



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 14, 2022 – 04:25 pm BST

PDB ID : 7ZWF  
Title : Pfs48/45 bound to scFv fragment of monoclonal antibody 32F3  
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Deposited on : 2022-05-19  
Resolution : 2.13 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.28.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.28.1

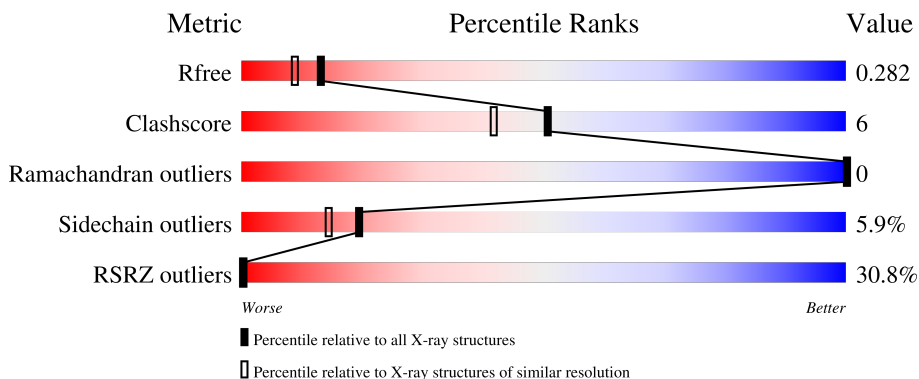
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.13 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))
$R_{free}$	130704	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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  $\geq 3$ , 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	428	
2	B	283	
3	C	2	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3983 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 Gametocyte surface protein P45/48.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	258	2074	1335	328	399	12	0	0	0

- Molecule 2 is a protein called 32F3scFv.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	239	1791	1122	304	358	7	0	0	0

- Molecule 3 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	2	24	14	1	9	0	0	0

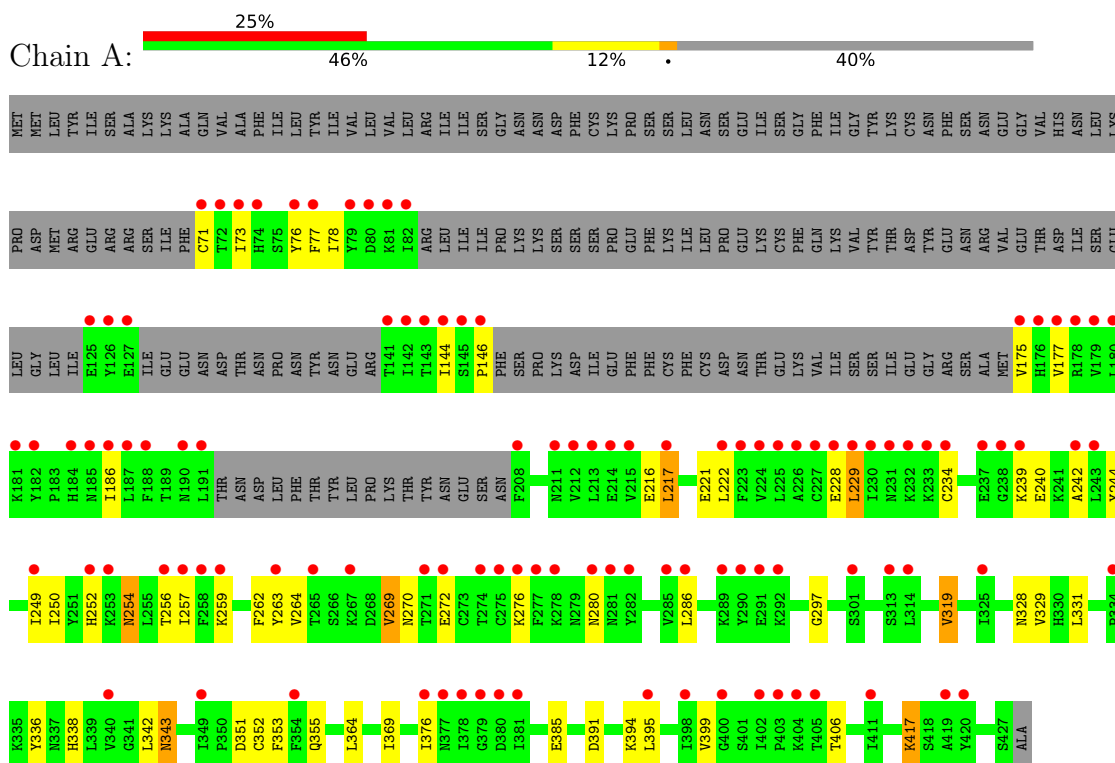
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	41	Total	O	0	0
			41	41		
4	B	53	Total	O	0	0
			53	53		

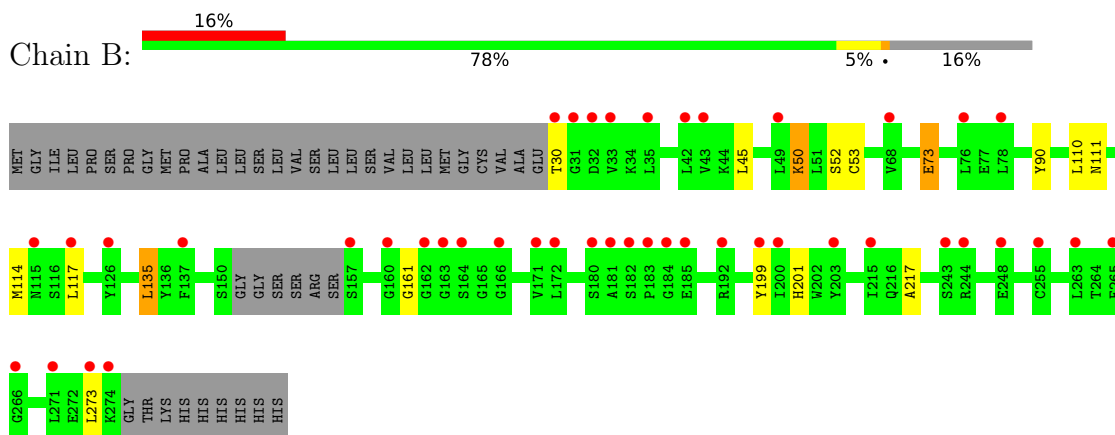
### 3 Residue-property plots [i](#)

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: Gametocyte surface protein P45/48



- Molecule 2: 32F3scFv



- Molecule 3: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose



3AG3  
FUC2

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.83Å 126.11Å 146.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.91 – 2.13 40.91 – 2.13	Depositor EDS
% Data completeness (in resolution range)	95.6 (40.91-2.13) 95.5 (40.91-2.13)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.30 (at 2.14Å)	Xtriage
Refinement program	BUSTER 2.10.4 (20-OCT-2021)	Depositor
R, $R_{free}$	0.276 , 0.286 0.265 , 0.282	Depositor DCC
$R_{free}$ test set	1964 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.2	Xtriage
Anisotropy	0.458	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3983	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: FUC, 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	0.39	0/2117	0.56	0/2860
2	B	0.47	0/1831	0.64	0/2480
All	All	0.43	0/3948	0.60	0/5340

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 [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	2074	0	2040	37	0
2	B	1791	0	1728	9	0
3	C	24	0	22	0	0
4	A	41	0	0	1	0
4	B	53	0	0	0	0
All	All	3983	0	3790	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 6.

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:242:ALA:HB1	1:A:269:VAL:HA	1.36	1.07
1:A:250:ILE:HB	1:A:257:ILE:HB	1.56	0.85
2:B:50:LYS:HE2	2:B:111:ASN:HB3	1.72	0.71
1:A:343:ASN:HD21	1:A:391:ASP:HB3	1.55	0.70
1:A:328:ASN:HB2	4:A:522:HOH:O	1.92	0.69
1:A:250:ILE:CG2	1:A:252:HIS:HD2	2.07	0.68
1:A:71:CYS:HB2	1:A:175:VAL:HG13	1.79	0.64
2:B:73:GLU:HG2	2:B:161:GLY:H	1.66	0.61
1:A:228:GLU:HA	1:A:254:ASN:HB3	1.83	0.60
1:A:385:GLU:HG2	1:A:394:LYS:HD3	1.84	0.59
2:B:135:LEU:HD22	2:B:217:ALA:HB2	1.86	0.58
2:B:114:MET:HB3	2:B:117:LEU:HD21	1.86	0.57
1:A:351:ASP:H	1:A:355:GLN:HE21	1.54	0.55
1:A:239:LYS:HB2	1:A:272:GLU:HB2	1.87	0.55
1:A:78:ILE:HG12	1:A:146:PRO:HG3	1.89	0.55
1:A:369:ILE:HD12	2:B:199:TYR:HB3	1.87	0.55
1:A:239:LYS:HE2	1:A:272:GLU:HG3	1.88	0.55
2:B:201:HIS:CE1	2:B:217:ALA:H	2.26	0.54
1:A:73:ILE:HB	1:A:177:VAL:HG13	1.89	0.54
1:A:217:LEU:HD23	1:A:221:GLU:HB3	1.89	0.54
1:A:229:LEU:HB3	1:A:276:LYS:HB2	1.89	0.53
1:A:250:ILE:CG2	1:A:252:HIS:CD2	2.90	0.51
1:A:336:TYR:HD1	1:A:338:HIS:CD2	2.30	0.49
2:B:53:CYS:HB3	2:B:110:LEU:HB3	1.94	0.49
1:A:242:ALA:CB	1:A:269:VAL:HA	2.25	0.49
1:A:77:PHE:HB3	1:A:144:ILE:HB	1.94	0.48
1:A:376:ILE:HD13	1:A:406:THR:HG21	1.95	0.48
1:A:250:ILE:HG22	1:A:252:HIS:HD2	1.75	0.48
1:A:250:ILE:O	1:A:256:THR:HA	2.15	0.47
1:A:262:PHE:CZ	1:A:399:VAL:HG21	2.50	0.46
1:A:331:LEU:HD23	1:A:338:HIS:HD2	1.81	0.46
1:A:319:VAL:O	1:A:417:LYS:HD2	2.16	0.46
1:A:319:VAL:HG22	1:A:417:LYS:HB3	1.97	0.46
1:A:364:LEU:HD23	2:B:90:TYR:HB3	1.98	0.44
1:A:250:ILE:HG23	1:A:252:HIS:CD2	2.52	0.43
1:A:264:VAL:HG21	1:A:269:VAL:HG11	2.00	0.43
1:A:186:ILE:HG23	1:A:222:LEU:HD23	2.00	0.43
1:A:352:CYS:HA	1:A:353:PHE:HA	1.84	0.43
2:B:73:GLU:HG2	2:B:161:GLY:N	2.34	0.43
1:A:331:LEU:HB3	1:A:336:TYR:CE1	2.54	0.42
1:A:249:ILE:HG23	1:A:249:ILE:O	2.20	0.41
1:A:297:GLY:HA2	1:A:329:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:228:GLU:HA	1:A:254:ASN:CB	2.50	0.41
1:A:331:LEU:HD23	1:A:338:HIS:CD2	2.56	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	A	248/428 (58%)	225 (91%)	23 (9%)	0	100	100
2	B	235/283 (83%)	223 (95%)	12 (5%)	0	100	100
All	All	483/711 (68%)	448 (93%)	35 (7%)	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	243/402 (60%)	224 (92%)	19 (8%)	12	7
2	B	194/230 (84%)	187 (96%)	7 (4%)	35	32
All	All	437/632 (69%)	411 (94%)	26 (6%)	19	14

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	TYR
1	A	216	GLU
1	A	217	LEU
1	A	229	LEU
1	A	234	CYS
1	A	240	GLU
1	A	244	TYR
1	A	254	ASN
1	A	259	LYS
1	A	263	TYR
1	A	269	VAL
1	A	270	ASN
1	A	280	ASN
1	A	286	LEU
1	A	319	VAL
1	A	342	LEU
1	A	343	ASN
1	A	395	LEU
1	A	417	LYS
2	B	30	THR
2	B	45	LEU
2	B	50	LYS
2	B	52	SER
2	B	73	GLU
2	B	135	LEU
2	B	273	LEU

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	74	HIS
1	A	252	HIS
1	A	280	ASN
1	A	328	ASN
1	A	343	ASN
1	A	355	GLN
2	B	111	ASN
2	B	143	GLN

### 5.3.3 RNA

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](#)

2 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	1,3	14,14,15	0.26	0	17,19,21	0.41	0
3	FUC	C	2	3	10,10,11	0.35	0	14,14,16	0.66	1 (7%)

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	1,3	-	0/6/23/26	0/1/1/1
3	FUC	C	2	3	-	-	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2	FUC	C1-C2-C3	2.01	112.14	109.67

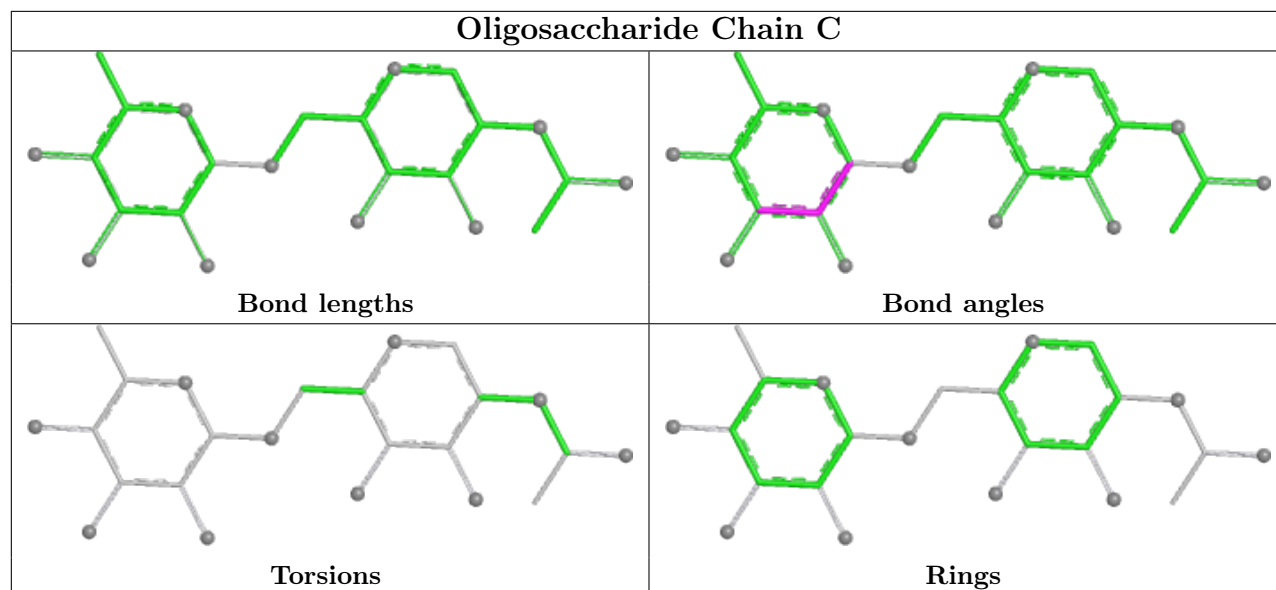
There are no chirality outliers.

There are no torsion outliers.

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	258/428 (60%)	2.53	109 (42%) <b>0</b> <b>0</b>	67, 109, 171, 210	0
2	B	239/283 (84%)	1.25	44 (18%) <b>1</b> <b>1</b>	51, 83, 116, 129	0
All	All	497/711 (69%)	1.91	153 (30%) <b>0</b> <b>0</b>	51, 92, 156, 210	0

All (153) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	179	VAL	14.5
1	A	277	PHE	12.7
1	A	82	ILE	12.3
1	A	177	VAL	11.1
1	A	215	VAL	10.8
1	A	77	PHE	10.6
1	A	227	CYS	10.2
1	A	230	ILE	10.0
1	A	252	HIS	9.6
1	A	226	ALA	9.2
1	A	398	ILE	9.2
1	A	142	ILE	9.0
1	A	182	TYR	8.9
1	A	125	GLU	8.7
1	A	143	THR	8.6
1	A	72	THR	8.4
1	A	144	ILE	8.4
2	B	30	THR	8.2
2	B	182	SER	8.1
1	A	378	ILE	7.6
1	A	282	TYR	7.4
1	A	223	PHE	7.2
1	A	127	GLU	7.2
1	A	176	HIS	6.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	253	LYS	6.6
1	A	74	HIS	6.2
1	A	184	HIS	6.1
1	A	79	TYR	6.1
1	A	73	ILE	6.0
1	A	228	GLU	5.8
2	B	271	LEU	5.8
1	A	181	LYS	5.7
1	A	257	ILE	5.6
2	B	43	VAL	5.4
1	A	145	SER	5.4
1	A	178	ARG	5.3
1	A	190	ASN	5.3
1	A	186	ILE	5.3
1	A	217	LEU	5.2
1	A	256	THR	5.1
1	A	225	LEU	5.1
2	B	160	GLY	5.0
1	A	229	LEU	4.9
2	B	157	SER	4.6
1	A	224	VAL	4.6
1	A	231	ASN	4.6
2	B	183	PRO	4.5
1	A	71	CYS	4.5
1	A	259	LYS	4.3
2	B	181	ALA	4.3
1	A	146	PRO	4.2
1	A	81	LYS	4.1
2	B	180	SER	4.1
1	A	141	THR	4.1
1	A	334	PRO	4.1
1	A	286	LEU	4.0
1	A	377	ASN	4.0
1	A	180	LEU	4.0
1	A	214	GLU	4.0
2	B	163	GLY	3.8
1	A	126	TYR	3.7
1	A	80	ASP	3.7
1	A	267	LYS	3.6
2	B	273	LEU	3.6
2	B	243	SER	3.6
1	A	292	LYS	3.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	380	ASP	3.4
1	A	175	VAL	3.3
2	B	184	GLY	3.3
1	A	290	TYR	3.3
1	A	301	SER	3.2
1	A	208	PHE	3.2
1	A	213	LEU	3.2
2	B	115	ASN	3.2
2	B	274	LYS	3.1
2	B	32	ASP	3.1
2	B	244	ARG	3.1
2	B	248	GLU	3.1
1	A	237	GLU	3.0
1	A	278	LYS	3.0
1	A	191	LEU	3.0
1	A	188	PHE	2.9
1	A	243	LEU	2.9
2	B	265	PHE	2.9
2	B	162	GLY	2.9
1	A	239	LYS	2.9
1	A	76	TYR	2.9
1	A	291	GLU	2.9
1	A	325	ILE	2.9
1	A	233	LYS	2.9
1	A	272	GLU	2.9
1	A	271	THR	2.8
1	A	212	VAL	2.8
1	A	411	ILE	2.8
1	A	211	ASN	2.8
2	B	42	LEU	2.7
2	B	76	LEU	2.7
2	B	117	LEU	2.7
1	A	249	ILE	2.7
1	A	242	ALA	2.7
1	A	281	ASN	2.6
1	A	222	LEU	2.6
1	A	185	ASN	2.6
1	A	381	ILE	2.6
1	A	314	LEU	2.6
1	A	232	LYS	2.6
2	B	164	SER	2.6
2	B	266	GLY	2.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	263	TYR	2.5
1	A	376	ILE	2.5
1	A	289	LYS	2.5
1	A	379	GLY	2.5
2	B	49	LEU	2.5
1	A	404	LYS	2.5
2	B	171	VAL	2.4
2	B	192	ARG	2.4
1	A	400	GLY	2.4
1	A	403	PRO	2.4
1	A	349	ILE	2.4
1	A	419	ALA	2.4
1	A	405	THR	2.4
1	A	395	LEU	2.4
1	A	275	CYS	2.4
2	B	185	GLU	2.4
1	A	420	TYR	2.4
2	B	68	VAL	2.3
1	A	285	VAL	2.3
2	B	31	GLY	2.3
1	A	354	PHE	2.3
1	A	238	GLY	2.3
2	B	78	LEU	2.2
1	A	340	VAL	2.2
2	B	203	TYR	2.2
1	A	234	CYS	2.2
2	B	172	LEU	2.2
1	A	274	THR	2.2
1	A	280	ASN	2.2
1	A	402	ILE	2.2
1	A	276	LYS	2.2
2	B	33	VAL	2.2
2	B	126	TYR	2.2
1	A	313	SER	2.2
2	B	35	LEU	2.1
1	A	187	LEU	2.1
2	B	199	TYR	2.1
2	B	263	LEU	2.1
2	B	137	PHE	2.1
2	B	255	CYS	2.1
2	B	200	ILE	2.1
1	A	258	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	265	THR	2.0
2	B	166	GLY	2.0
2	B	215	ILE	2.0

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

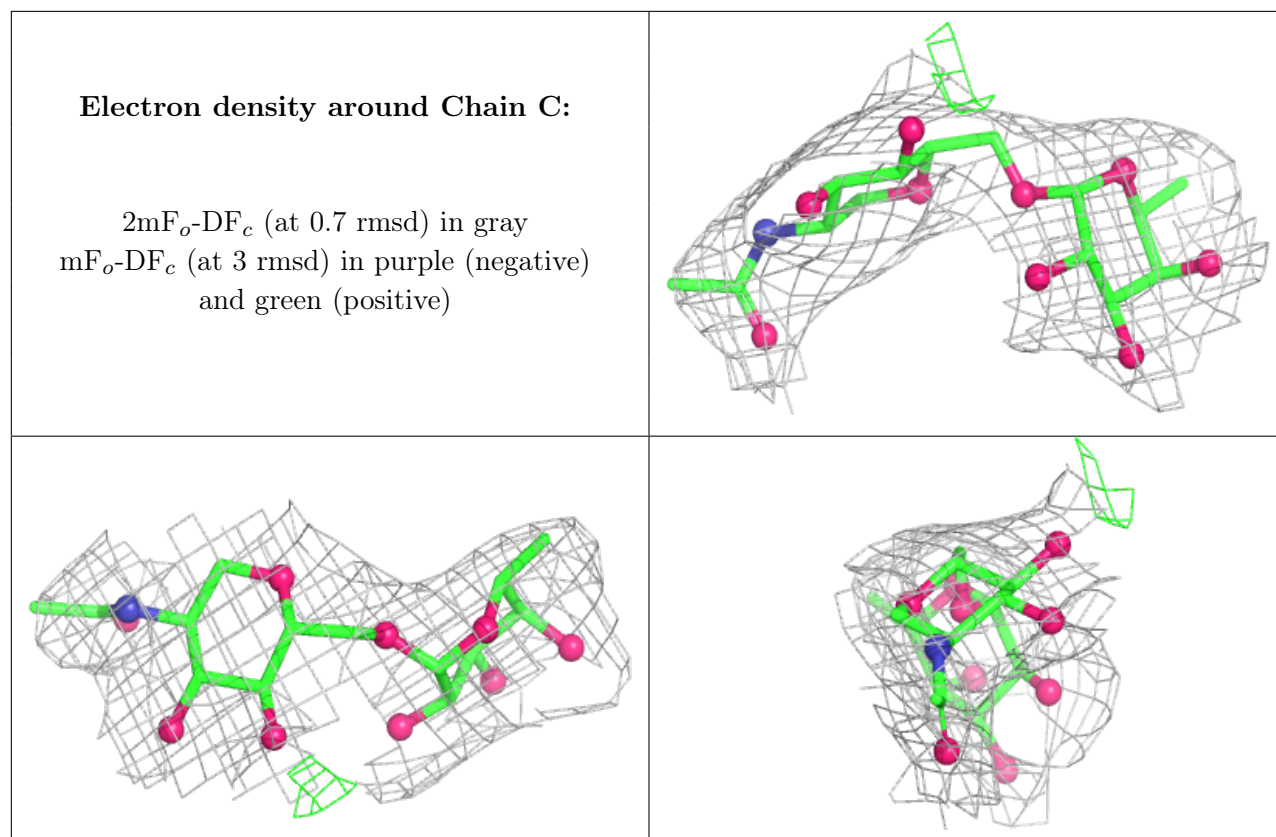
There are no non-standard protein/DNA/RNA residues in this entry.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	FUC	C	2	10/11	0.84	0.12	118,118,119,119	0
3	NAG	C	1	14/15	0.90	0.11	114,115,116,117	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.