



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:55 AM UTC

PDB ID : 5O4O / pdb_00005o4o
Title : HER3 in complex with Fab MF3178
Authors : De Nardis, C.; Gros, P.
Deposited on : 2017-05-30
Resolution : 3.40 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

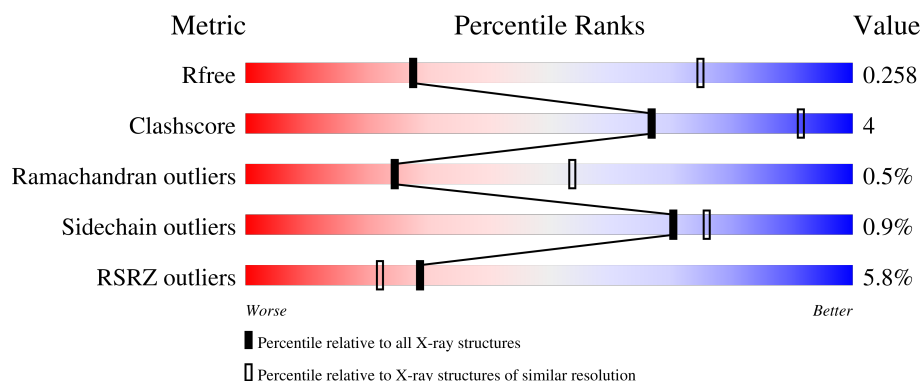
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	214	4% 86% 13% .
2	B	250	% 78% 8% 14%
3	C	649	5% 49% . 47%
4	D	2	50% 50%
4	E	2	50% 50%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6065 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 MF3178 FAB light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	213	Total	C	N	O	S	0	0	0
			1629	1017	272	335	5			

- Molecule 2 is a protein called MF3178 FAB heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	216	Total	C	N	O	S	0	0	0
			1661	1054	284	315	8			

- Molecule 3 is a protein called Receptor tyrosine-protein kinase erbB-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	347	Total	C	N	O	S	0	0	0
			2663	1648	486	496	33			

There are 6 discrepancies between the modelled and reference sequences:

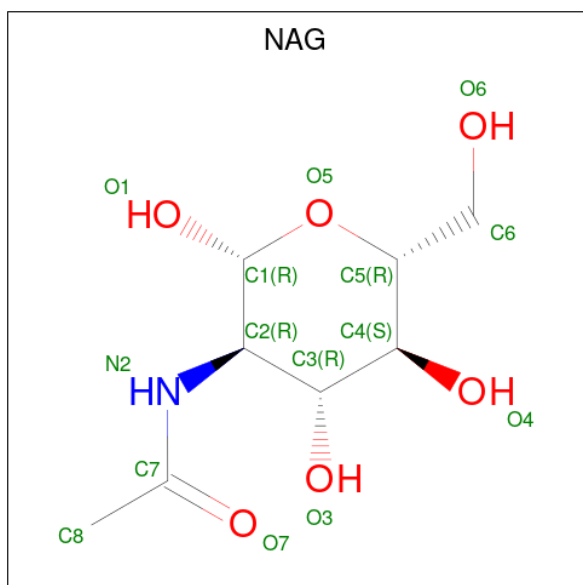
Chain	Residue	Modelled	Actual	Comment	Reference
C	644	HIS	-	expression tag	UNP P21860
C	645	HIS	-	expression tag	UNP P21860
C	646	HIS	-	expression tag	UNP P21860
C	647	HIS	-	expression tag	UNP P21860
C	648	HIS	-	expression tag	UNP P21860
C	649	HIS	-	expression tag	UNP P21860

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

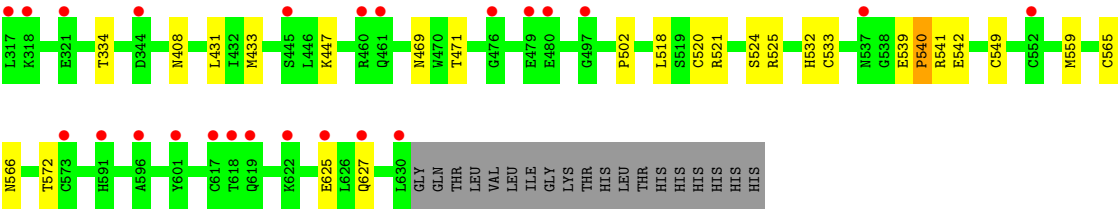


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total	C	N	O	0	0
			14	8	1	5		
5	C	1	Total	C	N	O	0	0
			14	8	1	5		
5	C	1	Total	C	N	O	0	0
			14	8	1	5		
5	C	1	Total	C	N	O	0	0
			14	8	1	5		



● Molecule 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-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	64.38Å 144.02Å 218.76Å 90.00° 97.91° 90.00°	Depositor
Resolution (Å)	59.97 – 3.40 59.97 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.1 (59.97-3.40) 99.1 (59.97-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 3.40Å)	Xtriage
Refinement program	PHENIX (1.11_2567: ???)	Depositor
R, R_{free}	0.215 , 0.261 0.216 , 0.258	Depositor DCC
R_{free} test set	1329 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	50.0	Xtriage
Anisotropy	0.726	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	6065	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.22% 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: 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	0.09	0/1664	0.28	0/2260
2	B	0.10	0/1709	0.26	0/2330
3	C	0.10	0/2730	0.29	0/3698
All	All	0.09	0/6103	0.28	0/8288

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	1629	0	1583	21	0
2	B	1661	0	1599	11	0
3	C	2663	0	2531	13	0
4	D	28	0	25	0	0
4	E	28	0	25	0	0
5	C	56	0	52	0	0
All	All	6065	0	5815	44	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 4.

All (44) 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:189:HIS:O	1:A:211:ARG:NH1	2.25	0.70
3:C:541:ARG:NH1	3:C:559:MET:O	2.26	0.69
1:A:94:THR:HG23	1:A:95:PRO:HD3	1.82	0.62
1:A:62:PHE:HA	1:A:75:ILE:HG22	1.85	0.59
3:C:539:GLU:HB2	3:C:540:PRO:HD3	1.83	0.59
1:A:37:GLN:HB2	1:A:47:LEU:HD11	1.85	0.58
3:C:532:HIS:ND1	3:C:533:CYS:O	2.33	0.58
3:C:542:GLU:OE1	3:C:549:CYS:HB3	2.05	0.56
1:A:96:PRO:HD2	2:B:47:TRP:CD2	2.39	0.56
1:A:6:GLN:HE21	1:A:102:THR:HG23	1.71	0.55
1:A:47:LEU:HA	1:A:58:VAL:HG21	1.89	0.54
2:B:206:ILE:HG12	2:B:221:ARG:HG2	1.92	0.51
1:A:145:LYS:HB3	1:A:197:THR:HB	1.92	0.51
2:B:11:VAL:HG21	2:B:158:PRO:HG3	1.92	0.51
1:A:6:GLN:NE2	1:A:102:THR:HG23	2.27	0.50
2:B:98:ARG:NH1	2:B:112:ASP:OD2	2.46	0.49
3:C:447:LYS:NZ	3:C:518:LEU:O	2.45	0.48
3:C:502:PRO:O	3:C:521:ARG:NH1	2.47	0.48
1:A:4:MET:HE3	1:A:90:GLN:HG2	1.95	0.47
1:A:21:ILE:HD11	1:A:73:LEU:HD23	1.96	0.47
2:B:97:ALA:HB1	2:B:111:PHE:HB3	1.96	0.47
3:C:539:GLU:H	3:C:539:GLU:CD	2.22	0.47
1:A:35:TRP:CD2	1:A:73:LEU:HB2	2.50	0.47
1:A:35:TRP:CE2	1:A:73:LEU:HB2	2.49	0.47
1:A:165:GLU:H	1:A:165:GLU:CD	2.23	0.47
1:A:120:PRO:HD3	1:A:132:VAL:HG22	1.98	0.46
3:C:525:ARG:HD3	3:C:542:GLU:OE2	2.14	0.46
1:A:11:LEU:HD23	1:A:104:VAL:HG12	1.98	0.46
1:A:113:PRO:HD3	1:A:198:HIS:ND1	2.31	0.45
2:B:210:ASN:HD21	2:B:217:LYS:HE2	1.81	0.45
1:A:21:ILE:HB	1:A:102:THR:HG21	1.99	0.45
3:C:625:GLU:OE1	3:C:627:GLN:NE2	2.50	0.44
3:C:520:CYS:SG	3:C:524:SER:HB3	2.58	0.43
1:A:89:GLN:HE21	1:A:96:PRO:HB3	1.84	0.42
3:C:469:ASN:OD1	3:C:471:THR:OG1	2.36	0.42
3:C:566:ASN:HB2	3:C:572:THR:HB	2.01	0.42
2:B:53:PRO:HA	2:B:72:ARG:HD3	2.02	0.42
2:B:67:ARG:HD2	2:B:85:ARG:HB3	2.02	0.42
3:C:431:LEU:HD21	3:C:433:MET:HE3	2.02	0.42
2:B:157:PHE:HA	2:B:158:PRO:HA	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:GLN:HE21	1:A:6:GLN:HB3	1.70	0.41
1:A:94:THR:O	1:A:96:PRO:HD3	2.20	0.41
2:B:100:HIS:CE1	2:B:110:GLY:H	2.37	0.41
2:B:99:ASP:OD1	2:B:107:SER:OG	2.38	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	211/214 (99%)	200 (95%)	8 (4%)	3 (1%)	9	31
2	B	212/250 (85%)	206 (97%)	6 (3%)	0	100	100
3	C	343/649 (53%)	309 (90%)	33 (10%)	1 (0%)	36	65
All	All	766/1113 (69%)	715 (93%)	47 (6%)	4 (0%)	24	54

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	540	PRO
1	A	138	ASN
1	A	2	ILE
1	A	95	PRO

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	188/189 (100%)	186 (99%)	2 (1%)	65	74
2	B	182/207 (88%)	181 (100%)	1 (0%)	81	81
3	C	300/560 (54%)	297 (99%)	3 (1%)	68	75
All	All	670/956 (70%)	664 (99%)	6 (1%)	70	76

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	ASP
1	A	94	THR
2	B	98	ARG
3	C	334	THR
3	C	408	ASN
3	C	565	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	138	ASN
1	A	199	GLN
2	B	59	ASN
3	C	369	ASN
3	C	614	HIS

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 ⓘ

4 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	D	1	3,4	14,14,15	0.37	0	17,19,21	0.73	1 (5%)
4	NAG	D	2	4	14,14,15	0.24	0	17,19,21	0.51	0
4	NAG	E	1	3,4	14,14,15	0.58	1 (7%)	17,19,21	0.55	0
4	NAG	E	2	4	14,14,15	0.20	0	17,19,21	0.37	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
4	NAG	D	1	3,4	-	1/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
4	NAG	E	1	3,4	-	2/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1	NAG	O5-C1	-2.04	1.40	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1	NAG	C1-O5-C5	2.31	115.28	112.19

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	2	NAG	O5-C5-C6-O6
4	E	1	NAG	O5-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6
4	E	2	NAG	O5-C5-C6-O6

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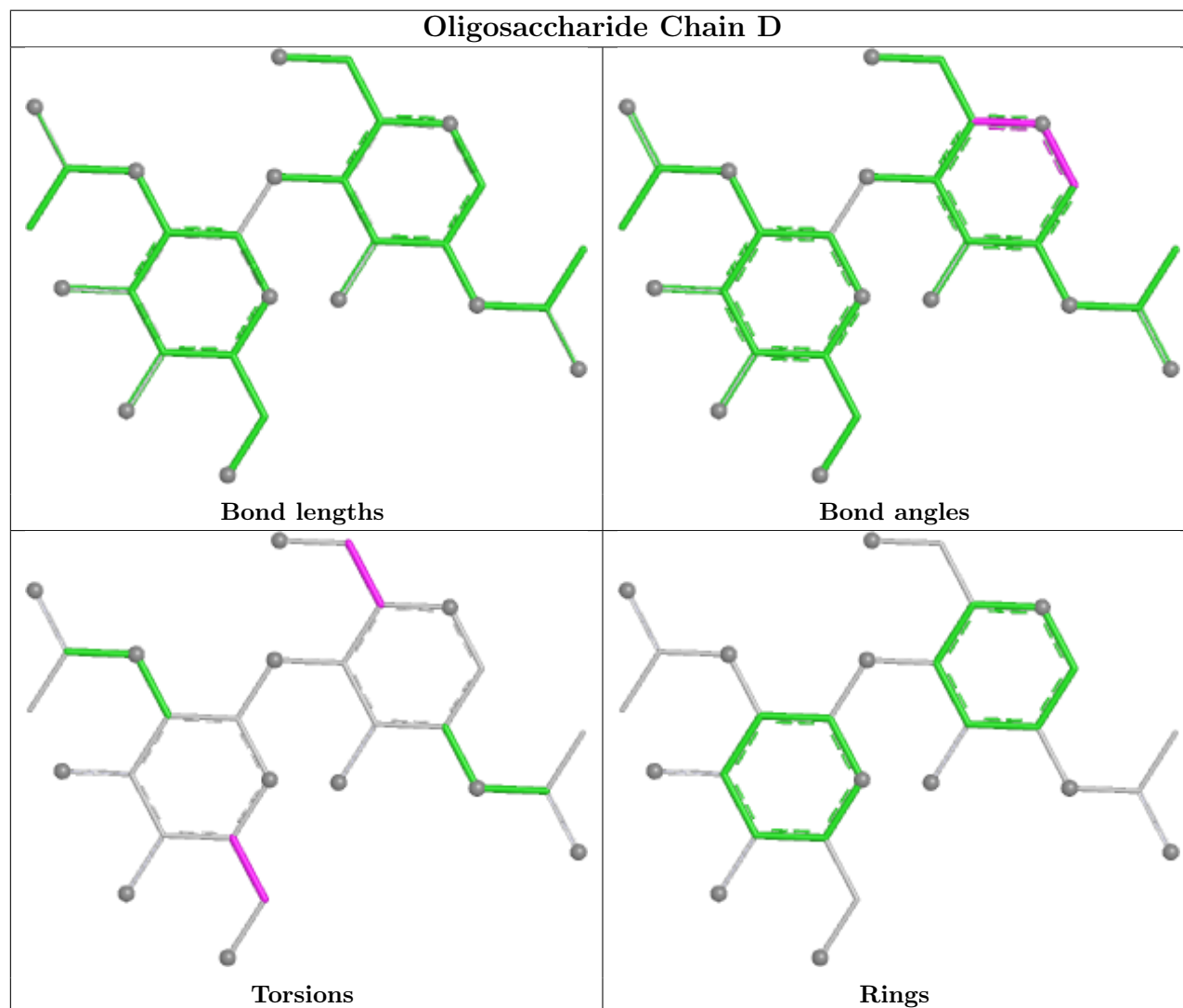
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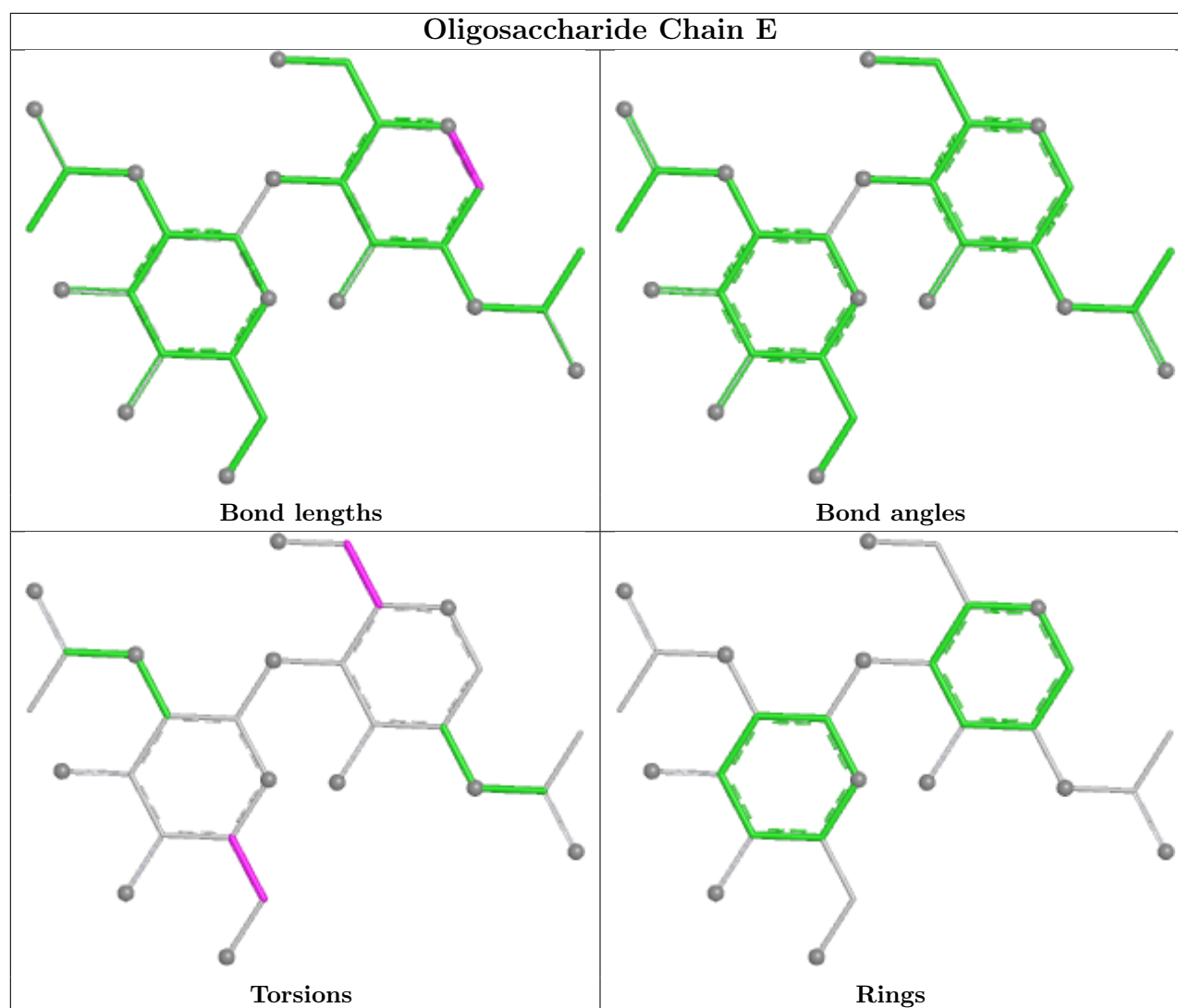
Mol	Chain	Res	Type	Atoms
4	E	2	NAG	C4-C5-C6-O6
4	E	1	NAG	C4-C5-C6-O6
4	D	1	NAG	O5-C5-C6-O6

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](#)

4 ligands 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	$\# Z > 2$
5	NAG	C	701	3	14,14,15	0.24	0	17,19,21	0.45	0
5	NAG	C	708	-	14,14,15	0.26	0	17,19,21	0.47	0
5	NAG	C	704	3	14,14,15	0.26	0	17,19,21	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	C	705	3	14,14,15	0.23	0	17,19,21	0.48	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
5	NAG	C	701	3	-	2/6/23/26	0/1/1/1
5	NAG	C	708	-	-	2/6/23/26	0/1/1/1
5	NAG	C	704	3	-	2/6/23/26	0/1/1/1
5	NAG	C	705	3	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	705	NAG	O5-C5-C6-O6
5	C	704	NAG	O5-C5-C6-O6
5	C	704	NAG	C4-C5-C6-O6
5	C	708	NAG	O5-C5-C6-O6
5	C	705	NAG	C4-C5-C6-O6
5	C	708	NAG	C4-C5-C6-O6
5	C	701	NAG	C1-C2-N2-C7
5	C	701	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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	213/214 (99%)	0.27	8 (3%) 44 31	19, 44, 73, 114	0
2	B	216/250 (86%)	0.06	3 (1%) 73 59	21, 37, 73, 89	0
3	C	347/649 (53%)	0.79	34 (9%) 13 13	25, 59, 115, 145	0
All	All	776/1113 (69%)	0.44	45 (5%) 29 22	19, 48, 104, 145	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	619	GLN	5.8
3	C	302	VAL	5.0
3	C	625	GLU	3.9
3	C	308	ASP	3.5
1	A	213	GLU	3.5
2	B	146	THR	3.4
3	C	622	LYS	3.2
3	C	268	LEU	3.1
3	C	344	ASP	3.0
3	C	263	LEU	3.0
3	C	460	ARG	3.0
1	A	210	ASN	3.0
3	C	261	GLN	2.9
3	C	307	PRO	2.8
3	C	596	ALA	2.8
3	C	618	THR	2.7
3	C	627	GLN	2.6
3	C	630	LEU	2.6
3	C	461	GLN	2.6
3	C	303	ARG	2.6
3	C	316	GLY	2.5
3	C	317	LEU	2.5
1	A	190	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	165	GLU	2.4
3	C	314	LYS	2.4
2	B	1	GLN	2.4
3	C	479	GLU	2.4
3	C	476	GLY	2.4
3	C	591	HIS	2.4
3	C	318	LYS	2.4
3	C	445	SER	2.4
2	B	137	PRO	2.4
1	A	94	THR	2.3
3	C	573	CYS	2.2
3	C	321	GLU	2.2
3	C	601	TYR	2.2
3	C	313	ASP	2.2
1	A	93	SER	2.2
1	A	203	SER	2.1
3	C	497	GLY	2.1
3	C	552	CYS	2.1
1	A	77	SER	2.1
3	C	480	GLU	2.1
3	C	617	CYS	2.1
3	C	537	ASN	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.

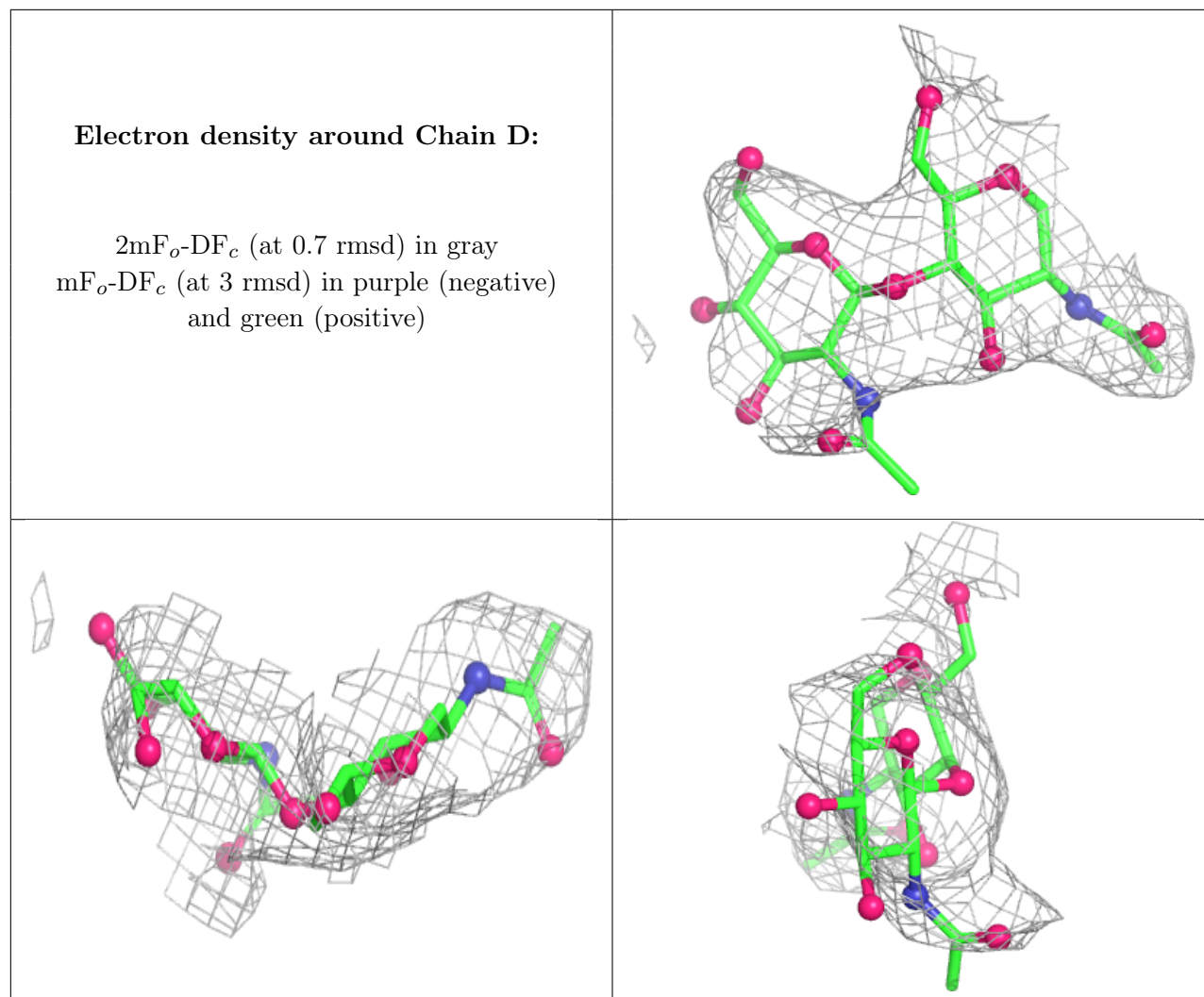
6.3 Carbohydrates [i](#)

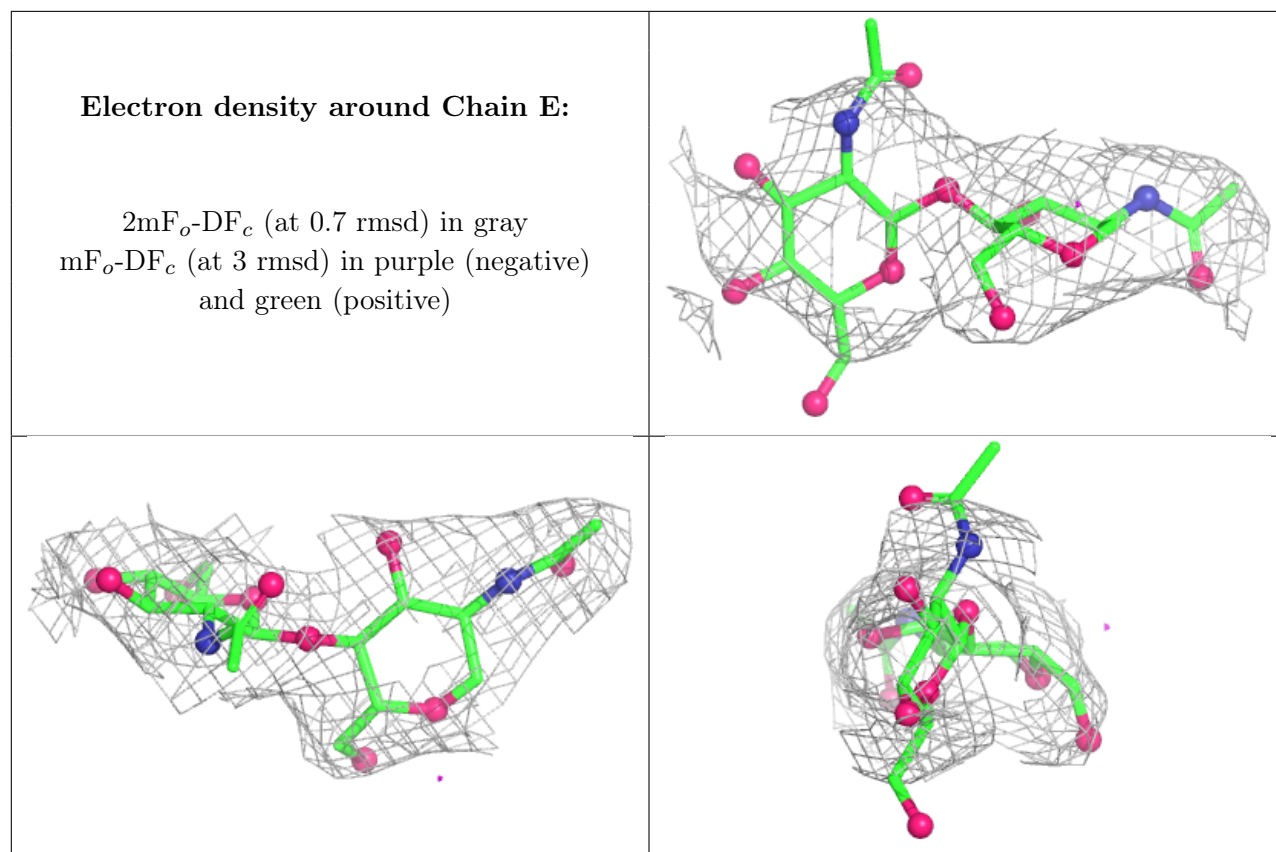
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	D	2	14/15	0.56	0.19	85,112,129,132	0
4	NAG	E	2	14/15	0.60	0.18	94,120,133,135	0
4	NAG	D	1	14/15	0.86	0.14	56,82,99,114	0
4	NAG	E	1	14/15	0.88	0.12	51,76,97,111	0

The following is a graphical depiction of the model fit to experimental electron density for oligosac-

charide. Each fit is shown from different orientation to approximate a three-dimensional view.





6.4 Ligands [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($\text{\AA}^2$)	Q<0.9
5	NAG	C	708	14/15	0.41	0.29	89,116,137,139	0
5	NAG	C	704	14/15	0.58	0.23	79,95,111,120	0
5	NAG	C	701	14/15	0.60	0.18	55,108,120,121	0
5	NAG	C	705	14/15	0.68	0.20	94,119,138,138	0

6.5 Other polymers [i](#)

There are no such residues in this entry.