



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:35 PM UTC

PDB ID : 8VQR / pdb_00008vqr
Title : Crystal structure of chimeric SARS-CoV-2 RBD complexed with chimeric raccoon dog ACE2
Authors : Hsueh, F.-C.; Shi, K.; Aihara, H.; Li, F.
Deposited on : 2024-01-19
Resolution : 2.56 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

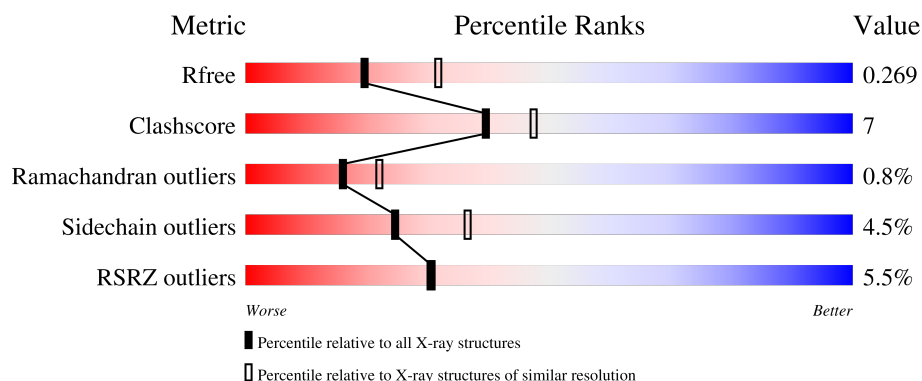
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.56 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.



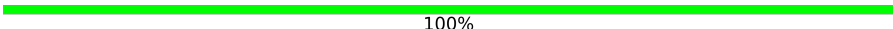
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1853 (2.58-2.54)
Clashscore	190562	1897 (2.58-2.54)
Ramachandran outliers	187476	1875 (2.58-2.54)
Sidechain outliers	187428	1875 (2.58-2.54)
RSRZ outliers	180081	1853 (2.58-2.54)

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	602	7% 76% 20% ..
1	B	602	3% 84% 14% ..
2	E	232	4% 66% 17% • 17%
2	F	232	7% 64% 17% • 16%
3	C	2	50% 50%

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Mol	Chain	Length	Quality of chain
4	D	5	 60% 40%
5	G	2	 50% 50%
5	I	2	 100%
6	H	4	 75% 25%
7	J	5	 60% 40%
8	K	3	 67% 33%

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 13126 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 Angiotensin-converting enzyme, Processed angiotensin-converting enzyme 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	594	Total	C	N	O	S	0	0	0
			4860	3108	804	920	28			
1	B	595	Total	C	N	O	S	0	0	0
			4866	3111	805	922	28			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	616	HIS	-	expression tag	UNP Q9BYF1
A	617	HIS	-	expression tag	UNP Q9BYF1
A	618	HIS	-	expression tag	UNP Q9BYF1
A	619	HIS	-	expression tag	UNP Q9BYF1
A	620	HIS	-	expression tag	UNP Q9BYF1
A	621	HIS	-	expression tag	UNP Q9BYF1
B	616	HIS	-	expression tag	UNP Q9BYF1
B	617	HIS	-	expression tag	UNP Q9BYF1
B	618	HIS	-	expression tag	UNP Q9BYF1
B	619	HIS	-	expression tag	UNP Q9BYF1
B	620	HIS	-	expression tag	UNP Q9BYF1
B	621	HIS	-	expression tag	UNP Q9BYF1

- Molecule 2 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	193	Total	C	N	O	S	0	0	0
			1524	982	246	287	9			
2	F	194	Total	C	N	O	S	0	0	0
			1531	984	248	290	9			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	321	VAL	GLN	engineered mutation	UNP P0DTC2
E	323	SER	THR	engineered mutation	UNP P0DTC2
E	324	GLY	GLU	engineered mutation	UNP P0DTC2
E	325	ASP	SER	engineered mutation	UNP P0DTC2
E	326	VAL	ILE	engineered mutation	UNP P0DTC2
E	346	LYS	ARG	variant	UNP P0DTC2
E	348	PRO	ALA	engineered mutation	UNP P0DTC2
E	354	GLU	ASN	engineered mutation	UNP P0DTC2
E	357	LYS	ARG	engineered mutation	UNP P0DTC2
E	372	THR	ALA	engineered mutation	UNP P0DTC2
E	373	PHE	SER	engineered mutation	UNP P0DTC2
E	384	ALA	PRO	engineered mutation	UNP P0DTC2
E	393	SER	THR	engineered mutation	UNP P0DTC2
E	402	VAL	ILE	engineered mutation	UNP P0DTC2
E	403	LYS	ARG	engineered mutation	UNP P0DTC2
E	406	ASP	GLU	engineered mutation	UNP P0DTC2
E	417	VAL	LYS	engineered mutation	UNP P0DTC2
E	430	MET	THR	engineered mutation	UNP P0DTC2
E	434	LEU	ILE	engineered mutation	UNP P0DTC2
E	438	THR	SER	engineered mutation	UNP P0DTC2
E	439	ARG	ASN	engineered mutation	UNP P0DTC2
E	441	ILE	LEU	engineered mutation	UNP P0DTC2
E	443	ALA	SER	engineered mutation	UNP P0DTC2
E	444	THR	LYS	variant	UNP P0DTC2
E	445	SER	VAL	engineered mutation	UNP P0DTC2
E	446	THR	GLY	engineered mutation	UNP P0DTC2
E	452	LYS	LEU	engineered mutation	UNP P0DTC2
E	519	ASN	HIS	engineered mutation	UNP P0DTC2
E	529	LEU	LYS	engineered mutation	UNP P0DTC2
E	532	ASP	ASN	engineered mutation	UNP P0DTC2
E	534	ILE	VAL	engineered mutation	UNP P0DTC2
E	536	SER	ASN	engineered mutation	UNP P0DTC2
E	537	GLY	-	expression tag	UNP P0DTC2
E	538	GLU	-	expression tag	UNP P0DTC2
E	539	ASN	-	expression tag	UNP P0DTC2
E	540	LEU	-	expression tag	UNP P0DTC2
E	541	TYR	-	expression tag	UNP P0DTC2
E	542	PHE	-	expression tag	UNP P0DTC2
E	543	GLN	-	expression tag	UNP P0DTC2
E	544	GLY	-	expression tag	UNP P0DTC2
E	545	HIS	-	expression tag	UNP P0DTC2
E	546	HIS	-	expression tag	UNP P0DTC2
E	547	HIS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	548	HIS	-	expression tag	UNP P0DTC2
E	549	HIS	-	expression tag	UNP P0DTC2
E	550	HIS	-	expression tag	UNP P0DTC2
F	321	VAL	GLN	engineered mutation	UNP P0DTC2
F	323	SER	THR	engineered mutation	UNP P0DTC2
F	324	GLY	GLU	engineered mutation	UNP P0DTC2
F	325	ASP	SER	engineered mutation	UNP P0DTC2
F	326	VAL	ILE	engineered mutation	UNP P0DTC2
F	346	LYS	ARG	variant	UNP P0DTC2
F	348	PRO	ALA	engineered mutation	UNP P0DTC2
F	354	GLU	ASN	engineered mutation	UNP P0DTC2
F	357	LYS	ARG	engineered mutation	UNP P0DTC2
F	372	THR	ALA	engineered mutation	UNP P0DTC2
F	373	PHE	SER	engineered mutation	UNP P0DTC2
F	384	ALA	PRO	engineered mutation	UNP P0DTC2
F	393	SER	THR	engineered mutation	UNP P0DTC2
F	402	VAL	ILE	engineered mutation	UNP P0DTC2
F	403	LYS	ARG	engineered mutation	UNP P0DTC2
F	406	ASP	GLU	engineered mutation	UNP P0DTC2
F	417	VAL	LYS	engineered mutation	UNP P0DTC2
F	430	MET	THR	engineered mutation	UNP P0DTC2
F	434	LEU	ILE	engineered mutation	UNP P0DTC2
F	438	THR	SER	engineered mutation	UNP P0DTC2
F	439	ARG	ASN	engineered mutation	UNP P0DTC2
F	441	ILE	LEU	engineered mutation	UNP P0DTC2
F	443	ALA	SER	engineered mutation	UNP P0DTC2
F	444	THR	LYS	variant	UNP P0DTC2
F	445	SER	VAL	engineered mutation	UNP P0DTC2
F	446	THR	GLY	engineered mutation	UNP P0DTC2
F	452	LYS	LEU	engineered mutation	UNP P0DTC2
F	519	ASN	HIS	engineered mutation	UNP P0DTC2
F	529	LEU	LYS	engineered mutation	UNP P0DTC2
F	532	ASP	ASN	engineered mutation	UNP P0DTC2
F	534	ILE	VAL	engineered mutation	UNP P0DTC2
F	536	SER	ASN	engineered mutation	UNP P0DTC2
F	537	GLY	-	expression tag	UNP P0DTC2
F	538	GLU	-	expression tag	UNP P0DTC2
F	539	ASN	-	expression tag	UNP P0DTC2
F	540	LEU	-	expression tag	UNP P0DTC2
F	541	TYR	-	expression tag	UNP P0DTC2
F	542	PHE	-	expression tag	UNP P0DTC2
F	543	GLN	-	expression tag	UNP P0DTC2

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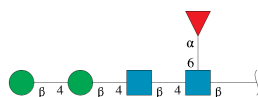
Chain	Residue	Modelled	Actual	Comment	Reference
F	544	GLY	-	expression tag	UNP P0DTC2
F	545	HIS	-	expression tag	UNP P0DTC2
F	546	HIS	-	expression tag	UNP P0DTC2
F	547	HIS	-	expression tag	UNP P0DTC2
F	548	HIS	-	expression tag	UNP P0DTC2
F	549	HIS	-	expression tag	UNP P0DTC2
F	550	HIS	-	expression tag	UNP P0DTC2

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



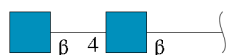
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	2	Total	C	N	O	0	0	0
			24	14	1	9			

- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-4)-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
4	D	5	Total	C	N	O	0	0	0
			60	34	2	24			

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



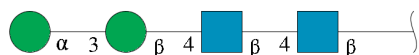
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

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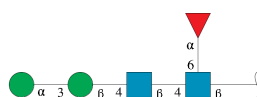
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 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.



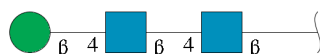
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	H	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-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.



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

- Molecule 8 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
8	K	3	Total	C	N	O	0	0	0
			39	22	2	15			

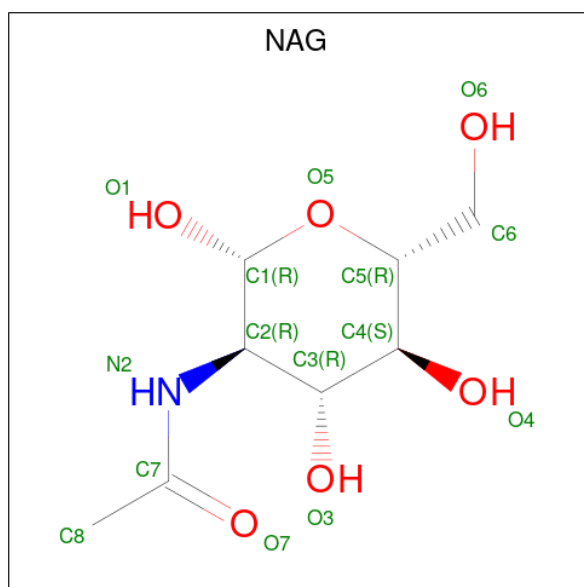
- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	Zn	0	0
			1	1		
9	B	1	Total	Zn	0	0
			1	1		

- Molecule 10 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

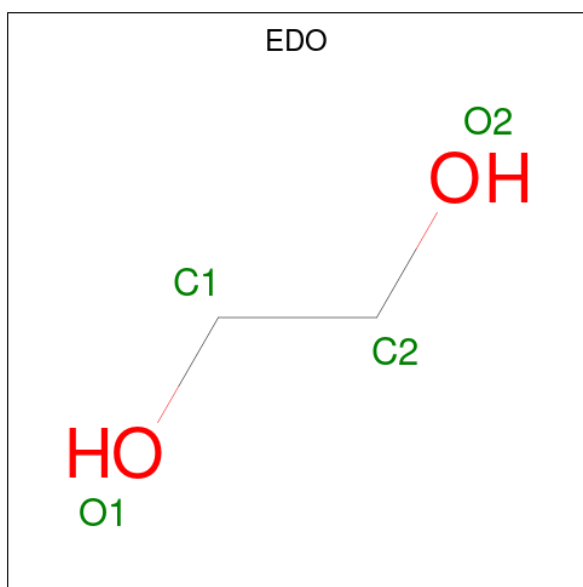
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1	Total	Cl	0	0
			1	1		
10	B	1	Total	Cl	0	0
			1	1		

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 12 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	B	1	Total	C	O	0	0
			4	2	2		
12	B	1	Total	C	O	0	0
			4	2	2		

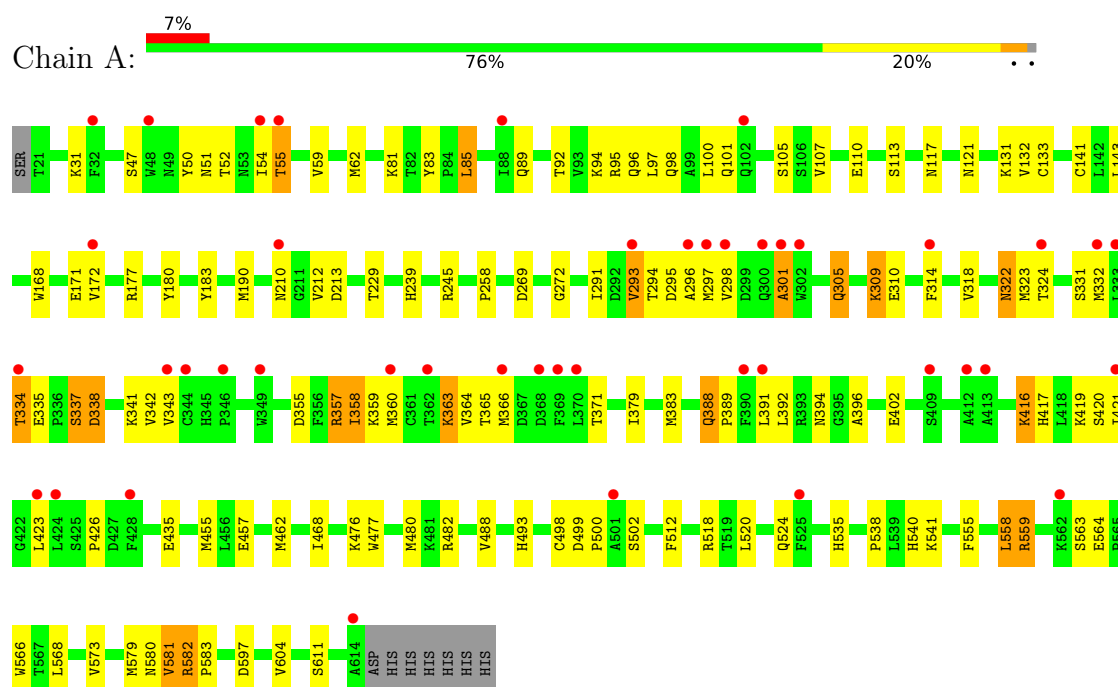
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	8	Total	O	0	0
			8	8		
13	B	6	Total	O	0	0
			6	6		
13	E	1	Total	O	0	0
			1	1		
13	F	1	Total	O	0	0
			1	1		

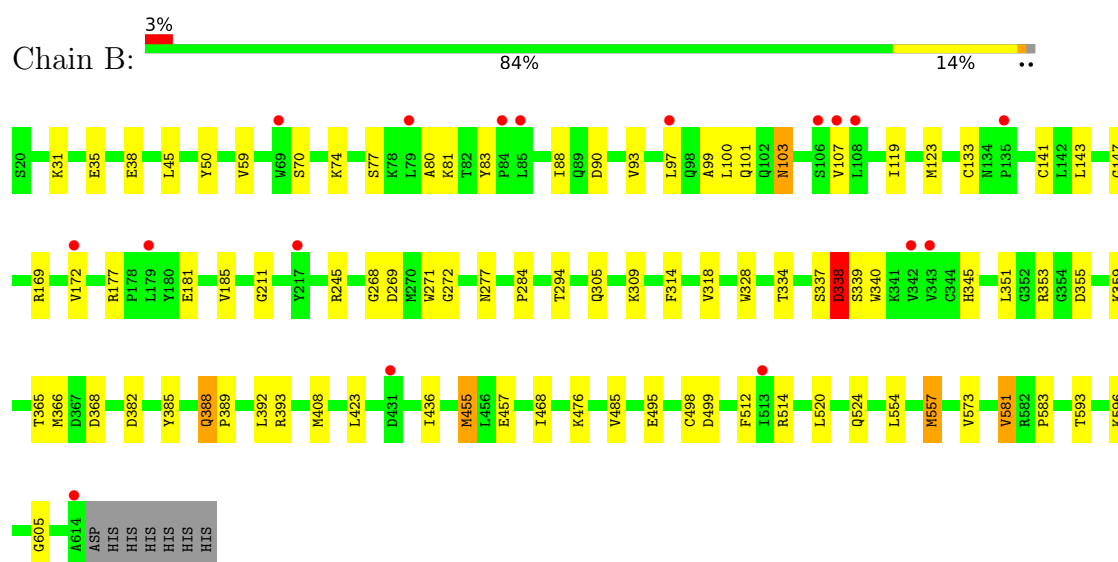
3 Residue-property plots [i](#)

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.

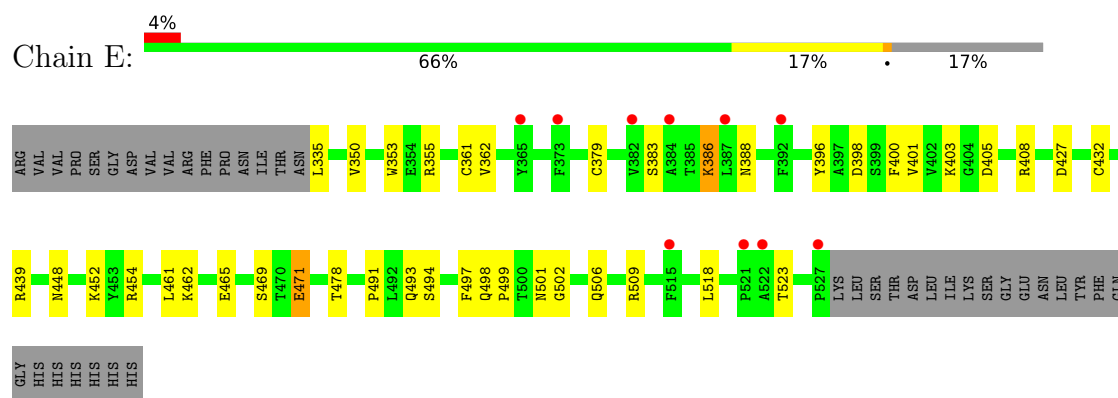
- Molecule 1: Angiotensin-converting enzyme, Processed angiotensin-converting enzyme 2



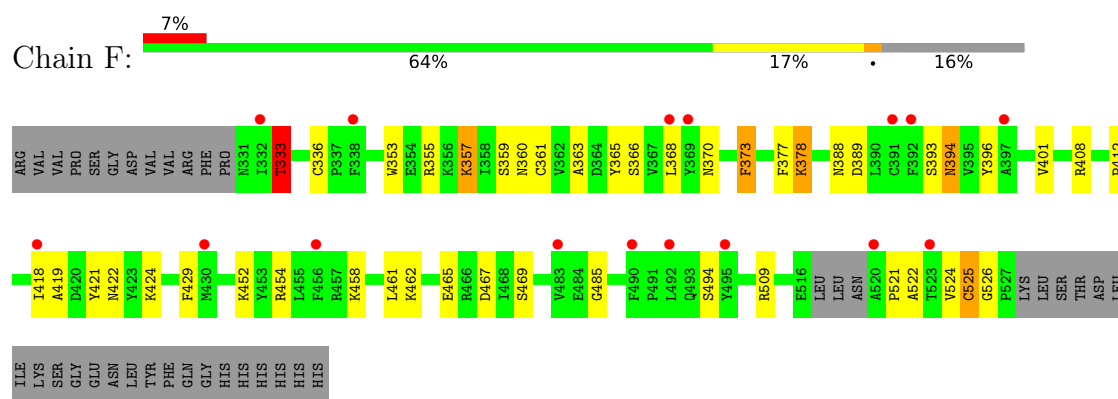
- Molecule 1: Angiotensin-converting enzyme, Processed angiotensin-converting enzyme 2



- Molecule 2: Spike protein S1



- Molecule 2: Spike protein S1



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



- Molecule 4: beta-D-mannopyranose-(1-4)-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



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  100%

MAG1
MAG2

- Molecule 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 H:  75% 25%

MAG1
MAG2
BMA3
MAN4

- Molecule 7: alpha-D-mannopyranose-(1-3)-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

Chain J:  60% 40%

MAG1
MAG2
BMA3
MAN4
FUC5

- Molecule 8: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  67% 33%

MAG1
MAG2
BMA3

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	80.96Å 118.11Å 112.23Å 90.00° 92.89° 90.00°	Depositor
Resolution (Å)	58.41 – 2.56 58.41 – 2.56	Depositor EDS
% Data completeness (in resolution range)	62.8 (58.41-2.56) 59.5 (58.41-2.56)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.214 , 0.264 0.228 , 0.269	Depositor DCC
R_{free} test set	2203 reflections (3.26%)	wwPDB-VP
Wilson B-factor (Å ²)	67.9	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13126	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.09	0/4998	0.28	0/6790
1	B	0.08	0/5004	0.25	0/6798
2	E	0.08	0/1568	0.25	0/2136
2	F	0.10	0/1574	0.28	0/2143
All	All	0.09	0/13144	0.27	0/17867

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4860	0	4626	74	0
1	B	4866	0	4631	47	0
2	E	1524	0	1437	22	0
2	F	1531	0	1440	28	0
3	C	24	0	22	1	0
4	D	60	0	52	0	0
5	G	28	0	25	1	0
5	I	28	0	25	0	0
6	H	50	0	43	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	J	60	0	52	0	0
8	K	39	0	34	1	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
10	A	1	0	0	0	0
10	B	1	0	0	1	0
11	A	14	0	13	0	0
11	B	14	0	13	0	0
12	B	8	0	12	0	0
13	A	8	0	0	0	0
13	B	6	0	0	0	0
13	E	1	0	0	0	0
13	F	1	0	0	0	0
All	All	13126	0	12425	172	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 7.

All (172) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:GLN:HE22	1:A:210:ASN:HD21	1.25	0.81
1:B:338:ASP:N	1:B:338:ASP:OD1	2.22	0.73
1:A:416:LYS:NZ	1:A:541:LYS:O	2.21	0.72
2:F:363:ALA:HB2	2:F:525:CYS:HB3	1.72	0.71
1:A:468:ILE:HD12	1:A:476:LYS:HG2	1.75	0.69
1:A:520:LEU:HD22	1:A:579:MET:HE2	1.77	0.67
2:E:335:LEU:HB3	2:E:362:VAL:H	1.60	0.65
2:E:454:ARG:NH2	2:E:469:SER:O	2.30	0.65
1:A:293:VAL:HG12	1:A:296:ALA:HB3	1.79	0.64
1:B:177:ARG:NH1	1:B:181:GLU:OE2	2.31	0.63
1:A:482:ARG:HH22	1:A:611:SER:HB3	1.64	0.62
1:A:555:PHE:HA	1:A:558:LEU:HD22	1.81	0.61
2:F:378:LYS:HA	2:F:378:LYS:HE3	1.81	0.61
1:B:83:TYR:O	1:B:101:GLN:NE2	2.31	0.61
1:A:420:SER:HB2	5:G:1:NAG:H62	1.84	0.60
1:B:177:ARG:NH2	1:B:495:GLU:OE1	2.36	0.58
2:F:365:TYR:HB2	2:F:388:ASN:HD22	1.68	0.58
2:E:383:SER:HB2	2:E:386:LYS:HG2	1.86	0.58
1:A:323:MET:HE1	1:A:379:ILE:HG21	1.84	0.58
2:E:448:ASN:HB3	2:E:497:PHE:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:455:MET:HE3	1:A:480:MET:HB2	1.87	0.57
1:B:70:SER:O	1:B:74:LYS:HG2	2.05	0.57
1:A:520:LEU:HD21	1:A:581:VAL:HG13	1.87	0.57
1:A:388:GLN:NE2	1:A:559:ARG:O	2.38	0.57
1:B:80:ALA:O	1:B:101:GLN:NE2	2.37	0.57
1:A:177:ARG:HD3	1:A:498:CYS:HB2	1.87	0.56
1:B:388:GLN:HG3	1:B:389:PRO:HD2	1.85	0.56
2:E:461:LEU:HD22	2:E:465:GLU:HB3	1.86	0.56
1:A:402:GLU:HB3	1:A:518:ARG:HH11	1.70	0.56
1:B:524:GLN:HG2	1:B:583:PRO:HG2	1.85	0.56
2:F:361:CYS:N	2:F:524:VAL:O	2.38	0.56
2:F:360:ASN:H	2:F:524:VAL:HA	1.70	0.56
2:F:333:THR:O	2:F:333:THR:OG1	2.22	0.56
1:A:524:GLN:HG2	1:A:583:PRO:HG2	1.88	0.55
1:B:99:ALA:O	1:B:103:ASN:HB2	2.06	0.55
2:E:335:LEU:HD23	2:E:361:CYS:HA	1.88	0.55
8:K:1:NAG:H83	8:K:1:NAG:H3	1.88	0.55
1:A:143:LEU:H	1:A:143:LEU:HD23	1.71	0.54
1:B:38:GLU:OE1	1:B:353:ARG:NH2	2.34	0.54
1:B:133:CYS:HA	1:B:141:CYS:HA	1.89	0.54
2:E:452:LYS:HG2	2:E:494:SER:HB3	1.89	0.54
1:A:331:SER:OG	1:A:358:ILE:O	2.25	0.54
1:B:245:ARG:NH2	1:B:605:GLY:O	2.41	0.54
2:F:461:LEU:HD22	2:F:465:GLU:HB3	1.89	0.54
1:A:324:THR:HG23	1:A:383:MET:HE2	1.89	0.54
1:A:294:THR:O	1:A:298:VAL:HG23	2.08	0.53
1:A:298:VAL:HG22	1:A:364:VAL:O	2.07	0.53
1:A:564:GLU:HB3	1:A:568:LEU:HD23	1.91	0.53
1:A:322:ASN:N	1:A:322:ASN:OD1	2.40	0.53
2:F:366:SER:OG	2:F:370:ASN:OD1	2.27	0.53
1:A:301:ALA:HA	1:A:364:VAL:HG11	1.91	0.52
1:A:435:GLU:HG3	1:A:540:HIS:CE1	2.43	0.52
1:A:51:ASN:HB3	1:A:359:LYS:HE2	1.90	0.52
1:B:88:ILE:HD11	1:B:97:LEU:HD23	1.91	0.52
1:B:337:SER:O	1:B:339:SER:N	2.42	0.52
1:B:455:MET:HE2	1:B:485:VAL:HG21	1.91	0.52
1:A:417:HIS:O	1:A:421:ILE:HG12	2.09	0.52
1:A:337:SER:OG	1:A:338:ASP:N	2.31	0.52
2:F:412:PRO:HG3	2:F:429:PHE:HB3	1.92	0.51
1:A:314:PHE:O	1:A:318:VAL:HG23	2.11	0.51
1:A:133:CYS:HA	1:A:141:CYS:HA	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:GLN:O	1:A:309:LYS:HB2	2.11	0.51
1:B:468:ILE:HD12	1:B:476:LYS:HG2	1.93	0.51
2:E:452:LYS:HA	2:E:494:SER:HA	1.92	0.51
1:A:168:TRP:CD1	1:A:502:SER:HB2	2.46	0.51
2:F:454:ARG:NH1	2:F:467:ASP:O	2.44	0.50
2:E:498:GLN:H	2:E:501:ASN:HD21	1.59	0.50
1:A:47:SER:HA	1:A:62:MET:HG3	1.93	0.50
1:B:143:LEU:HD23	1:B:143:LEU:H	1.77	0.50
1:A:343:VAL:HG23	1:A:359:LYS:NZ	2.27	0.50
2:E:439:ARG:HD2	2:E:499:PRO:HA	1.94	0.49
2:F:524:VAL:HG13	2:F:525:CYS:H	1.77	0.49
1:B:305:GLN:O	1:B:309:LYS:HB2	2.13	0.49
1:A:457:GLU:HG2	1:A:512:PHE:HB3	1.95	0.49
1:A:105:SER:OG	1:A:190:MET:SD	2.71	0.49
2:F:363:ALA:H	2:F:526:GLY:H	1.61	0.49
2:F:393:SER:HA	2:F:522:ALA:HA	1.95	0.48
2:E:350:VAL:HA	2:E:400:PHE:HB2	1.94	0.48
1:A:363:LYS:N	1:A:363:LYS:HD3	2.28	0.48
1:A:52:THR:HB	3:C:1:NAG:HN2	1.79	0.48
2:F:355:ARG:HD2	2:F:396:TYR:HD2	1.79	0.48
1:A:396:ALA:HB1	1:A:566:TRP:HA	1.94	0.47
2:E:462:LYS:HG2	2:E:465:GLU:OE1	2.14	0.47
1:A:55:THR:O	1:A:59:VAL:HG23	2.14	0.47
2:E:401:VAL:HG22	2:E:509:ARG:HG2	1.95	0.47
2:E:498:GLN:H	2:E:501:ASN:ND2	2.12	0.47
1:A:355:ASP:OD2	1:A:357:ARG:NH1	2.48	0.47
1:B:457:GLU:HG2	1:B:512:PHE:HB3	1.95	0.47
1:A:416:LYS:HE3	1:A:416:LYS:H	1.79	0.47
1:A:419:LYS:NZ	1:A:426:PRO:O	2.38	0.47
1:A:51:ASN:O	1:A:343:VAL:HG22	2.15	0.46
2:E:379:CYS:HA	2:E:432:CYS:HA	1.98	0.46
1:A:477:TRP:CE3	1:A:500:PRO:HG3	2.50	0.46
1:B:31:LYS:NZ	1:B:35:GLU:OE2	2.38	0.46
1:A:132:VAL:HG12	1:A:171:GLU:HG3	1.97	0.46
1:A:96:GLN:HB3	1:A:391:LEU:HD13	1.99	0.45
1:B:593:THR:HA	1:B:596:LYS:HE2	1.97	0.45
2:E:403:LYS:HE3	2:E:405:ASP:HB2	1.98	0.45
1:A:269:ASP:OD1	1:A:272:GLY:N	2.49	0.45
1:A:360:MET:HE1	1:A:371:THR:HB	1.98	0.45
1:A:389:PRO:HG2	1:A:392:LEU:HD22	1.99	0.45
1:B:309:LYS:HD2	1:B:328:TRP:CH2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:TYR:HA	1:A:183:TYR:HB3	1.99	0.45
1:A:239:HIS:CE1	1:A:604:VAL:HG11	2.52	0.45
1:B:365:THR:OG1	1:B:366:MET:N	2.50	0.45
1:B:455:MET:HE3	1:B:455:MET:HB3	1.84	0.44
2:F:524:VAL:HG13	2:F:525:CYS:N	2.32	0.44
1:B:557:MET:O	1:B:557:MET:HE2	2.17	0.44
1:B:177:ARG:HD3	1:B:498:CYS:HB2	2.00	0.44
1:B:365:THR:HG23	1:B:368:ASP:H	1.82	0.44
2:E:355:ARG:HD3	2:E:398:ASP:OD1	2.17	0.44
2:F:394:ASN:HA	2:F:524:VAL:HB	2.00	0.44
1:B:314:PHE:O	1:B:318:VAL:HG23	2.17	0.44
2:F:353:TRP:CD1	2:F:353:TRP:H	2.35	0.44
1:A:332:MET:HE2	1:A:342:VAL:HG21	1.98	0.44
1:A:488:VAL:HG21	1:A:611:SER:HA	2.00	0.44
1:A:81:LYS:HA	1:A:101:GLN:HE21	1.83	0.44
2:E:353:TRP:H	2:E:353:TRP:CD1	2.36	0.44
2:F:359:SER:HA	2:F:524:VAL:HG23	2.00	0.44
2:F:401:VAL:HG22	2:F:509:ARG:HG2	1.99	0.44
1:A:359:LYS:HE3	1:A:359:LYS:HB3	1.85	0.43
1:A:113:SER:O	1:A:117:ASN:ND2	2.51	0.43
1:B:382:ASP:OD1	1:B:385:TYR:OH	2.28	0.43
1:A:310:GLU:OE2	1:A:421:ILE:HD12	2.19	0.43
1:B:268:GLY:O	1:B:277:ASN:ND2	2.39	0.43
2:F:421:TYR:HB3	2:F:454:ARG:HG2	1.99	0.43
1:A:213:ASP:OD1	1:A:213:ASP:N	2.51	0.43
1:A:229:THR:HG22	1:A:581:VAL:HG22	2.00	0.43
1:A:493:HIS:ND1	1:A:499:ASP:OD2	2.51	0.43
1:B:284:PRO:HG2	1:B:436:ILE:HG22	2.01	0.43
1:B:50:TYR:CE1	1:B:59:VAL:HG22	2.53	0.43
1:B:408:MET:HE1	1:B:554:LEU:HD21	2.00	0.43
2:E:383:SER:OG	2:E:386:LYS:NZ	2.48	0.43
1:B:389:PRO:HG2	1:B:392:LEU:HD22	2.00	0.42
2:E:502:GLY:O	2:E:506:GLN:HG3	2.19	0.42
1:A:54:ILE:HB	1:A:341:LYS:HG2	2.01	0.42
1:A:245:ARG:HD3	1:A:258:PRO:HA	2.02	0.42
1:B:294:THR:HG23	1:B:365:THR:HA	2.02	0.42
2:F:373:PHE:HD1	2:F:373:PHE:HA	1.68	0.42
1:A:117:ASN:O	1:A:121:ASN:ND2	2.52	0.42
1:A:580:ASN:OD1	1:A:582:ARG:HG2	2.19	0.42
1:A:535:HIS:NE2	1:A:538:PRO:O	2.50	0.42
1:B:77:SER:O	1:B:81:LYS:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:345:HIS:O	1:B:359:LYS:NZ	2.52	0.41
1:A:83:TYR:HB2	1:A:97:LEU:HD21	2.02	0.41
1:B:119:ILE:HG22	1:B:123:MET:HE2	2.02	0.41
1:B:169:ARG:HH22	1:B:271:TRP:HA	1.85	0.41
1:B:90:ASP:HB2	1:B:93:VAL:HB	2.02	0.41
1:B:269:ASP:OD1	1:B:272:GLY:N	2.47	0.41
2:F:419:ALA:O	2:F:424:LYS:HD3	2.20	0.41
2:F:452:LYS:HA	2:F:494:SER:HA	2.02	0.41
1:A:50:TYR:CD1	1:A:59:VAL:HG22	2.56	0.41
1:A:92:THR:O	1:A:96:GLN:HG3	2.20	0.41
1:A:332:MET:HE3	1:A:332:MET:HB3	1.88	0.41
1:B:520:LEU:HD21	1:B:581:VAL:HG13	2.01	0.41
2:E:355:ARG:HD2	2:E:396:TYR:HB3	2.03	0.41
2:F:368:LEU:HB3	2:F:377:PHE:CZ	2.56	0.41
2:E:471:GLU:O	2:E:491:PRO:HG3	2.21	0.41
1:B:423:LEU:HD23	1:B:423:LEU:HA	1.93	0.41
1:A:85:LEU:HD13	1:A:94:LYS:NZ	2.35	0.41
2:F:357:LYS:NZ	2:F:357:LYS:HB3	2.36	0.41
2:F:394:ASN:OD1	2:F:394:ASN:N	2.51	0.41
1:A:95:ARG:HD3	1:A:563:SER:O	2.20	0.41
2:F:418:ILE:HA	2:F:422:ASN:HD22	1.87	0.40
1:A:462:MET:HE3	1:A:468:ILE:HD11	2.02	0.40
1:B:45:LEU:HD23	1:B:45:LEU:HA	1.95	0.40
2:F:454:ARG:NH2	2:F:469:SER:O	2.53	0.40
1:A:365:THR:OG1	1:A:366:MET:N	2.53	0.40
1:B:389:PRO:O	1:B:393:ARG:HG3	2.22	0.40
1:B:499:ASP:HB3	10:B:702:CL:CL	2.59	0.40
1:A:297:MET:HE2	1:A:423:LEU:HB3	2.03	0.40
1:B:351:LEU:HD12	1:B:355:ASP:OD2	2.21	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	592/602 (98%)	567 (96%)	21 (4%)	4 (1%)	18	25
1	B	593/602 (98%)	569 (96%)	20 (3%)	4 (1%)	18	25
2	E	191/232 (82%)	171 (90%)	19 (10%)	1 (0%)	24	33
2	F	190/232 (82%)	168 (88%)	19 (10%)	3 (2%)	7	9
All	All	1566/1668 (94%)	1475 (94%)	79 (5%)	12 (1%)	16	22

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	338	ASP
1	B	147	GLY
1	B	340	TRP
1	A	212	VAL
1	A	337	SER
2	F	333	THR
1	A	301	ALA
1	A	334	THR
2	E	518	LEU
2	F	485	GLY
1	B	211	GLY
2	F	521	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	527/535 (98%)	497 (94%)	30 (6%)	18	28
1	B	528/535 (99%)	515 (98%)	13 (2%)	42	58
2	E	166/203 (82%)	158 (95%)	8 (5%)	23	34
2	F	167/203 (82%)	156 (93%)	11 (7%)	15	21
All	All	1388/1476 (94%)	1326 (96%)	62 (4%)	24	36

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LYS
1	A	55	THR
1	A	85	LEU
1	A	89	GLN
1	A	100	LEU
1	A	107	VAL
1	A	110	GLU
1	A	131	LYS
1	A	172	VAL
1	A	291	ILE
1	A	293	VAL
1	A	295	ASP
1	A	305	GLN
1	A	309	LYS
1	A	322	ASN
1	A	334	THR
1	A	335	GLU
1	A	338	ASP
1	A	357	ARG
1	A	358	ILE
1	A	363	LYS
1	A	388	GLN
1	A	394	ASN
1	A	416	LYS
1	A	558	LEU
1	A	559	ARG
1	A	573	VAL
1	A	581	VAL
1	A	582	ARG
1	A	597	ASP
1	B	100	LEU
1	B	103	ASN
1	B	107	VAL
1	B	172	VAL
1	B	185	VAL
1	B	334	THR
1	B	338	ASP
1	B	388	GLN
1	B	455	MET
1	B	514	ARG
1	B	557	MET
1	B	573	VAL
1	B	581	VAL

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Mol	Chain	Res	Type
2	E	386	LYS
2	E	388	ASN
2	E	408	ARG
2	E	427	ASP
2	E	471	GLU
2	E	478	THR
2	E	493	GLN
2	E	523	THR
2	F	333	THR
2	F	336	CYS
2	F	357	LYS
2	F	373	PHE
2	F	378	LYS
2	F	389	ASP
2	F	394	ASN
2	F	408	ARG
2	F	458	LYS
2	F	462	LYS
2	F	525	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	117	ASN
1	A	121	ASN
1	A	194	ASN
1	A	210	ASN
1	A	388	GLN
1	A	472	GLN
1	B	42	GLN
1	B	58	ASN
1	B	117	ASN
1	B	121	ASN
1	B	137	ASN
1	B	194	ASN
1	B	388	GLN
1	B	442	GLN
2	E	360	ASN
2	E	370	ASN
2	E	493	GLN
2	E	498	GLN
2	E	501	ASN

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Mol	Chain	Res	Type
2	F	360	ASN
2	F	388	ASN
2	F	474	GLN
2	F	498	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 ⓘ

23 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	C	1	3,1	14,14,15	0.29	0	17,19,21	0.79	1 (5%)
3	FUC	C	2	3	10,10,11	0.71	0	14,14,16	0.91	0
4	NAG	D	1	1,4	14,14,15	0.35	0	17,19,21	0.55	0
4	NAG	D	2	4	14,14,15	0.50	0	17,19,21	0.67	0
4	BMA	D	3	4	11,11,12	1.42	2 (18%)	15,15,17	1.34	2 (13%)
4	BMA	D	4	4	11,11,12	0.94	0	15,15,17	0.98	1 (6%)
4	FUC	D	5	4	10,10,11	0.68	0	14,14,16	0.79	0
5	NAG	G	1	1,5	14,14,15	0.51	0	17,19,21	0.85	0
5	NAG	G	2	5	14,14,15	0.22	0	17,19,21	0.51	0
6	NAG	H	1	1,6	14,14,15	0.38	0	17,19,21	0.46	0
6	NAG	H	2	6	14,14,15	0.34	0	17,19,21	0.45	0
6	BMA	H	3	6	11,11,12	0.67	0	15,15,17	0.81	0
6	MAN	H	4	6	11,11,12	0.62	0	15,15,17	1.02	2 (13%)
5	NAG	I	1	1,5	14,14,15	0.30	0	17,19,21	0.60	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	I	2	5	14,14,15	0.40	0	17,19,21	0.52	0
7	NAG	J	1	1,7	14,14,15	0.30	0	17,19,21	0.55	0
7	NAG	J	2	7	14,14,15	0.19	0	17,19,21	0.49	0
7	BMA	J	3	7	11,11,12	1.41	2 (18%)	15,15,17	1.08	1 (6%)
7	MAN	J	4	7	11,11,12	0.77	0	15,15,17	1.35	2 (13%)
7	FUC	J	5	7	10,10,11	0.72	0	14,14,16	0.76	0
8	NAG	K	1	2,8	14,14,15	0.45	0	17,19,21	1.35	2 (11%)
8	NAG	K	2	8	14,14,15	0.32	0	17,19,21	0.45	0
8	BMA	K	3	8	11,11,12	0.58	0	15,15,17	0.81	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	C	1	3,1	-	4/6/23/26	0/1/1/1
3	FUC	C	2	3	-	-	0/1/1/1
4	NAG	D	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
4	BMA	D	3	4	-	1/2/19/22	0/1/1/1
4	BMA	D	4	4	-	2/2/19/22	0/1/1/1
4	FUC	D	5	4	-	-	0/1/1/1
5	NAG	G	1	1,5	-	3/6/23/26	0/1/1/1
5	NAG	G	2	5	-	2/6/23/26	0/1/1/1
6	NAG	H	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	H	2	6	-	2/6/23/26	0/1/1/1
6	BMA	H	3	6	-	0/2/19/22	0/1/1/1
6	MAN	H	4	6	-	0/2/19/22	0/1/1/1
5	NAG	I	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	I	2	5	-	3/6/23/26	0/1/1/1
7	NAG	J	1	1,7	-	0/6/23/26	0/1/1/1
7	NAG	J	2	7	-	2/6/23/26	0/1/1/1
7	BMA	J	3	7	-	2/2/19/22	0/1/1/1
7	MAN	J	4	7	-	0/2/19/22	1/1/1/1
7	FUC	J	5	7	-	-	0/1/1/1
8	NAG	K	1	2,8	-	4/6/23/26	0/1/1/1
8	NAG	K	2	8	-	0/6/23/26	0/1/1/1
8	BMA	K	3	8	-	0/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	J	3	BMA	C2-C3	3.36	1.57	1.52
4	D	3	BMA	C4-C3	2.80	1.59	1.52
4	D	3	BMA	C2-C3	2.46	1.56	1.52
7	J	3	BMA	O3-C3	2.38	1.48	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	K	1	NAG	C2-N2-C7	4.60	129.06	122.90
7	J	4	MAN	C1-O5-C5	4.35	118.02	112.19
4	D	3	BMA	C2-C3-C4	3.13	116.36	110.86
6	H	4	MAN	C1-O5-C5	2.75	115.88	112.19
3	C	1	NAG	C1-O5-C5	2.63	115.71	112.19
7	J	3	BMA	O3-C3-C2	2.36	114.88	110.05
4	D	3	BMA	C1-O5-C5	-2.22	109.21	112.19
8	K	1	NAG	C1-C2-N2	2.20	113.91	110.43
4	D	4	BMA	C2-C3-C4	2.20	114.73	110.86
7	J	4	MAN	O2-C2-C3	-2.20	105.60	110.15
6	H	4	MAN	O2-C2-C3	-2.18	105.63	110.15

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	G	2	NAG	O5-C5-C6-O6
5	G	2	NAG	C4-C5-C6-O6
4	D	4	BMA	O5-C5-C6-O6
5	I	1	NAG	O5-C5-C6-O6
4	D	2	NAG	O5-C5-C6-O6
4	D	4	BMA	C4-C5-C6-O6
3	C	1	NAG	O5-C5-C6-O6
5	I	1	NAG	C4-C5-C6-O6
4	D	1	NAG	C8-C7-N2-C2
4	D	1	NAG	O7-C7-N2-C2
6	H	1	NAG	C8-C7-N2-C2
6	H	1	NAG	O7-C7-N2-C2
6	H	2	NAG	C8-C7-N2-C2
6	H	2	NAG	O7-C7-N2-C2
8	K	1	NAG	C8-C7-N2-C2
8	K	1	NAG	O7-C7-N2-C2
3	C	1	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
7	J	2	NAG	O5-C5-C6-O6
7	J	3	BMA	C4-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6
4	D	3	BMA	O5-C5-C6-O6
5	I	2	NAG	O5-C5-C6-O6
5	G	1	NAG	O5-C5-C6-O6
7	J	3	BMA	O5-C5-C6-O6
5	I	2	NAG	C1-C2-N2-C7
3	C	1	NAG	C3-C2-N2-C7
5	G	1	NAG	C3-C2-N2-C7
5	I	2	NAG	C3-C2-N2-C7
7	J	2	NAG	C4-C5-C6-O6
3	C	1	NAG	C1-C2-N2-C7
5	G	1	NAG	C1-C2-N2-C7
8	K	1	NAG	C1-C2-N2-C7
8	K	1	NAG	C3-C2-N2-C7

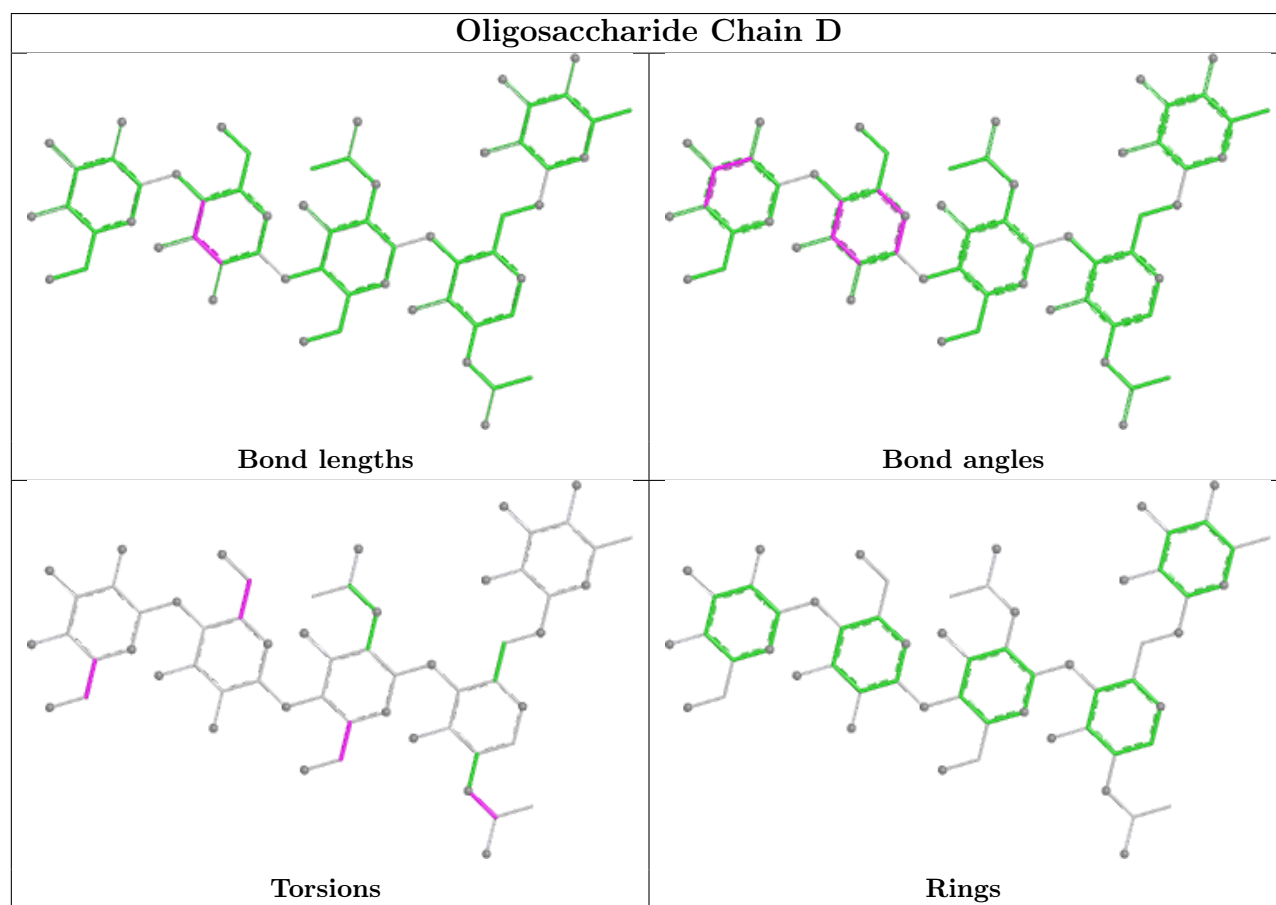
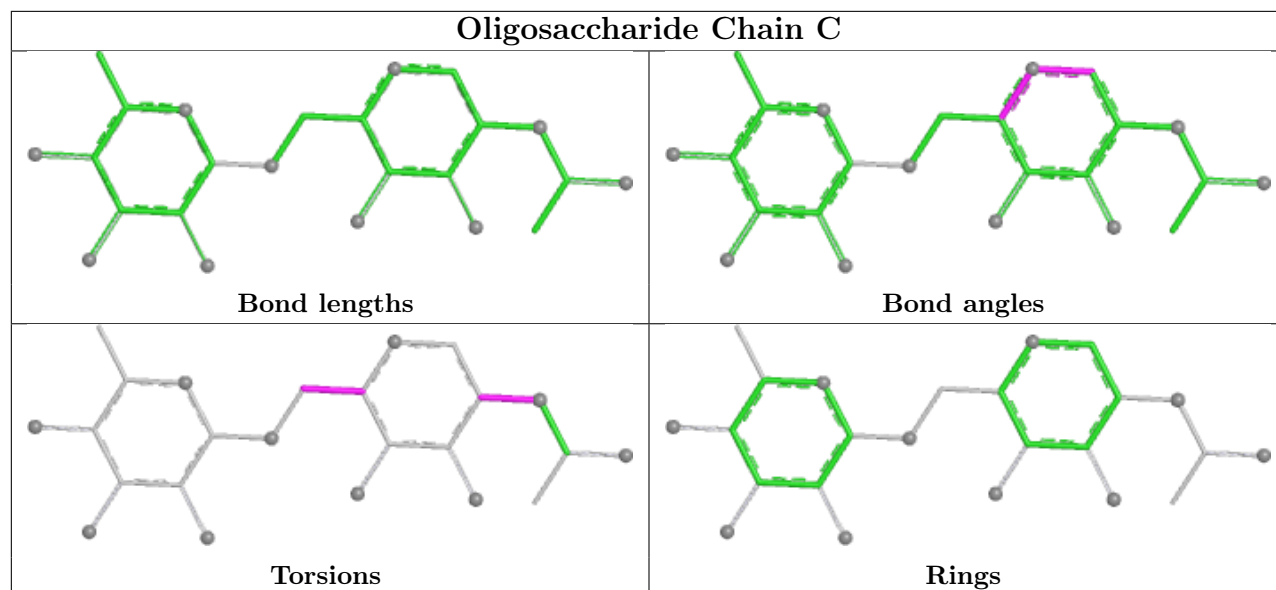
All (1) ring outliers are listed below:

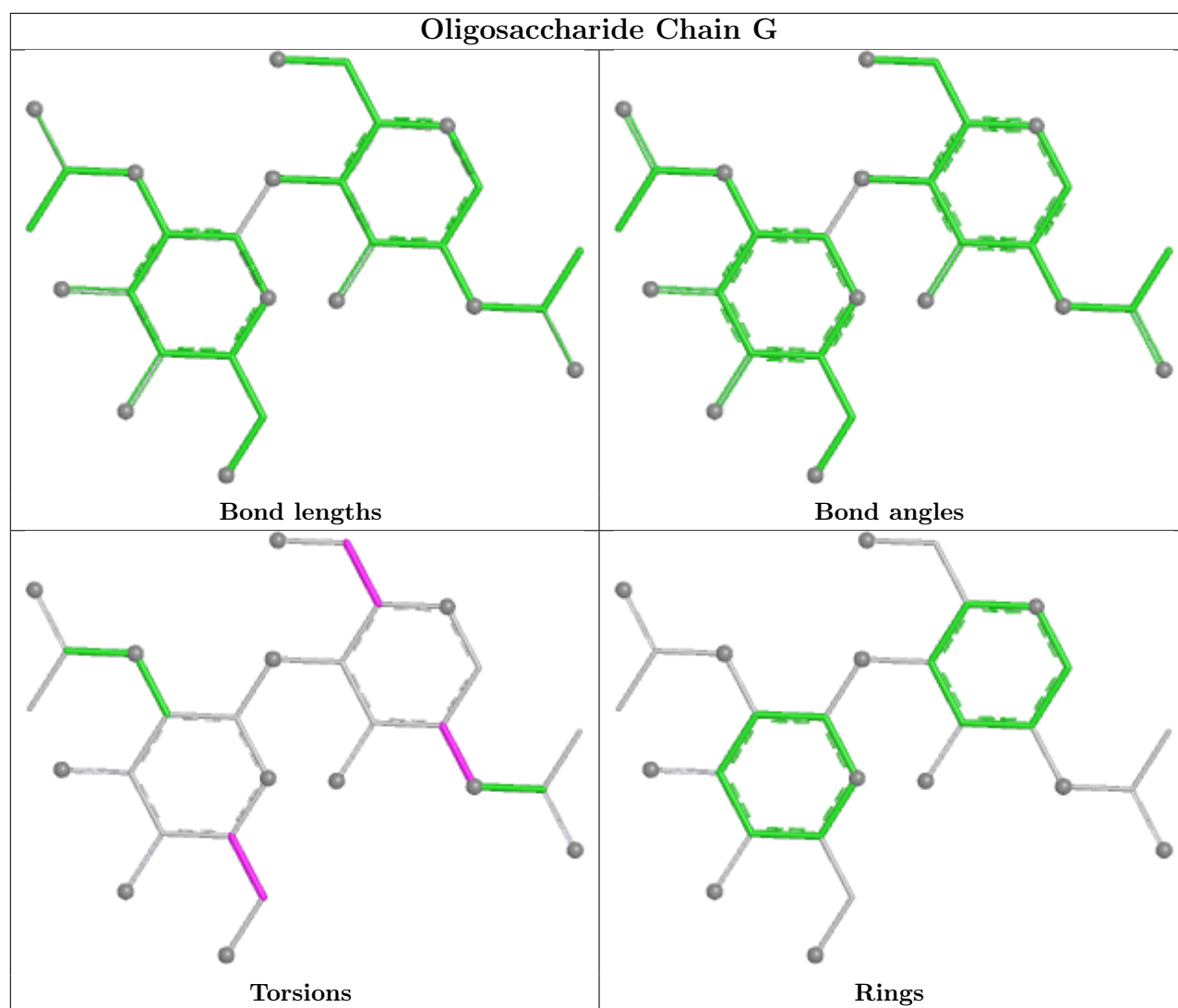
Mol	Chain	Res	Type	Atoms
7	J	4	MAN	C1-C2-C3-C4-C5-O5

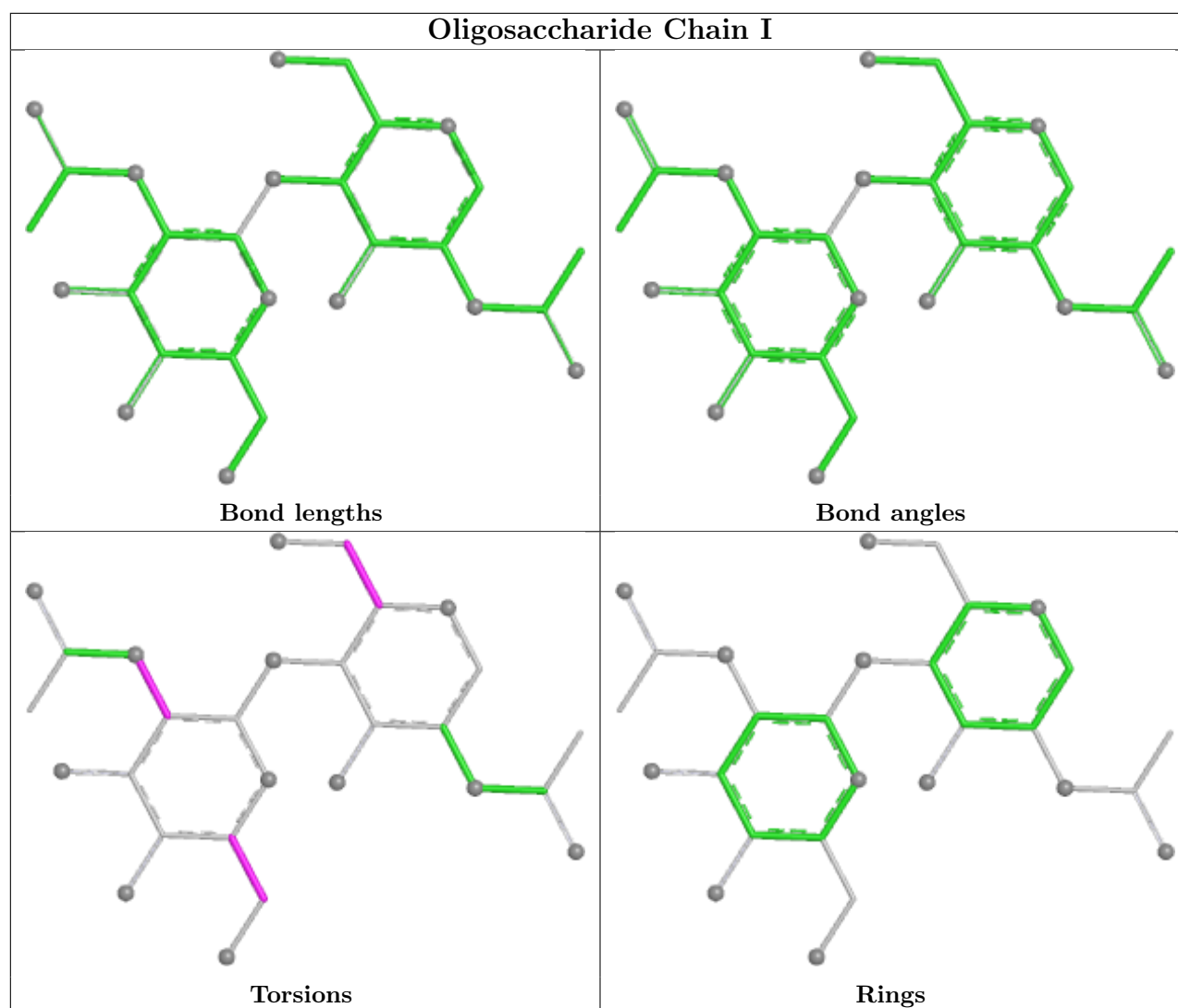
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	K	1	NAG	1	0
3	C	1	NAG	1	0
5	G	1	NAG	1	0

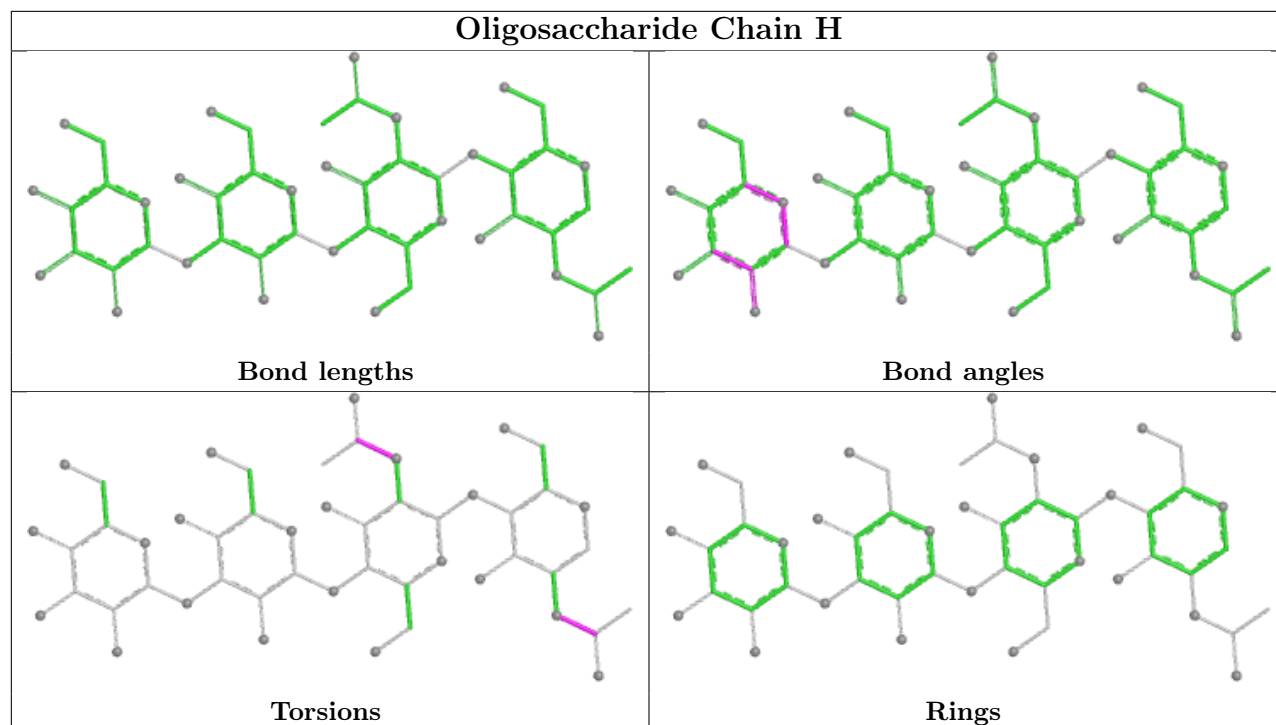
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



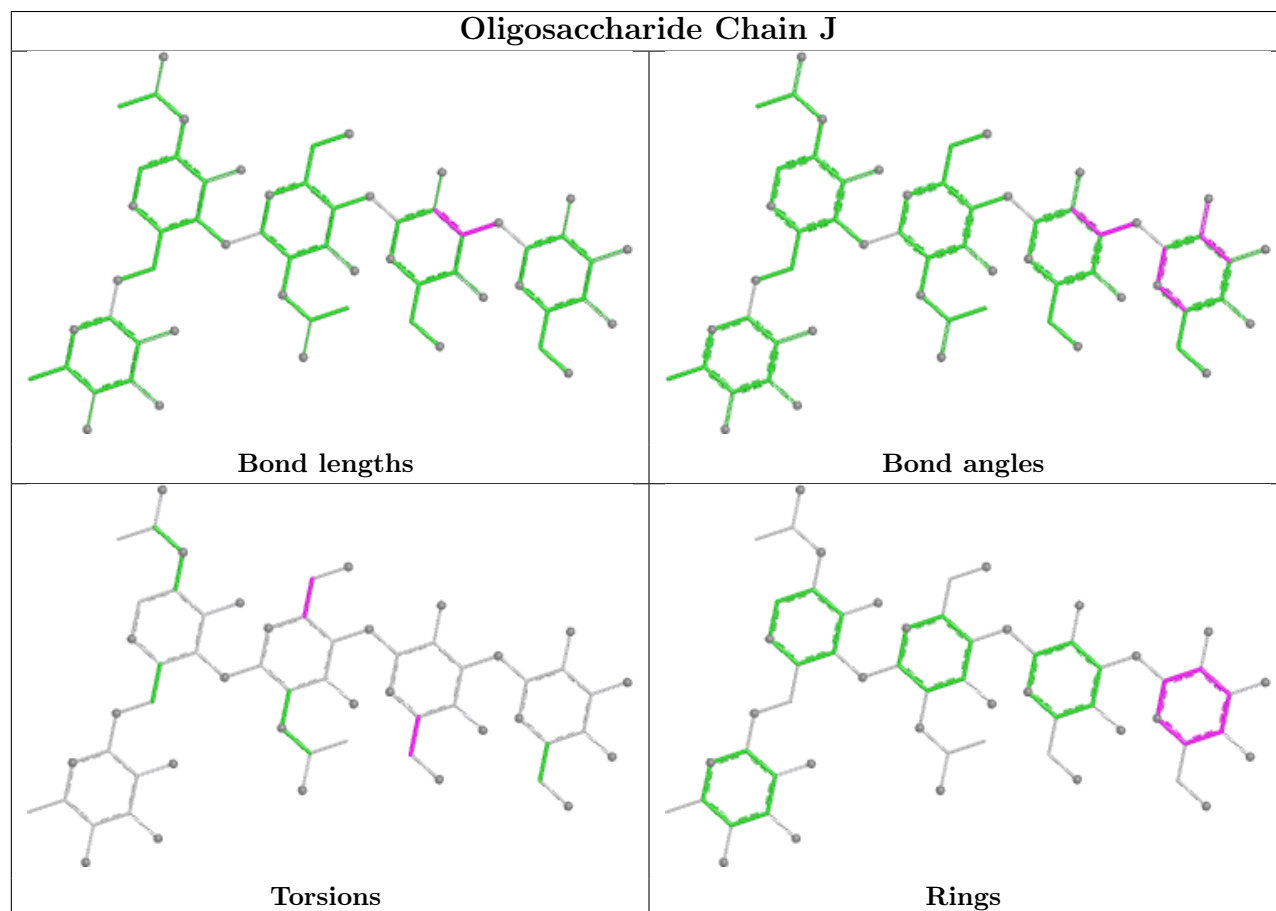


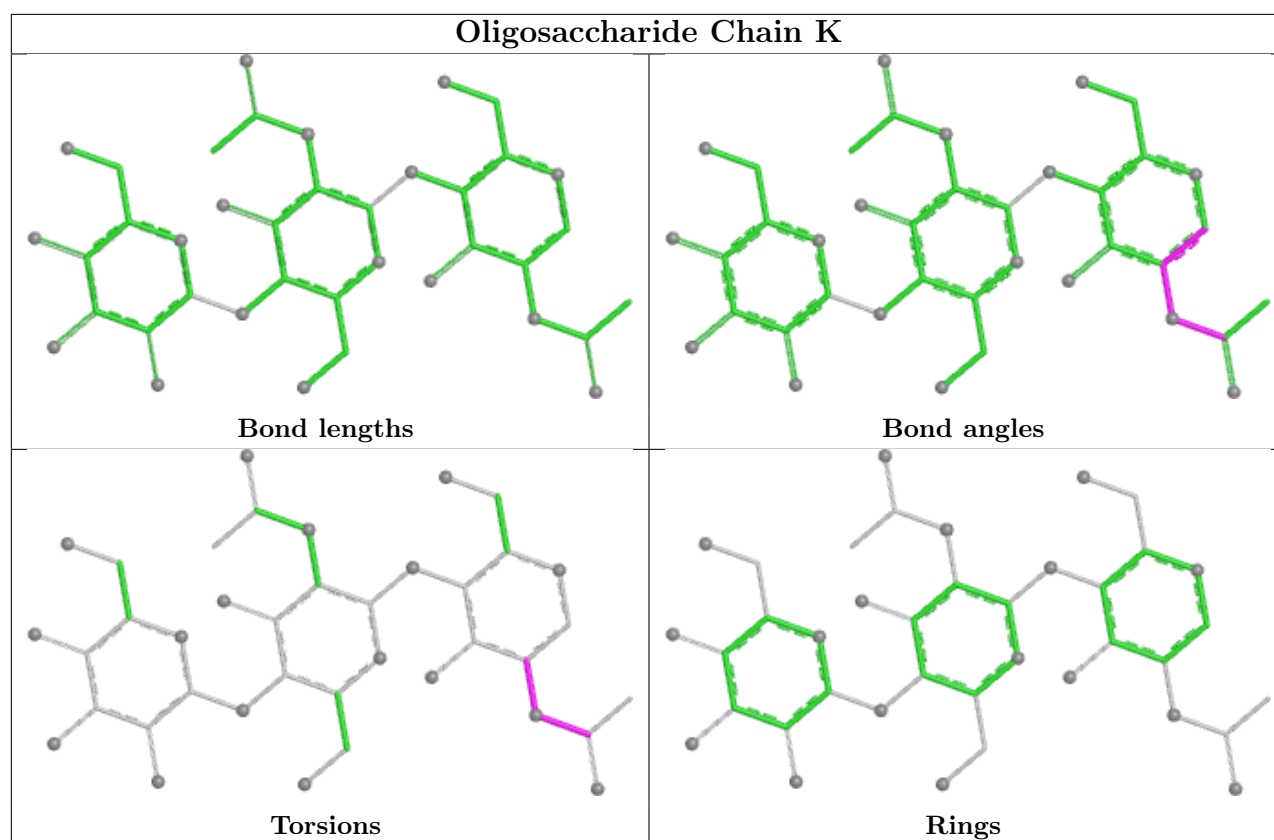


Oligosaccharide Chain H



Oligosaccharide Chain J





5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
11	NAG	A	703	1	14,14,15	0.26	0	17,19,21	0.45	0
11	NAG	B	705	1	14,14,15	0.28	0	17,19,21	0.48	0
12	EDO	B	704	-	3,3,3	0.42	0	2,2,2	0.39	0
12	EDO	B	703	-	3,3,3	0.42	0	2,2,2	0.39	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	NAG	A	703	1	-	2/6/23/26	0/1/1/1
11	NAG	B	705	1	-	4/6/23/26	0/1/1/1
12	EDO	B	704	-	-	1/1/1/1	-
12	EDO	B	703	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	703	NAG	C8-C7-N2-C2
11	A	703	NAG	O7-C7-N2-C2
11	B	705	NAG	C8-C7-N2-C2
11	B	705	NAG	O7-C7-N2-C2
11	B	705	NAG	C4-C5-C6-O6
11	B	705	NAG	O5-C5-C6-O6
12	B	704	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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	594/602 (98%)	0.56	43 (7%) 21 21	39, 83, 141, 203	0
1	B	595/602 (98%)	0.23	17 (2%) 53 55	37, 69, 134, 217	0
2	E	193/232 (83%)	0.40	10 (5%) 33 33	45, 77, 167, 277	0
2	F	194/232 (83%)	0.78	16 (8%) 17 17	59, 112, 183, 248	0
All	All	1576/1668 (94%)	0.44	86 (5%) 30 30	37, 80, 155, 277	0

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	333	LEU	4.5
1	A	362	THR	4.2
1	B	614	ALA	4.1
2	E	515	PHE	3.9
1	A	360	MET	3.9
1	A	390	PHE	3.5
2	E	387	LEU	3.5
1	A	424	LEU	3.4
2	F	456	PHE	3.4
1	A	370	LEU	3.4
1	A	346	PRO	3.3
1	A	413	ALA	3.3
1	A	409	SER	3.2
1	B	97	LEU	3.2
2	E	522	ALA	3.2
1	A	302	TRP	3.1
1	B	342	VAL	3.1
1	A	102	GLN	3.1
1	A	369	PHE	3.0
2	F	338	PHE	3.0
1	B	107	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
2	F	368	LEU	3.0
2	E	373	PHE	3.0
1	A	412	ALA	3.0
2	F	520	ALA	2.9
1	A	88	ILE	2.9
1	A	391	LEU	2.8
1	A	334	THR	2.8
2	F	483	VAL	2.8
2	F	490	PHE	2.8
1	A	368	ASP	2.7
1	A	298	VAL	2.7
2	E	365	TYR	2.7
1	A	349	TRP	2.7
1	B	108	LEU	2.6
1	A	55	THR	2.6
1	A	296	ALA	2.6
1	A	314	PHE	2.6
1	B	106	SER	2.6
1	A	343	VAL	2.5
1	B	172	VAL	2.5
2	E	527	PRO	2.5
1	B	69	TRP	2.5
2	E	382	VAL	2.5
2	F	391	CYS	2.5
1	B	217	TYR	2.5
2	F	392	PHE	2.5
1	B	84	PRO	2.4
1	B	85	LEU	2.4
1	A	210	ASN	2.4
1	A	293	VAL	2.4
1	A	423	LEU	2.4
1	B	343	VAL	2.4
1	B	513	ILE	2.3
2	F	332	ILE	2.3
1	A	428	PHE	2.3
2	E	384	ALA	2.3
2	E	392	PHE	2.3
1	A	614	ALA	2.2
1	A	562	LYS	2.2
2	F	430	MET	2.2
1	B	79	LEU	2.2
1	A	421	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	48	TRP	2.2
1	A	344	CYS	2.2
2	F	495	TYR	2.2
1	A	366	MET	2.2
2	F	418	ILE	2.2
1	B	431	ASP	2.2
1	A	525	PHE	2.2
1	A	501	ALA	2.2
2	E	521	PRO	2.2
2	F	397	ALA	2.1
1	B	179	LEU	2.1
2	F	492	LEU	2.1
1	A	54	ILE	2.1
1	A	172	VAL	2.1
1	A	297	MET	2.1
1	A	301	ALA	2.1
1	A	332	MET	2.1
1	A	300	GLN	2.1
1	B	135	PRO	2.0
1	A	32	PHE	2.0
1	A	324	THR	2.0
2	F	523	THR	2.0
2	F	369	TYR	2.0

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

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

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	C	1	14/15	-	-	129,138,147,152	0
3	FUC	C	2	10/11	-	-	117,141,146,147	0
4	NAG	D	1	14/15	-	-	120,128,136,138	0
4	NAG	D	2	14/15	-	-	88,119,130,134	0
4	BMA	D	3	11/12	-	-	114,122,138,138	0

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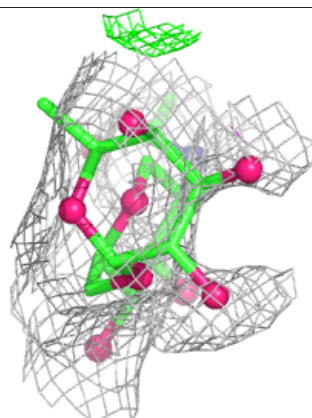
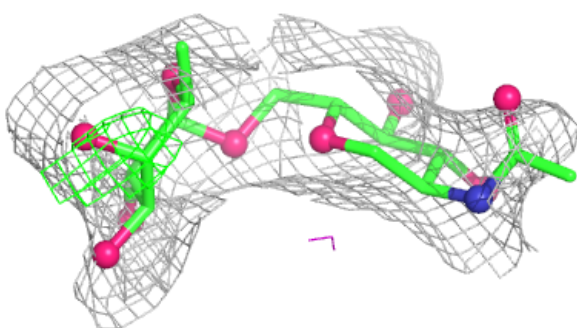
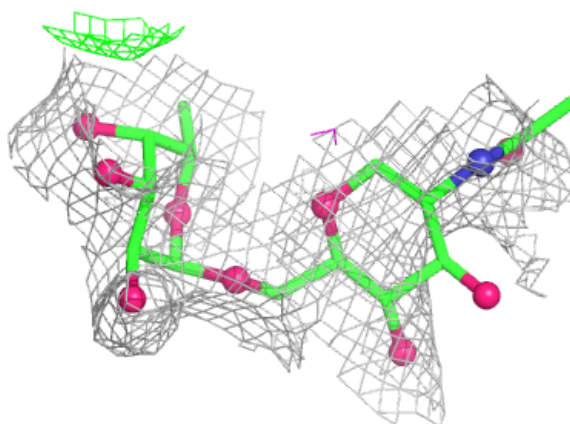
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	BMA	D	4	11/12	-	-	78,109,117,122	0
4	FUC	D	5	10/11	-	-	90,102,118,121	0
8	BMA	K	3	11/12	0.33	0.15	122,126,144,155	0
5	NAG	I	2	14/15	0.45	0.15	99,114,128,129	0
8	NAG	K	2	14/15	0.61	0.14	115,125,149,149	0
6	MAN	H	4	11/12	0.62	0.13	71,100,112,118	0
5	NAG	G	2	14/15	0.69	0.11	84,118,138,150	0
6	BMA	H	3	11/12	0.70	0.10	69,83,99,101	0
7	BMA	J	3	11/12	0.73	0.16	84,98,112,114	0
8	NAG	K	1	14/15	0.74	0.11	86,115,127,132	0
5	NAG	I	1	14/15	0.79	0.12	86,100,116,118	0
7	MAN	J	4	11/12	0.81	0.14	57,79,93,96	0
5	NAG	G	1	14/15	0.81	0.13	99,116,123,128	0
7	NAG	J	1	14/15	0.84	0.13	101,116,124,129	0
6	NAG	H	2	14/15	0.85	0.10	49,59,76,93	0
7	NAG	J	2	14/15	0.85	0.12	80,102,111,115	0
7	FUC	J	5	10/11	0.85	0.16	90,101,114,115	0
6	NAG	H	1	14/15	0.93	0.08	35,54,73,82	0

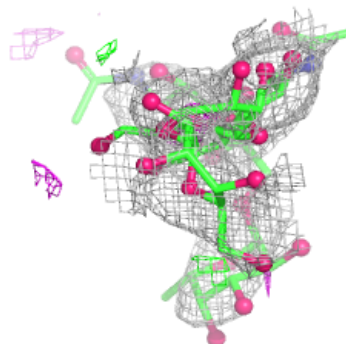
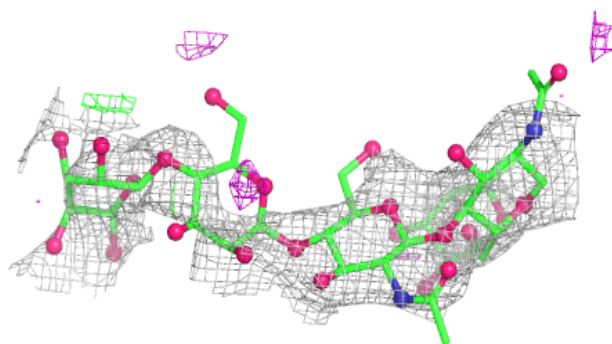
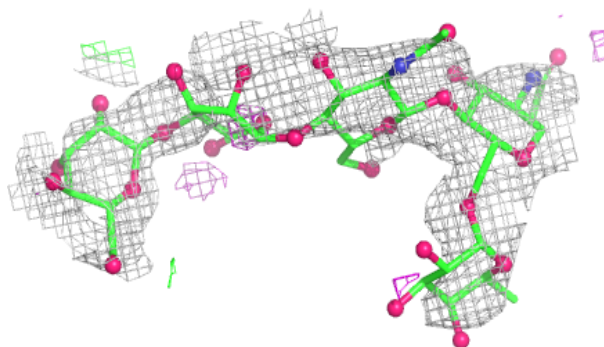
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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

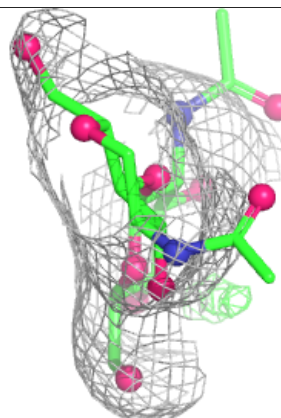
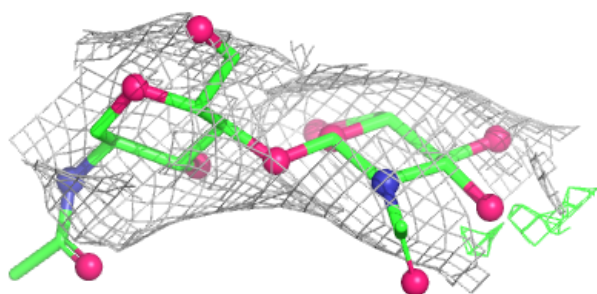
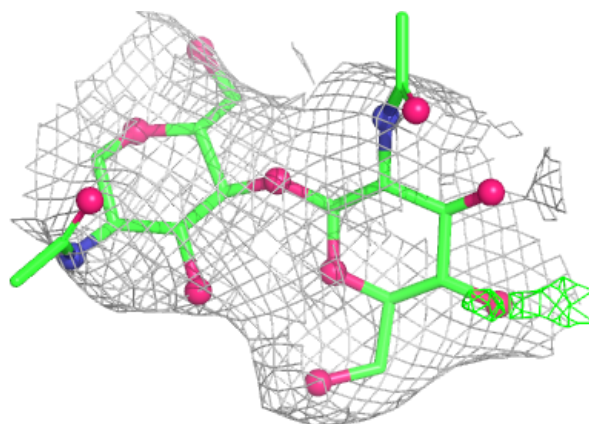
**Electron density around Chain D:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

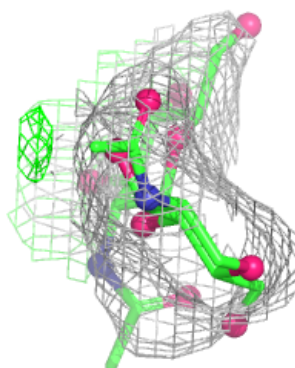
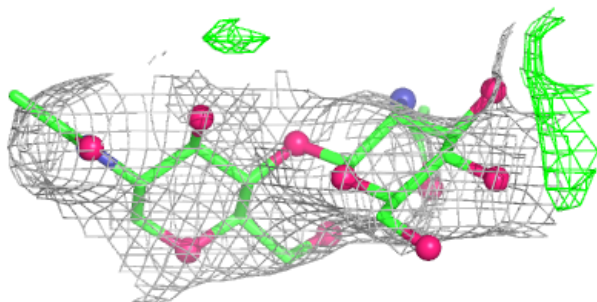


Electron density around Chain G:

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

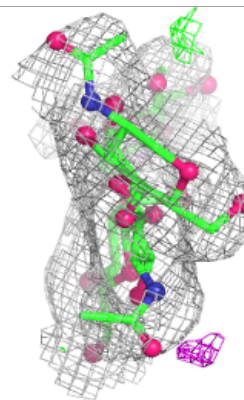
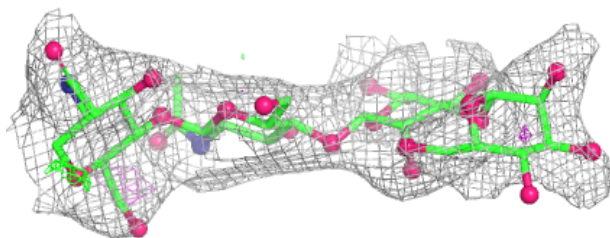
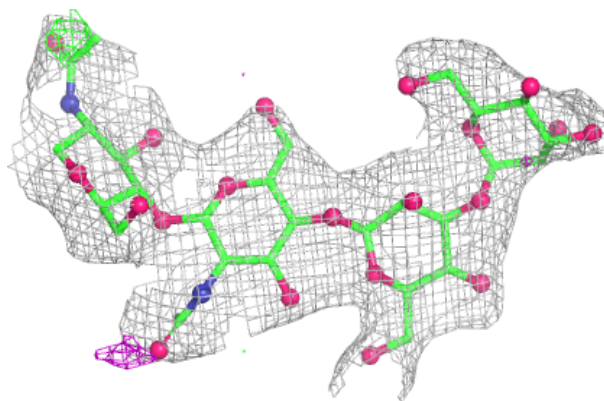
**Electron density around Chain I:**

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

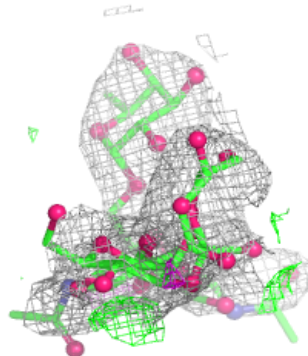
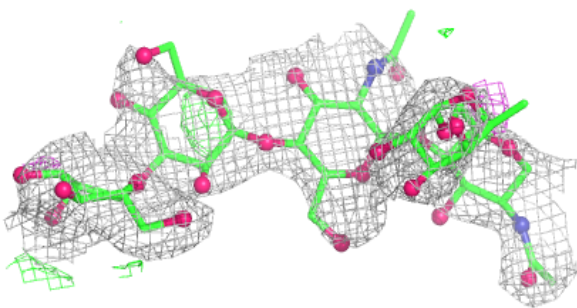
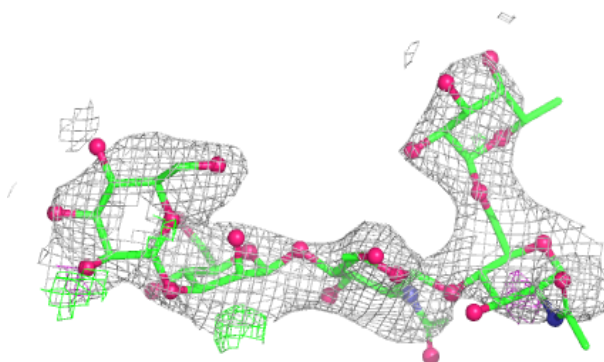


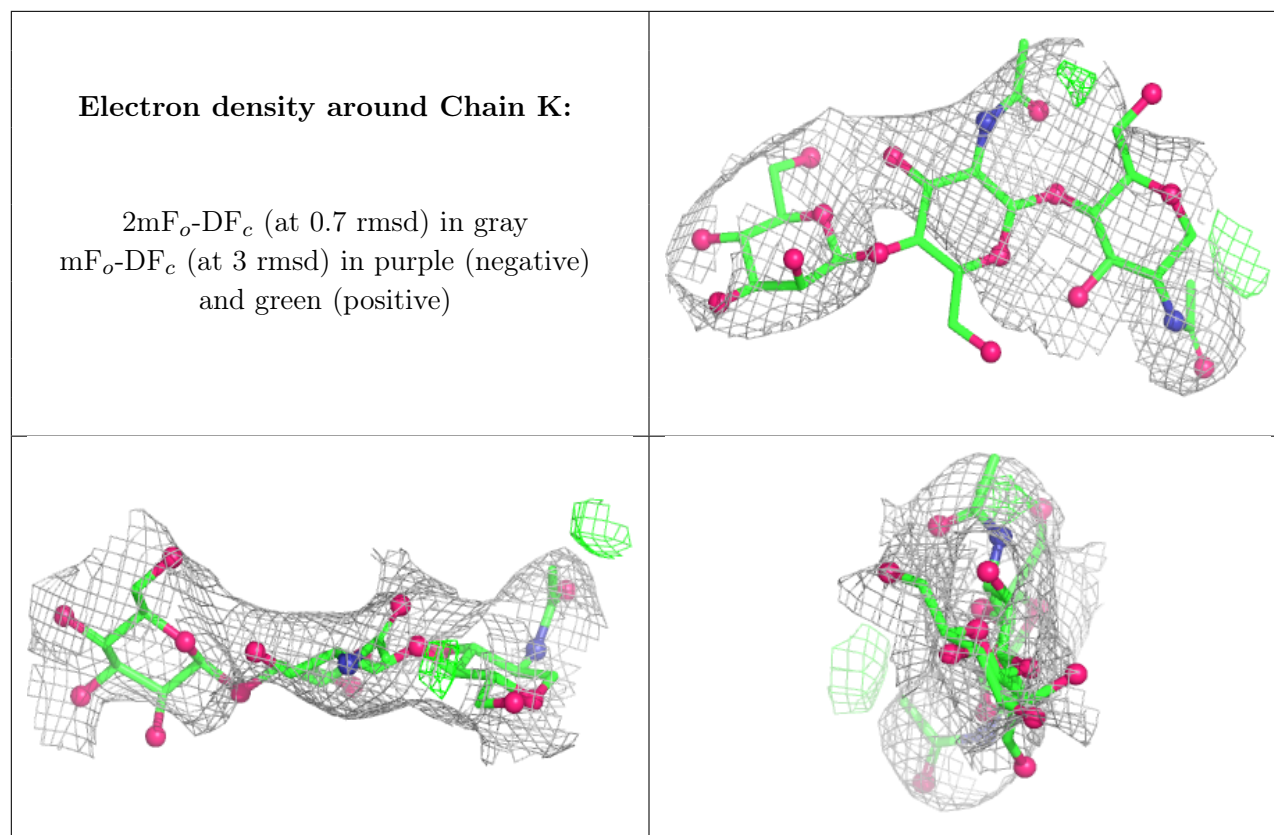
Electron density around Chain H:

$2mF_o-DF_c$ (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)





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
11	NAG	A	703	14/15	0.51	0.14	98,133,141,147	0
11	NAG	B	705	14/15	0.66	0.12	76,93,105,116	0
12	EDO	B	704	4/4	0.85	0.13	44,52,55,58	0
12	EDO	B	703	4/4	0.86	0.12	48,53,61,67	0
10	CL	B	702	1/1	0.91	0.09	75,75,75,75	0
9	ZN	B	701	1/1	0.93	0.08	85,85,85,85	0
10	CL	A	702	1/1	0.94	0.10	64,64,64,64	0
9	ZN	A	701	1/1	0.98	0.05	85,85,85,85	0

6.5 Other polymers [i](#)

There are no such residues in this entry.