



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 10:39 AM BST

PDB ID : 4OFY  
Title : Crystal Structure of the Complex of SYG-1 D1-D2 and SYG-2 D1-D4  
Authors : Ozkan, E.; Garcia, K.C.  
Deposited on : 2014-01-15  
Resolution : 3.30 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](mailto: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.

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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 : 2.13.1  
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) : 2.13.1

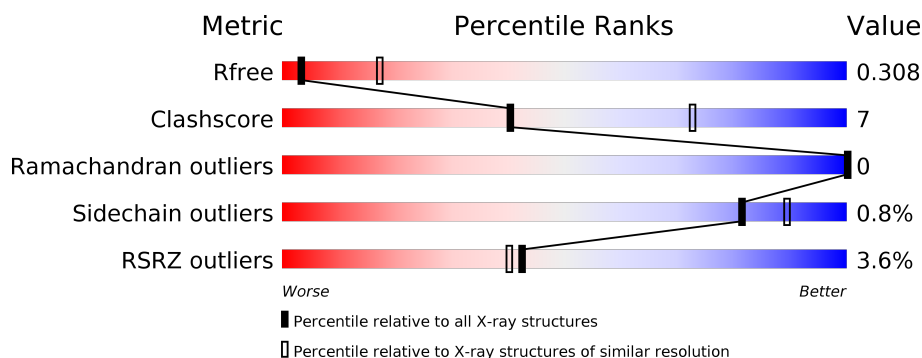
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.30 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	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	262	<div> <div>6%</div> <div> <div></div> <div>76%</div> <div>12%</div> <div>12%</div> </div> </div>
1	B	262	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>11%</div> <div>13%</div> </div> </div>
1	C	262	<div> <div>3%</div> <div> <div></div> <div>76%</div> <div>10%</div> <div>13%</div> </div> </div>
2	D	420	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>19%</div> <div>•</div> </div> </div>
2	E	420	<div> <div>4%</div> <div> <div></div> <div>76%</div> <div>20%</div> <div>•</div> </div> </div>
2	F	420	<div> <div>4%</div> <div> <div></div> <div>76%</div> <div>19%</div> <div>• •</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	G	2	 50%50%
3	H	2	 50%50%
3	I	2	 50%50%
3	J	2	 100%
3	K	2	 100%
3	L	2	 100%

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	G	1	-	-	-	X
3	NAG	G	2	-	-	-	X
3	NAG	H	2	-	-	-	X
3	NAG	I	1	-	-	-	X
3	NAG	I	2	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14816 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 Protein SYG-1, isoform b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1767	1109	310	340	8			
1	B	227	Total	C	N	O	S	0	0	0
			1752	1100	307	337	8			
1	C	227	Total	C	N	O	S	0	0	0
			1752	1100	307	337	8			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	ALA	-	expression tag	UNP B1Q236
A	17	ASP	-	expression tag	UNP B1Q236
A	18	PRO	-	expression tag	UNP B1Q236
A	272	HIS	-	expression tag	UNP B1Q236
A	273	HIS	-	expression tag	UNP B1Q236
A	274	HIS	-	expression tag	UNP B1Q236
A	275	HIS	-	expression tag	UNP B1Q236
A	276	HIS	-	expression tag	UNP B1Q236
A	277	HIS	-	expression tag	UNP B1Q236
B	16	ALA	-	expression tag	UNP B1Q236
B	17	ASP	-	expression tag	UNP B1Q236
B	18	PRO	-	expression tag	UNP B1Q236
B	272	HIS	-	expression tag	UNP B1Q236
B	273	HIS	-	expression tag	UNP B1Q236
B	274	HIS	-	expression tag	UNP B1Q236
B	275	HIS	-	expression tag	UNP B1Q236
B	276	HIS	-	expression tag	UNP B1Q236
B	277	HIS	-	expression tag	UNP B1Q236
C	16	ALA	-	expression tag	UNP B1Q236
C	17	ASP	-	expression tag	UNP B1Q236
C	18	PRO	-	expression tag	UNP B1Q236
C	272	HIS	-	expression tag	UNP B1Q236
C	273	HIS	-	expression tag	UNP B1Q236

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Chain	Residue	Modelled	Actual	Comment	Reference
C	274	HIS	-	expression tag	UNP B1Q236
C	275	HIS	-	expression tag	UNP B1Q236
C	276	HIS	-	expression tag	UNP B1Q236
C	277	HIS	-	expression tag	UNP B1Q236

- Molecule 2 is a protein called Protein SYG-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	407	Total	C	N	O	S	0	0	0
			3045	1912	520	598	15			
2	E	407	Total	C	N	O	S	0	0	0
			3042	1910	519	598	15			
2	F	407	Total	C	N	O	S	0	0	0
			3057	1921	522	599	15			

There are 30 discrepancies between the modelled and reference sequences:

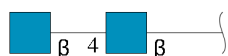
Chain	Residue	Modelled	Actual	Comment	Reference
D	17	ALA	-	expression tag	UNP Q9U3P2
D	18	ASP	-	expression tag	UNP Q9U3P2
D	19	PRO	-	expression tag	UNP Q9U3P2
D	391	CYS	ASN	engineered mutation	UNP Q9U3P2
D	431	HIS	-	expression tag	UNP Q9U3P2
D	432	HIS	-	expression tag	UNP Q9U3P2
D	433	HIS	-	expression tag	UNP Q9U3P2
D	434	HIS	-	expression tag	UNP Q9U3P2
D	435	HIS	-	expression tag	UNP Q9U3P2
D	436	HIS	-	expression tag	UNP Q9U3P2
E	17	ALA	-	expression tag	UNP Q9U3P2
E	18	ASP	-	expression tag	UNP Q9U3P2
E	19	PRO	-	expression tag	UNP Q9U3P2
E	391	CYS	ASN	engineered mutation	UNP Q9U3P2
E	431	HIS	-	expression tag	UNP Q9U3P2
E	432	HIS	-	expression tag	UNP Q9U3P2
E	433	HIS	-	expression tag	UNP Q9U3P2
E	434	HIS	-	expression tag	UNP Q9U3P2
E	435	HIS	-	expression tag	UNP Q9U3P2
E	436	HIS	-	expression tag	UNP Q9U3P2
F	17	ALA	-	expression tag	UNP Q9U3P2
F	18	ASP	-	expression tag	UNP Q9U3P2
F	19	PRO	-	expression tag	UNP Q9U3P2
F	391	CYS	ASN	engineered mutation	UNP Q9U3P2

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Chain	Residue	Modelled	Actual	Comment	Reference
F	431	HIS	-	expression tag	UNP Q9U3P2
F	432	HIS	-	expression tag	UNP Q9U3P2
F	433	HIS	-	expression tag	UNP Q9U3P2
F	434	HIS	-	expression tag	UNP Q9U3P2
F	435	HIS	-	expression tag	UNP Q9U3P2
F	436	HIS	-	expression tag	UNP Q9U3P2

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	H	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			
3	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	L	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



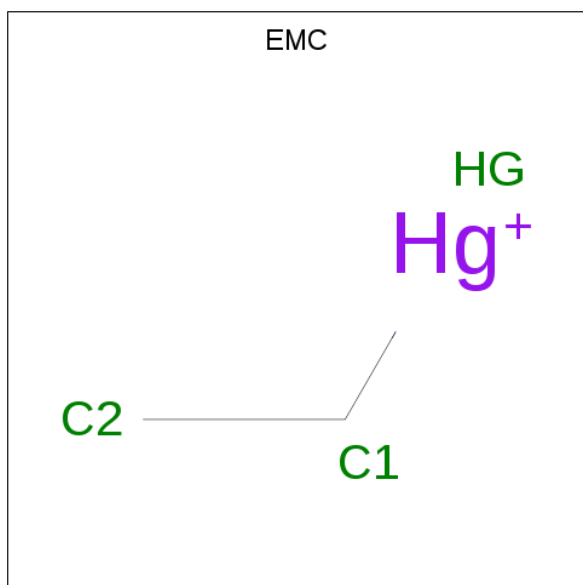
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1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

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

- Molecule 5 is ETHYL MERCURY ION (three-letter code: EMC) (formula: C<sub>2</sub>H<sub>5</sub>Hg).



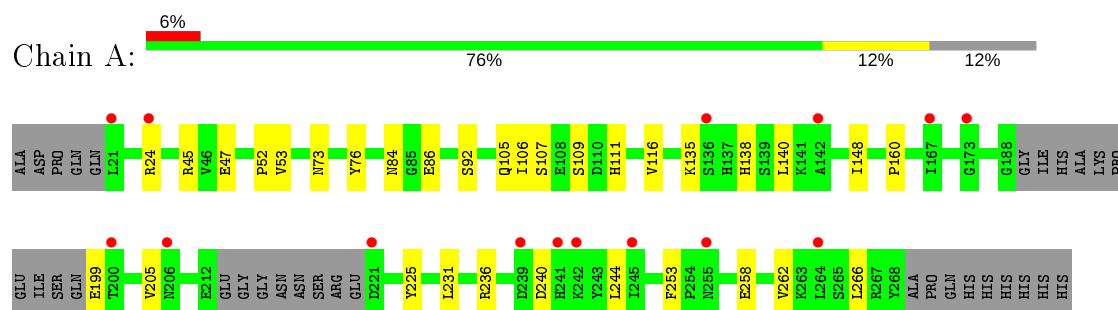
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	Hg	0	0
			3	2	1		
5	E	1	Total	C	Hg	0	0
			3	2	1		
5	F	1	Total	C	Hg	0	0
			3	2	1		



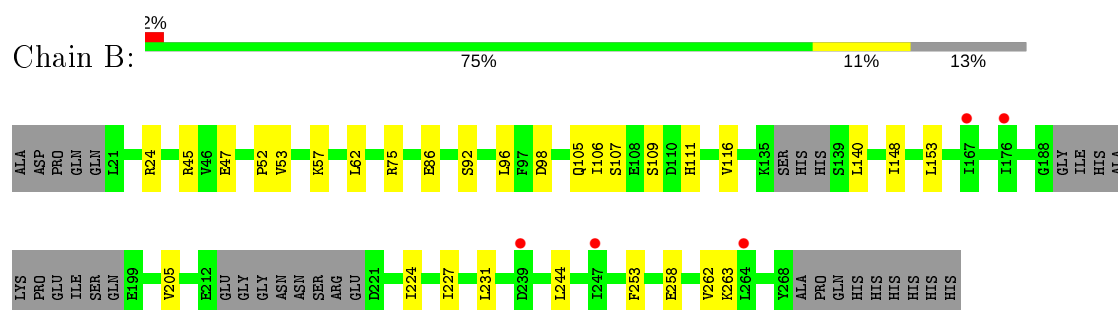
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

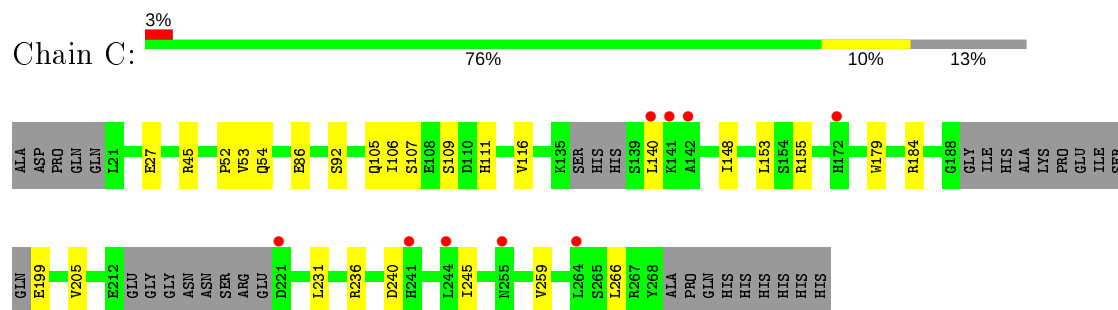
- Molecule 1: Protein SYG-1, isoform b



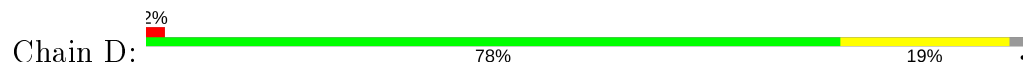
- Molecule 1: Protein SYG-1, isoform b

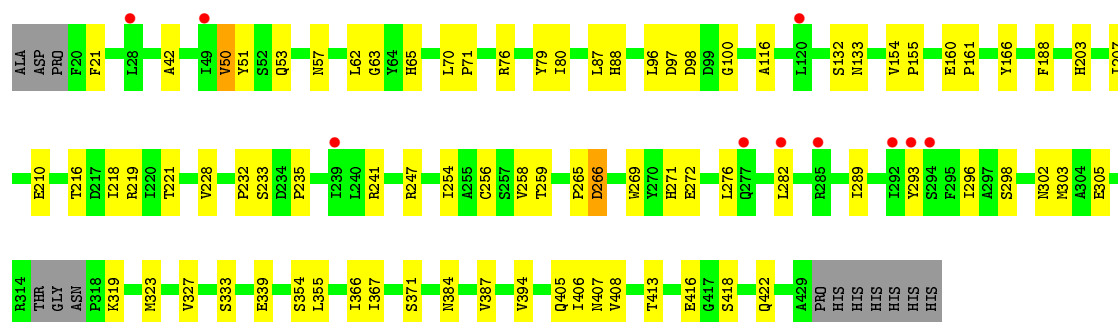


- Molecule 1: Protein SYG-1, isoform b

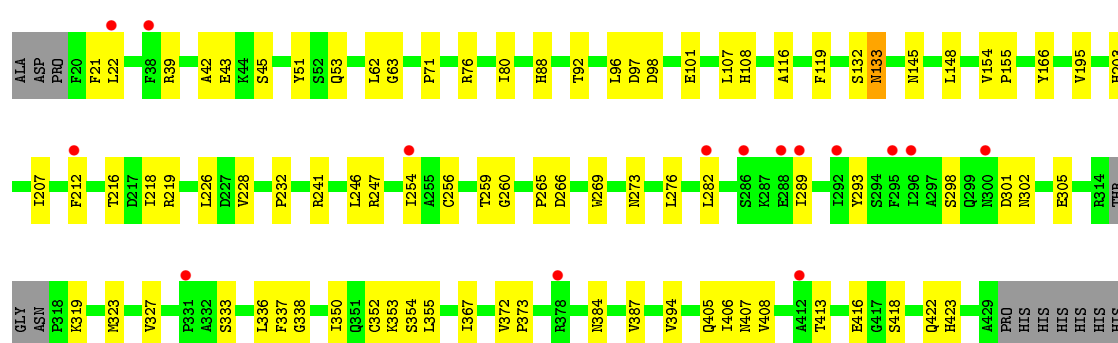
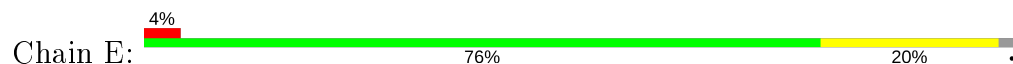


- Molecule 2: Protein SYG-2

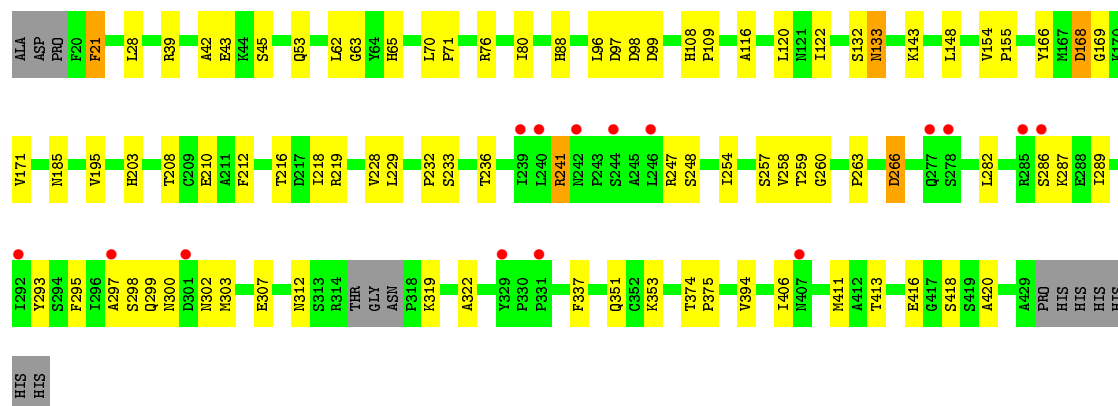
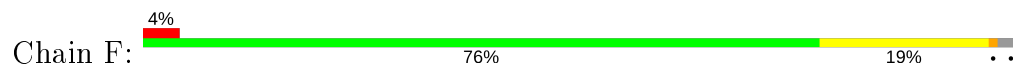




- Molecule 2: Protein SYG-2



- Molecule 2: Protein SYG-2



- 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

Chain H:  50% 50%

HA01  
HA02

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

Chain I:  50% 50%


HA01  
HA02

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

Chain J:  100%

HA01  
HA02

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

Chain K:  100%

HA01  
HA02

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

Chain L:  100%

HA01  
HA02

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	286.79Å 116.14Å 98.03Å 90.00° 107.62° 90.00°	Depositor
Resolution (Å)	41.06 – 3.30 41.06 – 3.29	Depositor EDS
% Data completeness (in resolution range)	95.3 (41.06-3.30) 95.6 (41.06-3.29)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.55 (at 3.32Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1593)	Depositor
R, $R_{free}$	0.259 , 0.306 0.262 , 0.308	Depositor DCC
$R_{free}$ test set	2266 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	90.9	Xtriage
Anisotropy	0.450	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 53.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h-2*k,l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	14816	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 52.25 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.9989e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, EMC

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	0.21	0/1801	0.41	0/2439
1	B	0.21	0/1785	0.41	0/2415
1	C	0.21	0/1785	0.41	0/2415
2	D	0.25	0/3116	0.49	0/4266
2	E	0.26	0/3113	0.50	0/4263
2	F	0.25	0/3128	0.50	0/4280
All	All	0.24	0/14728	0.47	0/20078

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1767	0	1751	19	0
1	B	1752	0	1744	17	0
1	C	1752	0	1743	16	0
2	D	3045	0	2835	48	2
2	E	3042	0	2820	50	3
2	F	3057	0	2857	59	0
3	G	28	0	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	28	0	25	1	0
3	I	28	0	25	1	0
3	J	28	0	25	0	0
3	K	28	0	25	0	0
3	L	28	0	25	0	0
4	C	14	0	13	0	0
4	D	70	0	65	1	0
4	E	70	0	65	0	0
4	F	70	0	65	0	0
5	D	3	0	0	0	0
5	E	3	0	0	0	0
5	F	3	0	0	0	0
All	All	14816	0	14108	208	3

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (208) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:282:LEU:HD13	2:E:289:ILE:HG13	1.61	0.82
2:F:39:ARG:HA	2:F:88:HIS:HD2	1.49	0.78
2:E:276:LEU:HD13	2:E:293:TYR:CE2	2.19	0.77
2:F:233:SER:HG	2:F:259:THR:HG1	1.25	0.76
2:F:53:GLN:HG3	2:F:63:GLY:HA3	1.68	0.76
1:A:140:LEU:HD21	1:A:148:ILE:HG21	1.67	0.75
2:F:21:PHE:HA	2:F:43:GLU:HG3	1.67	0.74
1:A:53:VAL:HG22	1:A:106:ILE:HG12	1.71	0.72
2:F:96:LEU:HA	2:F:122:ILE:HD13	1.72	0.72
2:F:21:PHE:HZ	2:F:116:ALA:HB2	1.54	0.71
2:D:53:GLN:HG3	2:D:63:GLY:HA3	1.74	0.70
2:D:216:THR:HB	2:D:218:ILE:HG22	1.73	0.70
2:D:233:SER:HG	2:D:259:THR:HG1	1.35	0.70
1:B:53:VAL:HG22	1:B:106:ILE:HG12	1.73	0.69
2:D:282:LEU:HD13	2:D:289:ILE:HG13	1.74	0.68
2:F:282:LEU:HD13	2:F:289:ILE:HG13	1.74	0.68
2:D:62:LEU:HG	2:D:70:LEU:HD23	1.76	0.68
2:F:216:THR:HB	2:F:218:ILE:HG22	1.75	0.67
2:E:216:THR:HB	2:E:218:ILE:HG22	1.75	0.67
1:B:140:LEU:HD21	1:B:148:ILE:HG21	1.76	0.66
2:D:21:PHE:HB2	2:D:42:ALA:HA	1.75	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:21:PHE:HB2	2:F:42:ALA:HA	1.77	0.66
2:E:21:PHE:HZ	2:E:116:ALA:HB2	1.61	0.66
2:E:21:PHE:HB2	2:E:42:ALA:HA	1.77	0.66
2:D:62:LEU:HD21	2:D:71:PRO:HD2	1.78	0.65
2:E:53:GLN:HG3	2:E:63:GLY:HA3	1.78	0.65
1:C:52:PRO:HD2	1:C:107:SER:HB2	1.80	0.64
2:D:276:LEU:HD13	2:D:293:TYR:CE2	2.34	0.62
2:D:247:ARG:NH1	2:D:416:GLU:OE2	2.32	0.62
2:E:51:TYR:HB2	2:E:107:LEU:HD13	1.81	0.62
1:A:52:PRO:HD2	1:A:107:SER:HB2	1.81	0.62
2:D:413:THR:HG23	2:D:418:SER:HB3	1.82	0.62
2:F:108:HIS:HD2	2:F:109:PRO:HD2	1.62	0.62
2:F:96:LEU:HD23	2:F:97:ASP:H	1.65	0.62
2:D:298:SER:N	2:D:302:ASN:OD1	2.25	0.61
1:A:24:ARG:NH1	1:A:47:GLU:OE2	2.34	0.61
2:E:39:ARG:HA	2:E:88:HIS:HD2	1.66	0.60
2:E:413:THR:HG23	2:E:418:SER:HB3	1.84	0.60
2:D:21:PHE:HZ	2:D:116:ALA:HB2	1.67	0.59
2:F:413:THR:HG23	2:F:418:SER:HB3	1.85	0.59
1:B:205:VAL:HG22	1:B:231:LEU:HA	1.85	0.59
2:F:80:ILE:HB	2:F:88:HIS:HB2	1.84	0.59
1:C:53:VAL:HG22	1:C:106:ILE:HG12	1.84	0.58
1:B:45:ARG:HG2	1:B:86:GLU:HG2	1.84	0.58
2:E:407:ASN:HB3	2:E:422:GLN:NE2	2.18	0.58
2:F:21:PHE:CZ	2:F:116:ALA:HB2	2.37	0.58
1:B:109:SER:O	1:B:111:HIS:N	2.36	0.57
2:E:247:ARG:NH1	2:E:416:GLU:OE2	2.37	0.57
1:C:140:LEU:HD21	1:C:148:ILE:HG21	1.87	0.57
2:E:96:LEU:HD23	2:E:97:ASP:H	1.69	0.57
2:D:266:ASP:N	2:D:266:ASP:OD1	2.30	0.56
2:F:62:LEU:HD21	2:F:71:PRO:HD2	1.87	0.56
1:C:199:GLU:O	1:C:236:ARG:NH1	2.39	0.55
2:D:210:GLU:HG3	2:D:221:THR:HG22	1.88	0.55
1:B:140:LEU:N	1:B:263:LYS:O	2.36	0.55
2:D:256:CYS:HB2	2:D:269:TRP:CZ2	2.42	0.55
2:D:394:VAL:HG11	2:D:406:ILE:HG21	1.89	0.54
1:C:109:SER:O	1:C:111:HIS:N	2.41	0.54
2:D:210:GLU:CD	2:D:219:ARG:HD2	2.28	0.54
2:E:336:LEU:HD13	2:E:423:HIS:HB2	1.90	0.54
1:A:199:GLU:O	1:A:236:ARG:NH1	2.40	0.53
1:A:45:ARG:HG2	1:A:86:GLU:HG2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:271:HIS:CD2	2:D:272:GLU:HG3	2.44	0.53
2:F:247:ARG:NH1	2:F:416:GLU:OE2	2.41	0.53
2:D:63:GLY:O	2:D:65:HIS:ND1	2.38	0.53
1:C:45:ARG:HG2	1:C:86:GLU:HG2	1.91	0.52
2:D:232:PRO:O	2:D:319:LYS:HD2	2.09	0.52
2:D:367:ILE:HD12	2:D:408:VAL:HG22	1.90	0.52
2:E:232:PRO:O	2:E:319:LYS:HD2	2.10	0.52
2:E:232:PRO:HG3	2:E:265:PRO:HG3	1.91	0.52
2:D:296:ILE:HD11	4:D:1506:NAG:H82	1.92	0.51
2:F:337:PHE:HE2	2:F:353:LYS:HG2	1.76	0.51
2:E:80:ILE:HB	2:E:88:HIS:HB2	1.93	0.51
1:A:109:SER:O	1:A:111:HIS:N	2.40	0.51
2:F:166:TYR:CE2	2:F:171:VAL:HG12	2.46	0.51
1:C:105:GLN:HG3	1:C:116:VAL:HG22	1.93	0.51
2:D:235:PRO:HB3	2:D:258:VAL:HG22	1.92	0.51
2:E:212:PHE:CD1	2:E:219:ARG:HD3	2.46	0.51
2:F:229:LEU:HD22	2:F:263:PRO:HD3	1.92	0.51
2:F:39:ARG:HA	2:F:88:HIS:CD2	2.39	0.51
2:E:62:LEU:HD21	2:E:71:PRO:HD2	1.93	0.51
2:F:286:SER:O	2:F:287:LYS:HG2	2.11	0.51
2:F:411:MET:HG3	2:F:420:ALA:HB2	1.93	0.50
1:C:92:SER:HB2	3:I:1:NAG:H82	1.94	0.50
2:E:407:ASN:HB3	2:E:422:GLN:HE21	1.75	0.50
2:F:21:PHE:N	2:F:21:PHE:CD1	2.79	0.50
2:E:203:HIS:HB2	2:E:228:VAL:HG22	1.93	0.50
1:A:205:VAL:HG22	1:A:231:LEU:HA	1.93	0.49
2:E:305:GLU:HA	2:E:323:MET:O	2.11	0.49
2:D:203:HIS:HB2	2:D:228:VAL:HG22	1.94	0.49
2:F:298:SER:O	2:F:302:ASN:HB2	2.13	0.49
1:B:92:SER:HB2	3:H:1:NAG:H82	1.94	0.48
2:F:233:SER:OG	2:F:259:THR:OG1	2.08	0.48
2:F:232:PRO:O	2:F:319:LYS:HD2	2.14	0.48
1:B:52:PRO:HD2	1:B:107:SER:HB2	1.96	0.48
2:E:39:ARG:HA	2:E:88:HIS:CD2	2.48	0.48
2:F:210:GLU:CD	2:F:219:ARG:HD2	2.34	0.48
2:F:210:GLU:OE2	2:F:219:ARG:HD2	2.13	0.48
2:F:236:THR:OG1	2:F:257:SER:HB3	2.13	0.48
2:F:394:VAL:HG11	2:F:406:ILE:HG21	1.96	0.48
1:C:27:GLU:OE1	1:C:45:ARG:NE	2.36	0.47
2:E:22:LEU:H	2:E:43:GLU:N	2.11	0.47
2:D:333:SER:H	2:D:355:LEU:HD12	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:50:VAL:HG23	2:D:51:TYR:CD2	2.49	0.47
2:F:45:SER:HB3	2:F:108:HIS:NE2	2.30	0.47
1:C:205:VAL:HG22	1:C:231:LEU:HA	1.97	0.47
1:C:54:GLN:NE2	2:F:53:GLN:OE1	2.44	0.47
1:B:24:ARG:NH1	1:B:47:GLU:OE2	2.46	0.47
2:D:305:GLU:HA	2:D:323:MET:O	2.15	0.47
2:F:299:GLN:HG3	2:F:300:ASN:H	1.80	0.47
2:F:76:ARG:NH1	2:F:98:ASP:OD2	2.48	0.47
1:A:73:ASN:HB3	1:A:76:TYR:CG	2.50	0.46
1:C:240:ASP:HB2	1:C:266:LEU:HD22	1.97	0.46
2:D:302:ASN:HB3	2:D:327:VAL:HG21	1.97	0.46
2:E:337:PHE:HE2	2:E:353:LYS:HG2	1.80	0.46
2:F:203:HIS:HB2	2:F:228:VAL:HG22	1.97	0.46
2:F:307:GLU:HA	2:F:322:ALA:HA	1.97	0.46
2:E:354:SER:O	2:E:387:VAL:HG13	2.16	0.46
2:E:298:SER:O	2:E:302:ASN:HB2	2.15	0.46
2:E:132:SER:HA	2:E:133:ASN:HA	1.49	0.46
2:F:99:ASP:HB2	2:F:122:ILE:HD12	1.97	0.46
2:D:354:SER:O	2:D:387:VAL:HG13	2.16	0.46
2:E:101:GLU:HB3	2:E:119:PHE:CE2	2.50	0.46
2:E:259:THR:OG1	2:E:260:GLY:N	2.48	0.46
2:F:298:SER:N	2:F:302:ASN:OD1	2.39	0.45
2:F:63:GLY:O	2:F:65:HIS:ND1	2.45	0.45
1:C:153:LEU:HD21	1:C:155:ARG:HD2	1.99	0.45
2:E:154:VAL:HA	2:E:155:PRO:HD3	1.75	0.45
2:E:246:LEU:HB2	2:E:327:VAL:HG22	1.98	0.45
2:F:185:ASN:OD1	2:F:185:ASN:N	2.49	0.45
1:A:240:ASP:HB2	1:A:266:LEU:HD22	1.99	0.45
2:D:232:PRO:HG3	2:D:265:PRO:HG3	1.99	0.45
2:E:254:ILE:HG13	2:E:293:TYR:HB3	1.99	0.45
1:A:253:PHE:CE2	1:A:258:GLU:HG3	2.52	0.45
2:D:166:TYR:O	2:D:207:ILE:HA	2.17	0.45
1:A:240:ASP:HA	1:A:266:LEU:HD13	1.99	0.44
1:B:153:LEU:HD12	1:B:227:ILE:O	2.17	0.44
1:B:253:PHE:CE2	1:B:258:GLU:HG3	2.52	0.44
2:F:374:THR:HA	2:F:375:PRO:HD3	1.81	0.44
1:B:96:LEU:HD11	1:B:224:ILE:HG23	1.99	0.44
2:F:154:VAL:HA	2:F:155:PRO:HD3	1.83	0.44
2:F:299:GLN:HG3	2:F:300:ASN:N	2.32	0.44
2:D:303:MET:HG3	2:D:384:ASN:HA	1.99	0.44
2:D:160:GLU:HB3	2:D:188:PHE:CG	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:80:ILE:HB	2:D:88:HIS:HB2	1.99	0.44
2:F:248:SER:O	2:F:297:ALA:HB3	2.17	0.44
1:A:84:ASN:HB3	1:A:86:GLU:HG3	1.99	0.44
1:C:245:ILE:HG23	1:C:259:VAL:HG13	1.99	0.43
2:D:96:LEU:HD23	2:D:97:ASP:H	1.83	0.43
2:D:366:ILE:HG12	2:D:371:SER:HA	2.00	0.43
2:E:336:LEU:HD23	2:E:352:CYS:HB2	1.99	0.43
2:E:333:SER:H	2:E:355:LEU:HD12	1.82	0.43
2:F:254:ILE:HG13	2:F:293:TYR:HB3	2.00	0.43
2:F:28:LEU:O	2:F:120:LEU:HA	2.18	0.43
2:F:132:SER:HA	2:F:133:ASN:HA	1.53	0.43
2:F:241:ARG:HB2	2:F:241:ARG:HE	1.38	0.43
2:E:21:PHE:CZ	2:E:116:ALA:HB2	2.49	0.43
2:E:76:ARG:HB3	2:E:92:THR:O	2.19	0.43
2:D:160:GLU:HA	2:D:161:PRO:HD3	1.86	0.43
2:E:256:CYS:HB2	2:E:269:TRP:CZ2	2.54	0.43
2:F:258:VAL:HG12	2:F:260:GLY:H	1.83	0.43
2:D:333:SER:N	2:D:355:LEU:HD12	2.34	0.43
2:E:301:ASP:H	2:E:384:ASN:ND2	2.17	0.43
2:D:339:GLU:HG3	2:D:339:GLU:H	1.64	0.42
1:A:105:GLN:HG3	1:A:116:VAL:HG22	2.02	0.42
2:D:154:VAL:HA	2:D:155:PRO:HD3	1.78	0.42
2:F:293:TYR:HE1	2:F:295:PHE:HB3	1.84	0.42
2:F:143:LYS:HA	2:F:229:LEU:HB2	2.01	0.42
1:A:105:GLN:HG2	1:A:106:ILE:N	2.34	0.42
2:E:45:SER:HB3	2:E:108:HIS:NE2	2.35	0.42
2:D:210:GLU:OE2	2:D:219:ARG:HD2	2.20	0.42
2:E:96:LEU:C	2:E:98:ASP:H	2.23	0.42
2:E:372:VAL:HB	2:E:373:PRO:HD2	2.01	0.42
2:F:166:TYR:HB2	2:F:208:THR:HB	2.02	0.42
2:F:232:PRO:HD3	2:F:312:ASN:ND2	2.34	0.42
2:F:62:LEU:HG	2:F:70:LEU:HD23	2.01	0.42
2:F:148:LEU:O	2:F:195:VAL:HA	2.19	0.41
2:F:266:ASP:N	2:F:266:ASP:OD1	2.43	0.41
2:E:21:PHE:N	2:E:21:PHE:CD1	2.89	0.41
2:E:333:SER:N	2:E:355:LEU:HD12	2.35	0.41
2:E:96:LEU:HD23	2:E:97:ASP:N	2.34	0.41
2:E:338:GLY:HA3	2:E:350:ILE:HD13	2.03	0.41
1:A:92:SER:HB2	3:G:1:NAG:H82	2.02	0.41
1:B:244:LEU:HB3	1:B:262:VAL:HG12	2.02	0.41
1:B:57:LYS:HB3	1:B:62:LEU:HD21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:96:LEU:HD23	2:F:97:ASP:N	2.32	0.41
2:E:394:VAL:HG11	2:E:406:ILE:HG21	2.03	0.41
1:B:105:GLN:HG2	1:B:106:ILE:N	2.35	0.41
1:C:179:TRP:CD1	1:C:184:ARG:HB2	2.55	0.41
2:D:407:ASN:HB3	2:D:422:GLN:NE2	2.35	0.41
2:D:254:ILE:HG21	2:D:323:MET:HE1	2.02	0.41
1:A:244:LEU:HB3	1:A:262:VAL:HG12	2.03	0.41
1:B:75:ARG:HH22	1:B:98:ASP:CG	2.24	0.41
1:C:105:GLN:HG2	1:C:106:ILE:N	2.36	0.41
2:D:76:ARG:NH1	2:D:98:ASP:OD2	2.52	0.41
1:A:160:PRO:HG3	1:A:225:TYR:CD1	2.56	0.40
1:B:105:GLN:HG3	1:B:116:VAL:HG22	2.03	0.40
2:D:21:PHE:CZ	2:D:116:ALA:HB2	2.51	0.40
2:F:337:PHE:HB2	2:F:351:GLN:HB3	2.03	0.40
2:D:57:ASN:HB2	2:D:100:GLY:HA3	2.03	0.40
2:E:148:LEU:O	2:E:195:VAL:HA	2.21	0.40
2:F:168:ASP:HB3	2:F:169:GLY:H	1.62	0.40
2:D:132:SER:HA	2:D:133:ASN:HA	1.47	0.40
2:D:79:TYR:CD2	2:D:87:LEU:HD11	2.56	0.40
2:E:166:TYR:O	2:E:207:ILE:HA	2.20	0.40
2:E:226:LEU:HD12	2:E:226:LEU:HA	1.85	0.40
2:E:367:ILE:HD12	2:E:408:VAL:HG22	2.03	0.40
1:A:135:LYS:HD2	1:A:138:HIS:HA	2.03	0.40

All (3) 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:D:405:GLN:NE2	2:E:422:GLN:OE1[1_452]	2.09	0.11
2:D:422:GLN:OE1	2:E:405:GLN:NE2[1_452]	2.09	0.11
2:E:145:ASN:O	2:E:273:ASN:ND2[2_658]	2.10	0.10

## 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	224/262 (86%)	212 (95%)	12 (5%)	0	100	100
1	B	219/262 (84%)	208 (95%)	11 (5%)	0	100	100
1	C	219/262 (84%)	208 (95%)	11 (5%)	0	100	100
2	D	403/420 (96%)	382 (95%)	21 (5%)	0	100	100
2	E	403/420 (96%)	382 (95%)	21 (5%)	0	100	100
2	F	403/420 (96%)	383 (95%)	20 (5%)	0	100	100
All	All	1871/2046 (91%)	1775 (95%)	96 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 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	197/228 (86%)	197 (100%)	0	100	100
1	B	197/228 (86%)	197 (100%)	0	100	100
1	C	197/228 (86%)	197 (100%)	0	100	100
2	D	331/380 (87%)	328 (99%)	3 (1%)	78	87
2	E	329/380 (87%)	326 (99%)	3 (1%)	78	87
2	F	333/380 (88%)	326 (98%)	7 (2%)	53	75
All	All	1584/1824 (87%)	1571 (99%)	13 (1%)	81	89

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	50	VAL
2	D	241	ARG
2	D	266	ASP
2	E	133	ASN

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Mol	Chain	Res	Type
2	E	241	ARG
2	E	266	ASP
2	F	21	PHE
2	F	133	ASN
2	F	168	ASP
2	F	212	PHE
2	F	241	ARG
2	F	266	ASP
2	F	303	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	D	422	GLN
2	E	88	HIS
2	E	422	GLN
2	F	88	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 ⓘ

12 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	NAG	G	1	1,3	14,14,15	0.41	0	17,19,21	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	G	2	3	14,14,15	0.22	0	17,19,21	0.36	0
3	NAG	H	1	1,3	14,14,15	0.43	0	17,19,21	0.51	0
3	NAG	H	2	3	14,14,15	0.23	0	17,19,21	0.35	0
3	NAG	I	1	1,3	14,14,15	0.38	0	17,19,21	0.53	0
3	NAG	I	2	3	14,14,15	0.28	0	17,19,21	0.38	0
3	NAG	J	1	3,2	14,14,15	0.29	0	17,19,21	0.47	0
3	NAG	J	2	3	14,14,15	0.29	0	17,19,21	0.48	0
3	NAG	K	1	3,2	14,14,15	0.41	0	17,19,21	0.46	0
3	NAG	K	2	3	14,14,15	0.31	0	17,19,21	0.49	0
3	NAG	L	1	3,2	14,14,15	0.20	0	17,19,21	0.51	0
3	NAG	L	2	3	14,14,15	0.24	0	17,19,21	0.41	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	G	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
3	NAG	H	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	1/6/23/26	0/1/1/1
3	NAG	I	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	I	2	3	-	0/6/23/26	0/1/1/1
3	NAG	J	1	3,2	-	2/6/23/26	0/1/1/1
3	NAG	J	2	3	-	2/6/23/26	0/1/1/1
3	NAG	K	1	3,2	-	2/6/23/26	0/1/1/1
3	NAG	K	2	3	-	2/6/23/26	0/1/1/1
3	NAG	L	1	3,2	-	2/6/23/26	0/1/1/1
3	NAG	L	2	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	J	2	NAG	O5-C5-C6-O6
3	K	1	NAG	O5-C5-C6-O6

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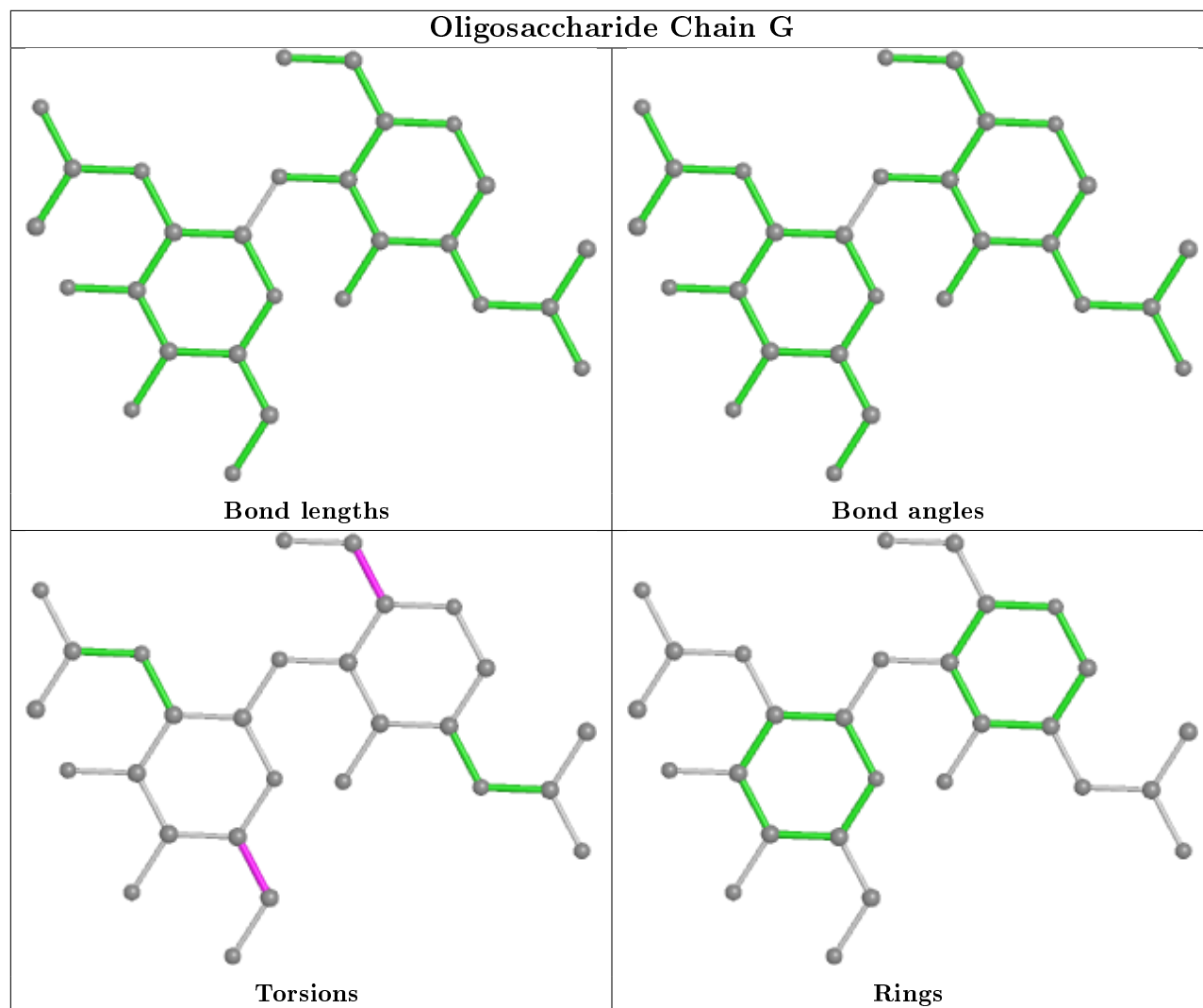
Mol	Chain	Res	Type	Atoms
3	J	1	NAG	O5-C5-C6-O6
3	K	2	NAG	O5-C5-C6-O6
3	H	1	NAG	O5-C5-C6-O6
3	I	1	NAG	O5-C5-C6-O6
3	K	2	NAG	C4-C5-C6-O6
3	J	1	NAG	C4-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
3	K	1	NAG	C4-C5-C6-O6
3	J	2	NAG	C4-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6
3	L	1	NAG	C4-C5-C6-O6
3	H	1	NAG	C4-C5-C6-O6
3	I	1	NAG	C4-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	L	1	NAG	O5-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6
3	H	2	NAG	C4-C5-C6-O6

There are no ring outliers.

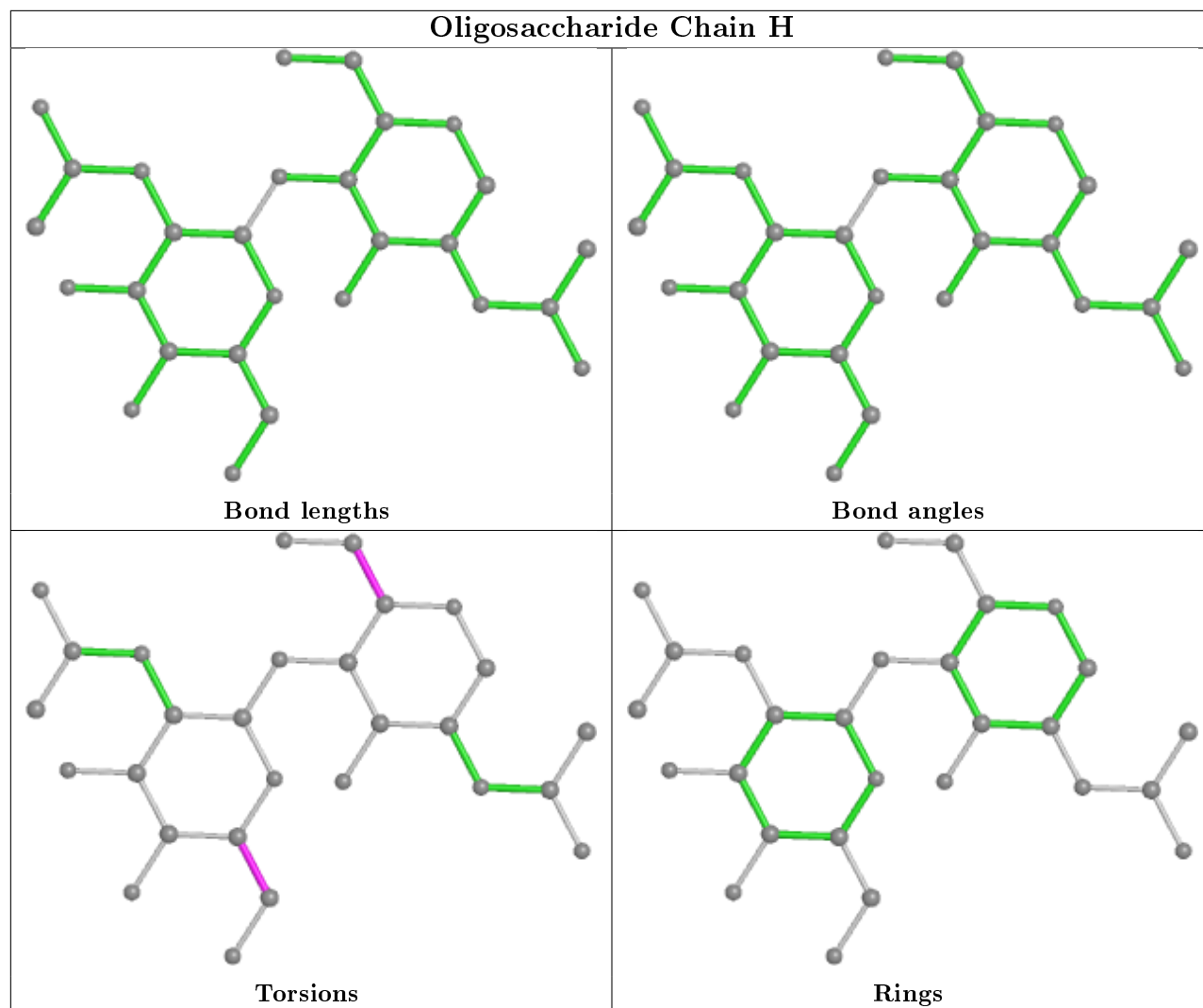
3 monomers are involved in 3 short contacts:

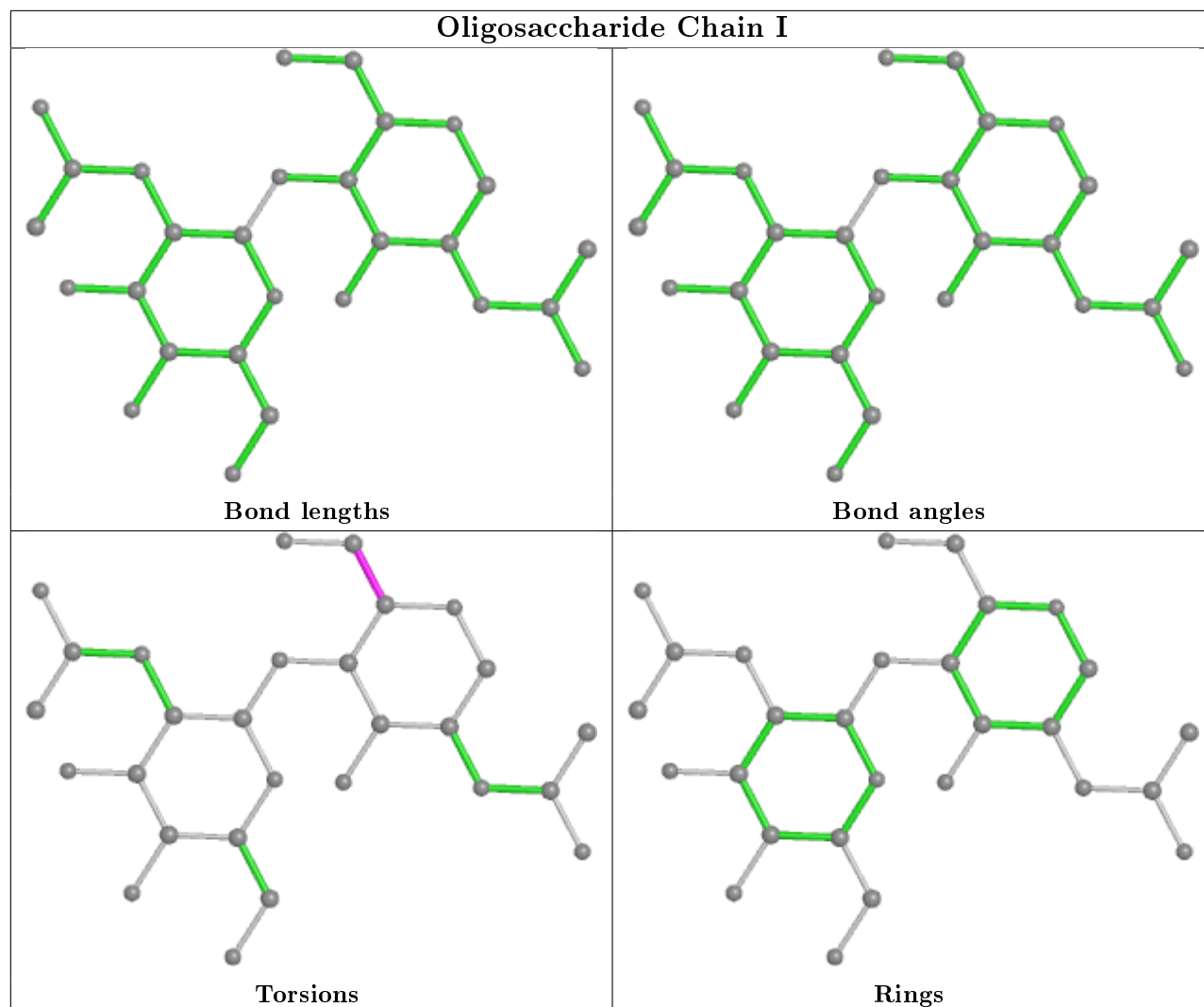
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	1	NAG	1	0
3	I	1	NAG	1	0
3	G	1	NAG	1	0

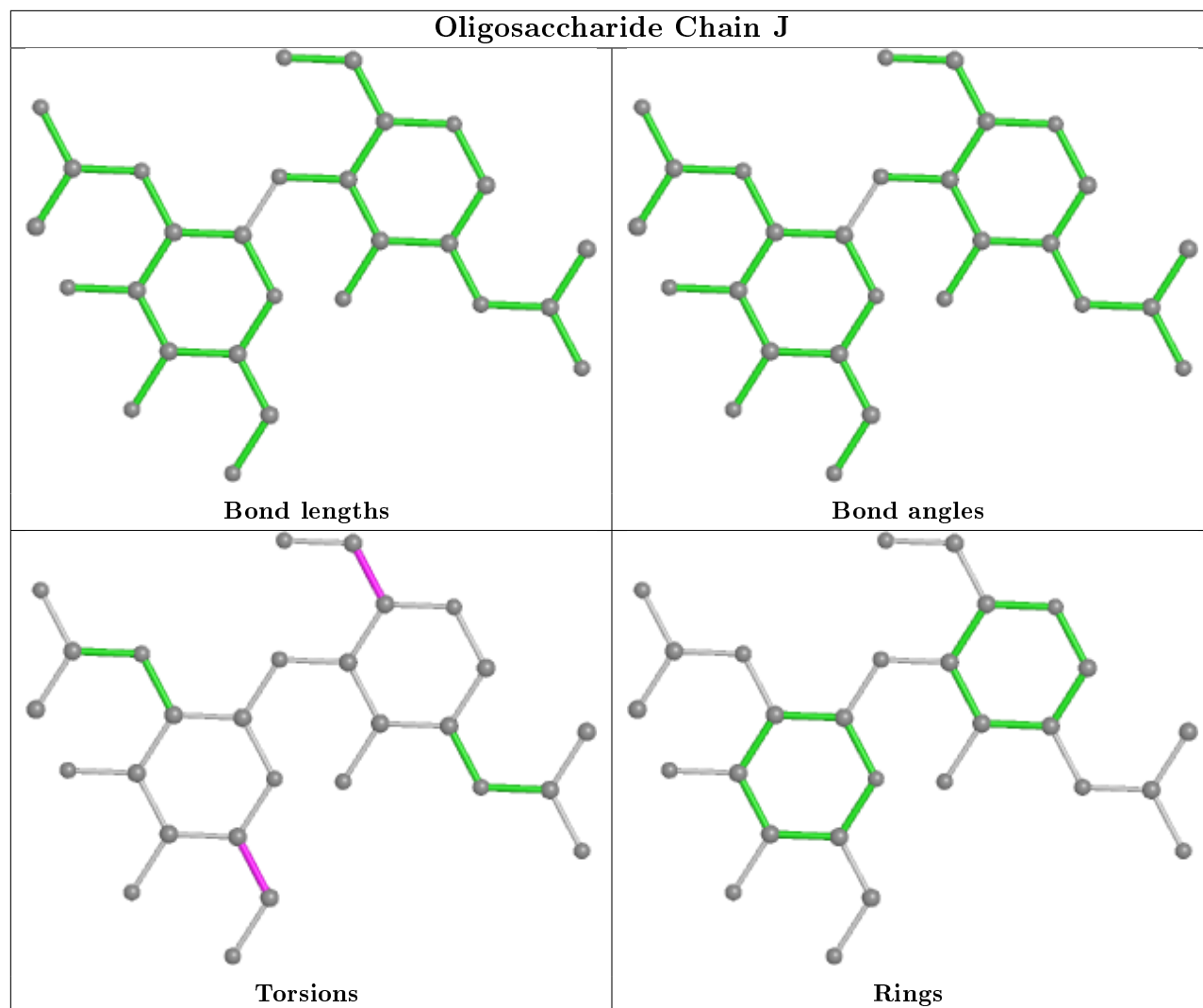
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

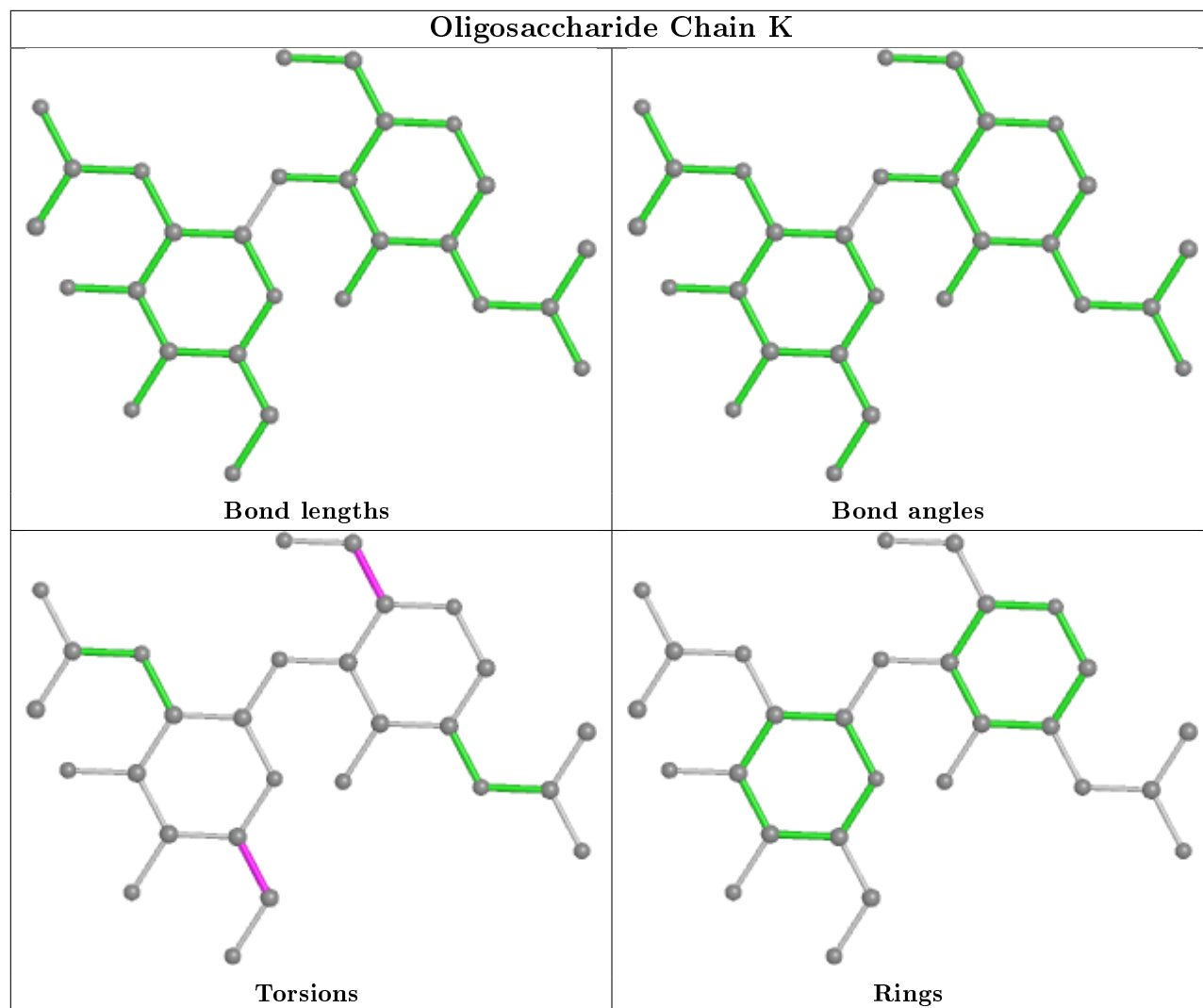


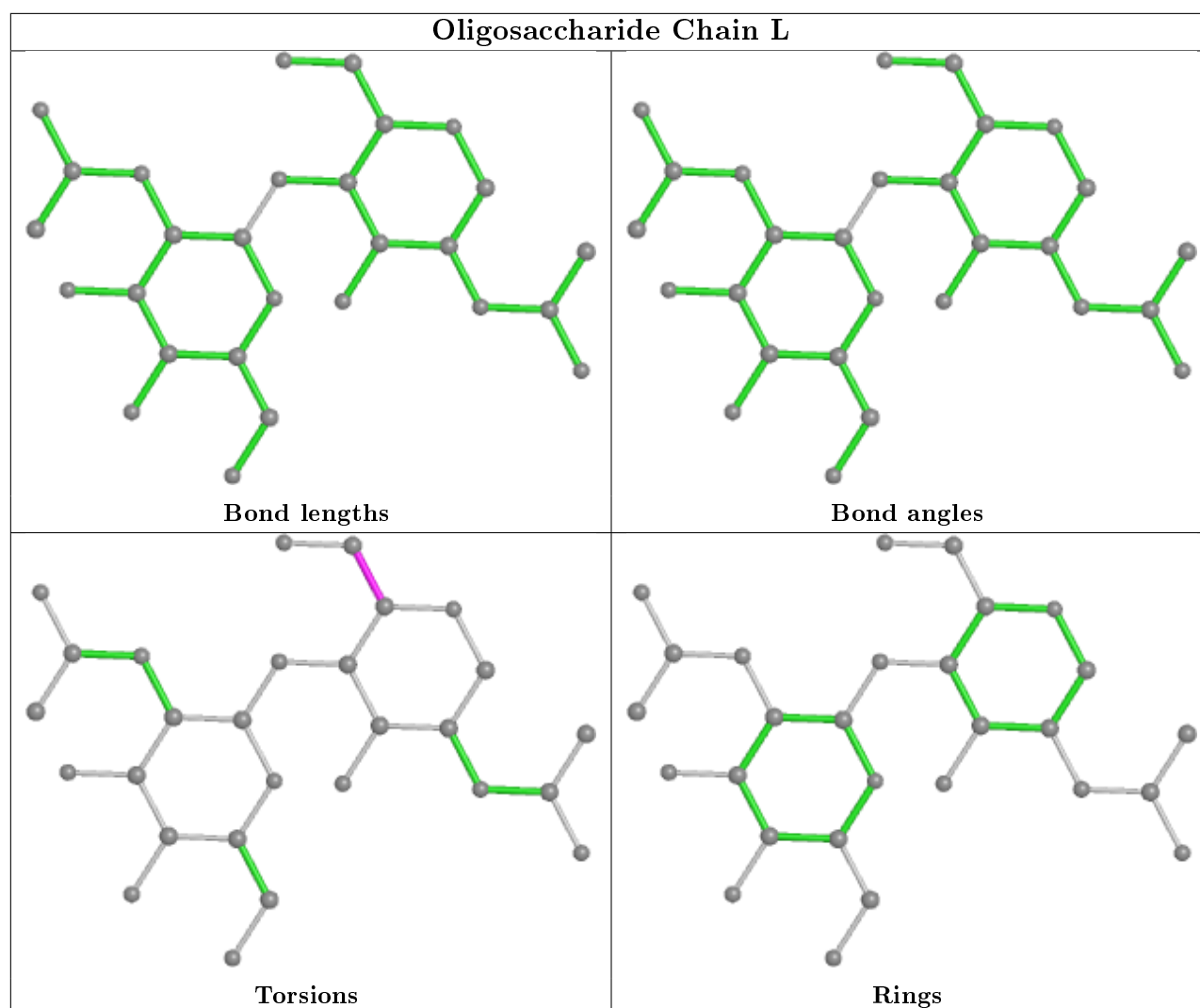












## 5.6 Ligand geometry ⓘ

19 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	$\# Z  > 2$
5	EMC	F	1508	2	1,2,2	0.04	0	-		
4	NAG	D	1505	2	14,14,15	0.26	0	17,19,21	0.45	0
4	NAG	F	1501	2	14,14,15	0.29	0	17,19,21	0.38	0
4	NAG	E	1507	2	14,14,15	0.21	0	17,19,21	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	C	803	1	14,14,15	0.38	0	17,19,21	0.39	0
5	EMC	E	1508	2	1,2,2	0.06	0	-		
4	NAG	F	1505	2	14,14,15	0.24	0	17,19,21	0.49	0
4	NAG	D	1502	2	14,14,15	0.30	0	17,19,21	0.46	0
4	NAG	F	1502	2	14,14,15	0.30	0	17,19,21	0.53	0
4	NAG	E	1502	2	14,14,15	0.32	0	17,19,21	0.52	0
4	NAG	D	1506	2	14,14,15	0.32	0	17,19,21	0.49	0
4	NAG	D	1501	2	14,14,15	0.28	0	17,19,21	0.48	0
4	NAG	F	1506	2	14,14,15	0.24	0	17,19,21	0.55	0
4	NAG	E	1506	2	14,14,15	0.35	0	17,19,21	0.57	0
4	NAG	F	1507	2	14,14,15	0.33	0	17,19,21	0.48	0
4	NAG	E	1501	2	14,14,15	0.27	0	17,19,21	0.49	0
4	NAG	E	1505	2	14,14,15	0.26	0	17,19,21	0.47	0
4	NAG	D	1507	2	14,14,15	0.29	0	17,19,21	0.52	0
5	EMC	D	1508	2	1,2,2	0.04	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	D	1505	2	-	0/6/23/26	0/1/1/1
4	NAG	F	1501	2	-	0/6/23/26	0/1/1/1
4	NAG	E	1507	2	-	0/6/23/26	0/1/1/1
4	NAG	C	803	1	-	1/6/23/26	0/1/1/1
4	NAG	F	1505	2	-	0/6/23/26	0/1/1/1
4	NAG	D	1502	2	-	2/6/23/26	0/1/1/1
4	NAG	F	1502	2	-	0/6/23/26	0/1/1/1
4	NAG	E	1502	2	-	0/6/23/26	0/1/1/1
4	NAG	D	1506	2	-	1/6/23/26	0/1/1/1
4	NAG	D	1501	2	-	0/6/23/26	0/1/1/1
4	NAG	F	1506	2	-	2/6/23/26	0/1/1/1
4	NAG	E	1506	2	-	0/6/23/26	0/1/1/1
4	NAG	F	1507	2	-	0/6/23/26	0/1/1/1
4	NAG	E	1501	2	-	0/6/23/26	0/1/1/1
4	NAG	E	1505	2	-	0/6/23/26	0/1/1/1
4	NAG	D	1507	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	1506	NAG	C4-C5-C6-O6
4	F	1506	NAG	O5-C5-C6-O6
4	D	1502	NAG	C4-C5-C6-O6
4	D	1502	NAG	O5-C5-C6-O6
4	D	1506	NAG	O5-C5-C6-O6
4	C	803	NAG	C1-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1506	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

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	230/262 (87%)	0.31	15 (6%)	18 18	58, 91, 153, 173	0
1	B	227/262 (86%)	0.13	5 (2%)	62 60	56, 82, 134, 153	0
1	C	227/262 (86%)	0.24	9 (3%)	38 36	57, 93, 136, 160	0
2	D	407/420 (96%)	0.08	10 (2%)	57 54	59, 89, 123, 163	0
2	E	407/420 (96%)	0.19	15 (3%)	41 38	58, 89, 131, 168	0
2	F	407/420 (96%)	0.24	15 (3%)	41 38	56, 92, 131, 181	0
All	All	1905/2046 (93%)	0.19	69 (3%)	42 40	56, 90, 137, 181	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	221	ASP	5.2
1	C	141	LYS	4.9
2	E	38	PHE	3.7
1	A	241	HIS	3.6
1	A	136	SER	3.4
1	A	264	LEU	3.4
1	B	264	LEU	3.4
2	F	239	ILE	3.4
2	F	292	ILE	3.2
2	F	240	LEU	3.2
2	F	244	SER	3.1
1	C	172	HIS	3.1
2	E	300	ASN	3.0
2	F	277	GLN	3.0
2	D	28	LEU	3.0
1	A	21	LEU	2.9
1	C	142	ALA	2.9
2	E	292	ILE	2.8
1	C	264	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	242	LYS	2.8
1	A	245	ILE	2.8
2	E	254	ILE	2.8
2	E	296	ILE	2.8
2	F	278	SER	2.7
1	A	239	ASP	2.7
2	F	297	ALA	2.7
2	D	292	ILE	2.7
2	F	242	ASN	2.7
1	C	255	ASN	2.7
1	A	255	ASN	2.6
2	D	49	ILE	2.6
2	F	331	PRO	2.6
1	B	239	ASP	2.6
2	D	294	SER	2.6
1	C	241	HIS	2.6
2	F	246	LEU	2.6
2	F	286	SER	2.6
1	C	221	ASP	2.6
2	E	282	LEU	2.6
1	A	167	ILE	2.5
2	F	329	TYR	2.5
2	D	120	LEU	2.5
2	E	331	PRO	2.5
1	A	24	ARG	2.4
1	A	206	ASN	2.4
1	A	142	ALA	2.4
2	E	286	SER	2.4
1	C	244	LEU	2.4
2	F	407	ASN	2.3
2	E	378	ARG	2.3
2	D	285	ARG	2.3
2	E	288	GLU	2.3
1	B	247	ILE	2.2
2	D	282	LEU	2.2
2	E	22	LEU	2.2
2	D	277	GLN	2.1
2	E	412	ALA	2.1
2	D	239	ILE	2.1
2	E	295	PHE	2.1
2	F	301	ASP	2.1
2	F	285	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	200	THR	2.1
2	E	289	ILE	2.1
1	A	173	GLY	2.0
2	E	212	PHE	2.0
1	B	167	ILE	2.0
2	D	293	TYR	2.0
1	C	140	LEU	2.0
1	B	176	ILE	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

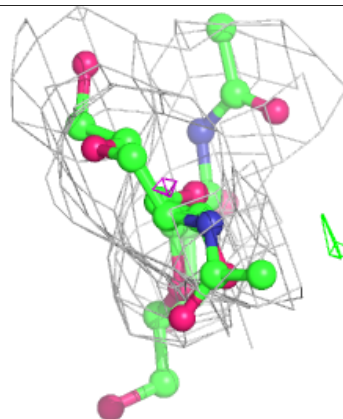
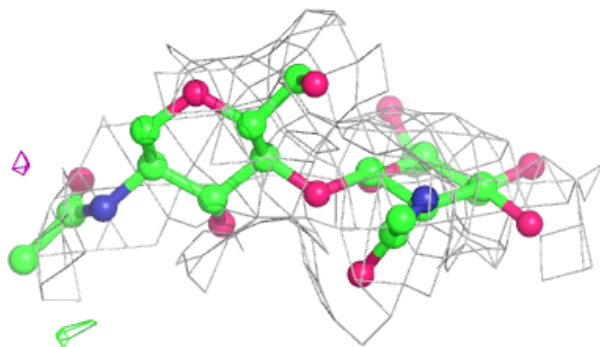
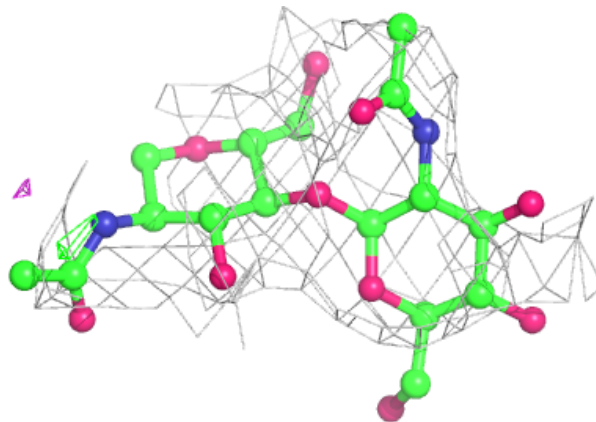
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	I	2	14/15	0.71	0.58	138,160,172,174	0
3	NAG	G	2	14/15	0.73	0.50	124,148,160,162	0
3	NAG	I	1	14/15	0.77	0.51	85,142,157,158	0
3	NAG	G	1	14/15	0.78	0.40	102,136,142,151	0
3	NAG	H	2	14/15	0.78	0.42	114,131,140,142	0
3	NAG	L	2	14/15	0.83	0.20	102,111,131,135	0
3	NAG	H	1	14/15	0.85	0.37	87,120,134,137	0
3	NAG	K	2	14/15	0.85	0.18	107,118,133,146	0
3	NAG	J	2	14/15	0.88	0.14	116,122,124,125	0
3	NAG	L	1	14/15	0.92	0.28	62,93,115,118	0
3	NAG	K	1	14/15	0.92	0.24	70,109,120,129	0
3	NAG	J	1	14/15	0.92	0.17	76,104,113,115	0

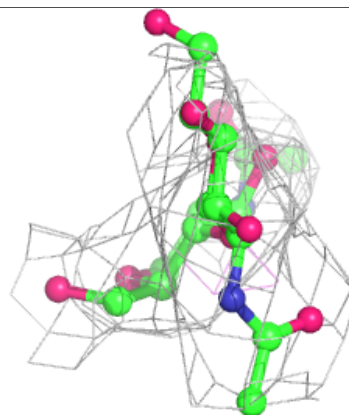
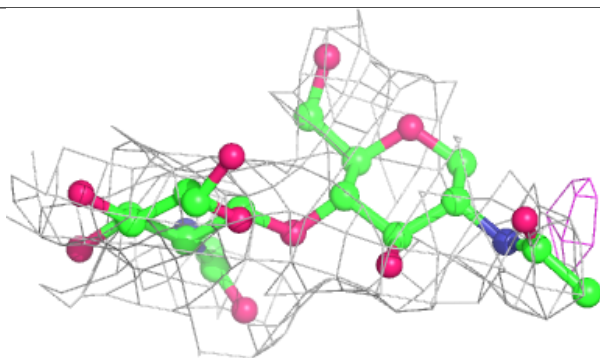
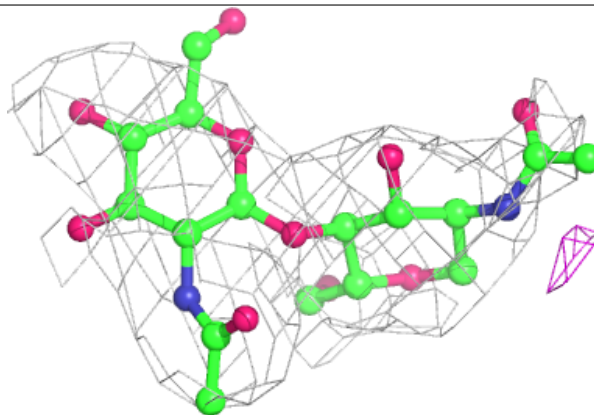
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around Chain G:**

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

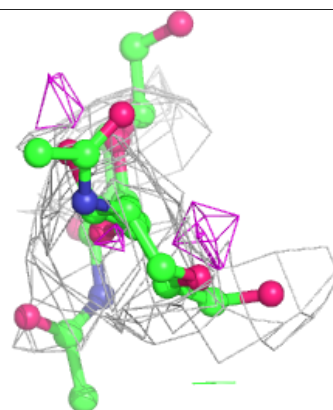
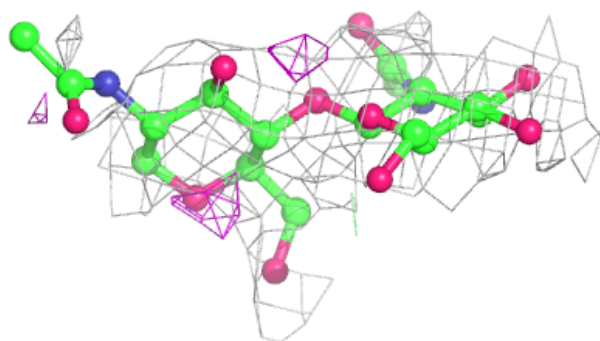
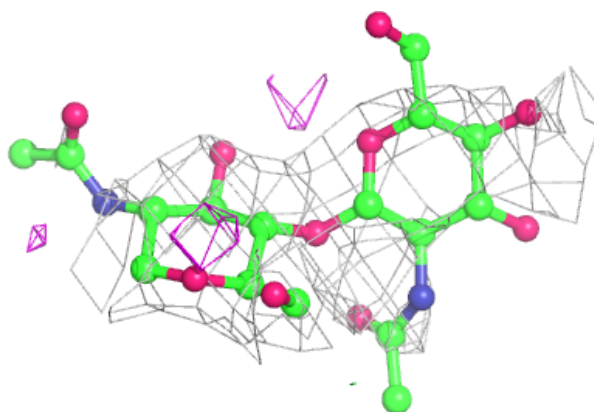
**Electron density around Chain H:**

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



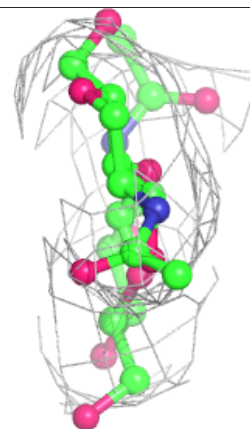
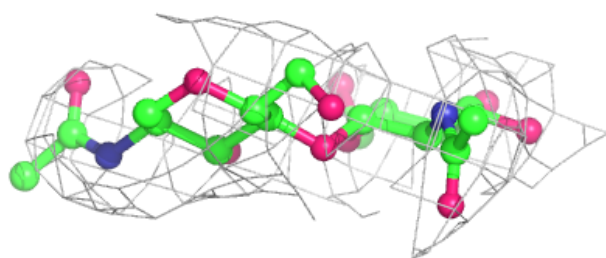
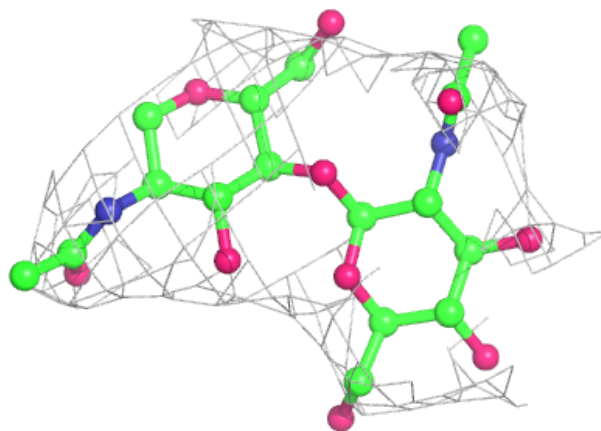
**Electron density around Chain I:**

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



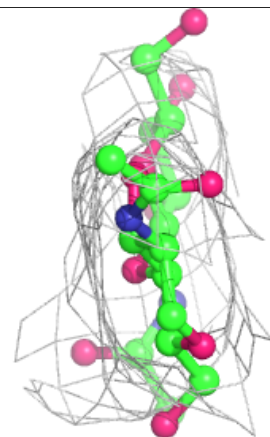
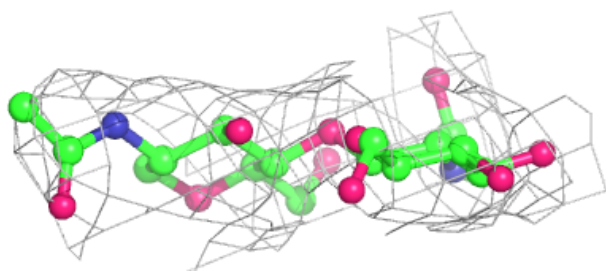
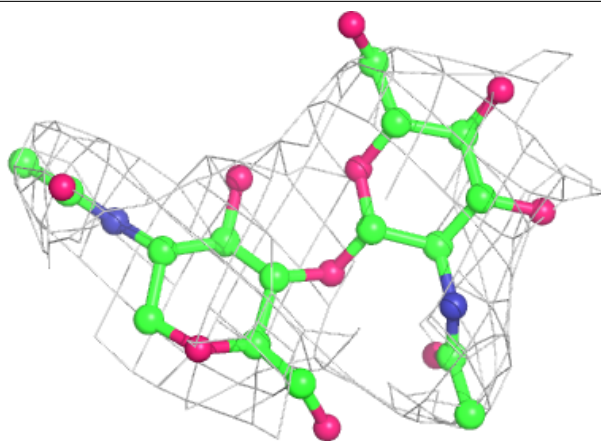
**Electron density around Chain J:**

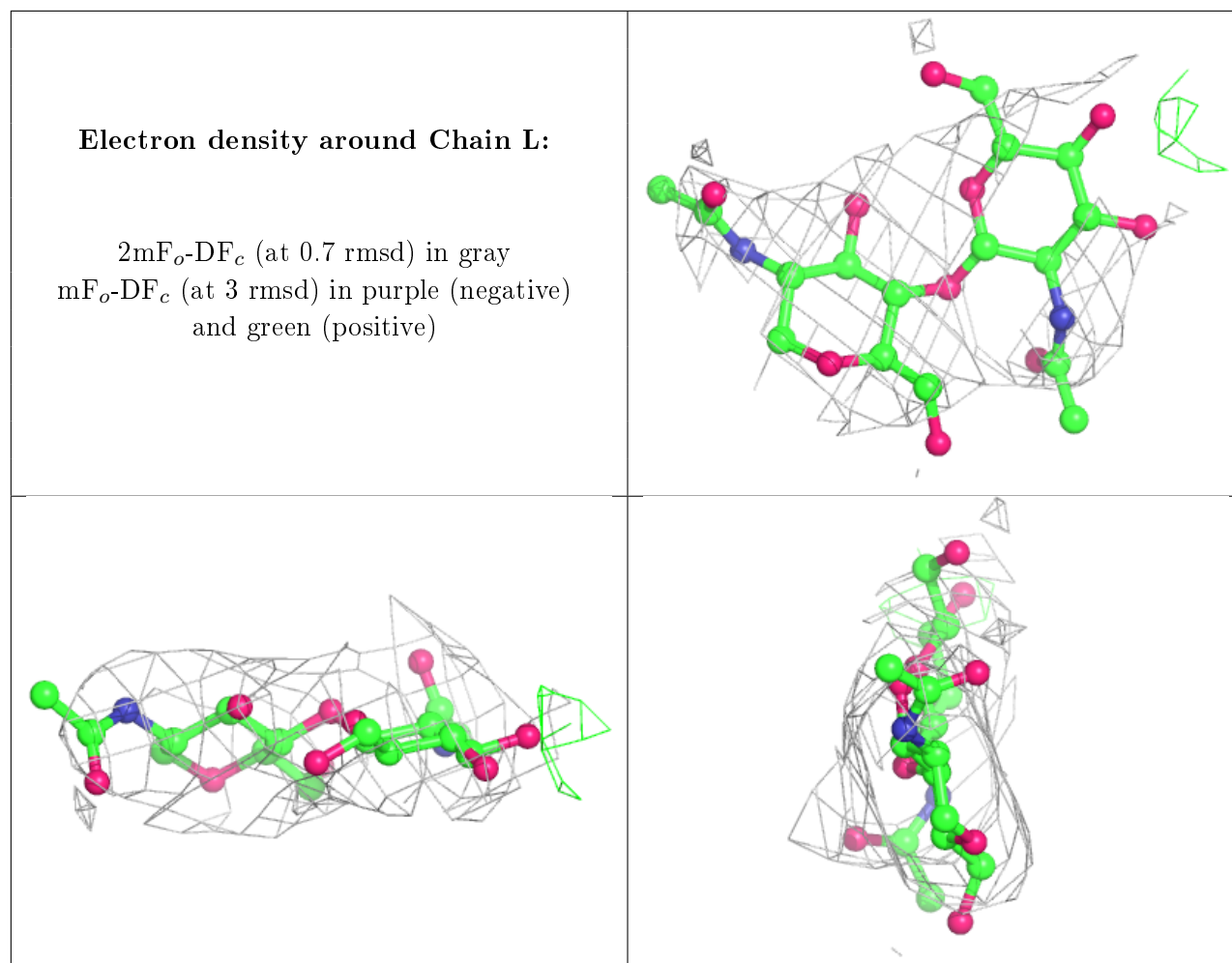
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain K:**

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





## 6.4 Ligands ⓘ

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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NAG	C	803	14/15	0.40	0.38	94,155,166,171	0
4	NAG	E	1506	14/15	0.60	0.22	100,127,140,140	0
4	NAG	F	1506	14/15	0.67	0.17	98,137,147,148	0
4	NAG	D	1507	14/15	0.67	0.37	122,139,155,168	0
4	NAG	D	1502	14/15	0.72	0.25	76,117,128,128	0
4	NAG	F	1501	14/15	0.73	0.20	80,103,114,127	0
4	NAG	E	1502	14/15	0.74	0.32	101,117,135,135	0
4	NAG	D	1506	14/15	0.76	0.21	113,135,139,141	0
4	NAG	E	1507	14/15	0.77	0.36	118,135,147,157	0
4	NAG	F	1507	14/15	0.78	0.27	99,130,145,152	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NAG	E	1501	14/15	0.81	0.18	87,106,123,131	0
5	EMC	E	1508	3/3	0.81	0.14	108,108,117,281	3
4	NAG	D	1501	14/15	0.84	0.15	99,109,130,138	0
4	NAG	E	1505	14/15	0.84	0.23	95,104,119,127	0
4	NAG	F	1502	14/15	0.84	0.19	83,104,111,115	0
5	EMC	D	1508	3/3	0.86	0.27	115,115,133,307	0
4	NAG	D	1505	14/15	0.87	0.18	71,96,112,118	0
4	NAG	F	1505	14/15	0.88	0.20	74,83,95,107	0
5	EMC	F	1508	3/3	0.90	0.20	166,166,187,321	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.