



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 11:57 AM BST

PDB ID : 5W0P  
Title : Crystal structure of rhodopsin bound to visual arrestin determined by X-ray free electron laser  
Authors : Zhou, X.E.; He, Y.; de Waal, P.W.; Gao, X.; Kang, Y.; Van Eps, N.; Yin, Y.; Pal, K.; Goswami, D.; White, T.A.; Barty, A.; Latorraca, N.R.; Chapman, H.N.; Hubbell, W.L.; Dror, R.O.; Stevens, R.C.; Cherezov, V.; Gurevich, V.V.; Griffin, P.R.; Ernst, O.P.; Melcher, K.; Xu, H.E.  
Deposited on : 2017-05-31  
Resolution : 3.01 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](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

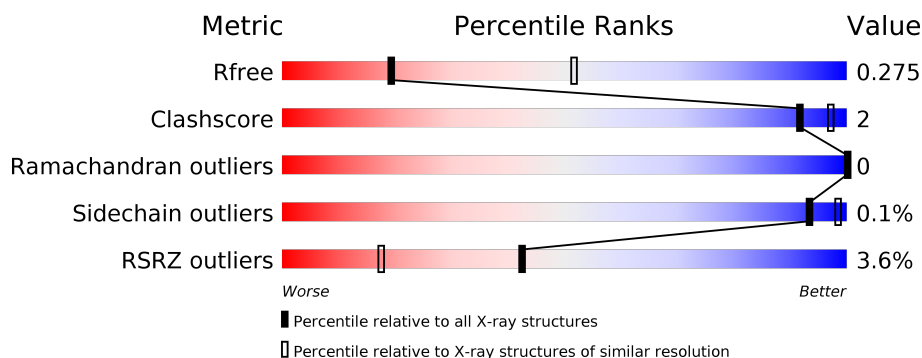
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.01 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	2399 (3.04-3.00)
Clashscore	141614	2734 (3.04-3.00)
Ramachandran outliers	138981	2640 (3.04-3.00)
Sidechain outliers	138945	2643 (3.04-3.00)
RSRZ outliers	127900	2287 (3.04-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	906	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>5%</div> <div>6%</div> </div> </div>
1	B	906	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>•</div> <div>11%</div> </div> </div>
2	C	906	<div> <div>3%</div> <div> <div></div> <div>91%</div> <div>•</div> <div>6%</div> </div> </div>
2	D	906	<div> <div>5%</div> <div> <div></div> <div>82%</div> <div>•</div> <div>15%</div> </div> </div>
3	E	2	<div> <div></div> <div> <div>50%</div> <div>50%</div> </div> </div>
3	F	2	<div> <div></div> <div> <div>50%</div> <div>50%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	G	2	 50%50%
3	H	2	 50%50%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 25976 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 Endolysin,Rhodopsin,S-arrestin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	849	Total	C	N	O	P	S	0	0	0
			6702	4337	1096	1227	2	40			
1	B	804	Total	C	N	O	P	S	0	0	0
			6351	4116	1035	1159	2	39			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-107	THR	CYS	engineered mutation	UNP A0A097J792
A	-64	ALA	CYS	engineered mutation	UNP A0A097J792
A	2	CYS	ASN	engineered mutation	UNP P08100
A	113	GLN	GLU	engineered mutation	UNP P08100
A	257	TYR	MET	engineered mutation	UNP P08100
A	282	CYS	ASN	engineered mutation	UNP P08100
A	1995	GLY	-	linker	UNP P08100
A	1996	SER	-	linker	UNP P08100
A	1997	ALA	-	linker	UNP P08100
A	1998	GLY	-	linker	UNP P08100
A	1999	SER	-	linker	UNP P08100
A	2000	ALA	-	linker	UNP P08100
A	2001	GLY	-	linker	UNP P08100
A	2002	SER	-	linker	UNP P08100
A	2003	ALA	-	linker	UNP P08100
A	2004	GLY	-	linker	UNP P08100
A	2005	SER	-	linker	UNP P08100
A	2006	ALA	-	linker	UNP P08100
A	2007	GLY	-	linker	UNP P08100
A	2008	SER	-	linker	UNP P08100
A	2009	ALA	-	linker	UNP P08100
A	2374	ALA	LEU	engineered mutation	UNP P20443
A	2375	ALA	VAL	engineered mutation	UNP P20443
A	2376	ALA	PHE	engineered mutation	UNP P20443
B	-107	THR	CYS	engineered mutation	UNP A0A097J792

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-64	ALA	CYS	engineered mutation	UNP A0A097J792
B	2	CYS	ASN	engineered mutation	UNP P08100
B	113	GLN	GLU	engineered mutation	UNP P08100
B	257	TYR	MET	engineered mutation	UNP P08100
B	282	CYS	ASN	engineered mutation	UNP P08100
B	1995	GLY	-	linker	UNP P08100
B	1996	SER	-	linker	UNP P08100
B	1997	ALA	-	linker	UNP P08100
B	1998	GLY	-	linker	UNP P08100
B	1999	SER	-	linker	UNP P08100
B	2000	ALA	-	linker	UNP P08100
B	2001	GLY	-	linker	UNP P08100
B	2002	SER	-	linker	UNP P08100
B	2003	ALA	-	linker	UNP P08100
B	2004	GLY	-	linker	UNP P08100
B	2005	SER	-	linker	UNP P08100
B	2006	ALA	-	linker	UNP P08100
B	2007	GLY	-	linker	UNP P08100
B	2008	SER	-	linker	UNP P08100
B	2009	ALA	-	linker	UNP P08100
B	2374	ALA	LEU	engineered mutation	UNP P20443
B	2375	ALA	VAL	engineered mutation	UNP P20443
B	2376	ALA	PHE	engineered mutation	UNP P20443

- Molecule 2 is a protein called Endolysin,Rhodopsin,S-arrestin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	850	Total	C	N	O	P	S	0	0	0
			6703	4340	1099	1223	1	40			
2	D	774	Total	C	N	O	P	S	0	0	0
			6108	3966	997	1106	1	38			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-107	THR	CYS	engineered mutation	UNP A0A097J792
C	-64	ALA	CYS	engineered mutation	UNP A0A097J792
C	2	CYS	ASN	engineered mutation	UNP P08100
C	113	GLN	GLU	engineered mutation	UNP P08100
C	257	TYR	MET	engineered mutation	UNP P08100
C	282	CYS	ASN	engineered mutation	UNP P08100
C	1995	GLY	-	linker	UNP P08100

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1996	SER	-	linker	UNP P08100
C	1997	ALA	-	linker	UNP P08100
C	1998	GLY	-	linker	UNP P08100
C	1999	SER	-	linker	UNP P08100
C	2000	ALA	-	linker	UNP P08100
C	2001	GLY	-	linker	UNP P08100
C	2002	SER	-	linker	UNP P08100
C	2003	ALA	-	linker	UNP P08100
C	2004	GLY	-	linker	UNP P08100
C	2005	SER	-	linker	UNP P08100
C	2006	ALA	-	linker	UNP P08100
C	2007	GLY	-	linker	UNP P08100
C	2008	SER	-	linker	UNP P08100
C	2009	ALA	-	linker	UNP P08100
C	2374	ALA	LEU	engineered mutation	UNP P20443
C	2375	ALA	VAL	engineered mutation	UNP P20443
C	2376	ALA	PHE	engineered mutation	UNP P20443
D	-107	THR	CYS	engineered mutation	UNP A0A097J792
D	-64	ALA	CYS	engineered mutation	UNP A0A097J792
D	2	CYS	ASN	engineered mutation	UNP P08100
D	113	GLN	GLU	engineered mutation	UNP P08100
D	257	TYR	MET	engineered mutation	UNP P08100
D	282	CYS	ASN	engineered mutation	UNP P08100
D	1995	GLY	-	linker	UNP P08100
D	1996	SER	-	linker	UNP P08100
D	1997	ALA	-	linker	UNP P08100
D	1998	GLY	-	linker	UNP P08100
D	1999	SER	-	linker	UNP P08100
D	2000	ALA	-	linker	UNP P08100
D	2001	GLY	-	linker	UNP P08100
D	2002	SER	-	linker	UNP P08100
D	2003	ALA	-	linker	UNP P08100
D	2004	GLY	-	linker	UNP P08100
D	2005	SER	-	linker	UNP P08100
D	2006	ALA	-	linker	UNP P08100
D	2007	GLY	-	linker	UNP P08100
D	2008	SER	-	linker	UNP P08100
D	2009	ALA	-	linker	UNP P08100
D	2374	ALA	LEU	engineered mutation	UNP P20443
D	2375	ALA	VAL	engineered mutation	UNP P20443
D	2376	ALA	PHE	engineered mutation	UNP P20443

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

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



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









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

Chain H:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.24Å 109.24Å 452.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.03 – 3.01 30.03 – 3.01	Depositor EDS
% Data completeness (in resolution range)	70.7 (30.03-3.01) 70.7 (30.03-3.01)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.91 (at 3.00Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.234 , 0.272 0.232 , 0.275	Depositor DCC
$R_{free}$ test set	3761 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	113.4	Xtriage
Anisotropy	0.566	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 138.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.35$ , $\langle L^2 \rangle = 0.18$	Xtriage
Estimated twinning fraction	0.499 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	25976	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	201.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.97% 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: TPO, NAG, SEP

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	0.26	0/6837	0.43	0/9285
1	B	0.29	0/6480	0.47	0/8804
2	C	0.27	0/6851	0.45	0/9306
2	D	0.28	0/6248	0.46	0/8495
All	All	0.28	0/26416	0.45	0/35890

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	6702	0	6749	27	0
1	B	6351	0	6385	19	0
2	C	6703	0	6755	15	0
2	D	6108	0	6152	21	0
3	E	28	0	25	0	0
3	F	28	0	25	0	0
3	G	28	0	25	1	0
3	H	28	0	25	2	0
All	All	25976	0	26141	83	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 2.

The worst 5 of 83 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2301:LYS:HG3	1:B:2302:HIS:H	1.51	0.74
2:D:2176:ARG:HG3	2:D:2300:ILE:HD11	1.70	0.72
1:B:72:LEU:HD12	1:B:2073:ILE:HD12	1.72	0.72
1:A:72:LEU:HB2	1:A:2073:ILE:HD11	1.74	0.68
2:C:-74:VAL:HA	2:C:-39:GLN:OE1	1.93	0.68

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	841/906 (93%)	827 (98%)	14 (2%)	0	100	100
1	B	794/906 (88%)	784 (99%)	10 (1%)	0	100	100
2	C	843/906 (93%)	831 (99%)	12 (1%)	0	100	100
2	D	767/906 (85%)	759 (99%)	8 (1%)	0	100	100
All	All	3245/3624 (90%)	3201 (99%)	44 (1%)	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	736/776 (95%)	736 (100%)	0	100	100
1	B	698/776 (90%)	697 (100%)	1 (0%)	93	98
2	C	737/777 (95%)	737 (100%)	0	100	100
2	D	673/777 (87%)	672 (100%)	1 (0%)	93	98
All	All	2844/3106 (92%)	2842 (100%)	2 (0%)	93	98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	2343	LEU
2	D	2340	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2244	GLN
1	A	2358	HIS
2	C	145	ASN
1	A	200	ASN
1	B	2244	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	SEP	B	338	1	8,9,10	1.46	1 (12%)	8,12,14	0.73	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SEP	C	338	2	8,9,10	1.46	1 (12%)	8,12,14	0.99	0
1	SEP	A	338	1	8,9,10	1.48	1 (12%)	8,12,14	0.81	0
1	TPO	B	336	1	8,10,11	1.63	1 (12%)	10,14,16	1.59	1 (10%)
1	TPO	A	336	1	8,10,11	1.12	0	10,14,16	1.53	1 (10%)
2	SEP	D	338	2	8,9,10	1.47	1 (12%)	8,12,14	0.70	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
1	SEP	B	338	1	-	0/5/8/10	-
2	SEP	C	338	2	-	0/5/8/10	-
1	SEP	A	338	1	-	0/5/8/10	-
1	TPO	B	336	1	-	1/9/11/13	-
1	TPO	A	336	1	-	3/9/11/13	-
2	SEP	D	338	2	-	0/5/8/10	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	336	TPO	P-O1P	3.26	1.61	1.50
1	A	338	SEP	P-O1P	3.21	1.60	1.50
2	D	338	SEP	P-O1P	3.18	1.60	1.50
1	B	338	SEP	P-O1P	3.17	1.60	1.50
2	C	338	SEP	P-O1P	3.14	1.60	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	336	TPO	P-OG1-CB	-4.52	109.56	123.21
1	A	336	TPO	P-OG1-CB	-4.21	110.48	123.21

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	336	TPO	N-CA-CB-OG1
1	A	336	TPO	N-CA-CB-OG1

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Mol	Chain	Res	Type	Atoms
1	A	336	TPO	CB-OG1-P-O3P
1	A	336	TPO	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates ⓘ

8 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
3	NAG	E	1	1,3	14,14,15	0.88	0	17,19,21	0.96	1 (5%)
3	NAG	E	2	3	14,14,15	0.55	0	17,19,21	0.52	0
3	NAG	F	1	1,3	14,14,15	0.72	0	17,19,21	0.88	0
3	NAG	F	2	3	14,14,15	1.00	1 (7%)	17,19,21	1.55	2 (11%)
3	NAG	G	1	3,2	14,14,15	0.91	0	17,19,21	0.95	1 (5%)
3	NAG	G	2	3	14,14,15	0.91	1 (7%)	17,19,21	0.86	1 (5%)
3	NAG	H	1	3,2	14,14,15	0.97	1 (7%)	17,19,21	1.22	1 (5%)
3	NAG	H	2	3	14,14,15	0.79	1 (7%)	17,19,21	0.74	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	E	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	E	2	3	-	1/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	F	2	3	-	3/6/23/26	0/1/1/1
3	NAG	G	1	3,2	-	5/6/23/26	0/1/1/1

*Continued on next page...*



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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	G	2	3	-	5/6/23/26	0/1/1/1
3	NAG	H	1	3,2	-	4/6/23/26	0/1/1/1
3	NAG	H	2	3	-	4/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	2	NAG	O5-C1	-3.05	1.38	1.43
3	H	1	NAG	C2-N2	-2.45	1.42	1.46
3	G	2	NAG	C1-C2	2.10	1.55	1.52
3	H	2	NAG	C1-C2	2.08	1.55	1.52

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	2	NAG	C1-C2-N2	-5.07	101.83	110.49
3	H	1	NAG	C2-N2-C7	3.38	127.72	122.90
3	F	2	NAG	C2-N2-C7	2.70	126.74	122.90
3	G	1	NAG	C4-C3-C2	2.16	114.18	111.02
3	G	2	NAG	C4-C3-C2	2.15	114.17	111.02

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

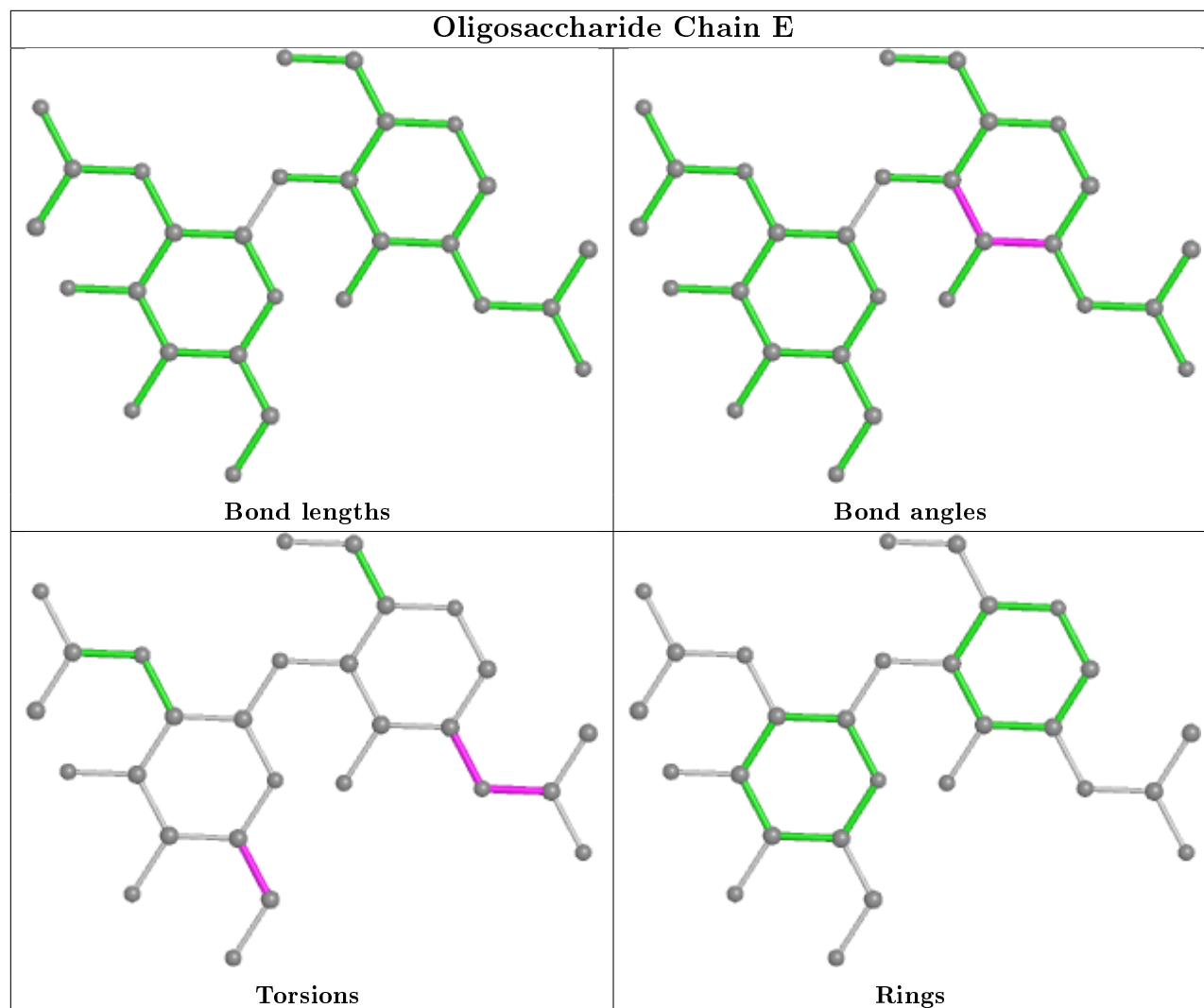
Mol	Chain	Res	Type	Atoms
3	G	2	NAG	C1-C2-N2-C7
3	H	2	NAG	C1-C2-N2-C7
3	G	1	NAG	C1-C2-N2-C7
3	F	1	NAG	C1-C2-N2-C7
3	E	1	NAG	C1-C2-N2-C7

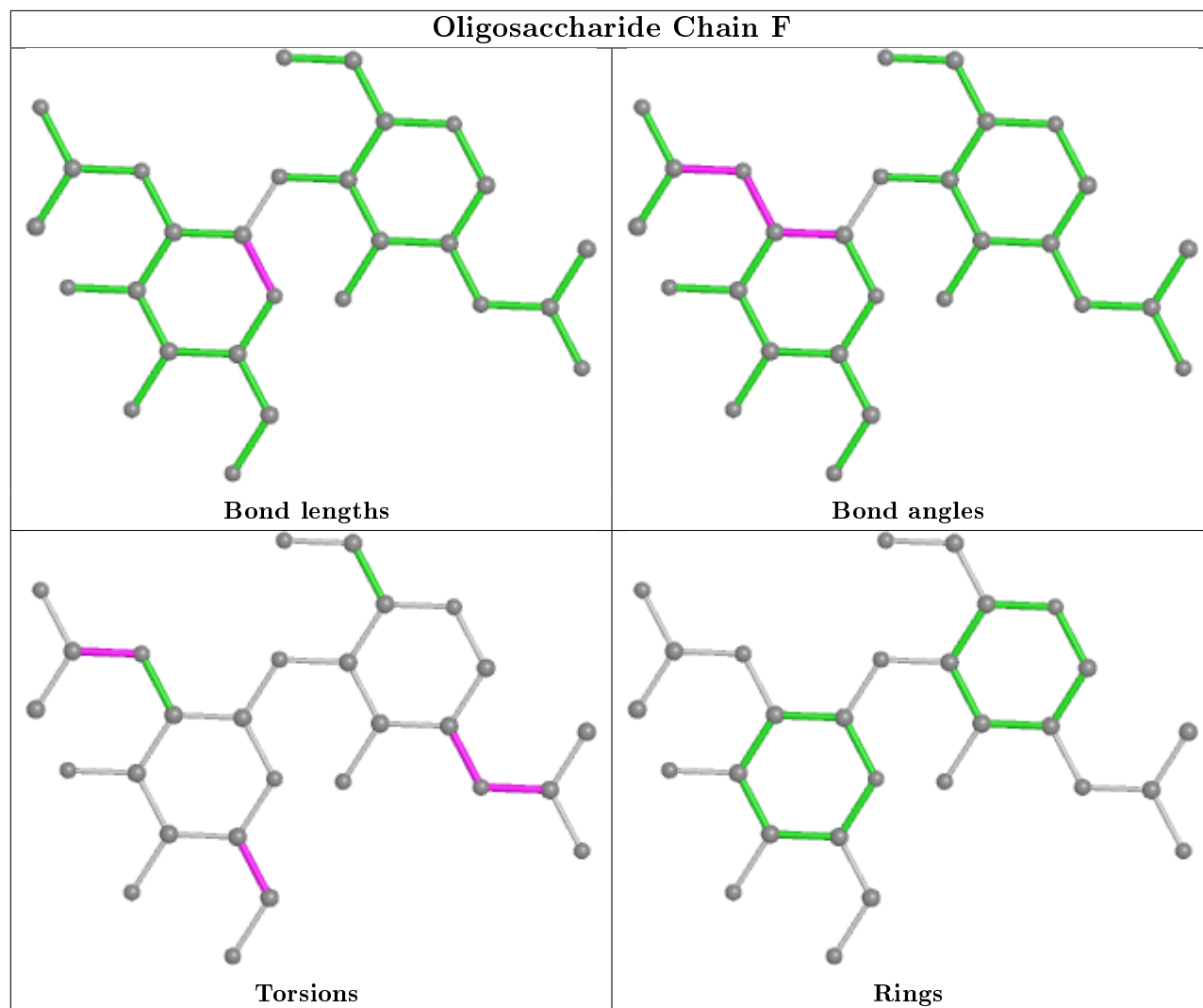
There are no ring outliers.

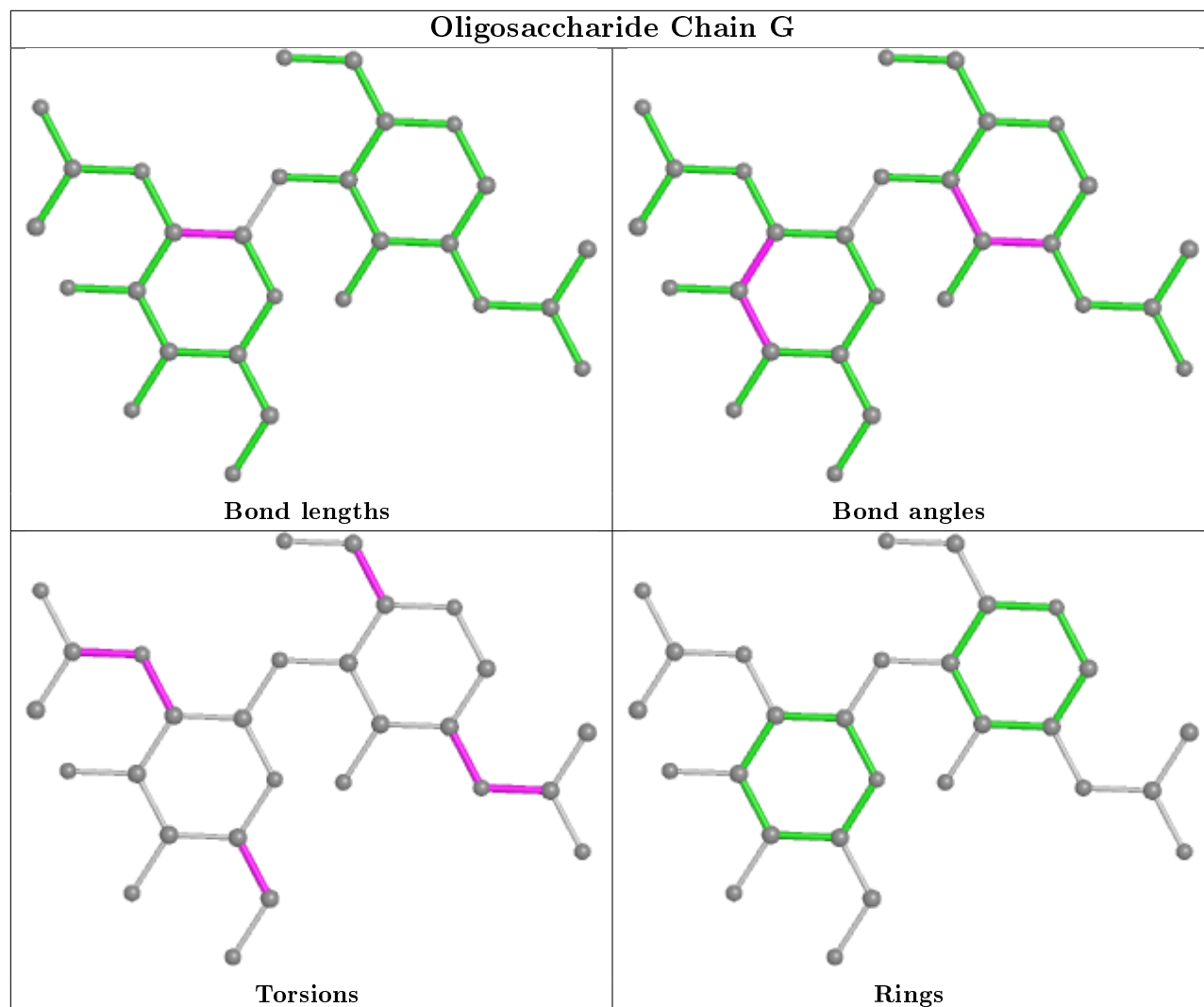
2 monomers are involved in 3 short contacts:

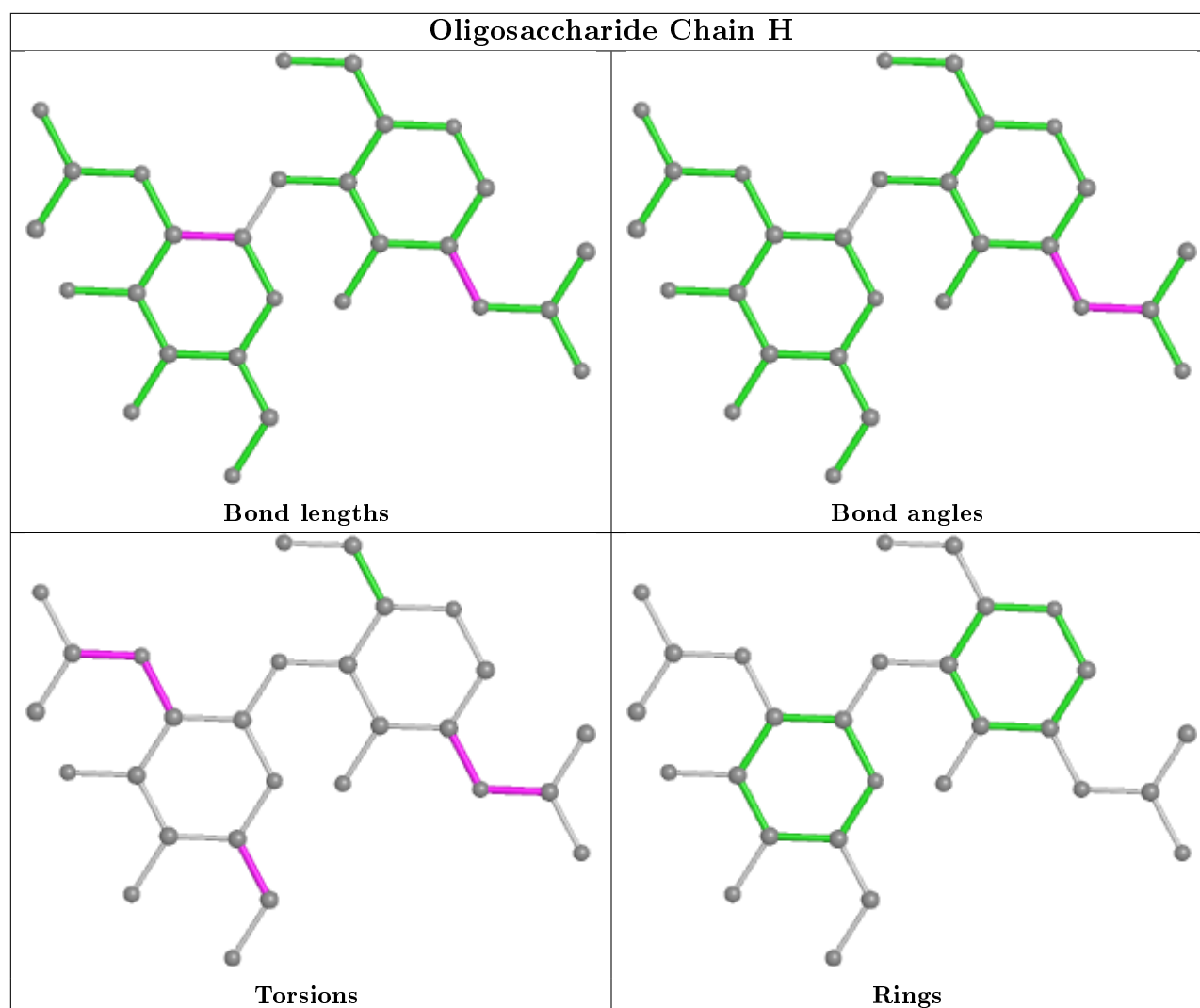
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	2	NAG	1	0
3	H	1	NAG	2	0

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









## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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, 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	847/906 (93%)	-0.02	26 (3%)	49	21	115, 194, 307, 335	0
1	B	802/906 (88%)	-0.08	26 (3%)	47	20	116, 196, 297, 321	0
2	C	849/906 (93%)	-0.11	23 (2%)	54	26	119, 190, 323, 347	0
2	D	773/906 (85%)	0.07	42 (5%)	25	9	83, 171, 341, 370	0
All	All	3271/3624 (90%)	-0.04	117 (3%)	42	17	83, 188, 311, 370	0

The worst 5 of 117 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	-124	PRO	8.9
2	C	-148	LEU	8.2
2	D	2336	VAL	7.8
2	D	-34	ASP	7.6
2	D	-82	LEU	6.6

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

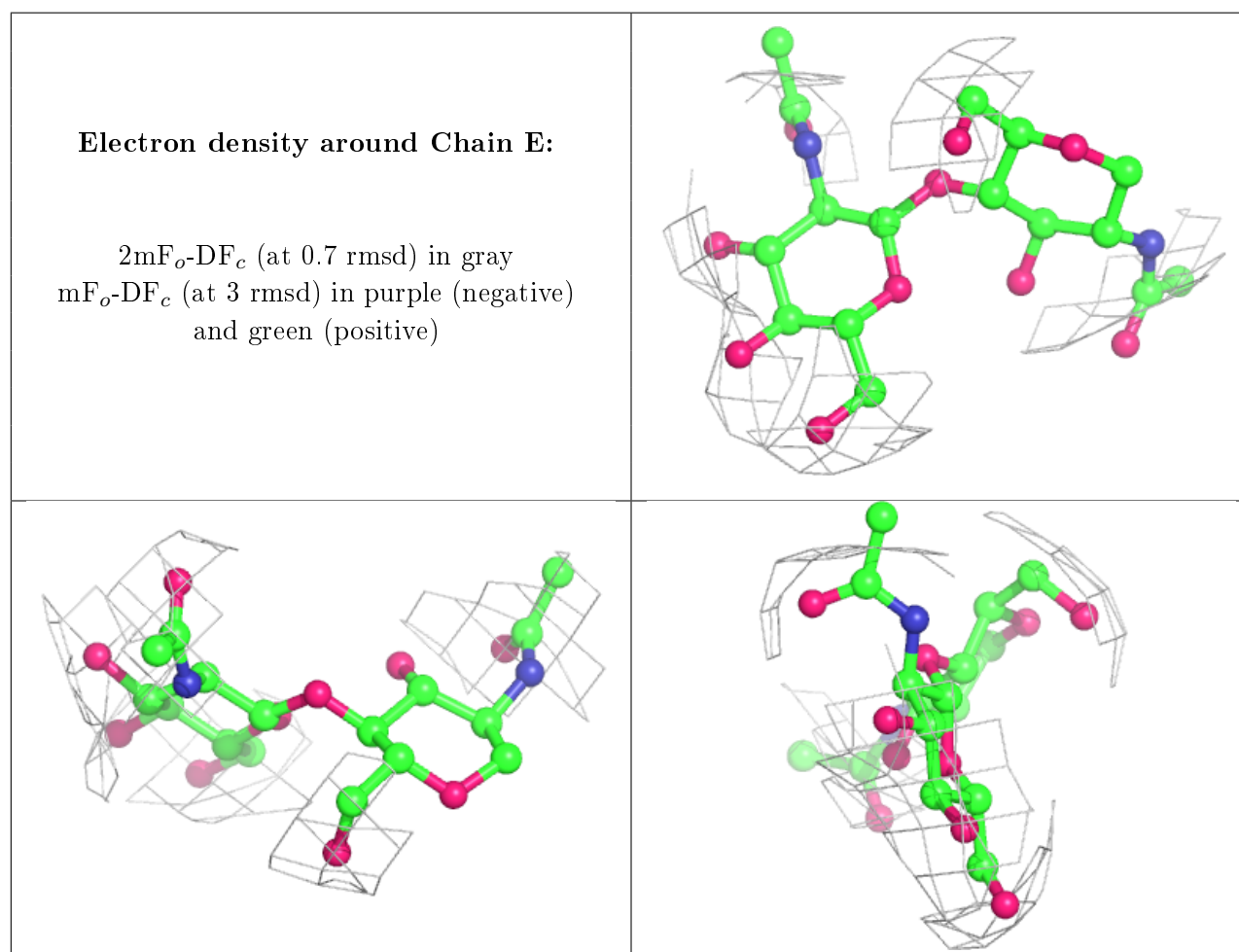
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
1	SEP	B	338	10/11	0.66	0.15	244,270,302,307	0
1	TPO	B	336	11/12	0.69	0.19	290,319,323,323	0
1	TPO	A	336	11/12	0.73	0.12	213,238,258,261	0
2	SEP	C	338	10/11	0.74	0.14	209,224,261,294	0
1	SEP	A	338	10/11	0.90	0.12	161,177,223,236	0
2	SEP	D	338	10/11	0.93	0.13	171,190,205,216	0

### 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.

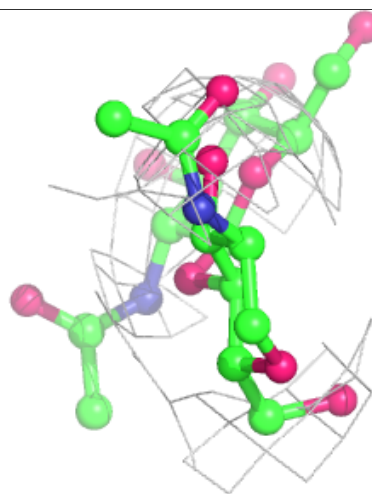
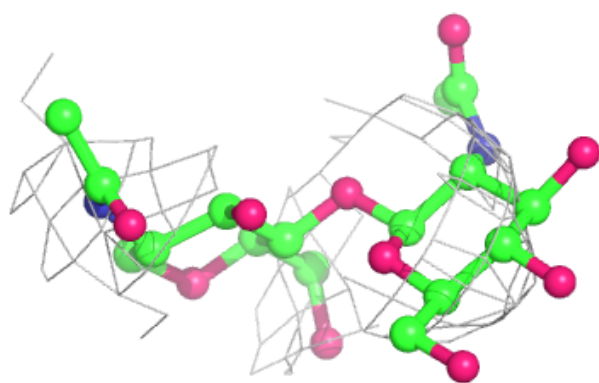
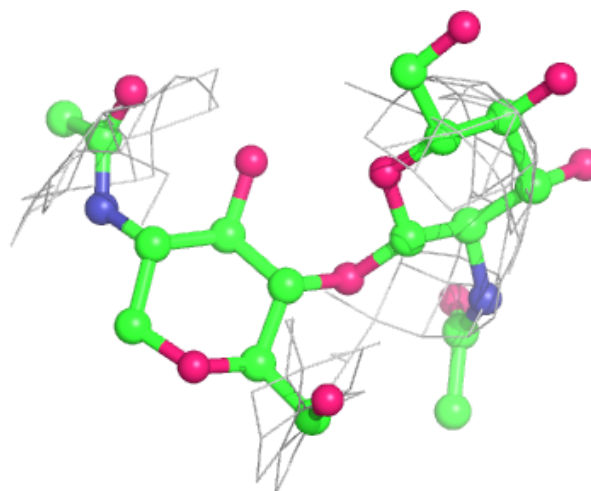
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	F	2	14/15	0.86	0.31	320,341,347,347	0
3	NAG	E	2	14/15	0.92	0.16	237,270,293,298	0
3	NAG	G	1	14/15	0.92	0.16	261,289,303,307	0
3	NAG	G	2	14/15	0.93	0.14	221,271,296,319	0
3	NAG	E	1	14/15	0.93	0.20	217,244,266,290	0
3	NAG	H	2	14/15	0.94	0.17	153,186,215,232	0
3	NAG	F	1	14/15	0.95	0.18	264,287,315,325	0
3	NAG	H	1	14/15	0.95	0.17	123,171,181,188	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 F:**

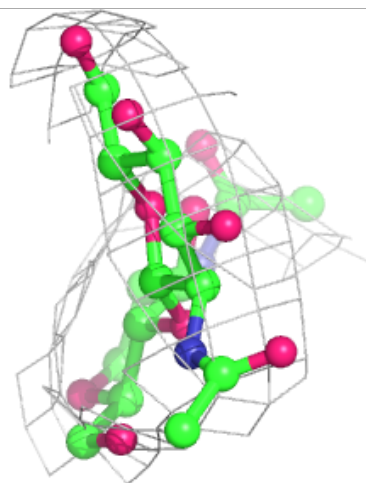
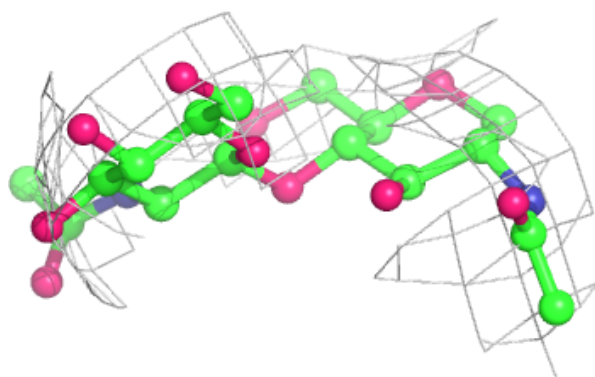
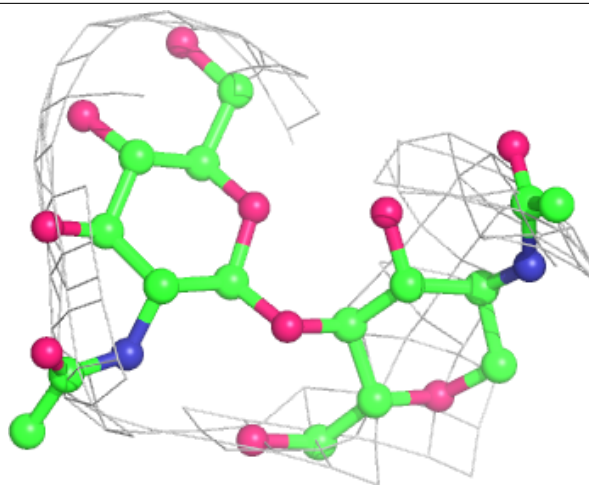
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

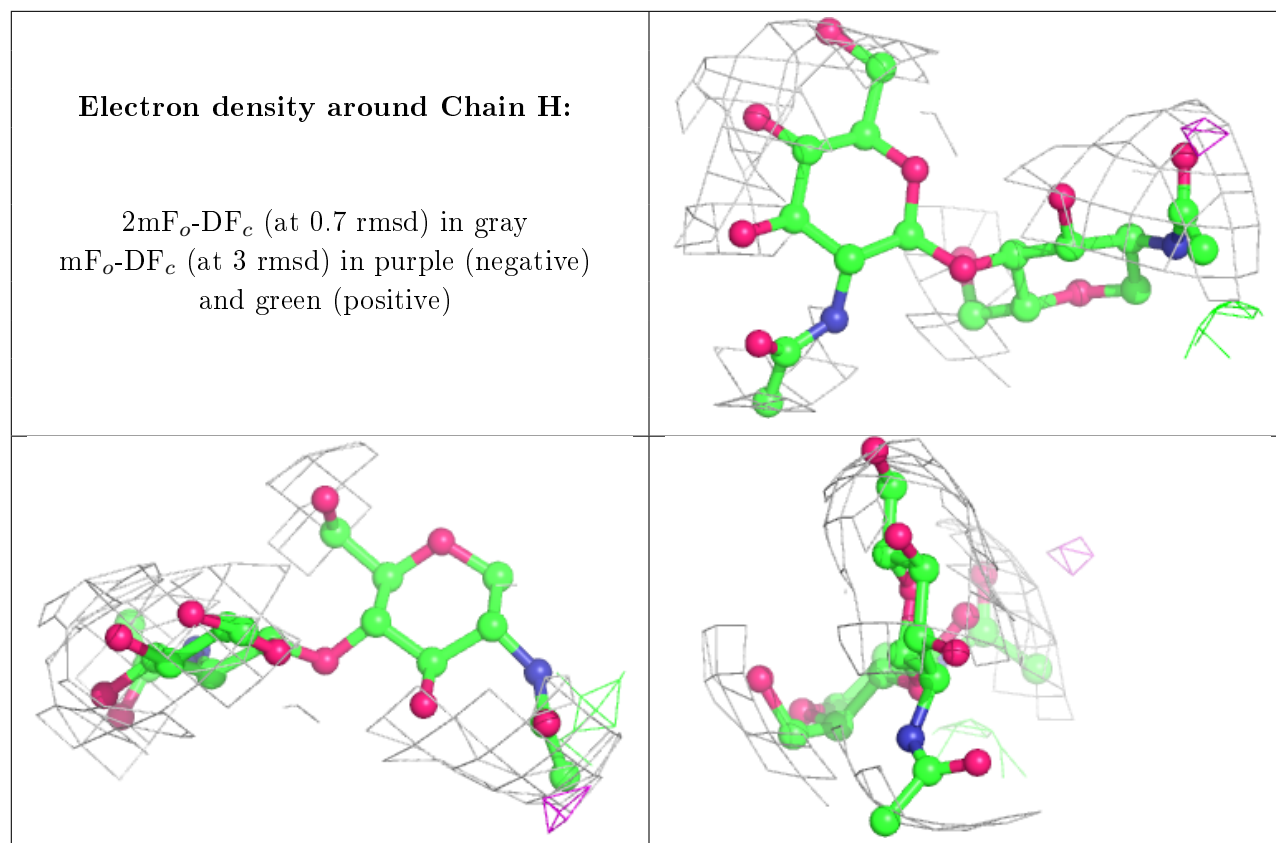




**Electron density around Chain G:**

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





## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.