



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 6, 2024 – 12:18 PM EDT

PDB ID : 9ATK
Title : BIFUNCTIONAL INHIBITION OF NEUTROPHIL ELASTASE AND
CATHEPSIN G by Eap4 of *S. aureus*
Authors : Mishra, N.B.; Herdendorf, T.J.; Geisbrecht, B.V.
Deposited on : 2024-02-27
Resolution : 2.11 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36.2
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) : 2.36.2

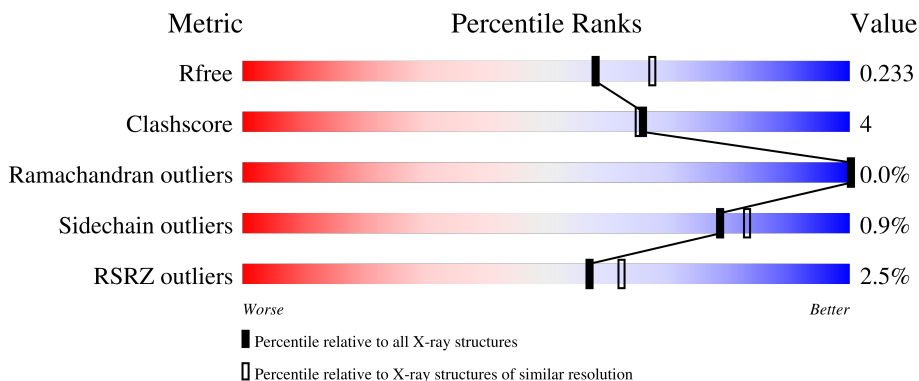
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

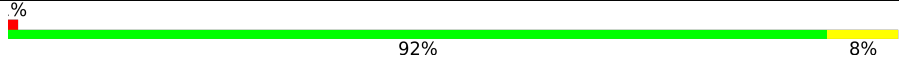
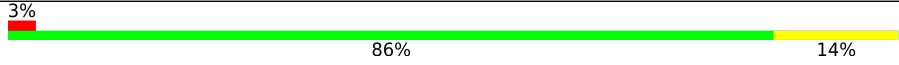
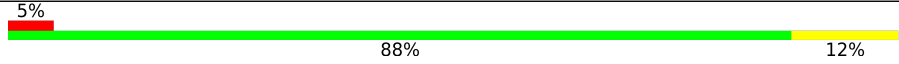
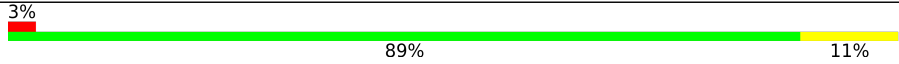
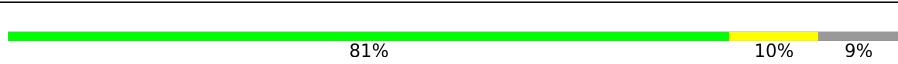
The reported resolution of this entry is 2.11 Å.

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	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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	218	 92% 8%
1	D	218	 86% 14% 3%
1	G	218	 88% 12% 5%
1	J	218	 89% 11% 3%
2	C	108	 81% 10% 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	108	% 81% 8% 9%
2	I	108	% 83% 6% 9%
2	L	108	% 77% 14% 9%
3	B	223	% 93% 7%
3	E	223	% 3% 90% 10%
3	H	223	% 4% 90% 9%
3	K	223	% 2% 89% 11%
4	M	4	% 75% 25%
4	O	4	% 50% 25% 25%
4	P	4	% 25% 75%
4	Q	4	% 100%
5	N	3	% 67% 33%
5	R	3	% 33% 67%
6	S	3	% 33% 67%
6	T	3	% 33% 33% 33%

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
6	NAG	T	2	-	-	-	X

2 Entry composition i

There are 8 unique types of molecules in this entry. The entry contains 17989 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 Neutrophil elastase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	218	Total 1635	C 1026	N 316	O 282	S 11	0	0	0
1	D	218	Total 1635	C 1026	N 316	O 282	S 11	0	0	0
1	G	218	Total 1635	C 1026	N 316	O 282	S 11	0	0	0
1	J	218	Total 1635	C 1026	N 316	O 282	S 11	0	0	0

- Molecule 2 is a protein called Extracellular Adherence Protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	98	Total 789	C 514	N 131	O 144	0	0	0
2	F	98	Total 789	C 514	N 131	O 144	0	0	0
2	I	98	Total 789	C 514	N 131	O 144	0	0	0
2	L	98	Total 789	C 514	N 131	O 144	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	369	GLY	-	expression tag	UNP Q99QS1
C	370	SER	-	expression tag	UNP Q99QS1
C	371	THR	-	expression tag	UNP Q99QS1
F	369	GLY	-	expression tag	UNP Q99QS1
F	370	SER	-	expression tag	UNP Q99QS1
F	371	THR	-	expression tag	UNP Q99QS1
I	369	GLY	-	expression tag	UNP Q99QS1
I	370	SER	-	expression tag	UNP Q99QS1

Continued on next page...

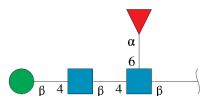
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	371	THR	-	expression tag	UNP Q99QS1
L	369	GLY	-	expression tag	UNP Q99QS1
L	370	SER	-	expression tag	UNP Q99QS1
L	371	THR	-	expression tag	UNP Q99QS1

- Molecule 3 is a protein called Cathepsin-G.

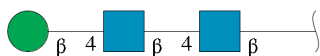
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	223	1780	1093	369	308	10	0	0	0
3	H	223	1780	1093	369	308	10	0	0	0
3	B	223	1780	1093	369	308	10	0	0	0
3	K	223	1780	1093	369	308	10	0	0	0

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



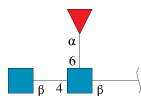
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	M	4	49	28	2	19	0	0	0
4	O	4	49	28	2	19	0	0	0
4	P	4	49	28	2	19	0	0	0
4	Q	4	49	28	2	19	0	0	0

- Molecule 5 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.



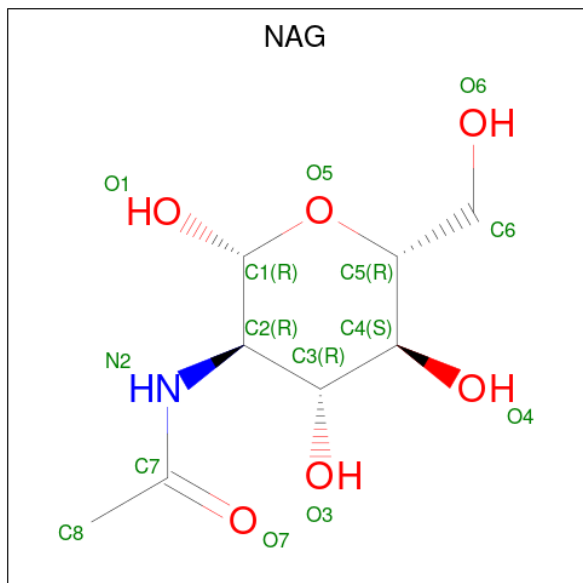
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	N	3	39	22	2	15	0	0	0
5	R	3	39	22	2	15	0	0	0

- Molecule 6 is an oligosaccharide called 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
			Total	C	N	O			
6	S	3	38	22	2	14	0	0	0
6	T	3	38	22	2	14	0	0	0

- 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
			Total	C	N	O		
7	E	1	14	8	1	5	0	0
7	H	1	14	8	1	5	0	0

Continued on next page...

Continued from previous page...

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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	94	Total	O	0	0
			94	94		
8	D	67	Total	O	0	0
			67	67		
8	C	48	Total	O	0	0
			48	48		
8	E	74	Total	O	0	0
			74	74		
8	F	63	Total	O	0	0
			63	63		
8	G	45	Total	O	0	0
			45	45		
8	H	68	Total	O	0	0
			68	68		
8	I	50	Total	O	0	0
			50	50		
8	B	95	Total	O	0	0
			95	95		
8	J	45	Total	O	0	0
			45	45		
8	K	75	Total	O	0	0
			75	75		
8	L	43	Total	O	0	0
			43	43		

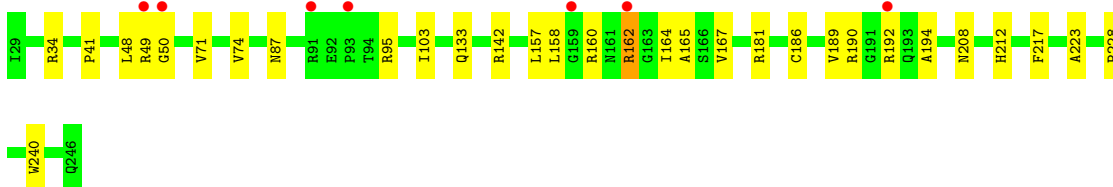
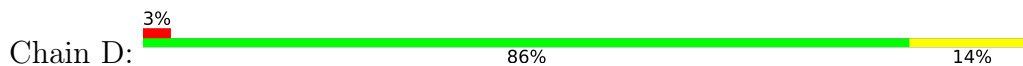
3 Residue-property plots [i](#)

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.

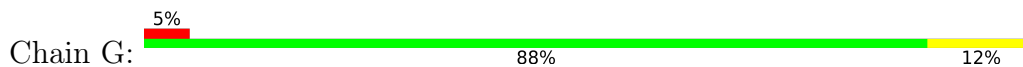
- Molecule 1: Neutrophil elastase



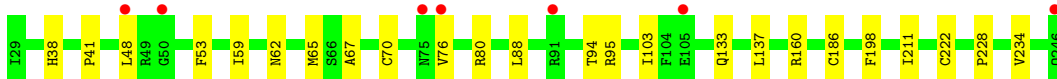
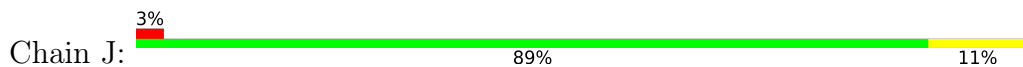
- Molecule 1: Neutrophil elastase



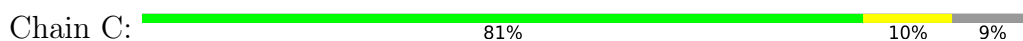
- Molecule 1: Neutrophil elastase

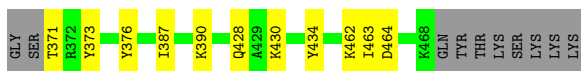


- Molecule 1: Neutrophil elastase

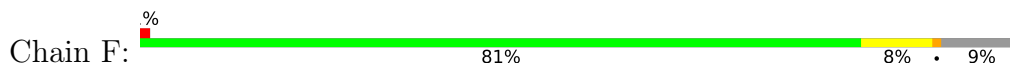


- Molecule 2: Extracellular Adherence Protein

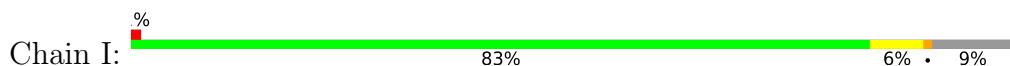




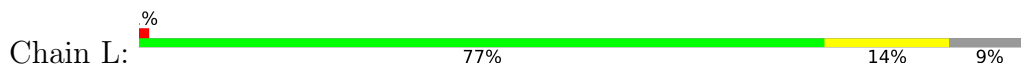
- Molecule 2: Extracellular Adherence Protein



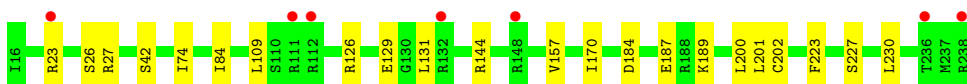
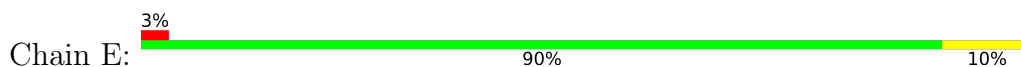
- Molecule 2: Extracellular Adherence Protein



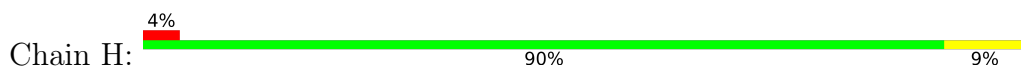
- Molecule 2: Extracellular Adherence Protein



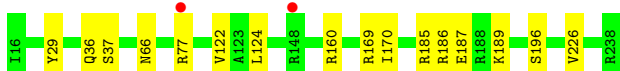
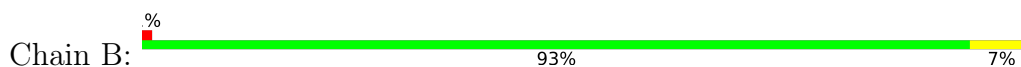
- Molecule 3: Cathepsin-G



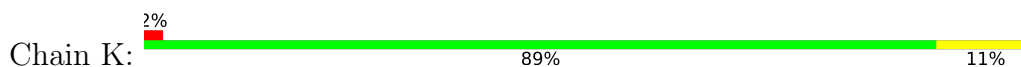
- Molecule 3: Cathepsin-G



- Molecule 3: Cathepsin-G

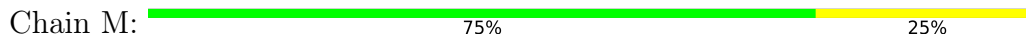


- Molecule 3: Cathepsin-G





- Molecule 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 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 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 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



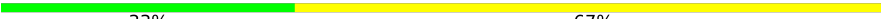
- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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




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

Chain S:  33% 67%

MAG1
MAG2
FUC3

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

Chain T:  33% 33% 33%

MAG1
MAG2
FUC3

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	82.21Å 85.53Å 89.54Å 82.77° 85.23° 83.60°	Depositor
Resolution (Å)	47.89 – 2.11 47.89 – 2.11	Depositor EDS
% Data completeness (in resolution range)	84.8 (47.89-2.11) 84.9 (47.89-2.11)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.10Å)	Xtrriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.179 , 0.233 0.181 , 0.233	Depositor DCC
R_{free} test set	1862 reflections (1.59%)	wwPDB-VP
Wilson B-factor (Å ²)	30.8	Xtrriage
Anisotropy	0.246	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.013 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17989	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% 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: BMA, NAG, FUC

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	0.43	0/1665	0.66	0/2263
1	D	0.39	0/1665	0.65	0/2263
1	G	0.36	0/1665	0.63	0/2263
1	J	0.34	0/1665	0.62	0/2263
2	C	0.45	0/801	0.58	0/1075
2	F	0.45	0/801	0.59	0/1075
2	I	0.42	0/801	0.57	0/1075
2	L	0.40	0/801	0.55	0/1075
3	B	0.43	0/1814	0.72	0/2447
3	E	0.39	0/1814	0.70	0/2447
3	H	0.39	0/1814	0.69	0/2447
3	K	0.41	0/1814	0.71	1/2447 (0.0%)
All	All	0.40	0/17120	0.66	1/23140 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	201	LEU	CA-CB-CG	-5.38	102.92	115.30

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	1635	0	1650	12	0
1	D	1635	0	1650	22	0
1	G	1635	0	1650	18	0
1	J	1635	0	1650	15	0
2	C	789	0	850	6	0
2	F	789	0	850	8	0
2	I	789	0	850	7	0
2	L	789	0	850	11	0
3	B	1780	0	1791	11	0
3	E	1780	0	1792	12	0
3	H	1780	0	1792	11	0
3	K	1780	0	1792	17	0
4	M	49	0	43	0	0
4	O	49	0	43	1	0
4	P	49	0	43	0	0
4	Q	49	0	43	0	0
5	N	39	0	34	0	0
5	R	39	0	34	2	0
6	S	38	0	34	0	0
6	T	38	0	34	1	0
7	B	14	0	13	0	0
7	E	14	0	13	0	0
7	H	14	0	13	1	0
7	K	14	0	13	0	0
8	A	94	0	0	4	0
8	B	95	0	0	4	0
8	C	48	0	0	0	0
8	D	67	0	0	0	0
8	E	74	0	0	0	0
8	F	63	0	0	1	0
8	G	45	0	0	1	0
8	H	68	0	0	0	0
8	I	50	0	0	2	0
8	J	45	0	0	0	0
8	K	75	0	0	3	0
8	L	43	0	0	1	0
All	All	17989	0	17527	138	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 4.

All (138) 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:G:97:VAL:HG11	5:R:2:NAG:H82	1.49	0.94
1:G:89:SER:HB3	1:G:90:ARG:HH11	1.45	0.81
2:L:371:THR:N	2:L:396:LYS:HZ3	1.85	0.74
3:K:165:ARG:O	3:K:169:ARG:HG3	1.88	0.73
2:I:402:LYS:NZ	8:I:501:HOH:O	2.23	0.71
2:C:428:GLN:NE2	2:C:430:LYS:HE2	2.06	0.71
3:K:51:GLU:OE2	3:K:115:ARG:NH1	2.23	0.71
2:F:428:GLN:HG2	8:F:551:HOH:O	1.92	0.69
1:D:189:VAL:HG11	1:D:194:ALA:HB3	1.72	0.69
3:K:186:ARG:HB2	3:K:186:ARG:HH11	1.58	0.68
3:K:185:ARG:HA	3:K:219:PRO:HG2	1.75	0.68
3:B:185:ARG:HH11	3:B:186:ARG:NH1	1.94	0.66
3:H:23:ARG:HD2	3:H:24:PRO:HD2	1.77	0.65
1:G:33:ARG:NH1	8:G:302:HOH:O	2.30	0.64
2:F:372:ARG:NH2	2:F:460:ILE:O	2.32	0.62
3:K:163:ARG:HG3	3:K:163:ARG:HH11	1.64	0.62
1:A:162:ARG:NH1	8:A:301:HOH:O	2.24	0.62
1:A:34:ARG:NH1	8:A:303:HOH:O	2.32	0.61
1:D:181:ARG:HG2	2:I:421:LEU:HD23	1.82	0.60
2:I:371:THR:N	2:I:395:ASN:OD1	2.36	0.59
1:D:160:ARG:NH2	1:D:223:ALA:O	2.36	0.58
3:B:169:ARG:HG3	3:B:170:ILE:HG23	1.86	0.57
1:D:157:LEU:HD23	1:D:164:ILE:HG22	1.86	0.57
1:G:88:LEU:HA	1:G:95:ARG:HH22	1.70	0.57
3:K:178:ARG:NH2	8:K:401:HOH:O	2.38	0.56
1:J:59:ILE:HD13	1:J:65:MET:HB3	1.89	0.54
3:E:84:ILE:HG21	3:E:109:LEU:HB3	1.90	0.54
1:D:189:VAL:HG22	1:D:192:ARG:HB2	1.90	0.53
5:R:2:NAG:H61	5:R:3:BMA:H2	1.90	0.53
1:D:186:CYS:HB3	1:D:228:PRO:HB2	1.90	0.53
1:J:137:LEU:HD22	1:J:234:VAL:HG11	1.90	0.53
1:D:71:VAL:HA	1:D:74:VAL:HG22	1.91	0.53
3:E:184:ASP:HB3	3:E:187:GLU:HG3	1.91	0.53
3:B:77:ARG:NH1	8:B:403:HOH:O	2.41	0.53
3:B:36:GLN:HG3	3:B:37:SER:N	2.25	0.52
3:B:124:LEU:HD22	3:B:226:VAL:HG11	1.92	0.52
1:J:186:CYS:HB3	1:J:228:PRO:HB2	1.90	0.52
1:D:240:TRP:HE1	3:B:160:ARG:HH21	1.57	0.51
3:K:98:ARG:HG3	2:L:418:ILE:HD11	1.92	0.51
2:I:442:VAL:HG12	8:I:536:HOH:O	2.11	0.50
2:C:387:ILE:HA	8:B:419:HOH:O	2.10	0.50
3:B:160:ARG:NE	8:B:406:HOH:O	2.45	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:164:ILE:HD12	1:G:165:ALA:H	1.77	0.49
3:H:29:TYR:CG	3:H:122:VAL:HB	2.47	0.49
3:K:196:SER:HA	3:K:210:VAL:HB	1.94	0.49
3:B:196:SER:HB2	8:B:419:HOH:O	2.13	0.49
2:L:396:LYS:NZ	8:L:504:HOH:O	2.45	0.49
1:D:48:LEU:O	1:D:50:GLY:N	2.46	0.49
3:H:16:ILE:N	3:H:195:ASP:OD2	2.46	0.49
1:G:60:ALA:HB3	1:G:63:PHE:HB2	1.96	0.48
1:D:41:PRO:HB2	1:D:133:GLN:HG3	1.96	0.48
2:F:391:LEU:H	2:F:391:LEU:HD23	1.77	0.48
1:G:88:LEU:HA	1:G:95:ARG:NH2	2.28	0.48
1:G:106:ASN:HB2	1:G:240:TRP:CE2	2.49	0.48
3:E:131:LEU:HD11	3:E:202:CYS:SG	2.53	0.48
1:J:137:LEU:HD23	1:J:211:ILE:HB	1.95	0.48
3:H:98:ARG:HG2	2:I:416:ARG:O	2.13	0.47
1:A:160:ARG:NH2	1:A:222:CYS:O	2.47	0.47
2:F:403:TYR:CZ	2:F:407:LYS:HE2	2.50	0.47
3:K:137:CYS:HB2	3:K:200:LEU:HD11	1.96	0.47
1:A:142:ARG:HG2	8:A:384:HOH:O	2.13	0.47
3:E:200:LEU:HB2	3:E:223:PHE:CE2	2.50	0.47
1:A:159:GLY:HA3	1:A:162:ARG:HD3	1.95	0.47
1:A:88:LEU:HA	1:A:95:ARG:HH22	1.78	0.47
1:D:142:ARG:NH2	1:D:212:HIS:HE1	2.12	0.47
1:A:157:LEU:HD23	1:A:164:ILE:HG22	1.96	0.46
1:D:208:ASN:H	4:O:4:FUC:C4	2.29	0.46
1:J:88:LEU:HA	1:J:95:ARG:NH2	2.31	0.46
1:J:48:LEU:HG	1:J:53:PHE:CE2	2.51	0.46
3:B:187:GLU:HB3	3:B:189:LYS:HG3	1.98	0.46
1:J:198:PHE:CD1	2:L:452:PRO:HA	2.51	0.46
1:D:157:LEU:HD22	1:D:162:ARG:O	2.16	0.45
1:D:158:LEU:HD21	1:D:165:ALA:HB2	1.99	0.45
1:D:240:TRP:HE1	3:B:160:ARG:NH2	2.14	0.45
2:C:462:LYS:HE3	2:C:464:ASP:OD2	2.17	0.44
1:J:38:HIS:NE2	1:J:94:THR:HG21	2.32	0.44
1:G:45:SER:HB3	1:G:82:VAL:HG22	2.00	0.44
2:C:434:TYR:CD1	2:C:462:LYS:HE2	2.52	0.44
1:J:76:VAL:HG11	1:J:103:ILE:HD11	2.00	0.44
3:K:219:PRO:HB3	8:K:418:HOH:O	2.17	0.44
1:A:144:LEU:HD11	1:A:212:HIS:CG	2.53	0.43
1:D:87:ASN:O	1:D:95:ARG:NH2	2.51	0.43
1:D:48:LEU:HD23	1:D:48:LEU:HA	1.74	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:58:ALA:HA	3:H:105:MET:HB2	1.99	0.43
1:D:34:ARG:HG2	1:D:167:VAL:HG11	2.00	0.43
1:A:181:ARG:HG3	2:L:421:LEU:HD23	2.00	0.43
1:G:198:PHE:CD1	2:I:452:PRO:HA	2.54	0.43
3:H:96:ASN:HB3	3:H:101:GLN:HG2	2.01	0.43
1:D:217:PHE:HA	2:F:452:PRO:HD3	1.99	0.43
3:E:42:SER:HA	2:F:388:LEU:O	2.19	0.43
3:E:157:VAL:HG21	3:E:189:LYS:HB3	1.99	0.43
1:A:77:ARG:NH1	8:A:308:HOH:O	2.52	0.43
1:A:83:LEU:O	1:A:95:ARG:HA	2.19	0.43
2:C:373:TYR:HB3	2:C:390:LYS:HB3	2.01	0.43
2:L:408:VAL:HG13	2:L:465:ILE:HD13	2.00	0.42
3:E:227:SER:HA	3:E:230:LEU:HD23	2.01	0.42
3:H:36:GLN:HB3	7:H:301:NAG:H83	2.01	0.42
1:A:36:ARG:HB2	1:A:39:ALA:HB2	2.01	0.42
3:K:163:ARG:HG3	3:K:163:ARG:NH1	2.33	0.42
2:L:402:LYS:HD2	2:L:450:PHE:CZ	2.55	0.42
1:G:241:ILE:O	1:G:245:ILE:HG12	2.19	0.42
3:E:126:ARG:HG2	3:E:129:GLU:OE1	2.19	0.42
3:H:227:SER:HA	3:H:230:LEU:HD23	2.01	0.42
3:K:127:ALA:HB2	3:K:230:LEU:HD12	2.01	0.42
1:J:88:LEU:HA	1:J:95:ARG:HH21	1.85	0.42
2:C:376:TYR:HA	2:C:463:ILE:O	2.20	0.42
3:E:23:ARG:HB2	3:E:26:SER:HB3	2.00	0.42
1:G:162:ARG:HG3	1:G:163:GLY:N	2.35	0.42
1:G:100:VAL:HG13	1:G:120:LEU:HB3	2.02	0.41
1:G:217:PHE:HA	2:I:452:PRO:HD3	2.01	0.41
1:D:162:ARG:N	1:D:162:ARG:HD3	2.35	0.41
1:J:160:ARG:HG3	1:J:222:CYS:HB2	2.03	0.41
3:E:74:ILE:H	3:E:74:ILE:HG13	1.68	0.41
3:E:27:ARG:NH1	3:E:201:LEU:HD13	2.36	0.41
1:G:164:ILE:HD12	1:G:164:ILE:HA	1.85	0.41
1:J:62:ASN:OD1	1:J:62:ASN:N	2.53	0.41
1:J:80:ARG:HE	6:T:2:NAG:C8	2.34	0.41
1:J:67:ALA:O	1:J:70:CYS:HB2	2.21	0.41
3:K:229:PHE:O	3:K:233:ILE:HG13	2.21	0.41
2:L:393:ILE:HG23	2:L:403:TYR:HE2	1.86	0.41
3:K:92:HIS:HB2	3:K:104:ILE:HG23	2.01	0.41
1:D:190:ARG:O	1:D:192:ARG:NH2	2.43	0.40
1:G:146:ASN:OD1	1:G:176:VAL:HA	2.19	0.40
3:H:34:GLN:HB2	3:H:66:ASN:HB2	2.02	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:29:TYR:CG	3:B:122:VAL:HB	2.56	0.40
1:J:41:PRO:HB2	1:J:133:GLN:HG3	2.03	0.40
2:F:371:THR:HB	2:F:395:ASN:OD1	2.20	0.40
3:H:218:VAL:HA	3:H:219:PRO:HD3	1.98	0.40
3:K:192:PHE:CE2	3:K:193:LYS:HD3	2.57	0.40
3:K:196:SER:HB3	2:L:386:PRO:HG2	2.04	0.40
3:E:144:ARG:HD3	2:F:388:LEU:HD21	2.01	0.40
1:G:157:LEU:HD12	1:G:164:ILE:HD13	2.04	0.40
3:H:225:ARG:HG2	3:H:228:SER:OG	2.22	0.40
3:K:87:ARG:NH2	8:K:408:HOH:O	2.54	0.40
2:L:373:TYR:HB3	2:L:390:LYS:HB3	2.03	0.40
1:D:34:ARG:HG2	1:D:167:VAL:CG1	2.51	0.40
1:G:119:ILE:HG21	1:G:244:ILE:HG21	2.03	0.40
2:L:404:LEU:HD23	2:L:404:LEU:HA	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	216/218 (99%)	210 (97%)	6 (3%)	0	100	100
1	D	216/218 (99%)	209 (97%)	6 (3%)	1 (0%)	29	25
1	G	216/218 (99%)	207 (96%)	9 (4%)	0	100	100
1	J	216/218 (99%)	207 (96%)	9 (4%)	0	100	100
2	C	96/108 (89%)	96 (100%)	0	0	100	100
2	F	96/108 (89%)	96 (100%)	0	0	100	100
2	I	96/108 (89%)	95 (99%)	1 (1%)	0	100	100
2	L	96/108 (89%)	96 (100%)	0	0	100	100
3	B	221/223 (99%)	217 (98%)	4 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	E	221/223 (99%)	214 (97%)	7 (3%)	0	100	100
3	H	221/223 (99%)	211 (96%)	10 (4%)	0	100	100
3	K	221/223 (99%)	215 (97%)	6 (3%)	0	100	100
All	All	2132/2196 (97%)	2073 (97%)	58 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	49	ARG

5.3.2 Protein sidechains [i](#)

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	172/172 (100%)	171 (99%)	1 (1%)	86	90
1	D	172/172 (100%)	170 (99%)	2 (1%)	71	77
1	G	172/172 (100%)	172 (100%)	0	100	100
1	J	172/172 (100%)	172 (100%)	0	100	100
2	C	91/100 (91%)	90 (99%)	1 (1%)	73	79
2	F	91/100 (91%)	90 (99%)	1 (1%)	73	79
2	I	91/100 (91%)	89 (98%)	2 (2%)	52	55
2	L	91/100 (91%)	91 (100%)	0	100	100
3	B	190/190 (100%)	189 (100%)	1 (0%)	88	92
3	E	190/190 (100%)	189 (100%)	1 (0%)	88	92
3	H	190/190 (100%)	185 (97%)	5 (3%)	46	49
3	K	190/190 (100%)	188 (99%)	2 (1%)	73	79
All	All	1812/1848 (98%)	1796 (99%)	16 (1%)	78	83

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	190	ARG
1	D	103	ILE
1	D	162	ARG
2	C	371	THR
3	E	170	ILE
2	F	371	THR
3	H	36	GLN
3	H	41	GLN
3	H	66	ASN
3	H	160	ARG
3	H	225	ARG
2	I	371	THR
2	I	372	ARG
3	B	66	ASN
3	K	147	MET
3	K	201	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	212	HIS
2	C	428	GLN
3	H	97	GLN
3	B	94	GLN
1	J	149	GLN
3	K	162	GLN
3	K	166	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

28 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	0.25	0	17,19,21	0.50	0
4	NAG	M	2	4	14,14,15	0.52	0	17,19,21	0.41	0
4	BMA	M	3	4	11,11,12	1.04	0	15,15,17	0.87	0
4	FUC	M	4	4	10,10,11	1.21	1 (10%)	14,14,16	0.89	0
5	NAG	N	1	1,5	14,14,15	0.56	0	17,19,21	0.46	0
5	NAG	N	2	5	14,14,15	0.34	0	17,19,21	0.60	0
5	BMA	N	3	5	11,11,12	1.22	2 (18%)	15,15,17	1.16	1 (6%)
4	NAG	O	1	1,4	14,14,15	0.25	0	17,19,21	0.51	0
4	NAG	O	2	4	14,14,15	0.57	0	17,19,21	0.51	0
4	BMA	O	3	4	11,11,12	1.33	1 (9%)	15,15,17	1.17	1 (6%)
4	FUC	O	4	4	10,10,11	1.60	4 (40%)	14,14,16	1.76	4 (28%)
4	NAG	P	1	1,4	14,14,15	0.65	1 (7%)	17,19,21	0.64	0
4	NAG	P	2	4	14,14,15	0.64	0	17,19,21	0.64	0
4	BMA	P	3	4	11,11,12	1.07	1 (9%)	15,15,17	1.13	1 (6%)
4	FUC	P	4	4	10,10,11	1.45	1 (10%)	14,14,16	0.84	0
4	NAG	Q	1	1,4	14,14,15	0.25	0	17,19,21	0.68	1 (5%)
4	NAG	Q	2	4	14,14,15	0.34	0	17,19,21	0.77	1 (5%)
4	BMA	Q	3	4	11,11,12	0.82	0	15,15,17	1.01	1 (6%)
4	FUC	Q	4	4	10,10,11	1.32	1 (10%)	14,14,16	1.26	2 (14%)
5	NAG	R	1	1,5	14,14,15	0.33	0	17,19,21	0.53	0
5	NAG	R	2	5	14,14,15	0.37	0	17,19,21	0.73	1 (5%)
5	BMA	R	3	5	11,11,12	1.24	1 (9%)	15,15,17	0.84	0
6	NAG	S	1	1,6	14,14,15	0.40	0	17,19,21	0.52	0
6	NAG	S	2	6	14,14,15	0.41	0	17,19,21	0.61	1 (5%)
6	FUC	S	3	6	10,10,11	1.71	2 (20%)	14,14,16	1.42	2 (14%)
6	NAG	T	1	1,6	14,14,15	0.38	0	17,19,21	0.34	0
6	NAG	T	2	6	14,14,15	0.24	0	17,19,21	0.68	1 (5%)
6	FUC	T	3	6	10,10,11	1.04	1 (10%)	14,14,16	0.91	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
4	NAG	M	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	M	2	4	-	0/6/23/26	0/1/1/1
4	BMA	M	3	4	-	0/2/19/22	0/1/1/1
4	FUC	M	4	4	-	-	0/1/1/1
5	NAG	N	1	1,5	-	1/6/23/26	0/1/1/1
5	NAG	N	2	5	-	0/6/23/26	0/1/1/1
5	BMA	N	3	5	-	0/2/19/22	0/1/1/1
4	NAG	O	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	O	2	4	-	0/6/23/26	0/1/1/1
4	BMA	O	3	4	-	2/2/19/22	0/1/1/1
4	FUC	O	4	4	-	-	0/1/1/1
4	NAG	P	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	P	2	4	-	0/6/23/26	0/1/1/1
4	BMA	P	3	4	-	0/2/19/22	0/1/1/1
4	FUC	P	4	4	-	-	0/1/1/1
4	NAG	Q	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	1/6/23/26	0/1/1/1
4	BMA	Q	3	4	-	2/2/19/22	0/1/1/1
4	FUC	Q	4	4	-	-	0/1/1/1
5	NAG	R	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	R	2	5	-	0/6/23/26	0/1/1/1
5	BMA	R	3	5	-	2/2/19/22	0/1/1/1
6	NAG	S	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	S	2	6	-	0/6/23/26	0/1/1/1
6	FUC	S	3	6	-	-	0/1/1/1
6	NAG	T	1	1,6	-	0/6/23/26	0/1/1/1
6	NAG	T	2	6	-	2/6/23/26	0/1/1/1
6	FUC	T	3	6	-	-	0/1/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	S	3	FUC	C1-C2	4.59	1.62	1.52
4	Q	4	FUC	C1-C2	3.55	1.60	1.52
4	P	4	FUC	O5-C1	-3.51	1.38	1.43
4	O	3	BMA	C4-C5	2.91	1.59	1.53
4	O	4	FUC	O5-C1	-2.90	1.39	1.43
5	R	3	BMA	C4-C5	2.38	1.58	1.53
5	N	3	BMA	C1-C2	2.31	1.57	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	3	BMA	C4-C3	2.24	1.58	1.52
4	P	1	NAG	C1-C2	2.23	1.55	1.52
4	M	4	FUC	O2-C2	-2.14	1.38	1.43
6	S	3	FUC	O5-C1	-2.13	1.40	1.43
4	O	4	FUC	C6-C5	2.07	1.56	1.51
5	N	3	BMA	C2-C3	2.06	1.55	1.52
4	O	4	FUC	C4-C5	2.06	1.57	1.52
4	O	4	FUC	C2-C3	2.04	1.55	1.52
6	T	3	FUC	C4-C5	2.00	1.57	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	O	4	FUC	O3-C3-C4	-3.60	102.03	110.35
6	S	3	FUC	C1-C2-C3	3.56	114.05	109.67
4	O	3	BMA	C1-C2-C3	-3.20	105.73	109.67
4	Q	3	BMA	C1-O5-C5	3.02	116.29	112.19
4	Q	4	FUC	C1-C2-C3	2.95	113.29	109.67
4	O	4	FUC	O2-C2-C1	2.66	114.59	109.15
4	P	3	BMA	C1-C2-C3	-2.61	106.46	109.67
4	Q	2	NAG	C1-O5-C5	2.60	115.72	112.19
6	S	3	FUC	O2-C2-C1	2.56	114.38	109.15
4	O	4	FUC	C2-C3-C4	2.36	114.98	110.89
6	T	2	NAG	C1-O5-C5	2.20	115.18	112.19
4	Q	4	FUC	O2-C2-C1	2.15	113.55	109.15
5	N	3	BMA	C1-O5-C5	2.08	115.01	112.19
4	O	4	FUC	C3-C4-C5	2.08	113.01	109.77
6	S	2	NAG	C1-O5-C5	2.06	114.98	112.19
5	R	2	NAG	C1-O5-C5	2.05	114.97	112.19
4	Q	1	NAG	C1-O5-C5	2.00	114.90	112.19

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	O	1	NAG	C4-C5-C6-O6
4	O	3	BMA	O5-C5-C6-O6
4	O	1	NAG	O5-C5-C6-O6
4	O	3	BMA	C4-C5-C6-O6
5	R	3	BMA	O5-C5-C6-O6
6	T	2	NAG	C4-C5-C6-O6
5	R	3	BMA	C4-C5-C6-O6

Continued on next page...

Continued from previous page...

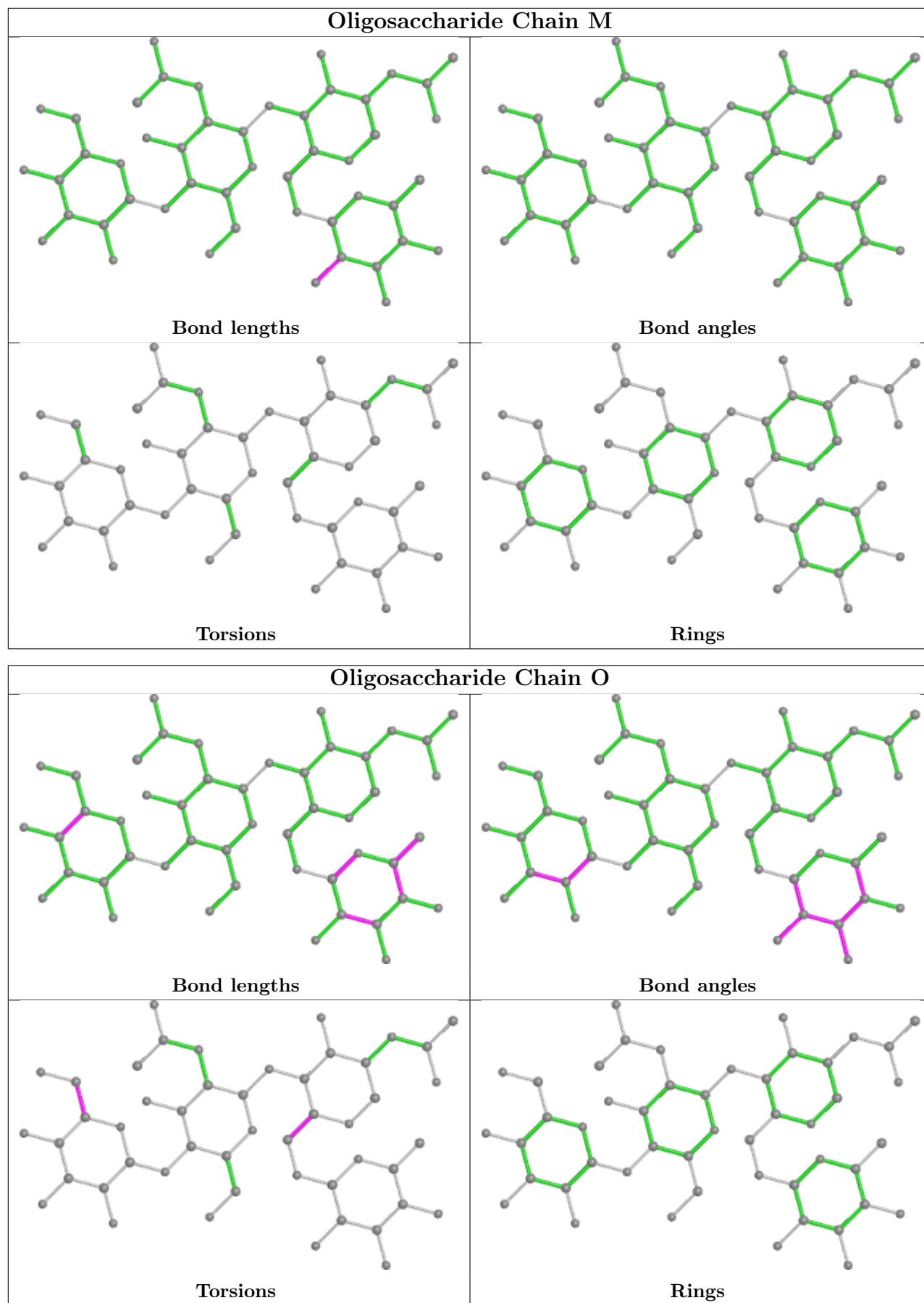
Mol	Chain	Res	Type	Atoms
6	T	2	NAG	O5-C5-C6-O6
4	Q	3	BMA	C4-C5-C6-O6
4	Q	1	NAG	C4-C5-C6-O6
5	R	1	NAG	C4-C5-C6-O6
4	P	1	NAG	C4-C5-C6-O6
4	Q	1	NAG	O5-C5-C6-O6
4	Q	3	BMA	O5-C5-C6-O6
5	R	1	NAG	O5-C5-C6-O6
4	P	1	NAG	O5-C5-C6-O6
6	S	1	NAG	C4-C5-C6-O6
5	N	1	NAG	C4-C5-C6-O6
6	S	1	NAG	O5-C5-C6-O6
4	Q	2	NAG	C4-C5-C6-O6

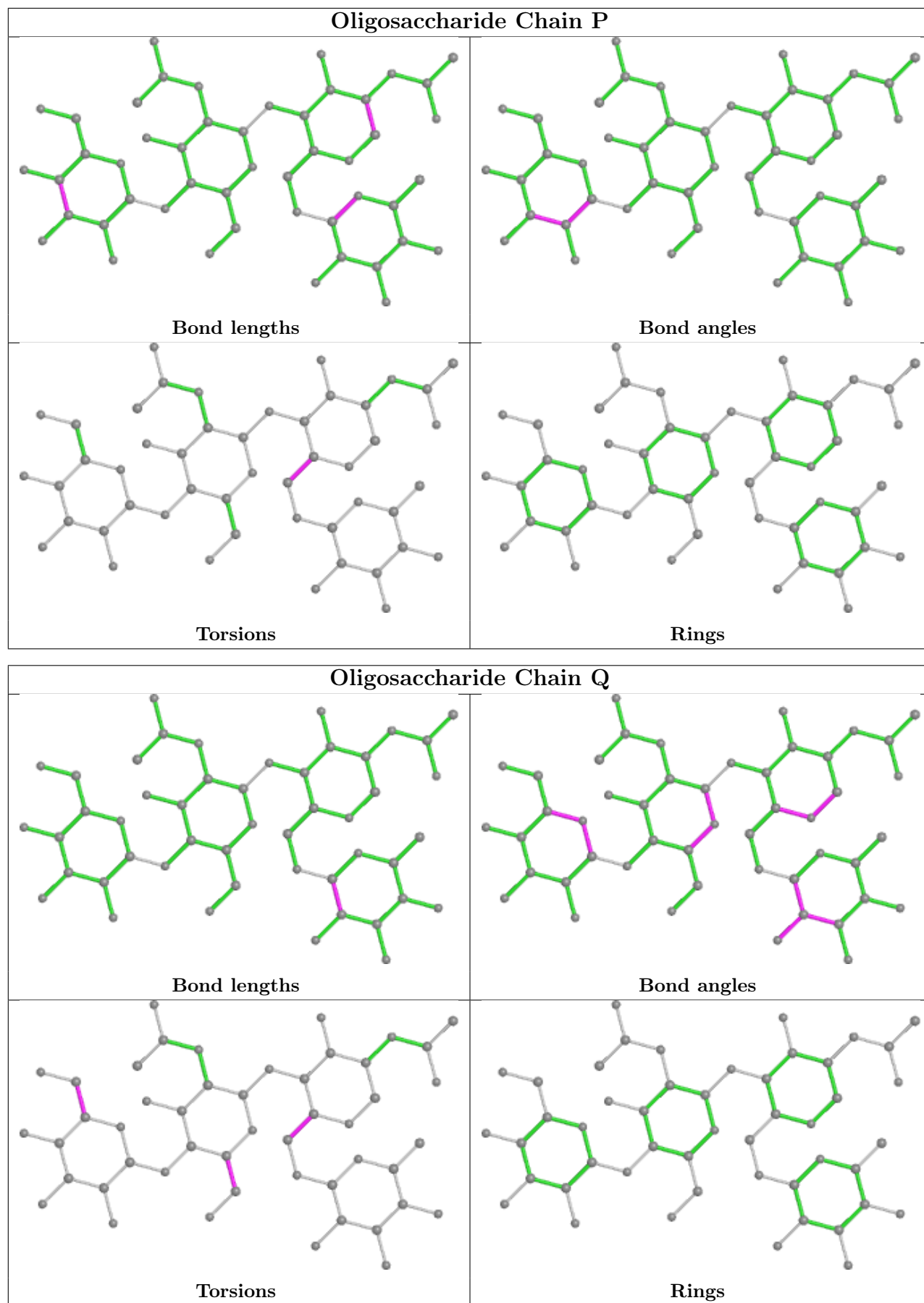
There are no ring outliers.

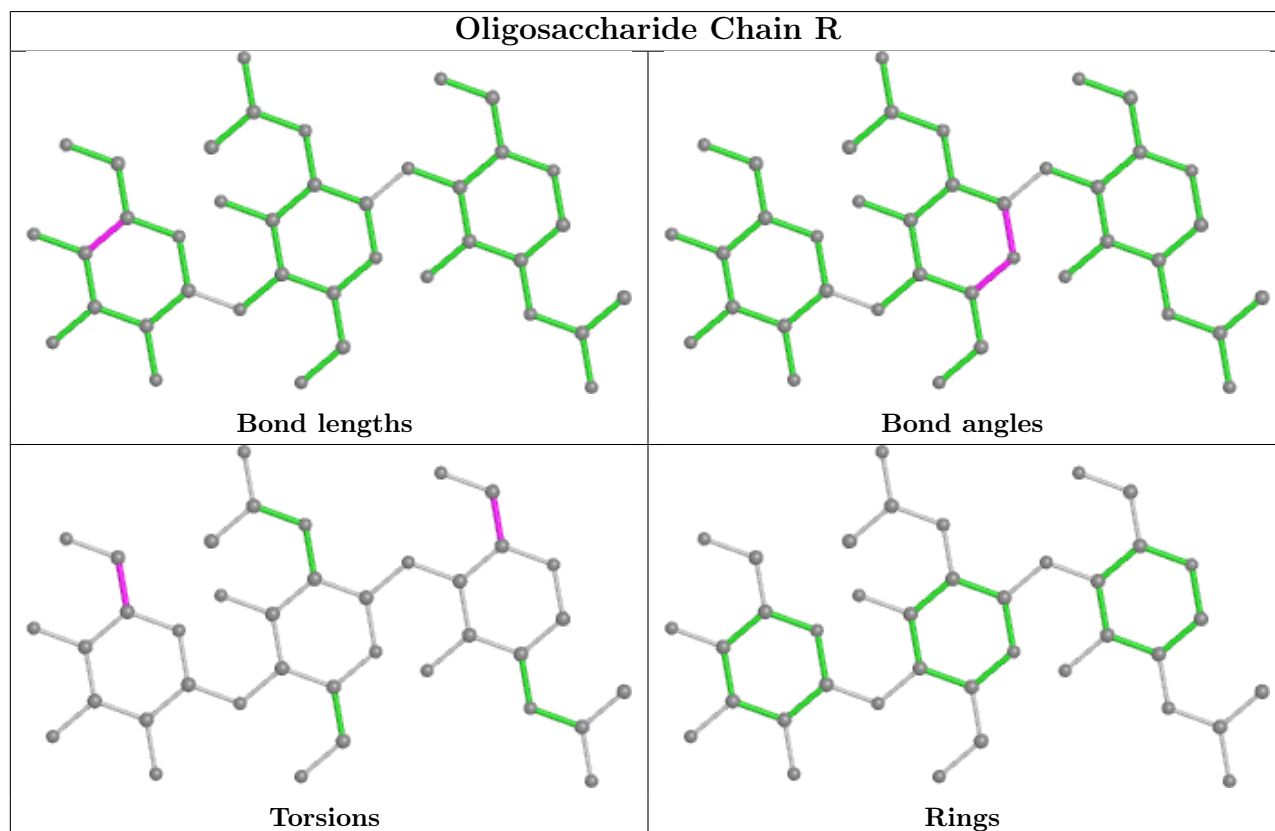
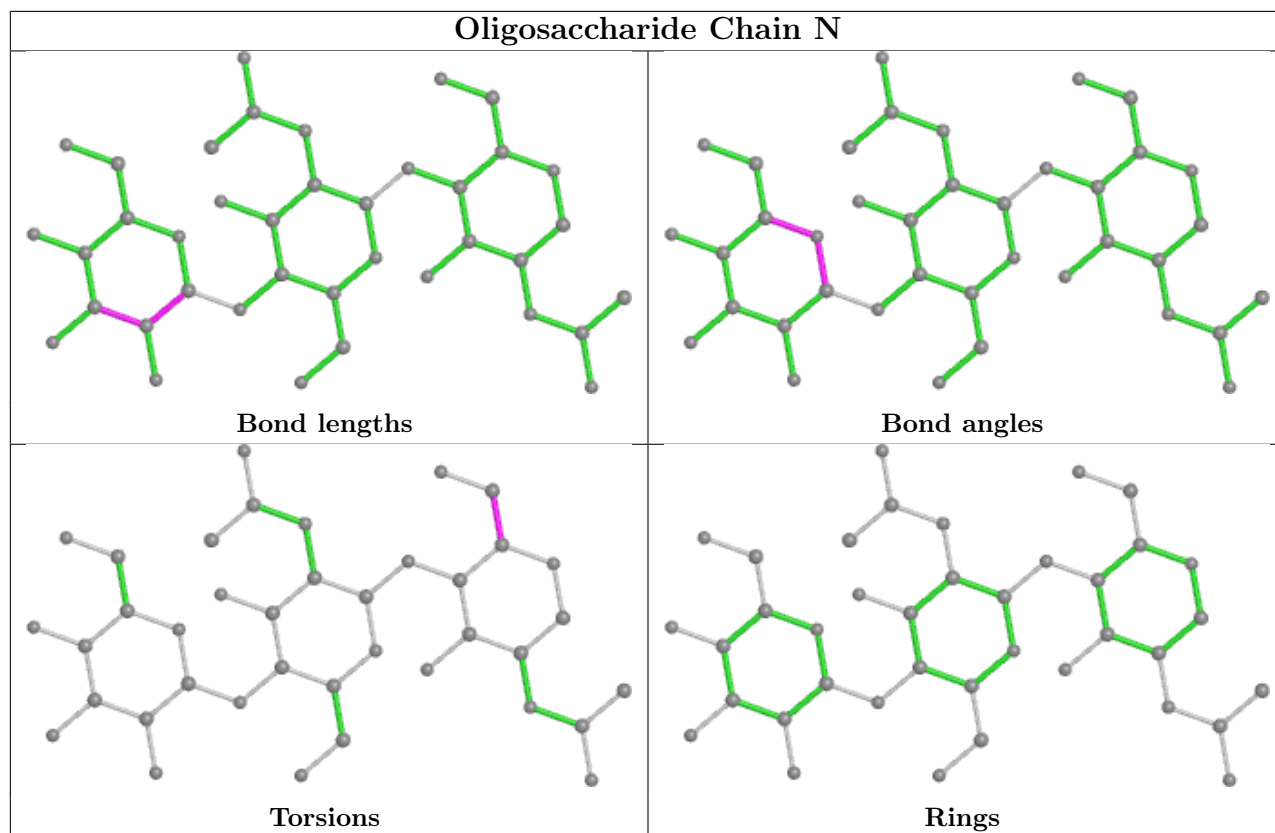
4 monomers are involved in 4 short contacts:

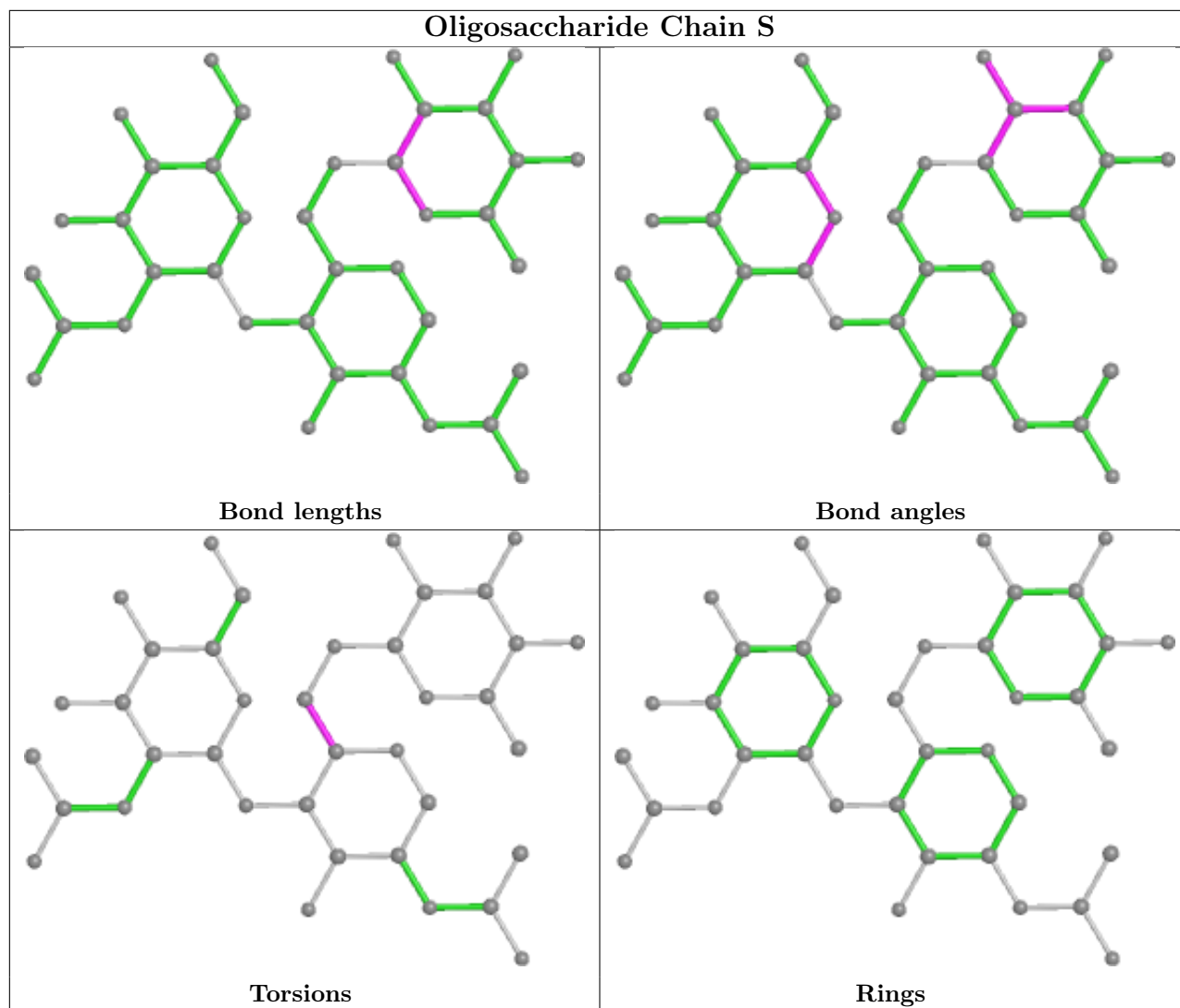
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	O	4	FUC	1	0
5	R	2	NAG	2	0
6	T	2	NAG	1	0
5	R	3	BMA	1	0

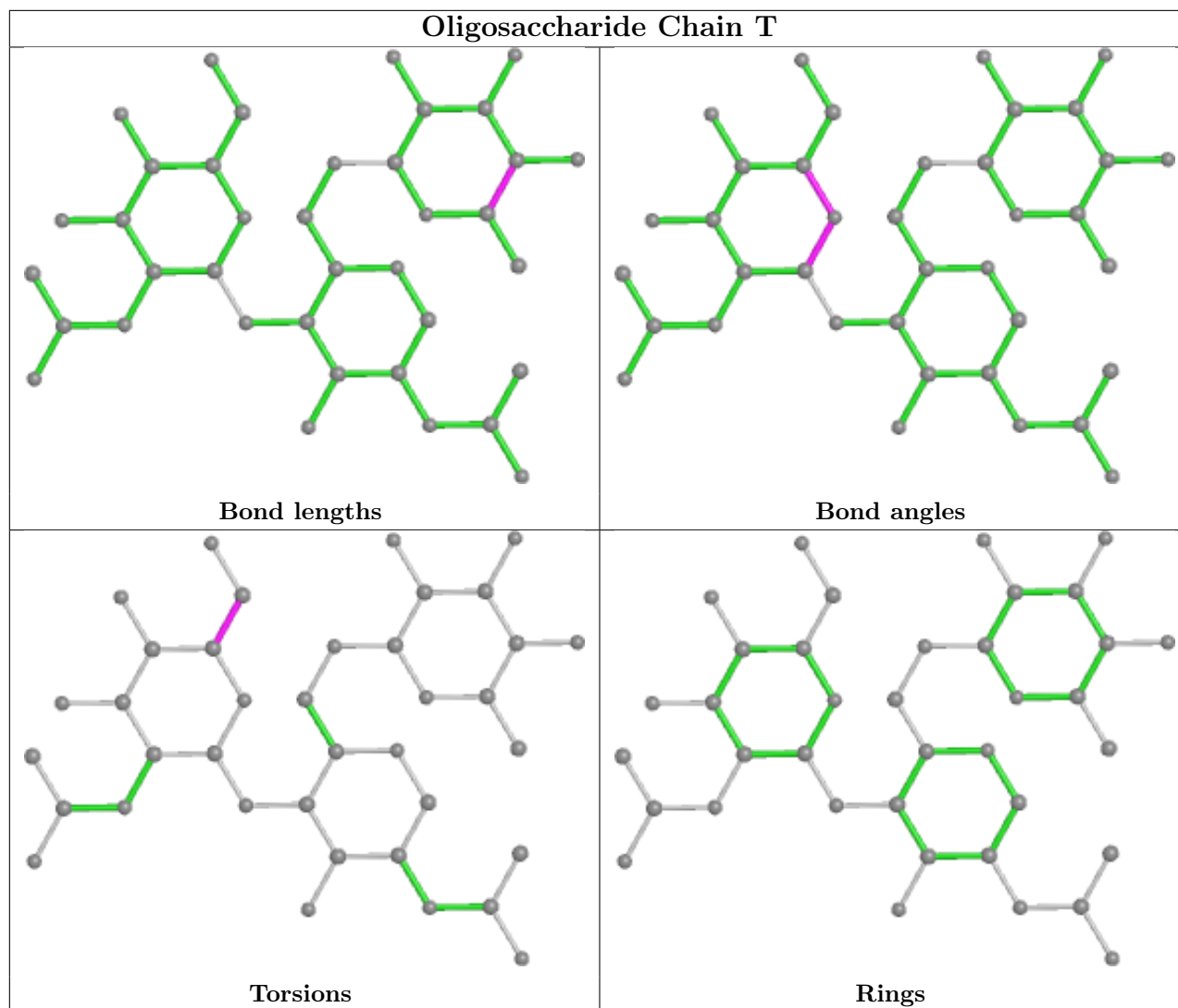
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	E	301	3	14,14,15	1.01	1 (7%)	17,19,21	0.81	1 (5%)
7	NAG	H	301	3	14,14,15	0.70	1 (7%)	17,19,21	0.91	1 (5%)
7	NAG	K	301	3	14,14,15	0.42	0	17,19,21	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	B	301	3	14,14,15	0.51	0	17,19,21	0.56	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	E	301	3	-	2/6/23/26	0/1/1/1
7	NAG	H	301	3	-	2/6/23/26	0/1/1/1
7	NAG	K	301	3	-	2/6/23/26	0/1/1/1
7	NAG	B	301	3	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	E	301	NAG	O5-C1	3.40	1.49	1.43
7	H	301	NAG	O5-C1	2.28	1.47	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	H	301	NAG	C1-O5-C5	2.67	115.81	112.19
7	E	301	NAG	C1-O5-C5	2.33	115.36	112.19

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	H	301	NAG	C4-C5-C6-O6
7	H	301	NAG	O5-C5-C6-O6
7	E	301	NAG	C8-C7-N2-C2
7	E	301	NAG	O7-C7-N2-C2
7	K	301	NAG	O5-C5-C6-O6
7	K	301	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	H	301	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	218/218 (100%)	0.05	3 (1%) 75 78	20, 34, 52, 74	0
1	D	218/218 (100%)	0.18	7 (3%) 47 54	21, 38, 60, 107	0
1	G	218/218 (100%)	0.36	11 (5%) 28 34	26, 49, 73, 109	0
1	J	218/218 (100%)	0.18	7 (3%) 47 54	27, 49, 74, 97	0
2	C	98/108 (90%)	-0.11	0 100 100	23, 30, 47, 61	0
2	F	98/108 (90%)	-0.03	1 (1%) 82 85	22, 29, 44, 58	0
2	I	98/108 (90%)	-0.06	1 (1%) 82 85	26, 35, 58, 70	0
2	L	98/108 (90%)	-0.15	1 (1%) 82 85	27, 34, 54, 61	0
3	B	223/223 (100%)	-0.06	2 (0%) 84 86	19, 32, 52, 84	0
3	E	223/223 (100%)	0.13	7 (3%) 49 55	25, 42, 65, 98	0
3	H	223/223 (100%)	0.02	8 (3%) 42 49	26, 40, 60, 96	0
3	K	223/223 (100%)	-0.04	5 (2%) 62 66	25, 38, 58, 78	0
All	All	2156/2196 (98%)	0.07	53 (2%) 57 62	19, 38, 65, 109	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	238	ARG	5.0
1	D	91	ARG	4.4
1	G	91	ARG	4.0
1	G	50	GLY	3.9
1	G	49	ARG	3.9
1	D	162	ARG	3.8
1	D	50	GLY	3.6
1	A	50	GLY	3.6
3	E	111	ARG	3.5
1	J	48	LEU	3.4
3	E	112	ARG	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
3	H	77	ARG	3.3
3	K	77	ARG	3.2
3	E	148	ARG	3.2
1	G	48	LEU	3.1
1	G	88	LEU	3.0
1	G	210	LEU	2.9
3	H	98	ARG	2.9
3	E	238	ARG	2.8
1	D	192	ARG	2.8
1	J	76	VAL	2.8
3	H	163	ARG	2.7
3	H	132	ARG	2.7
3	H	148	ARG	2.5
1	G	244	ILE	2.5
1	G	80	ARG	2.4
1	G	182	ARG	2.4
1	A	36	ARG	2.4
1	G	162	ARG	2.4
1	J	105	GLU	2.3
1	D	49	ARG	2.3
3	B	77	ARG	2.3
2	L	373	TYR	2.2
3	K	165	ARG	2.2
3	H	147	MET	2.2
3	K	169	ARG	2.2
1	J	50	GLY	2.2
3	E	236	THR	2.2
1	D	159	GLY	2.2
1	J	246	GLN	2.2
3	B	148	ARG	2.2
3	K	238	ARG	2.2
1	J	75	ASN	2.1
3	H	20	ARG	2.1
2	F	428	GLN	2.1
1	G	90	ARG	2.1
1	D	93	PRO	2.1
1	J	91	ARG	2.1
3	E	23	ARG	2.1
2	I	396	LYS	2.1
3	K	74	ILE	2.0
1	A	80	ARG	2.0
3	E	132	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

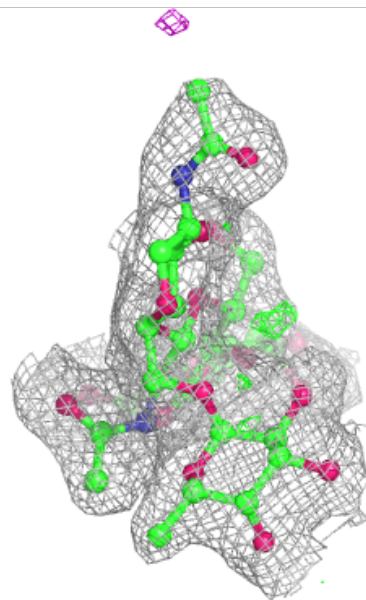
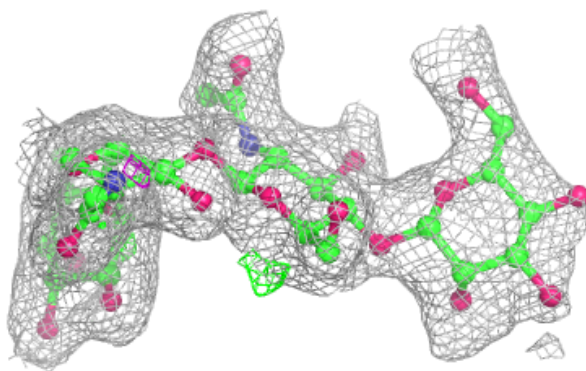
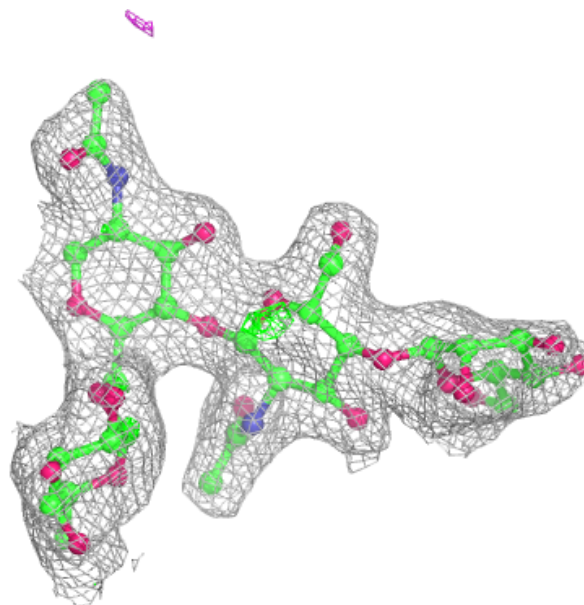
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	BMA	R	3	11/12	0.58	0.35	75,81,84,85	0
4	BMA	O	3	11/12	0.67	0.29	64,67,69,69	0
6	NAG	T	2	14/15	0.71	0.48	80,83,86,86	0
4	BMA	P	3	11/12	0.74	0.38	73,77,82,83	0
4	BMA	M	3	11/12	0.75	0.25	65,69,71,75	0
6	NAG	T	1	14/15	0.76	0.19	70,73,80,81	0
5	NAG	N	2	14/15	0.76	0.33	60,65,67,67	0
5	NAG	R	2	14/15	0.77	0.28	77,81,82,85	0
4	BMA	Q	3	11/12	0.78	0.21	73,75,76,76	0
6	FUC	T	3	10/11	0.78	0.31	72,80,82,82	0
4	FUC	O	4	10/11	0.81	0.20	40,48,50,51	0
4	NAG	Q	2	14/15	0.83	0.18	52,64,70,75	0
4	NAG	P	2	14/15	0.83	0.27	64,69,75,77	0
6	NAG	S	2	14/15	0.84	0.20	57,67,69,71	0
5	NAG	N	1	14/15	0.85	0.29	51,56,62,63	0
4	FUC	P	4	10/11	0.85	0.25	65,69,71,71	0
4	NAG	Q	1	14/15	0.87	0.15	48,53,60,62	0
6	NAG	S	1	14/15	0.87	0.16	52,59,62,63	0
5	NAG	R	1	14/15	0.88	0.21	67,71,76,77	0
4	NAG	O	2	14/15	0.88	0.20	48,57,62,66	0
6	FUC	S	3	10/11	0.89	0.17	49,55,57,64	0
5	BMA	N	3	11/12	0.89	0.26	59,61,64,65	0
4	NAG	P	1	14/15	0.90	0.12	54,59,64,65	0
4	FUC	Q	4	10/11	0.90	0.14	49,51,55,59	0
4	NAG	M	2	14/15	0.91	0.11	41,52,57,64	0
4	NAG	O	1	14/15	0.93	0.18	43,47,52,56	0
4	NAG	M	1	14/15	0.97	0.07	34,41,46,48	0
4	FUC	M	4	10/11	0.98	0.10	34,36,39,41	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.

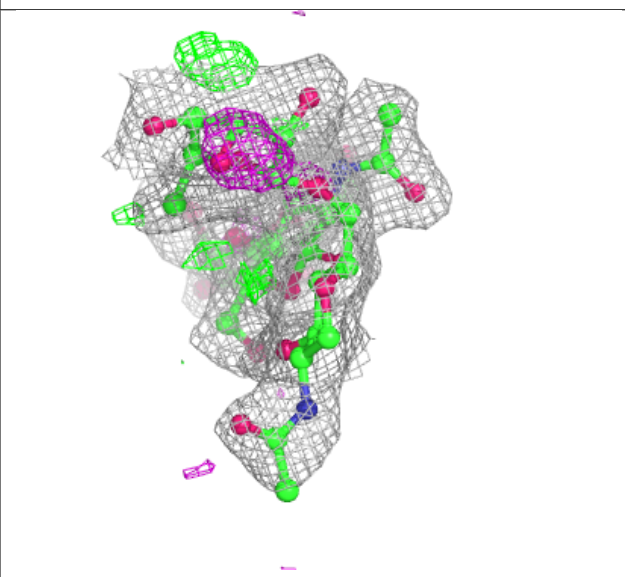
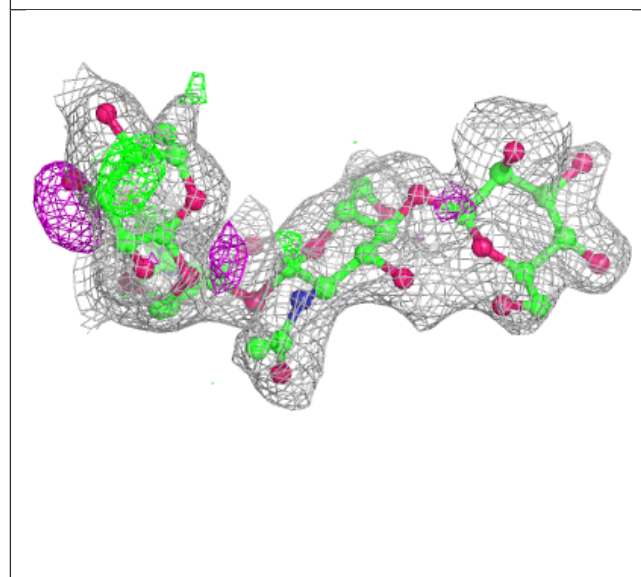
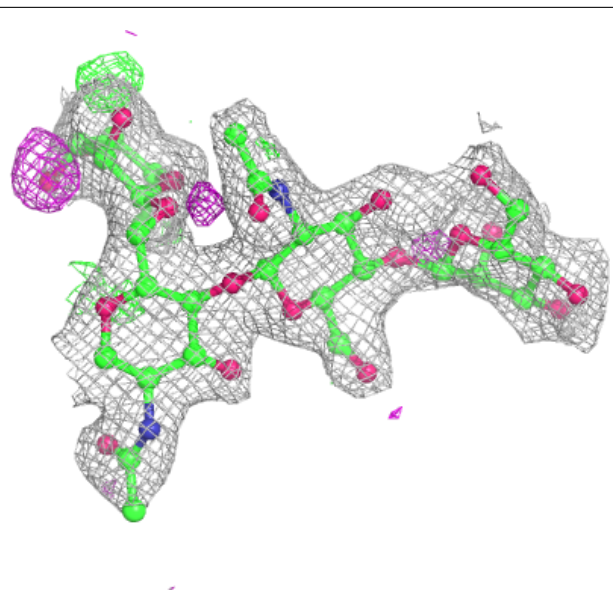
Electron density around Chain M:

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



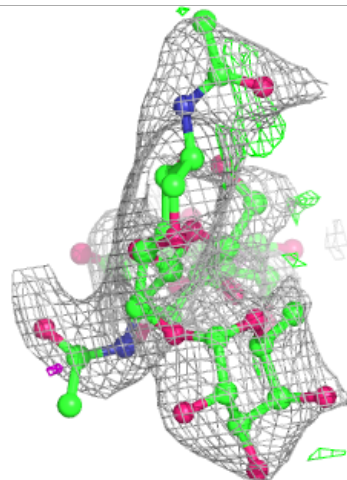
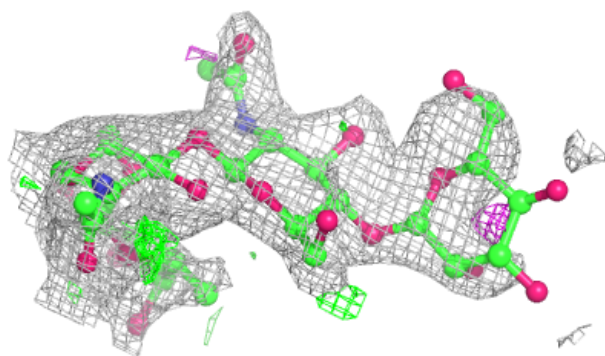
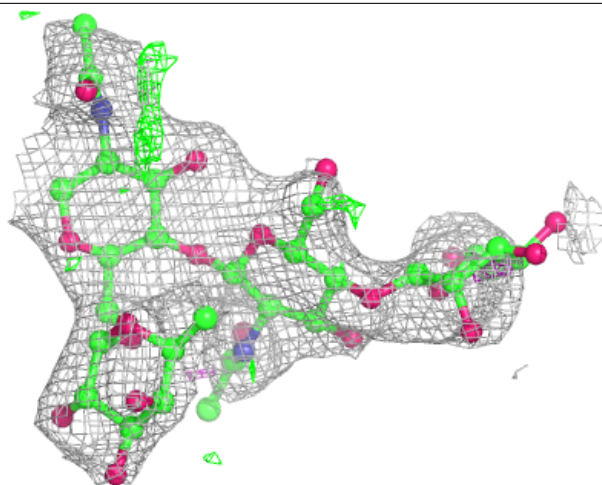
Electron density around Chain O:

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



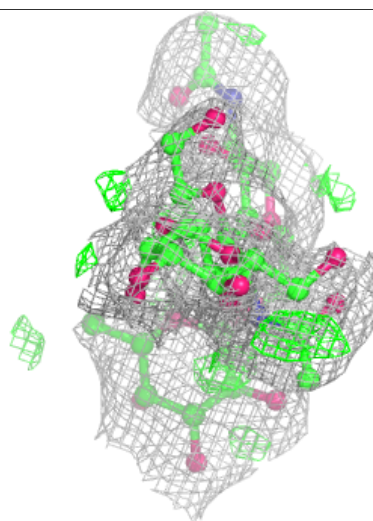
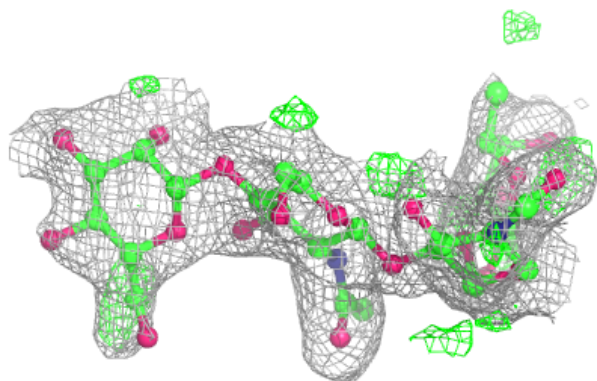
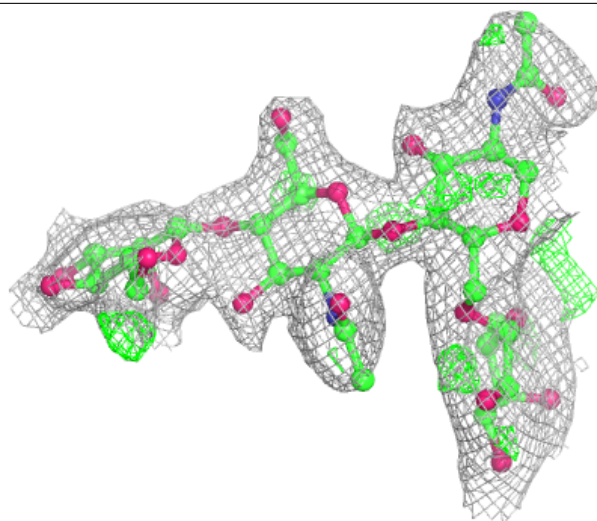
Electron density around Chain P:

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



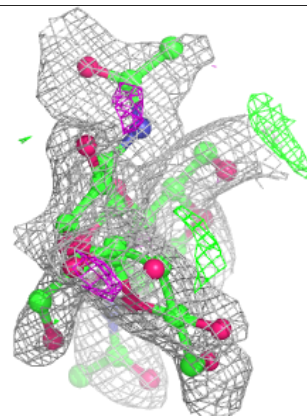
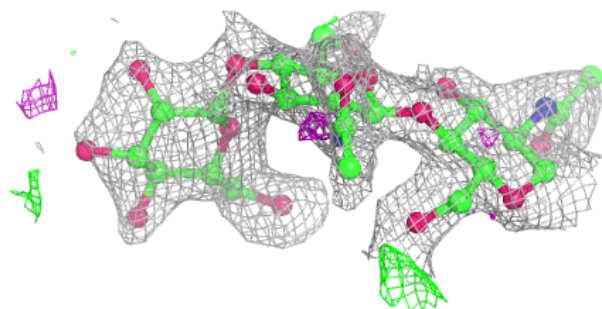
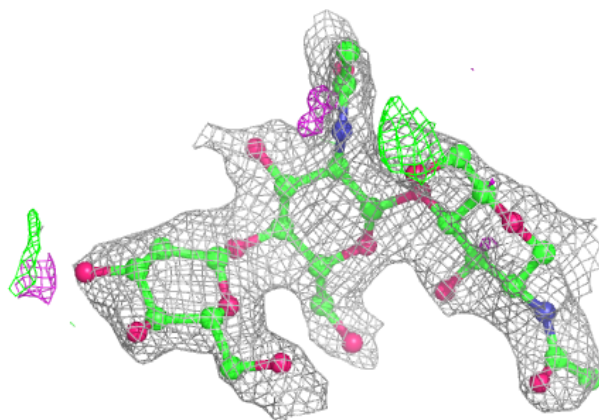
Electron density around Chain Q:

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

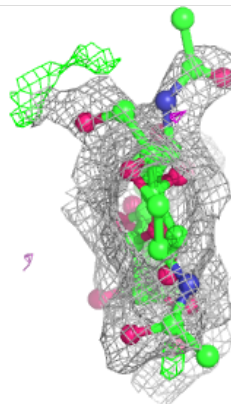
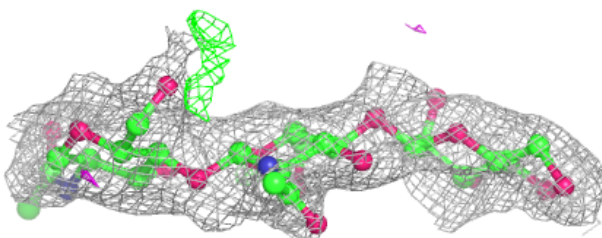
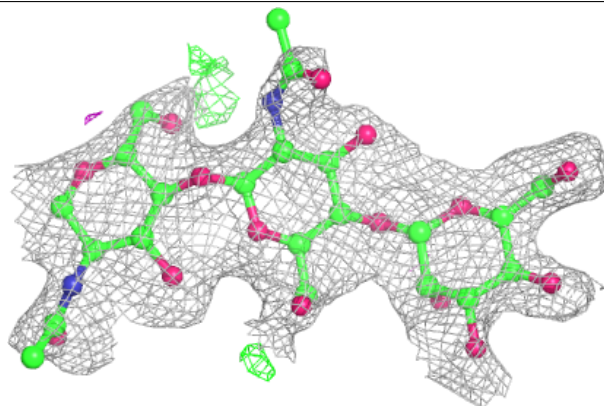


Electron density around Chain N:

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

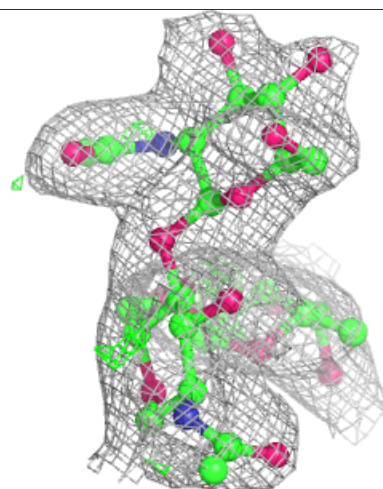
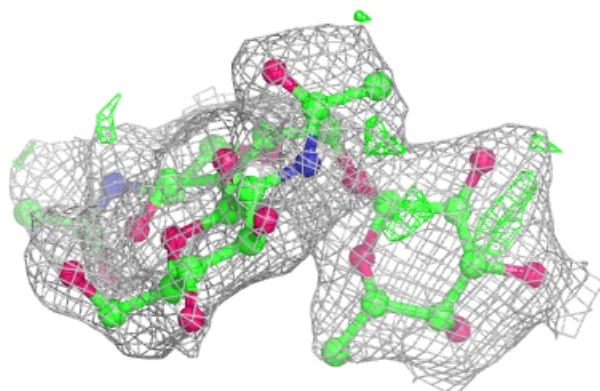
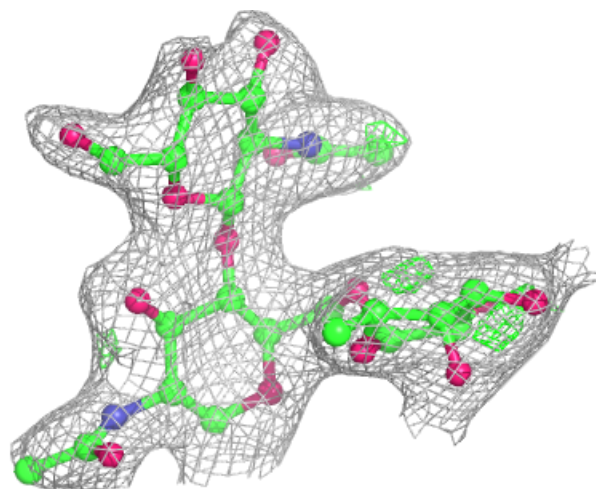
**Electron density around Chain R:**

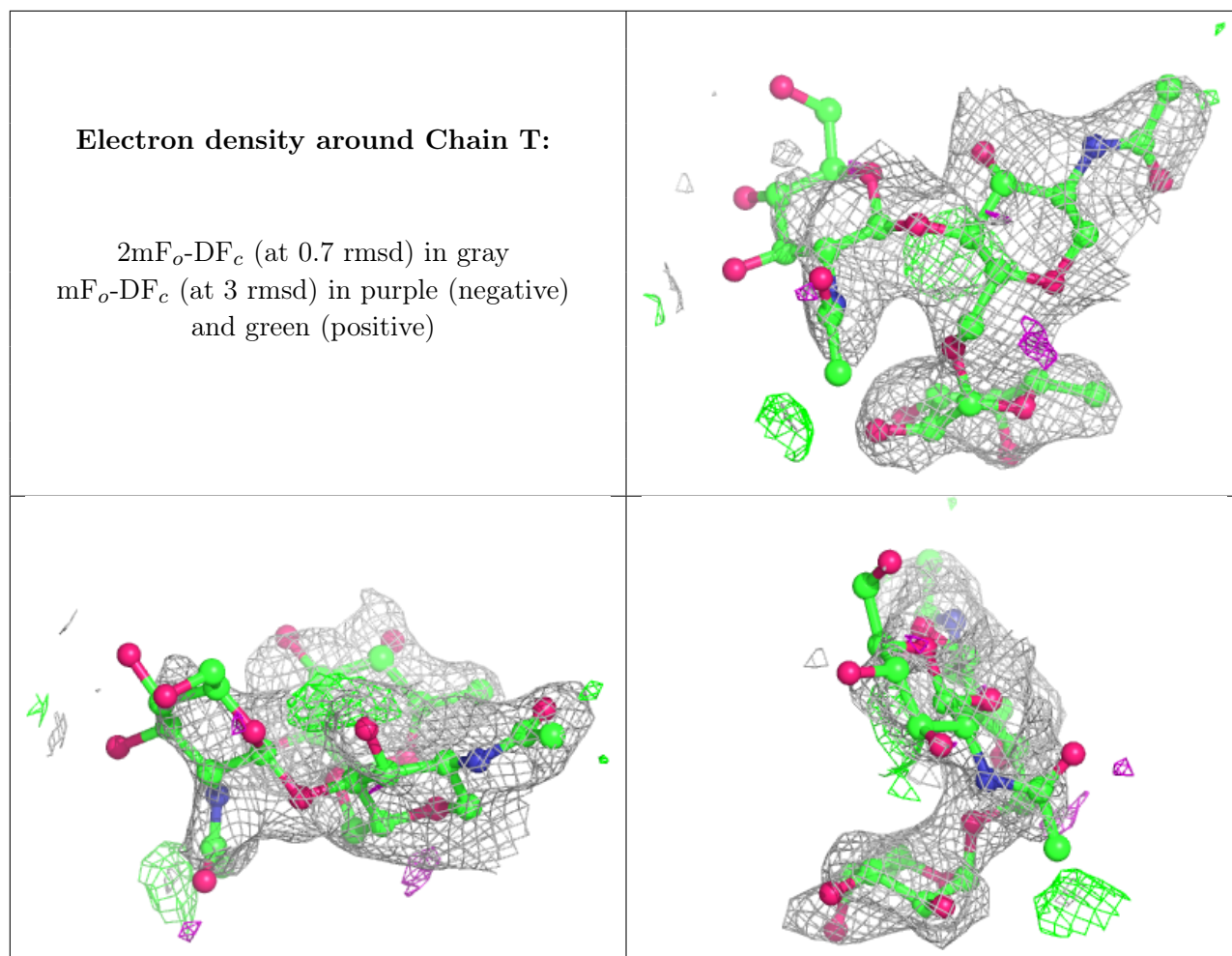
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain S:

$2mF_o-DF_c$ (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	H	301	14/15	0.69	0.40	47,65,68,69	0
7	NAG	E	301	14/15	0.79	0.26	50,66,70,76	0
7	NAG	B	301	14/15	0.81	0.23	43,59,63,65	0
7	NAG	K	301	14/15	0.85	0.30	46,62,70,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.