



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:32 PM UTC

PDB ID : 8UDZ / pdb_00008udz
Title : The Structure of LTBP-49247 Fab Bound to TGFbeta1 Small Latent Complex
Authors : Streich Jr., F.C.; Nicholls, S.B.; Boston, C.J.; Ramachandran, S.
Deposited on : 2023-09-29
Resolution : 2.21 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

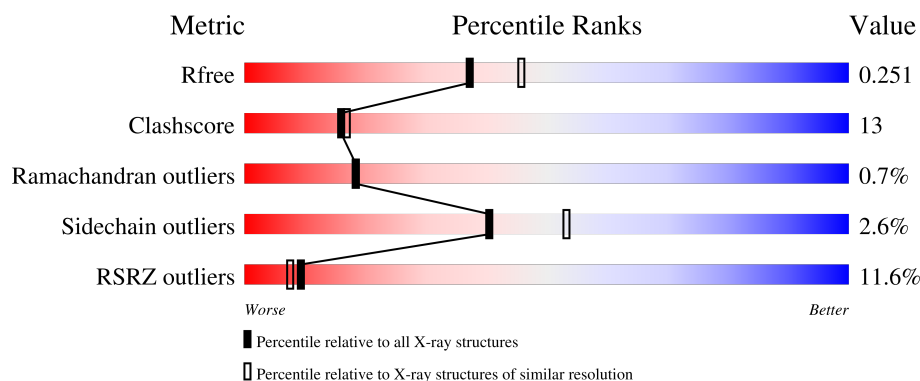
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.21 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	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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	361	14% 46% 24% • 29%
1	B	361	11% 58% 23% • 19%
2	C	233	21% 69% 24% • 6%
2	E	233	5% 74% 22% •
3	D	218	5% 77% 21% •

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Mol	Chain	Length	Quality of chain
3	F	218	2% 88% 9% ..
4	G	5	20% 80%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11329 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 Transforming growth factor beta-1 proprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	0	0	0
			2062	1315	360	371	16			
1	B	294	Total	C	N	O	S	0	1	0
			2374	1520	413	424	17			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	SER	CYS	engineered mutation	UNP P01137
A	278	ALA	ARG	engineered mutation	UNP P01137
B	33	SER	CYS	engineered mutation	UNP P01137
B	278	ALA	ARG	engineered mutation	UNP P01137

- Molecule 2 is a protein called LTBP-49247 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	220	Total	C	N	O	S	0	0	0
			1654	1044	291	313	6			
2	E	223	Total	C	N	O	S	0	0	0
			1676	1057	295	318	6			

- Molecule 3 is a protein called LTBP-49247 Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	214	Total	C	N	O	S	0	0	0
			1621	1006	270	340	5			
3	F	214	Total	C	N	O	S	0	0	0
			1621	1006	270	340	5			

- Molecule 4 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
4	G	5	Total	C	N	O	0	0	0
			61	34	2	25			

- 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	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is water.

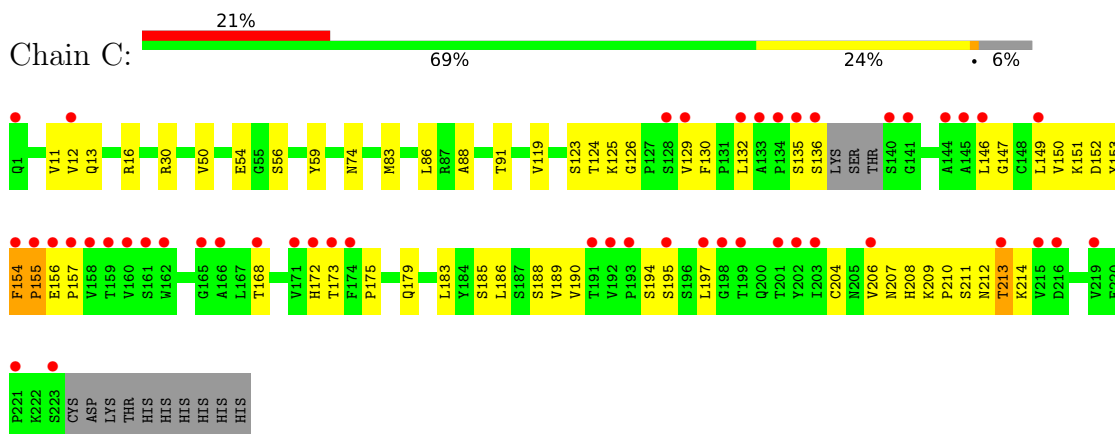
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	26	Total	O	0	0
			26	26		
6	B	30	Total	O	0	0
			30	30		
6	C	21	Total	O	0	0
			21	21		
6	D	30	Total	O	0	0
			30	30		

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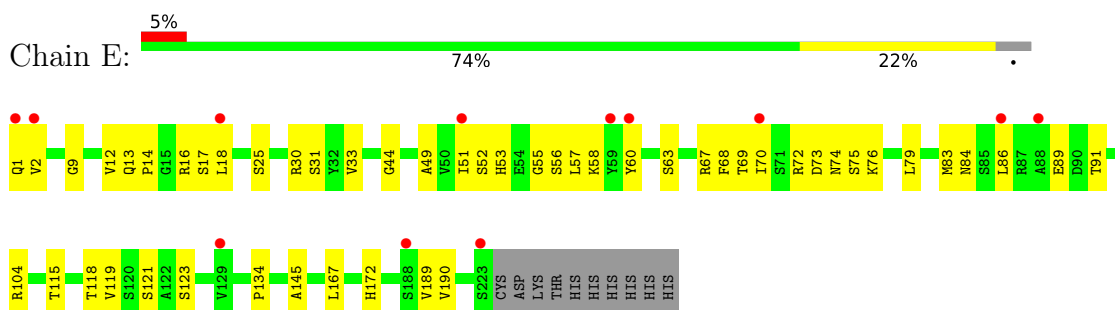
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	28	Total	O	0	0
			28	28		
6	F	97	Total	O	0	0
			97	97		

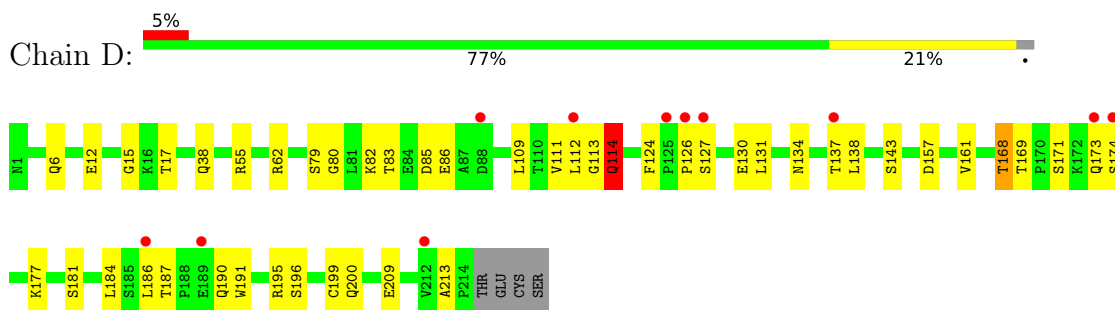
- Molecule 2: LTBP-49247 Fab Heavy Chain



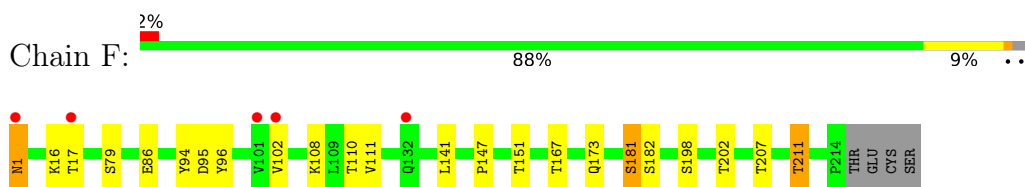
- Molecule 2: LTBP-49247 Fab Heavy Chain



- Molecule 3: LTBP-49247 Fab Light Chain



- Molecule 3: LTBP-49247 Fab Light Chain



- Molecule 4: 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





4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	73.50Å 141.91Å 186.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.50 – 2.21 73.50 – 2.21	Depositor EDS
% Data completeness (in resolution range)	99.5 (73.50-2.21) 99.5 (73.50-2.21)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.99 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.232 , 0.264 (Not available) , 0.251	Depositor DCC
R_{free} test set	4924 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	62.3	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 53.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11329	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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, 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	0.44	0/2102	0.71	2/2838 (0.1%)
1	B	0.40	0/2432	0.61	0/3292
2	C	0.43	0/1693	0.63	1/2300 (0.0%)
2	E	0.35	0/1716	0.57	0/2332
3	D	0.40	0/1660	0.64	0/2267
3	F	0.47	0/1660	0.71	0/2267
All	All	0.41	0/11263	0.65	3/15296 (0.0%)

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	A	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	230	ASN	N-CA-C	-9.88	100.54	112.59
2	C	155	PRO	N-CA-C	-5.96	101.73	111.15
1	A	229	ASP	O-C-N	5.47	124.88	120.83

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	110	ARG	Sidechain

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	2062	0	2067	88	0
1	B	2374	0	2373	72	0
2	C	1654	0	1641	49	0
2	E	1676	0	1667	42	0
3	D	1621	0	1544	37	0
3	F	1621	0	1544	23	0
4	G	61	0	52	0	0
5	A	14	0	13	0	0
5	B	14	0	13	0	0
6	A	26	0	0	1	0
6	B	30	0	0	1	0
6	C	21	0	0	0	0
6	D	30	0	0	1	0
6	E	28	0	0	0	0
6	F	97	0	0	2	0
All	All	11329	0	10914	291	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 13.

The worst 5 of 291 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:F:17:THR:HG22	3:F:79:SER:CA	1.75	1.16
3:F:17:THR:CG2	3:F:79:SER:HA	1.88	1.03
3:F:17:THR:HG22	3:F:79:SER:HA	0.97	0.97
2:C:30:ARG:HG3	2:C:74:ASN:ND2	1.83	0.94
2:E:49:ALA:HB1	2:E:70:ILE:HD11	1.55	0.88

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	237/361 (66%)	223 (94%)	11 (5%)	3 (1%)	9	7
1	B	281/361 (78%)	258 (92%)	20 (7%)	3 (1%)	11	9
2	C	216/233 (93%)	204 (94%)	11 (5%)	1 (0%)	24	26
2	E	221/233 (95%)	211 (96%)	9 (4%)	1 (0%)	24	26
3	D	212/218 (97%)	201 (95%)	10 (5%)	1 (0%)	24	26
3	F	212/218 (97%)	205 (97%)	7 (3%)	0	100	100
All	All	1379/1624 (85%)	1302 (94%)	68 (5%)	9 (1%)	18	18

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	175	SER
2	C	154	PHE
1	A	313	GLU
2	E	56	SER
1	B	251	HIS

5.3.2 Protein sidechains

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	143/321 (44%)	137 (96%)	6 (4%)	26	34
1	B	260/321 (81%)	257 (99%)	3 (1%)	63	76
2	C	170/195 (87%)	165 (97%)	5 (3%)	37	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	185/195 (95%)	182 (98%)	3 (2%)	55	70
3	D	187/191 (98%)	179 (96%)	8 (4%)	26	33
3	F	187/191 (98%)	183 (98%)	4 (2%)	47	61
All	All	1132/1414 (80%)	1103 (97%)	29 (3%)	40	53

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	6	GLN
3	F	181	SER
3	D	127	SER
2	E	123	SER
3	D	114	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	200	GLN
2	E	13	GLN
3	F	203	HIS
2	E	82	GLN
2	C	53	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 ⓘ

5 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	G	1	1,4	14,14,15	0.37	0	17,19,21	0.67	0
4	NAG	G	2	4	14,14,15	0.36	0	17,19,21	0.77	1 (5%)
4	BMA	G	3	4	11,11,12	1.01	0	15,15,17	1.29	2 (13%)
4	MAN	G	4	4	11,11,12	1.57	3 (27%)	15,15,17	1.11	2 (13%)
4	MAN	G	5	4	11,11,12	1.54	3 (27%)	15,15,17	1.43	3 (20%)

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

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	5	MAN	C2-C3	3.39	1.57	1.52
4	G	4	MAN	C1-C2	3.09	1.59	1.52
4	G	4	MAN	O5-C5	2.56	1.48	1.43
4	G	5	MAN	C1-C2	2.47	1.58	1.52
4	G	5	MAN	O5-C5	2.25	1.47	1.43

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	5	MAN	C1-O5-C5	3.64	117.07	112.19
4	G	4	MAN	C1-O5-C5	3.17	116.43	112.19
4	G	2	NAG	C1-O5-C5	2.62	115.69	112.19
4	G	3	BMA	C1-O5-C5	2.60	115.67	112.19
4	G	5	MAN	C1-C2-C3	2.29	112.98	109.64

There are no chirality outliers.

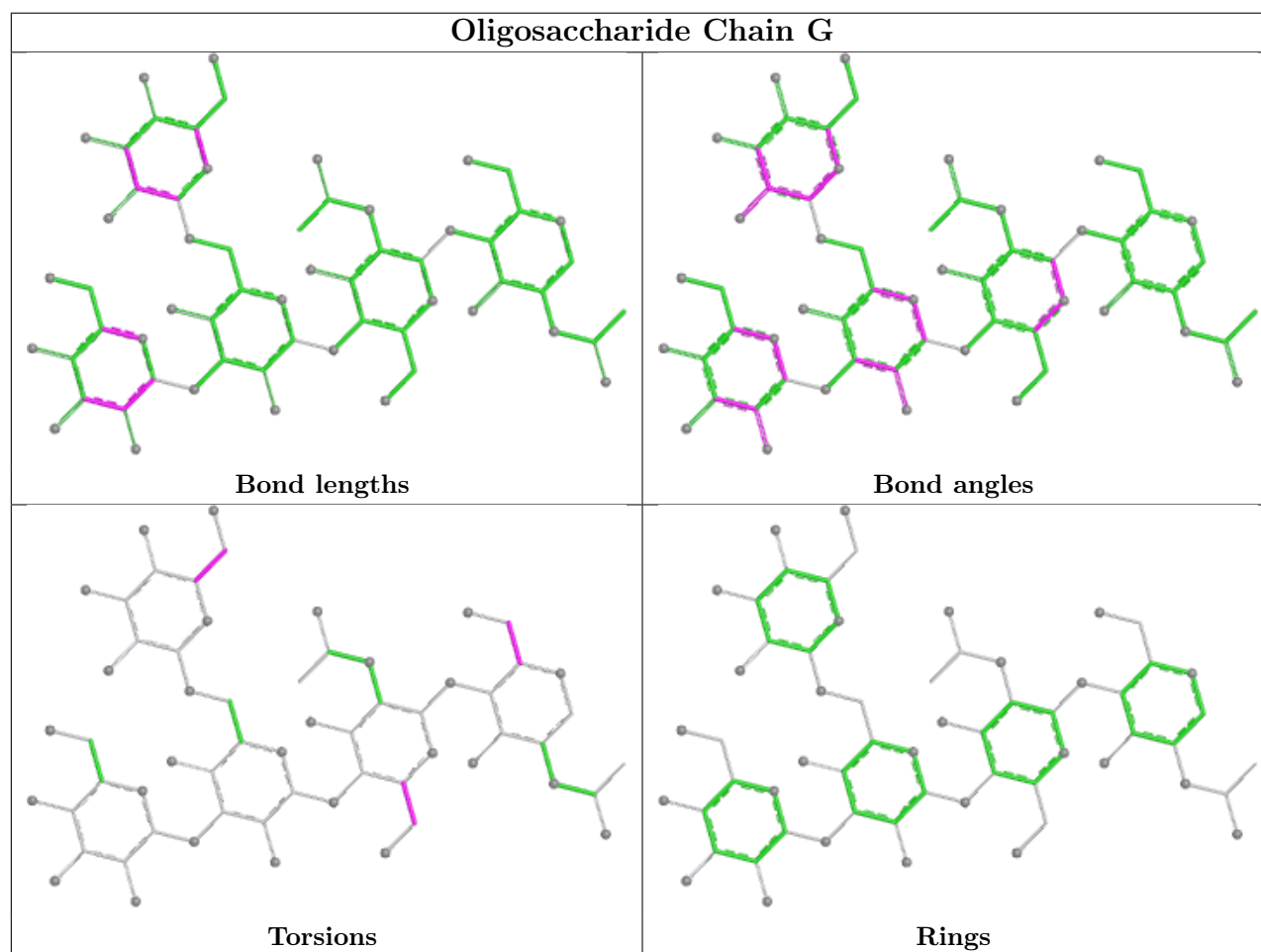
5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	2	NAG	O5-C5-C6-O6
4	G	5	MAN	O5-C5-C6-O6
4	G	2	NAG	C4-C5-C6-O6
4	G	1	NAG	C4-C5-C6-O6
4	G	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](#)

2 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	B	401	1	14,14,15	0.75	1 (7%)	17,19,21	0.69	1 (5%)
5	NAG	A	401	1	14,14,15	0.38	0	17,19,21	0.51	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	B	401	1	-	2/6/23/26	0/1/1/1
5	NAG	A	401	1	-	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)
5	B	401	NAG	C1-C2	2.07	1.55	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	401	NAG	C1-O5-C5	2.35	115.33	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	401	NAG	C4-C5-C6-O6
5	A	401	NAG	O5-C5-C6-O6
5	B	401	NAG	O5-C5-C6-O6
5	B	401	NAG	C4-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 [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	257/361 (71%)	1.11	49 (19%) 3 2	30, 95, 128, 136	0
1	B	294/361 (81%)	0.92	40 (13%) 7 5	39, 76, 119, 140	1 (0%)
2	C	220/233 (94%)	1.05	48 (21%) 2 1	44, 88, 159, 186	0
2	E	223/233 (95%)	0.59	12 (5%) 31 28	54, 79, 114, 132	0
3	D	214/218 (98%)	0.56	11 (5%) 33 30	45, 78, 131, 158	0
3	F	214/218 (98%)	-0.01	5 (2%) 61 59	43, 55, 81, 112	0
All	All	1422/1624 (87%)	0.73	165 (11%) 9 7	30, 76, 132, 186	1 (0%)

The worst 5 of 165 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	124	PHE	7.4
1	A	327	PRO	5.7
2	C	215	VAL	5.5
1	B	121	TYR	5.4
1	B	120	ILE	5.3

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

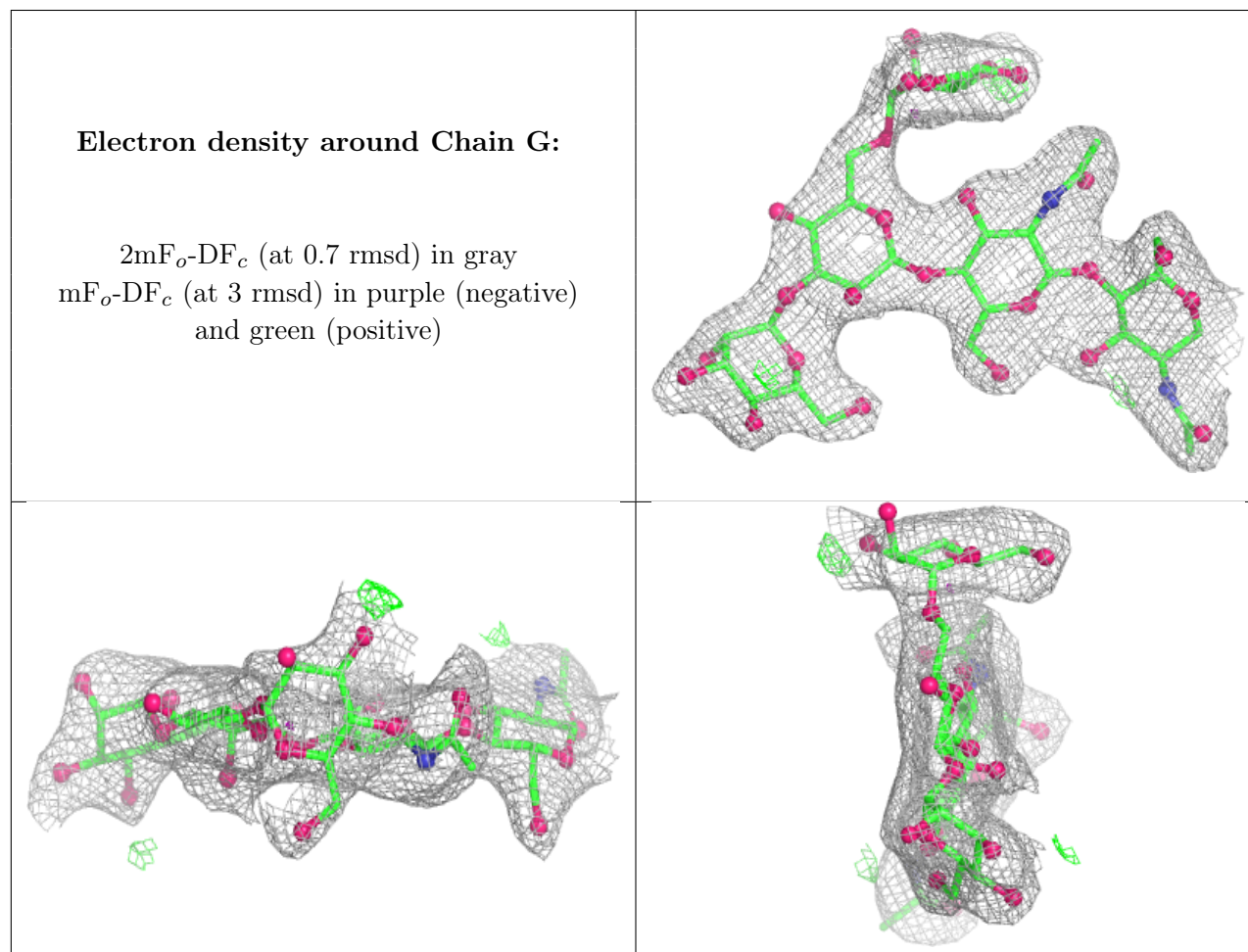
There are no non-standard protein/DNA/RNA residues in this entry.

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($\text{\AA}^2$)	Q<0.9
4	MAN	G	5	11/12	0.56	0.17	107,113,115,120	0
4	BMA	G	3	11/12	0.84	0.11	86,91,100,110	0
4	NAG	G	2	14/15	0.89	0.10	78,85,93,95	0
4	MAN	G	4	11/12	0.91	0.09	79,81,86,86	0
4	NAG	G	1	14/15	0.93	0.09	66,72,79,84	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 ⓘ

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	A	401	14/15	0.62	0.15	110,120,125,125	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	NAG	B	401	14/15	0.71	0.16	104,111,120,120	0

6.5 Other polymers [i](#)

There are no such residues in this entry.