



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 8, 2021 – 11:50 AM EST

PDB ID : 7LEN
Title : Crystal structure of the epidermal growth factor receptor extracellular region with R84K mutation in complex with epiregulin crystallized with trehalose
Authors : Hu, C.; Leche II, C.A.; Stayrook, S.E.; Ferguson, K.M.; Lemmon, M.A.
Deposited on : 2021-01-14
Resolution : 2.90 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 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 : 2.23.2
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) : 2.23.2

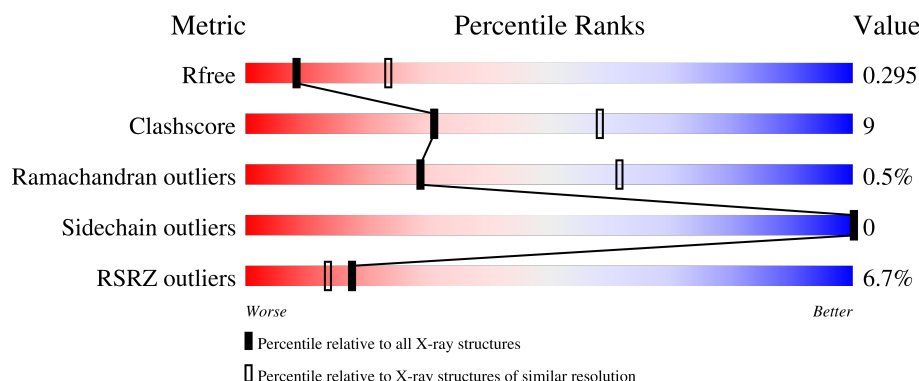
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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.




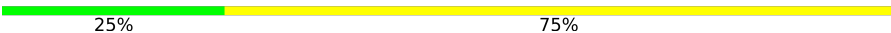
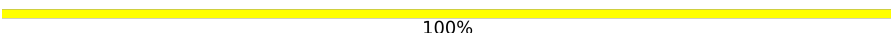

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	507	<div> <div>10%</div> <div>80%</div> <div>18%</div> <div>.</div> </div>
1	B	507	<div> <div>4%</div> <div>80%</div> <div>18%</div> <div>.</div> </div>
2	C	48	<div> <div>6%</div> <div>71%</div> <div>27%</div> <div>.</div> </div>
2	D	48	<div> <div>83%</div> <div>15%</div> <div>.</div> </div>
3	E	2	<div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
3	I	2	 50% 50%
4	F	4	 25% 75%
5	G	2	 100%
6	H	5	 80% 20%

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
3	NAG	E	2	-	-	-	X
5	NAG	G	1	-	-	-	X
7	NAG	A	4201	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8423 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 Isoform 4 of Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	500	Total	C	N	O	S	0	0	0
			3707	2302	647	716	42			
1	B	499	Total	C	N	O	S	0	0	0
			3765	2335	658	730	42			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	84	LYS	ARG	engineered mutation	UNP P00533
A	502	HIS	-	expression tag	UNP P00533
A	503	HIS	-	expression tag	UNP P00533
A	504	HIS	-	expression tag	UNP P00533
A	505	HIS	-	expression tag	UNP P00533
A	506	HIS	-	expression tag	UNP P00533
A	507	HIS	-	expression tag	UNP P00533
B	84	LYS	ARG	engineered mutation	UNP P00533
B	502	HIS	-	expression tag	UNP P00533
B	503	HIS	-	expression tag	UNP P00533
B	504	HIS	-	expression tag	UNP P00533
B	505	HIS	-	expression tag	UNP P00533
B	506	HIS	-	expression tag	UNP P00533
B	507	HIS	-	expression tag	UNP P00533

- Molecule 2 is a protein called Proepiregulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	47	Total	C	N	O	S	0	0	0
			358	219	61	70	8			
2	D	47	Total	C	N	O	S	0	0	0
			370	230	62	70	8			

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

cetamido-2-deoxy-beta-D-glucopyranose.



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

- 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.



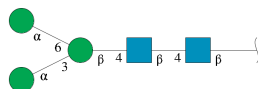
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



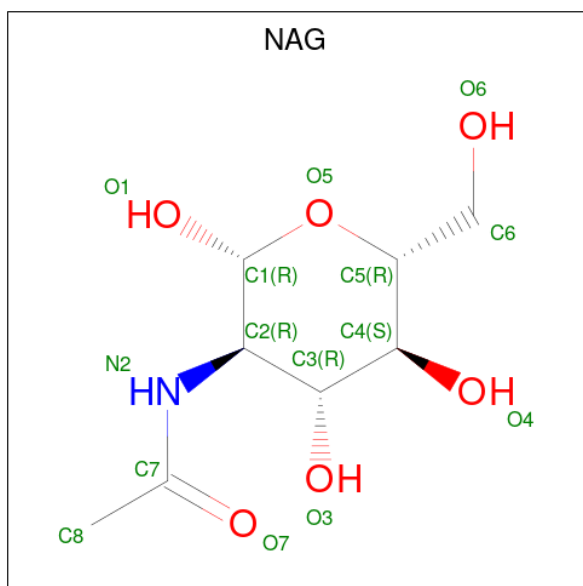
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	G	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 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
6	H	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

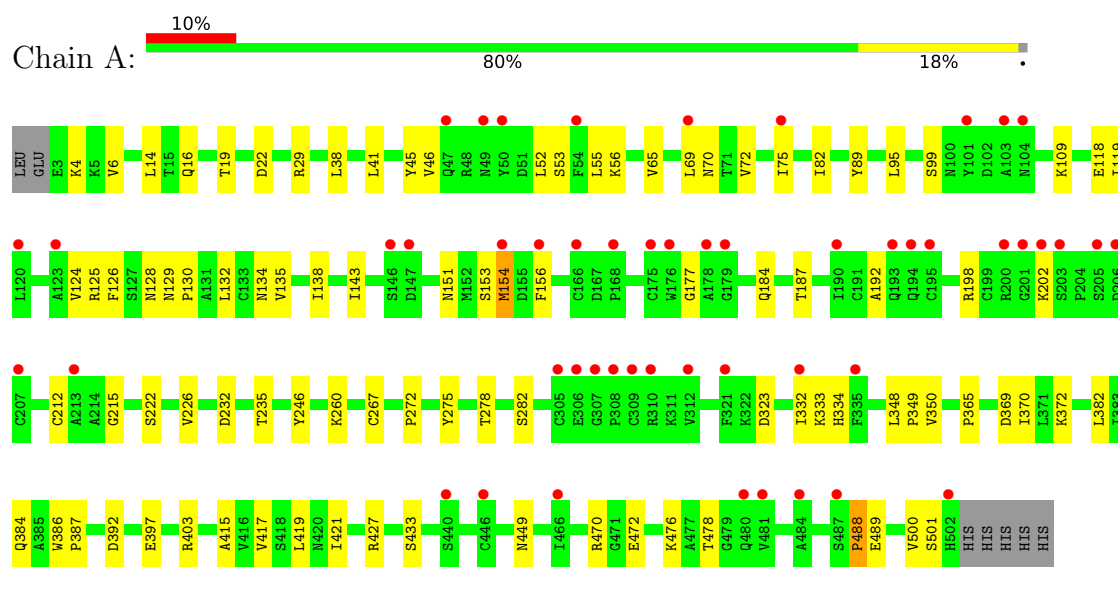


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	B	1	Total	C	N	O	0	0
			14	8	1	5		

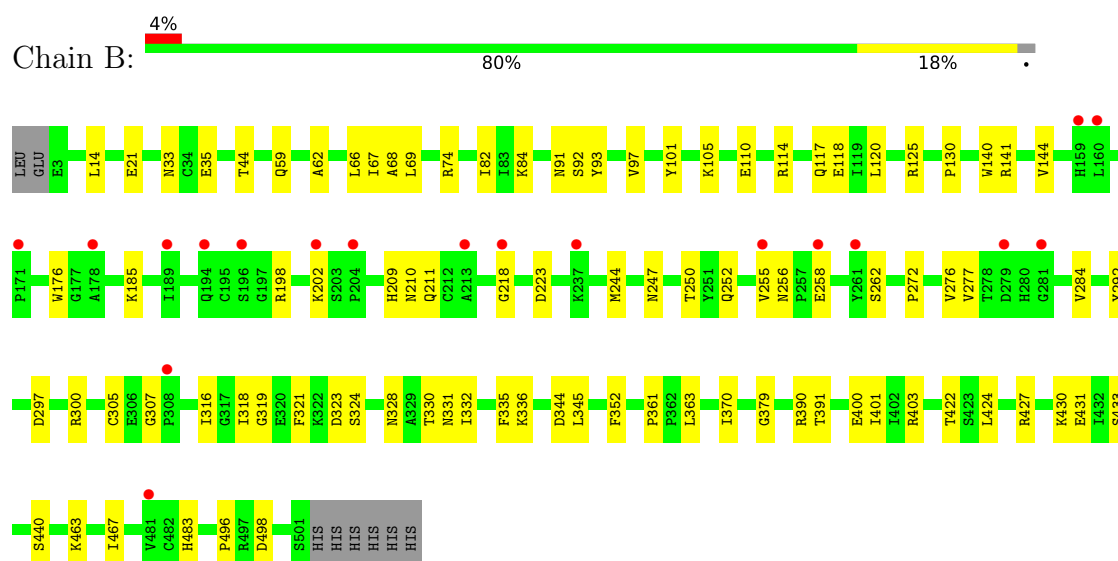
3 Residue-property plots

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.

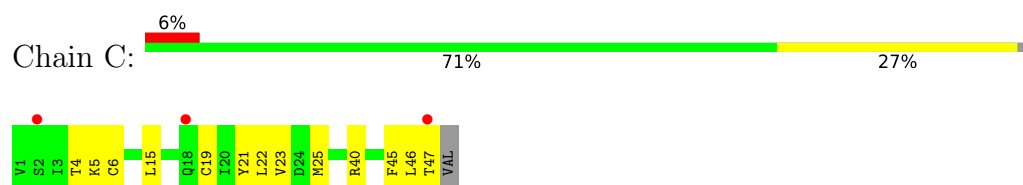
- Molecule 1: Isoform 4 of Epidermal growth factor receptor



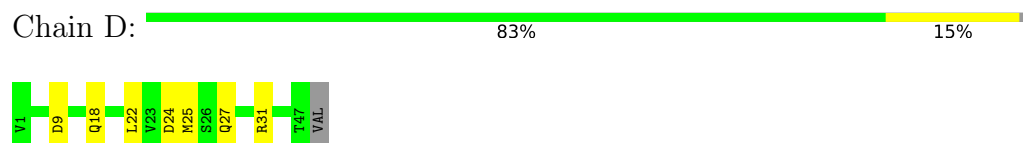
- Molecule 1: Isoform 4 of Epidermal growth factor receptor



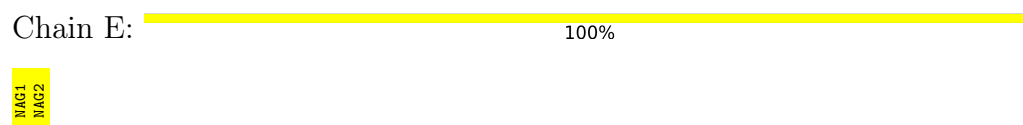
- Molecule 2: Proepiregulin



• Molecule 2: Proepiregulin



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



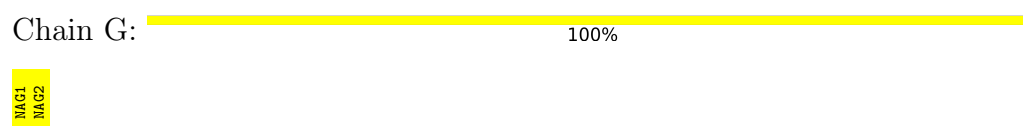
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



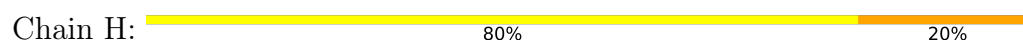
• Molecule 4: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 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





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	77.74Å 86.60Å 197.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.48 – 2.90 43.48 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (43.48-2.90) 99.8 (43.48-2.90)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 2.90Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.237 , 0.295 0.237 , 0.295	Depositor DCC
R_{free} test set	1473 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	89.4	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 68.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8423	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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, MAN, BMA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.34	0/3778	0.60	1/5135 (0.0%)
1	B	0.35	0/3836	0.60	0/5203
2	C	0.33	0/364	0.67	0/491
2	D	0.30	0/377	0.63	0/507
All	All	0.34	0/8355	0.60	1/11336 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	154	MET	CB-CG-SD	-5.22	96.74	112.40

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	3707	0	3452	72	0
1	B	3765	0	3565	66	0
2	C	358	0	318	11	0
2	D	370	0	343	6	0
3	E	28	0	25	1	0
3	I	28	0	25	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	50	0	43	1	0
5	G	28	0	25	1	0
6	H	61	0	52	4	0
7	A	14	0	13	0	0
7	B	14	0	13	0	0
All	All	8423	0	7874	148	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 9.

All (148) 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:154:MET:HE1	1:A:156:PHE:CE2	1.81	1.15
1:A:154:MET:CE	1:A:156:PHE:CE2	2.33	1.11
1:A:154:MET:HE1	1:A:156:PHE:CZ	1.85	1.11
1:A:154:MET:CE	1:A:156:PHE:CZ	2.33	1.09
1:A:95:LEU:HB3	1:A:124:VAL:HG12	1.51	0.89
1:A:154:MET:HE2	1:A:156:PHE:CE2	2.10	0.85
1:A:489:GLU:HB2	1:A:500:VAL:HG11	1.58	0.84
1:A:82:ILE:HG21	1:A:226:VAL:HG11	1.65	0.77
1:B:101:TYR:OH	2:D:24:ASP:OD1	2.09	0.70
1:B:209:HIS:HD2	1:B:211:GLN:H	1.37	0.70
1:A:470:ARG:HH22	1:A:478:THR:HG21	1.58	0.67
1:B:352:PHE:HE1	1:B:363:LEU:HD23	1.59	0.67
1:A:134:ASN:HD22	1:A:177:GLY:HA2	1.60	0.66
1:B:297:ASP:O	1:B:297:ASP:OD1	2.14	0.66
1:A:41:LEU:HB3	1:A:65:VAL:HG22	1.77	0.65
1:B:35:GLU:OE2	1:B:59:GLN:NE2	2.30	0.65
1:B:401:ILE:HG13	1:B:431:GLU:HB3	1.77	0.65
1:B:117:GLN:HE21	1:B:185:LYS:HB2	1.62	0.64
1:A:488:PRO:HG2	1:A:501:SER:HB2	1.79	0.63
1:B:202:LYS:N	1:B:202:LYS:HD3	2.14	0.63
1:B:218:GLY:H	1:B:223:ASP:HB3	1.62	0.63
1:B:318:ILE:O	1:B:321:PHE:HB2	1.99	0.63
1:A:272:PRO:HG2	1:A:275:TYR:CD1	2.34	0.63
1:A:449:ASN:HD22	1:A:472:GLU:HG3	1.64	0.63
1:B:69:LEU:HD11	2:D:22:LEU:HD21	1.81	0.62
3:I:1:NAG:H62	3:I:2:NAG:C7	2.29	0.62
1:A:16:GLN:HB2	1:A:45:TYR:HE2	1.65	0.61
1:A:384:GLN:HG2	1:A:417:VAL:HG22	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:321:PHE:HE1	1:B:335:PHE:CZ	2.19	0.60
1:A:397:GLU:HB2	1:A:427:ARG:NH1	2.19	0.57
1:B:352:PHE:CE1	1:B:363:LEU:HD23	2.38	0.57
1:A:70:ASN:HB3	1:A:72:VAL:HG22	1.87	0.57
1:B:250:THR:O	1:B:252:GLN:N	2.37	0.57
1:A:129:ASN:HB3	1:A:132:LEU:HB2	1.86	0.56
1:A:99:SER:HA	1:A:128:ASN:O	2.06	0.56
1:B:440:SER:HA	1:B:467:ILE:O	2.05	0.56
1:A:16:GLN:HB2	1:A:45:TYR:CE2	2.40	0.56
1:B:91:ASN:HB3	5:G:2:NAG:HN2	1.71	0.56
1:A:187:THR:OG1	1:A:198:ARG:NH1	2.32	0.56
1:B:244:MET:HE2	1:B:255:VAL:HA	1.86	0.56
1:A:365:PRO:HB3	1:A:387:PRO:HG3	1.88	0.55
1:B:316:ILE:HD13	1:B:321:PHE:HD1	1.71	0.55
1:A:6:VAL:HG13	1:A:38:LEU:HD21	1.89	0.55
1:B:118:GLU:OE1	1:B:198:ARG:HD2	2.07	0.55
1:A:154:MET:HE3	1:A:156:PHE:CZ	2.35	0.54
1:A:350:VAL:HG11	2:C:15:LEU:CD1	2.36	0.54
1:B:332:ILE:HG13	1:B:370:ILE:HD11	1.90	0.54
1:A:119:ILE:HG12	1:A:143:ILE:HG22	1.89	0.53
1:A:449:ASN:OD1	1:A:449:ASN:N	2.41	0.53
1:A:489:GLU:HB2	1:A:500:VAL:CG1	2.34	0.53
1:B:82:ILE:HD11	1:B:120:LEU:HD13	1.89	0.53
1:B:209:HIS:CD2	1:B:211:GLN:H	2.24	0.53
1:A:272:PRO:HD2	1:A:275:TYR:HB2	1.91	0.52
1:B:276:VAL:HG13	1:B:284:VAL:HG23	1.90	0.52
1:A:369:ASP:HB3	1:A:372:LYS:HD2	1.91	0.52
1:B:483:HIS:CD2	1:B:496:PRO:HD3	2.45	0.51
2:C:25:MET:SD	2:C:25:MET:N	2.84	0.51
1:A:350:VAL:HG11	2:C:15:LEU:HD12	1.92	0.50
1:A:278:THR:HG1	1:A:282:SER:HG	1.58	0.50
1:A:350:VAL:CG1	2:C:15:LEU:HD12	2.42	0.50
1:A:45:TYR:HE1	1:A:69:LEU:HD12	1.77	0.49
2:D:25:MET:O	2:D:27:GLN:HG3	2.13	0.49
1:B:328:ASN:HD22	6:H:1:NAG:C7	2.26	0.48
1:A:419:LEU:HB2	1:A:421:ILE:HG12	1.96	0.47
1:A:46:VAL:HG11	1:A:52:LEU:HD21	1.95	0.47
2:C:22:LEU:HB3	2:C:25:MET:HE2	1.97	0.47
1:B:336:LYS:HA	1:B:370:ILE:HD12	1.94	0.47
1:A:29:ARG:HH22	2:C:45:PHE:HE2	1.61	0.47
1:A:118:GLU:OE1	1:A:198:ARG:NH2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:ASN:OD1	3:E:1:NAG:H2	2.14	0.47
1:A:403:ARG:HA	1:A:433:SER:HB2	1.97	0.47
1:B:140:TRP:O	1:B:144:VAL:HG12	2.15	0.47
1:B:247:ASN:HB3	1:B:250:THR:O	2.15	0.47
1:B:44:THR:HA	1:B:68:ALA:O	2.15	0.47
1:B:114:ARG:HA	1:B:176:TRP:CD1	2.50	0.46
1:B:118:GLU:HG2	1:B:120:LEU:HD12	1.96	0.46
1:B:141:ARG:N	1:B:141:ARG:HD3	2.30	0.46
1:A:135:VAL:HA	1:A:138:ILE:CD1	2.45	0.46
1:A:154:MET:HE2	1:A:156:PHE:CD2	2.51	0.46
2:C:21:TYR:CE2	2:C:23:VAL:HG12	2.51	0.46
1:B:292:TYR:HE1	1:B:305:CYS:HA	1.79	0.46
2:C:15:LEU:CD2	2:C:40:ARG:HB3	2.46	0.46
1:A:6:VAL:HG13	1:A:38:LEU:CD2	2.45	0.46
1:A:53:SER:O	1:A:56:LYS:HG3	2.15	0.45
1:B:344:ASP:OD1	1:B:379:GLY:HA3	2.17	0.45
1:A:138:ILE:HG23	1:A:184:GLN:OE1	2.17	0.45
1:B:324:SER:OG	6:H:1:NAG:H61	2.17	0.45
1:A:332:ILE:HG13	1:A:370:ILE:HD12	1.99	0.45
1:B:14:LEU:CD1	1:B:66:LEU:HD21	2.46	0.45
1:B:93:TYR:CE1	1:B:125:ARG:HB2	2.51	0.44
1:B:209:HIS:CD2	1:B:210:ASN:N	2.85	0.44
1:B:210:ASN:OD1	1:B:211:GLN:HG2	2.18	0.44
1:B:14:LEU:HD12	1:B:66:LEU:HD21	1.99	0.44
1:A:126:PHE:CD2	1:A:154:MET:HE3	2.52	0.44
1:A:472:GLU:O	1:A:476:LYS:HG3	2.18	0.44
1:A:212:CYS:HB3	1:A:215:GLY:O	2.17	0.44
1:A:138:ILE:HD12	1:A:138:ILE:H	1.83	0.44
1:A:55:LEU:HD23	1:A:75:ILE:HG23	1.99	0.44
1:A:14:LEU:HD11	1:A:89:TYR:OH	2.17	0.44
1:A:128:ASN:O	1:A:130:PRO:HD3	2.18	0.43
1:B:330:THR:HG23	1:B:361:PRO:HD2	2.00	0.43
1:B:483:HIS:CE1	1:B:496:PRO:HG3	2.53	0.43
1:B:292:TYR:HD1	1:B:305:CYS:SG	2.42	0.43
1:A:232:ASP:OD1	1:A:232:ASP:C	2.57	0.43
1:A:449:ASN:HD22	1:A:472:GLU:CG	2.31	0.43
1:B:118:GLU:OE1	1:B:198:ARG:NH1	2.50	0.43
1:A:222:SER:HB3	1:A:235:THR:HG22	2.00	0.43
2:D:18:GLN:OE1	2:D:31:ARG:NH2	2.52	0.43
1:B:74:ARG:HG3	1:B:110:GLU:CB	2.48	0.43
1:B:331:ASN:HB3	6:H:1:NAG:O6	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:33:ASN:ND2	3:I:1:NAG:O5	2.35	0.43
1:B:321:PHE:HE1	1:B:335:PHE:CE2	2.37	0.43
1:B:391:THR:OG1	1:B:422:THR:OG1	2.34	0.43
1:B:400:GLU:O	1:B:430:LYS:HG2	2.19	0.43
1:B:14:LEU:HD23	2:D:22:LEU:CD2	2.48	0.43
1:B:256:ASN:OD1	1:B:258:GLU:N	2.52	0.43
1:A:134:ASN:HD22	1:A:177:GLY:CA	2.31	0.42
1:A:348:LEU:HB3	1:A:349:PRO:HD2	2.01	0.42
1:B:319:GLY:C	1:B:321:PHE:H	2.22	0.42
1:A:386:TRP:CG	1:A:387:PRO:HD2	2.54	0.42
1:B:403:ARG:HA	1:B:433:SER:HB2	2.01	0.42
1:A:333:LYS:HG3	1:A:334:HIS:CD2	2.54	0.42
1:B:323:ASP:HB2	6:H:2:NAG:H5	2.01	0.42
2:C:4:THR:HG22	2:C:5:LYS:H	1.84	0.42
2:D:9:ASP:OD2	2:D:9:ASP:N	2.53	0.42
1:A:246:TYR:CD2	1:B:262:SER:HB3	2.55	0.42
1:B:424:LEU:HD23	1:B:424:LEU:HA	1.94	0.42
2:C:46:LEU:HD12	2:C:47:THR:N	2.35	0.42
1:B:117:GLN:NE2	1:B:185:LYS:HB2	2.32	0.41
2:C:6:CYS:HB2	2:C:19:CYS:HB3	1.90	0.41
1:A:109:LYS:HA	1:A:132:LEU:HA	2.03	0.41
1:A:260:LYS:HB3	1:A:267:CYS:HB3	2.02	0.41
1:B:344:ASP:O	1:B:345:LEU:HD23	2.20	0.41
1:A:125:ARG:HG3	1:A:153:SER:O	2.21	0.41
1:B:67:ILE:O	1:B:97:VAL:HA	2.20	0.41
1:A:192:ALA:HB2	1:A:202:LYS:O	2.21	0.41
1:B:105:LYS:HD2	1:B:130:PRO:HG3	2.03	0.41
1:A:382:LEU:HD13	1:A:415:ALA:HB3	2.03	0.40
1:B:390:ARG:HD2	1:B:390:ARG:HA	1.85	0.40
1:A:19:THR:HG22	1:A:22:ASP:OD2	2.21	0.40
1:B:62:ALA:HA	1:B:84:LYS:HB2	2.03	0.40
1:B:427:ARG:HG2	1:B:498:ASP:HA	2.03	0.40
1:A:323:ASP:HB2	4:F:2:NAG:H5	2.03	0.40
1:B:277:VAL:HG12	1:B:300:ARG:O	2.21	0.40
1:A:4:LYS:O	1:A:6:VAL:HG23	2.22	0.40
1:A:392:ASP:OD2	1:A:392:ASP:C	2.59	0.40
1:A:449:ASN:ND2	1:A:472:GLU:HG3	2.35	0.40
1:B:463:LYS:HD3	1:B:463:LYS:HA	1.91	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	498/507 (98%)	462 (93%)	35 (7%)	1 (0%)	47	78
1	B	497/507 (98%)	468 (94%)	25 (5%)	4 (1%)	19	51
2	C	45/48 (94%)	40 (89%)	5 (11%)	0	100	100
2	D	45/48 (94%)	42 (93%)	3 (7%)	0	100	100
All	All	1085/1110 (98%)	1012 (93%)	68 (6%)	5 (0%)	29	61

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	21	GLU
1	B	307	GLY
1	B	92	SER
1	A	488	PRO
1	B	272	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	399/446 (90%)	399 (100%)	0	100	100
1	B	416/446 (93%)	416 (100%)	0	100	100
2	C	40/44 (91%)	40 (100%)	0	100	100
2	D	43/44 (98%)	43 (100%)	0	100	100
All	All	898/980 (92%)	898 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	134	ASN
1	A	139	GLN
1	A	182	ASN
1	B	117	GLN
1	B	209	HIS
1	B	444	ASN
1	B	480	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 ⓘ

15 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	E	1	1,3	14,14,15	0.69	0	17,19,21	0.48	0
3	NAG	E	2	3	14,14,15	0.63	1 (7%)	17,19,21	1.16	1 (5%)
4	NAG	F	1	1,4	14,14,15	0.36	0	17,19,21	0.50	0
4	NAG	F	2	4	14,14,15	0.20	0	17,19,21	0.62	0
4	BMA	F	3	4	11,11,12	1.01	0	15,15,17	1.08	1 (6%)
4	MAN	F	4	4	11,11,12	0.68	0	15,15,17	1.01	2 (13%)
5	NAG	G	1	1,5	14,14,15	0.80	1 (7%)	17,19,21	0.53	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	G	2	5	14,14,15	0.27	0	17,19,21	0.42	0
6	NAG	H	1	1,6	14,14,15	0.32	0	17,19,21	0.61	0
6	NAG	H	2	6	14,14,15	0.41	0	17,19,21	1.09	1 (5%)
6	BMA	H	3	6	11,11,12	1.39	3 (27%)	15,15,17	2.35	4 (26%)
6	MAN	H	4	6	11,11,12	0.94	1 (9%)	15,15,17	1.30	2 (13%)
6	MAN	H	5	6	11,11,12	0.92	1 (9%)	15,15,17	1.32	1 (6%)
3	NAG	I	1	1,3	14,14,15	0.48	0	17,19,21	0.47	0
3	NAG	I	2	3	14,14,15	0.53	0	17,19,21	0.74	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
3	NAG	E	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	3/6/23/26	0/1/1/1
4	NAG	F	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
4	BMA	F	3	4	-	0/2/19/22	0/1/1/1
4	MAN	F	4	4	-	1/2/19/22	0/1/1/1
5	NAG	G	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	G	2	5	-	1/6/23/26	0/1/1/1
6	NAG	H	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	H	2	6	-	0/6/23/26	0/1/1/1
6	BMA	H	3	6	-	2/2/19/22	0/1/1/1
6	MAN	H	4	6	-	1/2/19/22	0/1/1/1
6	MAN	H	5	6	-	1/2/19/22	1/1/1/1
3	NAG	I	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	I	2	3	-	1/6/23/26	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	H	3	BMA	O5-C5	2.79	1.49	1.43
5	G	1	NAG	C1-C2	2.53	1.56	1.52
6	H	5	MAN	O5-C1	-2.45	1.39	1.43
6	H	3	BMA	C1-C2	2.30	1.57	1.52
6	H	4	MAN	C1-C2	2.07	1.56	1.52
3	E	2	NAG	O5-C1	2.03	1.47	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	H	3	BMA	O5-C1	2.02	1.46	1.43

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	3	BMA	C1-O5-C5	7.52	122.38	112.19
3	E	2	NAG	C1-O5-C5	4.19	117.86	112.19
6	H	5	MAN	C1-O5-C5	4.11	117.76	112.19
6	H	4	MAN	C1-O5-C5	3.80	117.34	112.19
6	H	2	NAG	C1-O5-C5	3.50	116.94	112.19
4	F	4	MAN	C1-O5-C5	2.60	115.71	112.19
3	I	2	NAG	C1-O5-C5	2.49	115.56	112.19
6	H	3	BMA	O5-C1-C2	2.23	114.22	110.77
6	H	3	BMA	C1-C2-C3	2.21	112.38	109.67
4	F	4	MAN	O2-C2-C3	-2.12	105.89	110.14
6	H	3	BMA	O5-C5-C6	2.12	110.53	107.20
6	H	4	MAN	O2-C2-C3	-2.12	105.89	110.14
4	F	3	BMA	O3-C3-C4	2.08	115.16	110.35

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	I	1	NAG	O5-C5-C6-O6
6	H	3	BMA	C4-C5-C6-O6
5	G	1	NAG	C4-C5-C6-O6
5	G	1	NAG	O5-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6
3	I	1	NAG	C4-C5-C6-O6
6	H	3	BMA	O5-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
4	F	4	MAN	O5-C5-C6-O6
6	H	5	MAN	O5-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6
6	H	4	MAN	O5-C5-C6-O6
3	E	2	NAG	C3-C2-N2-C7
5	G	2	NAG	C4-C5-C6-O6

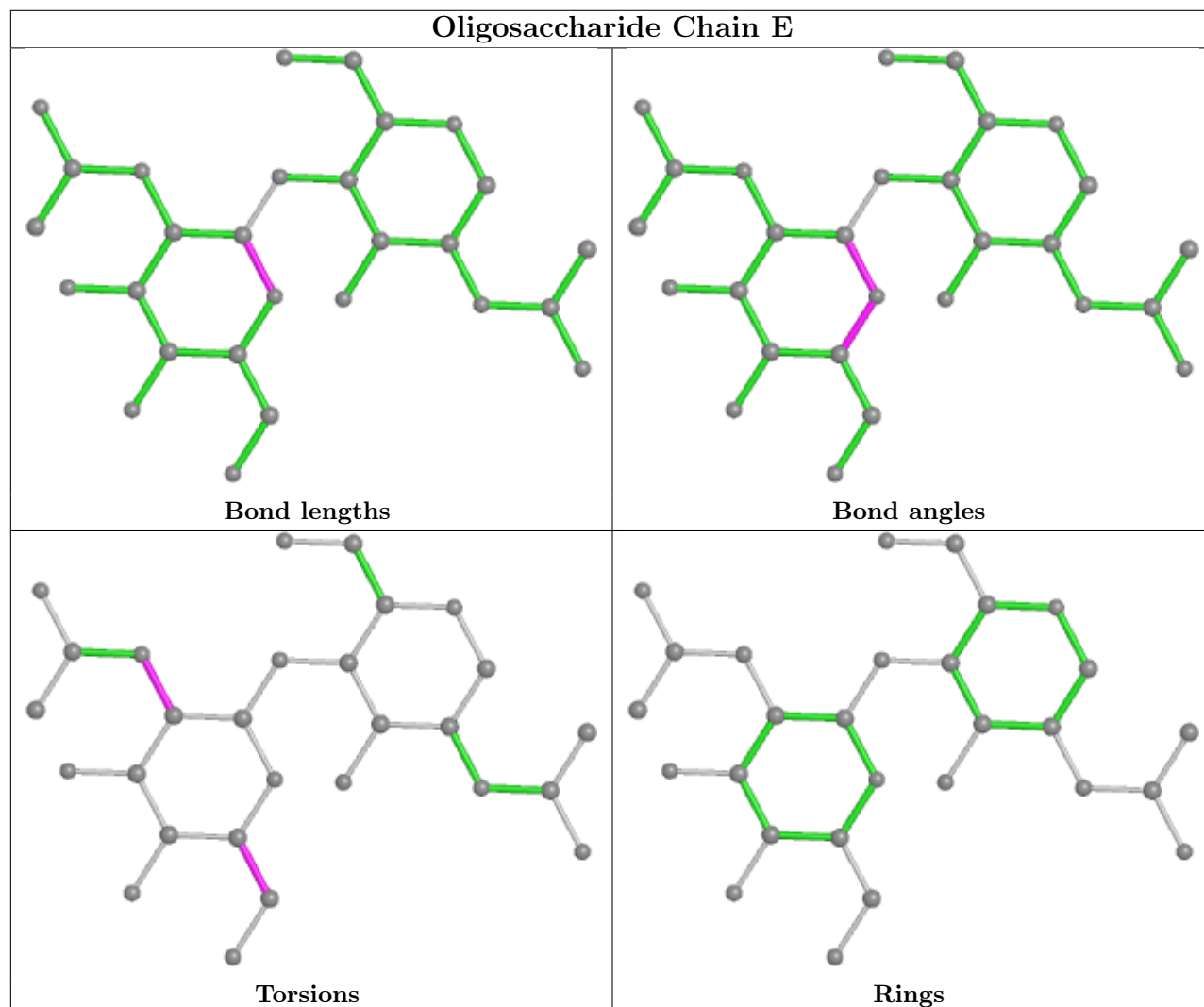
All (1) ring outliers are listed below:

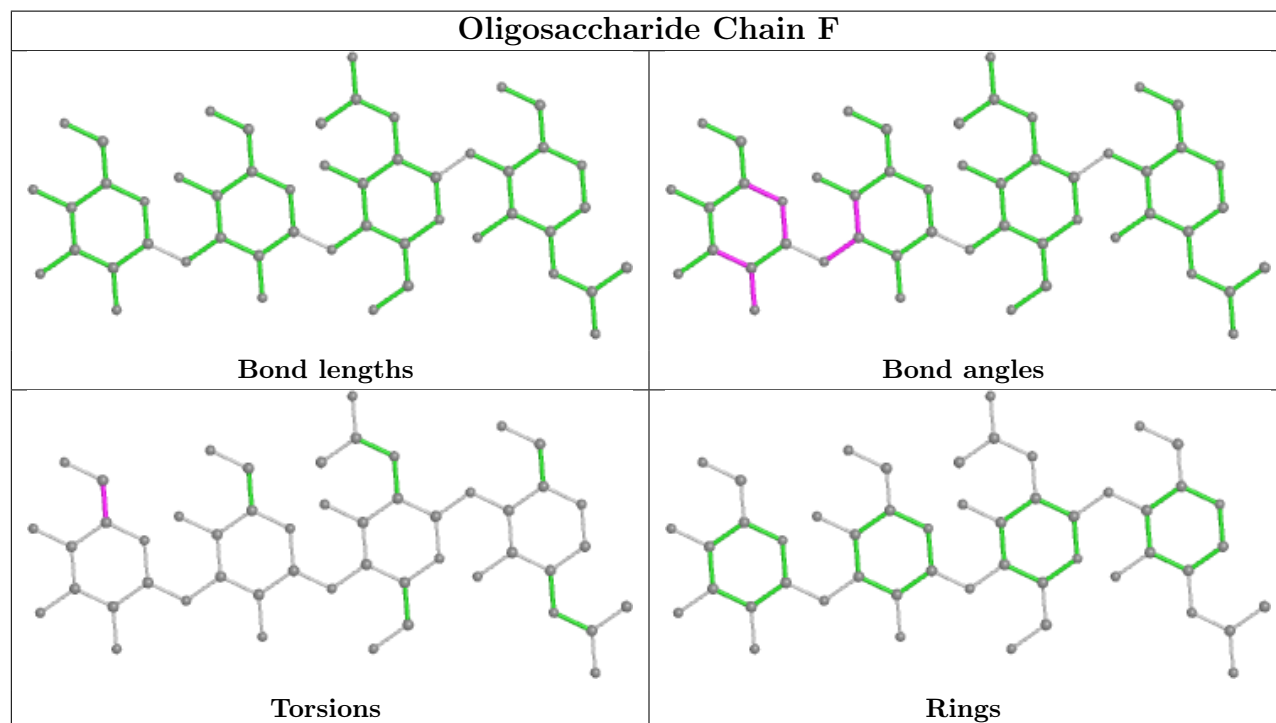
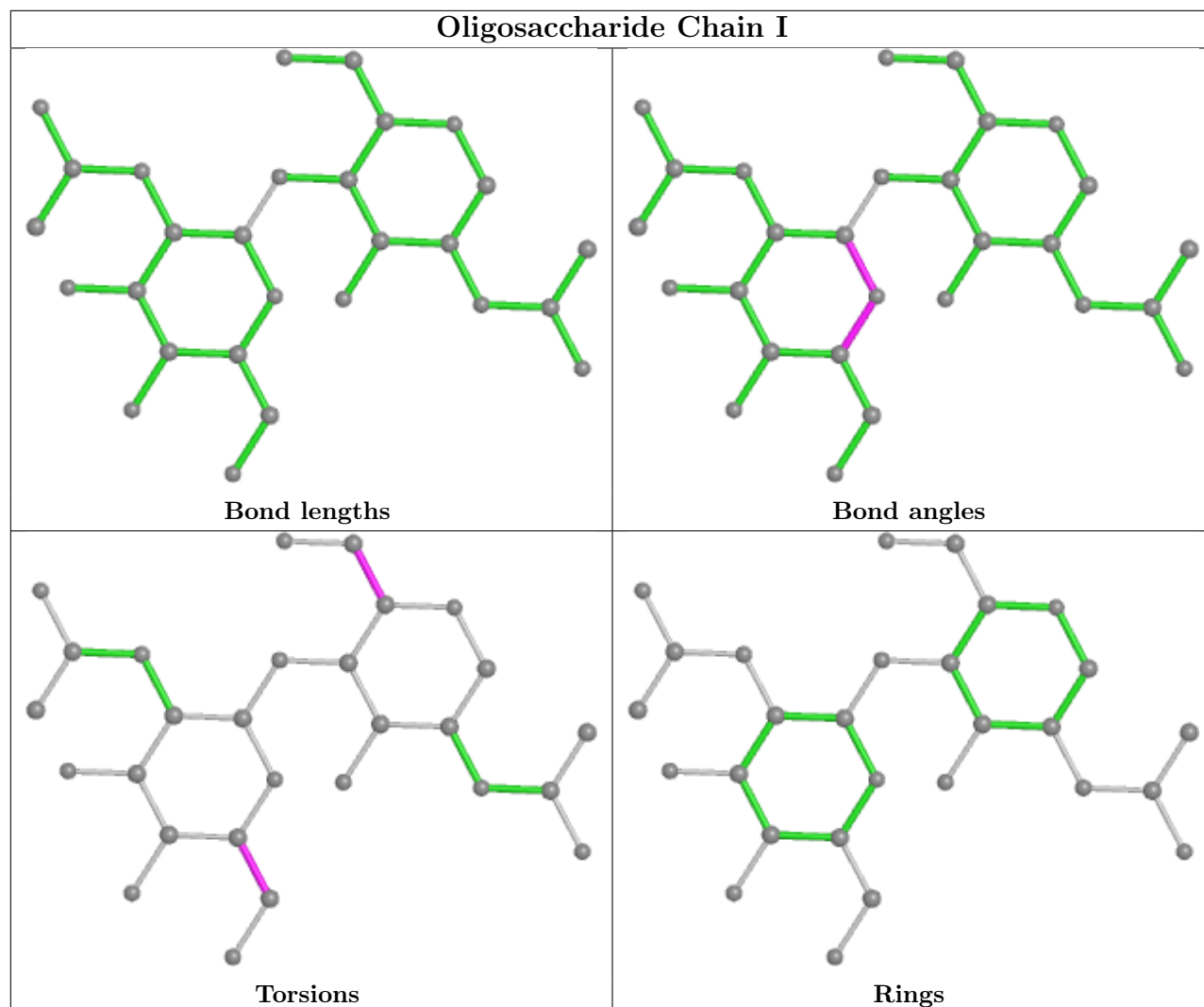
Mol	Chain	Res	Type	Atoms
6	H	5	MAN	C1-C2-C3-C4-C5-O5

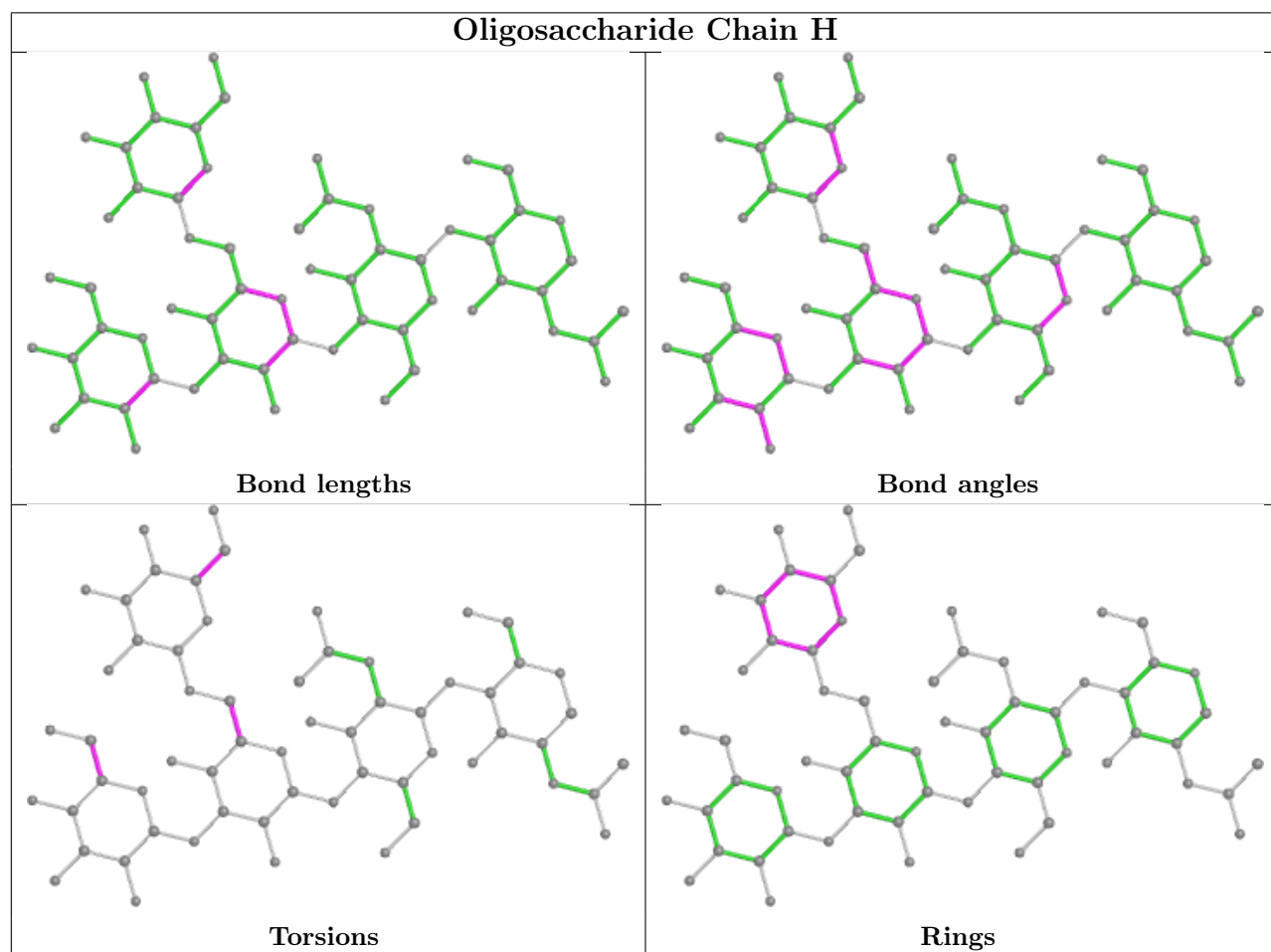
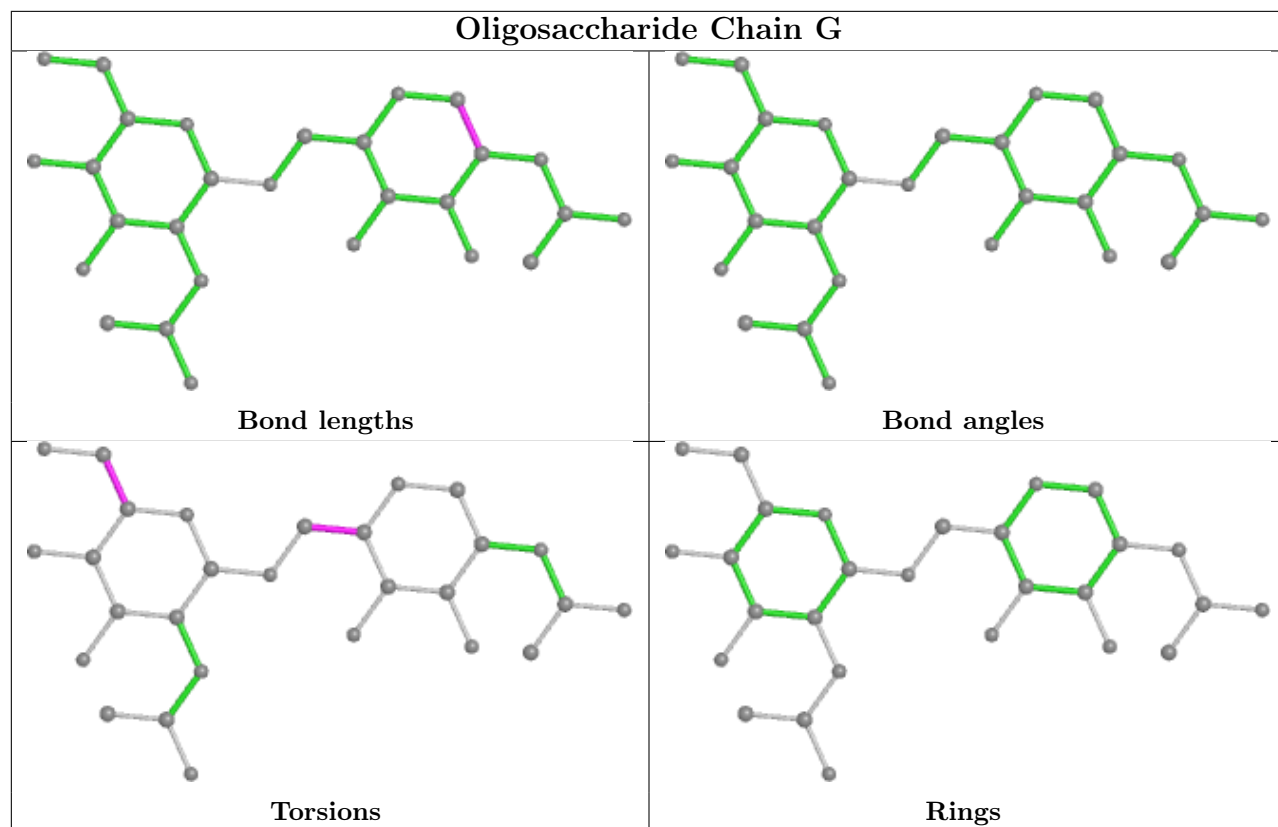
7 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	H	1	NAG	3	0
3	E	1	NAG	1	0
3	I	2	NAG	1	0
4	F	2	NAG	1	0
6	H	2	NAG	1	0
5	G	2	NAG	1	0
3	I	1	NAG	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

2 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	$\# Z > 2$
7	NAG	A	4201	1	14,14,15	0.29	0	17,19,21	0.68	1 (5%)
7	NAG	B	901	1	14,14,15	0.21	0	17,19,21	0.52	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
7	NAG	A	4201	1	-	2/6/23/26	0/1/1/1
7	NAG	B	901	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	4201	NAG	C1-O5-C5	2.14	115.09	112.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	4201	NAG	O5-C5-C6-O6
7	A	4201	NAG	C4-C5-C6-O6

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	500/507 (98%)	0.70	51 (10%) 6 5	59, 91, 135, 159	0
1	B	499/507 (98%)	0.45	19 (3%) 40 36	48, 77, 113, 159	0
2	C	47/48 (97%)	0.64	3 (6%) 19 15	64, 90, 114, 119	0
2	D	47/48 (97%)	0.35	0 100 100	52, 68, 93, 96	0
All	All	1093/1110 (98%)	0.56	73 (6%) 17 13	48, 84, 127, 159	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	306	GLU	4.8
1	B	196	SER	4.8
1	A	190	ILE	4.5
1	A	207	CYS	4.4
1	A	156	PHE	4.3
1	A	309	CYS	4.1
1	A	179	GLY	4.1
1	B	160	LEU	4.0
1	A	168	PRO	4.0
1	A	178	ALA	3.9
2	C	2	SER	3.9
1	B	204	PRO	3.8
1	A	103	ALA	3.7
1	A	194	GLN	3.6
1	B	281	GLY	3.6
1	A	502	HIS	3.4
1	A	487	SER	3.4
1	B	194	GLN	3.4
1	A	47	GLN	3.3
1	A	49	ASN	3.2
1	A	213	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	205	SER	3.1
1	A	308	PRO	3.1
1	B	218	GLY	3.1
1	B	159	HIS	3.0
1	A	195	CYS	2.9
1	A	146	SER	2.8
1	A	201	GLY	2.7
1	A	120	LEU	2.7
2	C	18	GLN	2.6
1	A	312	VAL	2.6
1	A	206	ASP	2.6
1	A	75	ILE	2.5
2	C	47	THR	2.5
1	B	213	ALA	2.5
1	B	237	LYS	2.5
1	A	200	ARG	2.5
1	A	203	SER	2.4
1	A	310	ARG	2.4
1	B	189	ILE	2.4
1	A	446	CYS	2.4
1	A	147	ASP	2.4
1	B	308	PRO	2.3
1	A	154	MET	2.3
1	A	484	ALA	2.3
1	A	481	VAL	2.3
1	A	466	ILE	2.3
1	B	255	VAL	2.3
1	A	307	GLY	2.3
1	A	321	PHE	2.3
1	A	54	PHE	2.2
1	A	69	LEU	2.2
1	A	50	TYR	2.2
1	A	166	CYS	2.2
1	A	305	CYS	2.2
1	A	202	LYS	2.2
1	B	258	GLU	2.2
1	B	202	LYS	2.2
1	B	279	ASP	2.1
1	B	261	TYR	2.1
1	A	335	PHE	2.1
1	A	193	GLN	2.1
1	A	480	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	178	ALA	2.1
1	A	440	SER	2.1
1	A	175	CYS	2.1
1	A	123	ALA	2.1
1	A	176	TRP	2.1
1	B	171	PRO	2.0
1	A	101	TYR	2.0
1	A	104	ASN	2.0
1	B	481	VAL	2.0
1	A	332	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

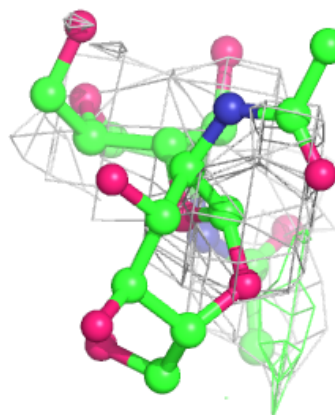
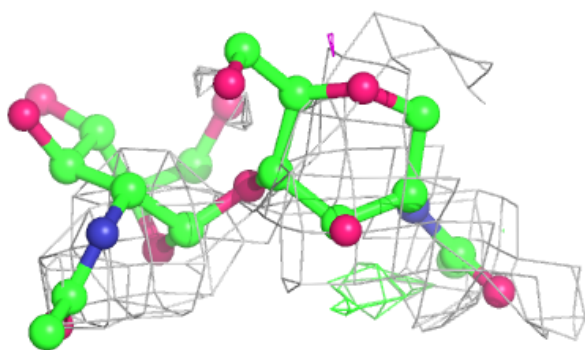
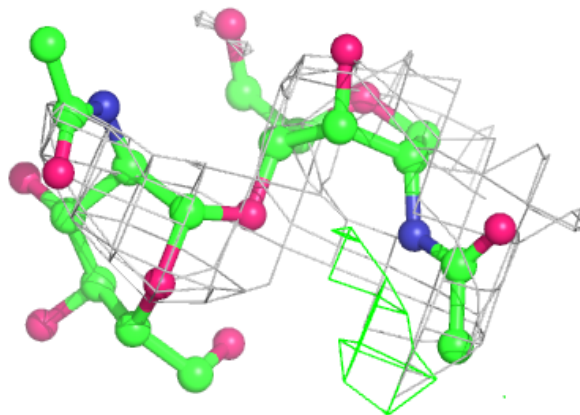
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	I	2	14/15	0.21	0.38	129,151,164,170	0
6	MAN	H	4	11/12	0.31	0.35	135,153,169,177	0
3	NAG	E	1	14/15	0.47	0.37	125,159,178,187	0
5	NAG	G	1	14/15	0.50	0.44	96,129,147,147	0
5	NAG	G	2	14/15	0.54	0.37	95,143,157,159	0
6	BMA	H	3	11/12	0.64	0.24	132,147,159,167	0
3	NAG	E	2	14/15	0.64	0.76	161,195,200,204	0
3	NAG	I	1	14/15	0.65	0.23	97,117,131,150	0
6	MAN	H	5	11/12	0.75	0.25	75,118,133,141	0
4	BMA	F	3	11/12	0.83	0.26	99,110,119,124	0
4	MAN	F	4	11/12	0.84	0.34	83,106,121,124	0
4	NAG	F	2	14/15	0.91	0.24	79,92,98,107	0
6	NAG	H	2	14/15	0.92	0.20	76,90,106,114	0
4	NAG	F	1	14/15	0.96	0.25	57,72,90,93	0
6	NAG	H	1	14/15	0.97	0.23	56,71,84,92	0

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

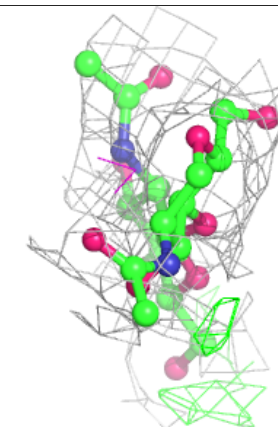
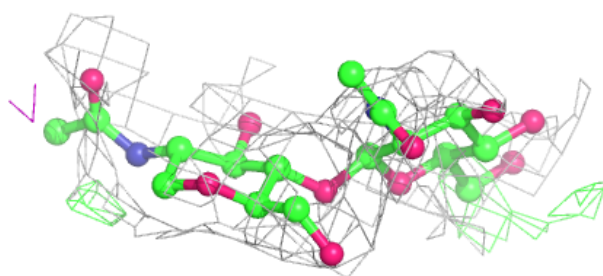
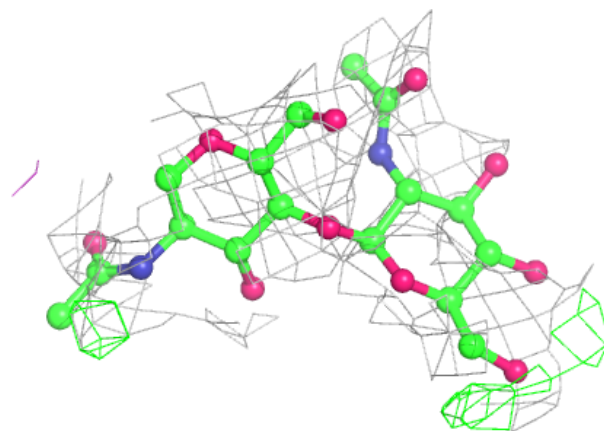
Electron density around Chain E:

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

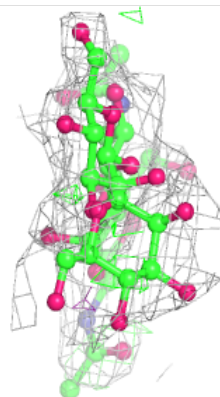
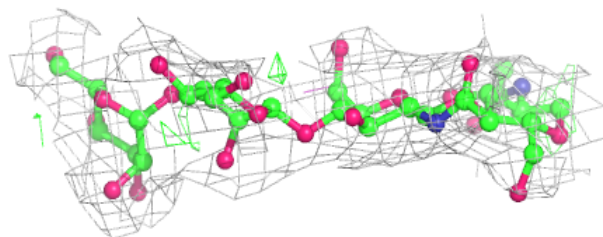


Electron density around Chain I:

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

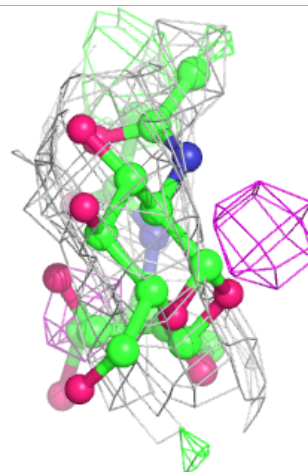
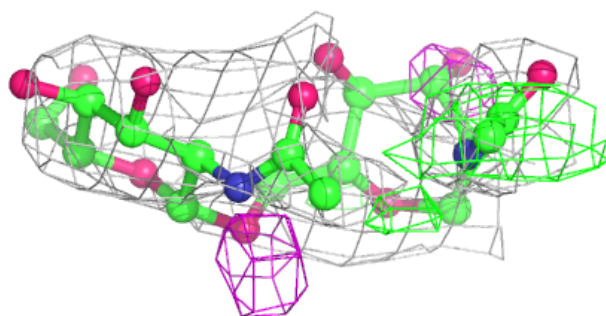
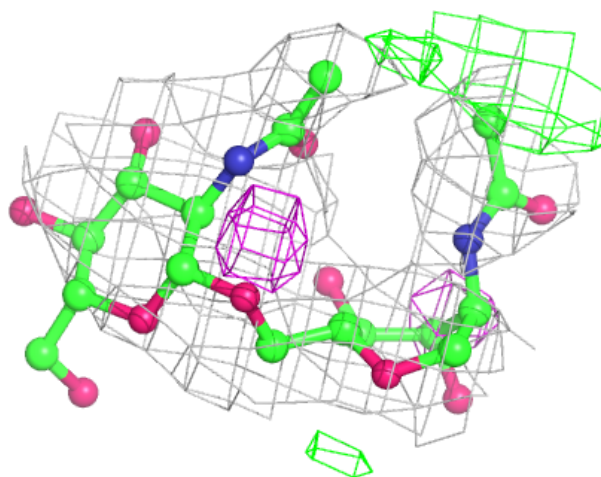
**Electron density around Chain F:**

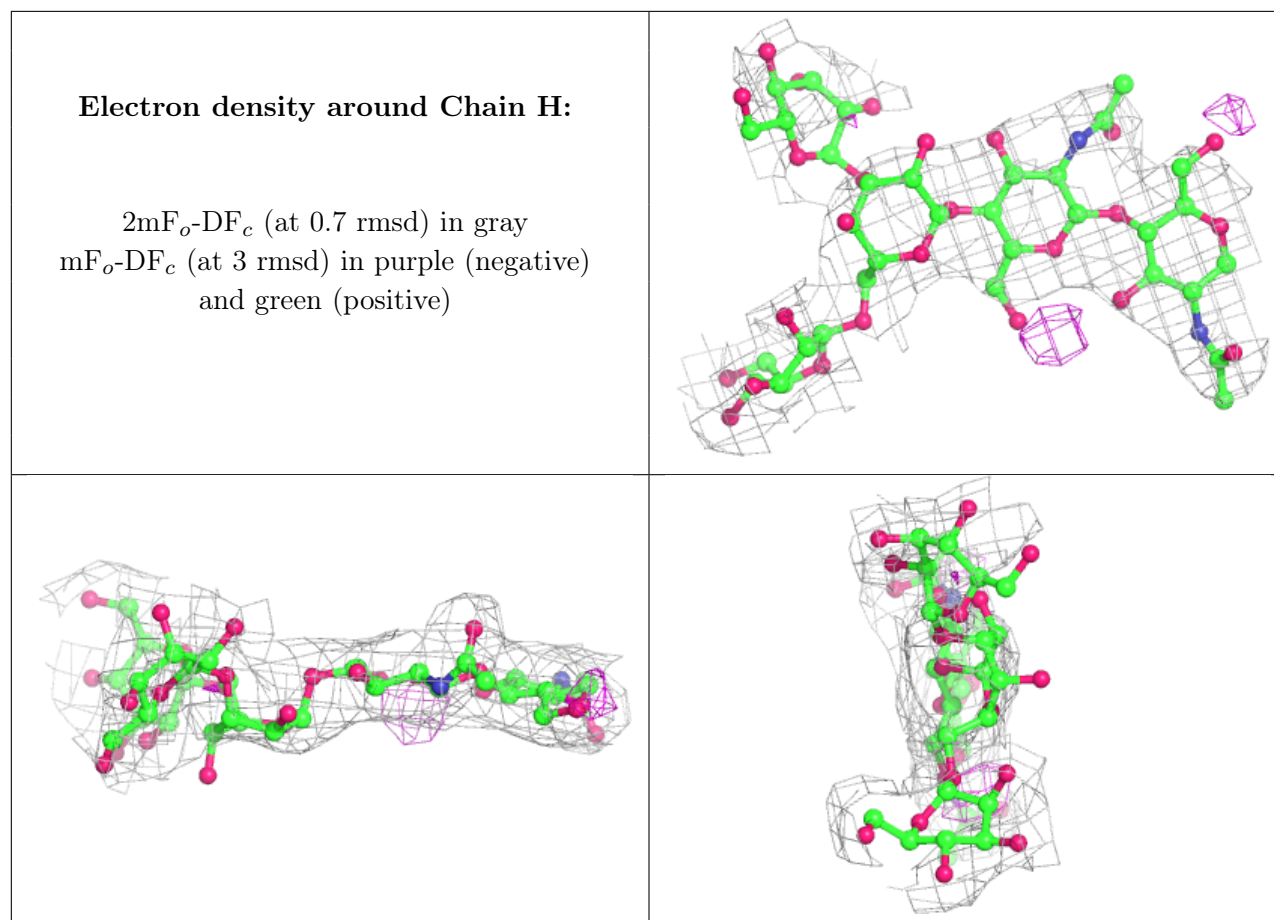
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain G:

$2mF_o-DF_c$ (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
7	NAG	B	901	14/15	0.70	0.27	117,127,137,139	0
7	NAG	A	4201	14/15	0.72	0.40	97,119,131,134	0

6.5 Other polymers [i](#)

There are no such residues in this entry.