Full wwPDB X-ray Structure Validation Report ⓘ

Jan 2, 2024 – 06:24 pm GMT

PDB ID	:	5JIK
Title	:	Crystal structure of HER2 binding IgG1-Fc (Fcab H10-03-6)
Authors	:	Humm, A.; Lobner, E.; Mlynek, G.; Obinger, C.; Djinovic-Carugo, K.
Deposited on	:	2016-04-22
Resolution	:	1.82 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:

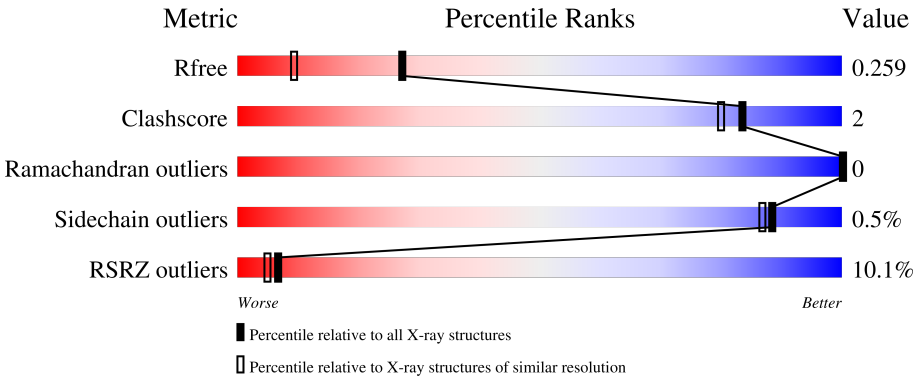
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.82 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	7484 (1.84-1.80)
Clashscore	141614	8401 (1.84-1.80)
Ramachandran outliers	138981	8290 (1.84-1.80)
Sidechain outliers	138945	8290 (1.84-1.80)
RSRZ outliers	127900	7371 (1.84-1.80)

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 <=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	227	2%, 84%, ·, 11%
1	B	227	16%, 84%, 6%, 10%
2	C	6	33%, 50%, 17%
3	D	5	40%, 60%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6754 atoms, of which 3272 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	201	Total	C	H	N	O	S	71	1	0
			3186	1032	1575	265	308	6			
1	B	204	Total	C	H	N	O	S	180	0	0
			3210	1041	1581	271	311	6			

There are 30 discrepancies between the modelled and reference sequences:

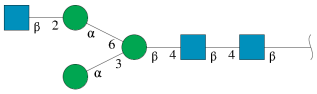
Chain	Residue	Modelled	Actual	Comment	Reference
A	358	TYR	LEU	engineered mutation	UNP P01857
A	359	LEU	THR	engineered mutation	UNP P01857
A	360	TYR	LYS	engineered mutation	UNP P01857
A	361	GLY	ASN	engineered mutation	UNP P01857
A	362	ASP	GLN	engineered mutation	UNP P01857
A	413	PRO	ASP	engineered mutation	UNP P01857
A	414	ARG	LYS	engineered mutation	UNP P01857
A	415	HIS	SER	engineered mutation	UNP P01857
A	415A	SER	-	insertion	UNP P01857
A	415B	ALA	-	insertion	UNP P01857
A	415C	ARG	-	insertion	UNP P01857
A	415D	MET	-	insertion	UNP P01857
A	415E	TRP	-	insertion	UNP P01857
A	418	ALA	GLN	engineered mutation	UNP P01857
A	419	HIS	GLN	engineered mutation	UNP P01857
B	358	TYR	LEU	engineered mutation	UNP P01857
B	359	LEU	THR	engineered mutation	UNP P01857
B	360	TYR	LYS	engineered mutation	UNP P01857
B	361	GLY	ASN	engineered mutation	UNP P01857
B	362	ASP	GLN	engineered mutation	UNP P01857
B	413	PRO	ASP	engineered mutation	UNP P01857
B	414	ARG	LYS	engineered mutation	UNP P01857
B	415	HIS	SER	engineered mutation	UNP P01857
B	415A	SER	-	insertion	UNP P01857
B	415B	ALA	-	insertion	UNP P01857

Continued on next page...

Continued from previous page...

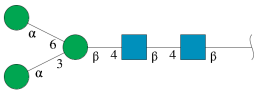
Chain	Residue	Modelled	Actual	Comment	Reference
B	415C	ARG	-	insertion	UNP P01857
B	415D	MET	-	insertion	UNP P01857
B	415E	TRP	-	insertion	UNP P01857
B	418	ALA	GLN	engineered mutation	UNP P01857
B	419	HIS	GLN	engineered mutation	UNP P01857

- 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)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	6	Total	C	H	N	O	0	0	0
			139	42	64	3	30			

- 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	4	0	0
			113	34	52	2	25			

- Molecule 4 is water.

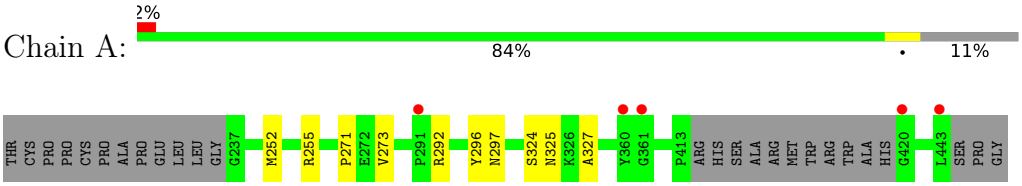
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	62	Total	O	0	0
			62	62		
4	B	44	Total	O	0	0
			44	44		

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.

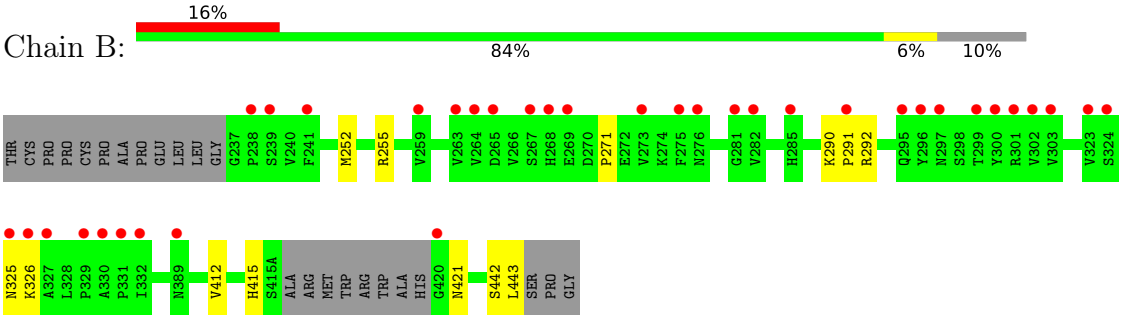
• Molecule 1: Ig gamma-1 chain C region

Chain A:



• Molecule 1: Ig gamma-1 chain C region

Chain B:

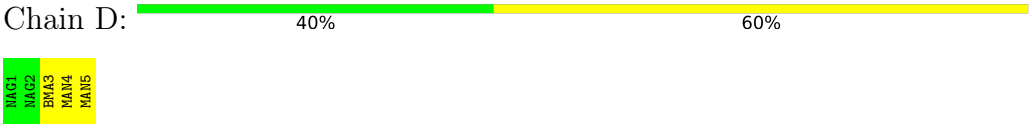


• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:

• 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

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	49.74Å 79.81Å 140.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.90 – 1.82 46.90 – 1.82	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.90-1.82) 99.8 (46.90-1.82)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.04 (at 1.82Å)	Xtriage
Refinement program	PHENIX dev_2247	Depositor
R, R_{free}	0.225 , 0.259 0.225 , 0.259	Depositor DCC
R_{free} test set	3682 reflections (7.21%)	wwPDB-VP
Wilson B-factor (Å^2)	44.2	Xtriage
Anisotropy	0.308	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 58.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6754	wwPDB-VP
Average B, all atoms (Å^2)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.35% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: NAG, BMA, 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	0.34	0/1657	0.53	0/2259
1	B	0.33	0/1676	0.52	0/2285
All	All	0.33	0/3333	0.53	0/4544

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	1611	1575	1574	6	0
1	B	1629	1581	1586	8	0
2	C	75	64	64	3	0
3	D	61	52	52	0	0
4	A	62	0	0	1	0
4	B	44	0	0	1	0
All	All	3482	3272	3276	15	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.

All (15) 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)
4:A:601:HOH:O	2:C:1:NAG:O6	2.06	0.73
1:B:415:HIS:O	4:B:601:HOH:O	2.13	0.66
1:A:297:ASN:HD21	2:C:1:NAG:C1	2.17	0.58
1:B:271:PRO:O	1:B:292:ARG:NH2	2.42	0.50
1:B:325:ASN:OD1	1:B:326:LYS:N	2.45	0.50
1:B:290:LYS:HB3	1:B:291:PRO:HD2	1.94	0.49
1:B:421:ASN:O	1:B:442:SER:O	2.31	0.48
1:A:252:MET:CE	1:A:255:ARG:HD2	2.45	0.47
1:A:271:PRO:HB2	1:A:292:ARG:NH1	2.30	0.46
1:A:297:ASN:ND2	2:C:1:NAG:C1	2.80	0.44
1:B:271:PRO:O	1:B:292:ARG:NH1	2.47	0.43
1:B:442:SER:O	1:B:443:LEU:HB3	2.20	0.42
1:A:273:VAL:HA	1:A:324:SER:O	2.20	0.42
1:A:325:ASN:OD1	1:A:327:ALA:HB3	2.20	0.41
1:B:252:MET:CE	1:B:255:ARG:HD2	2.51	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	198/227 (87%)	195 (98%)	3 (2%)	0	100	100
1	B	200/227 (88%)	196 (98%)	4 (2%)	0	100	100
All	All	398/454 (88%)	391 (98%)	7 (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	187/207 (90%)	186 (100%)	1 (0%)	88 87
1	B	189/207 (91%)	188 (100%)	1 (0%)	88 87
All	All	376/414 (91%)	374 (100%)	2 (0%)	88 87

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

Mol	Chain	Res	Type
1	A	296	TYR
1	B	412	VAL

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

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	2	14,14,15	0.80	1 (7%)	17,19,21	0.77	0
2	NAG	C	2	2	14,14,15	0.63	1 (7%)	17,19,21	0.36	0
2	BMA	C	3	2	11,11,12	0.72	0	15,15,17	1.01	0
2	MAN	C	4	2	11,11,12	0.65	0	15,15,17	1.17	1 (6%)
2	NAG	C	5	2	14,14,15	0.20	0	17,19,21	0.51	0
2	MAN	C	6	2	11,11,12	1.06	1 (9%)	15,15,17	0.88	1 (6%)
3	NAG	D	1	1,3	14,14,15	0.18	0	17,19,21	0.59	0
3	NAG	D	2	3	14,14,15	0.24	0	17,19,21	0.52	0
3	BMA	D	3	3	11,11,12	0.86	0	15,15,17	1.00	1 (6%)
3	MAN	D	4	3	11,11,12	0.97	1 (9%)	15,15,17	1.10	1 (6%)
3	MAN	D	5	3	11,11,12	1.18	1 (9%)	15,15,17	1.98	1 (6%)

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

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	5	MAN	O5-C5	2.74	1.49	1.43
2	C	1	NAG	O5-C1	-2.67	1.39	1.43
2	C	6	MAN	O5-C1	-2.60	1.39	1.43
3	D	4	MAN	O5-C1	-2.48	1.39	1.43
2	C	2	NAG	O5-C1	-2.11	1.40	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	5	MAN	C1-O5-C5	6.97	121.64	112.19
3	D	4	MAN	O2-C2-C3	-2.80	104.53	110.14
3	D	3	BMA	O5-C5-C6	2.61	111.29	107.20
2	C	6	MAN	O2-C2-C3	-2.36	105.42	110.14
2	C	4	MAN	C1-C2-C3	-2.07	107.12	109.67

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	5	NAG	O5-C5-C6-O6
3	D	2	NAG	O5-C5-C6-O6
3	D	3	BMA	O5-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
2	C	5	NAG	C4-C5-C6-O6
3	D	3	BMA	C4-C5-C6-O6
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2
3	D	1	NAG	C8-C7-N2-C2
3	D	1	NAG	O7-C7-N2-C2
2	C	1	NAG	C4-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6
3	D	4	MAN	O5-C5-C6-O6
3	D	5	MAN	O5-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6

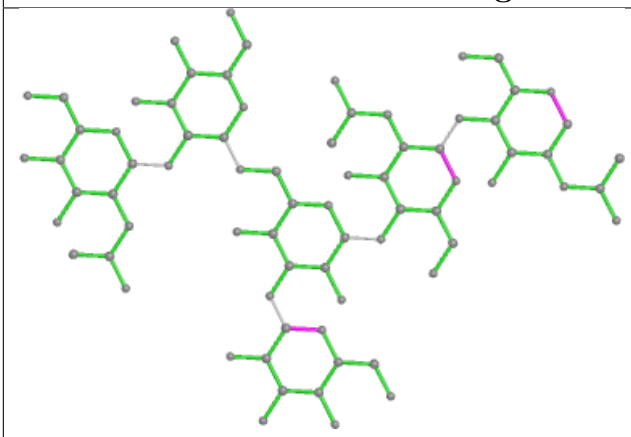
There are no ring outliers.

1 monomer is involved in 3 short contacts:

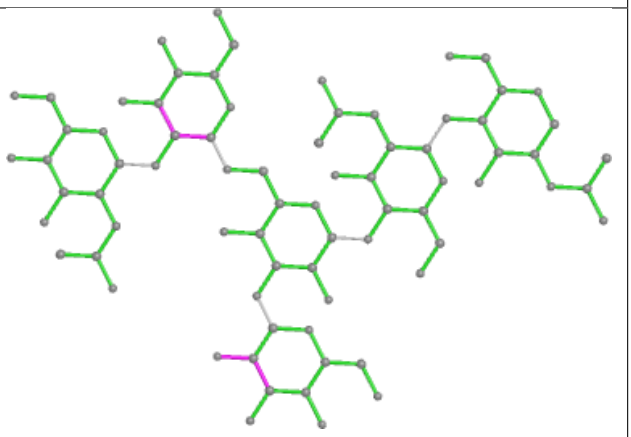
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	NAG	3	0

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

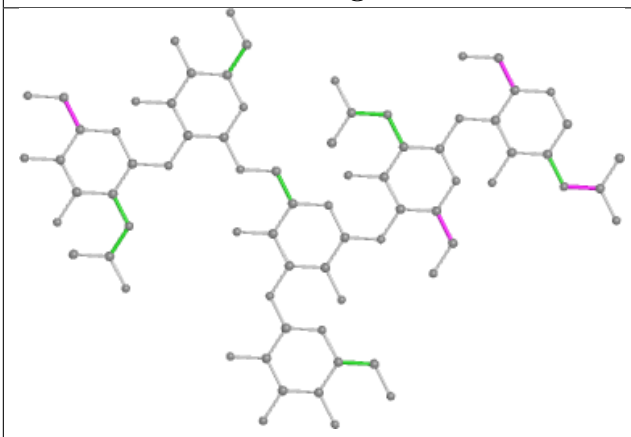
Oligosaccharide Chain C



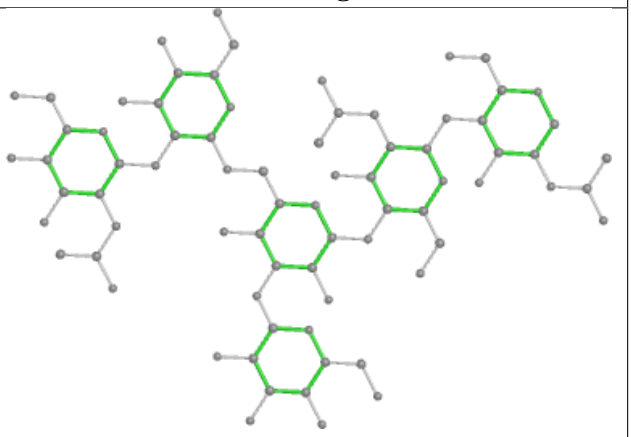
Bond lengths



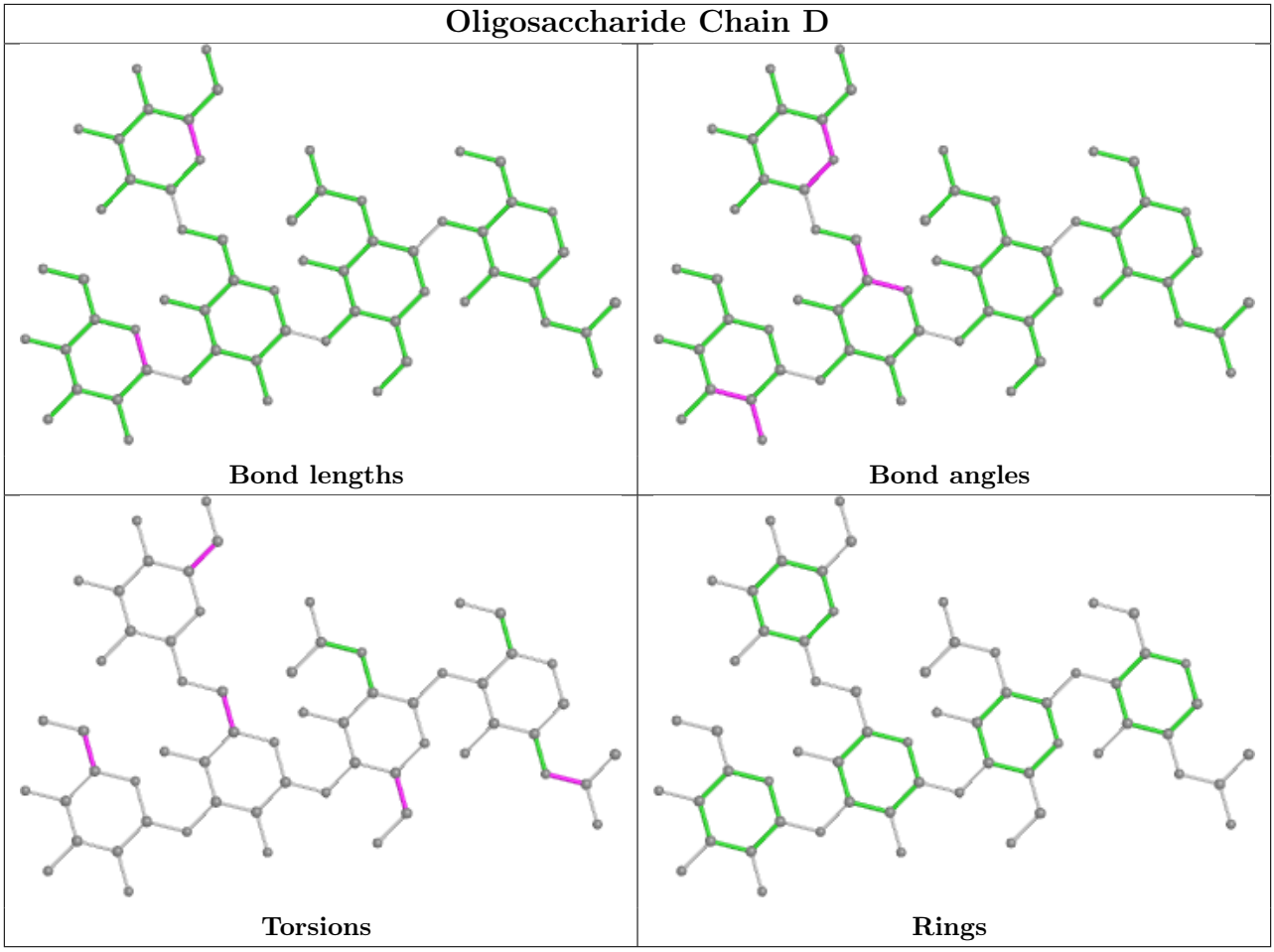
Bond angles



Torsions



Rings



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, 95^{th} 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	201/227 (88%)	0.48	5 (2%) 57 52	40, 64, 101, 133	9 (4%)
1	B	204/227 (89%)	1.06	36 (17%) 1 0	42, 78, 130, 166	21 (10%)
All	All	405/454 (89%)	0.77	41 (10%) 7 5	40, 69, 126, 166	30 (7%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	TYR	7.4
1	B	299	THR	7.0
1	A	361	GLY	6.1
1	B	291	PRO	5.7
1	B	273	VAL	5.0
1	A	420	GLY	4.7
1	B	297	ASN	4.6
1	B	238	PRO	4.5
1	B	324	SER	4.4
1	B	329	PRO	4.4
1	B	323	VAL	4.4
1	B	281	GLY	4.3
1	B	296	TYR	4.2
1	B	268	HIS	3.8
1	B	301	ARG	3.7
1	B	264	VAL	3.6
1	B	420	GLY	3.5
1	B	302	VAL	3.4
1	A	291	PRO	3.2
1	B	326	LYS	3.2
1	A	443	LEU	3.2
1	B	332	ILE	3.0
1	B	303	VAL	3.0
1	B	282	VAL	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	327	ALA	2.9
1	A	360	TYR	2.8
1	B	265	ASP	2.6
1	B	389	ASN	2.6
1	B	241	PHE	2.5
1	B	275	PHE	2.5
1	B	239	SER	2.5
1	B	330	ALA	2.5
1	B	263	VAL	2.4
1	B	295	GLN	2.4
1	B	269	GLU	2.3
1	B	285	HIS	2.3
1	B	331	PRO	2.2
1	B	267	SER	2.1
1	B	276	ASN	2.1
1	B	325	ASN	2.0
1	B	259	VAL	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)

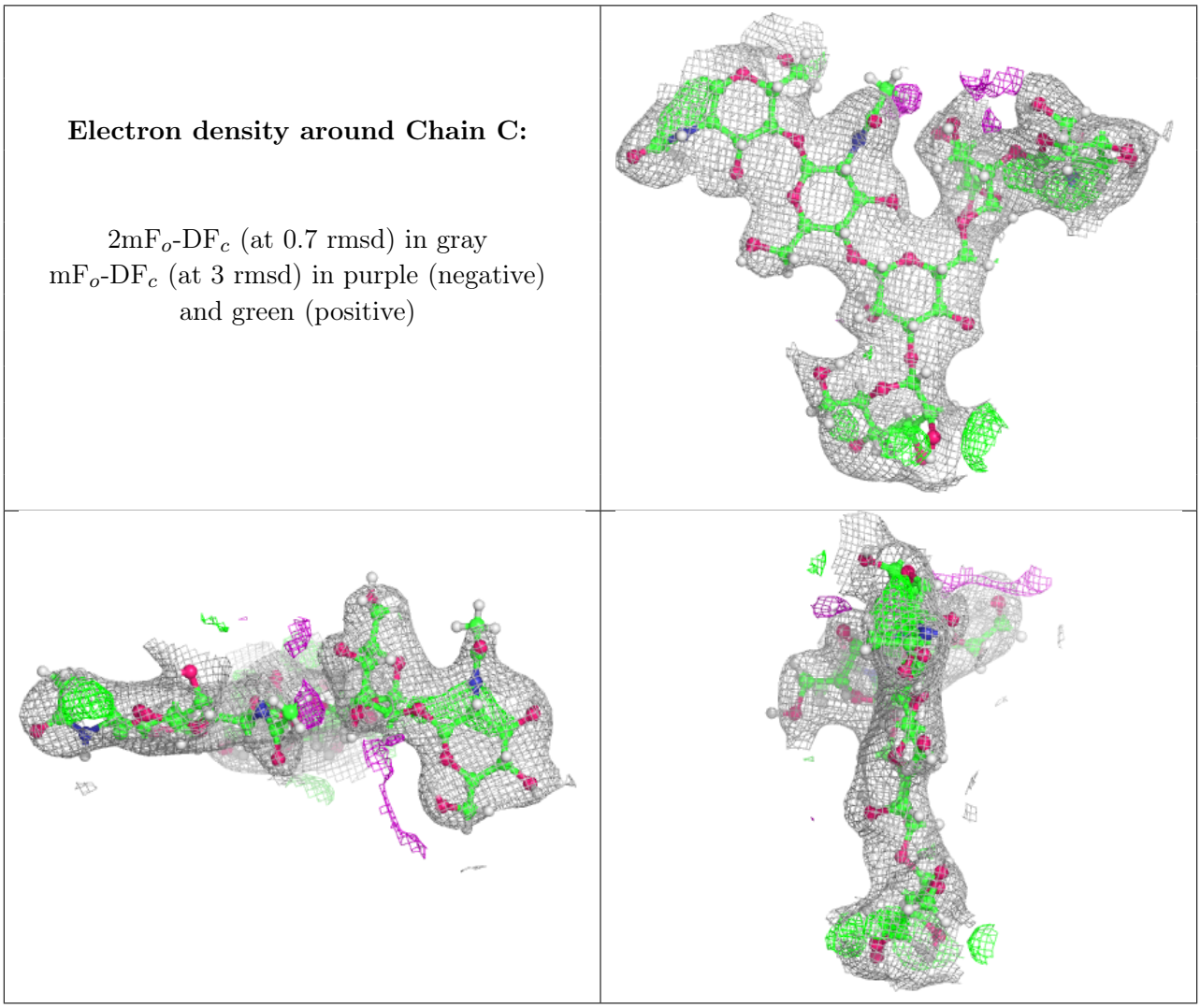
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	NAG	D	1	14/15	0.48	0.23	84,120,149,166	4
3	MAN	D	5	11/12	0.67	0.16	78,104,124,140	0
3	MAN	D	4	11/12	0.80	0.12	75,101,119,131	0
3	NAG	D	2	14/15	0.80	0.22	106,202,246,268	0
2	NAG	C	1	14/15	0.82	0.09	89,108,128,131	0
2	MAN	C	6	11/12	0.86	0.12	77,91,107,109	0
3	BMA	D	3	11/12	0.86	0.11	108,137,175,176	0
2	MAN	C	4	11/12	0.90	0.10	72,89,109,109	0
2	NAG	C	5	14/15	0.90	0.14	69,96,220,220	0
2	NAG	C	2	14/15	0.93	0.12	72,91,104,104	0
2	BMA	C	3	11/12	0.93	0.09	54,69,88,95	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.

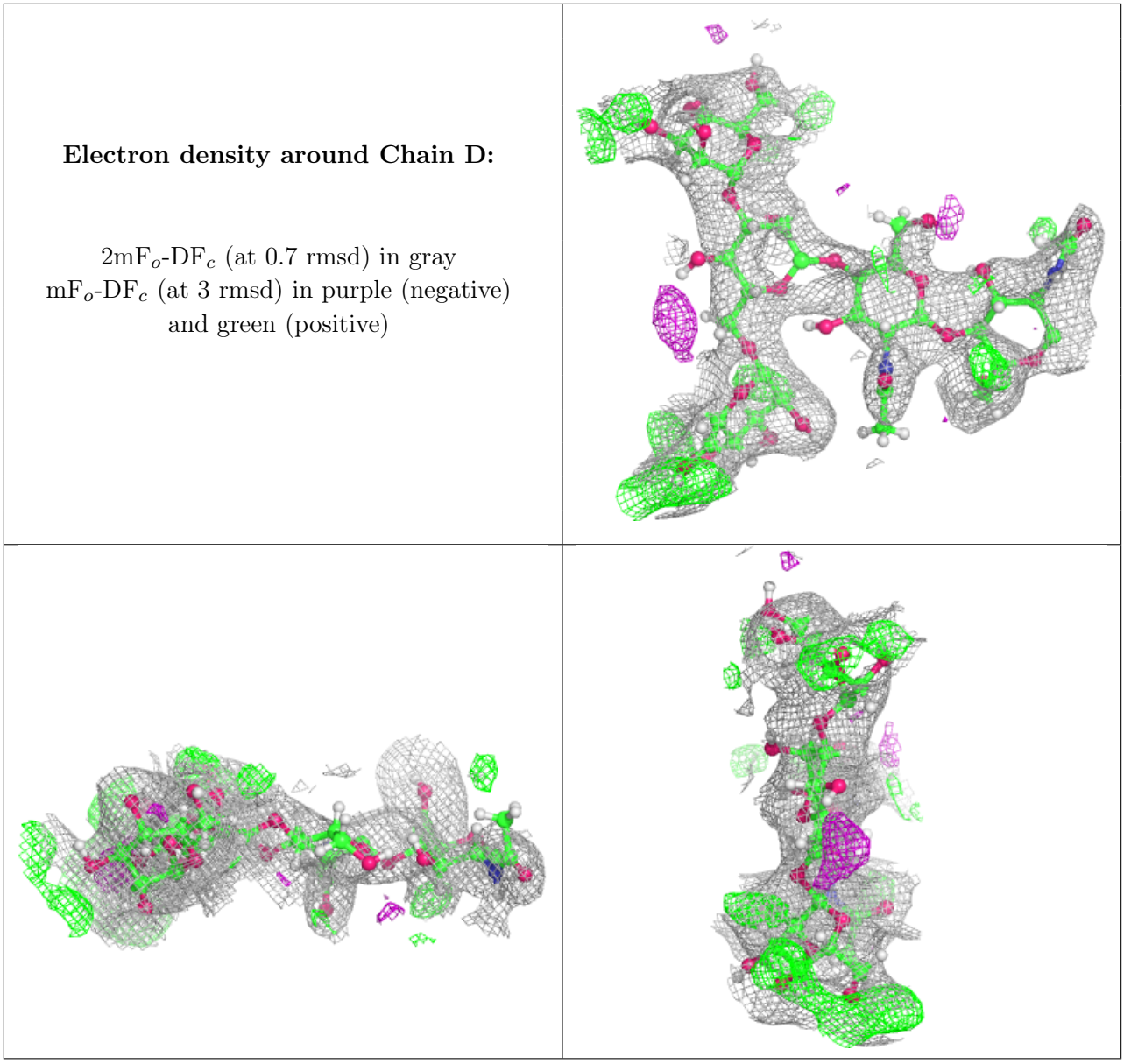
Electron density around Chain C:

$2mF_o$-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)



6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.