



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:01 AM UTC

PDB ID : 7BPS / pdb\_00007bps  
Title : Crystal structure of mouse TEX101  
Authors : Masutani, M.; Sakurai, S.; Shimizu, T.; Ohto, U.  
Deposited on : 2020-03-23  
Resolution : 2.35 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

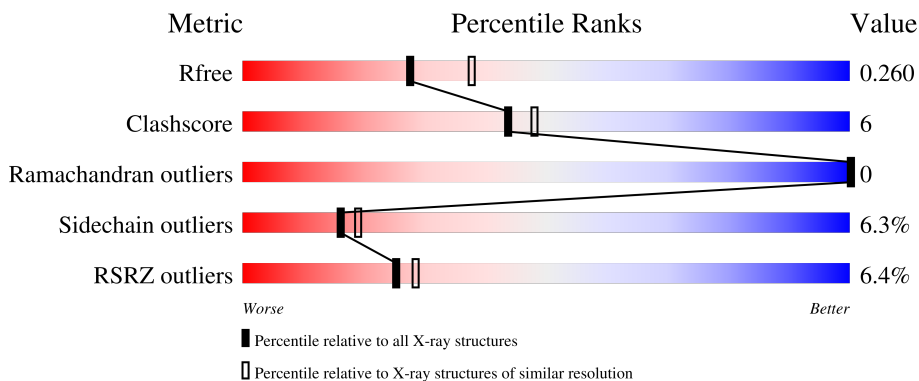
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



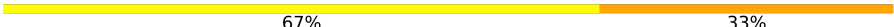
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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  $\geq 3$ , 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	211	
1	B	211	
2	C	2	
3	D	3	
3	E	3	

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Mol	Chain	Length	Quality of chain
3	F	3	 67% 33%

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 2885 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 Testis-expressed protein 101.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	178	1306	800	220	267	19	0	0	0
1	B	180	1323	809	225	270	19	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

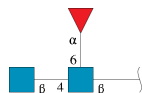
Chain	Residue	Modelled	Actual	Comment	Reference
A	22	ARG	-	expression tag	UNP Q9JMI7
A	23	SER	-	expression tag	UNP Q9JMI7
A	24	PRO	-	expression tag	UNP Q9JMI7
A	25	TRP	-	expression tag	UNP Q9JMI7
A	225	GLU	-	expression tag	UNP Q9JMI7
A	226	PHE	-	expression tag	UNP Q9JMI7
A	227	LEU	-	expression tag	UNP Q9JMI7
A	228	GLU	-	expression tag	UNP Q9JMI7
A	229	VAL	-	expression tag	UNP Q9JMI7
A	230	LEU	-	expression tag	UNP Q9JMI7
A	231	PHE	-	expression tag	UNP Q9JMI7
A	232	GLN	-	expression tag	UNP Q9JMI7
B	22	ARG	-	expression tag	UNP Q9JMI7
B	23	SER	-	expression tag	UNP Q9JMI7
B	24	PRO	-	expression tag	UNP Q9JMI7
B	25	TRP	-	expression tag	UNP Q9JMI7
B	225	GLU	-	expression tag	UNP Q9JMI7
B	226	PHE	-	expression tag	UNP Q9JMI7
B	227	LEU	-	expression tag	UNP Q9JMI7
B	228	GLU	-	expression tag	UNP Q9JMI7
B	229	VAL	-	expression tag	UNP Q9JMI7
B	230	LEU	-	expression tag	UNP Q9JMI7
B	231	PHE	-	expression tag	UNP Q9JMI7
B	232	GLN	-	expression tag	UNP Q9JMI7

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



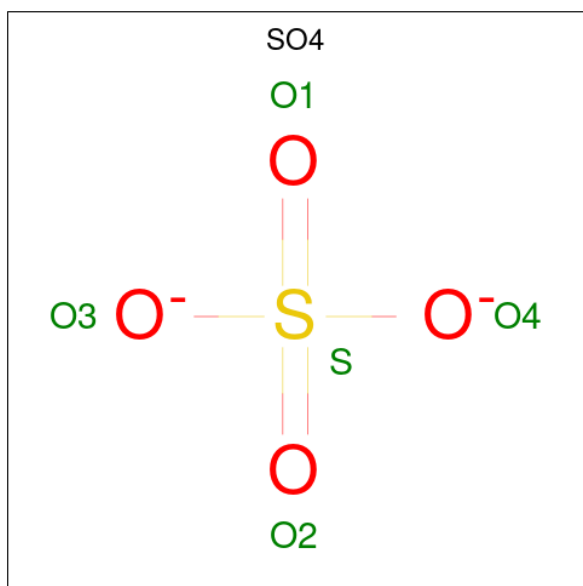
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	2	24	14	1	9	0	0	0

- Molecule 3 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			
3	D	3	38	22	2	14	0	0	0
3	E	3	38	22	2	14	0	0	0
3	F	3	38	22	2	14	0	0	0

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0

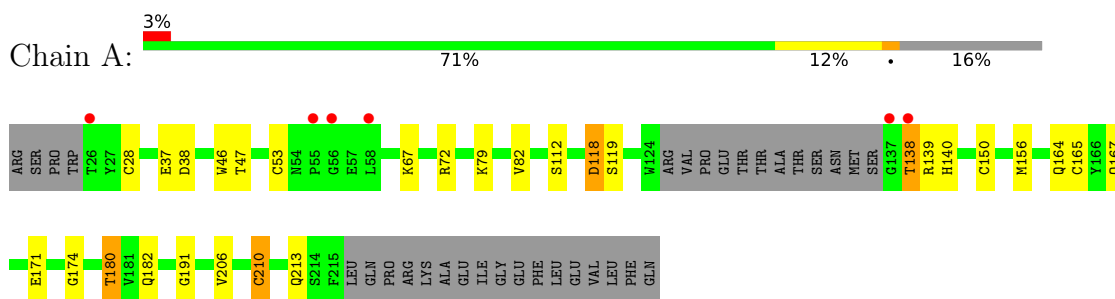
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	65	Total O 65 65	0	0
5	B	38	Total O 38 38	0	0

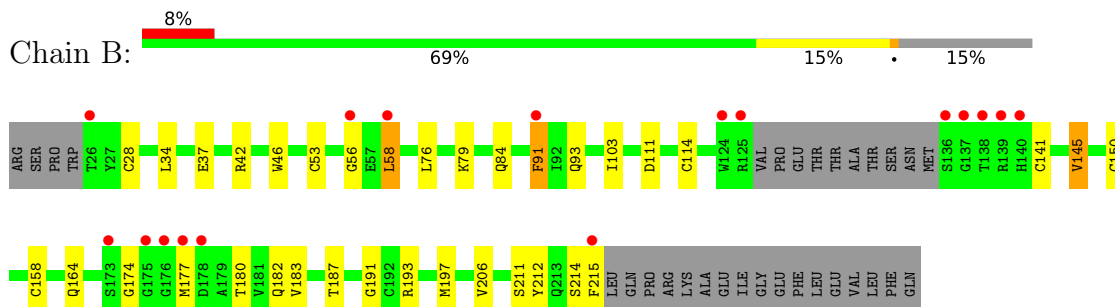
### 3 Residue-property plots [i](#)

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.

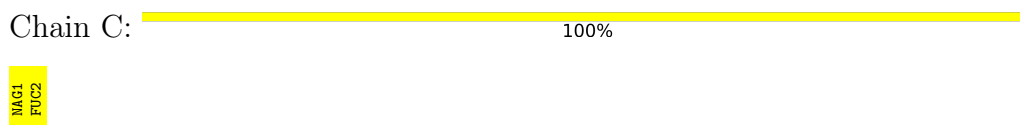
- Molecule 1: Testis-expressed protein 101



- Molecule 1: Testis-expressed protein 101




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



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose




- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%

MAG1  
MAG2  
FUC3

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  67% 33%

MAG1  
MAG2  
FUC3

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	138.60Å 211.54Å 37.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.08 – 2.35 42.08 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.08-2.35) 99.9 (42.08-2.35)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.52 (at 2.34Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.199 , 0.250 0.205 , 0.260	Depositor DCC
$R_{free}$ test set	1131 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.3	Xtrriage
Anisotropy	0.020	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 32.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2885	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.64% of the height of the origin peak. No significant pseudotranslation is detected.*

<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: FUC, NAG, SO4

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	1.05	0/1327	1.34	2/1802 (0.1%)
1	B	0.99	0/1344	1.33	3/1824 (0.2%)
All	All	1.02	0/2671	1.33	5/3626 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	215	PHE	CA-C-O	6.24	131.41	120.80
1	B	91	PHE	CA-CB-CG	6.12	119.92	113.80
1	B	174	GLY	CA-C-O	-5.52	117.82	122.29
1	A	174	GLY	CA-C-O	-5.18	118.09	122.29
1	A	138	THR	CB-CA-C	5.17	118.36	109.51

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	210	CYS	Peptide

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Mol	Chain	Res	Type	Group
1	B	56	GLY	Peptide

## 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	1306	0	1245	14	0
1	B	1323	0	1263	19	0
2	C	24	0	22	0	0
3	D	38	0	34	2	0
3	E	38	0	34	0	0
3	F	38	0	34	2	0
4	A	10	0	0	0	0
4	B	5	0	0	0	0
5	A	65	0	0	2	0
5	B	38	0	0	2	0
All	All	2885	0	2632	33	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 6.

All (33) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:GLN:HE22	1:A:213:GLN:HE22	1.29	0.81
1:A:164:GLN:HE22	1:A:191:GLY:H	1.29	0.79
1:B:164:GLN:HE22	1:B:191:GLY:H	1.29	0.78
1:A:150:CYS:H	1:A:182:GLN:HE21	1.32	0.76
1:B:150:CYS:H	1:B:182:GLN:HE21	1.33	0.72
1:B:212:TYR:OH	3:D:2:NAG:H61	1.99	0.61
1:A:171:GLU:OE2	1:A:180:THR:HG23	2.01	0.60
1:B:42:ARG:NH1	5:B:402:HOH:O	2.39	0.55
1:B:58:LEU:CD2	3:F:1:NAG:H82	2.37	0.54
1:B:93:GLN:HE21	1:B:103:ILE:HD11	1.74	0.52
1:A:150:CYS:H	1:A:182:GLN:NE2	2.07	0.51
1:B:193:ARG:NH2	3:D:1:NAG:O3	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:58:LEU:HD23	3:F:1:NAG:H82	1.96	0.48
1:B:141:CYS:SG	1:B:158:CYS:SG	3.13	0.47
1:B:34:LEU:HD13	1:B:76:LEU:HG	1.95	0.47
1:B:28:CYS:SG	1:B:53:CYS:SG	3.12	0.47
1:B:145:VAL:HG23	1:B:183:VAL:HG22	1.98	0.46
1:B:150:CYS:H	1:B:182:GLN:NE2	2.07	0.45
1:B:187:THR:HA	5:B:409:HOH:O	2.16	0.45
1:A:28:CYS:SG	1:A:53:CYS:SG	3.16	0.43
1:A:164:GLN:HE22	1:A:191:GLY:N	2.06	0.43
1:A:165:CYS:HB2	1:A:213:GLN:NE2	2.34	0.43
1:B:193:ARG:HD3	1:B:197:MET:SD	2.59	0.43
1:A:47:THR:OG1	1:A:118:ASP:HB2	2.18	0.42
1:A:67:LYS:NZ	5:A:404:HOH:O	2.51	0.42
1:B:164:GLN:NE2	1:B:191:GLY:H	2.08	0.41
1:B:164:GLN:HE22	1:B:191:GLY:N	2.07	0.41
1:B:46:TRP:CD1	1:B:79:LYS:HE3	2.54	0.41
1:A:82:VAL:HG21	5:A:438:HOH:O	2.19	0.41
1:A:140:HIS:HA	1:A:156:MET:O	2.21	0.40
1:A:46:TRP:CD1	1:A:79:LYS:HE3	2.56	0.40
1:B:111:ASP:O	1:B:114:CYS:SG	2.80	0.40
1:A:38:ASP:OD1	1:A:72:ARG:NE	2.52	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	174/211 (82%)	171 (98%)	3 (2%)	0	100	100
1	B	176/211 (83%)	171 (97%)	5 (3%)	0	100	100
All	All	350/422 (83%)	342 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	150/180 (83%)	141 (94%)	9 (6%)	17	21
1	B	152/180 (84%)	142 (93%)	10 (7%)	15	17
All	All	302/360 (84%)	283 (94%)	19 (6%)	16	19

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	GLU
1	A	112	SER
1	A	118	ASP
1	A	119	SER
1	A	138	THR
1	A	139	ARG
1	A	180	THR
1	A	206	VAL
1	A	210	CYS
1	B	37	GLU
1	B	58	LEU
1	B	84	GLN
1	B	91	PHE
1	B	145	VAL
1	B	177	MET
1	B	180	THR
1	B	206	VAL
1	B	211	SER
1	B	214	SER

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

Mol	Chain	Res	Type
1	A	164	GLN

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Mol	Chain	Res	Type
1	A	182	GLN
1	A	213	GLN
1	B	93	GLN
1	B	107	ASN
1	B	164	GLN
1	B	182	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](#)

11 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
2	NAG	C	1	1,2	14,14,15	1.01	1 (7%)	17,19,21	1.49	3 (17%)
2	FUC	C	2	2	10,10,11	0.79	0	14,14,16	2.04	4 (28%)
3	NAG	D	1	1,3	14,14,15	0.67	0	17,19,21	1.56	2 (11%)
3	NAG	D	2	3	14,14,15	1.78	5 (35%)	17,19,21	1.76	5 (29%)
3	FUC	D	3	3	10,10,11	0.60	0	14,14,16	1.10	1 (7%)
3	NAG	E	1	1,3	14,14,15	0.34	0	17,19,21	1.32	2 (11%)
3	NAG	E	2	3	14,14,15	1.70	4 (28%)	17,19,21	2.43	6 (35%)
3	FUC	E	3	3	10,10,11	0.69	0	14,14,16	1.62	3 (21%)
3	NAG	F	1	1,3	14,14,15	0.63	0	17,19,21	1.11	1 (5%)
3	NAG	F	2	3	14,14,15	0.65	0	17,19,21	1.72	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	FUC	F	3	3	10,10,11	0.72	0	14,14,16	1.85	2 (14%)

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
2	NAG	C	1	1,2	-	2/6/23/26	0/1/1/1
2	FUC	C	2	2	-	-	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	FUC	D	3	3	-	-	0/1/1/1
3	NAG	E	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	FUC	E	3	3	-	-	0/1/1/1
3	NAG	F	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	2/6/23/26	0/1/1/1
3	FUC	F	3	3	-	-	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	2	NAG	O4-C4	2.93	1.50	1.43
3	E	2	NAG	C1-C2	2.86	1.56	1.52
3	D	2	NAG	C1-C2	2.86	1.56	1.52
3	D	2	NAG	O5-C5	2.71	1.48	1.43
3	E	2	NAG	O5-C5	2.71	1.48	1.43
3	E	2	NAG	O5-C1	2.70	1.48	1.43
3	D	2	NAG	O4-C4	2.58	1.49	1.43
2	C	1	NAG	C1-C2	2.34	1.55	1.52
3	D	2	NAG	C3-C2	2.34	1.57	1.52
3	D	2	NAG	C2-N2	2.13	1.49	1.46

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	2	NAG	C1-O5-C5	5.76	119.91	112.19
2	C	2	FUC	O5-C5-C4	4.81	118.21	109.55
3	E	2	NAG	O3-C3-C2	-4.65	99.74	109.40
3	D	2	NAG	O4-C4-C5	4.45	120.29	109.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1	NAG	C4-C3-C2	-4.32	104.69	111.02
3	F	2	NAG	O5-C1-C2	4.20	117.78	111.29
3	F	3	FUC	C3-C4-C5	3.81	115.60	109.81
2	C	2	FUC	C3-C4-C5	3.66	115.37	109.81
3	E	3	FUC	O5-C5-C6	3.65	115.32	107.40
3	F	3	FUC	O5-C1-C2	3.59	119.36	110.79
3	E	2	NAG	O4-C4-C3	3.52	118.67	110.38
3	D	2	NAG	C3-C4-C5	-3.50	103.88	110.23
3	E	2	NAG	C3-C4-C5	-3.42	104.03	110.23
3	F	2	NAG	C1-O5-C5	3.40	116.74	112.19
3	E	3	FUC	C3-C4-C5	-3.09	105.11	109.81
2	C	1	NAG	C1-C2-N2	2.99	115.14	110.43
2	C	1	NAG	O5-C5-C6	2.84	113.18	107.66
3	D	2	NAG	C4-C3-C2	-2.76	106.98	111.02
3	F	1	NAG	C4-C3-C2	-2.69	107.07	111.02
3	E	1	NAG	C1-O5-C5	-2.51	108.82	112.19
3	E	2	NAG	C6-C5-C4	-2.45	107.00	113.02
3	D	1	NAG	C8-C7-N2	-2.42	112.10	116.12
2	C	2	FUC	O2-C2-C3	2.37	115.05	110.15
2	C	2	FUC	C1-C2-C3	-2.25	106.36	109.64
3	D	2	NAG	C1-O5-C5	2.22	115.16	112.19
3	D	2	NAG	O5-C1-C2	-2.14	107.97	111.29
2	C	1	NAG	O3-C3-C2	2.13	113.82	109.40
3	E	1	NAG	O7-C7-N2	2.12	125.73	121.98
3	F	2	NAG	O3-C3-C2	-2.09	105.06	109.40
3	D	3	FUC	O5-C5-C6	2.09	111.93	107.40
3	E	2	NAG	C4-C3-C2	2.08	114.06	111.02
3	E	3	FUC	O4-C4-C5	2.06	114.28	109.74

There are no chirality outliers.

All (8) torsion outliers are listed below:

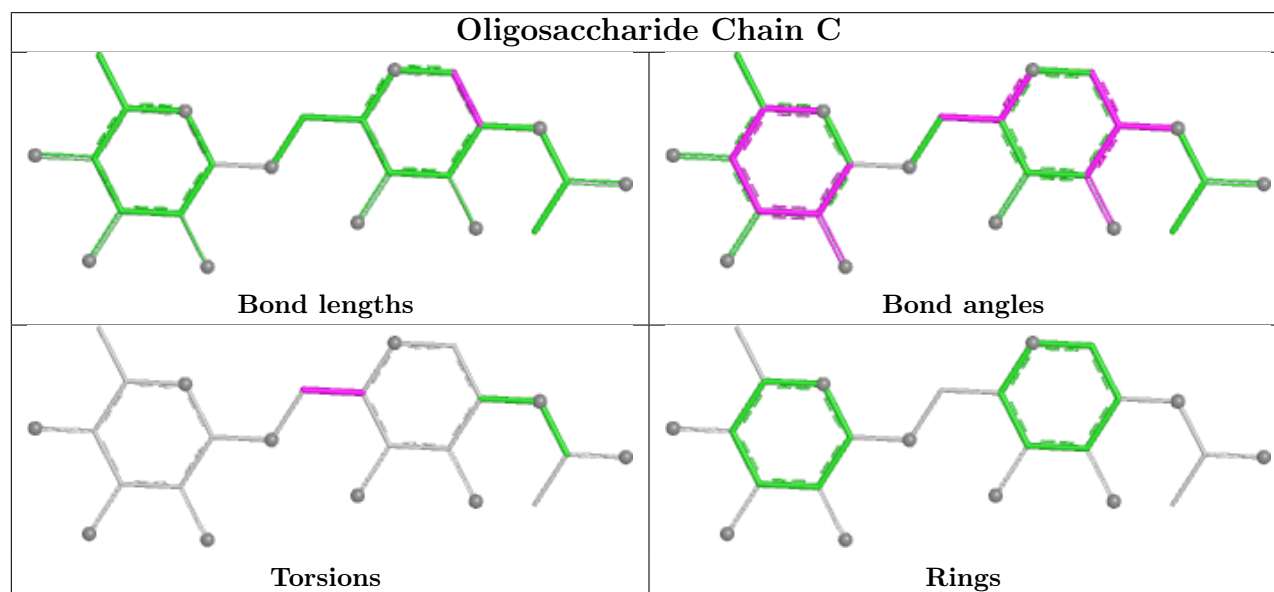
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	O5-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6
3	F	1	NAG	C4-C5-C6-O6

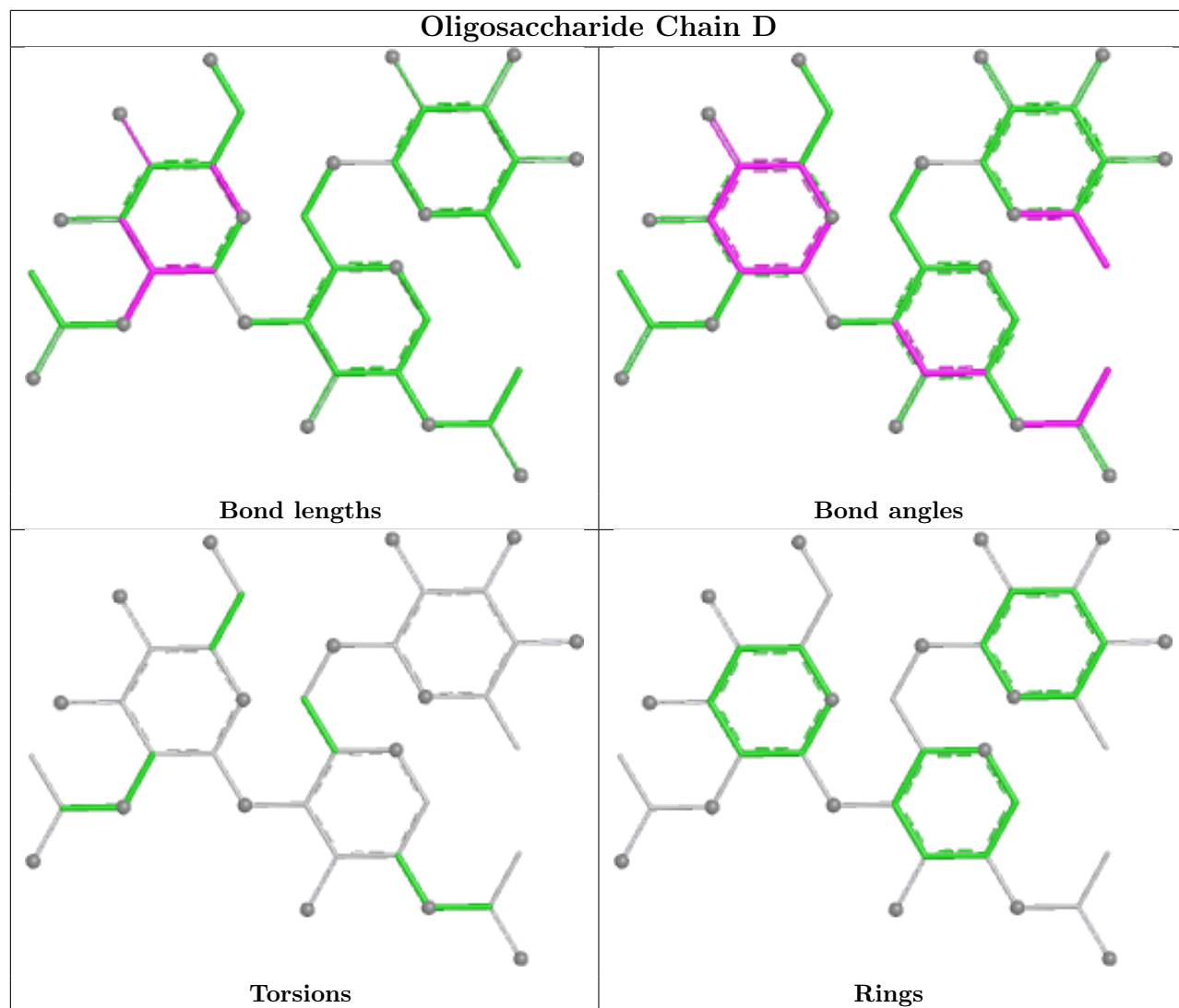
There are no ring outliers.

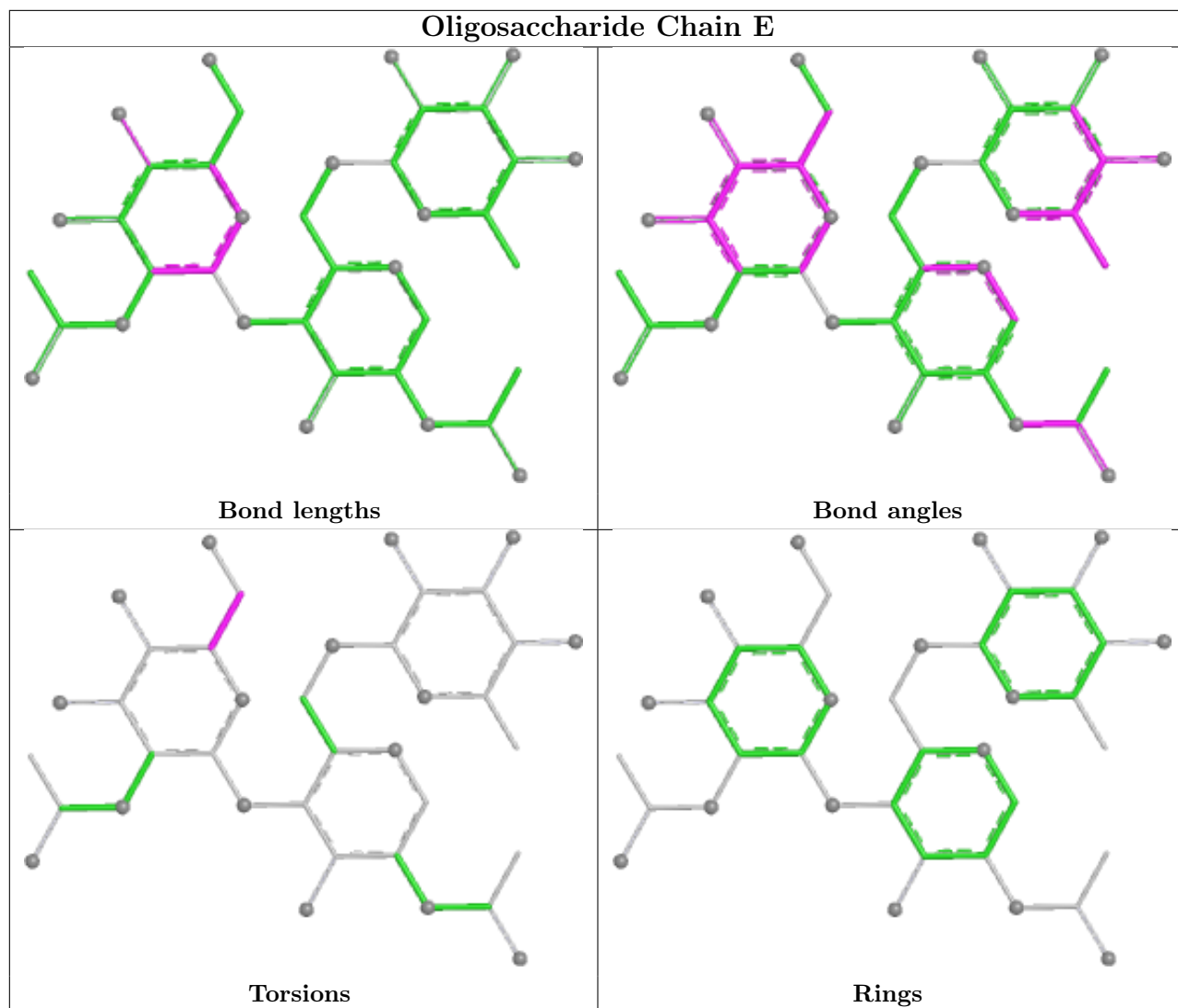
3 monomers are involved in 4 short contacts:

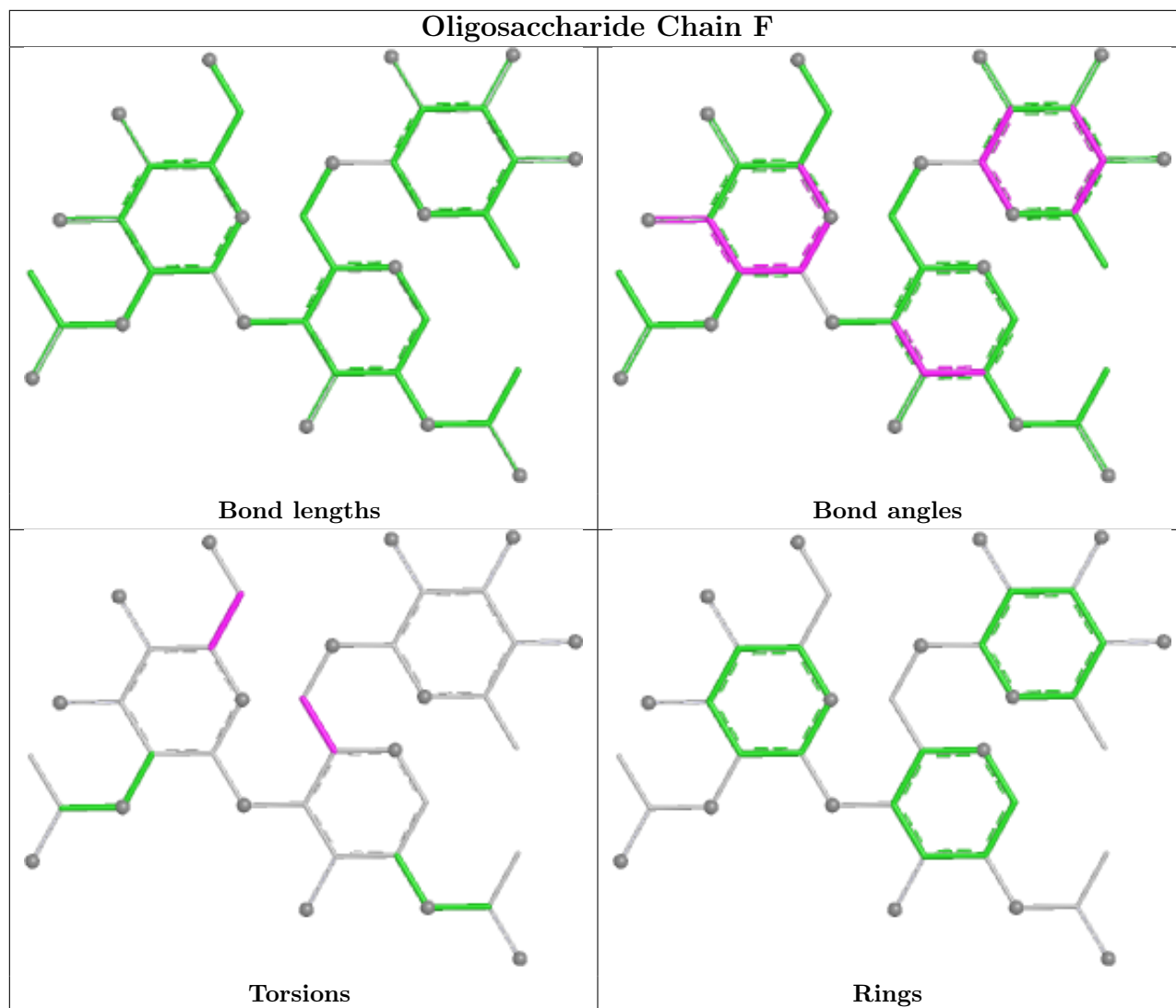
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	1	NAG	2	0
3	D	1	NAG	1	0
3	D	2	NAG	1	0

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 [i](#)

3 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	$\# Z  > 2$
4	SO4	B	307	-	4,4,4	0.31	0	6,6,6	0.10	0
4	SO4	A	307	-	4,4,4	0.29	0	6,6,6	0.13	0
4	SO4	A	306	-	4,4,4	0.30	0	6,6,6	0.11	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	178/211 (84%)	0.05	6 (3%) 48 55	27, 39, 70, 101	0
1	B	180/211 (85%)	0.51	17 (9%) 14 16	35, 51, 83, 108	0
All	All	358/422 (84%)	0.28	23 (6%) 25 28	27, 46, 78, 108	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	137	GLY	5.5
1	A	26	THR	5.0
1	B	138	THR	4.9
1	A	56	GLY	4.8
1	A	55	PRO	4.3
1	B	137	GLY	3.8
1	B	136	SER	3.7
1	B	176	GLY	3.6
1	B	125	ARG	3.5
1	B	177	MET	3.2
1	B	175	GLY	3.1
1	B	215	PHE	2.9
1	B	91	PHE	2.9
1	B	56	GLY	2.7
1	B	26	THR	2.6
1	B	139	ARG	2.6
1	B	58	LEU	2.5
1	B	140	HIS	2.4
1	B	178	ASP	2.3
1	B	173	SER	2.3
1	A	58	LEU	2.2
1	B	124	TRP	2.1
1	A	138	THR	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](#)

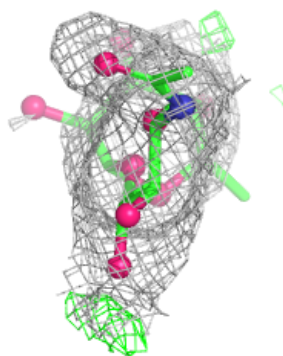
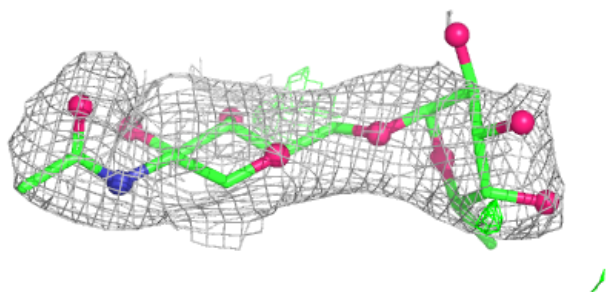
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	D	2	14/15	0.66	0.18	56,60,63,68	0
3	NAG	E	2	14/15	0.71	0.19	54,57,60,61	0
3	NAG	F	2	14/15	0.84	0.14	60,70,77,78	0
2	NAG	C	1	14/15	0.85	0.13	71,83,91,96	0
2	FUC	C	2	10/11	0.89	0.16	98,100,108,114	0
3	FUC	D	3	10/11	0.90	0.11	63,65,69,69	0
3	NAG	D	1	14/15	0.92	0.10	48,59,64,70	0
3	NAG	E	1	14/15	0.92	0.10	63,66,73,77	0
3	FUC	E	3	10/11	0.94	0.10	65,72,76,77	0
3	FUC	F	3	10/11	0.94	0.10	49,55,57,60	0
3	NAG	F	1	14/15	0.97	0.06	41,47,55,56	0

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

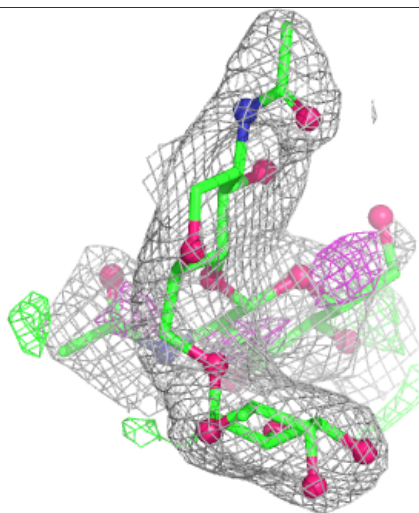
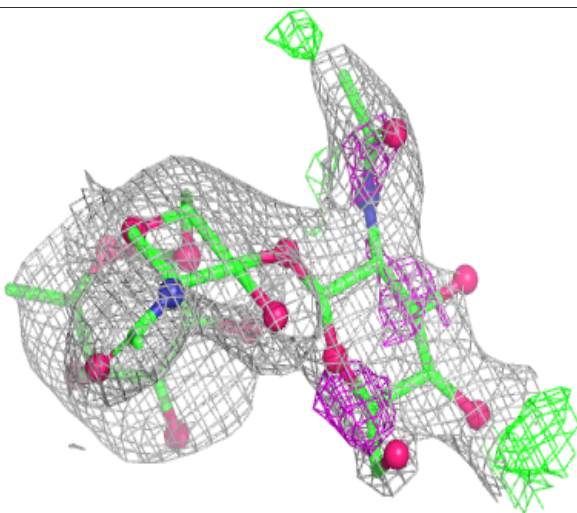
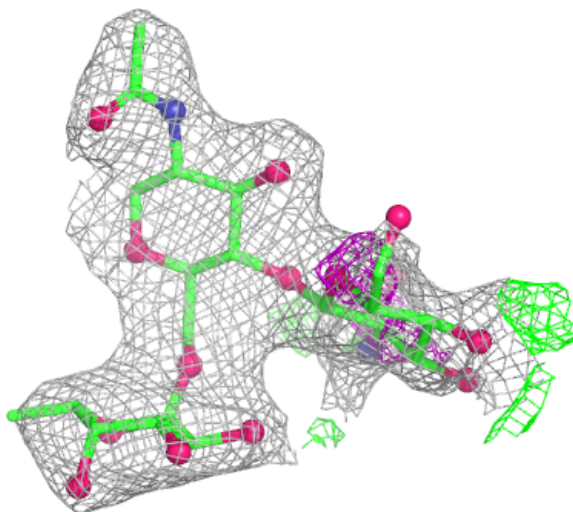
**Electron density around Chain C:**

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



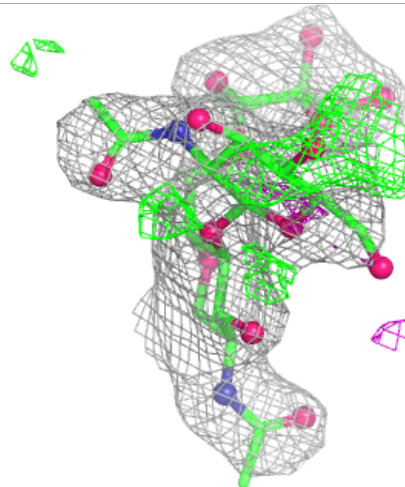
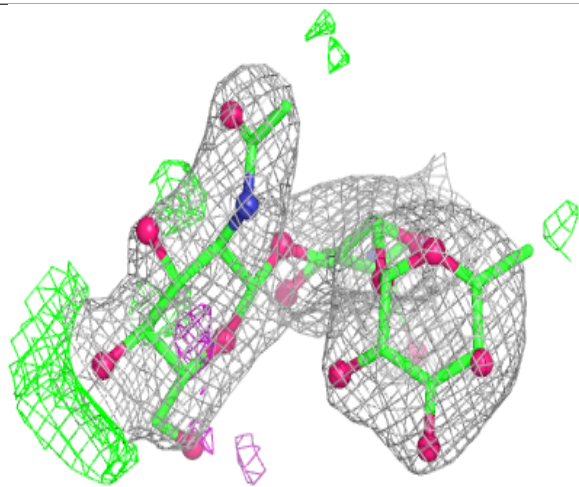
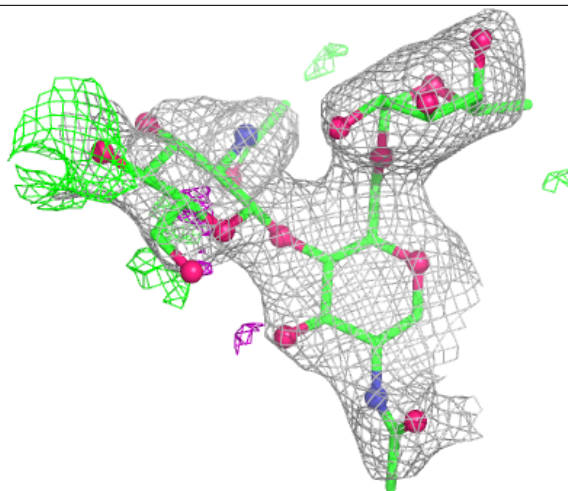
**Electron density around Chain D:**

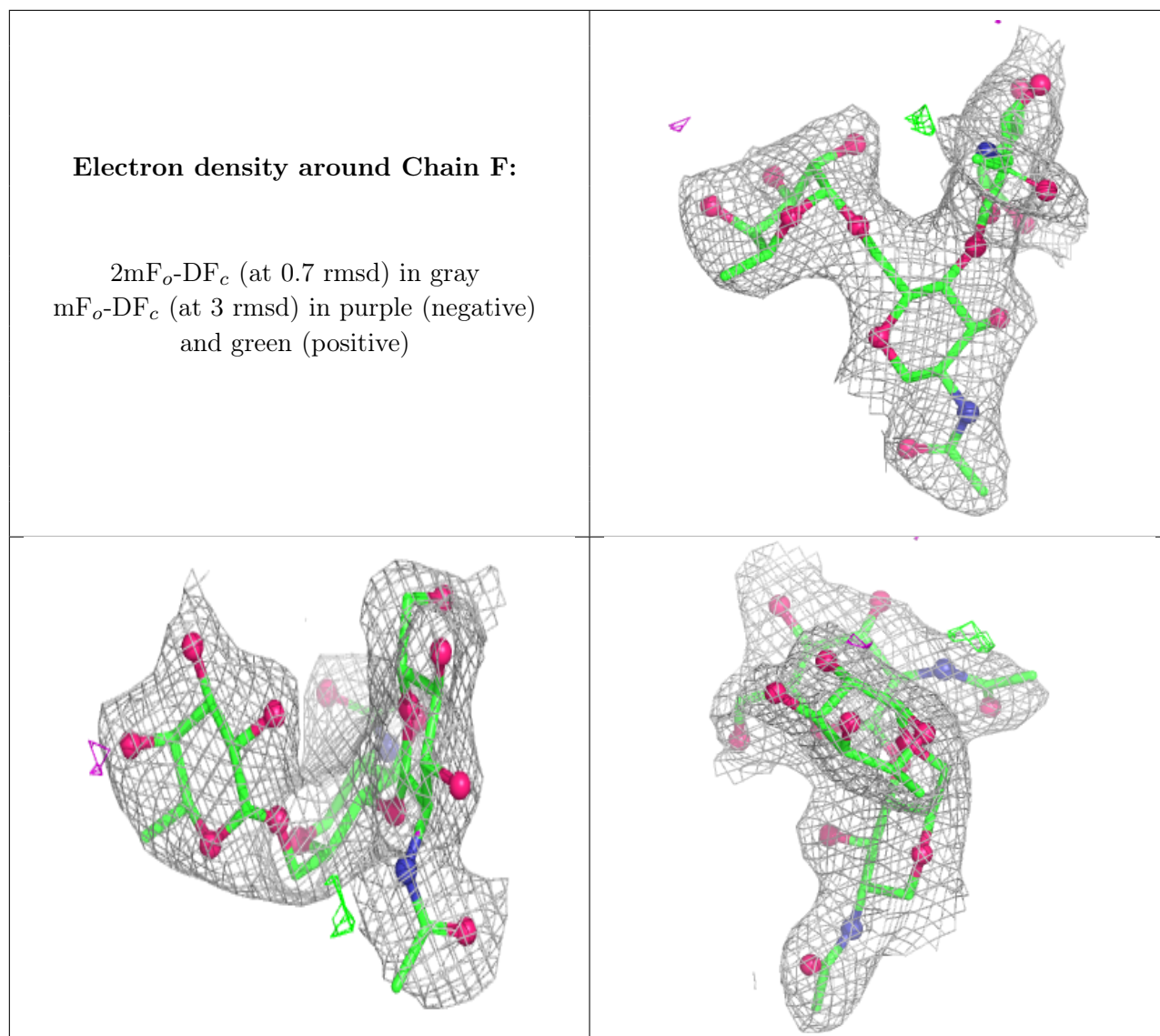
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain E:**

$2mF_o-DF_c$  (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, 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(Å <sup>2</sup> )	Q<0.9
4	SO4	B	307	5/5	0.71	0.20	125,132,135,147	0
4	SO4	A	307	5/5	0.76	0.12	82,89,107,112	0
4	SO4	A	306	5/5	0.82	0.11	84,88,96,97	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.