



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:40 PM UTC

PDB ID : 8A16 / pdb_00008a16
Title : Human PTPRM domains FN3-4, in spacegroup P212121
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Deposited on : 2022-05-31
Resolution : 2.89 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 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

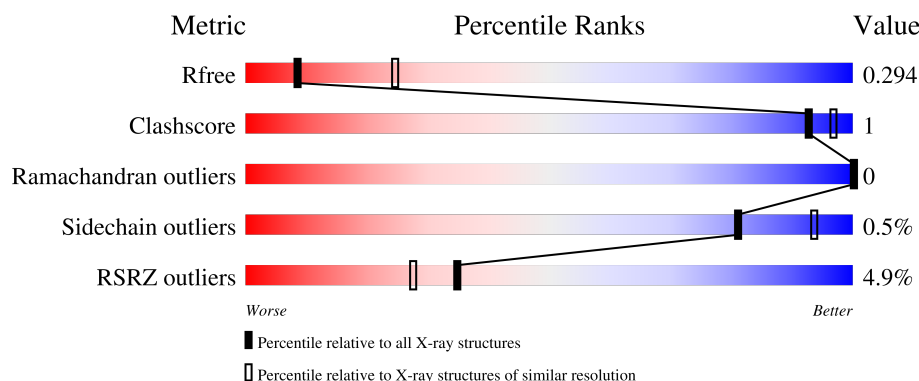
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.89 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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

Mol	Chain	Length	Quality of chain
1	A	258	4% 83% 5% 13%
1	B	258	5% 93% • 5%
2	C	4	100%
3	D	3	67% 33%
3	E	3	100%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3809 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.

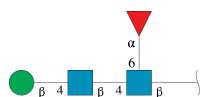
- Molecule 1 is a protein called Receptor-type tyrosine-protein phosphatase mu.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	0	0
			1763	1135	285	339	4			
1	B	244	Total	C	N	O	S	0	0	0
			1921	1234	316	367	4			

There are 24 discrepancies between the modelled and reference sequences:

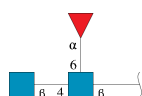
Chain	Residue	Modelled	Actual	Comment	Reference
A	475	GLU	-	cloning artifact	UNP P28827
A	476	THR	-	cloning artifact	UNP P28827
A	477	GLY	-	cloning artifact	UNP P28827
A	724	GLY	-	expression tag	UNP P28827
A	725	THR	-	expression tag	UNP P28827
A	726	LYS	-	expression tag	UNP P28827
A	727	HIS	-	expression tag	UNP P28827
A	728	HIS	-	expression tag	UNP P28827
A	729	HIS	-	expression tag	UNP P28827
A	730	HIS	-	expression tag	UNP P28827
A	731	HIS	-	expression tag	UNP P28827
A	732	HIS	-	expression tag	UNP P28827
B	475	GLU	-	cloning artifact	UNP P28827
B	476	THR	-	cloning artifact	UNP P28827
B	477	GLY	-	cloning artifact	UNP P28827
B	724	GLY	-	expression tag	UNP P28827
B	725	THR	-	expression tag	UNP P28827
B	726	LYS	-	expression tag	UNP P28827
B	727	HIS	-	expression tag	UNP P28827
B	728	HIS	-	expression tag	UNP P28827
B	729	HIS	-	expression tag	UNP P28827
B	730	HIS	-	expression tag	UNP P28827
B	731	HIS	-	expression tag	UNP P28827
B	732	HIS	-	expression tag	UNP P28827

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



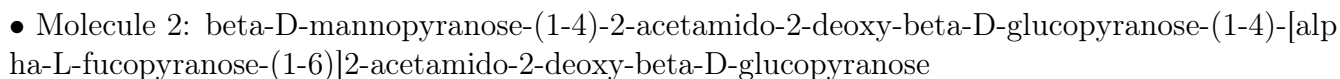
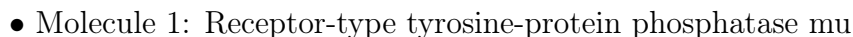
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	4	Total	C	N	O	0	0	0
			49	28	2	19			

- 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
3	D	3	Total	C	N	O	0	0	0
			38	22	2	14			
3	E	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 1: Receptor-type tyrosine-protein phosphatase mu



MAG1
MAG2
FUC3

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.68Å 89.64Å 128.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.48 – 2.89 73.48 – 2.89	Depositor EDS
% Data completeness (in resolution range)	99.5 (73.48-2.89) 89.5 (73.48-2.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.90 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487, PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.234 , 0.288 0.241 , 0.294	Depositor DCC
R_{free} test set	674 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	55.9	Xtriage
Anisotropy	0.384	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3809	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, FUC, NAG

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	0.16	0/1813	0.47	0/2473
1	B	0.16	0/1975	0.46	0/2694
All	All	0.16	0/3788	0.46	0/5167

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

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	1763	0	1700	8	0
1	B	1921	0	1872	3	0
2	C	49	0	43	0	0
3	D	38	0	34	0	0
3	E	38	0	34	0	0
All	All	3809	0	3683	11	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 1.

All (11) 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:598:ASN:OD1	1:A:605:THR:HB	1.95	0.66
1:B:510:TYR:HE2	1:B:569:LYS:HZ2	1.55	0.54
1:A:604:VAL:O	1:A:678:ILE:N	2.40	0.50
1:A:668:ASP:O	1:A:671:GLN:HG3	2.13	0.48
1:A:604:VAL:CG2	1:A:722:LYS:HD2	2.44	0.47
1:A:604:VAL:HG23	1:A:722:LYS:HD2	1.96	0.47
1:A:598:ASN:OD1	1:A:598:ASN:N	2.48	0.47
1:A:484:ALA:HB2	1:A:573:PRO:HG2	1.98	0.45
1:A:567:THR:HG22	1:A:568:ALA:N	2.33	0.43
1:B:510:TYR:HE2	1:B:569:LYS:NZ	2.17	0.42
1:B:597:LEU:HD11	1:B:607:MET:HE2	2.03	0.41

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	219/258 (85%)	216 (99%)	3 (1%)	0	100	100
1	B	242/258 (94%)	235 (97%)	7 (3%)	0	100	100
All	All	461/516 (89%)	451 (98%)	10 (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	192/223 (86%)	191 (100%)	1 (0%)	81	93
1	B	209/223 (94%)	208 (100%)	1 (0%)	81	93
All	All	401/446 (90%)	399 (100%)	2 (0%)	81	93

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

Mol	Chain	Res	Type
1	A	665	PHE
1	B	665	PHE

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	671	GLN
1	B	491	GLN
1	B	535	GLN
1	B	656	ASN
1	B	658	GLN
1	B	685	ASN
1	B	718	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

10 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	2,1	14,14,15	0.35	0	17,19,21	0.64	0
2	NAG	C	2	2	14,14,15	0.32	0	17,19,21	0.44	0
2	BMA	C	3	2	11,11,12	0.52	0	15,15,17	0.73	0
2	FUC	C	4	2	10,10,11	0.63	0	14,14,16	0.75	0
3	NAG	D	1	3,1	14,14,15	0.44	0	17,19,21	0.44	0
3	NAG	D	2	3	14,14,15	0.31	0	17,19,21	0.71	1 (5%)
3	FUC	D	3	3	10,10,11	0.81	0	14,14,16	0.68	0
3	NAG	E	1	3,1	14,14,15	0.24	0	17,19,21	0.45	0
3	NAG	E	2	3	14,14,15	0.20	0	17,19,21	0.64	0
3	FUC	E	3	3	10,10,11	0.68	0	14,14,16	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
2	NAG	C	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	FUC	C	4	2	-	-	0/1/1/1
3	NAG	D	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	1/6/23/26	0/1/1/1
3	FUC	D	3	3	-	-	0/1/1/1
3	NAG	E	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	FUC	E	3	3	-	-	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	2	NAG	C1-O5-C5	2.39	115.39	112.19

There are no chirality outliers.

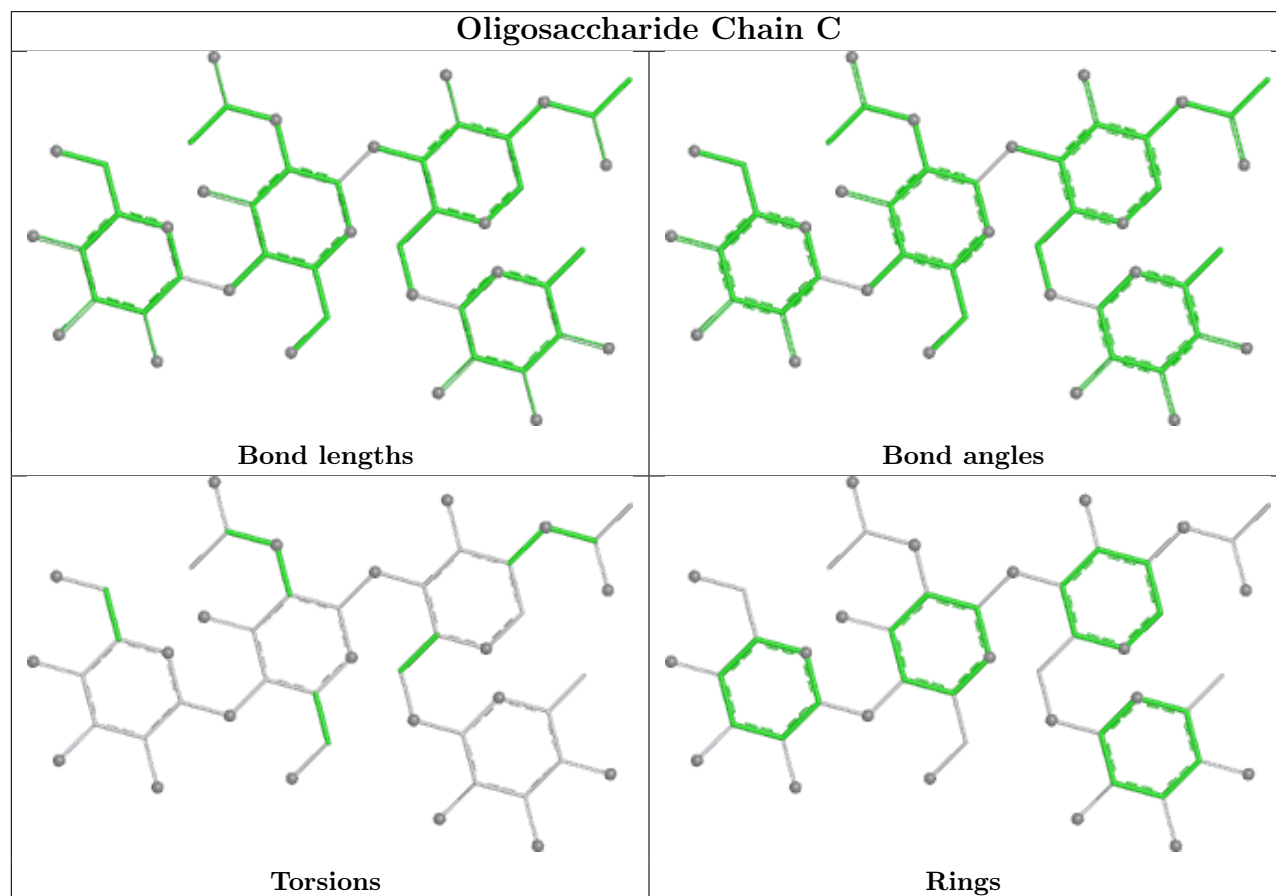
All (1) torsion outliers are listed below:

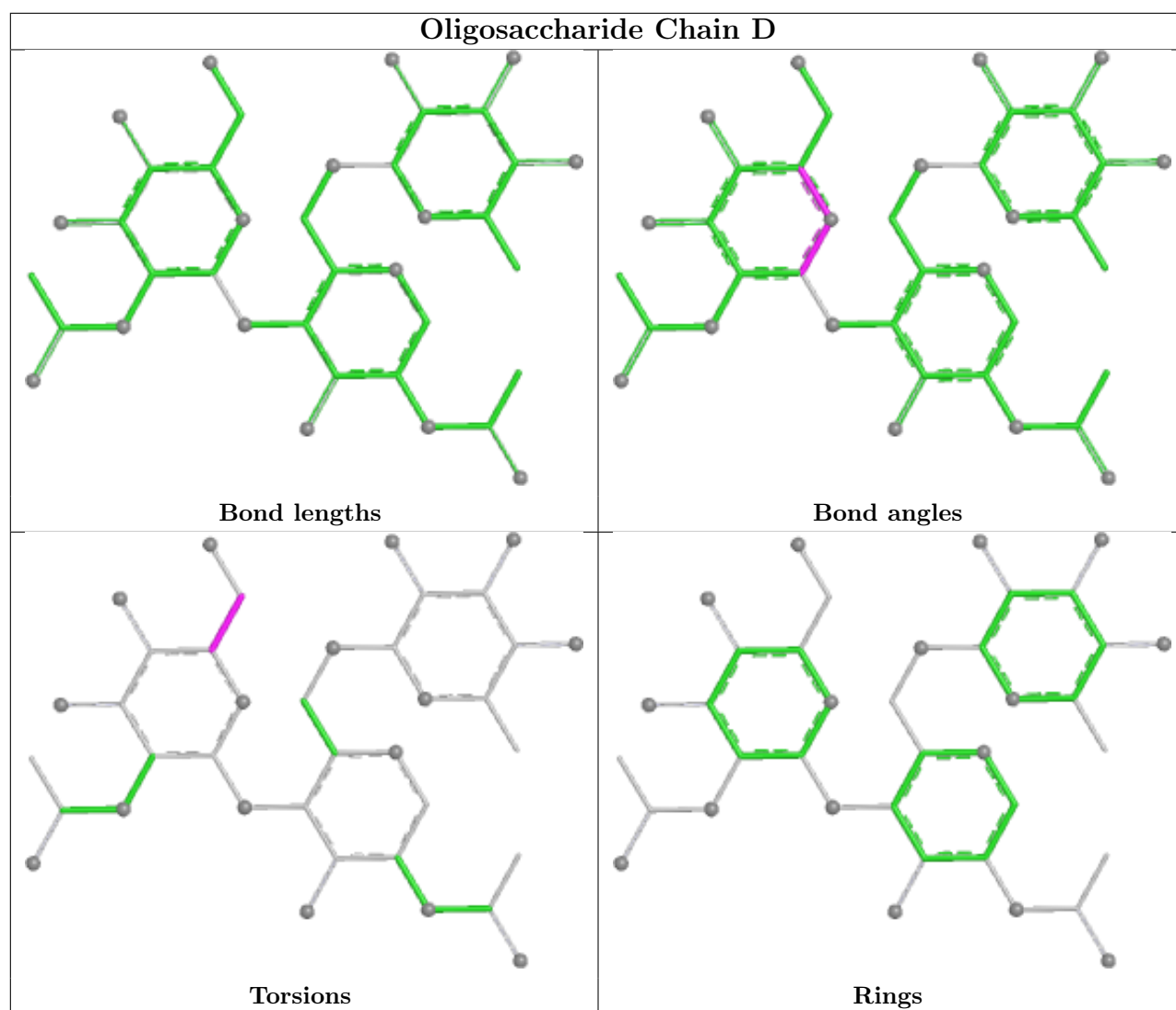
Mol	Chain	Res	Type	Atoms
3	D	2	NAG	C4-C5-C6-O6

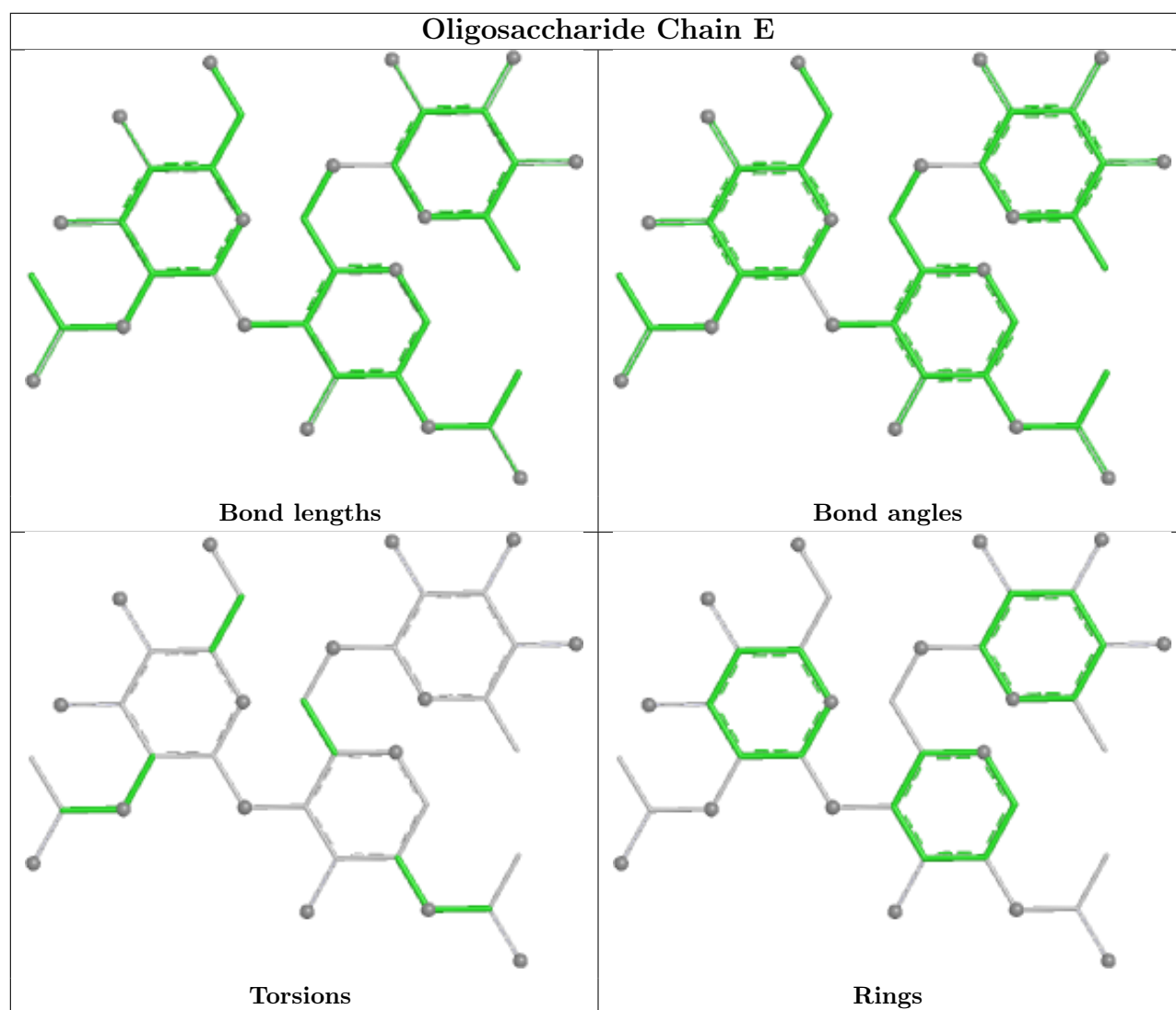
There are no ring outliers.

No monomer is involved in short contacts.

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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	225/258 (87%)	0.51	11 (4%) 35 27	52, 71, 102, 132	0
1	B	244/258 (94%)	0.59	12 (4%) 35 27	51, 74, 103, 143	0
All	All	469/516 (90%)	0.55	23 (4%) 35 27	51, 72, 103, 143	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	510	TYR	4.0
1	B	638	GLU	3.1
1	A	508	GLN	3.0
1	A	598	ASN	2.9
1	A	628	GLU	2.7
1	B	711	GLU	2.7
1	B	510	TYR	2.6
1	A	596	PRO	2.5
1	B	630	PRO	2.3
1	A	590	ALA	2.3
1	B	542	LEU	2.3
1	B	639	ILE	2.3
1	B	599	GLN	2.2
1	A	554	TYR	2.2
1	B	511	GLY	2.2
1	A	488	GLU	2.2
1	B	531	ASP	2.1
1	B	594	GLU	2.1
1	A	531	ASP	2.1
1	B	530	ILE	2.1
1	A	505	GLU	2.1
1	A	711	GLU	2.1
1	B	593	LEU	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 ⓘ

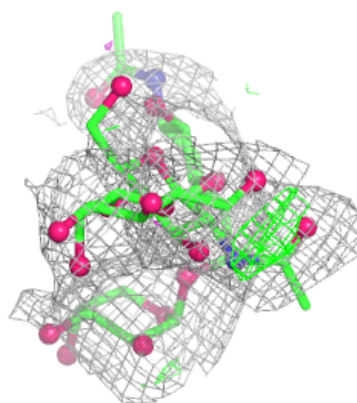
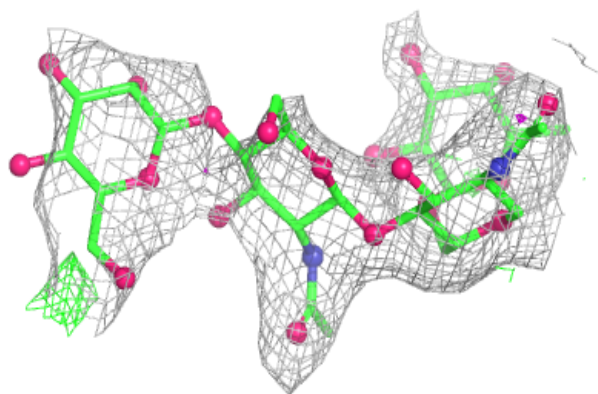
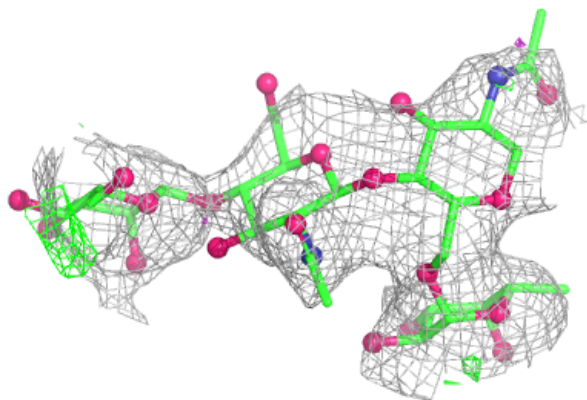
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BMA	C	3	11/12	0.12	0.17	93,109,115,117	0
3	FUC	D	3	10/11	0.57	0.17	93,99,104,104	0
2	FUC	C	4	10/11	0.69	0.17	78,95,97,99	0
2	NAG	C	2	14/15	0.72	0.15	66,96,110,114	0
3	NAG	E	2	14/15	0.73	0.13	85,97,105,105	0
3	NAG	D	2	14/15	0.76	0.13	87,103,110,112	0
3	FUC	E	3	10/11	0.78	0.14	95,105,112,118	0
3	NAG	D	1	14/15	0.82	0.14	81,88,100,103	0
2	NAG	C	1	14/15	0.87	0.14	70,80,92,93	0
3	NAG	E	1	14/15	0.88	0.10	76,84,93,94	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.

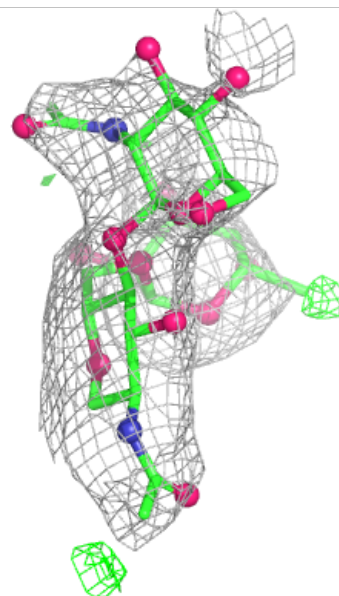
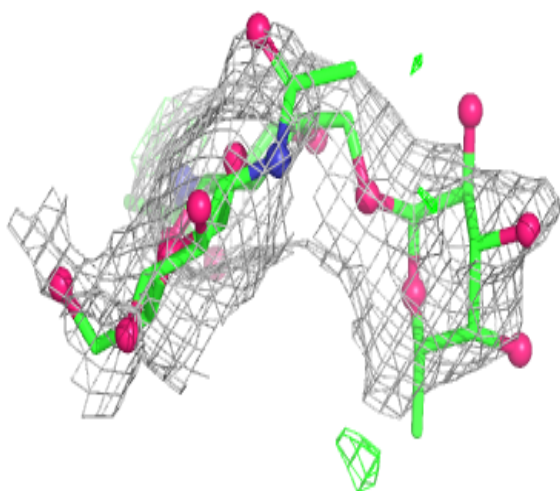
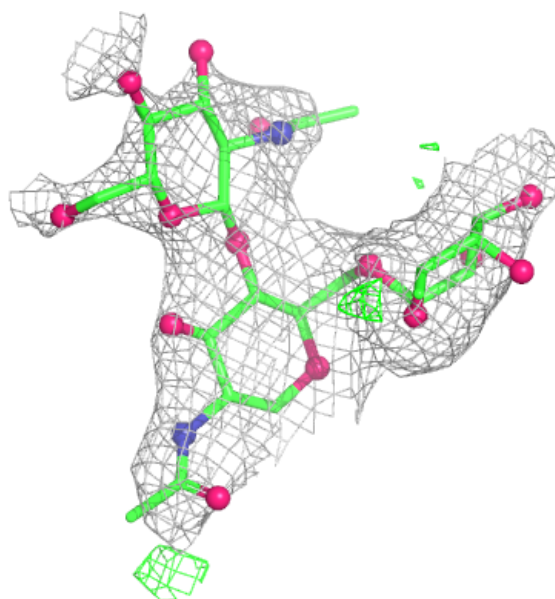
Electron density around Chain C:

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



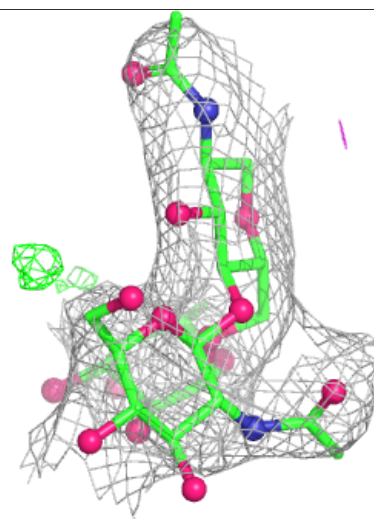
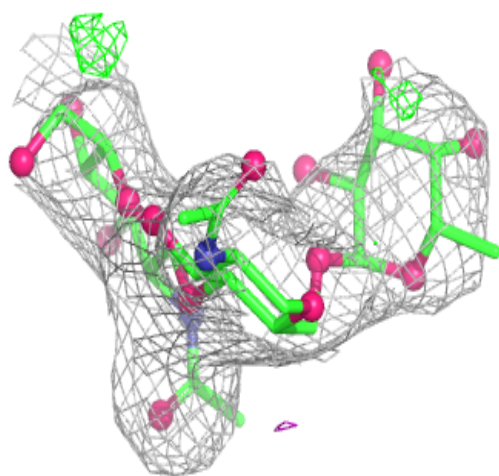
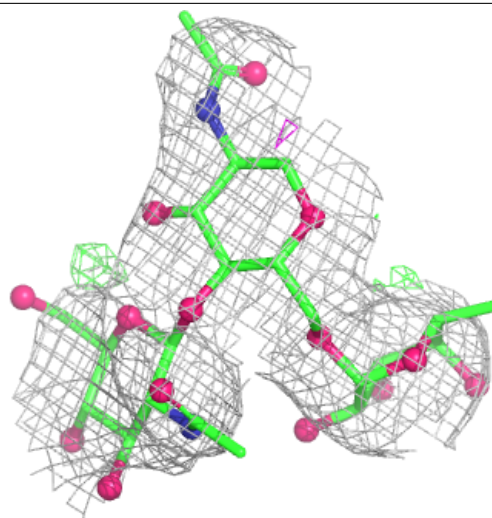
Electron density around Chain D:

$2mF_o-DF_c$ (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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.