



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:18 PM UTC

PDB ID : 7KX0 / pdb_00007kx0
Title : Crystal structure of the CD27:CD70 co-stimulatory complex
Authors : Maben, Z.; Liu, W.; Mosyak, L.; Chaparro-Riggers, J.
Deposited on : 2020-12-02
Resolution : 2.69 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

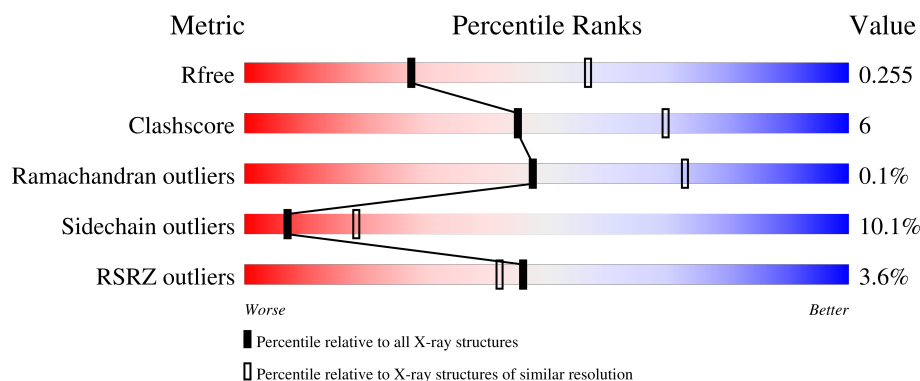
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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	158	4% 70% 17% 11%
1	B	158	2% 66% 20% 11%
1	C	158	4% 69% 18% 11%
2	D	114	7% 70% 16% 12%
2	E	114	0% 68% 17% 13%

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Mol	Chain	Length	Quality of chain
2	F	114	2% 64% 22% 13%
3	G	4	75% 25%
3	I	4	50% 50%
4	H	4	75% 25%
5	J	5	80% 20%
5	L	5	60% 40%
6	K	5	80% 20%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6093 atoms, of which 12 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 CD70 antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	140	Total	C	N	O	S	0	0	0
			1083	678	203	197	5			
1	B	140	Total	C	N	O	S	0	0	0
			1083	678	203	197	5			
1	C	140	Total	C	N	O	S	0	0	0
			1083	678	203	197	5			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	36	HIS	-	expression tag	UNP P32970
A	37	HIS	-	expression tag	UNP P32970
A	38	HIS	-	expression tag	UNP P32970
A	39	HIS	-	expression tag	UNP P32970
A	40	HIS	-	expression tag	UNP P32970
A	41	HIS	-	expression tag	UNP P32970
A	42	GLY	-	expression tag	UNP P32970
A	43	SER	-	expression tag	UNP P32970
A	44	GLY	-	expression tag	UNP P32970
B	36	HIS	-	expression tag	UNP P32970
B	37	HIS	-	expression tag	UNP P32970
B	38	HIS	-	expression tag	UNP P32970
B	39	HIS	-	expression tag	UNP P32970
B	40	HIS	-	expression tag	UNP P32970
B	41	HIS	-	expression tag	UNP P32970
B	42	GLY	-	expression tag	UNP P32970
B	43	SER	-	expression tag	UNP P32970
B	44	GLY	-	expression tag	UNP P32970
C	36	HIS	-	expression tag	UNP P32970
C	37	HIS	-	expression tag	UNP P32970
C	38	HIS	-	expression tag	UNP P32970
C	39	HIS	-	expression tag	UNP P32970
C	40	HIS	-	expression tag	UNP P32970

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Chain	Residue	Modelled	Actual	Comment	Reference
C	41	HIS	-	expression tag	UNP P32970
C	42	GLY	-	expression tag	UNP P32970
C	43	SER	-	expression tag	UNP P32970
C	44	GLY	-	expression tag	UNP P32970

- Molecule 2 is a protein called CD27 antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	100	Total	C	N	O	S	0	0	0
			775	465	149	144	17			
2	E	99	Total	C	N	O	S	0	0	0
			766	459	147	143	17			
2	F	99	Total	C	N	O	S	0	0	0
			766	459	147	143	17			

There are 27 discrepancies between the modelled and reference sequences:

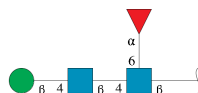
Chain	Residue	Modelled	Actual	Comment	Reference
D	128	GLY	-	expression tag	UNP P26842
D	129	SER	-	expression tag	UNP P26842
D	130	GLY	-	expression tag	UNP P26842
D	131	HIS	-	expression tag	UNP P26842
D	132	HIS	-	expression tag	UNP P26842
D	133	HIS	-	expression tag	UNP P26842
D	134	HIS	-	expression tag	UNP P26842
D	135	HIS	-	expression tag	UNP P26842
D	136	HIS	-	expression tag	UNP P26842
E	128	GLY	-	expression tag	UNP P26842
E	129	SER	-	expression tag	UNP P26842
E	130	GLY	-	expression tag	UNP P26842
E	131	HIS	-	expression tag	UNP P26842
E	132	HIS	-	expression tag	UNP P26842
E	133	HIS	-	expression tag	UNP P26842
E	134	HIS	-	expression tag	UNP P26842
E	135	HIS	-	expression tag	UNP P26842
E	136	HIS	-	expression tag	UNP P26842
F	128	GLY	-	expression tag	UNP P26842
F	129	SER	-	expression tag	UNP P26842
F	130	GLY	-	expression tag	UNP P26842
F	131	HIS	-	expression tag	UNP P26842
F	132	HIS	-	expression tag	UNP P26842
F	133	HIS	-	expression tag	UNP P26842

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Chain	Residue	Modelled	Actual	Comment	Reference
F	134	HIS	-	expression tag	UNP P26842
F	135	HIS	-	expression tag	UNP P26842
F	136	HIS	-	expression tag	UNP P26842

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



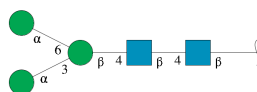
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	4	Total	C	N	O	0	0	0
			49	28	2	19			
3	I	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 4 is an oligosaccharide called 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	H	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 5 is an oligosaccharide called 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.



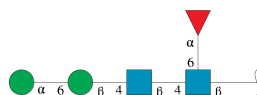
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	J	5	Total	C	N	O	0	0	0
			61	34	2	25			

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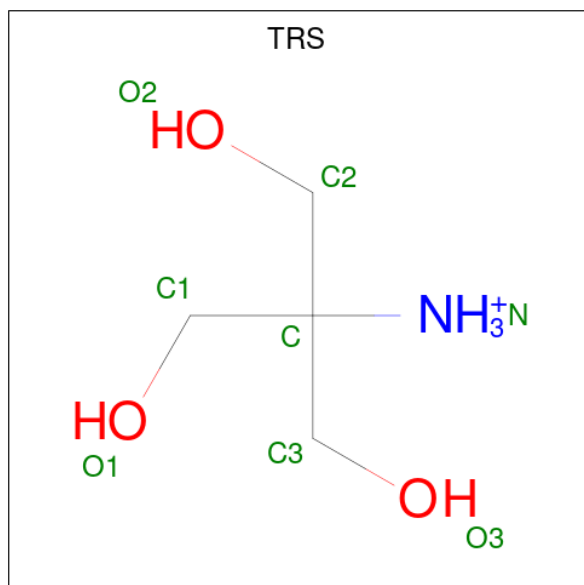
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	L	5	Total	C	N	O	0	0	0
			61	34	2	25			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	K	5	Total	C	N	O	0	0	0
			60	34	2	24			

- Molecule 7 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	C	1	Total	C	H	N	O	0	0
			20	4	12	1	3		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

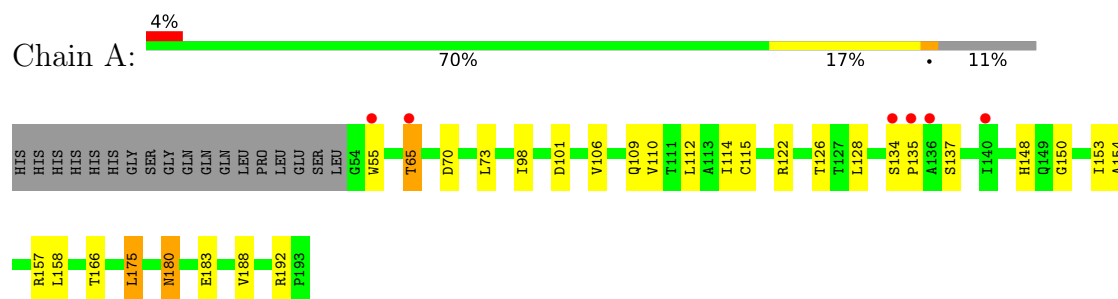
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	27	Total	O	0	0
			27	27		
9	B	33	Total	O	0	0
			33	33		
9	C	28	Total	O	0	0
			28	28		
9	D	17	Total	O	0	0
			17	17		
9	E	13	Total	O	0	0
			13	13		
9	F	27	Total	O	0	0
			27	27		

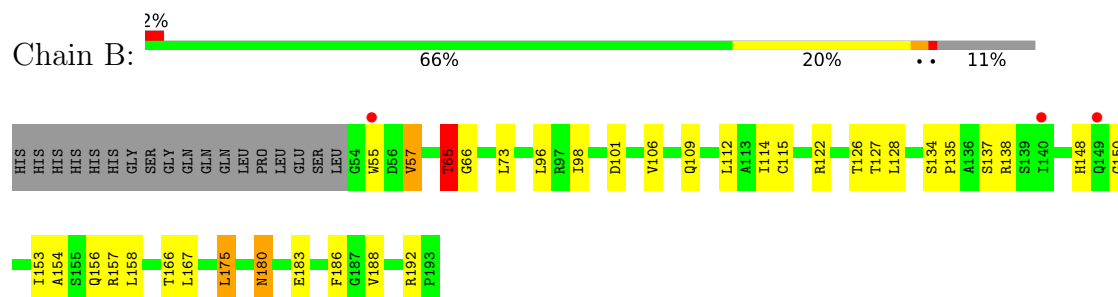
3 Residue-property plots [i](#)

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.

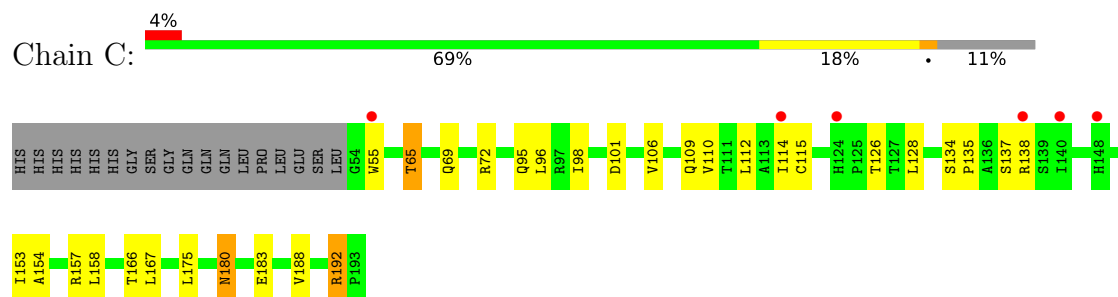
- Molecule 1: CD70 antigen



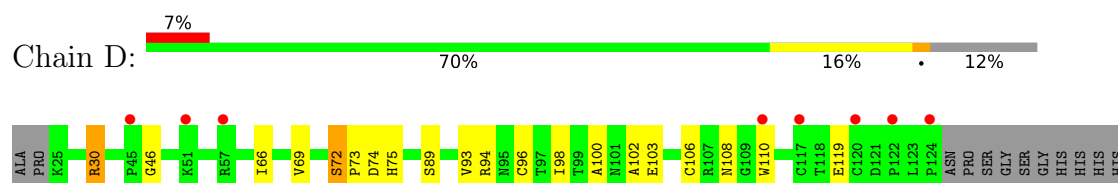
- Molecule 1: CD70 antigen



- Molecule 1: CD70 antigen



- Molecule 2: CD27 antigen



HIS
HIS

- Molecule 2: CD27 antigen



ALA	PRO	LYS	S26	C27	P28	E29	R30	H31	K37	G46	T47	F49	I66	V69	S72	H75	C81	S89	V93	C96	T97	I98	A102	E103	C106	R107	N108	G109	W110	E119	P124	ASN	PRO	SER	GLY	SER	GLY	HIS	HIS	HIS	HIS	HIS	HIS
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- Molecule 2: CD27 antigen



ALA	PRO	LYS	S26	R30	H31	Y32	K37	L38	C39	C40	C43	E44	P45	G46	Q61	I66	V69	S72	P73	D74	H75	R85	S89	V93	R94	N95	C96	T97	I98	T99	A100	N101	A102	C106	R107	N108	G109	W110	E119	P124	ASN	PRO	SER	GLY	SER	GLY
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HIS
HIS
HIS
HIS
HIS
HIS

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

MAG1
MAG2
BMA3
FUC4

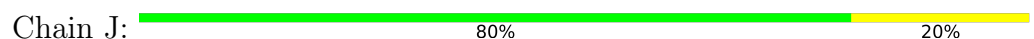
- Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

MAG1
MAG2
BMA3
FUC4

- Molecule 4: 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

MAG1
MAG2
BMA3
MAN4

- 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





- 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 L:  60% 40%



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

Chain K:  80% 20%



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	109.53Å 113.63Å 163.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.72 – 2.69 36.72 – 2.69	Depositor EDS
% Data completeness (in resolution range)	64.9 (36.72-2.69) 60.2 (36.72-2.69)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.98 (at 2.69Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.200 , 0.236 0.213 , 0.255	Depositor DCC
R_{free} test set	915 reflections (3.19%)	wwPDB-VP
Wilson B-factor (Å ²)	54.4	Xtriage
Anisotropy	0.119	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 89.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for $-1/2^*h+1/2^*k+1/2^*l, 1/2^*h-1/2^*k+1/2^*l, h+k$ 0.025 for $-1/2^*h+1/2^*k-1/2^*l, 1/2^*h-1/2^*k-1/2^*l, -h-k$ 0.001 for $k, h, -l$ 0.044 for $-1/2^*h-1/2^*k+1/2^*l, -1/2^*h-1/2^*k-1/2^*l, h-k$ 0.019 for $-1/2^*h-1/2^*k-1/2^*l, -1/2^*h-1/2^*k+1/2^*l, -h+k$	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6093	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, TRS, BMA, FUC, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.80	0/1110	1.22	4/1513 (0.3%)
1	B	0.80	0/1110	1.24	4/1513 (0.3%)
1	C	0.81	0/1110	1.21	3/1513 (0.2%)
2	D	0.74	0/795	1.22	0/1076
2	E	0.75	0/786	1.22	2/1065 (0.2%)
2	F	0.74	0/786	1.18	0/1065
All	All	0.78	0/5697	1.22	13/7745 (0.2%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	65	THR	N-CA-C	-6.32	98.91	108.96
1	A	65	THR	N-CA-C	-5.99	99.44	108.96
1	C	180	ASN	CA-C-N	5.50	127.66	120.28
1	C	180	ASN	C-N-CA	5.50	127.66	120.28
1	A	180	ASN	CA-C-N	5.50	127.65	120.28
1	A	180	ASN	C-N-CA	5.50	127.65	120.28
2	E	107	ARG	CA-C-N	5.46	129.01	120.82
2	E	107	ARG	C-N-CA	5.46	129.01	120.82
1	B	180	ASN	CA-C-N	5.42	127.55	120.28
1	B	180	ASN	C-N-CA	5.42	127.55	120.28
1	A	70	ASP	CA-CB-CG	5.17	117.77	112.60
1	C	65	THR	N-CA-C	-5.12	100.95	109.46
1	B	186	PHE	CA-CB-CG	5.10	118.90	113.80

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	1083	0	1067	11	0
1	B	1083	0	1067	14	0
1	C	1083	0	1067	14	0
2	D	775	0	705	13	0
2	E	766	0	692	9	0
2	F	766	0	692	12	0
3	G	49	0	43	0	0
3	I	49	0	43	0	0
4	H	50	0	43	0	0
5	J	61	0	52	0	0
5	L	61	0	52	0	0
6	K	60	0	52	0	0
7	C	8	12	12	1	0
8	D	14	0	13	0	0
8	E	14	0	13	0	0
8	F	14	0	13	0	0
9	A	27	0	0	0	0
9	B	33	0	0	1	0
9	C	28	0	0	0	0
9	D	17	0	0	0	0
9	E	13	0	0	0	0
9	F	27	0	0	0	0
All	All	6081	12	5626	68	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 6.

All (68) 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:D:30:ARG:HH22	2:D:75:HIS:HD2	1.18	0.91
2:D:30:ARG:HH22	2:D:75:HIS:CD2	1.94	0.85
1:B:57:VAL:HG21	1:C:192:ARG:HG3	1.67	0.76
2:F:45:PRO:HD3	2:F:75:HIS:CE1	2.30	0.66
2:D:89:SER:HB3	2:D:119:GLU:HA	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:ALA:H	7:C:201:TRS:H31	1.69	0.57
1:A:112:LEU:HD21	1:A:126:THR:HG21	1.86	0.57
2:D:30:ARG:HH11	2:D:30:ARG:HB2	1.70	0.57
1:B:112:LEU:HD21	1:B:126:THR:HG21	1.87	0.56
1:C:72:ARG:HD2	1:C:95:GLN:NE2	2.22	0.55
1:A:134:SER:OG	1:A:135:PRO:HD3	2.07	0.55
2:E:46:GLY:H	2:E:72:SER:HB3	1.71	0.54
1:A:180:ASN:HB2	1:A:183:GLU:HG2	1.89	0.54
1:C:134:SER:OG	1:C:135:PRO:HD3	2.07	0.54
1:B:180:ASN:HB2	1:B:183:GLU:HG2	1.90	0.53
1:C:180:ASN:HB2	1:C:183:GLU:HG2	1.89	0.52
2:F:89:SER:HB3	2:F:119:GLU:HA	1.91	0.52
1:B:134:SER:OG	1:B:135:PRO:HD3	2.10	0.52
2:D:30:ARG:HB2	2:D:30:ARG:NH1	2.24	0.52
2:E:89:SER:HB3	2:E:119:GLU:HA	1.92	0.51
1:A:128:LEU:HD22	1:A:153:ILE:HD11	1.93	0.51
1:B:128:LEU:HD22	1:B:153:ILE:HD11	1.93	0.51
2:E:96:CYS:HB2	2:E:102:ALA:HB2	1.94	0.49
2:E:48:PHE:HD2	2:E:81:CYS:SG	2.36	0.48
1:B:138:ARG:HH11	2:F:73:PRO:HD2	1.79	0.48
2:F:32:TYR:CE1	2:F:40:CYS:HB2	2.48	0.48
1:A:148:HIS:C	1:A:150:GLY:H	2.22	0.47
2:F:85:ARG:HB2	2:F:101:ASN:HD21	1.79	0.47
2:E:28:PRO:O	2:E:31:HIS:HB2	2.14	0.47
2:F:106:CYS:HB3	2:F:110:TRP:HB3	1.97	0.47
1:C:112:LEU:HD21	1:C:126:THR:HG21	1.97	0.47
1:C:109:GLN:HG3	1:C:154:ALA:HB2	1.97	0.46
1:B:148:HIS:C	1:B:150:GLY:H	2.24	0.46
2:D:30:ARG:HH12	2:D:75:HIS:HB3	1.81	0.46
2:F:46:GLY:H	2:F:72:SER:HB3	1.79	0.46
2:E:106:CYS:HB3	2:E:110:TRP:HB3	1.97	0.46
2:D:106:CYS:HB3	2:D:110:TRP:HB3	1.99	0.45
1:A:109:GLN:HG3	1:A:154:ALA:HB2	1.97	0.45
1:C:110:VAL:HG21	1:C:128:LEU:HD13	1.99	0.45
1:B:109:GLN:HG3	1:B:154:ALA:HB2	1.99	0.44
1:C:138:ARG:HH11	2:D:73:PRO:HD2	1.83	0.44
2:E:30:ARG:HH22	2:E:75:HIS:HD2	1.64	0.43
2:F:66:ILE:HB	2:F:69:VAL:HB	2.00	0.43
1:A:135:PRO:C	1:A:137:SER:H	2.27	0.43
2:D:46:GLY:H	2:D:72:SER:HB3	1.84	0.43
1:A:110:VAL:HG21	1:A:128:LEU:HD13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:LEU:HD23	1:B:175:LEU:HD13	2.02	0.42
1:C:134:SER:CB	1:C:166:THR:H	2.32	0.42
2:E:66:ILE:HB	2:E:69:VAL:HB	2.00	0.42
1:A:112:LEU:HD23	1:A:175:LEU:HD13	2.02	0.42
2:D:66:ILE:HB	2:D:69:VAL:HB	2.01	0.42
1:C:128:LEU:HD22	1:C:153:ILE:HD11	2.01	0.42
1:C:135:PRO:C	1:C:137:SER:H	2.27	0.42
2:F:46:GLY:HA2	2:F:98:ILE:O	2.19	0.42
1:C:96:LEU:HD23	1:C:167:LEU:HD12	2.01	0.41
2:D:96:CYS:HB2	2:D:102:ALA:HB2	2.01	0.41
1:C:137:SER:HB2	2:D:74:ASP:HB3	2.02	0.41
2:E:46:GLY:HA2	2:E:98:ILE:O	2.21	0.41
1:B:135:PRO:C	1:B:137:SER:H	2.28	0.41
1:B:57:VAL:CG2	1:C:192:ARG:HG3	2.45	0.41
1:B:65:THR:HG23	9:B:201:HOH:O	2.20	0.41
1:B:96:LEU:HD23	1:B:167:LEU:HD12	2.04	0.40
1:B:134:SER:CB	1:B:166:THR:H	2.34	0.40
2:F:43:CYS:O	2:F:75:HIS:HA	2.21	0.40
2:D:94:ARG:HH11	2:D:100:ALA:HB3	1.87	0.40
2:F:94:ARG:HH21	2:F:100:ALA:HB3	1.86	0.40
2:F:96:CYS:HB2	2:F:102:ALA:HB2	2.03	0.40
1:A:134:SER:CB	1:A:166:THR:H	2.33	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	138/158 (87%)	124 (90%)	14 (10%)	0	100	100
1	B	138/158 (87%)	124 (90%)	13 (9%)	1 (1%)	18	41
1	C	138/158 (87%)	123 (89%)	15 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	98/114 (86%)	94 (96%)	4 (4%)	0	100	100
2	E	97/114 (85%)	91 (94%)	6 (6%)	0	100	100
2	F	97/114 (85%)	90 (93%)	7 (7%)	0	100	100
All	All	706/816 (86%)	646 (92%)	59 (8%)	1 (0%)	48	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	66	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	119/135 (88%)	105 (88%)	14 (12%)	5	13
1	B	119/135 (88%)	102 (86%)	17 (14%)	3	8
1	C	119/135 (88%)	106 (89%)	13 (11%)	6	16
2	D	89/100 (89%)	83 (93%)	6 (7%)	15	36
2	E	88/100 (88%)	81 (92%)	7 (8%)	11	28
2	F	88/100 (88%)	82 (93%)	6 (7%)	14	35
All	All	622/705 (88%)	559 (90%)	63 (10%)	7	18

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	TRP
1	A	65	THR
1	A	73	LEU
1	A	98	ILE
1	A	101	ASP
1	A	106	VAL
1	A	114	ILE

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Mol	Chain	Res	Type
1	A	115	CYS
1	A	122	ARG
1	A	157	ARG
1	A	158	LEU
1	A	175	LEU
1	A	188	VAL
1	A	192	ARG
1	B	55	TRP
1	B	57	VAL
1	B	65	THR
1	B	73	LEU
1	B	98	ILE
1	B	101	ASP
1	B	106	VAL
1	B	114	ILE
1	B	115	CYS
1	B	122	ARG
1	B	127	THR
1	B	156	GLN
1	B	157	ARG
1	B	158	LEU
1	B	175	LEU
1	B	188	VAL
1	B	192	ARG
1	C	55	TRP
1	C	65	THR
1	C	69	GLN
1	C	98	ILE
1	C	101	ASP
1	C	106	VAL
1	C	114	ILE
1	C	115	CYS
1	C	157	ARG
1	C	158	LEU
1	C	175	LEU
1	C	188	VAL
1	C	192	ARG
2	D	30	ARG
2	D	72	SER
2	D	93	VAL
2	D	98	ILE
2	D	103	GLU

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Mol	Chain	Res	Type
2	D	108	ASN
2	E	30	ARG
2	E	37	LYS
2	E	72	SER
2	E	93	VAL
2	E	98	ILE
2	E	103	GLU
2	E	108	ASN
2	F	30	ARG
2	F	38	LEU
2	F	61	GLN
2	F	72	SER
2	F	93	VAL
2	F	108	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	GLN
1	A	64	HIS
1	A	76	GLN
1	A	99	HIS
1	A	107	HIS
1	A	109	GLN
1	A	189	GLN
1	B	61	GLN
1	B	76	GLN
1	B	99	HIS
1	B	107	HIS
1	B	109	GLN
1	B	149	GLN
1	B	189	GLN
1	C	61	GLN
1	C	76	GLN
1	C	95	GLN
1	C	99	HIS
1	C	107	HIS
1	C	109	GLN
1	C	148	HIS
1	C	149	GLN
1	C	189	GLN
2	D	56	HIS

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Mol	Chain	Res	Type
2	D	61	GLN
2	D	75	HIS
2	D	111	GLN
2	E	31	HIS
2	E	56	HIS
2	E	61	GLN
2	E	75	HIS
2	E	80	HIS
2	F	61	GLN
2	F	80	HIS

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 ⓘ

27 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	G	1	1,3	14,14,15	0.34	0	17,19,21	0.65	0
3	NAG	G	2	3	14,14,15	0.39	0	17,19,21	0.97	2 (11%)
3	BMA	G	3	3	11,11,12	0.33	0	15,15,17	0.53	0
3	FUC	G	4	3	10,10,11	0.42	0	14,14,16	0.77	0
4	NAG	H	1	1,4	14,14,15	0.34	0	17,19,21	0.78	0
4	NAG	H	2	4	14,14,15	0.32	0	17,19,21	0.81	0
4	BMA	H	3	4	11,11,12	0.33	0	15,15,17	0.86	1 (6%)
4	MAN	H	4	4	11,11,12	0.37	0	15,15,17	0.73	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	I	1	1,3	14,14,15	0.31	0	17,19,21	0.69	0
3	NAG	I	2	3	14,14,15	0.39	0	17,19,21	1.40	2 (11%)
3	BMA	I	3	3	11,11,12	0.32	0	15,15,17	0.76	1 (6%)
3	FUC	I	4	3	10,10,11	0.39	0	14,14,16	0.55	0
5	NAG	J	1	1,5	14,14,15	0.31	0	17,19,21	0.73	0
5	NAG	J	2	5	14,14,15	0.27	0	17,19,21	0.60	0
5	BMA	J	3	5	11,11,12	0.31	0	15,15,17	0.60	0
5	MAN	J	4	5	11,11,12	0.36	0	15,15,17	0.77	0
5	MAN	J	5	5	11,11,12	0.34	0	15,15,17	0.94	1 (6%)
6	NAG	K	1	1,6	14,14,15	0.31	0	17,19,21	0.59	0
6	NAG	K	2	6	14,14,15	0.25	0	17,19,21	0.50	0
6	BMA	K	3	6	11,11,12	0.32	0	15,15,17	0.63	0
6	MAN	K	4	6	11,11,12	0.35	0	15,15,17	0.75	1 (6%)
6	FUC	K	5	6	10,10,11	0.42	0	14,14,16	0.75	0
5	NAG	L	1	1,5	14,14,15	0.34	0	17,19,21	0.71	0
5	NAG	L	2	5	14,14,15	0.28	0	17,19,21	0.66	0
5	BMA	L	3	5	11,11,12	0.31	0	15,15,17	0.66	1 (6%)
5	MAN	L	4	5	11,11,12	0.38	0	15,15,17	0.79	0
5	MAN	L	5	5	11,11,12	0.31	0	15,15,17	0.73	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MAN	J	4	5	-	0/2/19/22	0/1/1/1
5	MAN	J	5	5	-	0/2/19/22	1/1/1/1
6	NAG	K	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	K	2	6	-	0/6/23/26	0/1/1/1
6	BMA	K	3	6	-	2/2/19/22	0/1/1/1
6	MAN	K	4	6	-	1/2/19/22	1/1/1/1
6	FUC	K	5	6	-	-	0/1/1/1
5	NAG	L	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	L	2	5	-	0/6/23/26	0/1/1/1
5	BMA	L	3	5	-	0/2/19/22	0/1/1/1
5	MAN	L	4	5	-	0/2/19/22	0/1/1/1
5	MAN	L	5	5	-	1/2/19/22	1/1/1/1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	2	NAG	C1-O5-C5	3.96	117.49	112.19
5	J	5	MAN	C1-O5-C5	3.28	116.58	112.19
3	I	2	NAG	C1-C2-N2	3.06	115.25	110.43
3	G	2	NAG	C1-O5-C5	2.74	115.86	112.19
4	H	3	BMA	C1-O5-C5	2.72	115.83	112.19
6	K	4	MAN	C1-O5-C5	2.72	115.83	112.19
5	L	5	MAN	C1-O5-C5	2.44	115.46	112.19
3	I	3	BMA	C1-O5-C5	2.42	115.43	112.19
3	G	2	NAG	O4-C4-C3	2.30	115.80	110.38
5	L	3	BMA	C1-O5-C5	2.13	115.04	112.19

There are no chirality outliers.

All (9) torsion outliers are listed below:

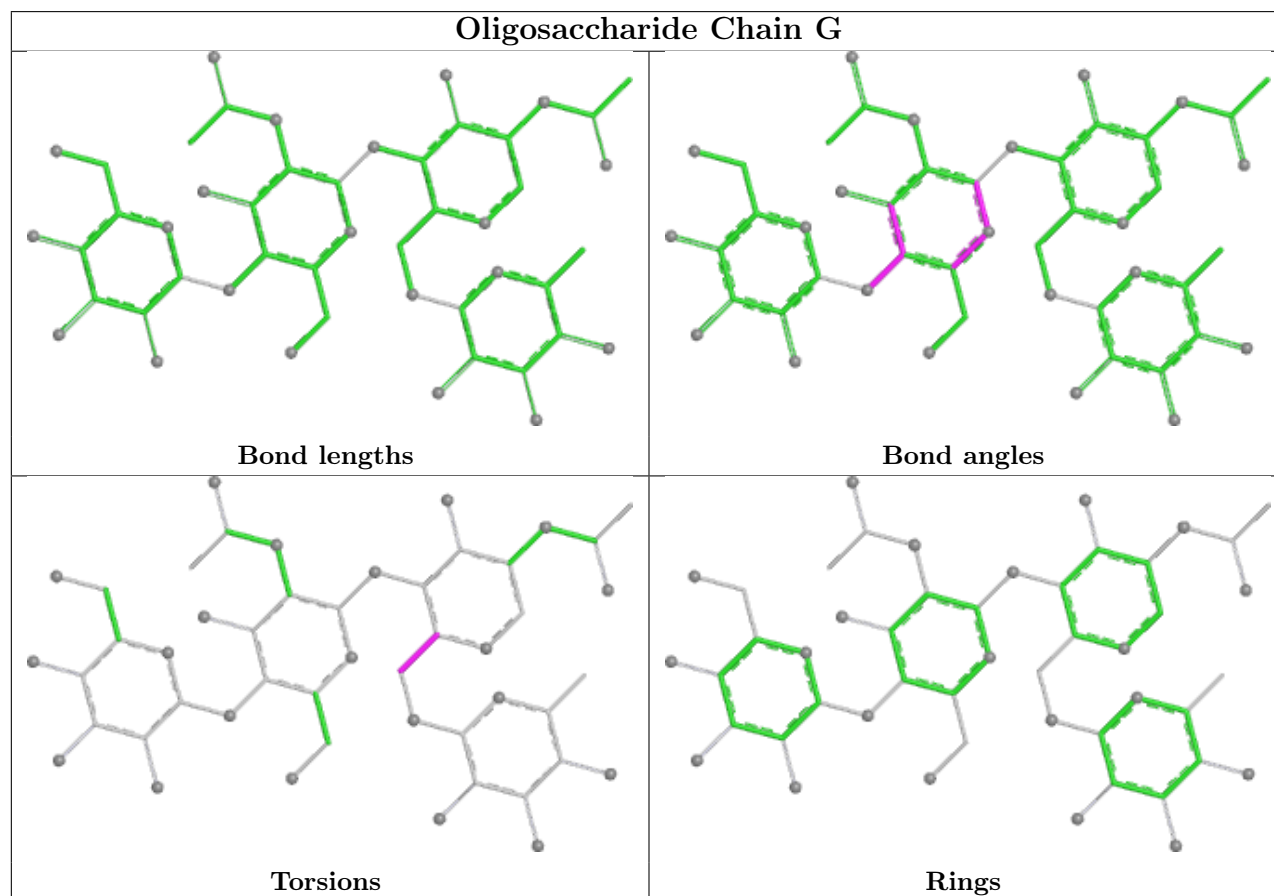
Mol	Chain	Res	Type	Atoms
6	K	4	MAN	O5-C5-C6-O6
5	L	5	MAN	O5-C5-C6-O6
6	K	3	BMA	C4-C5-C6-O6
3	I	1	NAG	C4-C5-C6-O6
6	K	1	NAG	C4-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
6	K	3	BMA	O5-C5-C6-O6
3	I	1	NAG	O5-C5-C6-O6
6	K	1	NAG	O5-C5-C6-O6

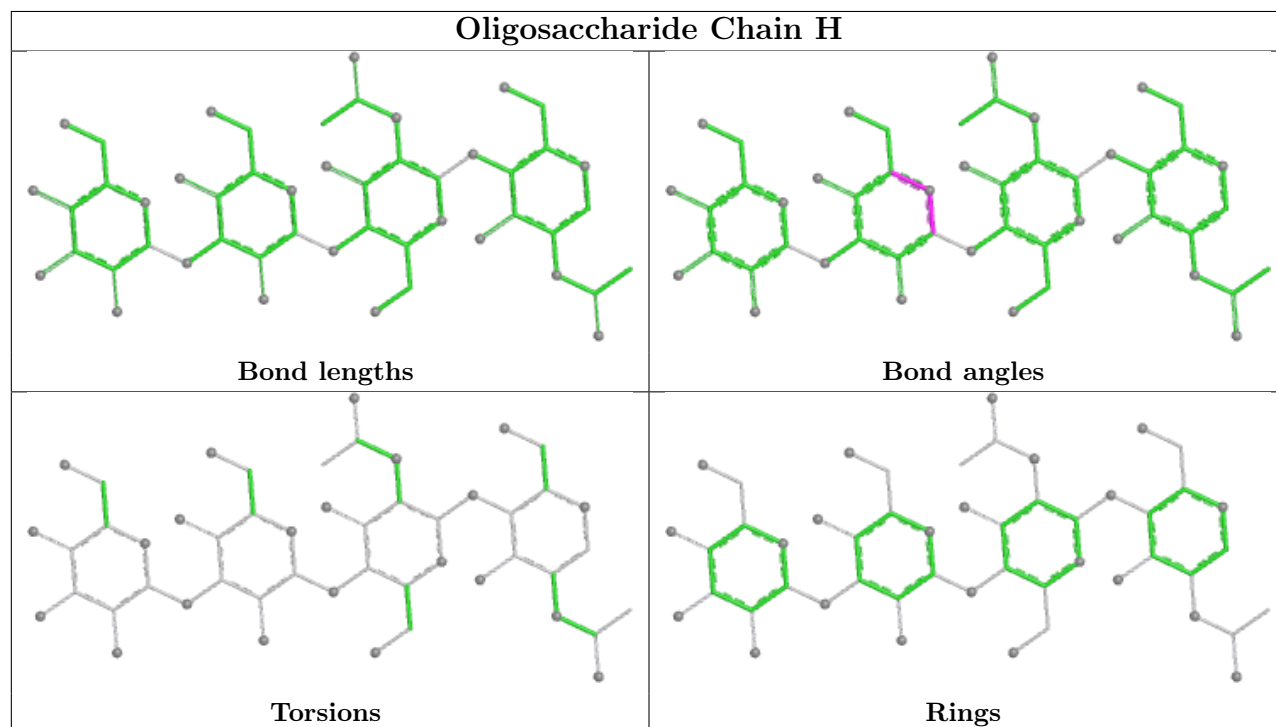
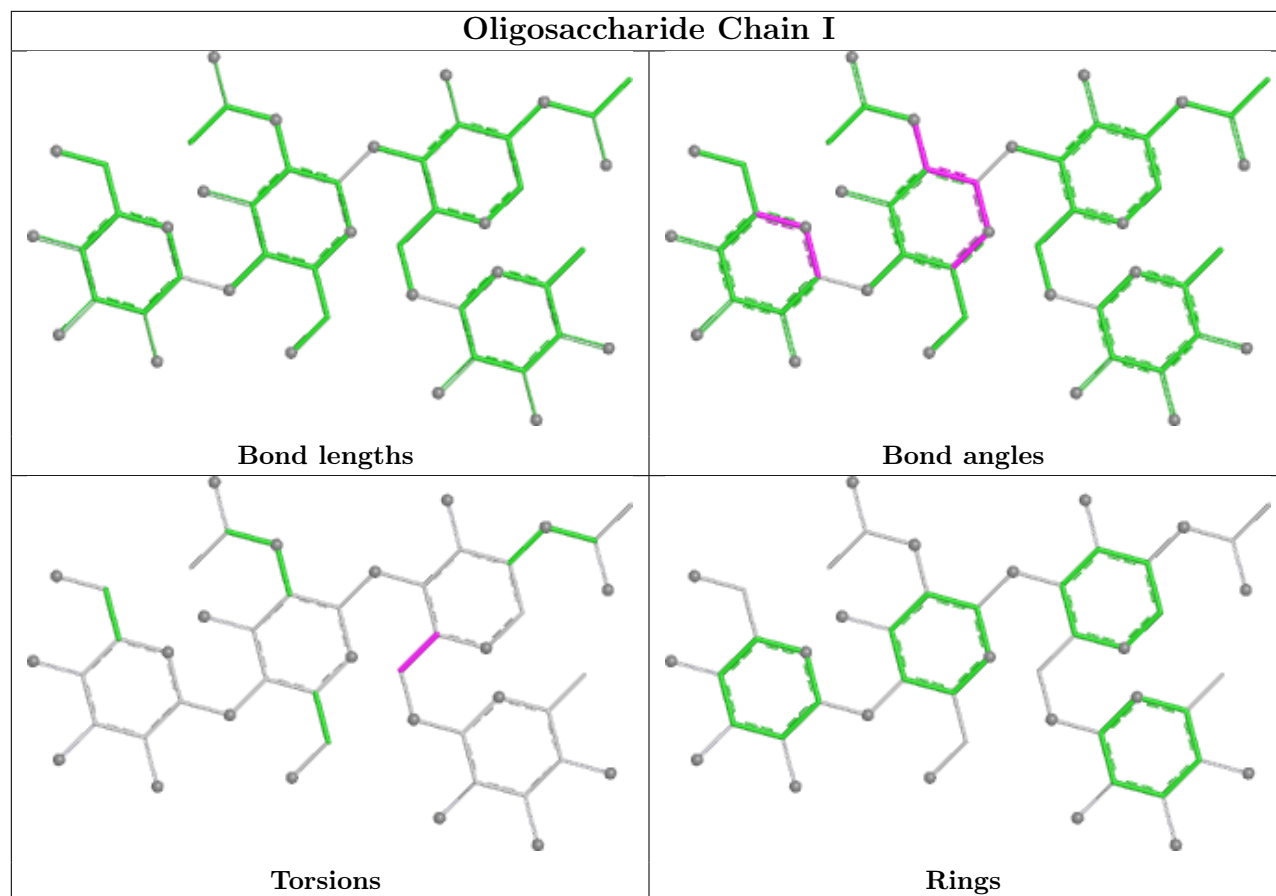
All (3) ring outliers are listed below:

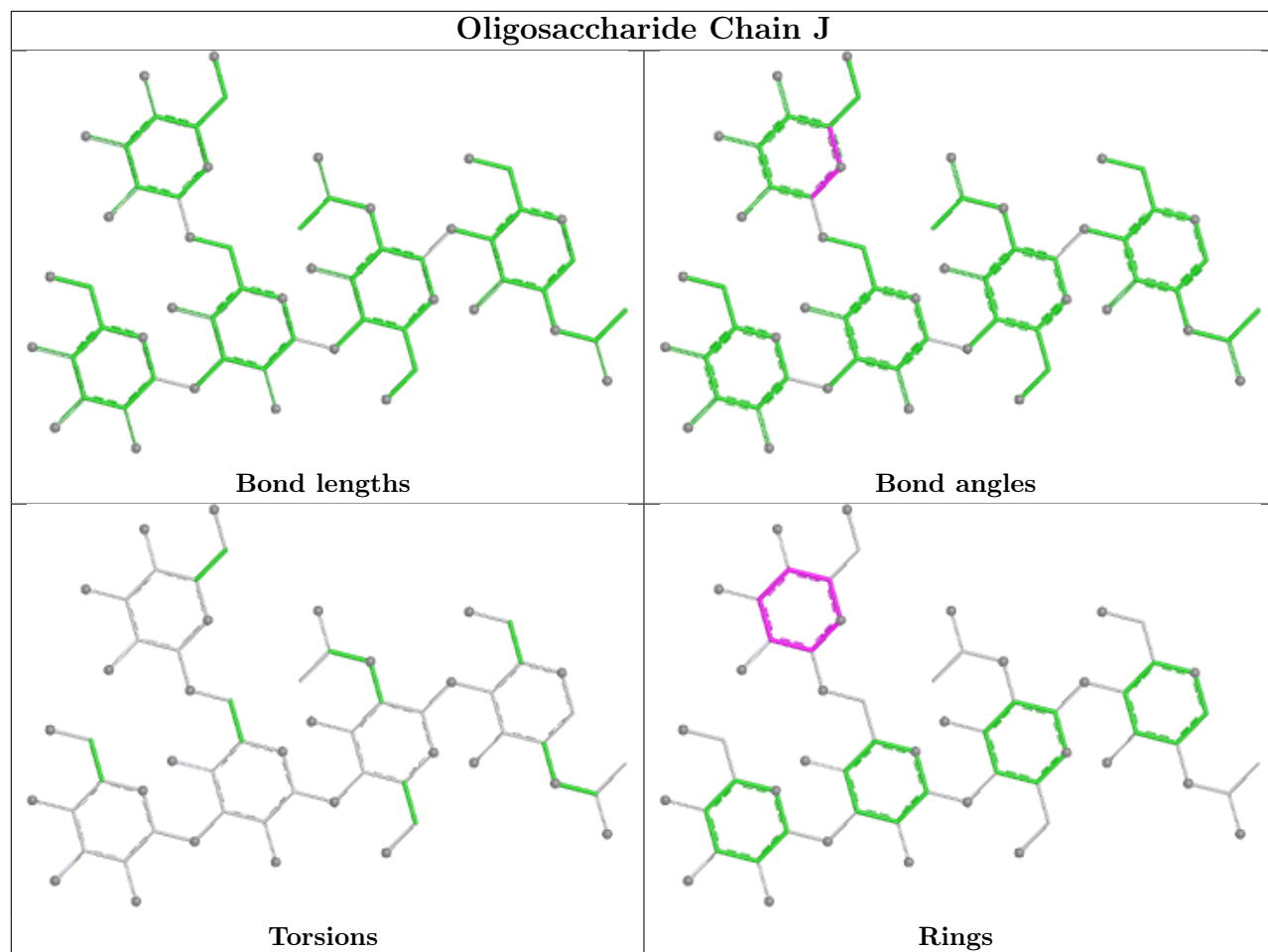
Mol	Chain	Res	Type	Atoms
5	L	5	MAN	C1-C2-C3-C4-C5-O5
5	J	5	MAN	C1-C2-C3-C4-C5-O5
6	K	4	MAN	C1-C2-C3-C4-C5-O5

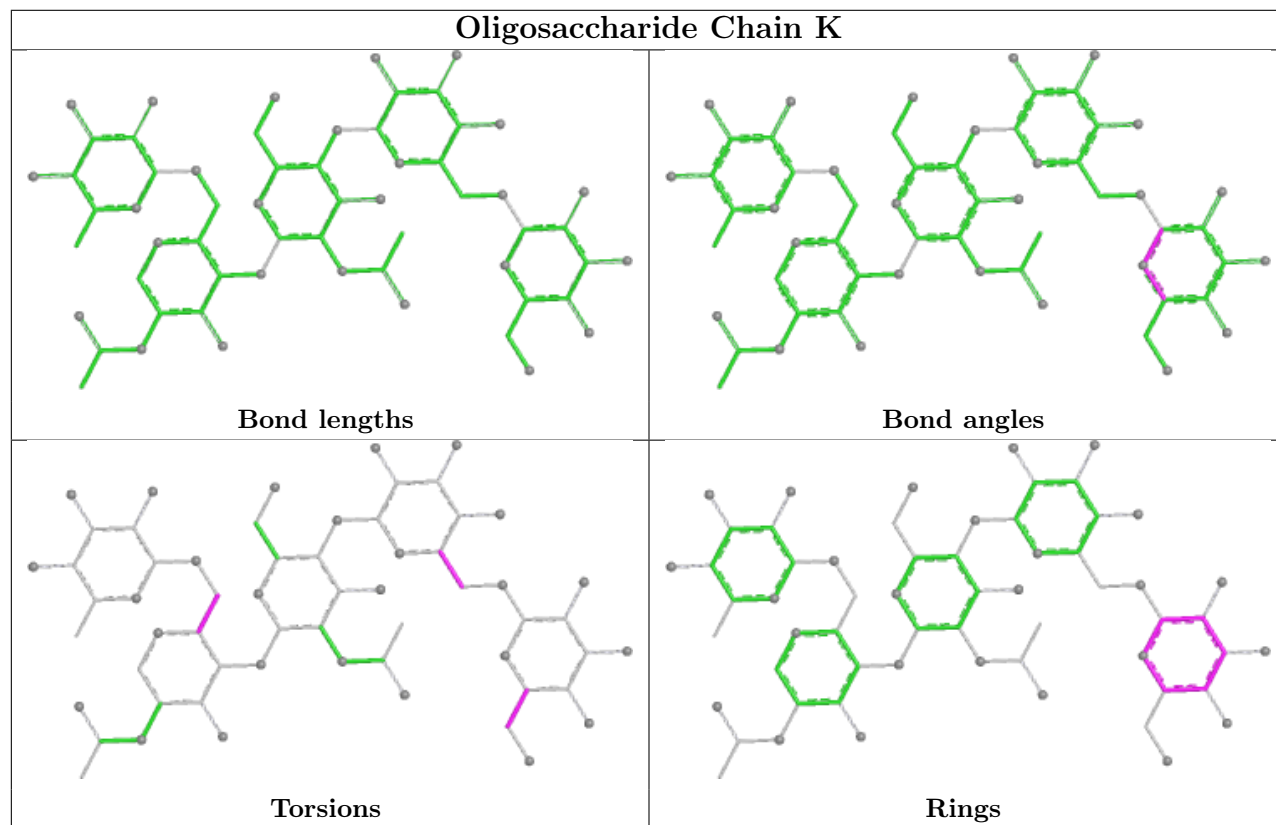
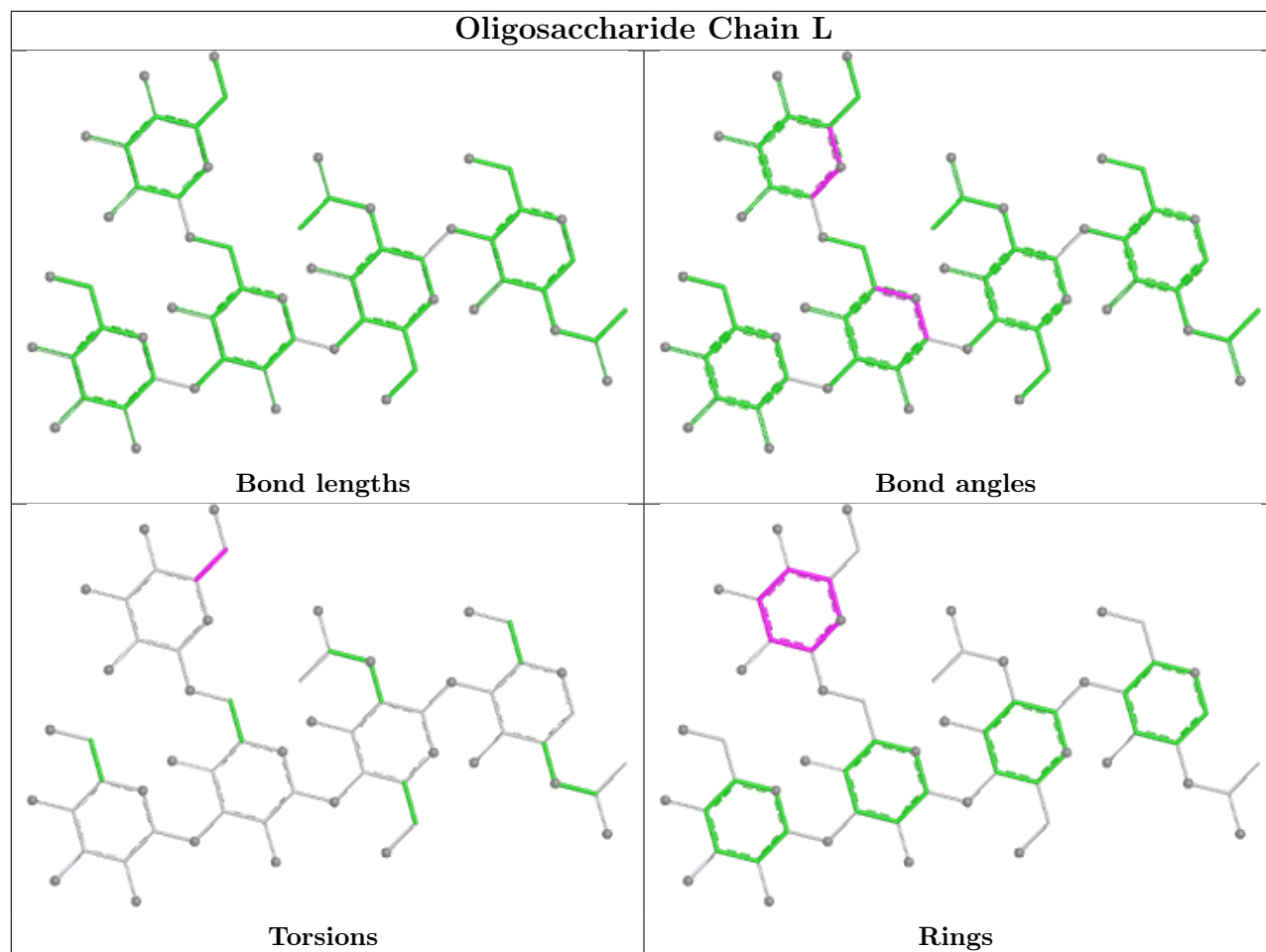
No monomer is involved in short contacts.

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









5.6 Ligand geometry

4 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
8	NAG	F	201	2	14,14,15	0.33	0	17,19,21	0.78	1 (5%)
8	NAG	D	201	2	14,14,15	0.31	0	17,19,21	0.75	1 (5%)
7	TRS	C	201	-	7,7,7	0.32	0	9,9,9	0.29	0
8	NAG	E	201	2	14,14,15	0.32	0	17,19,21	0.76	1 (5%)

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
8	NAG	F	201	2	-	0/6/23/26	0/1/1/1
8	NAG	D	201	2	-	0/6/23/26	0/1/1/1
7	TRS	C	201	-	-	6/9/9/9	-
8	NAG	E	201	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	F	201	NAG	C1-O5-C5	2.70	115.80	112.19
8	D	201	NAG	C1-O5-C5	2.45	115.47	112.19
8	E	201	NAG	C1-O5-C5	2.32	115.29	112.19

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	201	TRS	C1-C-C3-O3

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Mol	Chain	Res	Type	Atoms
7	C	201	TRS	C2-C-C3-O3
7	C	201	TRS	N-C-C3-O3
7	C	201	TRS	C1-C-C2-O2
7	C	201	TRS	C3-C-C2-O2
7	C	201	TRS	N-C-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	201	TRS	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	140/158 (88%)	0.42	6 (4%) 40 36	58, 80, 119, 155	0
1	B	140/158 (88%)	0.39	3 (2%) 63 61	58, 81, 122, 174	0
1	C	140/158 (88%)	0.39	6 (4%) 40 36	60, 81, 122, 168	0
2	D	100/114 (87%)	0.68	8 (8%) 18 15	71, 97, 202, 267	0
2	E	99/114 (86%)	0.31	1 (1%) 79 78	68, 94, 150, 247	0
2	F	99/114 (86%)	0.30	2 (2%) 65 62	65, 87, 139, 231	0
All	All	718/816 (87%)	0.41	26 (3%) 46 42	58, 87, 142, 267	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	37	LYS	3.5
2	F	124	PRO	3.3
1	C	138	ARG	3.2
2	D	122	PRO	3.1
2	D	124	PRO	3.1
1	C	55	TRP	3.0
1	A	55	TRP	2.9
1	A	134	SER	2.9
2	D	120	CYS	2.8
2	E	124	PRO	2.7
1	A	136	ALA	2.7
2	D	117	CYS	2.5
2	D	45	PRO	2.4
1	A	140	ILE	2.3
1	C	114	ILE	2.3
2	D	51	LYS	2.3
1	A	135	PRO	2.3
1	B	149	GLN	2.2
1	B	55	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
2	D	57	ARG	2.1
2	D	110	TRP	2.1
1	A	65	THR	2.1
1	B	140	ILE	2.1
1	C	140	ILE	2.1
1	C	124	HIS	2.0
1	C	148	HIS	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.

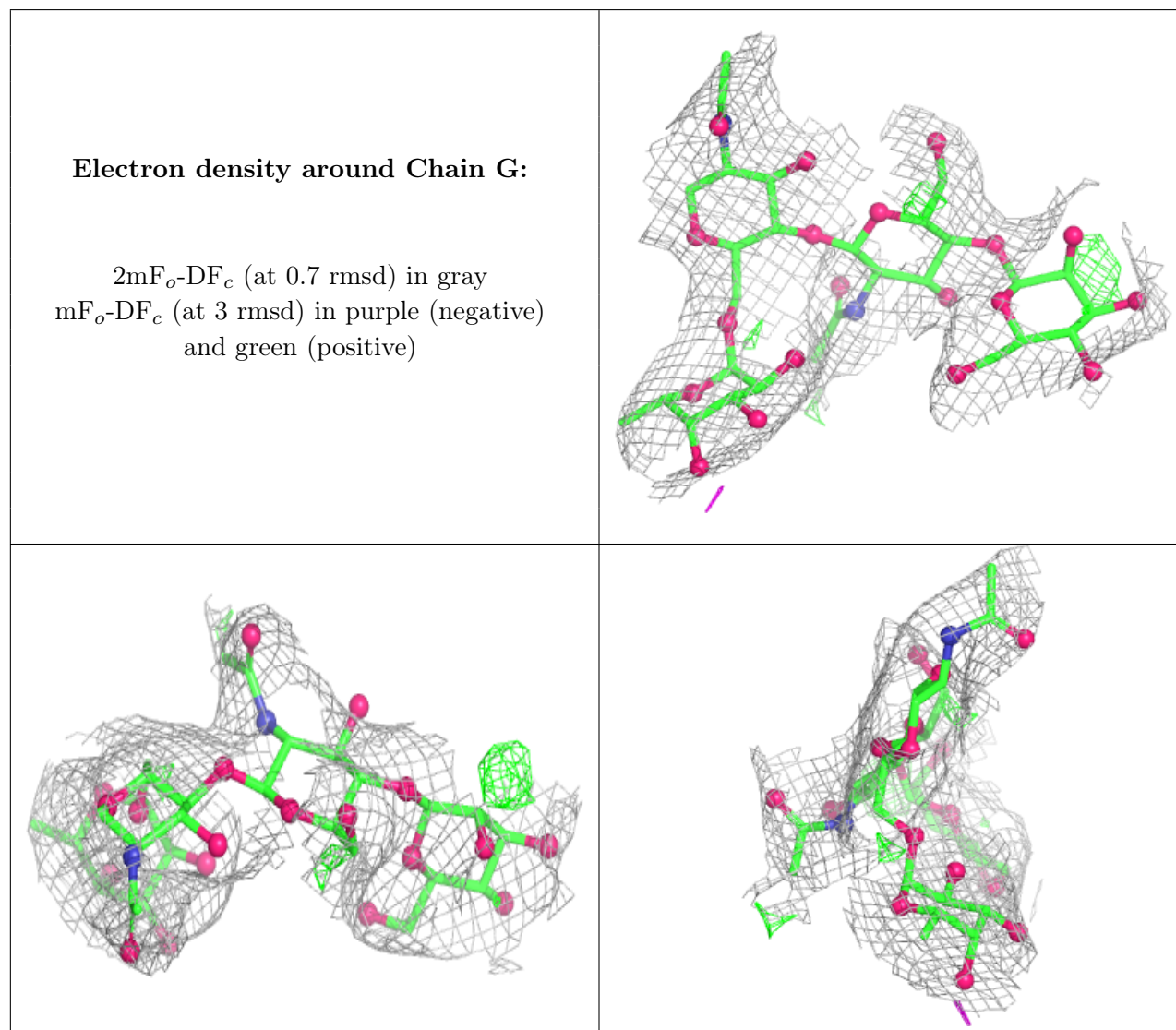
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MAN	J	5	11/12	0.25	0.22	242,244,247,249	0
3	BMA	I	3	11/12	0.28	0.16	241,248,252,255	0
3	BMA	G	3	11/12	0.36	0.14	238,241,250,250	0
4	BMA	H	3	11/12	0.37	0.18	233,239,246,252	0
5	MAN	L	5	11/12	0.39	0.24	253,255,258,260	0
5	BMA	L	3	11/12	0.44	0.20	250,256,263,275	0
6	MAN	K	4	11/12	0.50	0.15	242,248,254,257	0
3	NAG	G	2	14/15	0.52	0.17	169,206,228,231	0
6	BMA	K	3	11/12	0.53	0.12	230,237,241,245	0
4	MAN	H	4	11/12	0.61	0.29	256,265,275,276	0
5	BMA	J	3	11/12	0.64	0.21	244,249,260,269	0
3	NAG	I	2	14/15	0.64	0.19	212,226,232,236	0
6	NAG	K	2	14/15	0.66	0.17	191,215,223,224	0
5	MAN	L	4	11/12	0.70	0.24	279,283,287,287	0
5	MAN	J	4	11/12	0.74	0.26	273,277,279,281	0
4	NAG	H	2	14/15	0.76	0.23	142,159,207,224	0
5	NAG	J	2	14/15	0.77	0.20	150,181,222,236	0
3	FUC	G	4	10/11	0.77	0.16	129,132,136,138	0
5	NAG	L	2	14/15	0.82	0.23	158,210,233,243	0
6	FUC	K	5	10/11	0.83	0.15	136,137,139,147	0
3	FUC	I	4	10/11	0.85	0.16	136,138,142,159	0

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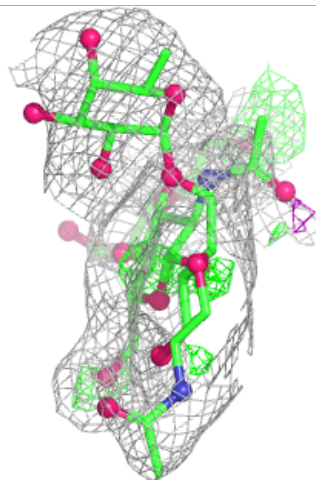
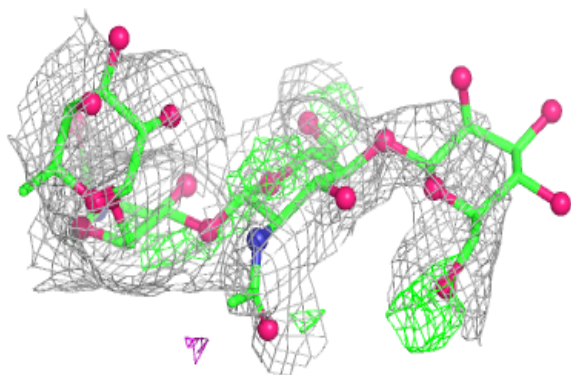
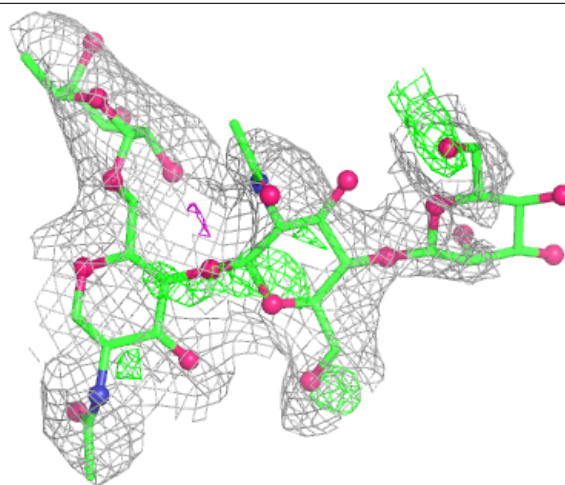
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	H	1	14/15	0.89	0.15	109,118,127,134	0
3	NAG	I	1	14/15	0.90	0.13	117,129,150,191	0
5	NAG	L	1	14/15	0.90	0.15	117,128,139,153	0
5	NAG	J	1	14/15	0.92	0.12	114,124,132,141	0
6	NAG	K	1	14/15	0.92	0.11	97,117,132,153	0
3	NAG	G	1	14/15	0.93	0.14	107,121,131,145	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.



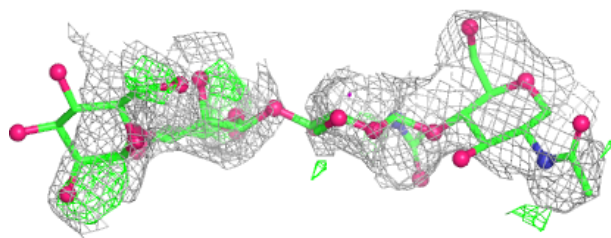
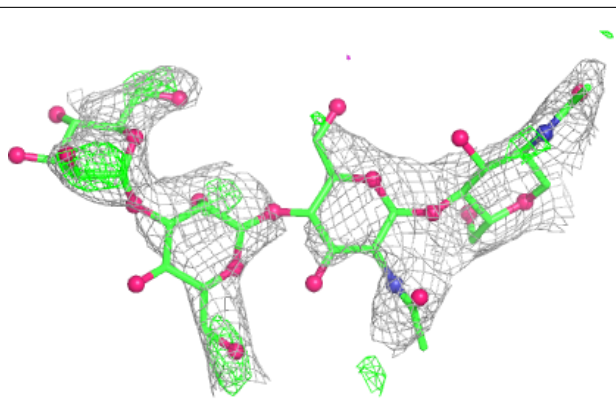
Electron density around Chain I:

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



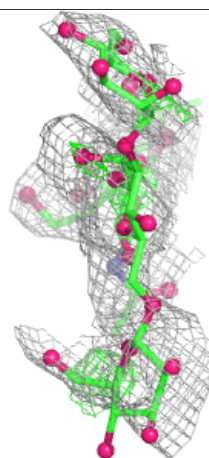
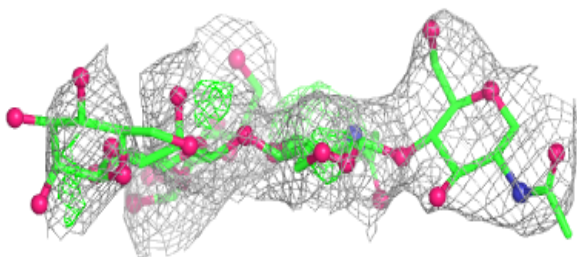
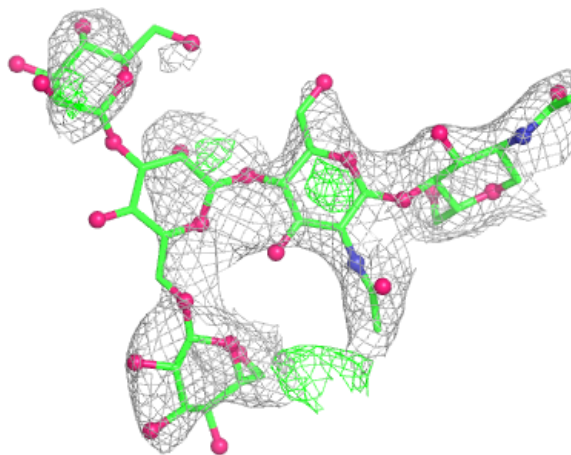
Electron density around Chain H:

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



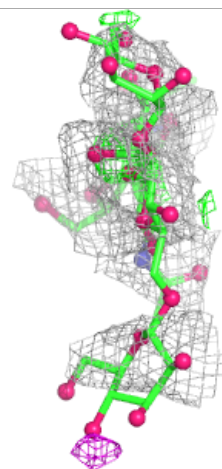
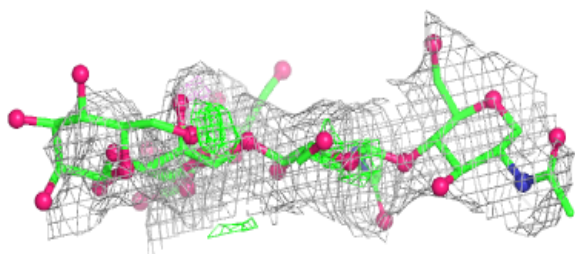
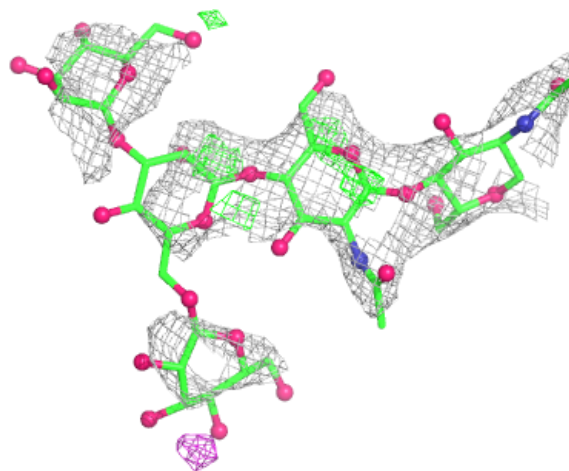
Electron density around Chain J:

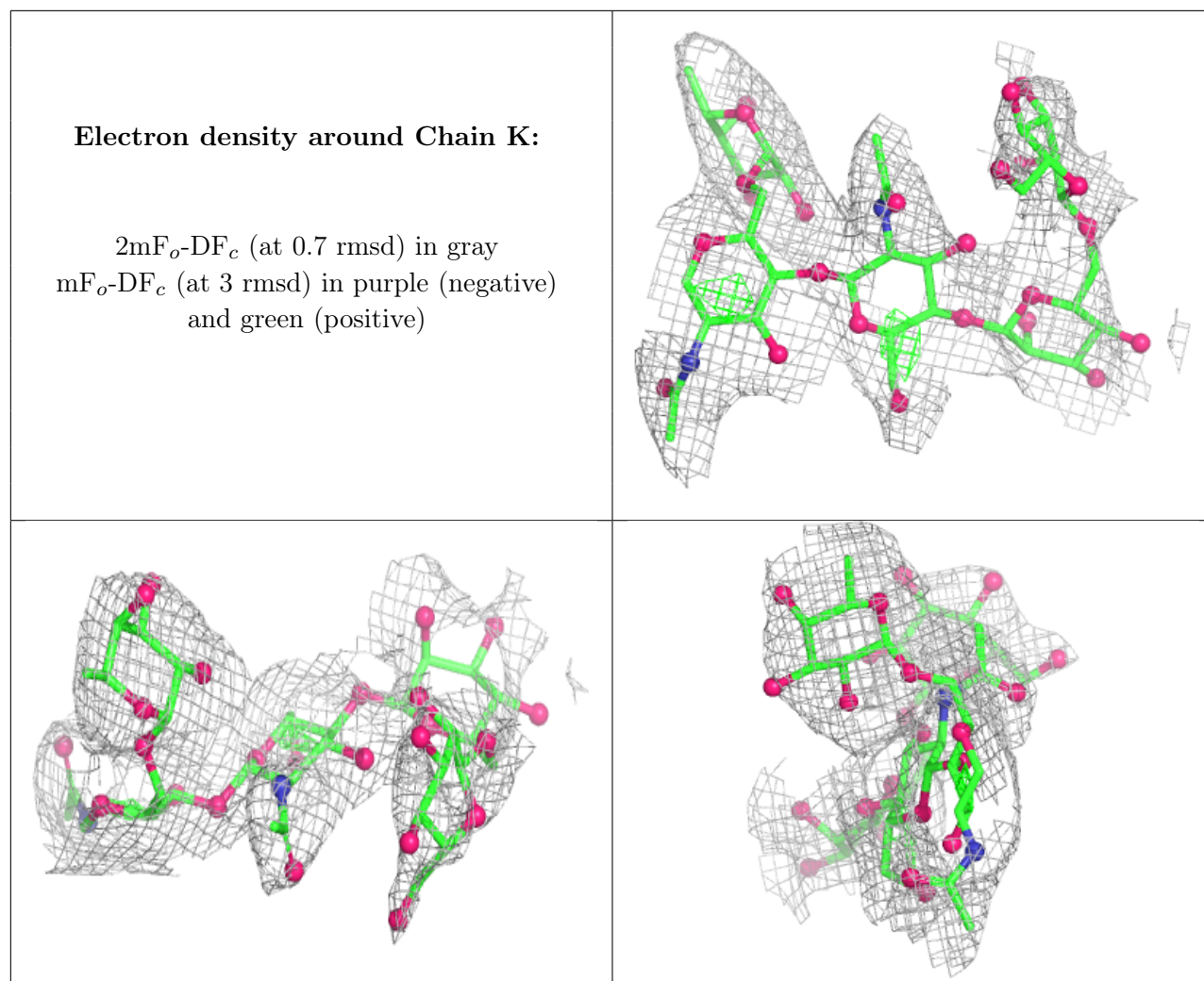
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain L:

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





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	NAG	D	201	14/15	0.67	0.25	200,229,253,254	0
8	NAG	E	201	14/15	0.69	0.14	158,201,237,239	0
8	NAG	F	201	14/15	0.80	0.13	127,134,147,148	0
7	TRS	C	201	8/8	0.88	0.15	37,39,41,41	20

6.5 Other polymers [i](#)

There are no such residues in this entry.