



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 6, 2025 – 04:09 PM EST

PDB ID : 9MVX / pdb_00009mvx
Title : Crystal structure of knob-in-hole immunoglobulin G1 Fc heterodimer with P374A
Authors : Choi, W.S.; Tilegenova, C.; Are, M.; Zwolak, A.; Shaffer, P.; Sharma, S.
Deposited on : 2025-01-16
Resolution : 1.84 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 : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

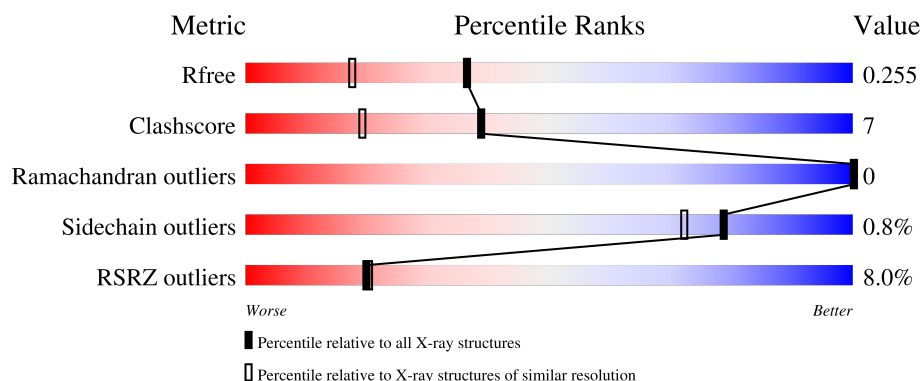
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.84 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}	164625	1150 (1.84-1.84)
Clashscore	180529	1248 (1.84-1.84)
Ramachandran outliers	177936	1240 (1.84-1.84)
Sidechain outliers	177891	1240 (1.84-1.84)
RSRZ outliers	164620	1149 (1.84-1.84)

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	227	<div> <div>13%</div> <div> <div></div> <div>78%</div> <div>15%</div> <div>7%</div> </div> </div>
2	B	227	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>12%</div> <div>7%</div> </div> </div>
3	C	7	<div> <div>29%</div> <div> <div></div> <div>57%</div> <div>14%</div> </div> </div>
4	D	8	<div> <div>75%</div> <div> <div></div> <div>25%</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3802 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 Isoform 1 of Immunoglobulin heavy constant gamma 1 HC1 (Hole).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	207	Total	C	N	O	S	0	5	0
			1618	1031	269	311	7			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	253	ASP	ILE	engineered mutation	UNP P01857
A	356	GLU	ASP	conflict	UNP P01857
A	358	MET	LEU	conflict	UNP P01857
A	366	SER	THR	engineered mutation	UNP P01857
A	368	ALA	LEU	engineered mutation	UNP P01857
A	374	ALA	PRO	engineered mutation	UNP P01857
A	407	VAL	TYR	engineered mutation	UNP P01857

- Molecule 2 is a protein called Isoform 1 of Immunoglobulin heavy constant gamma 1 HC2 (Knob).

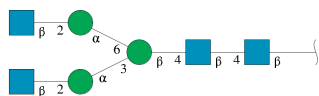
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	207	Total	C	N	O	S	0	7	0
			1700	1086	283	324	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	356	GLU	ASP	conflict	UNP P01857
B	358	MET	LEU	conflict	UNP P01857
B	366	TRP	THR	engineered mutation	UNP P01857
B	374	ALA	PRO	engineered mutation	UNP P01857

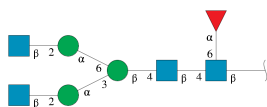
- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-man

nopyranose-(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	C	7	Total	C	N	O	0	0	0
			89	50	4	35			

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]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
4	D	8	Total	C	N	O	0	0	0
			99	56	4	39			

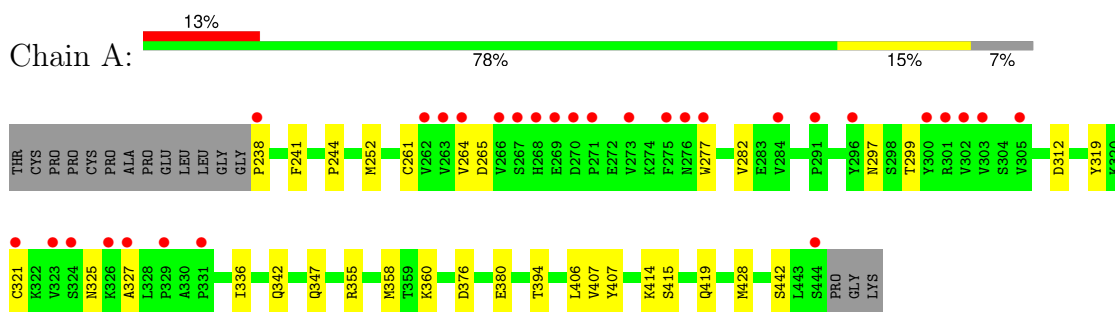
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	104	Total	O	0	0
			104	104		
5	B	192	Total	O	0	0
			192	192		

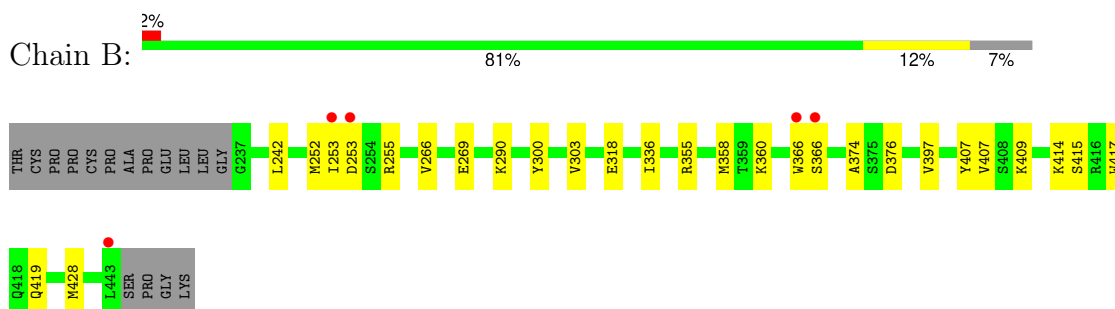
3 Residue-property plots [i](#)

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: Isoform 1 of Immunoglobulin heavy constant gamma 1 HC1 (Hole)



- Molecule 2: Isoform 1 of Immunoglobulin heavy constant gamma 1 HC2 (Knob)



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



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



MAG1	MAG2	MAN4	MAG5	MAG6	MAG7	FUC8

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	49.76Å 81.01Å 136.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.40 – 1.84 42.40 – 1.84	Depositor EDS
% Data completeness (in resolution range)	90.9 (42.40-1.84) 82.7 (42.40-1.84)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.82 (at 1.83Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.211 , 0.255 0.211 , 0.255	Depositor DCC
R_{free} test set	2201 reflections (4.50%)	wwPDB-VP
Wilson B-factor (Å ²)	36.3	Xtriage
Anisotropy	0.446	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 43.4	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	0.96	EDS
Total number of atoms	3802	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.85% 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, NAG, FUC, 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	0.33	0/1661	0.57	0/2267
2	B	0.40	0/1753	0.58	0/2384
All	All	0.37	0/3414	0.57	0/4651

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	1618	0	1515	26	0
2	B	1700	0	1654	19	0
3	C	89	0	76	5	0
4	D	99	0	85	0	0
5	A	104	0	0	3	0
5	B	192	0	0	4	0
All	All	3802	0	3330	43	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 7.

All (43) 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:419:GLN:NE2	5:A:501:HOH:O	2.30	0.65
2:B:366[B]:TRP:CH2	2:B:409:LYS:HD3	2.34	0.62
1:A:358:MET:HE3	1:A:414:LYS:HD2	1.82	0.61
1:A:415:SER:O	1:A:419:GLN:HG3	2.00	0.61
1:A:241:PHE:CE1	3:C:2:NAG:H4	2.38	0.58
1:A:297:ASN:OD1	1:A:299:THR:OG1	2.21	0.58
2:B:252:MET:HE3	2:B:255:ARG:HD3	1.84	0.58
2:B:269:GLU:OE2	2:B:269:GLU:N	2.30	0.57
1:A:264:VAL:HG21	3:C:1:NAG:O4	2.05	0.56
1:A:252:MET:HG2	1:A:428:MET:HE1	1.88	0.55
2:B:318:GLU:HG3	5:B:554:HOH:O	2.05	0.54
2:B:360:LYS:O	2:B:414:LYS:NZ	2.28	0.54
1:A:358:MET:O	1:A:414:LYS:HE3	2.07	0.54
1:A:360:LYS:N	1:A:360:LYS:HD2	2.24	0.53
1:A:264:VAL:HG22	1:A:265:ASP:H	1.74	0.53
1:A:355:ARG:HA	1:A:358:MET:HG2	1.90	0.52
1:A:347:GLN:OE1	2:B:360:LYS:HE3	2.10	0.51
1:A:325:ASN:OD1	1:A:327:ALA:N	2.43	0.51
1:A:376:ASP:HB2	5:A:575:HOH:O	2.11	0.51
1:A:238:PRO:HA	1:A:265:ASP:HB2	1.93	0.51
1:A:241:PHE:CE1	3:C:2:NAG:H61	2.46	0.51
2:B:358:MET:HE1	2:B:417:TRP:CD1	2.48	0.49
2:B:242:LEU:HD23	2:B:336[A]:ILE:HG23	1.95	0.49
1:A:407[B]:VAL:HG11	2:B:407[B]:TYR:CE2	2.49	0.48
1:A:244:PRO:HB3	1:A:336:ILE:HD11	1.96	0.47
1:A:342:GLN:NE2	5:A:509:HOH:O	2.47	0.47
1:A:261:CYS:HB2	1:A:277:TRP:CZ2	2.49	0.47
1:A:312:ASP:HB3	1:A:319:TYR:OH	2.16	0.46
1:A:241:PHE:HE1	3:C:2:NAG:H61	1.80	0.45
2:B:252:MET:CG	2:B:428:MET:HE1	2.47	0.45
2:B:253[B]:ILE:HG12	5:B:610:HOH:O	2.16	0.45
2:B:290:LYS:HE3	2:B:303:VAL:HB	2.00	0.44
1:A:261:CYS:HB2	1:A:277:TRP:CH2	2.52	0.44
2:B:415:SER:O	2:B:419:GLN:NE2	2.51	0.43
2:B:266:VAL:HB	2:B:300:TYR:HB2	2.01	0.43
2:B:252:MET:HG3	2:B:428:MET:HE1	2.00	0.43
1:A:277:TRP:CZ3	1:A:321:CYS:HB2	2.55	0.42
1:A:406:LEU:C	1:A:406:LEU:HD12	2.45	0.42
2:B:376:ASP:HB2	5:B:626:HOH:O	2.20	0.42
2:B:355:ARG:O	2:B:358:MET:HB2	2.20	0.41
2:B:374:ALA:HB3	5:B:626:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:2:NAG:O3	3:C:6:MAN:H3	2.21	0.41
1:A:394:THR:HA	2:B:397:VAL:HG21	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	202/227 (89%)	198 (98%)	4 (2%)	0	100	100
2	B	204/227 (90%)	203 (100%)	1 (0%)	0	100	100
All	All	406/454 (89%)	401 (99%)	5 (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	178/208 (86%)	174 (98%)	4 (2%)	47	31
2	B	197/208 (95%)	197 (100%)	0	100	100
All	All	375/416 (90%)	371 (99%)	4 (1%)	79	60

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	282	VAL
1	A	380[A]	GLU
1	A	380[B]	GLU
1	A	442	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	286	ASN
1	A	342	GLN
1	A	384	ASN
2	B	311	GLN
2	B	347	GLN
2	B	362	GLN
2	B	419	GLN
2	B	421	ASN

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](#)

15 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	C	1	3,1	14,14,15	0.22	0	17,19,21	0.53	0
3	NAG	C	2	3	14,14,15	0.21	0	17,19,21	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	BMA	C	3	3	11,11,12	0.96	0	15,15,17	0.96	0
3	MAN	C	4	3	11,11,12	0.93	0	15,15,17	1.03	2 (13%)
3	NAG	C	5	3	14,14,15	0.68	0	17,19,21	0.57	0
3	MAN	C	6	3	11,11,12	1.08	0	15,15,17	0.96	1 (6%)
3	NAG	C	7	3	14,14,15	0.21	0	17,19,21	0.91	1 (5%)
4	NAG	D	1	4,2	14,14,15	0.35	0	17,19,21	0.48	0
4	NAG	D	2	4	14,14,15	0.46	0	17,19,21	0.58	0
4	BMA	D	3	4	11,11,12	0.88	0	15,15,17	0.89	0
4	MAN	D	4	4	11,11,12	1.26	2 (18%)	15,15,17	1.60	2 (13%)
4	NAG	D	5	4	14,14,15	0.41	0	17,19,21	0.54	0
4	MAN	D	6	4	11,11,12	0.72	0	15,15,17	1.27	2 (13%)
4	NAG	D	7	4	14,14,15	0.53	0	17,19,21	0.58	0
4	FUC	D	8	4	10,10,11	0.79	0	14,14,16	0.73	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	C	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	1/2/19/22	0/1/1/1
3	MAN	C	4	3	-	2/2/19/22	0/1/1/1
3	NAG	C	5	3	-	0/6/23/26	0/1/1/1
3	MAN	C	6	3	-	0/2/19/22	0/1/1/1
3	NAG	C	7	3	-	2/6/23/26	0/1/1/1
4	NAG	D	1	4,2	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
4	BMA	D	3	4	-	0/2/19/22	0/1/1/1
4	MAN	D	4	4	-	1/2/19/22	0/1/1/1
4	NAG	D	5	4	-	4/6/23/26	0/1/1/1
4	MAN	D	6	4	-	0/2/19/22	0/1/1/1
4	NAG	D	7	4	-	0/6/23/26	0/1/1/1
4	FUC	D	8	4	-	-	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	4	MAN	C2-C3	-2.19	1.49	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	4	MAN	O2-C2	-2.09	1.39	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	4	MAN	O2-C2-C3	-4.12	101.62	110.15
4	D	6	MAN	O2-C2-C3	-3.91	102.06	110.15
4	D	4	MAN	C1-O5-C5	3.83	117.31	112.19
3	C	7	NAG	C1-O5-C5	3.24	116.53	112.19
3	C	4	MAN	O2-C2-C3	-2.74	104.48	110.15
4	D	6	MAN	C1-O5-C5	2.46	115.48	112.19
3	C	6	MAN	C1-O5-C5	2.25	115.20	112.19
3	C	4	MAN	C1-O5-C5	2.10	115.01	112.19

There are no chirality outliers.

All (12) torsion outliers are listed below:

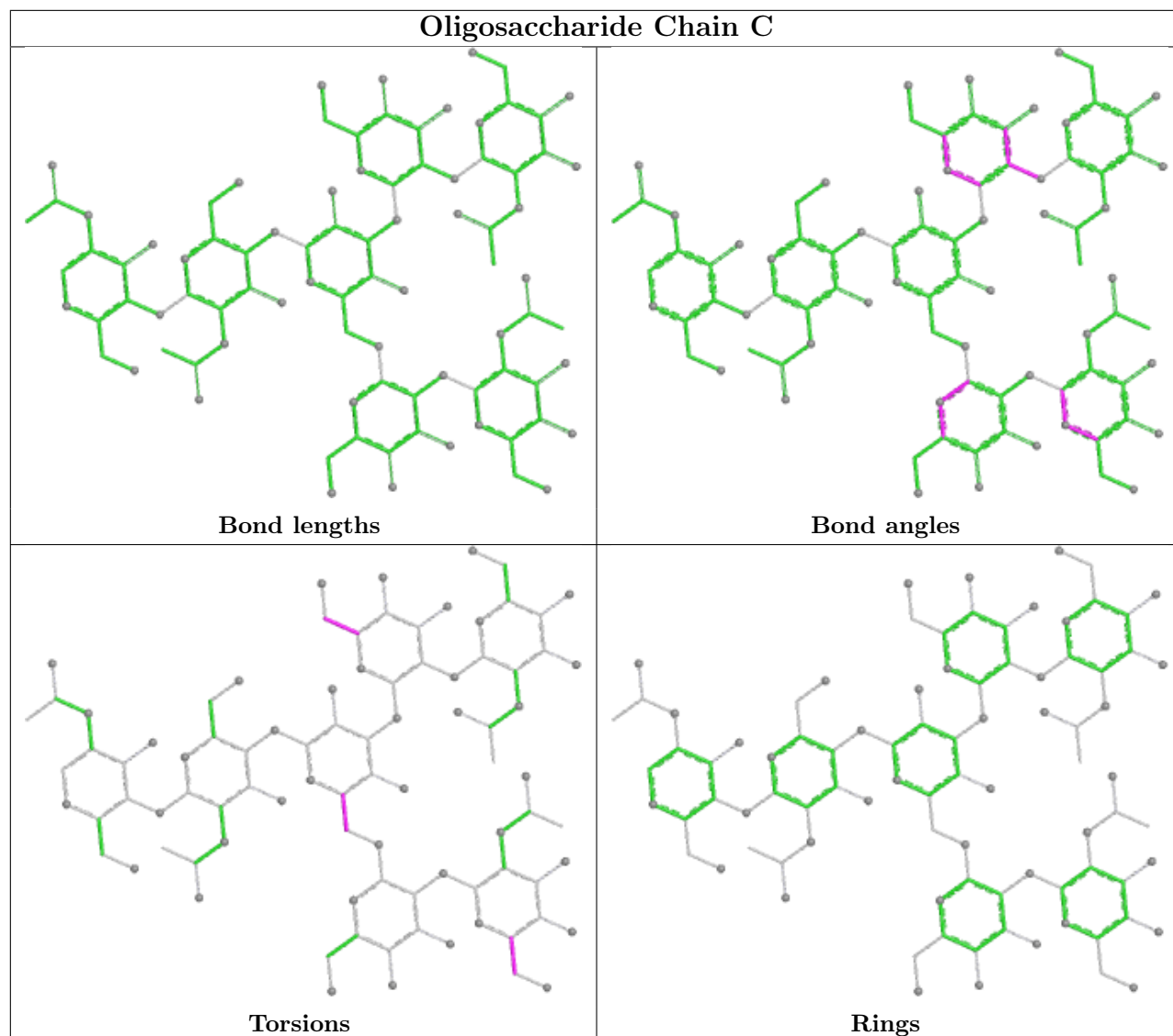
Mol	Chain	Res	Type	Atoms
3	C	7	NAG	O5-C5-C6-O6
3	C	4	MAN	C4-C5-C6-O6
3	C	4	MAN	O5-C5-C6-O6
4	D	5	NAG	O5-C5-C6-O6
4	D	5	NAG	C8-C7-N2-C2
4	D	5	NAG	O7-C7-N2-C2
4	D	2	NAG	O5-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6
4	D	5	NAG	C4-C5-C6-O6
3	C	7	NAG	C4-C5-C6-O6
4	D	4	MAN	C4-C5-C6-O6
3	C	3	BMA	O5-C5-C6-O6

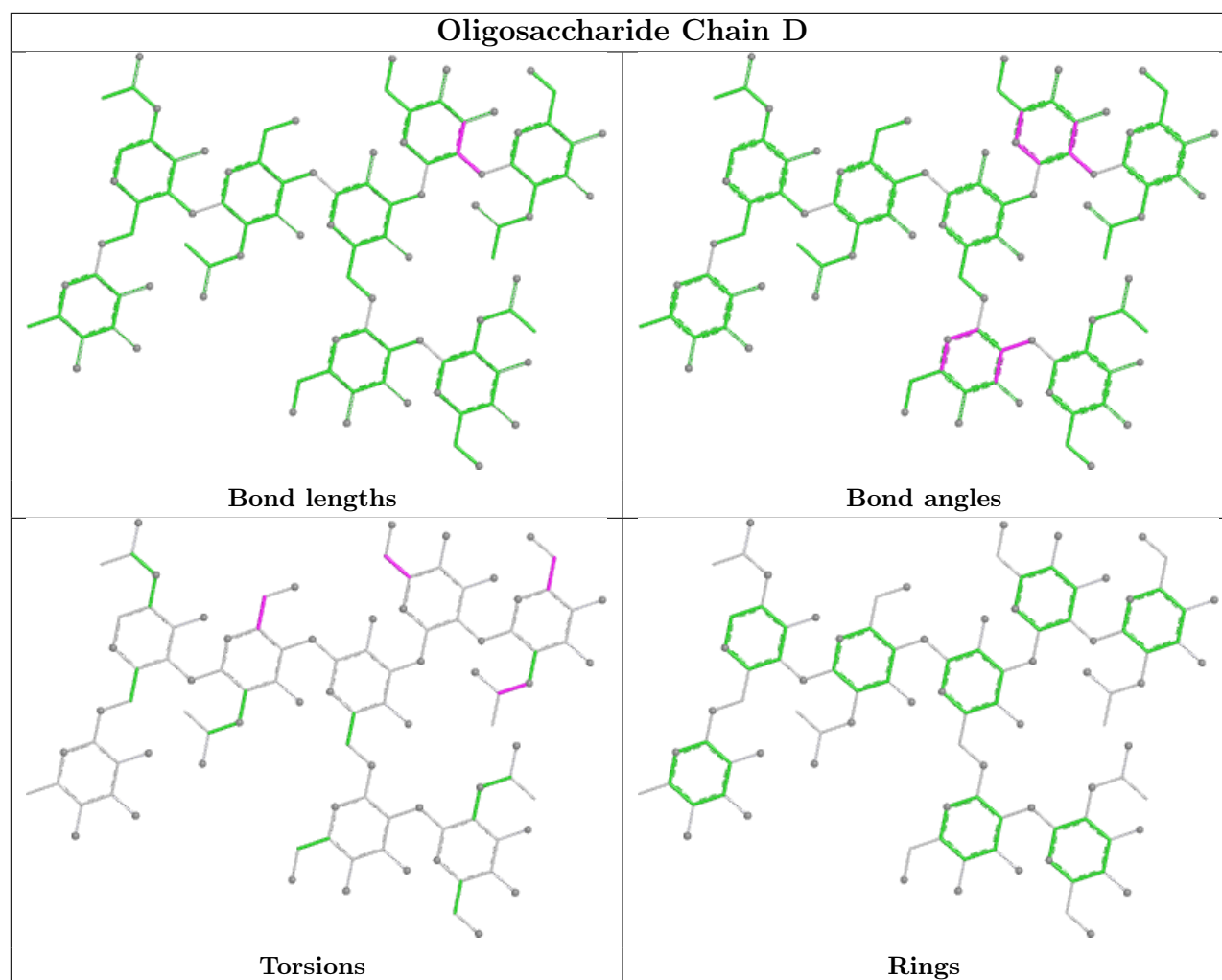
There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2	NAG	4	0
3	C	6	MAN	1	0
3	C	1	NAG	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 ⓘ

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	203/227 (89%)	0.75	30 (14%) 7 7	26, 60, 142, 363	1 (0%)
2	B	203/227 (89%)	0.00	1 (0%) 87 92	24, 45, 81, 110	3 (1%)
All	All	406/454 (89%)	0.37	31 (7%) 20 22	24, 50, 121, 363	4 (0%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	273	VAL	4.5
1	A	266	VAL	4.3
1	A	275	PHE	4.2
1	A	268	HIS	4.0
1	A	264	VAL	4.0
1	A	263	VAL	4.0
1	A	323	VAL	3.8
1	A	267	SER	3.7
1	A	296	TYR	3.7
1	A	271	PRO	3.5
1	A	262	VAL	3.5
1	A	300	TYR	3.3
1	A	270	ASP	3.1
1	A	238	PRO	3.0
1	A	284	VAL	2.9
1	A	302	VAL	2.8
1	A	321	CYS	2.8
1	A	303	VAL	2.7
1	A	327	ALA	2.6
1	A	276	ASN	2.4
1	A	326	LYS	2.4
1	A	269	GLU	2.3
1	A	291	PRO	2.3
1	A	301	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	331	PRO	2.2
1	A	305	VAL	2.2
1	A	324	SER	2.2
1	A	329	PRO	2.2
1	A	444	SER	2.1
1	A	277	TRP	2.1
2	B	443	LEU	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](#)

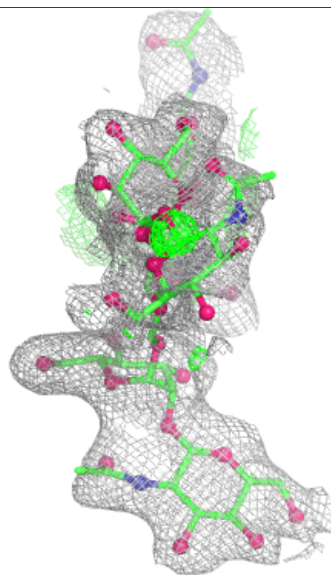
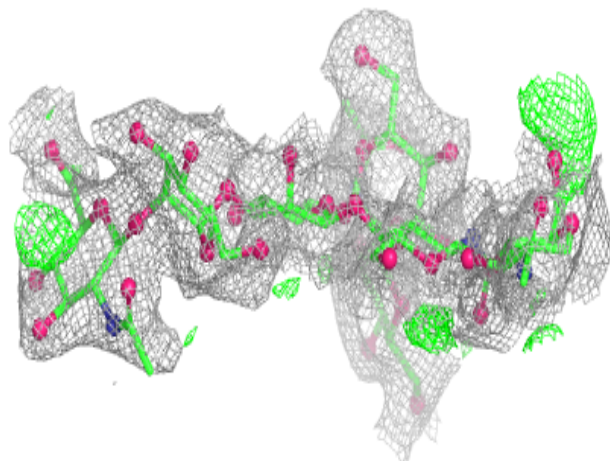
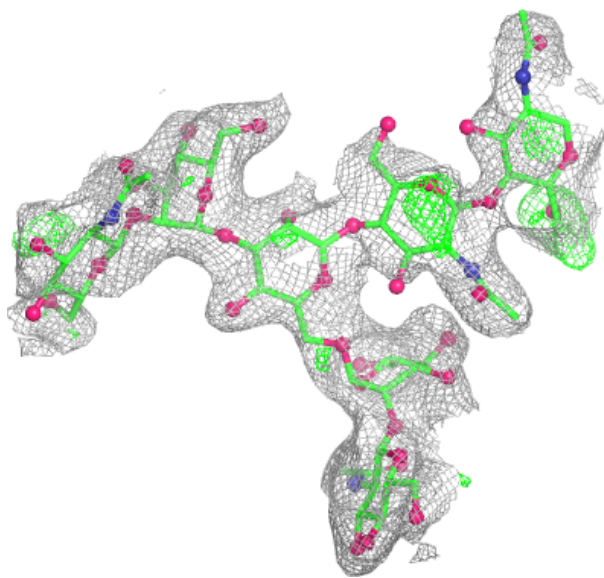
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

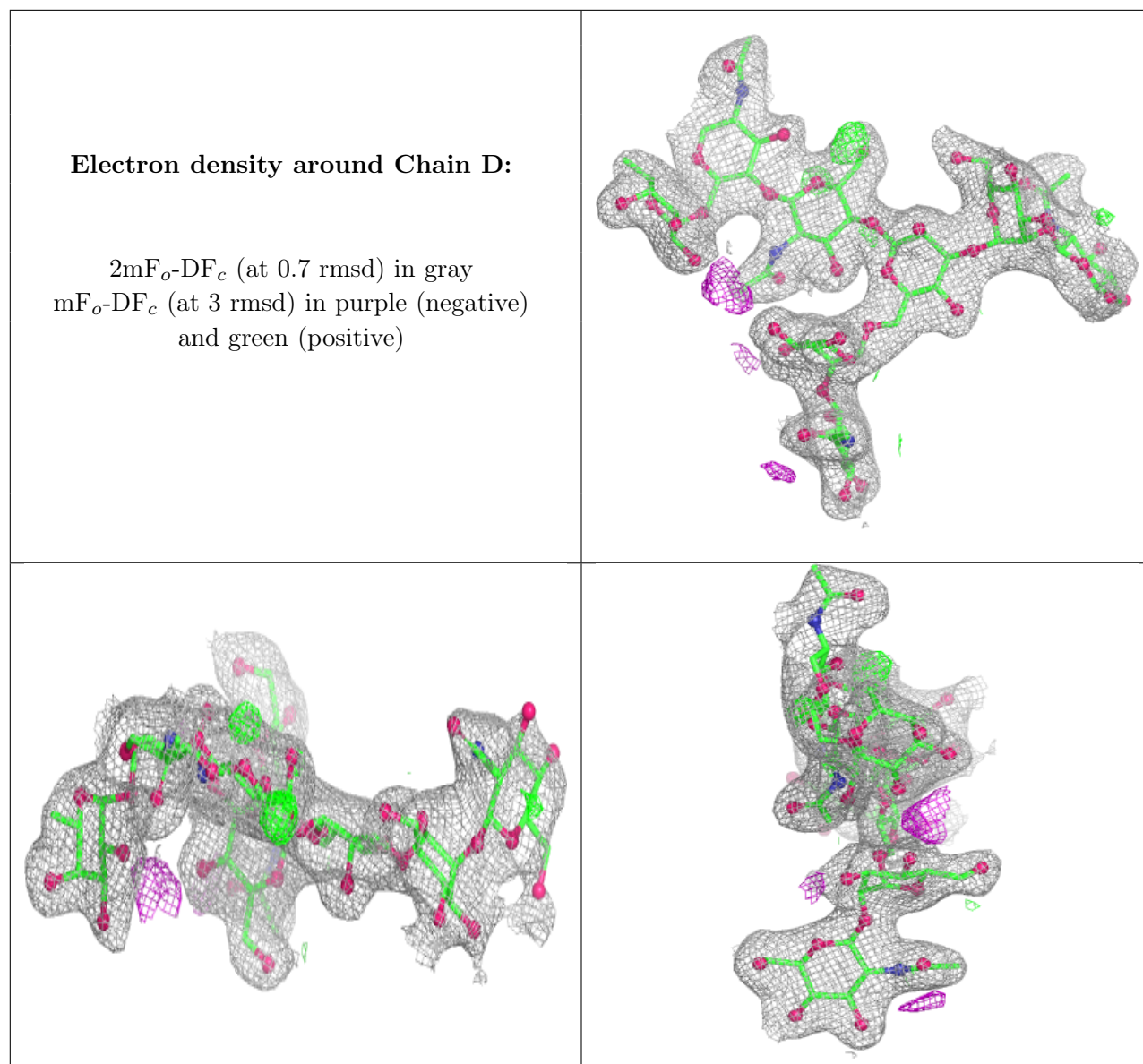
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	C	1	14/15	0.55	0.15	112,126,135,138	0
3	NAG	C	5	14/15	0.61	0.15	93,99,108,113	0
3	NAG	C	2	14/15	0.64	0.16	92,105,115,116	0
4	NAG	D	5	14/15	0.72	0.14	78,86,99,99	0
3	BMA	C	3	11/12	0.82	0.10	80,88,92,96	0
3	MAN	C	4	11/12	0.82	0.10	73,82,91,91	0
4	NAG	D	2	14/15	0.88	0.10	48,51,55,66	0
3	MAN	C	6	11/12	0.90	0.07	77,80,85,85	0
3	NAG	C	7	14/15	0.90	0.09	70,76,78,83	0
4	MAN	D	4	11/12	0.91	0.09	59,66,75,80	0
4	NAG	D	1	14/15	0.92	0.08	50,56,59,60	0
4	FUC	D	8	10/11	0.92	0.08	55,58,63,68	0
4	MAN	D	6	11/12	0.94	0.07	45,46,54,56	0
4	NAG	D	7	14/15	0.94	0.07	41,46,49,51	0
4	BMA	D	3	11/12	0.94	0.07	44,47,52,52	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)





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.