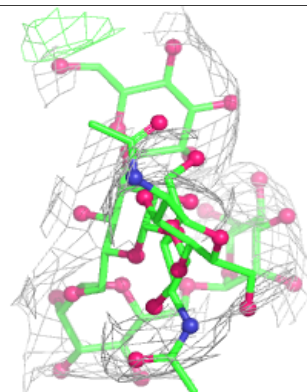
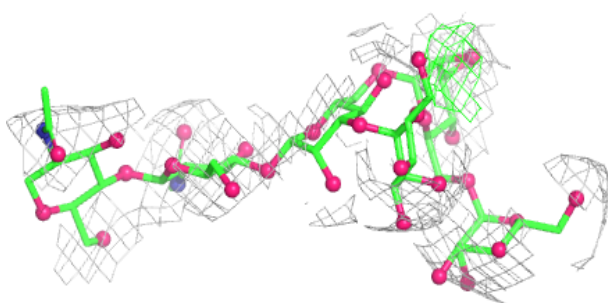
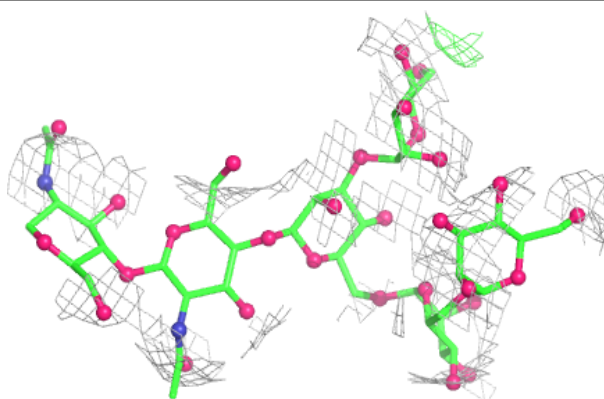


Electron density around Chain e:

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

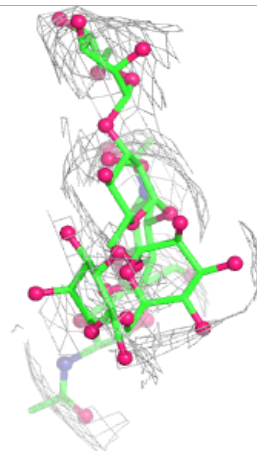
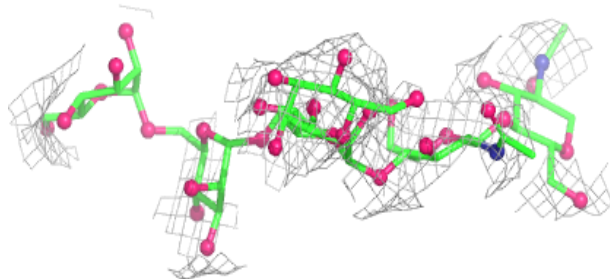
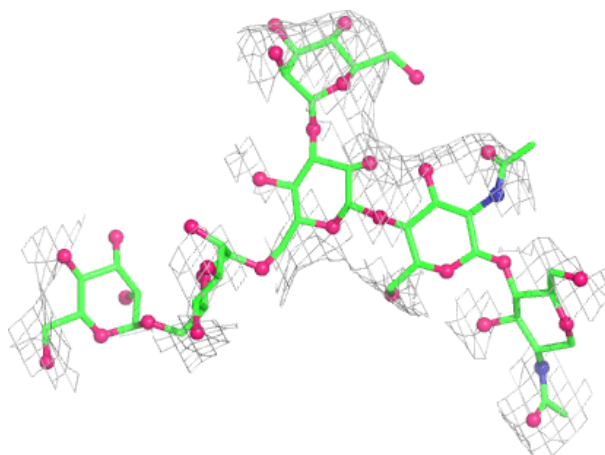
**Electron density around Chain f:**

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



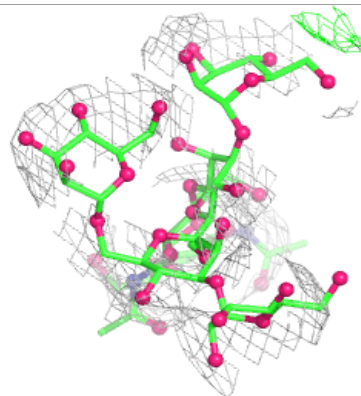
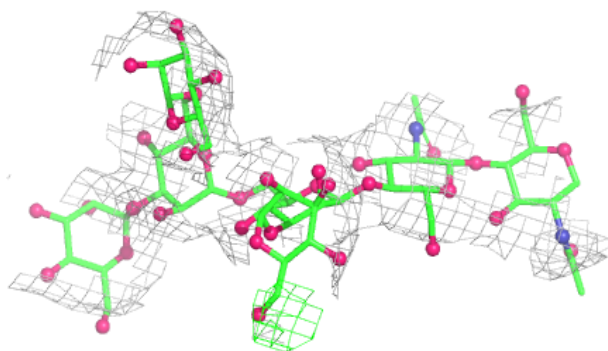
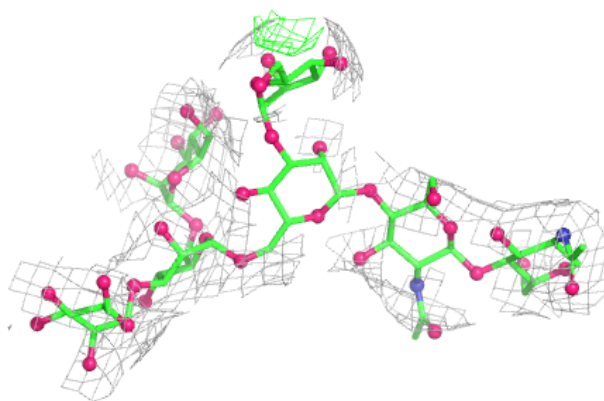
Electron density around Chain h:

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



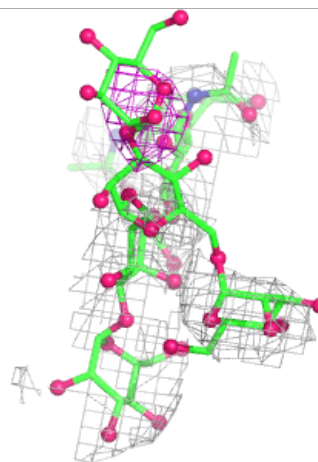
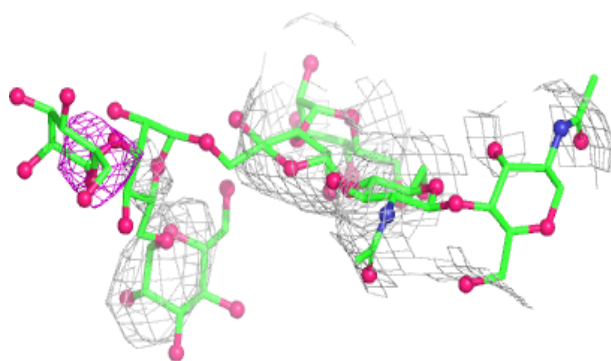
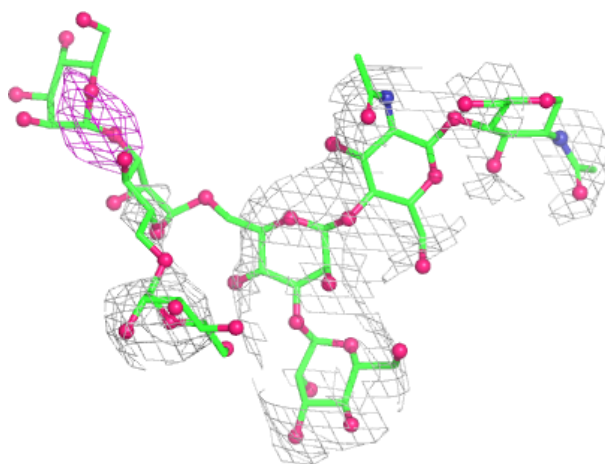
Electron density around Chain Z:

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



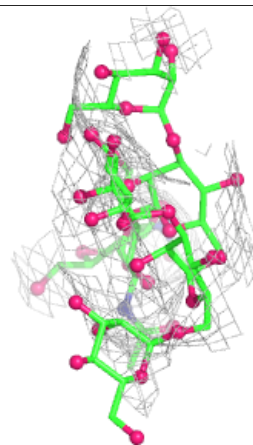
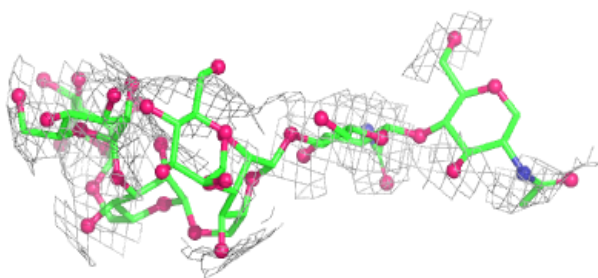
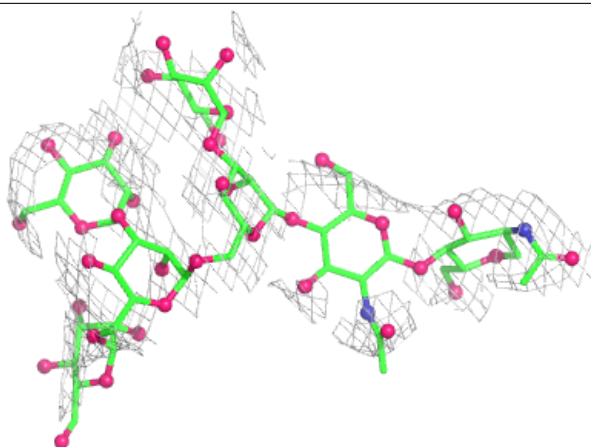
Electron density around Chain a:

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



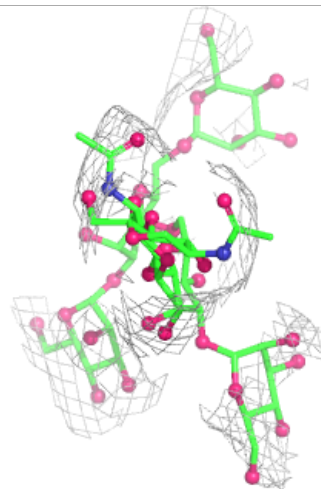
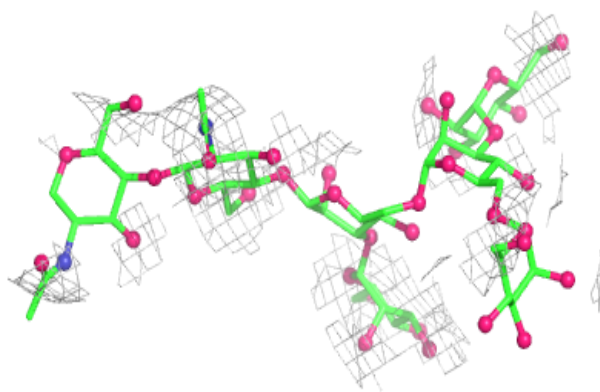
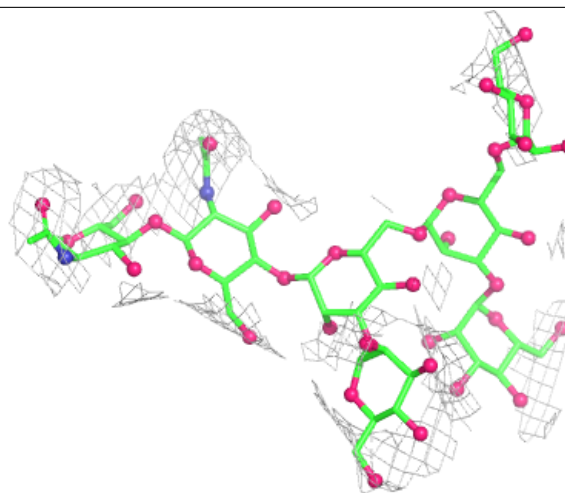
Electron density around Chain i:

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



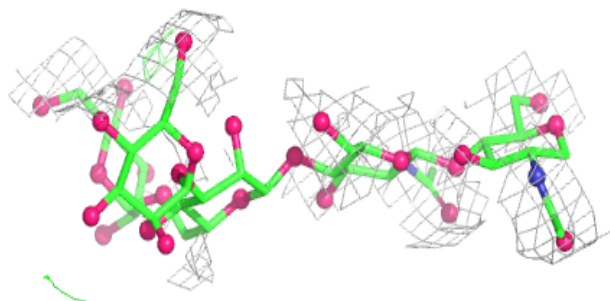
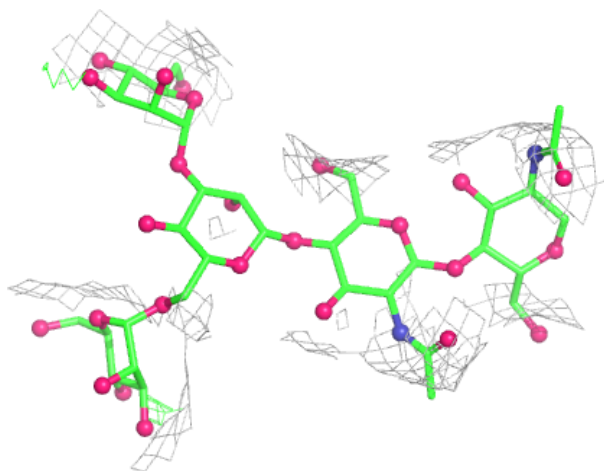
Electron density around Chain j:

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



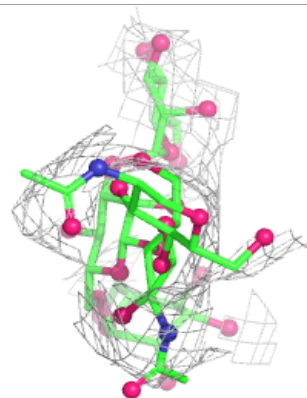
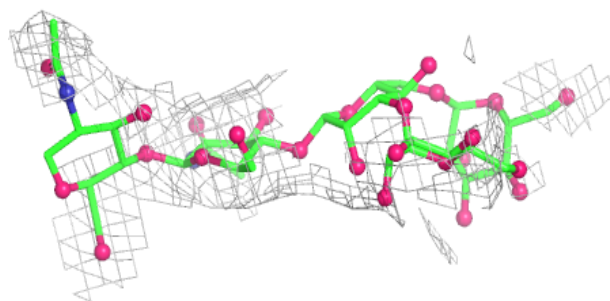
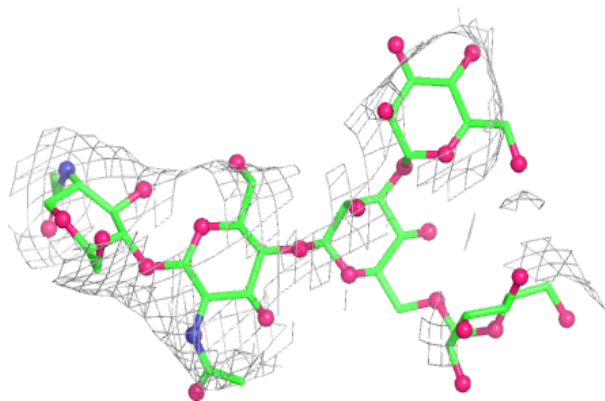
Electron density around Chain b:

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



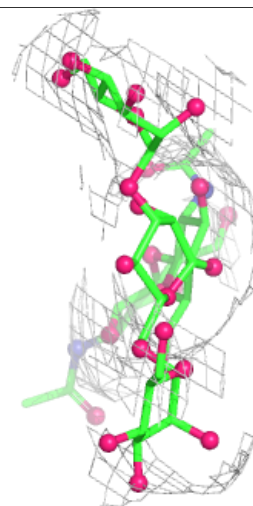
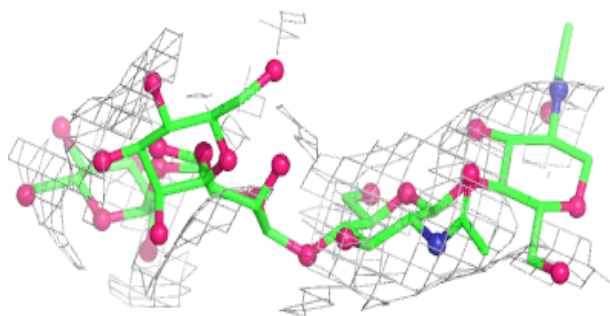
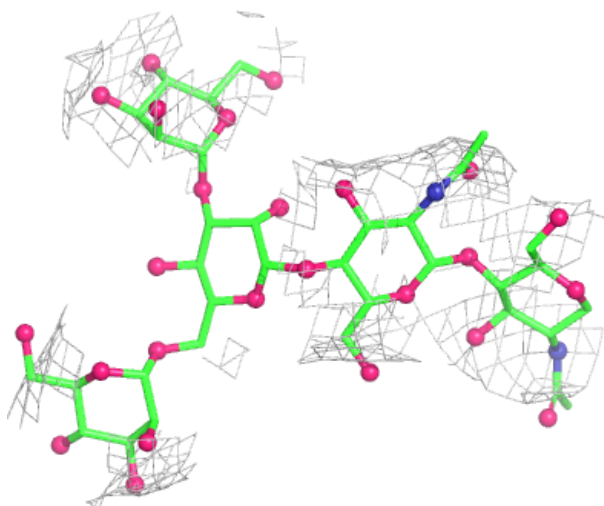
Electron density around Chain c:

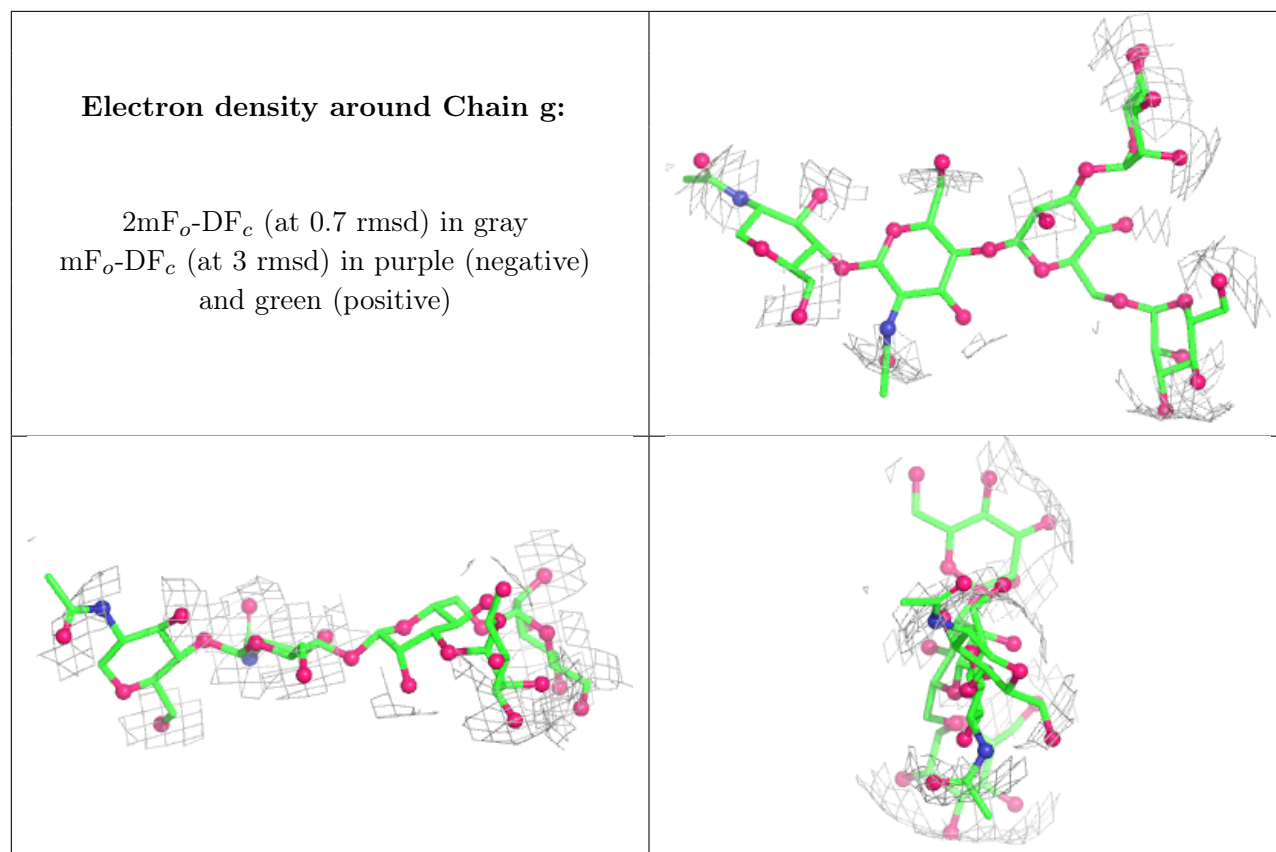
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain d:

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





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.