



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:15 PM UTC

PDB ID : 5HBT / pdb_00005hbt
Title : Complex structure of Fab35 and human nAChR alpha1
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Deposited on : 2016-01-02
Resolution : 2.61 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

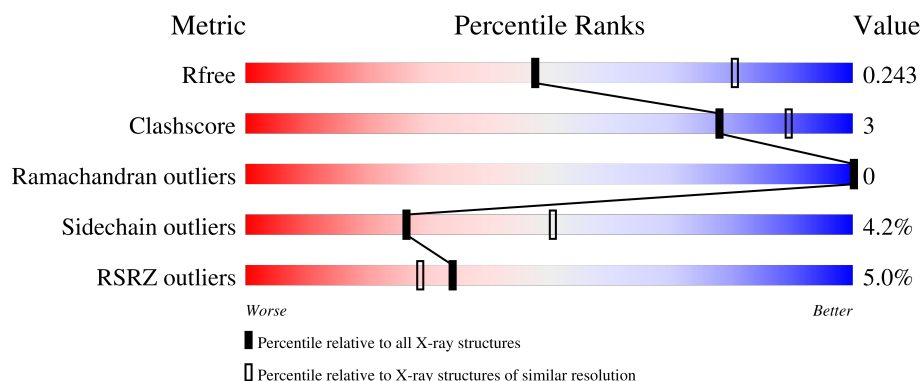
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	B	212	3% 95% ..
2	C	213	% 91% 8%
3	D	219	7% 85% 14% .
4	A	74	15% 91% 9%
5	E	9	11% 89%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5784 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 Acetylcholine receptor subunit alpha 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	212	Total	C	N	O	S	0	0	0
			1731	1108	290	326	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	LYS	-	expression tag	UNP G5E9G9
B	8	GLU	VAL	engineered mutation	UNP G5E9G9
B	149	ARG	TRP	engineered mutation	UNP G5E9G9
B	155	ALA	VAL	engineered mutation	UNP G5E9G9

- Molecule 2 is a protein called Fab35, Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	212	Total	C	N	O	S	0	0	0
			1628	1019	268	335	6			

- Molecule 3 is a protein called Fab35, Heavy Chain.

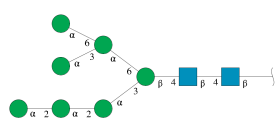
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	219	Total	C	N	O	S	0	0	0
			1671	1052	283	327	9			

- Molecule 4 is a protein called Alpha-bungarotoxin isoform V31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	74	Total	C	N	O	S	0	0	0
			547	337	94	105	11			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deox

y-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	9	Total	C	N	O	0	0	0
			105	58	2	45			

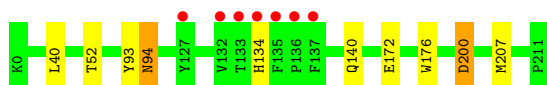
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	37	Total	O	0	0
			37	37		
6	C	23	Total	O	0	0
			23	23		
6	D	35	Total	O	0	0
			35	35		
6	A	7	Total	O	0	0
			7	7		

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.

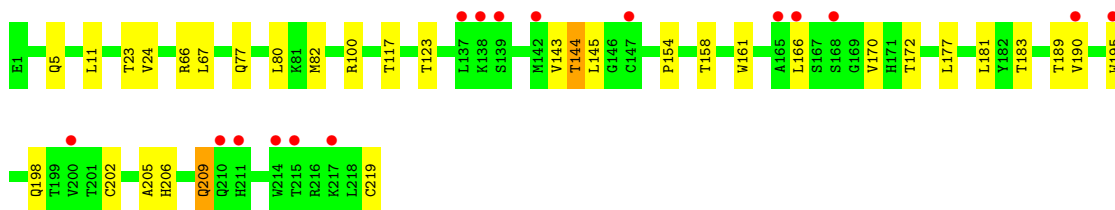
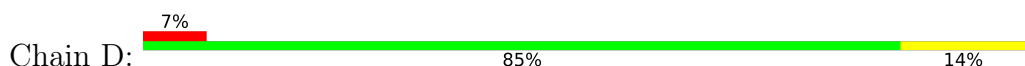
- Molecule 1: Acetylcholine receptor subunit alpha 1



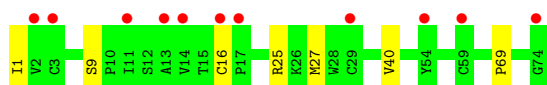
- Molecule 2: Fab35, Light Chain



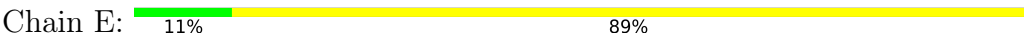
- Molecule 3: Fab35, Heavy Chain



- Molecule 4: Alpha-bungarotoxin isoform V31



- Molecule 5: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]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



MAN1
MAN2
MAN3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	160.01Å 42.14Å 136.49Å 90.00° 117.05° 90.00°	Depositor
Resolution (Å)	50.01 – 2.61 50.01 – 2.61	Depositor EDS
% Data completeness (in resolution range)	99.5 (50.01-2.61) 99.7 (50.01-2.61)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.207 , 0.260 (Not available) , 0.243	Depositor DCC
R_{free} test set	1231 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	48.6	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.1	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	0.94	EDS
Total number of atoms	5784	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% 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, MAN, BMA

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	B	0.60	0/1778	0.75	0/2422
2	C	0.58	0/1660	0.75	0/2257
3	D	0.60	0/1715	0.77	0/2346
4	A	0.63	0/561	0.83	0/763
All	All	0.60	0/5714	0.77	0/7788

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	93	TYR	Peptide

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	B	1731	0	1684	6	0
2	C	1628	0	1582	5	0
3	D	1671	0	1622	16	0
4	A	547	0	525	4	0
5	E	105	0	88	0	0
6	A	7	0	0	0	0
6	B	37	0	0	0	0
6	C	23	0	0	0	0
6	D	35	0	0	0	0
All	All	5784	0	5501	31	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 3.

All (31) 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)
3:D:23:THR:HG22	3:D:77:GLN:HE21	1.55	0.72
3:D:206:HIS:ND1	3:D:209:GLN:OE1	2.23	0.70
3:D:144:THR:HG22	3:D:189:THR:HG22	1.80	0.64
4:A:25:ARG:HD3	4:A:27:MET:HE3	1.82	0.61
1:B:94:ASN:O	1:B:94:ASN:ND2	2.34	0.60
4:A:27:MET:HE1	4:A:69:PRO:HG3	1.87	0.57
3:D:67:LEU:HD22	3:D:80:LEU:HD11	1.90	0.54
3:D:158:THR:HG22	3:D:205:ALA:HB3	1.89	0.54
3:D:166:LEU:HD12	3:D:170:VAL:HG21	1.90	0.54
4:A:27:MET:HE2	4:A:40:VAL:HG22	1.91	0.53
4:A:1:ILE:HG23	4:A:16:CYS:HB2	1.91	0.52
3:D:23:THR:CG2	3:D:77:GLN:HE21	2.24	0.50
3:D:66:ARG:CZ	3:D:82:MET:HE2	2.41	0.50
2:C:32:TYR:HB2	2:C:92:ILE:HG13	1.95	0.49
3:D:11:LEU:HD23	3:D:123:THR:HG23	1.94	0.48
3:D:209:GLN:HE21	3:D:209:GLN:C	2.21	0.48
3:D:144:THR:CG2	3:D:189:THR:HG22	2.44	0.48
2:C:78:LEU:HD11	2:C:103:LEU:HD21	1.94	0.47
3:D:143:VAL:N	3:D:190:VAL:O	2.47	0.47
3:D:158:THR:CG2	3:D:205:ALA:HB3	2.45	0.46
1:B:140:GLN:HE21	1:B:207:MET:HE2	1.83	0.43
2:C:178:LEU:HD11	2:C:180:LEU:HD21	2.00	0.43
3:D:154:PRO:O	3:D:206:HIS:NE2	2.45	0.43
2:C:12:SER:HA	2:C:104:GLU:O	2.19	0.43
1:B:176:TRP:CD1	1:B:207:MET:HE3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:145:LEU:HD21	3:D:195:TRP:CE2	2.54	0.42
3:D:161:TRP:CZ3	3:D:202:CYS:HB3	2.55	0.42
1:B:200:ASP:OD1	1:B:200:ASP:C	2.64	0.41
1:B:176:TRP:CG	1:B:207:MET:HE3	2.56	0.40
2:C:149:ILE:HD13	2:C:188:HIS:CD2	2.56	0.40
1:B:40:LEU:CD2	1:B:52:THR:HG22	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	B	210/212 (99%)	205 (98%)	5 (2%)	0	100	100
2	C	210/213 (99%)	200 (95%)	10 (5%)	0	100	100
3	D	217/219 (99%)	205 (94%)	12 (6%)	0	100	100
4	A	72/74 (97%)	69 (96%)	3 (4%)	0	100	100
All	All	709/718 (99%)	679 (96%)	30 (4%)	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	B	196/197 (100%)	192 (98%)	4 (2%)	48	73
2	C	186/189 (98%)	176 (95%)	10 (5%)	20	40
3	D	190/191 (100%)	178 (94%)	12 (6%)	16	34
4	A	65/66 (98%)	64 (98%)	1 (2%)	57	79
All	All	637/643 (99%)	610 (96%)	27 (4%)	26	50

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	94	ASN
1	B	134	HIS
1	B	172	GLU
1	B	200	ASP
2	C	22	THR
2	C	40	LEU
2	C	69	THR
2	C	92	ILE
2	C	99	THR
2	C	102	LYS
2	C	107	ARG
2	C	142	ASP
2	C	186	GLU
2	C	211	ASN
3	D	5	GLN
3	D	24	VAL
3	D	100	ARG
3	D	117	THR
3	D	144	THR
3	D	172	THR
3	D	177	LEU
3	D	181	LEU
3	D	183	THR
3	D	198	GLN
3	D	209	GLN
3	D	219	CYS
4	A	9	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	42	ASN

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Mol	Chain	Res	Type
1	B	47	ASN
1	B	64	ASN
1	B	140	GLN
2	C	27	GLN
2	C	137	ASN
2	C	189	ASN
2	C	209	ASN
3	D	77	GLN
3	D	171	HIS
3	D	198	GLN

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 ⓘ

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	$\# Z > 2$
5	NAG	E	1	5,1	14,14,15	0.33	0	17,19,21	1.00	1 (5%)
5	NAG	E	2	5	14,14,15	0.38	0	17,19,21	0.97	1 (5%)
5	BMA	E	3	5	11,11,12	0.41	0	15,15,17	0.64	0
5	MAN	E	4	5	11,11,12	0.44	0	15,15,17	1.53	2 (13%)
5	MAN	E	5	5	11,11,12	0.46	0	15,15,17	0.70	1 (6%)
5	MAN	E	6	5	11,11,12	0.39	0	15,15,17	0.78	1 (6%)
5	MAN	E	7	5	11,11,12	0.35	0	15,15,17	0.84	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	MAN	E	8	5	11,11,12	0.34	0	15,15,17	1.28	1 (6%)
5	MAN	E	9	5	11,11,12	0.39	0	15,15,17	0.93	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
5	NAG	E	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	E	2	5	-	2/6/23/26	0/1/1/1
5	BMA	E	3	5	-	0/2/19/22	0/1/1/1
5	MAN	E	4	5	-	1/2/19/22	0/1/1/1
5	MAN	E	5	5	-	2/2/19/22	0/1/1/1
5	MAN	E	6	5	-	0/2/19/22	0/1/1/1
5	MAN	E	7	5	-	0/2/19/22	0/1/1/1
5	MAN	E	8	5	-	0/2/19/22	0/1/1/1
5	MAN	E	9	5	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	4	MAN	C1-O5-C5	4.85	118.69	112.19
5	E	8	MAN	C1-O5-C5	4.28	117.92	112.19
5	E	2	NAG	C1-O5-C5	2.66	115.75	112.19
5	E	7	MAN	C1-O5-C5	2.47	115.50	112.19
5	E	1	NAG	O5-C1-C2	-2.36	107.64	111.29
5	E	9	MAN	C1-O5-C5	2.33	115.31	112.19
5	E	5	MAN	C1-O5-C5	2.15	115.07	112.19
5	E	4	MAN	C3-C4-C5	2.13	114.09	110.23
5	E	6	MAN	C1-O5-C5	2.12	115.03	112.19

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	5	MAN	O5-C5-C6-O6
5	E	5	MAN	C4-C5-C6-O6
5	E	2	NAG	C4-C5-C6-O6

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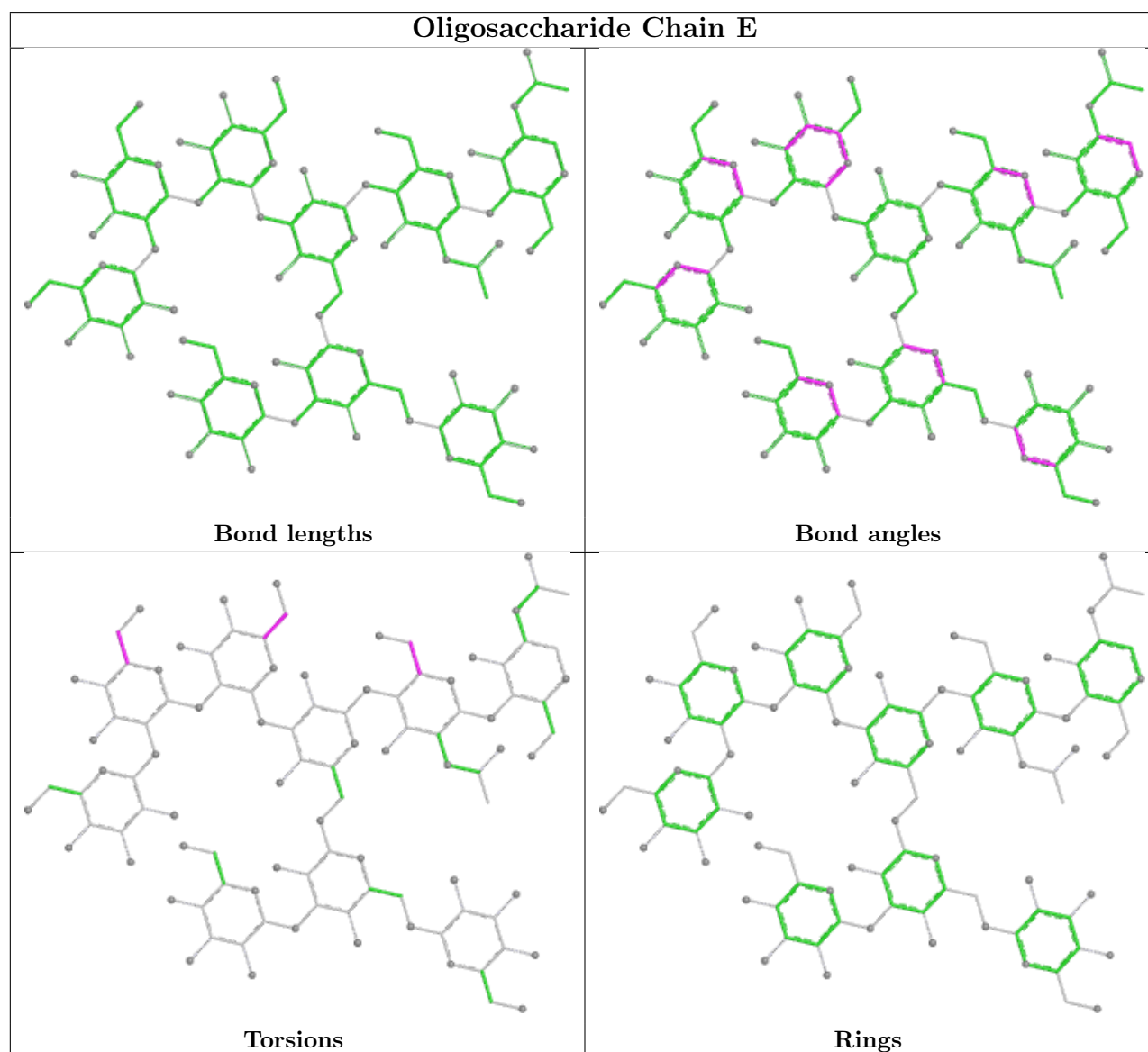
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Mol	Chain	Res	Type	Atoms
5	E	4	MAN	O5-C5-C6-O6
5	E	2	NAG	O5-C5-C6-O6

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](#)

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	B	212/212 (100%)	0.02	7 (3%) 49 44	29, 42, 74, 115	0
2	C	212/213 (99%)	0.12	2 (0%) 81 78	32, 56, 86, 112	0
3	D	219/219 (100%)	0.31	16 (7%) 21 17	31, 57, 108, 135	0
4	A	74/74 (100%)	1.15	11 (14%) 5 4	45, 89, 113, 118	0
All	All	717/718 (99%)	0.26	36 (5%) 34 29	29, 54, 103, 135	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	A	3	CYS	4.7
1	B	135	PHE	3.5
1	B	132	VAL	3.4
3	D	211	HIS	3.1
1	B	133	THR	3.1
3	D	215	THR	2.9
3	D	137	LEU	2.9
3	D	214	TRP	2.8
3	D	166	LEU	2.8
4	A	2	VAL	2.8
4	A	17	PRO	2.7
3	D	147	CYS	2.7
2	C	210	ARG	2.7
4	A	59	CYS	2.6
3	D	210	GLN	2.4
4	A	14	VAL	2.4
4	A	11	ILE	2.4
1	B	134	HIS	2.3
4	A	54	TYR	2.3
3	D	217	LYS	2.3
4	A	16	CYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	136	PRO	2.2
3	D	168	SER	2.2
3	D	142	MET	2.2
3	D	200	VAL	2.2
4	A	29	CYS	2.2
3	D	139	SER	2.2
4	A	13	ALA	2.1
1	B	137	PHE	2.1
1	B	127	TYR	2.1
2	C	212	GLU	2.1
3	D	165	ALA	2.1
3	D	190	VAL	2.1
3	D	195	TRP	2.0
4	A	74	GLY	2.0
3	D	138	LYS	2.0

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

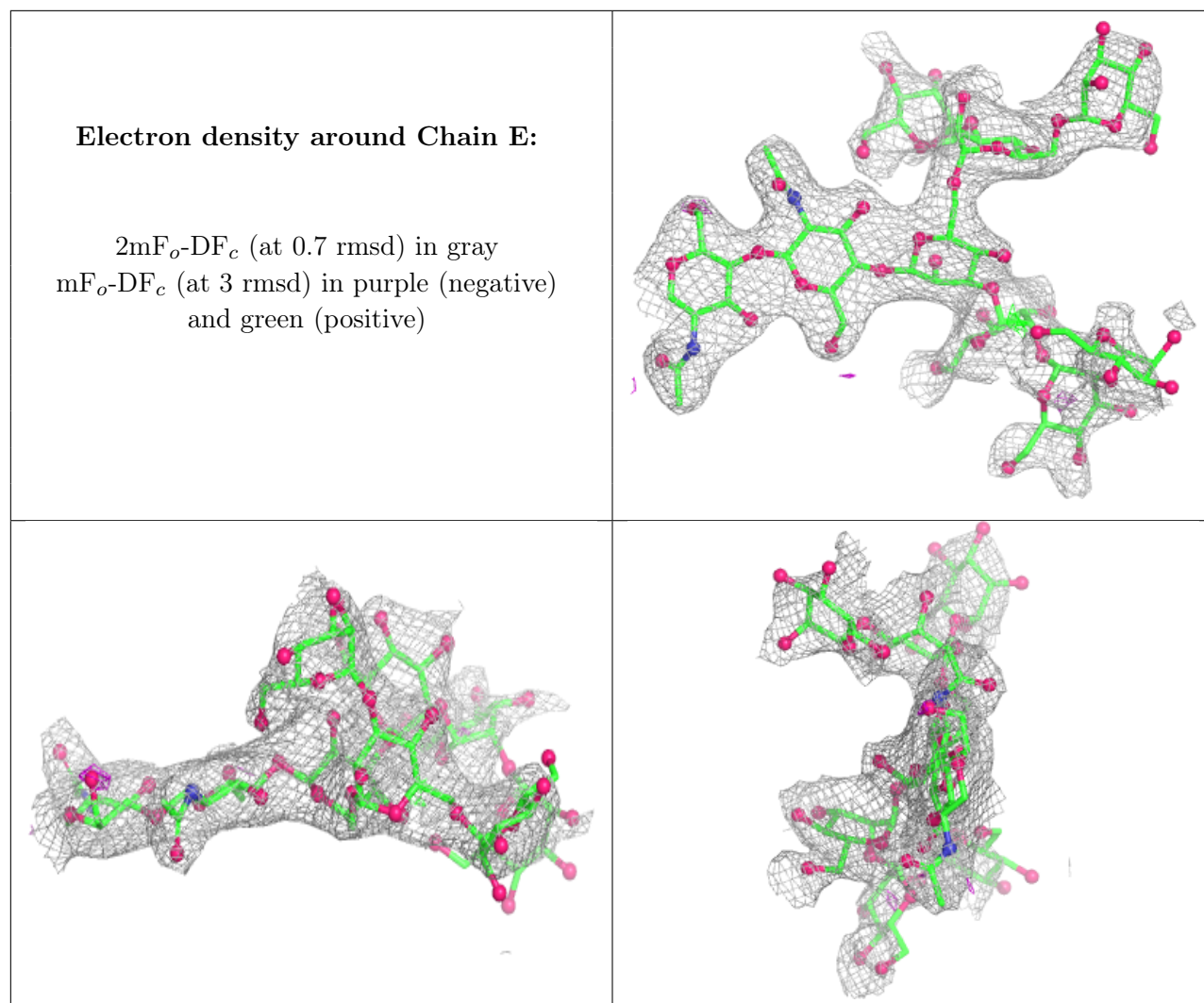
There are no non-standard protein/DNA/RNA residues in this entry.

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
5	MAN	E	6	11/12	0.38	0.15	122,125,126,126	0
5	MAN	E	5	11/12	0.44	0.14	111,113,115,121	0
5	MAN	E	4	11/12	0.62	0.12	90,93,94,102	0
5	MAN	E	8	11/12	0.72	0.14	89,91,92,92	0
5	MAN	E	7	11/12	0.87	0.09	76,78,81,84	0
5	NAG	E	1	14/15	0.89	0.11	42,43,45,47	0
5	MAN	E	9	11/12	0.89	0.09	84,85,88,88	0
5	BMA	E	3	11/12	0.94	0.06	64,71,74,81	0
5	NAG	E	2	14/15	0.95	0.07	46,47,51,57	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.