



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 10, 2023 – 12:24 PM EDT

PDB ID : 6WNA
Title : Next generation monomeric IgG4 Fc
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Deposited on : 2020-04-22
Resolution : 2.40 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

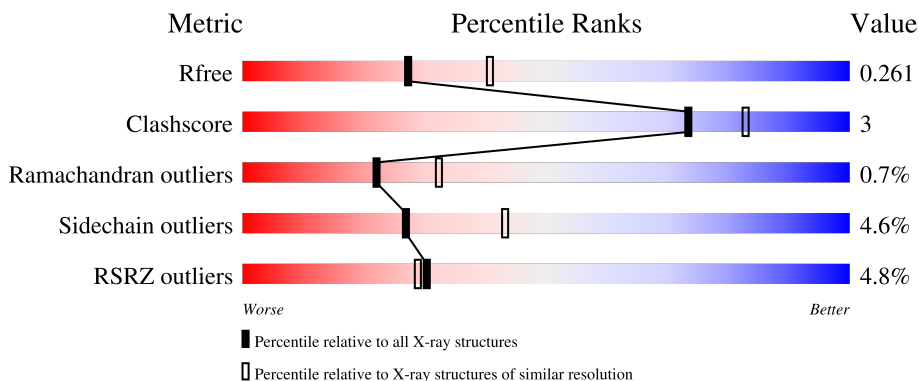
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	264	3% 85% 15%
2	B	99	3% 89% 11%
3	H	207	8% 87% 9% ..
4	C	9	100%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4728 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 IgG receptor FcRn large subunit p51.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	264	2080	1330	360	382	8	0	0	0

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	99	829	528	140	158	3	0	0	0

- Molecule 3 is a protein called Immunoglobulin heavy constant gamma 4.

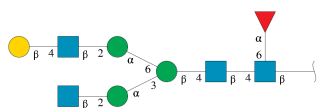
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	H	200	1621	1027	275	313	6	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	252	TYR	MET	engineered mutation	UNP P01861
H	254	THR	SER	engineered mutation	UNP P01861
H	256	GLU	THR	engineered mutation	UNP P01861
H	351	PHE	LEU	engineered mutation	UNP P01861
H	354	GLU	SER	engineered mutation	UNP P01861
H	366	ARG	THR	engineered mutation	UNP P01861
H	395	LYS	PRO	engineered mutation	UNP P01861
H	405	ARG	PHE	engineered mutation	UNP P01861
H	407	GLU	TYR	engineered mutation	UNP P01861

- Molecule 4 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-

-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	C	9	110	62	4	44	0	0	0

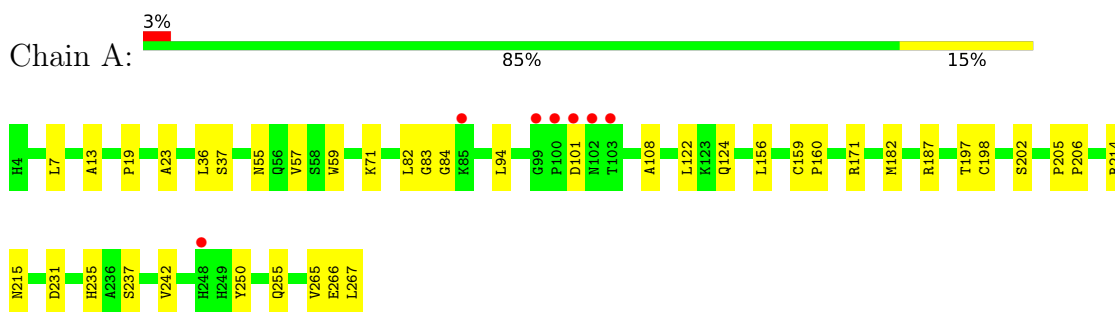
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	38	Total	O	0	0
			38	38		
5	B	21	Total	O	0	0
			21	21		
5	H	29	Total	O	0	0
			29	29		

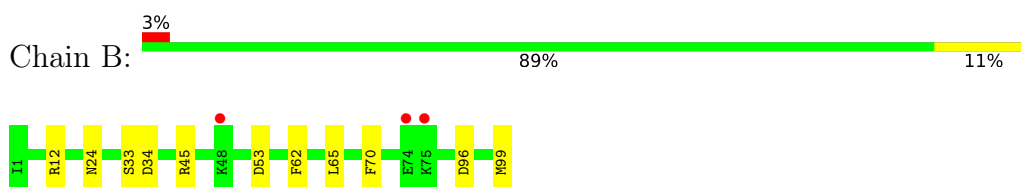
3 Residue-property plots [i](#)

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.

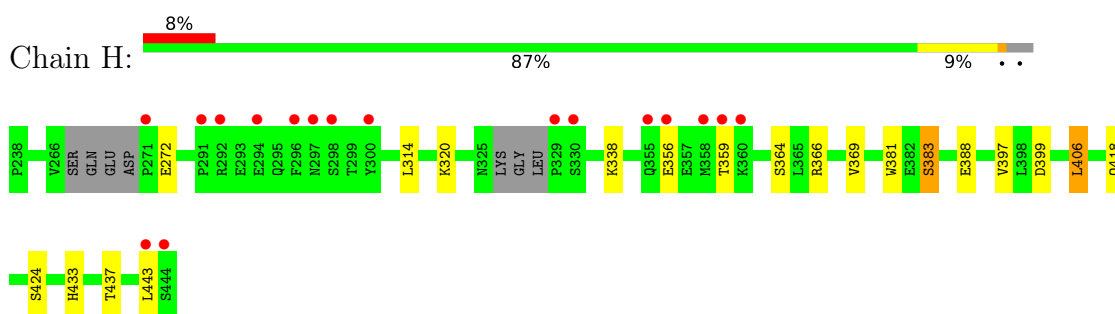
- Molecule 1: IgG receptor FcRn large subunit p51



- Molecule 2: Beta-2-microglobulin



- Molecule 3: Immunoglobulin heavy constant gamma 4



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



4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	68.09Å 122.10Å 179.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.00 – 2.40 36.15 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.3 (35.00-2.40) 99.3 (36.15-2.40)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.214 , 0.263 0.219 , 0.261	Depositor DCC
R_{free} test set	876 reflections (2.97%)	wwPDB-VP
Wilson B-factor (Å ²)	39.6	Xtrriage
Anisotropy	0.392	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 32.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.025 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.039 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4728	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.83% 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: GAL, NAG, MAN, BMA, FUC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.66	0/2146	0.80	0/2915
2	B	0.65	0/852	0.79	0/1152
3	H	0.65	0/1662	0.80	0/2254
All	All	0.66	0/4660	0.80	0/6321

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	2080	0	1990	21	0
2	B	829	0	794	6	0
3	H	1621	0	1576	7	0
4	C	110	0	92	0	0
5	A	38	0	0	0	0
5	B	21	0	0	0	0
5	H	29	0	0	0	0
All	All	4728	0	4452	30	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 3.

The worst 5 of 30 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:57:VAL:HG11	1:A:59:TRP:CE2	2.39	0.57
1:A:197:THR:HG21	2:B:99:MET:HG2	1.87	0.57
1:A:205:PRO:HB2	1:A:206:PRO:HD2	1.87	0.56
2:B:33:SER:HB3	2:B:62:PHE:CE2	2.40	0.56
3:H:314:LEU:HA	3:H:338:LYS:HE2	1.88	0.54

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	262/264 (99%)	249 (95%)	11 (4%)	2 (1%)	19	29
2	B	97/99 (98%)	93 (96%)	4 (4%)	0	100	100
3	H	194/207 (94%)	186 (96%)	6 (3%)	2 (1%)	15	23
All	All	553/570 (97%)	528 (96%)	21 (4%)	4 (1%)	22	32

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	83	GLY
1	A	55	ASN
3	H	356	GLU
3	H	359	THR

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	218/218 (100%)	209 (96%)	9 (4%)	30	48
2	B	94/94 (100%)	90 (96%)	4 (4%)	29	46
3	H	189/195 (97%)	179 (95%)	10 (5%)	22	37
All	All	501/507 (99%)	478 (95%)	23 (5%)	27	43

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	320	LYS
3	H	383	SER
3	H	366	ARG
3	H	397	VAL
1	A	202	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	215	ASN
3	H	433	HIS

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](#)

9 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	C	1	3,4	14,14,15	0.55	0	17,19,21	2.25	4 (23%)
4	NAG	C	2	4	14,14,15	0.43	0	17,19,21	1.09	1 (5%)
4	BMA	C	3	4	11,11,12	0.37	0	15,15,17	1.31	2 (13%)
4	MAN	C	4	4	11,11,12	0.47	0	15,15,17	1.68	1 (6%)
4	NAG	C	5	4	14,14,15	0.56	0	17,19,21	0.94	1 (5%)
4	GAL	C	6	4	11,11,12	0.65	0	15,15,17	1.38	2 (13%)
4	MAN	C	7	4	11,11,12	0.19	0	15,15,17	0.91	1 (6%)
4	NAG	C	8	4	14,14,15	0.53	0	17,19,21	0.97	1 (5%)
4	FUC	C	9	4	10,10,11	0.77	0	14,14,16	1.12	1 (7%)

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	C	1	3,4	-	2/6/23/26	0/1/1/1
4	NAG	C	2	4	-	0/6/23/26	0/1/1/1
4	BMA	C	3	4	-	0/2/19/22	0/1/1/1
4	MAN	C	4	4	-	0/2/19/22	0/1/1/1
4	NAG	C	5	4	-	0/6/23/26	0/1/1/1
4	GAL	C	6	4	-	2/2/19/22	0/1/1/1
4	MAN	C	7	4	-	1/2/19/22	0/1/1/1
4	NAG	C	8	4	-	1/6/23/26	0/1/1/1
4	FUC	C	9	4	-	-	0/1/1/1

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1	NAG	C1-O5-C5	5.54	119.69	112.19
4	C	4	MAN	C1-O5-C5	5.13	119.14	112.19
4	C	1	NAG	C4-C3-C2	-5.06	103.60	111.02
4	C	1	NAG	O5-C1-C2	-3.15	106.31	111.29
4	C	6	GAL	O5-C5-C6	3.13	112.11	107.20

There are no chirality outliers.

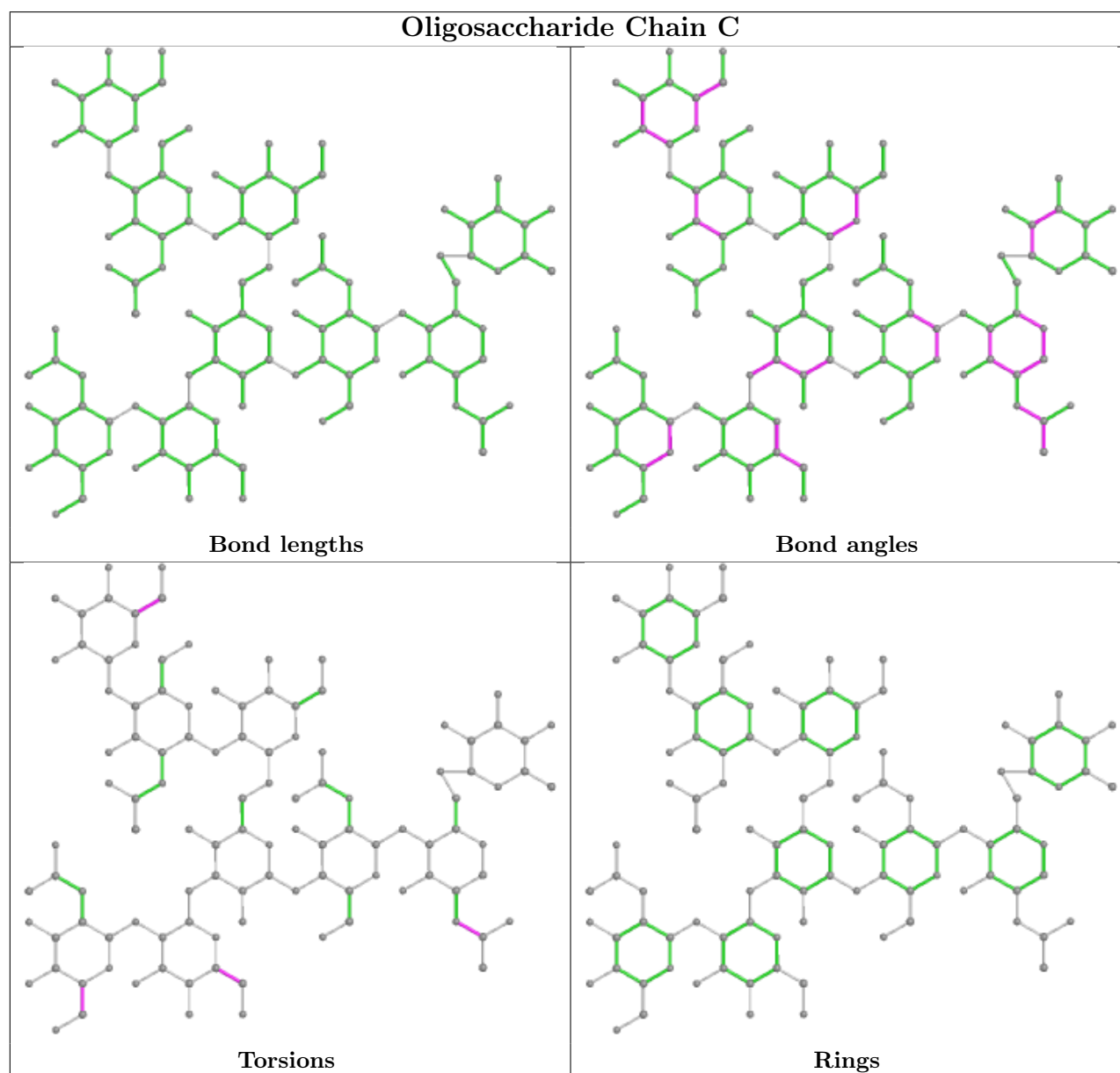
5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	6	GAL	O5-C5-C6-O6
4	C	6	GAL	C4-C5-C6-O6
4	C	1	NAG	C8-C7-N2-C2
4	C	1	NAG	O7-C7-N2-C2
4	C	8	NAG	O5-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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	264/264 (100%)	0.01	7 (2%) 54 52	23, 38, 76, 125	0
2	B	99/99 (100%)	-0.05	3 (3%) 50 49	25, 44, 79, 97	0
3	H	200/207 (96%)	0.20	17 (8%) 10 10	23, 50, 101, 117	0
All	All	563/570 (98%)	0.07	27 (4%) 30 29	23, 43, 90, 125	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	296	PHE	5.5
1	A	102	ASN	5.0
3	H	330	SER	4.7
3	H	300	TYR	4.2
1	A	248	HIS	3.9

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

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

6.3 Carbohydrates [i](#)

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

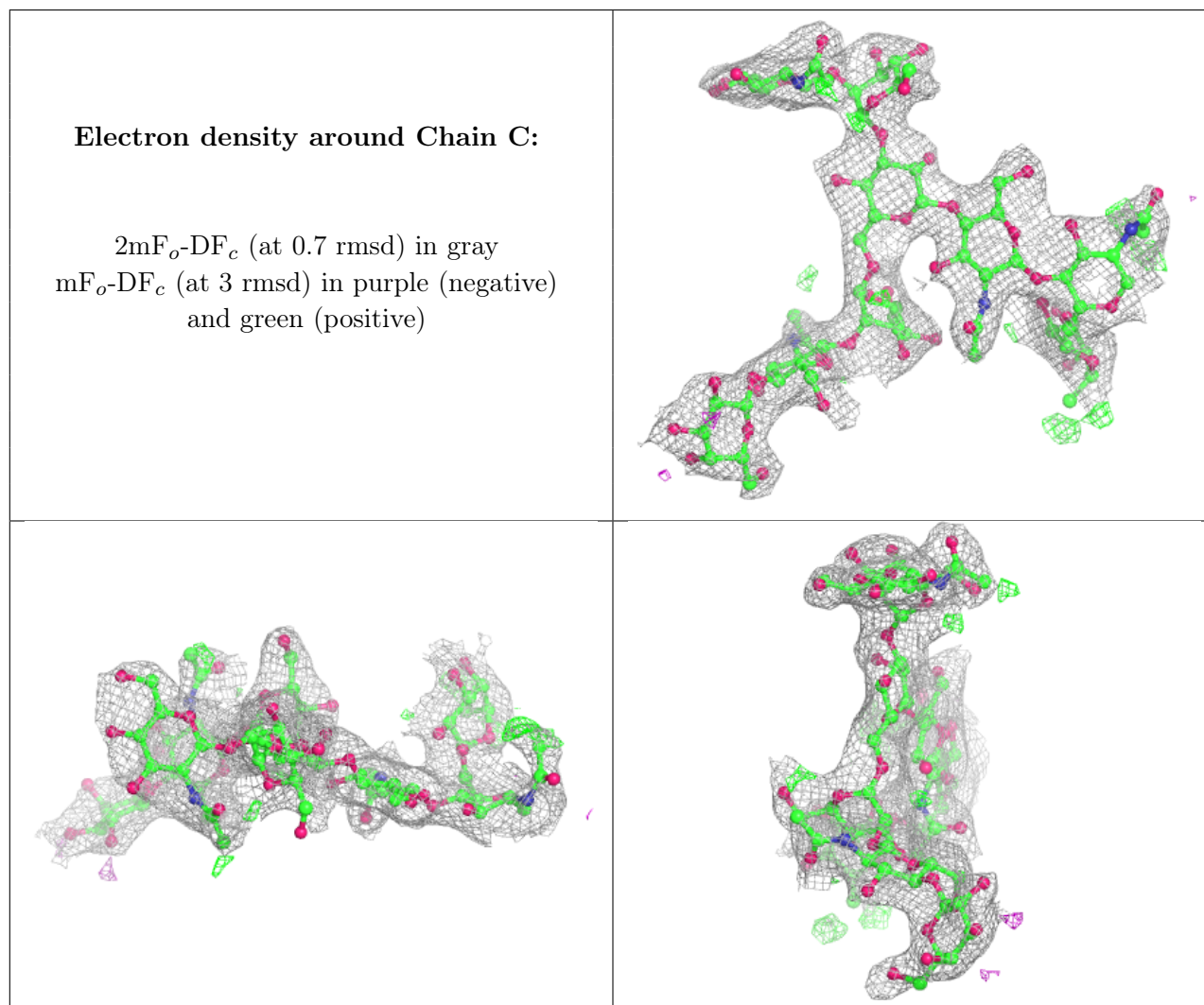
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	C	1	14/15	0.70	0.24	85,96,107,113	0
4	BMA	C	3	11/12	0.79	0.13	77,82,86,90	0
4	FUC	C	9	10/11	0.80	0.29	105,112,113,114	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	NAG	C	8	14/15	0.83	0.15	81,95,100,100	0
4	MAN	C	4	11/12	0.88	0.15	63,76,79,79	0
4	GAL	C	6	11/12	0.88	0.21	62,69,71,71	0
4	NAG	C	5	14/15	0.91	0.14	63,67,72,74	0
4	MAN	C	7	11/12	0.91	0.18	93,94,96,97	0
4	NAG	C	2	14/15	0.94	0.21	66,74,81,83	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.



6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.