



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 2, 2026 – 01:32 AM UTC

PDB ID : 5UDC / pdb\_00005udc  
Title : Crystal Structure of RSV F A2 Bound to MEDI8897  
Authors : McLellan, J.S.  
Deposited on : 2016-12-26  
Resolution : 3.45 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](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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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

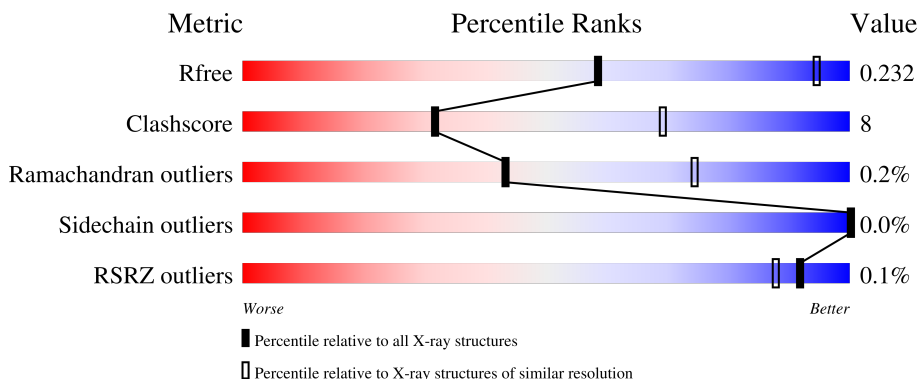
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.45 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.







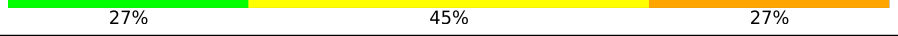
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1070 (3.50-3.42)
Clashscore	190562	1128 (3.50-3.42)
Ramachandran outliers	187476	1101 (3.50-3.42)
Sidechain outliers	187428	1102 (3.50-3.42)
RSRZ outliers	180081	1070 (3.50-3.42)

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	B	228	 79% 17% .
1	E	228	 77% 20% .
1	H	228	 83% 12% 5%
2	C	214	 81% 18% .
2	G	214	 83% 16%

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Mol	Chain	Length	Quality of chain
2	L	214	 80% 19%
3	A	568	 64% 15% 21%
3	D	568	 62% 17% 21%
3	F	568	 62% 17% 21%
4	I	11	 27% 45% 27%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 20324 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 MEDI8897 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	H	217	Total 1618	C 1025	N 264	O 321	S 8	0	0	0
1	B	218	Total 1630	C 1033	N 265	O 324	S 8	0	0	0
1	E	220	Total 1648	C 1044	N 269	O 327	S 8	0	0	0

- Molecule 2 is a protein called MEDI8897 Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	211	Total 1619	C 1014	N 269	O 331	S 5	0	0	0
2	C	211	Total 1619	C 1014	N 269	O 331	S 5	0	0	0
2	G	213	Total 1632	C 1021	N 271	O 335	S 5	0	0	0

- Molecule 3 is a protein called Fusion glycoprotein F0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	F	449	Total 3482	C 2202	N 573	O 684	S 23	0	0	0
3	A	448	Total 3474	C 2196	N 572	O 683	S 23	0	0	0
3	D	448	Total 3473	C 2197	N 571	O 682	S 23	0	0	0

There are 186 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	102	ALA	PRO	conflict	UNP P03420
F	155	CYS	SER	engineered mutation	UNP P03420

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Chain	Residue	Modelled	Actual	Comment	Reference
F	190	PHE	SER	engineered mutation	UNP P03420
F	207	LEU	VAL	engineered mutation	UNP P03420
F	290	CYS	SER	engineered mutation	UNP P03420
F	379	VAL	ILE	conflict	UNP P03420
F	447	VAL	MET	conflict	UNP P03420
F	514	SER	-	expression tag	UNP P03420
F	515	ALA	-	expression tag	UNP P03420
F	516	ILE	-	expression tag	UNP P03420
F	517	GLY	-	expression tag	UNP P03420
F	518	GLY	-	expression tag	UNP P03420
F	519	TYR	-	expression tag	UNP P03420
F	520	ILE	-	expression tag	UNP P03420
F	521	PRO	-	expression tag	UNP P03420
F	522	GLU	-	expression tag	UNP P03420
F	523	ALA	-	expression tag	UNP P03420
F	524	PRO	-	expression tag	UNP P03420
F	525	ARG	-	expression tag	UNP P03420
F	526	ASP	-	expression tag	UNP P03420
F	527	GLY	-	expression tag	UNP P03420
F	528	GLN	-	expression tag	UNP P03420
F	529	ALA	-	expression tag	UNP P03420
F	530	TYR	-	expression tag	UNP P03420
F	531	VAL	-	expression tag	UNP P03420
F	532	ARG	-	expression tag	UNP P03420
F	533	LYS	-	expression tag	UNP P03420
F	534	ASP	-	expression tag	UNP P03420
F	535	GLY	-	expression tag	UNP P03420
F	536	GLU	-	expression tag	UNP P03420
F	537	TRP	-	expression tag	UNP P03420
F	538	VAL	-	expression tag	UNP P03420
F	539	LEU	-	expression tag	UNP P03420
F	540	LEU	-	expression tag	UNP P03420
F	541	SER	-	expression tag	UNP P03420
F	542	THR	-	expression tag	UNP P03420
F	543	PHE	-	expression tag	UNP P03420
F	544	LEU	-	expression tag	UNP P03420
F	545	GLY	-	expression tag	UNP P03420
F	546	GLY	-	expression tag	UNP P03420
F	547	LEU	-	expression tag	UNP P03420
F	548	VAL	-	expression tag	UNP P03420
F	549	PRO	-	expression tag	UNP P03420
F	550	ARG	-	expression tag	UNP P03420

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Chain	Residue	Modelled	Actual	Comment	Reference
F	551	GLY	-	expression tag	UNP P03420
F	552	SER	-	expression tag	UNP P03420
F	553	HIS	-	expression tag	UNP P03420
F	554	HIS	-	expression tag	UNP P03420
F	555	HIS	-	expression tag	UNP P03420
F	556	HIS	-	expression tag	UNP P03420
F	557	HIS	-	expression tag	UNP P03420
F	558	HIS	-	expression tag	UNP P03420
F	559	SER	-	expression tag	UNP P03420
F	560	ALA	-	expression tag	UNP P03420
F	561	TRP	-	expression tag	UNP P03420
F	562	SER	-	expression tag	UNP P03420
F	563	HIS	-	expression tag	UNP P03420
F	564	PRO	-	expression tag	UNP P03420
F	565	GLN	-	expression tag	UNP P03420
F	566	PHE	-	expression tag	UNP P03420
F	567	GLU	-	expression tag	UNP P03420
F	568	LYS	-	expression tag	UNP P03420
A	102	ALA	PRO	conflict	UNP P03420
A	155	CYS	SER	engineered mutation	UNP P03420
A	190	PHE	SER	engineered mutation	UNP P03420
A	207	LEU	VAL	engineered mutation	UNP P03420
A	290	CYS	SER	engineered mutation	UNP P03420
A	379	VAL	ILE	conflict	UNP P03420
A	447	VAL	MET	conflict	UNP P03420
A	514	SER	-	expression tag	UNP P03420
A	515	ALA	-	expression tag	UNP P03420
A	516	ILE	-	expression tag	UNP P03420
A	517	GLY	-	expression tag	UNP P03420
A	518	GLY	-	expression tag	UNP P03420
A	519	TYR	-	expression tag	UNP P03420
A	520	ILE	-	expression tag	UNP P03420
A	521	PRO	-	expression tag	UNP P03420
A	522	GLU	-	expression tag	UNP P03420
A	523	ALA	-	expression tag	UNP P03420
A	524	PRO	-	expression tag	UNP P03420
A	525	ARG	-	expression tag	UNP P03420
A	526	ASP	-	expression tag	UNP P03420
A	527	GLY	-	expression tag	UNP P03420
A	528	GLN	-	expression tag	UNP P03420
A	529	ALA	-	expression tag	UNP P03420
A	530	TYR	-	expression tag	UNP P03420

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Chain	Residue	Modelled	Actual	Comment	Reference
A	531	VAL	-	expression tag	UNP P03420
A	532	ARG	-	expression tag	UNP P03420
A	533	LYS	-	expression tag	UNP P03420
A	534	ASP	-	expression tag	UNP P03420
A	535	GLY	-	expression tag	UNP P03420
A	536	GLU	-	expression tag	UNP P03420
A	537	TRP	-	expression tag	UNP P03420
A	538	VAL	-	expression tag	UNP P03420
A	539	LEU	-	expression tag	UNP P03420
A	540	LEU	-	expression tag	UNP P03420
A	541	SER	-	expression tag	UNP P03420
A	542	THR	-	expression tag	UNP P03420
A	543	PHE	-	expression tag	UNP P03420
A	544	LEU	-	expression tag	UNP P03420
A	545	GLY	-	expression tag	UNP P03420
A	546	GLY	-	expression tag	UNP P03420
A	547	LEU	-	expression tag	UNP P03420
A	548	VAL	-	expression tag	UNP P03420
A	549	PRO	-	expression tag	UNP P03420
A	550	ARG	-	expression tag	UNP P03420
A	551	GLY	-	expression tag	UNP P03420
A	552	SER	-	expression tag	UNP P03420
A	553	HIS	-	expression tag	UNP P03420
A	554	HIS	-	expression tag	UNP P03420
A	555	HIS	-	expression tag	UNP P03420
A	556	HIS	-	expression tag	UNP P03420
A	557	HIS	-	expression tag	UNP P03420
A	558	HIS	-	expression tag	UNP P03420
A	559	SER	-	expression tag	UNP P03420
A	560	ALA	-	expression tag	UNP P03420
A	561	TRP	-	expression tag	UNP P03420
A	562	SER	-	expression tag	UNP P03420
A	563	HIS	-	expression tag	UNP P03420
A	564	PRO	-	expression tag	UNP P03420
A	565	GLN	-	expression tag	UNP P03420
A	566	PHE	-	expression tag	UNP P03420
A	567	GLU	-	expression tag	UNP P03420
A	568	LYS	-	expression tag	UNP P03420
D	102	ALA	PRO	conflict	UNP P03420
D	155	CYS	SER	engineered mutation	UNP P03420
D	190	PHE	SER	engineered mutation	UNP P03420
D	207	LEU	VAL	engineered mutation	UNP P03420

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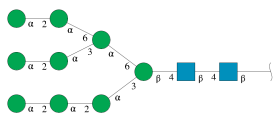
Chain	Residue	Modelled	Actual	Comment	Reference
D	290	CYS	SER	engineered mutation	UNP P03420
D	379	VAL	ILE	conflict	UNP P03420
D	447	VAL	MET	conflict	UNP P03420
D	514	SER	-	expression tag	UNP P03420
D	515	ALA	-	expression tag	UNP P03420
D	516	ILE	-	expression tag	UNP P03420
D	517	GLY	-	expression tag	UNP P03420
D	518	GLY	-	expression tag	UNP P03420
D	519	TYR	-	expression tag	UNP P03420
D	520	ILE	-	expression tag	UNP P03420
D	521	PRO	-	expression tag	UNP P03420
D	522	GLU	-	expression tag	UNP P03420
D	523	ALA	-	expression tag	UNP P03420
D	524	PRO	-	expression tag	UNP P03420
D	525	ARG	-	expression tag	UNP P03420
D	526	ASP	-	expression tag	UNP P03420
D	527	GLY	-	expression tag	UNP P03420
D	528	GLN	-	expression tag	UNP P03420
D	529	ALA	-	expression tag	UNP P03420
D	530	TYR	-	expression tag	UNP P03420
D	531	VAL	-	expression tag	UNP P03420
D	532	ARG	-	expression tag	UNP P03420
D	533	LYS	-	expression tag	UNP P03420
D	534	ASP	-	expression tag	UNP P03420
D	535	GLY	-	expression tag	UNP P03420
D	536	GLU	-	expression tag	UNP P03420
D	537	TRP	-	expression tag	UNP P03420
D	538	VAL	-	expression tag	UNP P03420
D	539	LEU	-	expression tag	UNP P03420
D	540	LEU	-	expression tag	UNP P03420
D	541	SER	-	expression tag	UNP P03420
D	542	THR	-	expression tag	UNP P03420
D	543	PHE	-	expression tag	UNP P03420
D	544	LEU	-	expression tag	UNP P03420
D	545	GLY	-	expression tag	UNP P03420
D	546	GLY	-	expression tag	UNP P03420
D	547	LEU	-	expression tag	UNP P03420
D	548	VAL	-	expression tag	UNP P03420
D	549	PRO	-	expression tag	UNP P03420
D	550	ARG	-	expression tag	UNP P03420
D	551	GLY	-	expression tag	UNP P03420
D	552	SER	-	expression tag	UNP P03420

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Chain	Residue	Modelled	Actual	Comment	Reference
D	553	HIS	-	expression tag	UNP P03420
D	554	HIS	-	expression tag	UNP P03420
D	555	HIS	-	expression tag	UNP P03420
D	556	HIS	-	expression tag	UNP P03420
D	557	HIS	-	expression tag	UNP P03420
D	558	HIS	-	expression tag	UNP P03420
D	559	SER	-	expression tag	UNP P03420
D	560	ALA	-	expression tag	UNP P03420
D	561	TRP	-	expression tag	UNP P03420
D	562	SER	-	expression tag	UNP P03420
D	563	HIS	-	expression tag	UNP P03420
D	564	PRO	-	expression tag	UNP P03420
D	565	GLN	-	expression tag	UNP P03420
D	566	PHE	-	expression tag	UNP P03420
D	567	GLU	-	expression tag	UNP P03420
D	568	LYS	-	expression tag	UNP P03420

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-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.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	I	11	127	70	2	55	0	0	0

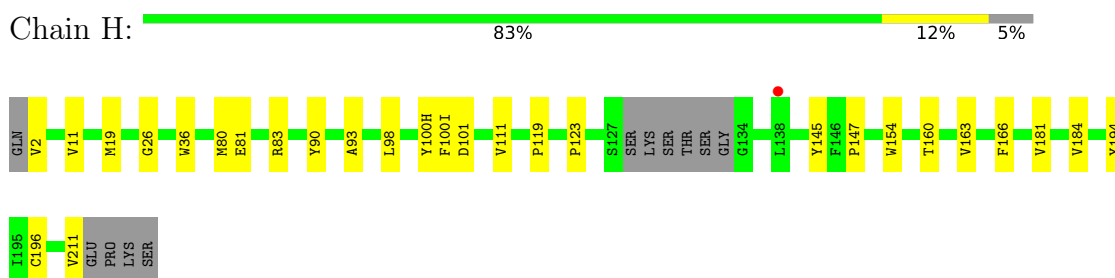
- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
5	F	1	1	1	0	0
5	A	1	1	1	0	0

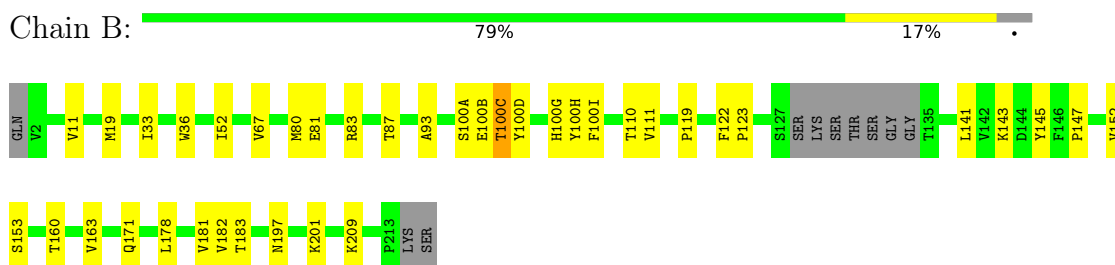
### 3 Residue-property plots [i](#)

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.

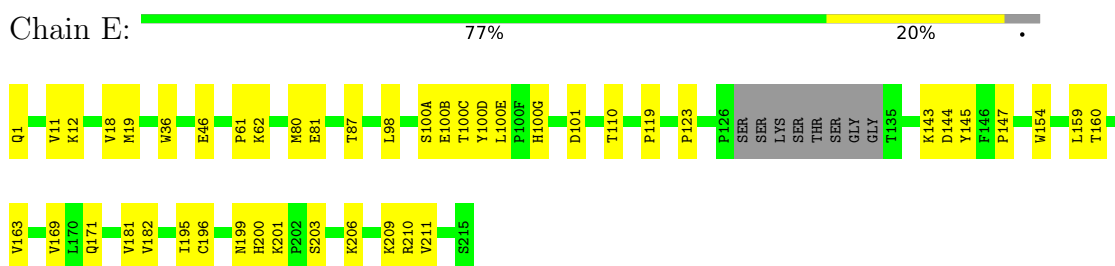
- Molecule 1: MEDI8897 Fab Heavy Chain



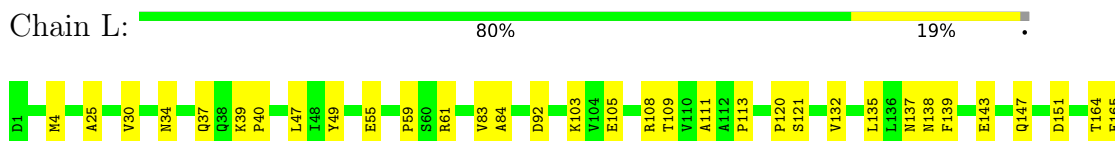
- Molecule 1: MEDI8897 Fab Heavy Chain

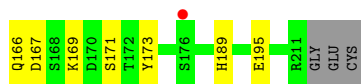


- Molecule 1: MEDI8897 Fab Heavy Chain



- Molecule 2: MEDI8897 Fab Light Chain





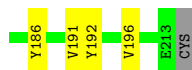
- Molecule 2: MEDI8897 Fab Light Chain

Chain C: 81% 18%



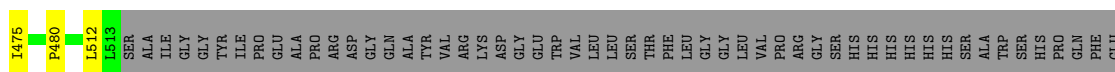
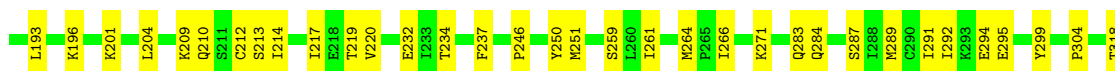
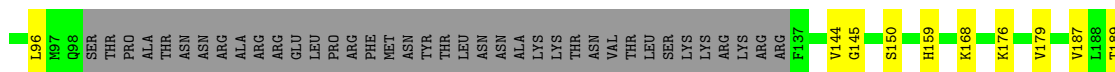
- Molecule 2: MEDI8897 Fab Light Chain

Chain G: 83% 16%



- Molecule 3: Fusion glycoprotein F0

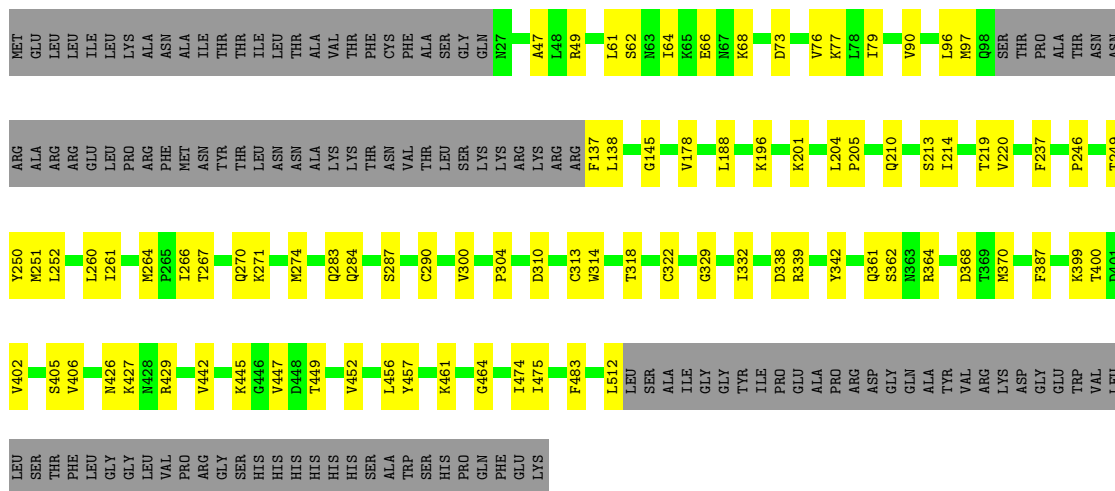
Chain F: 62% 17% 21%



LYS

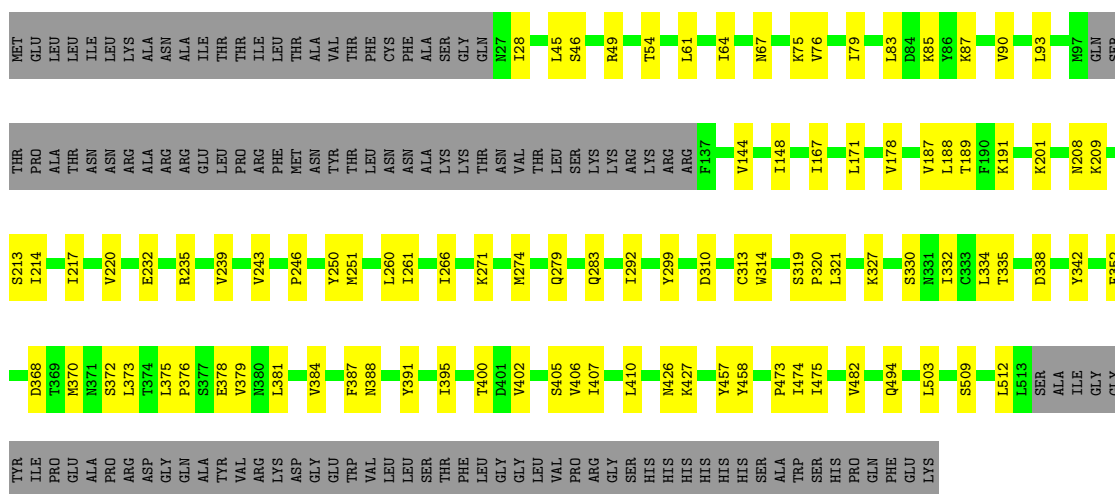
- Molecule 3: Fusion glycoprotein F0

Chain A: 64% 15% 21%



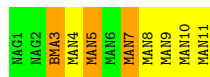
- Molecule 3: Fusion glycoprotein F0

Chain D: 62% 17% 21%



- Molecule 4: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-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

Chain I: 27% 45% 27%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.78Å 126.31Å 162.31Å 90.00° 102.56° 90.00°	Depositor
Resolution (Å)	43.14 – 3.45 43.14 – 3.45	Depositor EDS
% Data completeness (in resolution range)	98.9 (43.14-3.45) 98.8 (43.14-3.45)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.17 (at 3.48Å)	Xtrriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, $R_{free}$	0.175 , 0.232 0.179 , 0.232	Depositor DCC
$R_{free}$ test set	2653 reflections (4.30%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	111.2	Xtrriage
Anisotropy	0.582	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 88.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	20324	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	138.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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: MAN, CL, BMA, 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	B	0.25	0/1670	0.49	0/2285
1	E	0.28	0/1688	0.50	0/2308
1	H	0.26	0/1657	0.51	0/2266
2	C	0.22	0/1652	0.47	0/2247
2	G	0.23	0/1665	0.50	0/2264
2	L	0.20	0/1652	0.44	0/2247
3	A	0.29	0/3524	0.53	0/4773
3	D	0.32	0/3523	0.55	0/4772
3	F	0.36	0/3532	0.59	0/4784
All	All	0.29	0/20563	0.52	0/27946

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	B	1630	0	1590	26	0
1	E	1648	0	1614	31	0
1	H	1618	0	1580	21	0
2	C	1619	0	1579	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	1632	0	1588	21	0
2	L	1619	0	1579	26	0
3	A	3474	0	3515	67	0
3	D	3473	0	3518	76	0
3	F	3482	0	3525	73	0
4	I	127	0	106	3	0
5	A	1	0	0	0	0
5	F	1	0	0	0	0
All	All	20324	0	20194	327	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 8.

The worst 5 of 327 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:A:66:GLU:OE2	3:A:68:LYS:HG3	1.10	1.22
3:A:66:GLU:OE2	3:A:68:LYS:CG	2.01	1.09
3:D:407:ILE:HD11	3:D:457:TYR:HB3	1.44	1.00
3:F:214:ILE:HD11	3:F:219:THR:HB	1.47	0.94
3:A:246:PRO:HB3	3:A:283:GLN:HA	1.56	0.87

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	214/228 (94%)	207 (97%)	6 (3%)	1 (0%)	24	57
1	E	216/228 (95%)	209 (97%)	7 (3%)	0	100	100
1	H	213/228 (93%)	207 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	209/214 (98%)	198 (95%)	10 (5%)	1 (0%)	24	57
2	G	211/214 (99%)	201 (95%)	9 (4%)	1 (0%)	24	57
2	L	209/214 (98%)	198 (95%)	10 (5%)	1 (0%)	24	57
3	A	444/568 (78%)	427 (96%)	17 (4%)	0	100	100
3	D	444/568 (78%)	424 (96%)	20 (4%)	0	100	100
3	F	445/568 (78%)	429 (96%)	16 (4%)	0	100	100
All	All	2605/3030 (86%)	2500 (96%)	101 (4%)	4 (0%)	43	74

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	100(C)	THR
2	L	30	VAL
2	C	30	VAL
2	G	30	VAL

### 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	185/193 (96%)	185 (100%)	0	100	100
1	E	187/193 (97%)	187 (100%)	0	100	100
1	H	183/193 (95%)	183 (100%)	0	100	100
2	C	186/188 (99%)	186 (100%)	0	100	100
2	G	187/188 (100%)	187 (100%)	0	100	100
2	L	186/188 (99%)	186 (100%)	0	100	100
3	A	409/510 (80%)	409 (100%)	0	100	100
3	D	409/510 (80%)	409 (100%)	0	100	100
3	F	410/510 (80%)	409 (100%)	1 (0%)	87	84
All	All	2342/2673 (88%)	2341 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	79	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	276	ASN
3	D	227	ASN
3	A	361	GLN
3	D	262	ASN
2	G	138	ASN

### 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](#)

11 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	I	1	4,3	14,14,15	0.30	0	17,19,21	0.52	0
4	MAN	I	10	4	11,11,12	1.13	0	15,15,17	1.05	1 (6%)
4	MAN	I	11	4	11,11,12	0.89	1 (9%)	15,15,17	1.31	2 (13%)
4	NAG	I	2	4	14,14,15	0.25	0	17,19,21	0.77	0
4	BMA	I	3	4	11,11,12	1.32	1 (9%)	15,15,17	1.62	3 (20%)
4	MAN	I	4	4	11,11,12	0.72	0	15,15,17	1.03	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	MAN	I	5	4	11,11,12	0.80	0	15,15,17	1.30	2 (13%)
4	MAN	I	6	4	11,11,12	0.96	0	15,15,17	0.79	0
4	MAN	I	7	4	11,11,12	1.80	4 (36%)	15,15,17	1.57	4 (26%)
4	MAN	I	8	4	11,11,12	0.68	0	15,15,17	1.47	2 (13%)
4	MAN	I	9	4	11,11,12	0.76	0	15,15,17	1.37	2 (13%)

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	I	1	4,3	-	0/6/23/26	0/1/1/1
4	MAN	I	10	4	-	2/2/19/22	0/1/1/1
4	MAN	I	11	4	-	2/2/19/22	0/1/1/1
4	NAG	I	2	4	-	2/6/23/26	0/1/1/1
4	BMA	I	3	4	-	1/2/19/22	0/1/1/1
4	MAN	I	4	4	-	2/2/19/22	0/1/1/1
4	MAN	I	5	4	-	1/2/19/22	0/1/1/1
4	MAN	I	6	4	-	0/2/19/22	0/1/1/1
4	MAN	I	7	4	-	0/2/19/22	0/1/1/1
4	MAN	I	8	4	-	2/2/19/22	0/1/1/1
4	MAN	I	9	4	-	0/2/19/22	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	I	7	MAN	O5-C1	-3.94	1.37	1.43
4	I	3	BMA	O5-C1	-3.28	1.38	1.43
4	I	7	MAN	C2-C3	2.65	1.56	1.52
4	I	7	MAN	C1-C2	2.46	1.58	1.52
4	I	7	MAN	C4-C3	2.15	1.57	1.52

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	8	MAN	C1-O5-C5	4.46	118.16	112.19
4	I	3	BMA	C1-O5-C5	3.97	117.50	112.19
4	I	11	MAN	C1-O5-C5	3.84	117.33	112.19
4	I	5	MAN	C1-O5-C5	3.72	117.18	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	7	MAN	C1-C2-C3	2.95	113.94	109.64

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

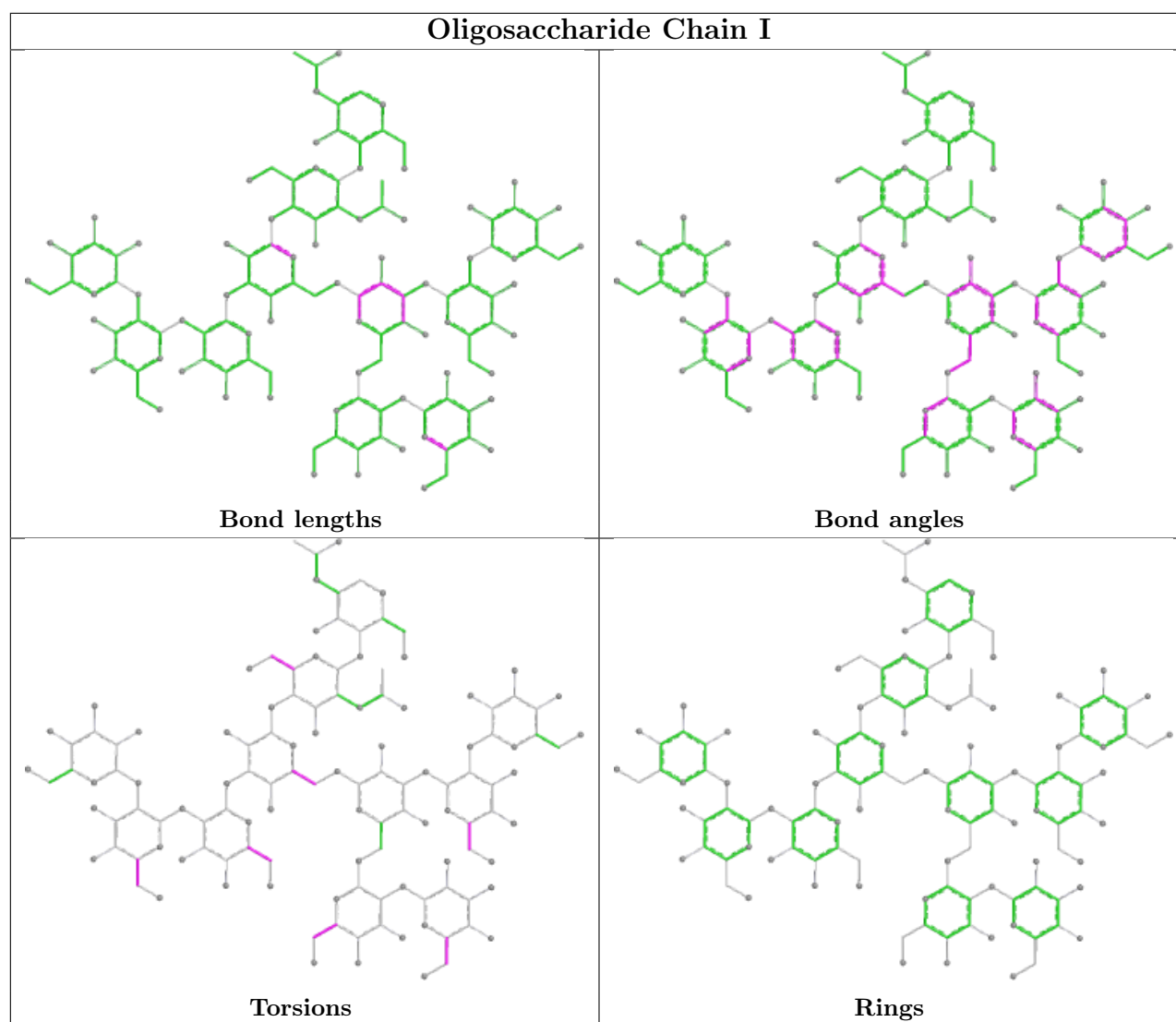
Mol	Chain	Res	Type	Atoms
4	I	8	MAN	O5-C5-C6-O6
4	I	11	MAN	O5-C5-C6-O6
4	I	8	MAN	C4-C5-C6-O6
4	I	2	NAG	C4-C5-C6-O6
4	I	4	MAN	O5-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	3	BMA	2	0
4	I	5	MAN	1	0
4	I	7	MAN	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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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, 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	B	218/228 (95%)	-0.65	0 <a href="#">100</a> <a href="#">100</a>	90, 132, 185, 210	0
1	E	220/228 (96%)	-0.66	0 <a href="#">100</a> <a href="#">100</a>	90, 131, 188, 224	0
1	H	217/228 (95%)	-0.55	1 (0%) <a href="#">87</a> <a href="#">70</a>	84, 144, 253, 311	0
2	C	211/214 (98%)	-0.69	0 <a href="#">100</a> <a href="#">100</a>	94, 155, 203, 245	0
2	G	213/214 (99%)	-0.66	0 <a href="#">100</a> <a href="#">100</a>	98, 153, 210, 247	0
2	L	211/214 (98%)	-0.50	1 (0%) <a href="#">87</a> <a href="#">70</a>	88, 203, 286, 336	0
3	A	448/568 (78%)	-0.66	0 <a href="#">100</a> <a href="#">100</a>	70, 127, 198, 245	0
3	D	448/568 (78%)	-0.63	0 <a href="#">100</a> <a href="#">100</a>	74, 118, 188, 242	0
3	F	449/568 (79%)	-0.66	0 <a href="#">100</a> <a href="#">100</a>	62, 104, 173, 243	0
All	All	2635/3030 (86%)	-0.63	2 (0%) <a href="#">92</a> <a href="#">88</a>	62, 131, 227, 336	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	138	LEU	2.1
2	L	176	SER	2.1

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

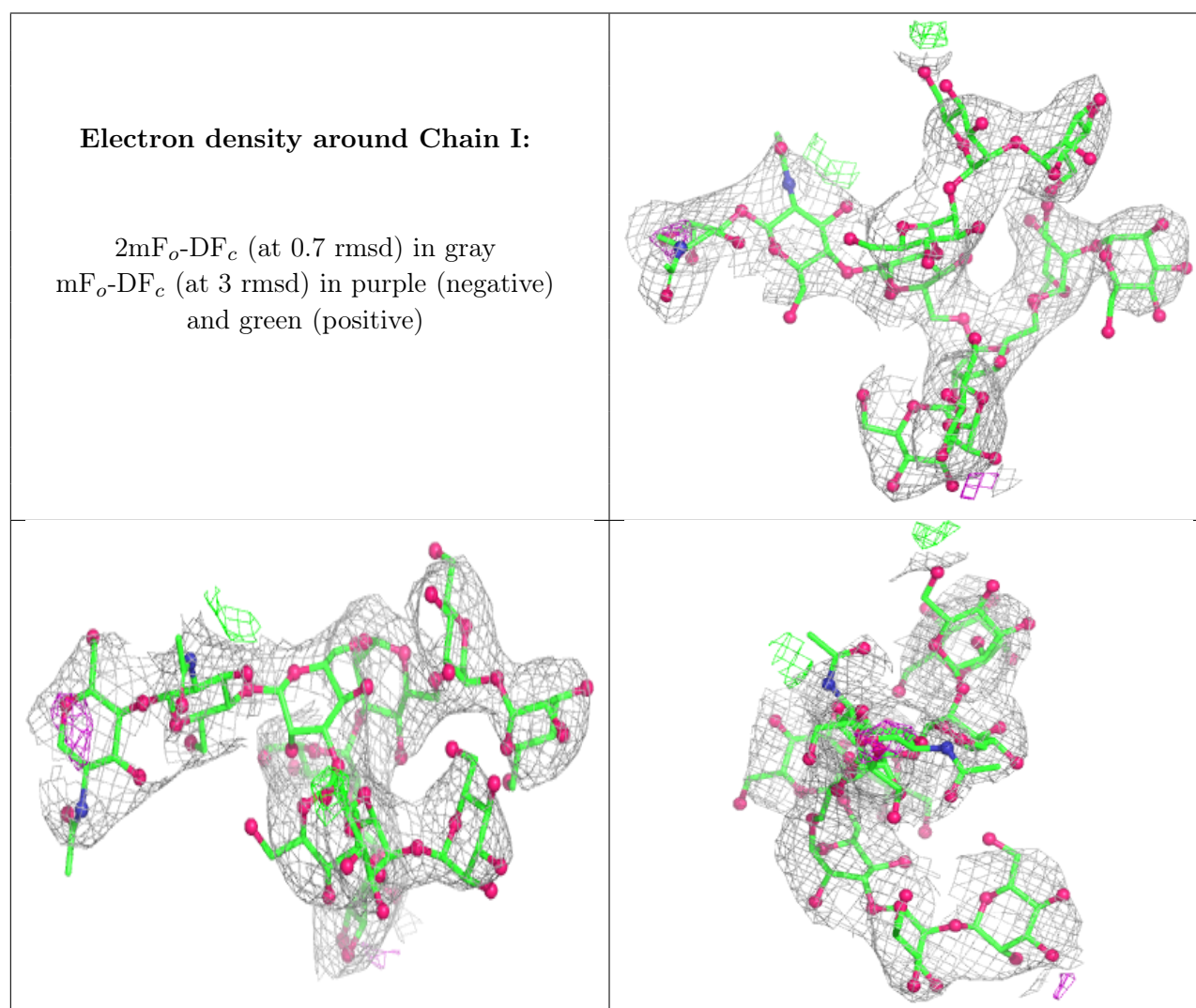
There are no non-standard protein/DNA/RNA residues in this entry.

### 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( $\text{\AA}^2$ )	Q<0.9
4	NAG	I	1	14/15	-	-	130,144,150,156	0
4	NAG	I	2	14/15	-	-	141,158,164,168	0
4	BMA	I	3	11/12	-	-	158,168,170,171	0
4	MAN	I	4	11/12	-	-	170,172,179,181	0
4	MAN	I	5	11/12	-	-	175,180,185,185	0
4	MAN	I	6	11/12	-	-	173,181,184,185	0
4	MAN	I	7	11/12	-	-	129,147,152,156	0
4	MAN	I	8	11/12	-	-	153,161,167,171	0
4	MAN	I	9	11/12	-	-	158,160,164,169	0
4	MAN	I	10	11/12	-	-	124,126,140,151	0
4	MAN	I	11	11/12	-	-	142,144,152,154	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](#)

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
5	CL	A	601	1/1	0.92	0.10	146,146,146,146	0
5	CL	F	612	1/1	0.95	0.08	95,95,95,95	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.