



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 15, 2021 – 02:05 PM EST

PDB ID : 7SHZ
Title : IgE-Fc in complex with HAE
Authors : Pennington, L.F.; Jardetzky, T.J.; Kleinboelting, S.
Deposited on : 2021-10-11
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.24
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.24

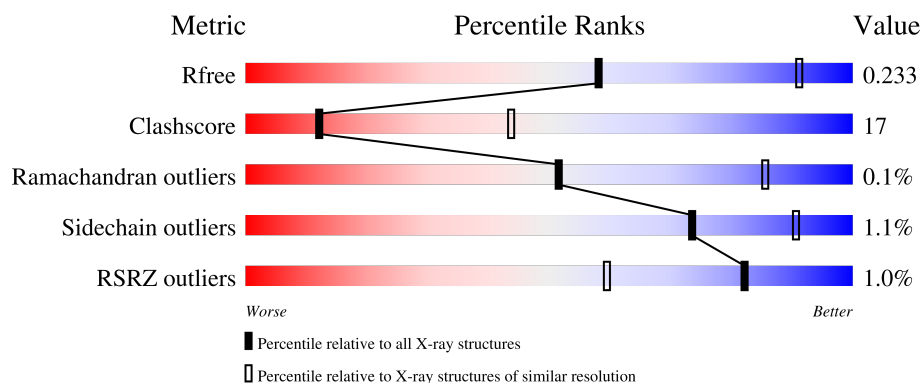
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	247	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%; height: 10px; background-color: red;"></div> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px; background-color: green;"></div> <div style="position: absolute; bottom: 0; left: 67%; width: 33%; height: 10px; background-color: yellow;"></div> <div style="position: absolute; bottom: 0; left: 95%; width: 5%; height: 10px; background-color: grey;"></div> </div> <div>67% 18% 15%</div> </div>
1	B	247	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px; background-color: green;"></div> <div style="position: absolute; bottom: 0; left: 50%; width: 50%; height: 10px; background-color: yellow;"></div> <div style="position: absolute; bottom: 0; left: 95%; width: 5%; height: 10px; background-color: grey;"></div> </div> <div>50% 34% 15%</div> </div>
1	G	247	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%; height: 10px; background-color: red;"></div> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px; background-color: green;"></div> <div style="position: absolute; bottom: 0; left: 56%; width: 44%; height: 10px; background-color: yellow;"></div> <div style="position: absolute; bottom: 0; left: 95%; width: 5%; height: 10px; background-color: grey;"></div> </div> <div>4% 56% 26% 18%</div> </div>
1	H	247	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px; background-color: green;"></div> <div style="position: absolute; bottom: 0; left: 63%; width: 37%; height: 10px; background-color: yellow;"></div> <div style="position: absolute; bottom: 0; left: 95%; width: 5%; height: 10px; background-color: grey;"></div> </div> <div>63% 23% 15%</div> </div>
2	C	123	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px; background-color: green;"></div> <div style="position: absolute; bottom: 0; left: 68%; width: 32%; height: 10px; background-color: yellow;"></div> <div style="position: absolute; bottom: 0; left: 95%; width: 5%; height: 10px; background-color: grey;"></div> </div> <div>68% 31% .</div> </div>

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Mol	Chain	Length	Quality of chain
2	E	123	
2	I	123	
2	K	123	
3	D	135	
3	F	135	
3	J	135	
3	L	135	
4	M	7	
5	N	4	
6	O	6	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MAN	M	5	-	-	-	X
6	BMA	O	3	-	-	X	-
6	MAN	O	6	-	-	X	-

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 14087 atoms, of which 23 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 IgE Fc.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	209	Total	C	N	O	S	0	0	0
			1654	1035	305	308	6			
1	A	210	Total	C	N	O	S	0	0	0
			1651	1033	304	308	6			
1	H	211	Total	C	N	O	S	0	0	0
			1650	1034	302	308	6			
1	G	202	Total	C	N	O	S	0	0	0
			1594	1001	290	297	6			

There are 116 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	299	ALA	-	expression tag	UNP P01854
B	300	PRO	-	expression tag	UNP P01854
B	301	MET	-	expression tag	UNP P01854
B	302	ALA	-	expression tag	UNP P01854
B	303	GLU	-	expression tag	UNP P01854
B	304	GLY	-	expression tag	UNP P01854
B	305	GLY	-	expression tag	UNP P01854
B	306	GLY	-	expression tag	UNP P01854
B	307	GLN	-	expression tag	UNP P01854
B	308	ASN	-	expression tag	UNP P01854
B	309	HIS	-	expression tag	UNP P01854
B	310	HIS	-	expression tag	UNP P01854
B	311	HIS	-	expression tag	UNP P01854
B	312	HIS	-	expression tag	UNP P01854
B	313	HIS	-	expression tag	UNP P01854
B	314	HIS	-	expression tag	UNP P01854
B	315	HIS	-	expression tag	UNP P01854
B	316	HIS	-	expression tag	UNP P01854
B	317	GLY	-	expression tag	UNP P01854
B	318	GLY	-	expression tag	UNP P01854
B	319	GLU	-	expression tag	UNP P01854

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Chain	Residue	Modelled	Actual	Comment	Reference
B	320	ASN	-	expression tag	UNP P01854
B	321	LEU	-	expression tag	UNP P01854
B	322	TYR	-	expression tag	UNP P01854
B	323	PHE	-	expression tag	UNP P01854
B	324	GLN	-	expression tag	UNP P01854
B	325	GLY	-	expression tag	UNP P01854
B	326	GLY	-	expression tag	UNP P01854
B	327	SER	-	expression tag	UNP P01854
A	299	ALA	-	expression tag	UNP P01854
A	300	PRO	-	expression tag	UNP P01854
A	301	MET	-	expression tag	UNP P01854
A	302	ALA	-	expression tag	UNP P01854
A	303	GLU	-	expression tag	UNP P01854
A	304	GLY	-	expression tag	UNP P01854
A	305	GLY	-	expression tag	UNP P01854
A	306	GLY	-	expression tag	UNP P01854
A	307	GLN	-	expression tag	UNP P01854
A	308	ASN	-	expression tag	UNP P01854
A	309	HIS	-	expression tag	UNP P01854
A	310	HIS	-	expression tag	UNP P01854
A	311	HIS	-	expression tag	UNP P01854
A	312	HIS	-	expression tag	UNP P01854
A	313	HIS	-	expression tag	UNP P01854
A	314	HIS	-	expression tag	UNP P01854
A	315	HIS	-	expression tag	UNP P01854
A	316	HIS	-	expression tag	UNP P01854
A	317	GLY	-	expression tag	UNP P01854
A	318	GLY	-	expression tag	UNP P01854
A	319	GLU	-	expression tag	UNP P01854
A	320	ASN	-	expression tag	UNP P01854
A	321	LEU	-	expression tag	UNP P01854
A	322	TYR	-	expression tag	UNP P01854
A	323	PHE	-	expression tag	UNP P01854
A	324	GLN	-	expression tag	UNP P01854
A	325	GLY	-	expression tag	UNP P01854
A	326	GLY	-	expression tag	UNP P01854
A	327	SER	-	expression tag	UNP P01854
H	299	ALA	-	expression tag	UNP P01854
H	300	PRO	-	expression tag	UNP P01854
H	301	MET	-	expression tag	UNP P01854
H	302	ALA	-	expression tag	UNP P01854
H	303	GLU	-	expression tag	UNP P01854

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Chain	Residue	Modelled	Actual	Comment	Reference
H	304	GLY	-	expression tag	UNP P01854
H	305	GLY	-	expression tag	UNP P01854
H	306	GLY	-	expression tag	UNP P01854
H	307	GLN	-	expression tag	UNP P01854
H	308	ASN	-	expression tag	UNP P01854
H	309	HIS	-	expression tag	UNP P01854
H	310	HIS	-	expression tag	UNP P01854
H	311	HIS	-	expression tag	UNP P01854
H	312	HIS	-	expression tag	UNP P01854
H	313	HIS	-	expression tag	UNP P01854
H	314	HIS	-	expression tag	UNP P01854
H	315	HIS	-	expression tag	UNP P01854
H	316	HIS	-	expression tag	UNP P01854
H	317	GLY	-	expression tag	UNP P01854
H	318	GLY	-	expression tag	UNP P01854
H	319	GLU	-	expression tag	UNP P01854
H	320	ASN	-	expression tag	UNP P01854
H	321	LEU	-	expression tag	UNP P01854
H	322	TYR	-	expression tag	UNP P01854
H	323	PHE	-	expression tag	UNP P01854
H	324	GLN	-	expression tag	UNP P01854
H	325	GLY	-	expression tag	UNP P01854
H	326	GLY	-	expression tag	UNP P01854
H	327	SER	-	expression tag	UNP P01854
G	299	ALA	-	expression tag	UNP P01854
G	300	PRO	-	expression tag	UNP P01854
G	301	MET	-	expression tag	UNP P01854
G	302	ALA	-	expression tag	UNP P01854
G	303	GLU	-	expression tag	UNP P01854
G	304	GLY	-	expression tag	UNP P01854
G	305	GLY	-	expression tag	UNP P01854
G	306	GLY	-	expression tag	UNP P01854
G	307	GLN	-	expression tag	UNP P01854
G	308	ASN	-	expression tag	UNP P01854
G	309	HIS	-	expression tag	UNP P01854
G	310	HIS	-	expression tag	UNP P01854
G	311	HIS	-	expression tag	UNP P01854
G	312	HIS	-	expression tag	UNP P01854
G	313	HIS	-	expression tag	UNP P01854
G	314	HIS	-	expression tag	UNP P01854
G	315	HIS	-	expression tag	UNP P01854
G	316	HIS	-	expression tag	UNP P01854

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Chain	Residue	Modelled	Actual	Comment	Reference
G	317	GLY	-	expression tag	UNP P01854
G	318	GLY	-	expression tag	UNP P01854
G	319	GLU	-	expression tag	UNP P01854
G	320	ASN	-	expression tag	UNP P01854
G	321	LEU	-	expression tag	UNP P01854
G	322	TYR	-	expression tag	UNP P01854
G	323	PHE	-	expression tag	UNP P01854
G	324	GLN	-	expression tag	UNP P01854
G	325	GLY	-	expression tag	UNP P01854
G	326	GLY	-	expression tag	UNP P01854
G	327	SER	-	expression tag	UNP P01854

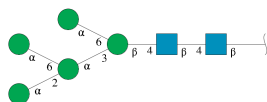
- Molecule 2 is a protein called HAE Variable fragment Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	K	121	Total	C	N	O	S	0	0	0
			941	597	164	177	3			
2	C	122	Total	C	N	O	S	0	0	0
			946	600	165	178	3			
2	I	119	Total	C	N	O	S	0	0	0
			929	591	162	173	3			
2	E	122	Total	C	N	O	S	0	0	0
			945	599	165	178	3			

- Molecule 3 is a protein called HAE Variable fragment Light chain.

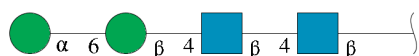
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	113	Total	C	N	O	S	0	0	0
			854	535	139	178	2			
3	D	114	Total	C	N	O	S	0	0	0
			859	537	140	180	2			
3	J	113	Total	C	N	O	S	0	0	0
			854	535	139	178	2			
3	F	114	Total	C	N	O	S	0	0	0
			863	540	141	180	2			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-[alpha-D-mannopyranose-(1-6)]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.



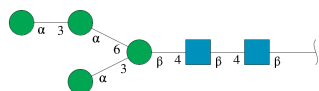
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	M	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 5 is an oligosaccharide called 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.



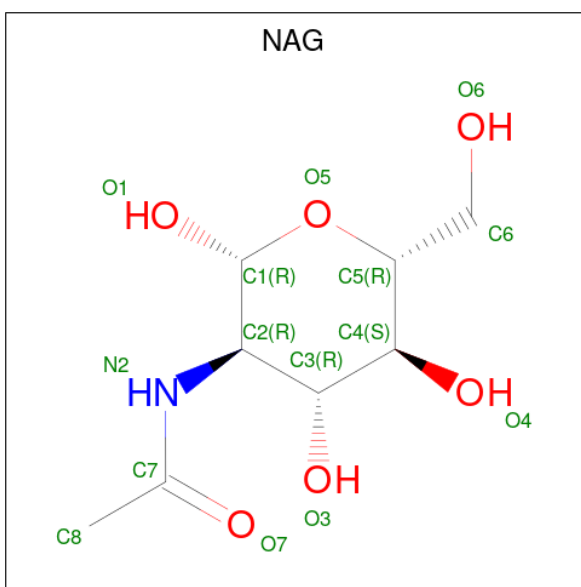
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	N	4	Total	C	N	O	0	0	0
			50	28	2	20			

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



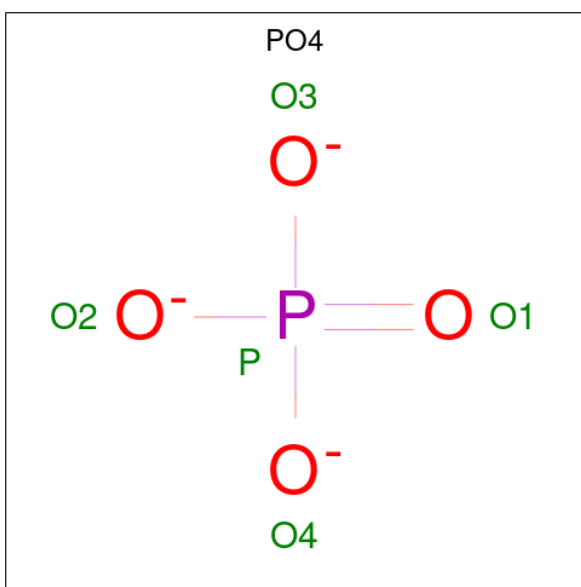
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	O	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 8 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



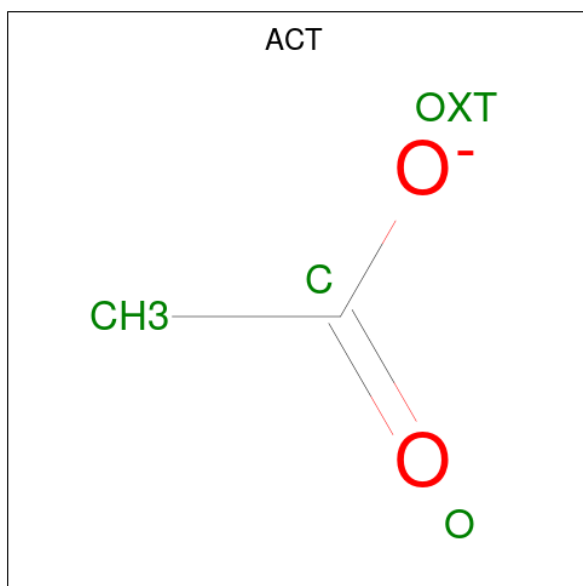
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	O	P	0	0
			5	4	1		

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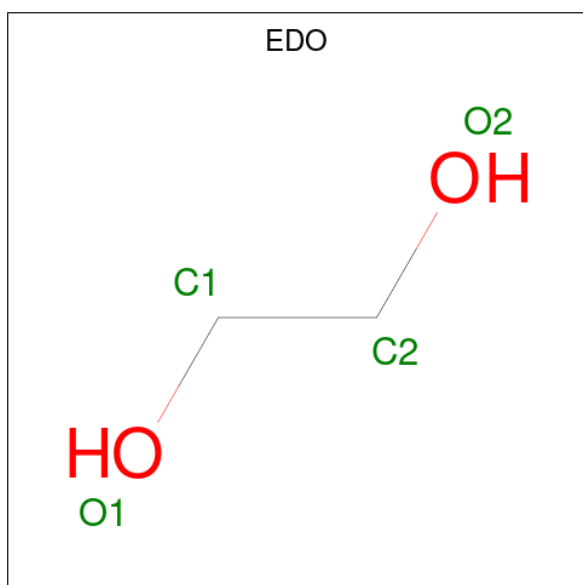
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	O	P	0	0
			5	4	1		

- Molecule 9 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



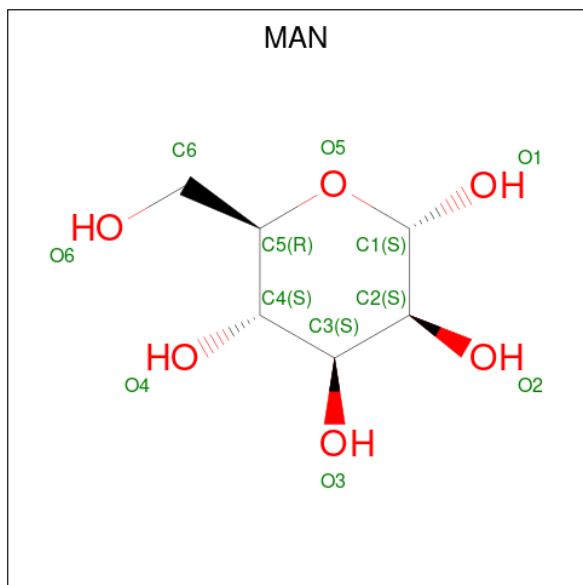
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	C	1	Total	C	H	O	0	0
			7	2	3	2		

- Molecule 10 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	D	1	Total	C	H	O	0	0
			10	2	6	2		
10	E	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 11 is alpha-D-mannopyranose (three-letter code: MAN) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			11	6	5		
11	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 12 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	A	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	B	2	Total	O	0	0
			2	2		
13	K	3	Total	O	0	0
			3	3		
13	C	1	Total	O	0	0
			1	1		
13	I	1	Total	O	0	0
			1	1		
13	L	2	Total	O	0	0
			2	2		
13	D	4	Total	O	0	0
			4	4		
13	J	1	Total	O	0	0
			1	1		
13	A	5	Total	O	0	0
			5	5		
13	H	3	Total	O	0	0
			3	3		
13	G	2	Total	O	0	0
			2	2		
13	E	1	Total	O	0	0
			1	1		

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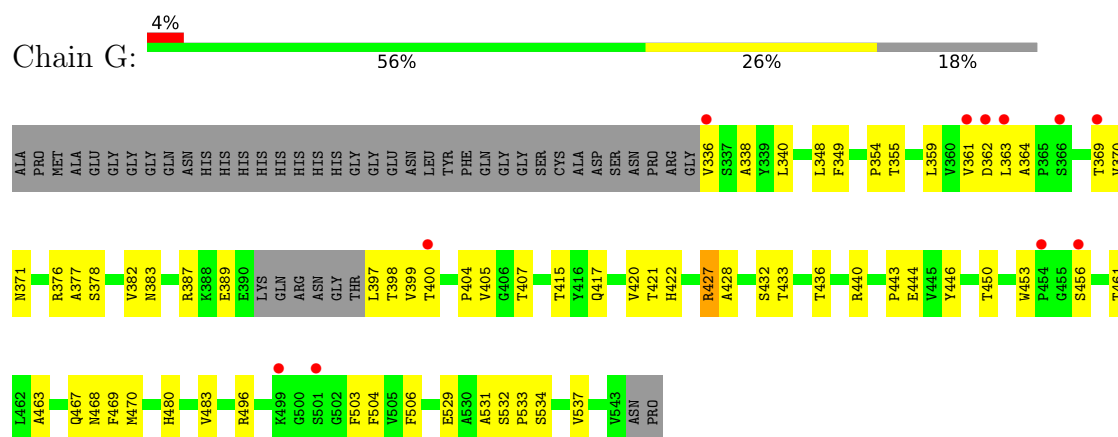
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	F	2	Total	O	0	0
			2	2		

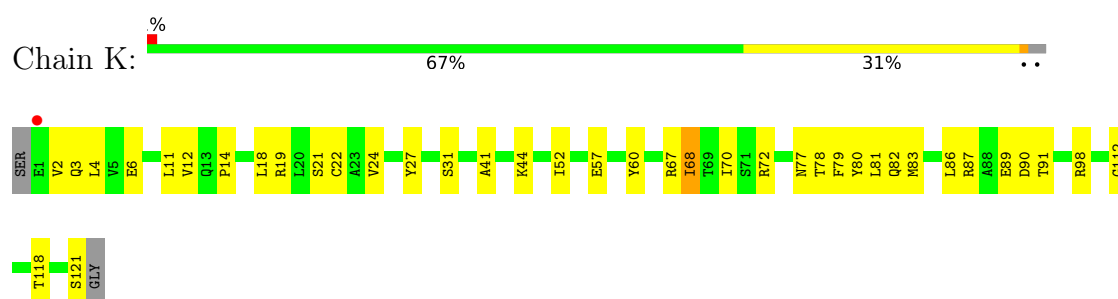
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Chain B:  50% 34% 1% 15%

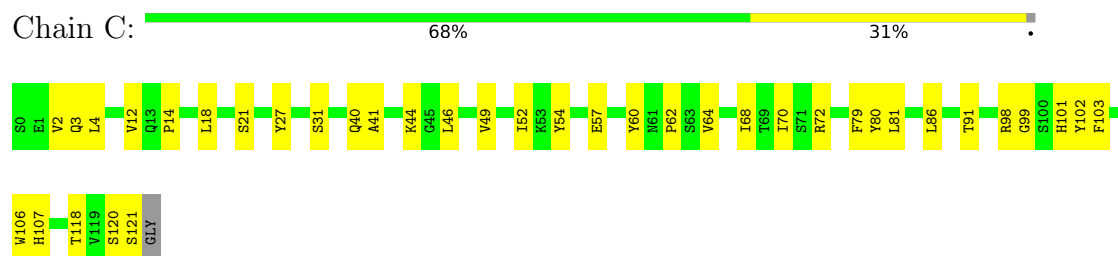




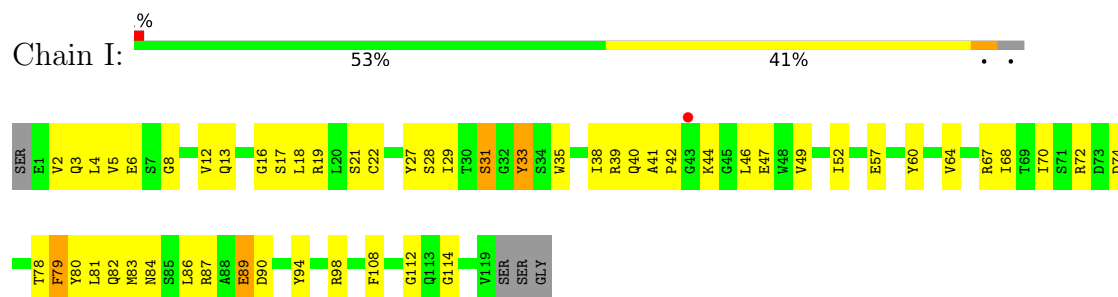
• Molecule 2: HAE Variable fragment Heavy chain



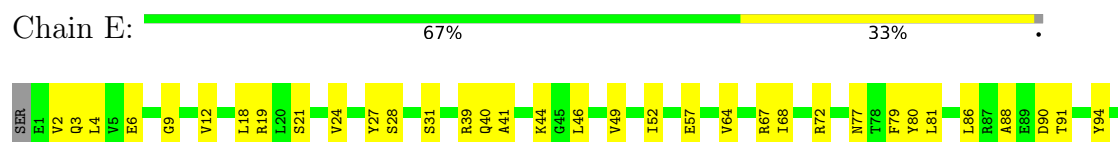
• Molecule 2: HAE Variable fragment Heavy chain



• Molecule 2: HAE Variable fragment Heavy chain

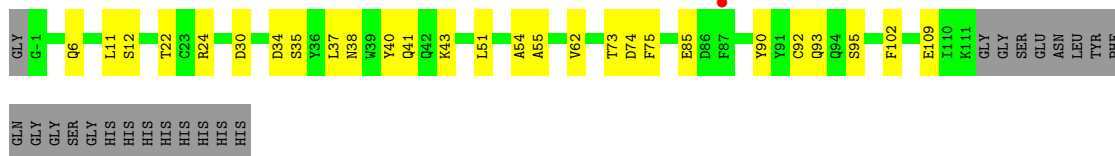


• Molecule 2: HAE Variable fragment Heavy chain





- Molecule 3: HAE Variable fragment Light chain



- Molecule 3: HAE Variable fragment Light chain



- Molecule 3: HAE Variable fragment Light chain



- Molecule 3: HAE Variable fragment Light chain



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

Chain N:  50% 50%



● Molecule 6: alpha-D-mannopyranose-(1-3)-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 O:  33% 67%



4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	93.34Å 187.34Å 148.83Å 90.00° 103.13° 90.00°	Depositor
Resolution (Å)	47.35 – 3.00 47.35 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.2 (47.35-3.00) 98.2 (47.35-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.186 , 0.235 0.183 , 0.233	Depositor DCC
R_{free} test set	1995 reflections (4.08%)	wwPDB-VP
Wilson B-factor (Å ²)	91.4	Xtriage
Anisotropy	0.634	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 79.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14087	wwPDB-VP
Average B, all atoms (Å ²)	112.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.49% 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: BMA, MAN, PO4, ACT, NAG, EDO, GOL

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	0.33	0/1693	0.53	0/2306
1	B	0.37	0/1695	0.57	0/2306
1	G	0.31	0/1635	0.53	0/2228
1	H	0.36	0/1692	0.59	0/2305
2	C	0.42	0/972	0.61	0/1319
2	E	0.36	0/971	0.59	0/1317
2	I	0.34	0/955	0.56	0/1296
2	K	0.41	0/967	0.60	0/1312
3	D	0.39	0/879	0.61	0/1194
3	F	0.36	0/883	0.57	0/1198
3	J	0.33	0/874	0.55	0/1188
3	L	0.40	0/874	0.63	0/1188
All	All	0.36	0/14090	0.57	0/19157

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

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	1651	0	1625	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1654	0	1635	107	0
1	G	1594	0	1570	46	1
1	H	1650	0	1621	47	0
2	C	946	0	903	41	0
2	E	945	0	904	33	0
2	I	929	0	891	53	1
2	K	941	0	901	31	0
3	D	859	0	811	18	0
3	F	863	0	822	16	1
3	J	854	0	805	12	1
3	L	854	0	805	18	0
4	M	83	0	70	8	0
5	N	50	0	43	8	0
6	O	72	0	60	11	0
7	B	14	0	13	0	0
7	G	14	0	13	2	0
7	H	14	0	13	5	0
8	C	10	0	0	0	0
9	C	4	3	3	0	0
10	D	4	6	6	0	0
10	E	4	6	6	0	0
11	A	22	0	20	3	0
12	A	6	8	8	1	0
13	A	5	0	0	0	0
13	B	2	0	0	0	0
13	C	1	0	0	0	0
13	D	4	0	0	0	0
13	E	1	0	0	0	0
13	F	2	0	0	0	0
13	G	2	0	0	0	0
13	H	3	0	0	0	0
13	I	1	0	0	0	0
13	J	1	0	0	0	0
13	K	3	0	0	0	0
13	L	2	0	0	0	0
All	All	14064	23	13548	472	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

The worst 5 of 472 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:B:427:ARG:NH2	3:F:35:SER:OG	1.79	1.15
2:I:68:ILE:HD11	2:I:81:LEU:HD11	1.21	1.14
2:C:68:ILE:HD11	2:C:81:LEU:HD11	1.30	1.10
2:E:68:ILE:HD11	2:E:81:LEU:HD11	1.39	1.02
1:G:389:GLU:HB3	1:G:397:LEU:HD11	1.40	1.01

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:74:ASP:OD2	1:G:534:SER:OG[2_755]	2.02	0.18
3:J:18:ARG:NH2	3:F:74:ASP:OD2[4_645]	2.18	0.02

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	208/247 (84%)	202 (97%)	6 (3%)	0	100	100
1	B	206/247 (83%)	200 (97%)	6 (3%)	0	100	100
1	G	198/247 (80%)	192 (97%)	5 (2%)	1 (0%)	29	68
1	H	209/247 (85%)	204 (98%)	5 (2%)	0	100	100
2	C	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
2	E	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
2	I	117/123 (95%)	115 (98%)	2 (2%)	0	100	100
2	K	119/123 (97%)	118 (99%)	1 (1%)	0	100	100
3	D	112/135 (83%)	108 (96%)	4 (4%)	0	100	100
3	F	112/135 (83%)	106 (95%)	6 (5%)	0	100	100
3	J	111/135 (82%)	107 (96%)	4 (4%)	0	100	100
3	L	111/135 (82%)	106 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1743/2020 (86%)	1695 (97%)	47 (3%)	1 (0%)	51 85

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	383	ASN

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	183/212 (86%)	183 (100%)	0	100 100
1	B	185/212 (87%)	180 (97%)	5 (3%)	44 77
1	G	178/212 (84%)	177 (99%)	1 (1%)	86 95
1	H	182/212 (86%)	181 (100%)	1 (0%)	88 96
2	C	99/100 (99%)	99 (100%)	0	100 100
2	E	99/100 (99%)	99 (100%)	0	100 100
2	I	97/100 (97%)	92 (95%)	5 (5%)	23 59
2	K	99/100 (99%)	98 (99%)	1 (1%)	76 91
3	D	95/112 (85%)	94 (99%)	1 (1%)	73 90
3	F	96/112 (86%)	95 (99%)	1 (1%)	76 91
3	J	94/112 (84%)	93 (99%)	1 (1%)	73 90
3	L	94/112 (84%)	93 (99%)	1 (1%)	73 90
All	All	1501/1696 (88%)	1484 (99%)	17 (1%)	73 90

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	384	HIS
3	F	34	ASP
2	I	33	TYR

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Mol	Chain	Res	Type
2	I	79	PHE
2	I	84	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	424	HIS
2	K	82	GLN
1	A	424	HIS
1	H	371	ASN
1	H	424	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 ⓘ

17 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	NAG	M	1	1,4	14,14,15	1.32	1 (7%)	17,19,21	1.60	3 (17%)
4	NAG	M	2	4	14,14,15	0.62	1 (7%)	17,19,21	0.66	0
4	BMA	M	3	4	11,11,12	1.07	1 (9%)	15,15,17	0.91	0
4	MAN	M	4	4	11,11,12	0.85	0	15,15,17	1.29	1 (6%)
4	MAN	M	5	4	11,11,12	2.23	3 (27%)	15,15,17	2.09	4 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MAN	M	6	4	11,11,12	0.98	0	15,15,17	1.39	4 (26%)
4	MAN	M	7	4	11,11,12	1.16	1 (9%)	15,15,17	1.09	2 (13%)
5	NAG	N	1	1,5	14,14,15	0.17	0	17,19,21	0.39	0
5	NAG	N	2	5	14,14,15	0.48	0	17,19,21	0.52	0
5	BMA	N	3	5	11,11,12	0.86	0	15,15,17	0.93	1 (6%)
5	MAN	N	4	5	11,11,12	2.27	4 (36%)	15,15,17	2.37	5 (33%)
6	NAG	O	1	1,6	14,14,15	0.57	0	17,19,21	0.64	0
6	NAG	O	2	6	14,14,15	0.20	0	17,19,21	0.63	1 (5%)
6	BMA	O	3	6	11,11,12	1.19	1 (9%)	15,15,17	1.21	2 (13%)
6	MAN	O	4	6	11,11,12	1.01	1 (9%)	15,15,17	1.19	1 (6%)
6	MAN	O	5	6	11,11,12	1.28	2 (18%)	15,15,17	0.92	0
6	MAN	O	6	6	11,11,12	1.41	2 (18%)	15,15,17	1.88	1 (6%)

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

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

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	M	1	NAG	O5-C1	-4.80	1.36	1.43
4	M	5	MAN	C2-C3	4.39	1.59	1.52
5	N	4	MAN	C1-C2	4.21	1.61	1.52
5	N	4	MAN	O5-C1	3.58	1.49	1.43
5	N	4	MAN	O5-C5	3.49	1.50	1.43

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	N	4	MAN	C1-O5-C5	6.88	121.52	112.19
6	O	6	MAN	C1-O5-C5	6.19	120.57	112.19
4	M	1	NAG	C1-O5-C5	-4.77	105.73	112.19
4	M	5	MAN	C1-C2-C3	4.75	115.50	109.67
4	M	5	MAN	C2-C3-C4	4.22	118.19	110.89

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	N	3	BMA	O5-C5-C6-O6
4	M	2	NAG	O5-C5-C6-O6
4	M	5	MAN	O5-C5-C6-O6
5	N	4	MAN	O5-C5-C6-O6
5	N	2	NAG	C4-C5-C6-O6

There are no ring outliers.

14 monomers are involved in 27 short contacts:

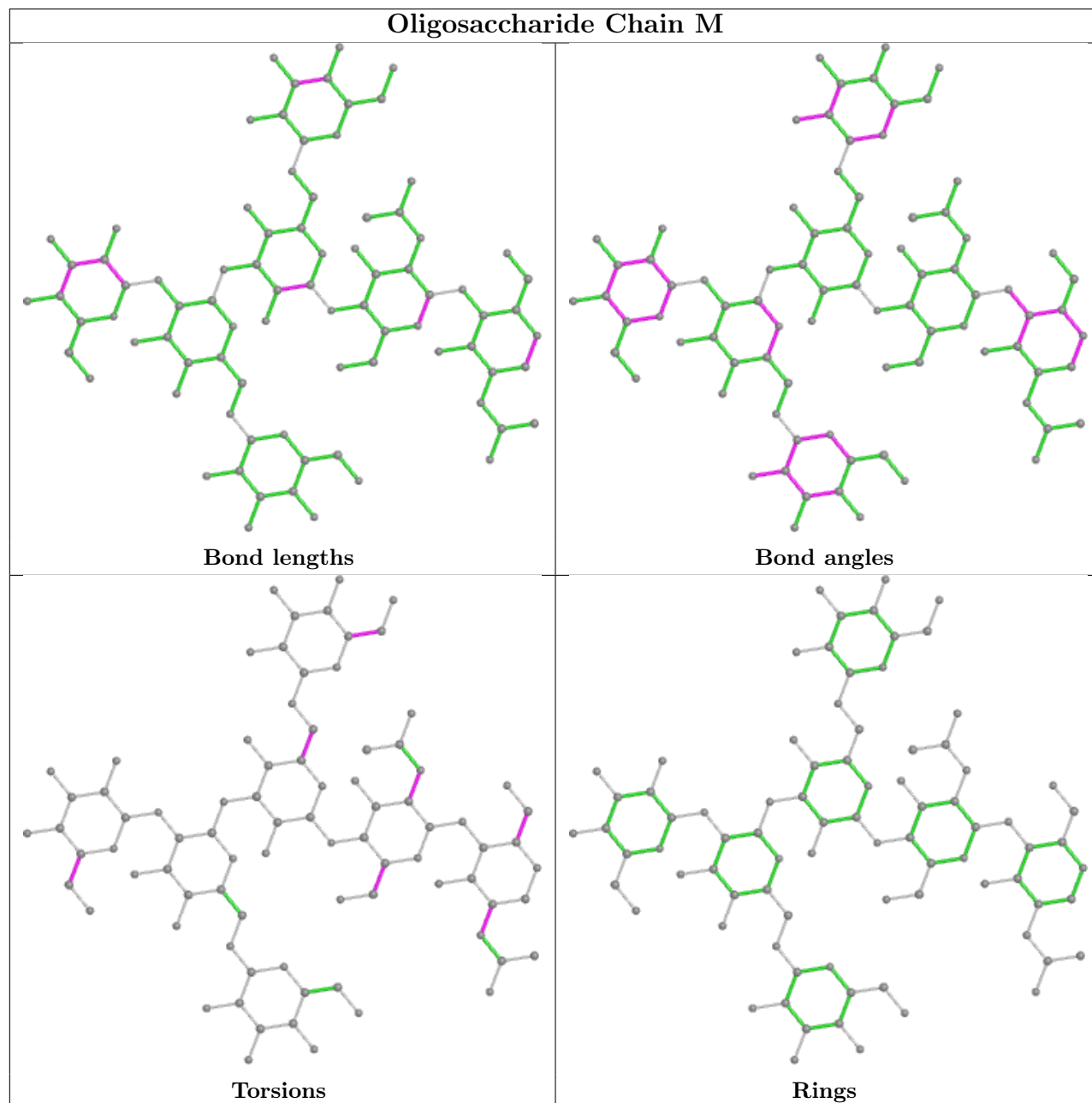
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	M	6	MAN	1	0
5	N	3	BMA	2	0
4	M	5	MAN	2	0
4	M	2	NAG	4	0
4	M	4	MAN	2	0
5	N	1	NAG	3	0
5	N	2	NAG	5	0
5	N	4	MAN	2	0
6	O	1	NAG	1	0
4	M	1	NAG	1	0
6	O	3	BMA	10	0
6	O	6	MAN	7	0
6	O	2	NAG	2	0

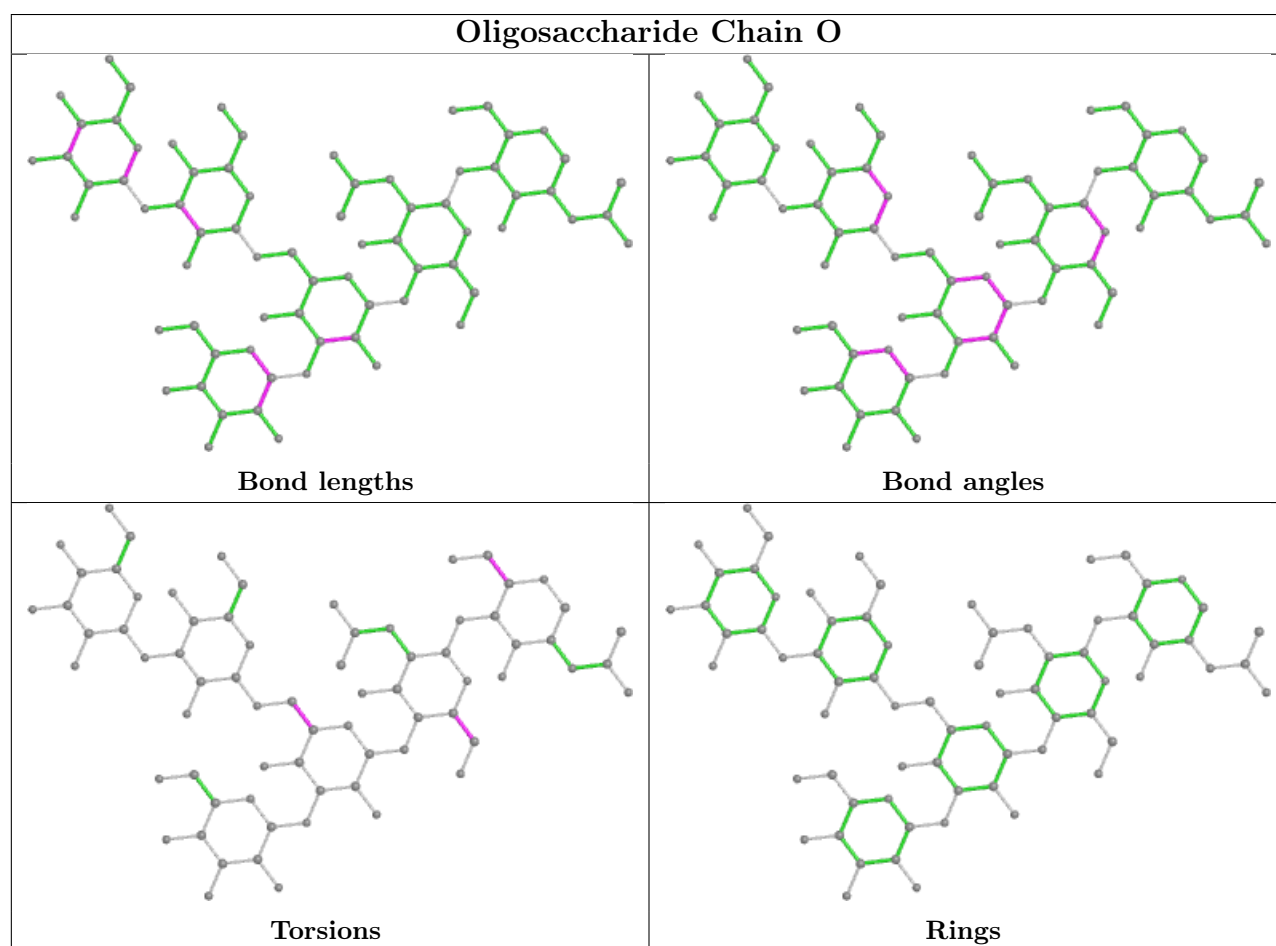
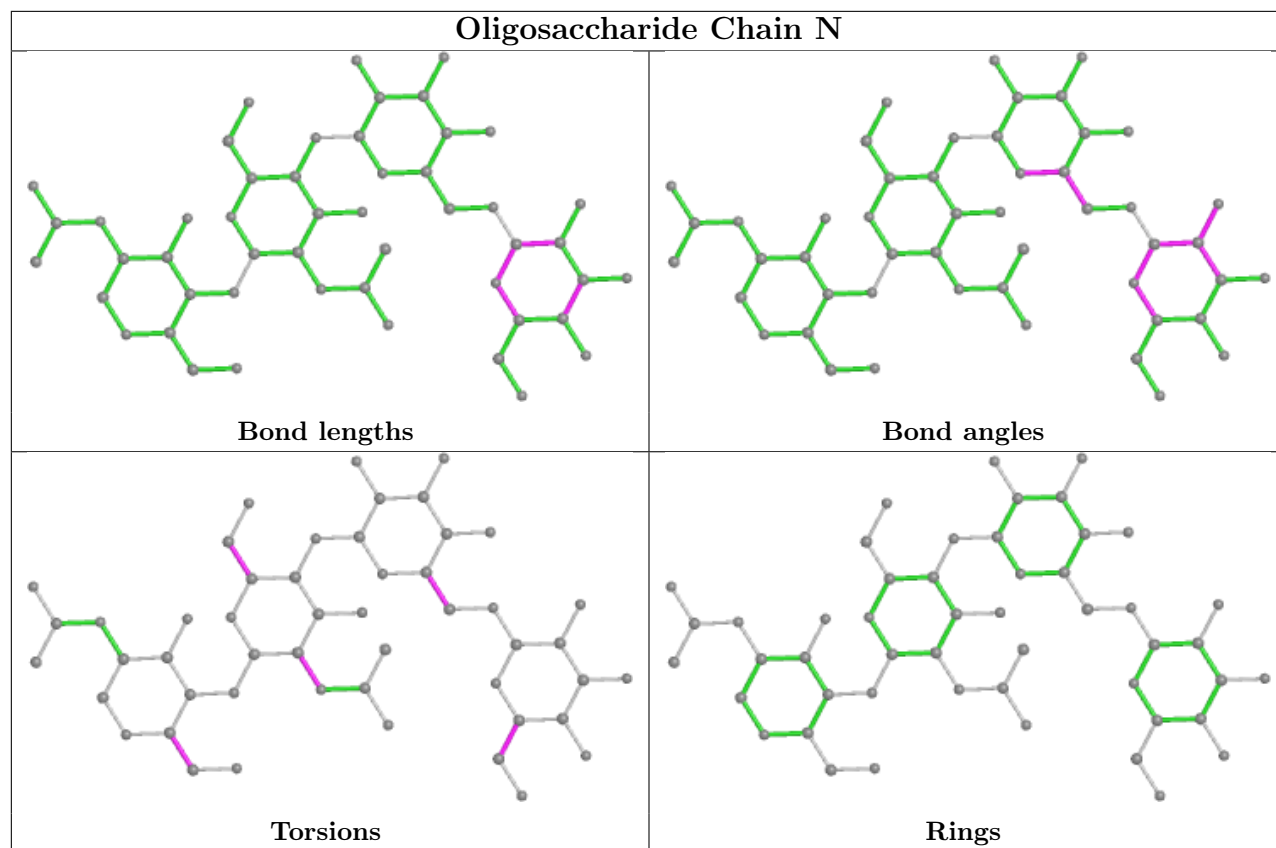
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	O	4	MAN	2	0

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

11 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
9	ACT	C	203	-	1,3,3	2.29	1 (100%)	0,3,3	-	-
10	EDO	E	201	-	3,3,3	0.53	0	2,2,2	0.10	0
7	NAG	B	601	1	14,14,15	0.39	0	17,19,21	0.49	0
8	PO4	C	202	-	4,4,4	0.65	0	6,6,6	1.01	0
7	NAG	H	601	-	14,14,15	0.60	1 (7%)	17,19,21	0.99	2 (11%)
11	MAN	A	602	-	11,11,12	1.10	0	15,15,17	1.12	1 (6%)
12	GOL	A	603	-	5,5,5	0.38	0	5,5,5	0.66	0
7	NAG	G	601	-	14,14,15	0.55	0	17,19,21	0.46	0
8	PO4	C	201	-	4,4,4	0.94	0	6,6,6	0.35	0
10	EDO	D	201	-	3,3,3	0.49	0	2,2,2	0.24	0
11	MAN	A	601	-	11,11,12	1.43	1 (9%)	15,15,17	1.35	2 (13%)

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
10	EDO	E	201	-	-	0/1/1/1	-
7	NAG	B	601	1	-	1/6/23/26	0/1/1/1
11	MAN	A	602	-	-	1/2/19/22	0/1/1/1
7	NAG	H	601	-	-	3/6/23/26	0/1/1/1
12	GOL	A	603	-	-	0/4/4/4	-
7	NAG	G	601	-	-	3/6/23/26	0/1/1/1
10	EDO	D	201	-	-	0/1/1/1	-
11	MAN	A	601	-	-	0/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	601	MAN	C2-C3	2.90	1.56	1.52
9	C	203	ACT	CH3-C	2.29	1.51	1.48
7	H	601	NAG	O5-C1	2.02	1.46	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	601	MAN	C1-O5-C5	2.65	115.79	112.19
7	H	601	NAG	C2-N2-C7	2.59	126.60	122.90
11	A	602	MAN	O2-C2-C3	-2.52	105.09	110.14
7	H	601	NAG	C1-O5-C5	2.41	115.46	112.19
11	A	601	MAN	O5-C1-C2	2.17	114.12	110.77

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	H	601	NAG	C3-C2-N2-C7
7	H	601	NAG	O5-C5-C6-O6
7	H	601	NAG	C4-C5-C6-O6
7	G	601	NAG	C1-C2-N2-C7
7	B	601	NAG	O5-C5-C6-O6

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	H	601	NAG	5	0
11	A	602	MAN	1	0
12	A	603	GOL	1	0
7	G	601	NAG	2	0
11	A	601	MAN	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	543:VAL	C	544:ASN	N	2.84

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	210/247 (85%)	-0.07	2 (0%) 82 59	69, 133, 191, 276	0
1	B	209/247 (84%)	-0.28	0 100 100	66, 104, 166, 228	0
1	G	202/247 (81%)	0.29	11 (5%) 25 9	86, 133, 230, 306	0
1	H	211/247 (85%)	-0.17	0 100 100	63, 109, 179, 222	0
2	C	122/123 (99%)	-0.31	0 100 100	57, 78, 128, 174	0
2	E	122/123 (99%)	-0.27	0 100 100	59, 88, 154, 182	0
2	I	119/123 (96%)	-0.15	1 (0%) 86 65	94, 129, 185, 223	0
2	K	121/123 (98%)	-0.26	1 (0%) 86 65	54, 73, 128, 157	0
3	D	114/135 (84%)	-0.46	0 100 100	58, 85, 118, 136	0
3	F	114/135 (84%)	-0.37	1 (0%) 84 63	72, 93, 142, 178	0
3	J	113/135 (83%)	-0.34	0 100 100	80, 109, 146, 176	0
3	L	113/135 (83%)	-0.46	1 (0%) 84 63	57, 78, 104, 169	0
All	All	1770/2020 (87%)	-0.20	17 (0%) 82 59	54, 104, 177, 306	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	363	LEU	6.4
1	G	366	SER	4.9
1	G	361	VAL	4.8
1	G	501	SER	4.6
1	G	499	LYS	4.1

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 ⓘ

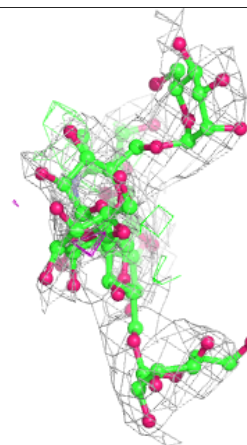
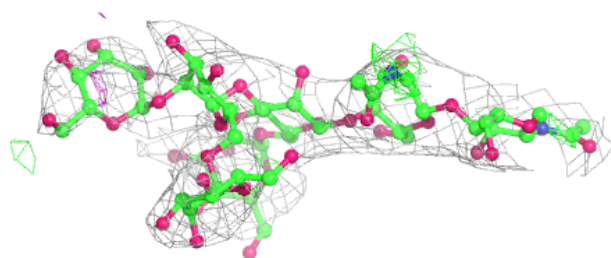
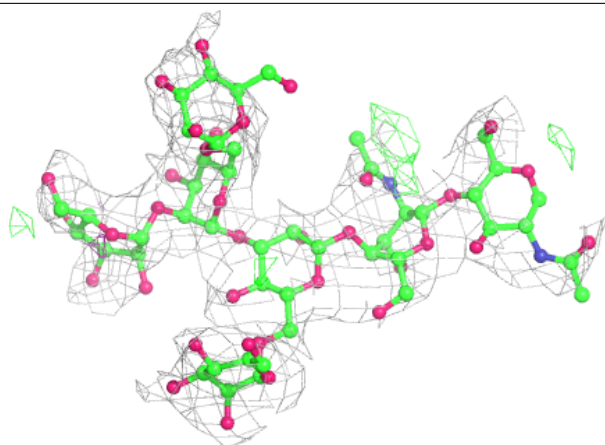
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MAN	M	5	11/12	0.62	0.41	137,151,170,170	0
5	MAN	N	4	11/12	0.67	0.19	103,149,154,154	0
6	MAN	O	5	11/12	0.73	0.25	147,171,190,190	0
5	BMA	N	3	11/12	0.81	0.18	149,155,162,165	0
4	MAN	M	4	11/12	0.81	0.17	145,156,164,165	0
6	BMA	O	3	11/12	0.81	0.20	178,182,184,187	0
5	NAG	N	1	14/15	0.81	0.28	137,163,172,175	0
4	MAN	M	6	11/12	0.82	0.29	142,158,168,171	0
6	NAG	O	2	14/15	0.83	0.22	137,165,176,180	0
6	MAN	O	4	11/12	0.85	0.12	131,155,169,174	0
4	BMA	M	3	11/12	0.85	0.16	140,151,159,165	0
6	MAN	O	6	11/12	0.86	0.15	149,161,172,176	0
4	MAN	M	7	11/12	0.87	0.17	140,150,154,155	0
6	NAG	O	1	14/15	0.88	0.23	153,173,177,179	0
5	NAG	N	2	14/15	0.90	0.25	153,162,168,171	0
4	NAG	M	2	14/15	0.92	0.20	132,151,163,170	0
4	NAG	M	1	14/15	0.93	0.11	128,147,156,160	0

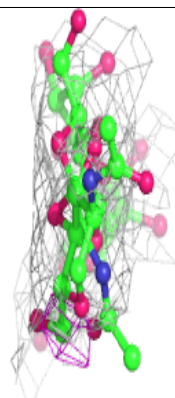
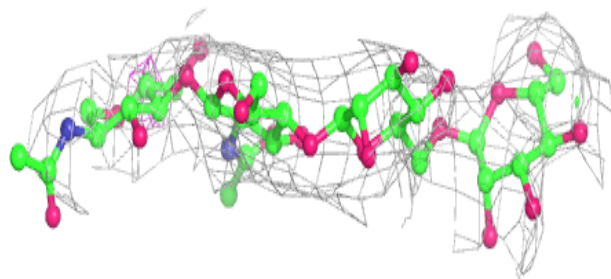
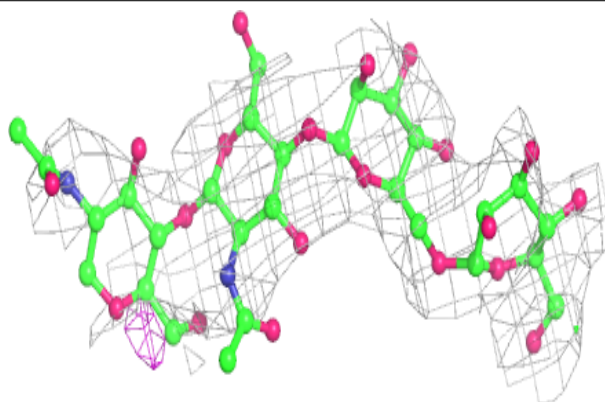
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

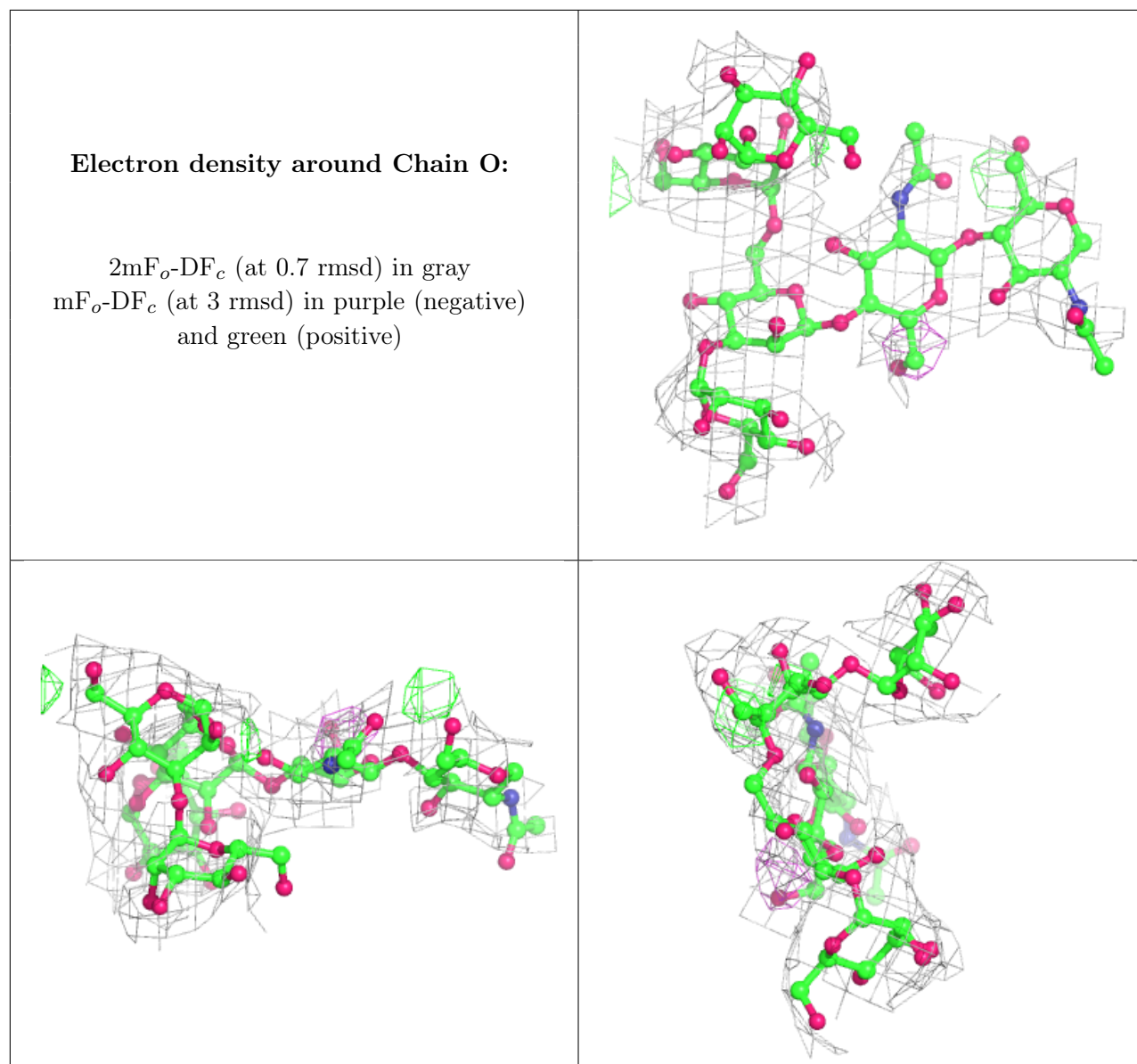
Electron density around Chain M:

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

**Electron density around Chain N:**

$2mF_o-DF_c$ (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	MAN	A	601	11/12	0.60	0.33	135,149,162,163	0
8	PO4	C	201	5/5	0.72	0.33	239,240,241,241	5
12	GOL	A	603	6/6	0.72	0.20	124,149,158,160	0
8	PO4	C	202	5/5	0.76	0.27	207,207,209,212	0
10	EDO	E	201	4/4	0.76	0.33	104,125,135,138	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	NAG	G	601	14/15	0.78	0.20	133,155,166,166	0
7	NAG	B	601	14/15	0.78	0.34	136,153,158,158	0
7	NAG	H	601	14/15	0.79	0.28	146,168,181,187	0
9	ACT	C	203	4/4	0.85	0.25	90,100,120,120	0
10	EDO	D	201	4/4	0.87	0.40	112,135,138,139	0
11	MAN	A	602	11/12	0.91	0.13	129,139,152,153	0

6.5 Other polymers [i](#)

There are no such residues in this entry.