



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:03 PM UTC

PDB ID : 6UQR / pdb_00006uqr
Title : Complex of IgE and Ligelizumab
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Deposited on : 2019-10-21
Resolution : 3.65 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	:	4-5-2 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

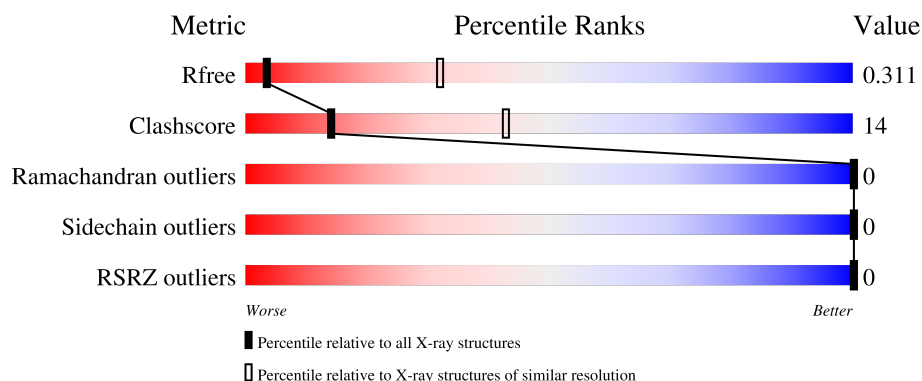
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

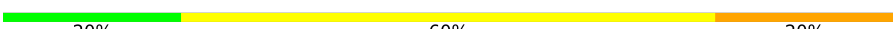
The reported resolution of this entry is 3.65 Å.

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	1062 (3.78-3.54)
Clashscore	190562	1009 (3.76-3.56)
Ramachandran outliers	187476	1054 (3.78-3.54)
Sidechain outliers	187428	1052 (3.78-3.54)
RSRZ outliers	180081	1061 (3.78-3.54)

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	268	
1	C	268	
2	B	247	
2	D	247	
3	E	5	

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Mol	Chain	Length	Quality of chain
4	F	4	 50%50%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6822 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 Ligelizumab.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	0	0	0
			1738	1102	284	344	8			
1	C	221	Total	C	N	O	S	0	0	0
			1691	1075	276	333	7			

- Molecule 2 is a protein called IgE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	212	Total	C	N	O	S	0	0	0
			1643	1027	299	311	6			
2	D	212	Total	C	N	O	S	0	0	0
			1639	1025	299	309	6			

There are 58 discrepancies between the modelled and reference sequences:

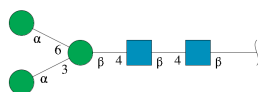
Chain	Residue	Modelled	Actual	Comment	Reference
B	299	ALA	-	expression tag	UNP P01854
B	300	PRO	-	expression tag	UNP P01854
B	301	MET	-	expression tag	UNP P01854
B	302	ALA	-	expression tag	UNP P01854
B	303	GLU	-	expression tag	UNP P01854
B	304	GLY	-	expression tag	UNP P01854
B	305	GLY	-	expression tag	UNP P01854
B	306	GLY	-	expression tag	UNP P01854
B	307	GLN	-	expression tag	UNP P01854
B	308	ASN	-	expression tag	UNP P01854
B	309	HIS	-	expression tag	UNP P01854
B	310	HIS	-	expression tag	UNP P01854
B	311	HIS	-	expression tag	UNP P01854
B	312	HIS	-	expression tag	UNP P01854
B	313	HIS	-	expression tag	UNP P01854
B	314	HIS	-	expression tag	UNP P01854

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Chain	Residue	Modelled	Actual	Comment	Reference
B	315	HIS	-	expression tag	UNP P01854
B	316	HIS	-	expression tag	UNP P01854
B	317	GLY	-	expression tag	UNP P01854
B	318	GLY	-	expression tag	UNP P01854
B	319	GLU	-	expression tag	UNP P01854
B	320	ASN	-	expression tag	UNP P01854
B	321	LEU	-	expression tag	UNP P01854
B	322	TYR	-	expression tag	UNP P01854
B	323	PHE	-	expression tag	UNP P01854
B	324	GLN	-	expression tag	UNP P01854
B	325	GLY	-	expression tag	UNP P01854
B	326	GLY	-	expression tag	UNP P01854
B	327	SER	-	expression tag	UNP P01854
D	299	ALA	-	expression tag	UNP P01854
D	300	PRO	-	expression tag	UNP P01854
D	301	MET	-	expression tag	UNP P01854
D	302	ALA	-	expression tag	UNP P01854
D	303	GLU	-	expression tag	UNP P01854
D	304	GLY	-	expression tag	UNP P01854
D	305	GLY	-	expression tag	UNP P01854
D	306	GLY	-	expression tag	UNP P01854
D	307	GLN	-	expression tag	UNP P01854
D	308	ASN	-	expression tag	UNP P01854
D	309	HIS	-	expression tag	UNP P01854
D	310	HIS	-	expression tag	UNP P01854
D	311	HIS	-	expression tag	UNP P01854
D	312	HIS	-	expression tag	UNP P01854
D	313	HIS	-	expression tag	UNP P01854
D	314	HIS	-	expression tag	UNP P01854
D	315	HIS	-	expression tag	UNP P01854
D	316	HIS	-	expression tag	UNP P01854
D	317	GLY	-	expression tag	UNP P01854
D	318	GLY	-	expression tag	UNP P01854
D	319	GLU	-	expression tag	UNP P01854
D	320	ASN	-	expression tag	UNP P01854
D	321	LEU	-	expression tag	UNP P01854
D	322	TYR	-	expression tag	UNP P01854
D	323	PHE	-	expression tag	UNP P01854
D	324	GLN	-	expression tag	UNP P01854
D	325	GLY	-	expression tag	UNP P01854
D	326	GLY	-	expression tag	UNP P01854
D	327	SER	-	expression tag	UNP P01854

- 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	E	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 4 is an oligosaccharide called 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.

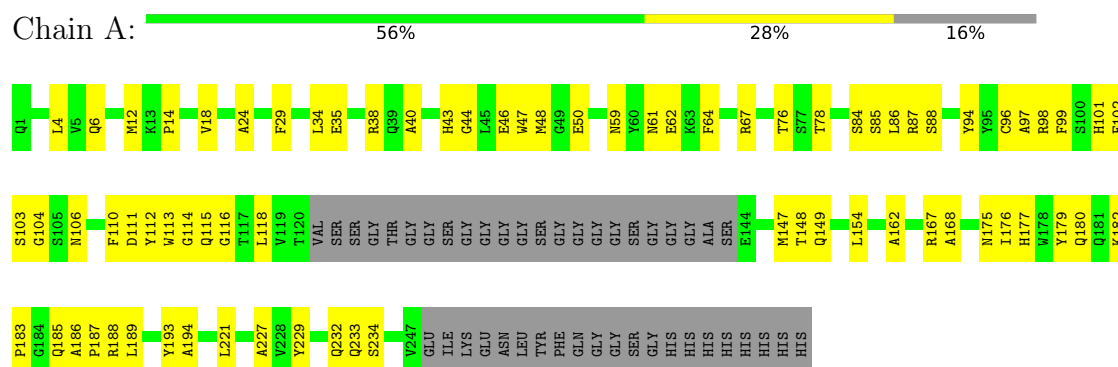


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	4	Total	C	N	O	0	0	0
			50	28	2	20			

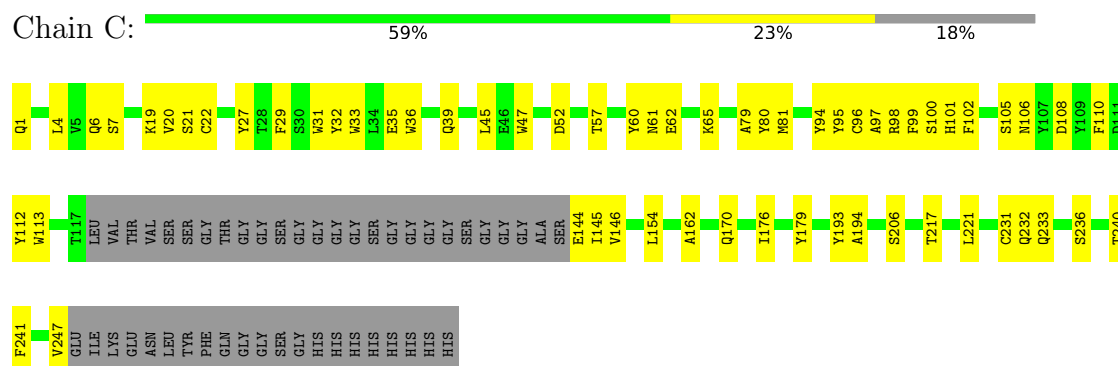
3 Residue-property plots

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.

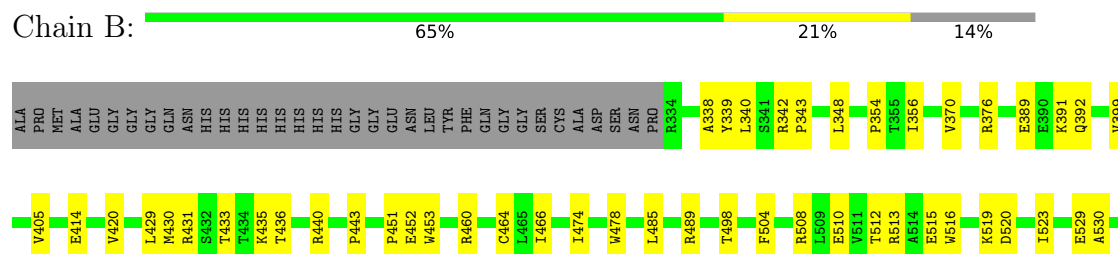
• Molecule 1: Ligelizumab



• Molecule 1: Ligelizumab



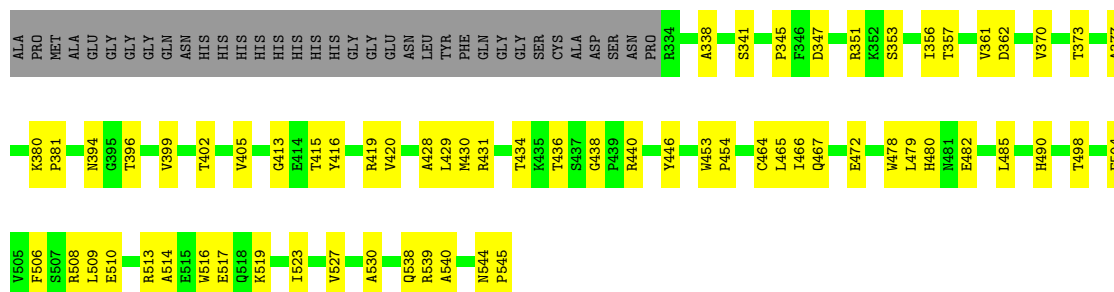
• Molecule 2: IgE





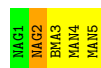
- Molecule 2: IgE

Chain D: 59% 27% 14%



- 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 E: 20% 60% 20%



- Molecule 4: 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 F: 50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.96Å 103.18Å 124.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.95 – 3.65 19.95 – 3.65	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.95-3.65) 99.2 (19.95-3.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 3.67Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.290 , 0.295 0.299 , 0.311	Depositor DCC
R_{free} test set	562 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	112.2	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 53.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	6822	wwPDB-VP
Average B, all atoms (Å ²)	113.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% 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: 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	0.20	0/1788	0.53	1/2436 (0.0%)
1	C	0.21	0/1741	0.53	0/2374
2	B	0.20	0/1686	0.50	0/2303
2	D	0.21	0/1682	0.53	0/2298
All	All	0.21	0/6897	0.52	1/9411 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	227	ALA	N-CA-C	5.16	115.16	107.88

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	1738	0	1613	54	0
1	C	1691	0	1550	55	0
2	B	1643	0	1585	38	0
2	D	1639	0	1581	50	0
3	E	61	0	52	2	0
4	F	50	0	43	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6822	0	6424	190	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 14.

The worst 5 of 190 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:C:176:ILE:HG23	1:C:194:ALA:HB2	1.74	0.69
2:D:380:LYS:HB3	2:D:381:PRO:HD2	1.75	0.69
1:C:61:ASN:OD1	1:C:62:GLU:N	2.27	0.68
1:C:39:GLN:HB2	1:C:45:LEU:HD23	1.76	0.67
2:B:343:PRO:HD3	2:B:356:ILE:HG22	1.76	0.67

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	220/268 (82%)	213 (97%)	7 (3%)	0	100	100
1	C	217/268 (81%)	209 (96%)	8 (4%)	0	100	100
2	B	210/247 (85%)	205 (98%)	5 (2%)	0	100	100
2	D	210/247 (85%)	207 (99%)	3 (1%)	0	100	100
All	All	857/1030 (83%)	834 (97%)	23 (3%)	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	186/215 (86%)	186 (100%)	0	100	100
1	C	177/215 (82%)	177 (100%)	0	100	100
2	B	180/212 (85%)	180 (100%)	0	100	100
2	D	179/212 (84%)	179 (100%)	0	100	100
All	All	722/854 (84%)	722 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	392	GLN

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
3	NAG	E	1	2,3	14,14,15	0.59	0	17,19,21	0.60	0
3	NAG	E	2	3	14,14,15	0.82	1 (7%)	17,19,21	1.34	1 (5%)
3	BMA	E	3	3	11,11,12	1.28	1 (9%)	15,15,17	1.35	1 (6%)
3	MAN	E	4	3	11,11,12	1.35	2 (18%)	15,15,17	1.15	2 (13%)
3	MAN	E	5	3	11,11,12	1.33	2 (18%)	15,15,17	1.20	2 (13%)
4	NAG	F	1	4,2	14,14,15	1.16	1 (7%)	17,19,21	1.56	2 (11%)
4	NAG	F	2	4	14,14,15	0.13	0	17,19,21	0.51	0
4	BMA	F	3	4	11,11,12	1.50	3 (27%)	15,15,17	1.40	3 (20%)
4	MAN	F	4	4	11,11,12	1.51	3 (27%)	15,15,17	0.94	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	E	1	2,3	-	1/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	BMA	E	3	3	-	2/2/19/22	0/1/1/1
3	MAN	E	4	3	-	2/2/19/22	0/1/1/1
3	MAN	E	5	3	-	2/2/19/22	0/1/1/1
4	NAG	F	1	4,2	-	1/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	BMA	F	3	4	-	2/2/19/22	0/1/1/1
4	MAN	F	4	4	-	0/2/19/22	1/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	1	NAG	O5-C1	4.16	1.50	1.43
4	F	3	BMA	O5-C5	-3.06	1.37	1.43
3	E	4	MAN	C1-C2	3.00	1.59	1.52
3	E	3	BMA	O5-C1	-2.93	1.38	1.43
4	F	4	MAN	O5-C5	2.90	1.49	1.43

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	1	NAG	C1-O5-C5	4.99	118.88	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	2	NAG	C1-O5-C5	4.87	118.71	112.19
3	E	3	BMA	C1-O5-C5	3.10	116.34	112.19
4	F	1	NAG	C2-N2-C7	2.92	126.81	122.90
4	F	3	BMA	O3-C3-C2	-2.37	105.22	110.05

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	1	NAG	C3-C2-N2-C7
3	E	3	BMA	C4-C5-C6-O6
3	E	3	BMA	O5-C5-C6-O6
4	F	3	BMA	O5-C5-C6-O6
4	F	3	BMA	C4-C5-C6-O6

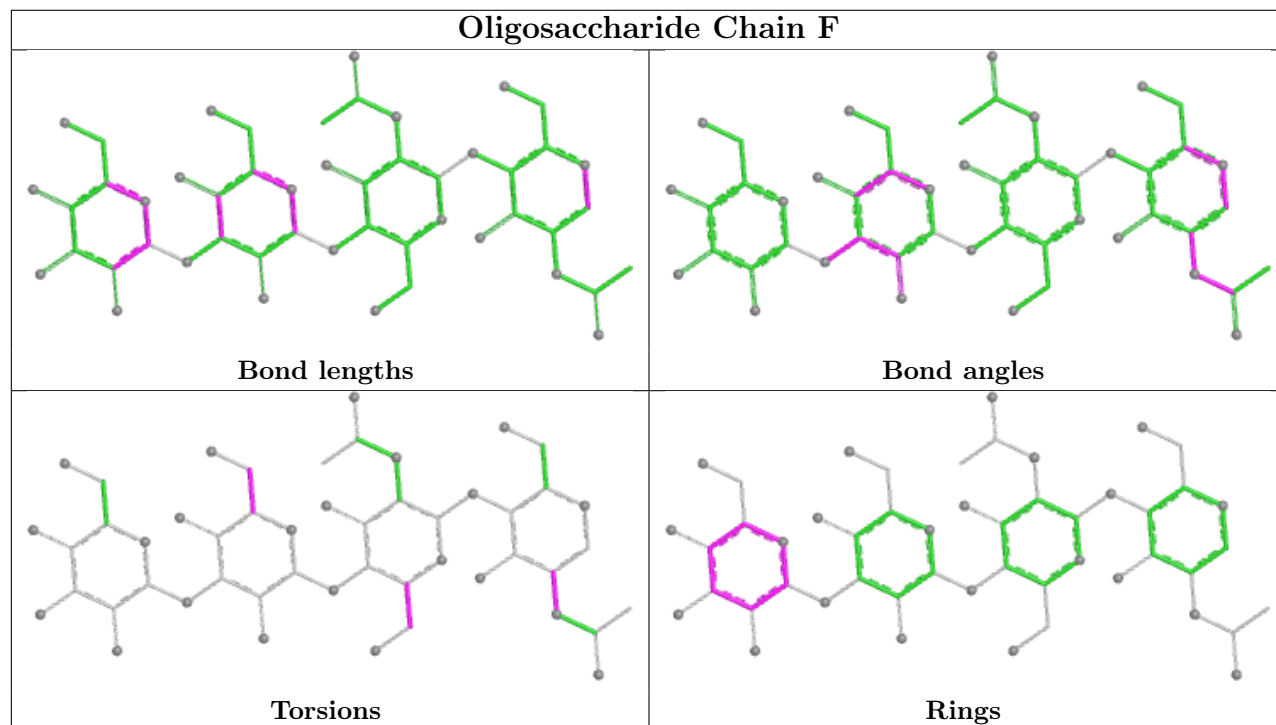
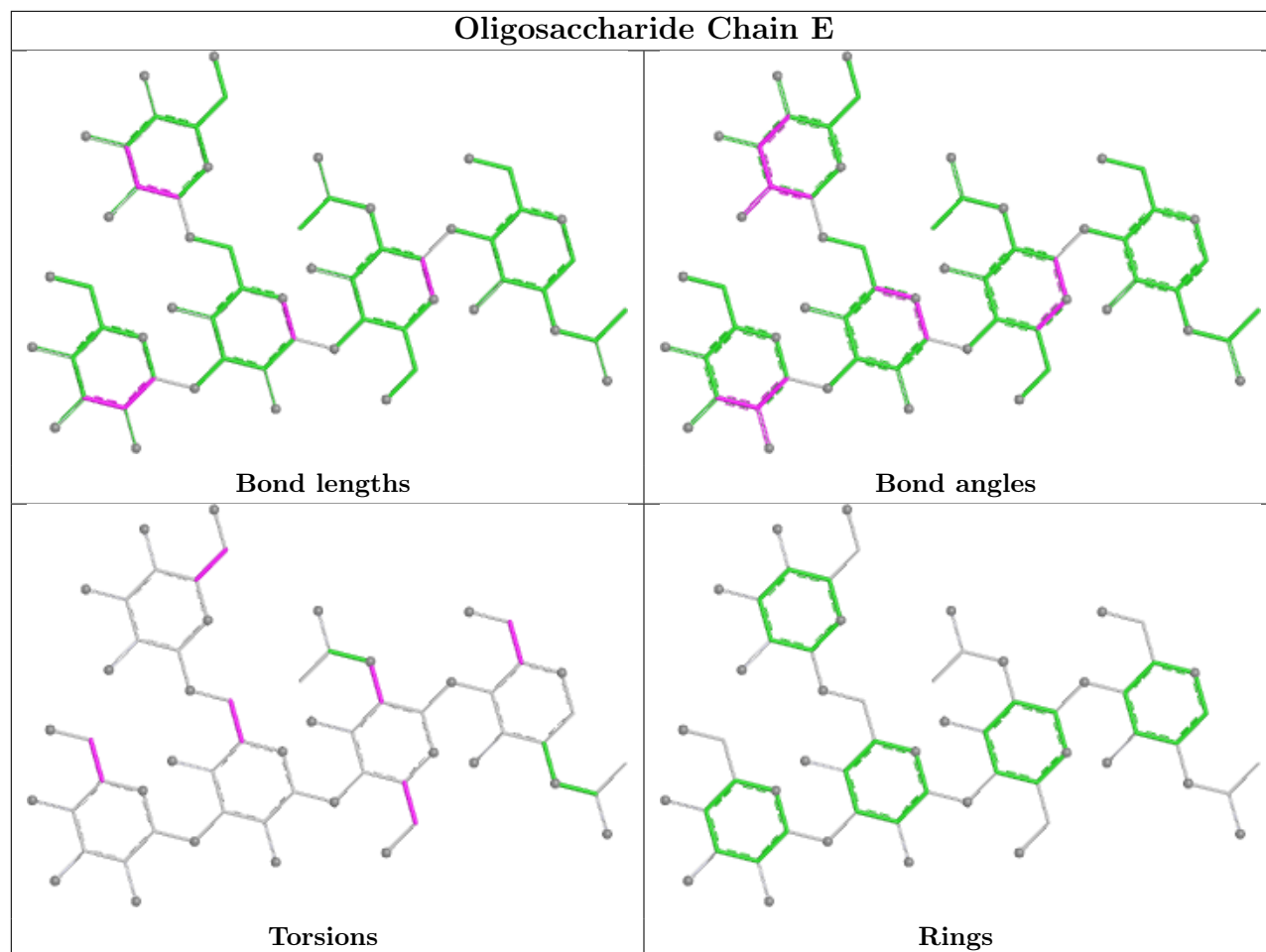
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	4	MAN	C1-C2-C3-C4-C5-O5

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	3	BMA	1	0
4	F	2	NAG	1	0
3	E	2	NAG	2	0
4	F	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 [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	224/268 (83%)	-0.21	0 100 100	75, 96, 124, 135	0
1	C	221/268 (82%)	-0.09	0 100 100	88, 125, 151, 170	0
2	B	212/247 (85%)	-0.21	0 100 100	84, 106, 130, 146	0
2	D	212/247 (85%)	-0.19	0 100 100	95, 118, 154, 167	0
All	All	869/1030 (84%)	-0.17	0 100 100	75, 111, 147, 170	0

There are no RSRZ outliers to report.

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

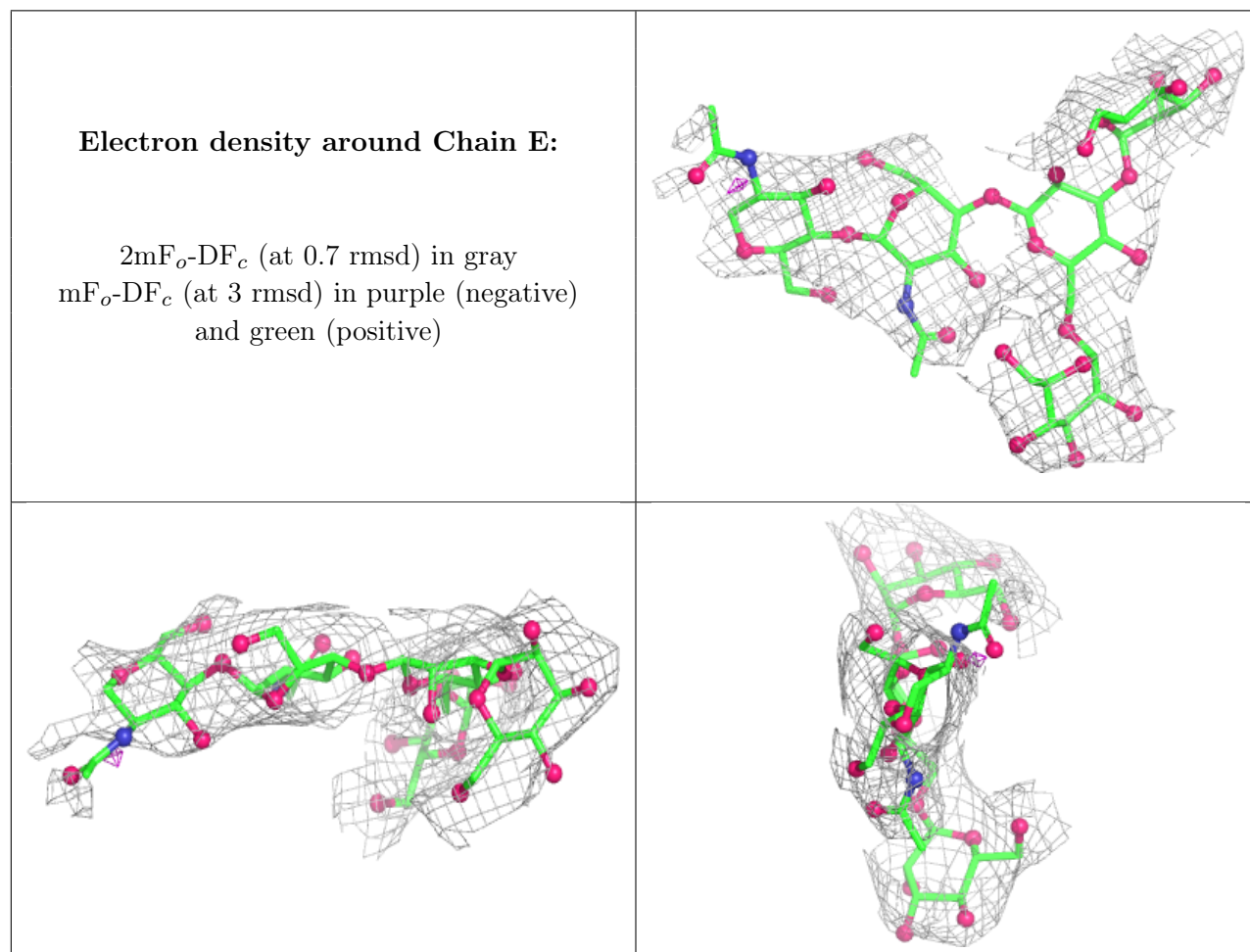
There are no non-standard protein/DNA/RNA residues in this entry.

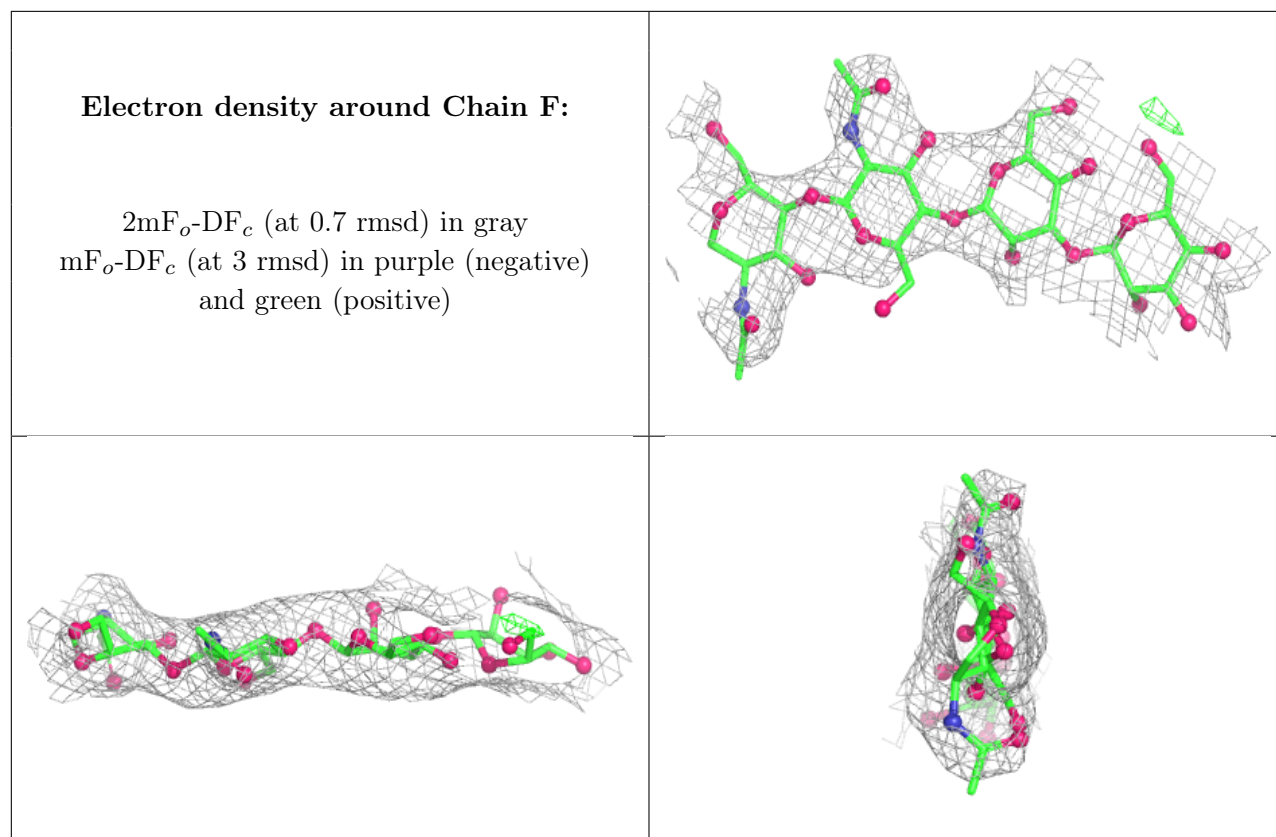
6.3 Carbohydrates [i](#)

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	MAN	F	4	11/12	0.30	0.12	119,119,119,119	0
3	MAN	E	5	11/12	0.43	0.08	119,119,119,119	0
3	NAG	E	1	14/15	0.52	0.12	123,123,123,123	0
3	MAN	E	4	11/12	0.53	0.08	132,132,132,132	0
4	NAG	F	1	14/15	0.66	0.09	130,130,130,130	0
4	BMA	F	3	11/12	0.68	0.08	116,116,116,116	0
3	NAG	E	2	14/15	0.78	0.08	119,119,119,119	0
4	NAG	F	2	14/15	0.78	0.08	124,124,124,124	0
3	BMA	E	3	11/12	0.82	0.05	123,123,123,123	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.