



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 21, 2020 – 07:15 AM BST

PDB ID : 5K65
Title : Crystal structure of VEGF binding IgG1-Fc (Fcab CT6)
Authors : Humm, A.; Lobner, E.; Kitzmuller, M.; Mlynek, G.; Obinger, C.; Djjinovic-Carugo, K.
Deposited on : 2016-05-24
Resolution : 2.50 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 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

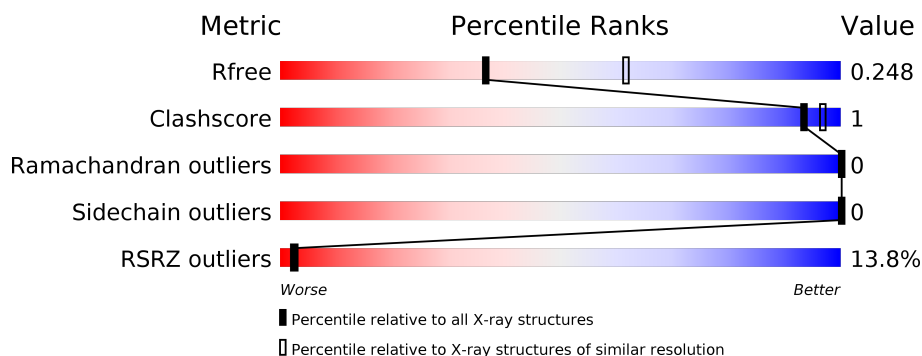
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 ≥ 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	228	<div> <div>5%</div> <div>92%</div> <div>6%</div> </div>
1	B	228	<div> <div>21%</div> <div>89%</div> <div>7%</div> </div>
2	C	7	<div> <div>71%</div> <div>29%</div> </div>
3	D	5	<div> <div>40%</div> <div>40%</div> <div>20%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7195 atoms, of which 3499 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 Ig gamma-1 chain C region.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	215	Total	C	H	N	O	S	0	0	0
			3435	1124	1693	288	323	7			
1	B	212	Total	C	H	N	O	S	0	0	0
			3408	1115	1681	285	320	7			

There are 50 discrepancies between the modelled and reference sequences:

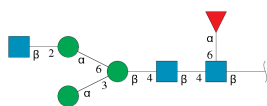
Chain	Residue	Modelled	Actual	Comment	Reference
A	359	ARG	THR	engineered mutation	UNP P01857
A	360	PHE	LYS	engineered mutation	UNP P01857
A	361	TYR	ASN	engineered mutation	UNP P01857
A	388	ASP	GLU	engineered mutation	UNP P01857
A	389	ILE	ASN	engineered mutation	UNP P01857
A	389A	PHE	-	insertion	UNP P01857
A	389B	PRO	-	insertion	UNP P01857
A	389C	ASN	-	insertion	UNP P01857
A	389D	GLY	-	insertion	UNP P01857
A	389E	LEU	-	insertion	UNP P01857
A	413	PRO	ASP	engineered mutation	UNP P01857
A	414	TYR	LYS	engineered mutation	UNP P01857
A	415	PRO	SER	engineered mutation	UNP P01857
A	416	SER	ARG	engineered mutation	UNP P01857
A	418	LEU	GLN	engineered mutation	UNP P01857
A	419	MET	GLN	engineered mutation	UNP P01857
A	421	THR	ASN	engineered mutation	UNP P01857
A	422	ARG	VAL	engineered mutation	UNP P01857
A	440	HIS	SER	engineered mutation	UNP P01857
A	442	GLU	SER	engineered mutation	UNP P01857
A	443	TYR	LEU	engineered mutation	UNP P01857
A	444	GLN	SER	engineered mutation	UNP P01857
A	445	TRP	PRO	engineered mutation	UNP P01857
A	446	PRO	GLY	engineered mutation	UNP P01857
A	447	THR	LYS	engineered mutation	UNP P01857

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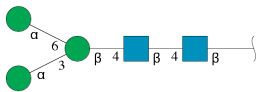
Chain	Residue	Modelled	Actual	Comment	Reference
B	359	ARG	THR	engineered mutation	UNP P01857
B	360	PHE	LYS	engineered mutation	UNP P01857
B	361	TYR	ASN	engineered mutation	UNP P01857
B	388	ASP	-	engineered mutation	UNP P01857
B	389	ILE	-	engineered mutation	UNP P01857
B	389A	PHE	-	insertion	UNP P01857
B	389B	PRO	-	insertion	UNP P01857
B	389C	ASN	-	insertion	UNP P01857
B	389D	GLY	GLU	insertion	UNP P01857
B	389E	LEU	ASN	insertion	UNP P01857
B	413	PRO	ASP	engineered mutation	UNP P01857
B	414	TYR	LYS	engineered mutation	UNP P01857
B	415	PRO	SER	engineered mutation	UNP P01857
B	416	SER	ARG	engineered mutation	UNP P01857
B	418	LEU	GLN	engineered mutation	UNP P01857
B	419	MET	GLN	engineered mutation	UNP P01857
B	421	THR	ASN	engineered mutation	UNP P01857
B	422	ARG	VAL	engineered mutation	UNP P01857
B	440	HIS	SER	engineered mutation	UNP P01857
B	442	GLU	SER	engineered mutation	UNP P01857
B	443	TYR	LEU	engineered mutation	UNP P01857
B	444	GLN	SER	engineered mutation	UNP P01857
B	445	TRP	PRO	engineered mutation	UNP P01857
B	446	PRO	GLY	engineered mutation	UNP P01857
B	447	THR	LYS	engineered mutation	UNP P01857

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[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
2	C	7	Total	C	H	N	O	0	0	0
			158	48	73	3	34			

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	5	Total	C	H	N	O	0	0	0
			113	34	52	2	25			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	39	Total	O	0	0
			39	39		
4	B	42	Total	O	0	0
			42	42		

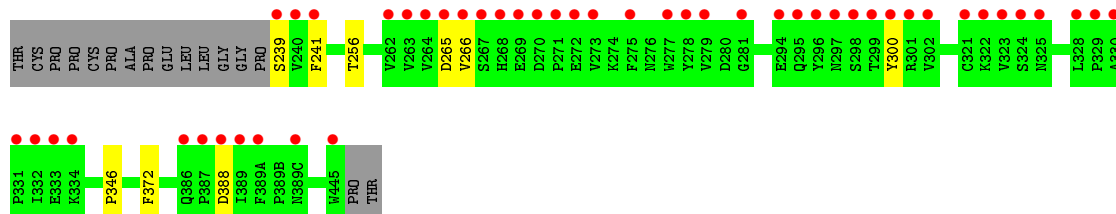
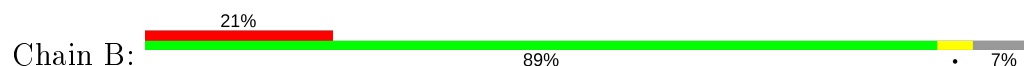
3 Residue-property plots [i](#)

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.

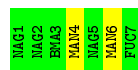
- Molecule 1: Ig gamma-1 chain C region



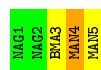
- Molecule 1: Ig gamma-1 chain C region



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	58.49 Å 72.00 Å 168.30 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.03 – 2.50 48.03 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.0 (48.03-2.50) 97.1 (48.03-2.50)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 2.51 Å)	Xtriage
Refinement program	PHENIX 1.10-2247	Depositor
R, R_{free}	0.221 , 0.246 0.222 , 0.248	Depositor DCC
R_{free} test set	1970 reflections (8.00%)	wwPDB-VP
Wilson B-factor (Å ²)	65.3	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 48.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7195	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0/1799	0.44	0/2456
1	B	0.25	0/1783	0.44	0/2434
All	All	0.26	0/3582	0.44	0/4890

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	1742	1693	1693	4	0
1	B	1727	1681	1681	6	0
2	C	85	73	73	0	0
3	D	61	52	52	1	0
4	A	39	0	0	3	0
4	B	42	0	0	1	0
All	All	3696	3499	3499	10	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.

The worst 5 of 10 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:239:SER:N	1:B:265:ASP:OD2	2.13	0.80
1:A:430:GLU:OE1	4:A:601:HOH:O	2.03	0.76
1:A:289:THR:OG1	4:A:602:HOH:O	2.06	0.74
1:A:272:GLU:O	1:A:325:ASN:ND2	2.27	0.67
1:B:256:THR:OG1	4:B:601:HOH:O	2.16	0.59

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	213/228 (93%)	211 (99%)	2 (1%)	0	100	100
1	B	210/228 (92%)	209 (100%)	1 (0%)	0	100	100
All	All	423/456 (93%)	420 (99%)	3 (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	199/211 (94%)	199 (100%)	0	100	100
1	B	198/211 (94%)	198 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	397/422 (94%)	397 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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	$\# Z > 2$
2	NAG	C	1	1,2	14,14,15	0.25	0	17,19,21	0.56	0
2	NAG	C	2	2	14,14,15	0.41	0	17,19,21	0.39	0
2	BMA	C	3	2	11,11,12	0.75	0	15,15,17	0.90	0
2	MAN	C	4	2	11,11,12	0.62	0	15,15,17	0.93	1 (6%)
2	NAG	C	5	2	14,14,15	0.29	0	17,19,21	0.45	0
2	MAN	C	6	2	11,11,12	1.16	1 (9%)	15,15,17	0.88	1 (6%)
2	FUC	C	7	2	10,10,11	0.78	0	14,14,16	0.86	0
3	NAG	D	1	3	14,14,15	0.33	0	17,19,21	0.51	0
3	NAG	D	2	3	14,14,15	0.26	0	17,19,21	0.41	0
3	BMA	D	3	3	11,11,12	0.78	0	15,15,17	0.85	1 (6%)
3	MAN	D	4	3	11,11,12	0.70	0	15,15,17	1.14	2 (13%)
3	MAN	D	5	3	11,11,12	0.89	1 (9%)	15,15,17	1.05	2 (13%)

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	-	4/6/23/26	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	MAN	C	4	2	-	2/2/19/22	0/1/1/1
2	NAG	C	5	2	-	2/6/23/26	0/1/1/1
2	MAN	C	6	2	-	2/2/19/22	0/1/1/1
2	FUC	C	7	2	-	-	0/1/1/1
3	NAG	D	1	3	-	3/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	BMA	D	3	3	-	2/2/19/22	0/1/1/1
3	MAN	D	4	3	-	0/2/19/22	0/1/1/1
3	MAN	D	5	3	-	1/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	6	MAN	O5-C1	-3.09	1.38	1.43
3	D	5	MAN	C1-C2	2.46	1.57	1.52

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	4	MAN	C1-O5-C5	3.33	116.70	112.19
3	D	5	MAN	C1-O5-C5	2.54	115.64	112.19
2	C	6	MAN	O2-C2-C3	-2.27	105.60	110.14
3	D	4	MAN	O2-C2-C3	-2.22	105.70	110.14
3	D	5	MAN	O2-C2-C3	-2.19	105.75	110.14

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	6	MAN	O5-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6
2	C	5	NAG	O5-C5-C6-O6
3	D	3	BMA	C4-C5-C6-O6

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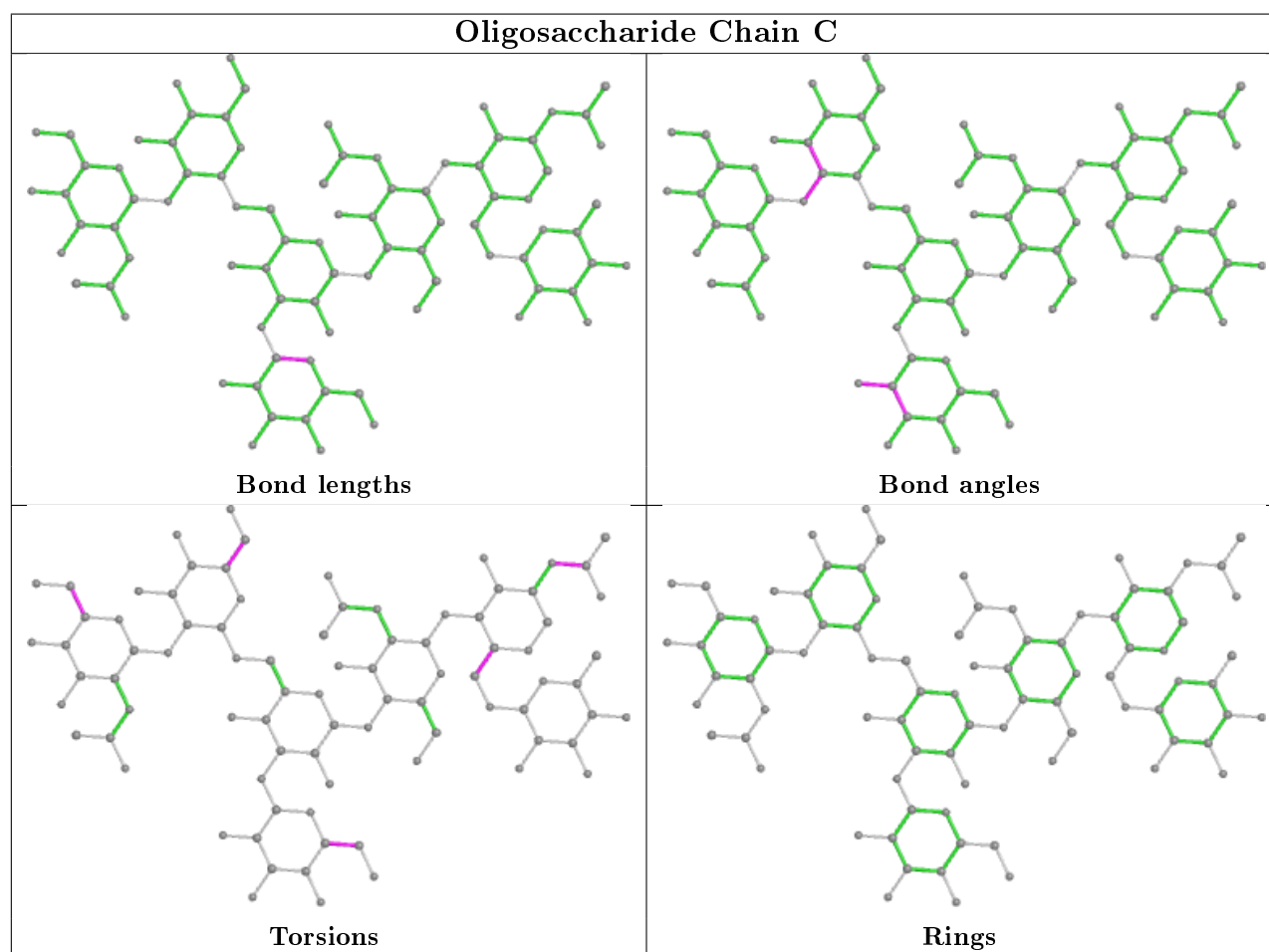
Mol	Chain	Res	Type	Atoms
3	D	3	BMA	O5-C5-C6-O6

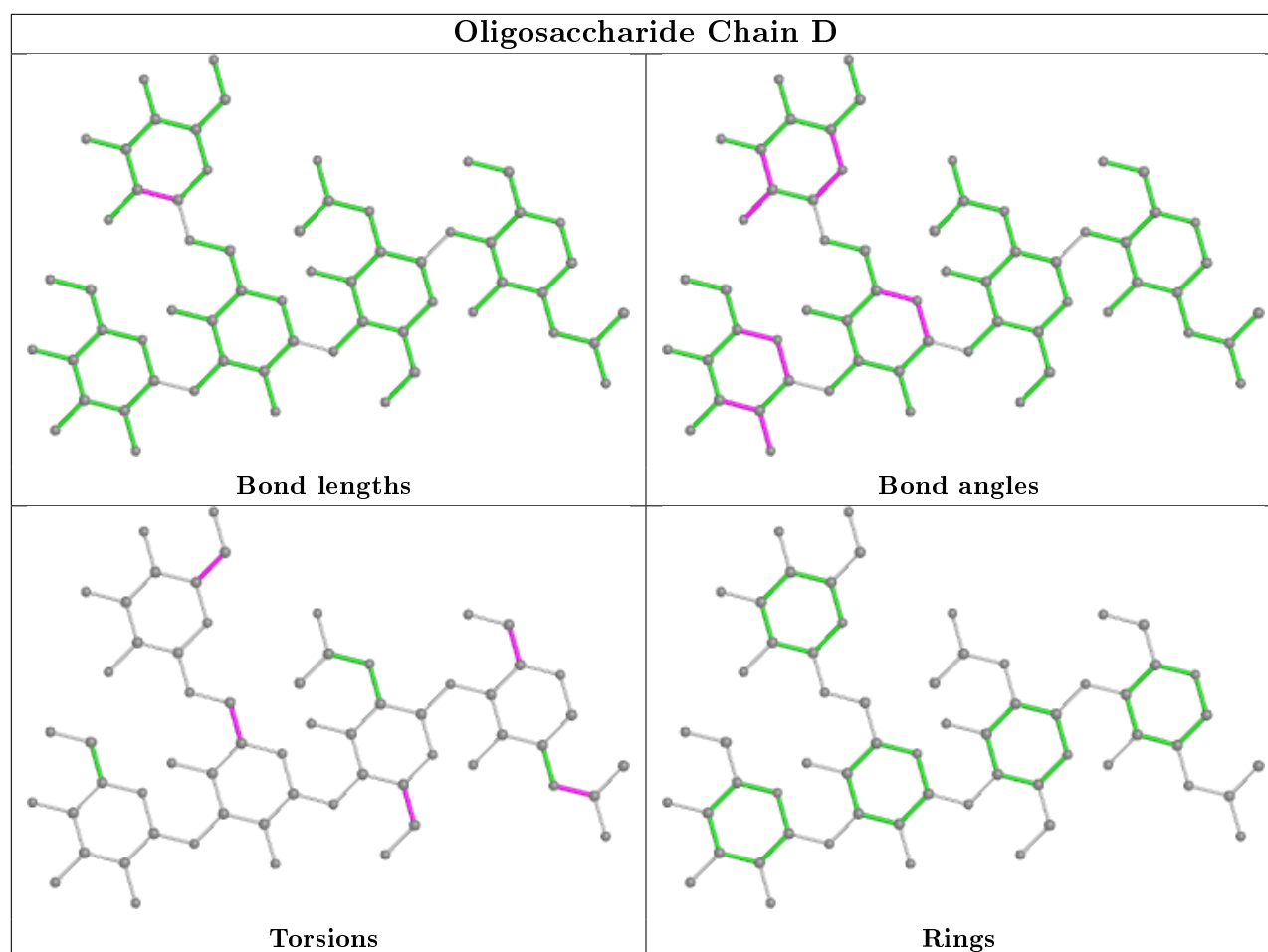
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	4	MAN	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](#)

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	215/228 (94%)	0.84	11 (5%) 28 29	44, 72, 113, 159	0
1	B	212/228 (92%)	1.50	48 (22%) 0 0	44, 77, 160, 301	0
All	All	427/456 (93%)	1.17	59 (13%) 2 2	44, 74, 149, 301	0

The worst 5 of 59 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	388	ASP	9.5
1	B	330	ALA	6.7
1	B	329	PRO	6.3
1	B	323	VAL	6.2
1	B	331	PRO	6.0

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, 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.

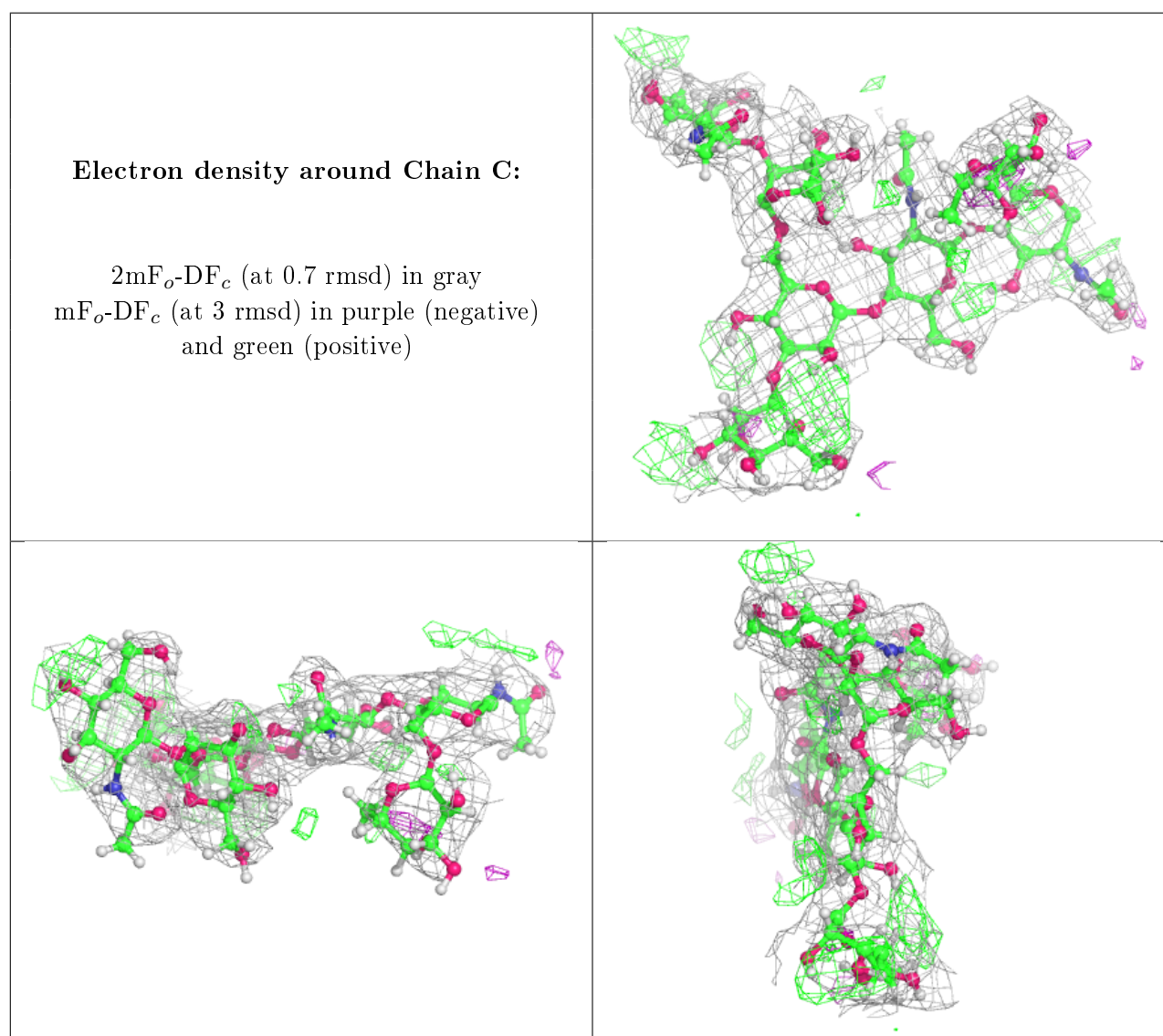
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MAN	D	4	11/12	0.54	0.21	117,119,142,143	0
3	MAN	D	5	11/12	0.62	0.23	106,108,128,129	0
3	NAG	D	1	14/15	0.72	0.24	116,119,143,144	0
2	MAN	C	6	11/12	0.77	0.18	87,90,108,109	0
3	BMA	D	3	11/12	0.78	0.11	110,117,141,141	0

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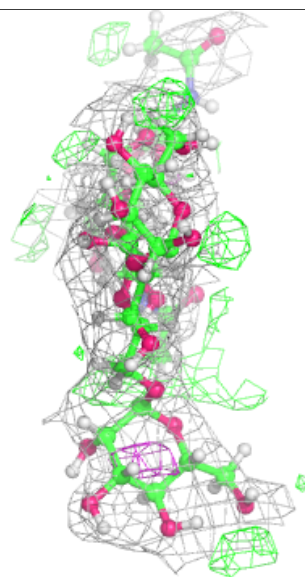
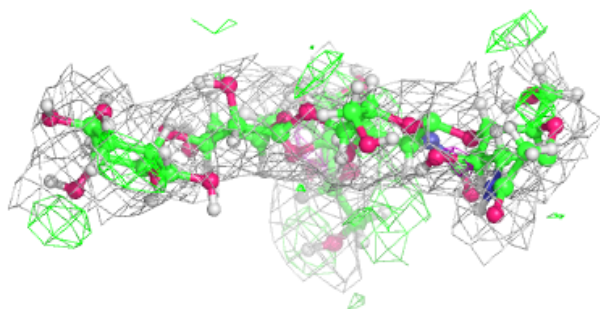
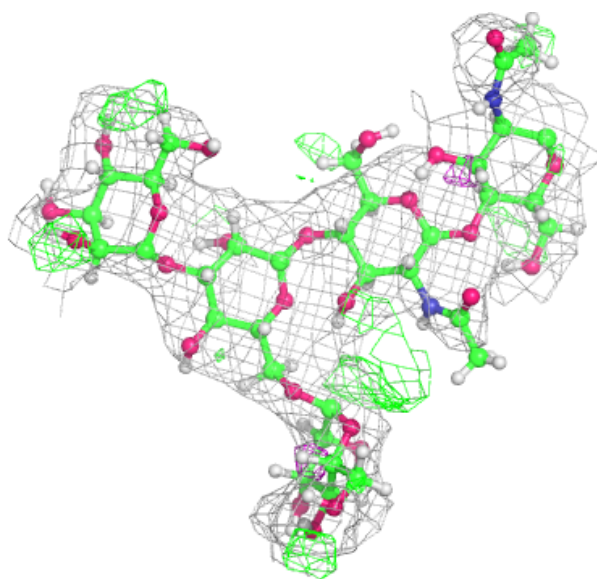
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	FUC	C	7	10/11	0.84	0.27	86,95,112,114	0
3	NAG	D	2	14/15	0.87	0.24	111,119,143,143	0
2	BMA	C	3	11/12	0.91	0.14	79,82,97,98	0
2	MAN	C	4	11/12	0.92	0.14	80,85,102,102	0
2	NAG	C	5	14/15	0.93	0.19	75,79,97,97	0
2	NAG	C	1	14/15	0.94	0.14	62,72,85,90	0
2	NAG	C	2	14/15	0.95	0.12	72,76,90,92	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 D:

$2mF_o-DF_c$ (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.