



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 21, 2020 – 04:50 PM BST

PDB ID : 2WSP  
Title : Thermotoga maritima alpha-L-fucosynthase, TmD224G, in complex with alpha-L-Fuc-(1-2)-beta-L-Fuc-N3  
Authors : Sulzenbacher, G.; Lipski, A.; Cobucci-Ponzano, B.; Conte, F.; Bedini, E.; Corsaro, M.M.; Parrilli, M.; Dal Piaz, F.; Lepore, L.; Rossi, M.; Moracci, M.  
Deposited on : 2009-09-08  
Resolution : 2.65 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.14.6  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.14.6

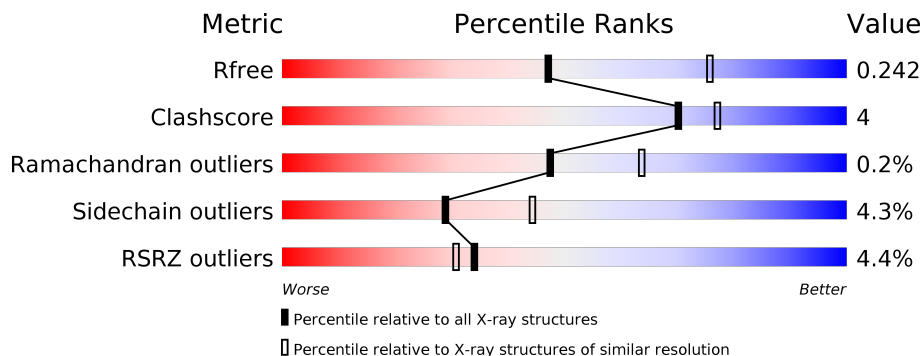
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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 on 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	449	
1	B	449	
2	C	2	
2	D	2	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7317 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 ALPHA-L-FUCOSIDASE, PUTATIVE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	435	Total 3586	C 2340	N 590	O 648	S 8	0	0	0
1	B	434	Total 3582	C 2338	N 589	O 647	S 8	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	224	GLY	ASP	engineered mutation	UNP Q9WYE2
B	224	GLY	ASP	engineered mutation	UNP Q9WYE2

- Molecule 2 is an oligosaccharide called alpha-L-fucopyranose-(1-2)-beta-L-fucosyl-azide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	2	Total 23	C 12	N 3	O 8	0	0	0
2	D	2	Total 23	C 12	N 3	O 8	0	0	0

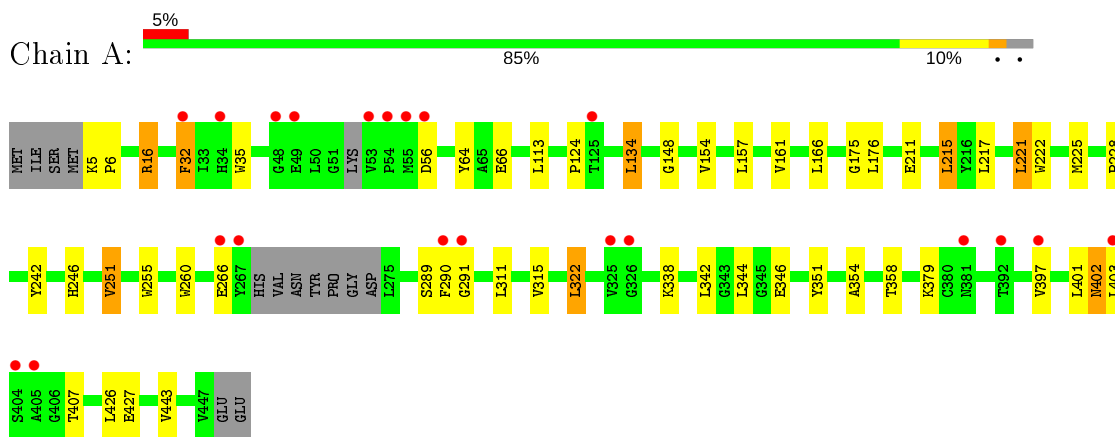
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	45	Total 45 O 45	0	0
3	B	58	Total 58 O 58	0	0

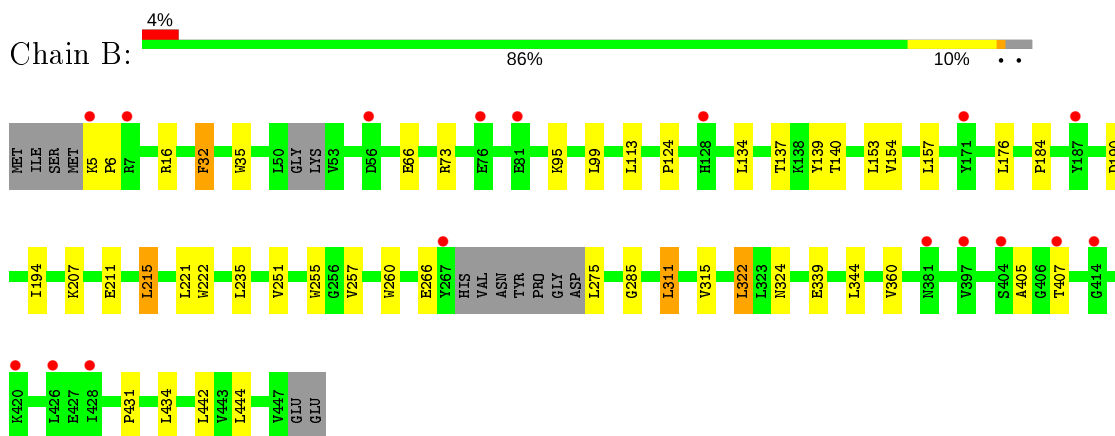
### 3 Residue-property plots [i](#)

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.

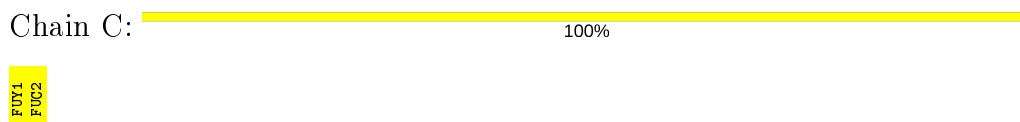
- Molecule 1: ALPHA-L-FUCOSIDASE, PUTATIVE



- Molecule 1: ALPHA-L-FUCOSIDASE, PUTATIVE



- Molecule 2: alpha-L-fucopyranose-(1-2)-beta-L-fucosyl-azide



- Molecule 2: alpha-L-fucopyranose-(1-2)-beta-L-fucosyl-azide



FU01  
FU02

## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	180.25Å 180.25Å 169.73Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	114.90 – 2.65 34.45 – 2.65	Depositor EDS
% Data completeness (in resolution range)	98.5 (114.90-2.65) 96.7 (34.45-2.65)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.03 (at 2.65Å)	Xtrriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.201 , 0.241 0.208 , 0.242	Depositor DCC
$R_{free}$ test set	1514 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	52.6	Xtrriage
Anisotropy	0.287	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 47.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7317	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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, FUY

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	0.34	0/3702	0.51	0/5026
1	B	0.34	0/3698	0.50	0/5021
All	All	0.34	0/7400	0.50	0/10047

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	3586	0	3465	30	0
1	B	3582	0	3462	25	0
2	C	23	0	21	1	0
2	D	23	0	21	0	0
3	A	45	0	0	0	0
3	B	58	0	0	1	0
All	All	7317	0	6969	51	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 4.

All (51) 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:16:ARG:HG2	1:B:260:TRP:CZ2	2.24	0.72
1:A:217:LEU:HD11	1:A:246:HIS:HB2	1.76	0.67
1:A:260:TRP:CZ2	1:B:16:ARG:HG2	2.37	0.60
1:B:35:TRP:O	1:B:134:LEU:HD11	2.05	0.56
1:A:311:LEU:O	1:A:315:VAL:HG23	2.06	0.56
1:A:5:LYS:N	1:A:6:PRO:CD	2.68	0.55
1:A:161:VAL:HG13	1:A:166:LEU:HB2	1.87	0.55
1:A:289:SER:OG	1:A:291:GLY:O	2.25	0.55
1:B:32:PHE:CD2	1:B:322:LEU:HD13	2.42	0.54
1:A:32:PHE:HB2	1:A:322:LEU:HD22	1.91	0.52
1:B:32:PHE:HB2	1:B:322:LEU:HD22	1.93	0.51
1:A:16:ARG:HG2	1:B:260:TRP:CE2	2.45	0.51
1:A:16:ARG:NH2	3:B:2005:HOH:O	2.30	0.50
1:B:211:GLU:HG2	1:B:215:LEU:HD22	1.93	0.50
1:A:211:GLU:HG2	1:A:215:LEU:HD22	1.95	0.48
1:A:397:VAL:HG22	1:A:427:GLU:HG2	1.95	0.48
1:B:190:ASP:HB3	1:B:194:ILE:HD12	1.96	0.48
1:A:32:PHE:CD2	1:A:322:LEU:HD13	2.49	0.48
1:A:403:LEU:HG	1:A:426:LEU:HD22	1.96	0.48
1:A:64:TYR:HA	1:A:289:SER:HB2	1.96	0.47
1:B:285:GLY:HA2	1:B:324:ASN:HB3	1.97	0.47
1:A:351:TYR:CD1	1:A:443:VAL:HG21	2.49	0.47
1:B:124:PRO:HG3	1:B:157:LEU:HD23	1.96	0.47
1:A:251:VAL:HG13	1:A:255:TRP:HE1	1.80	0.47
1:B:134:LEU:O	1:B:154:VAL:HG23	2.15	0.47
1:A:338:LYS:HE3	1:A:342:LEU:HD11	1.96	0.47
1:A:35:TRP:O	1:A:134:LEU:HD11	2.14	0.47
1:A:401:LEU:C	1:A:402:ASN:HD22	2.18	0.46
1:A:134:LEU:HD23	1:A:134:LEU:N	2.30	0.45
1:A:217:LEU:HD11	1:A:246:HIS:CB	2.44	0.45
1:B:275:LEU:HD22	1:B:360:VAL:HB	1.98	0.45
1:B:235:LEU:HD12	1:B:257:VAL:HG11	1.96	0.45
1:A:124:PRO:HG3	1:A:157:LEU:HD23	1.98	0.44
1:B:311:LEU:O	1:B:315:VAL:HG23	2.17	0.44
1:A:354:ALA:O	1:A:358:THR:HG21	2.17	0.44
1:B:5:LYS:N	1:B:6:PRO:HD2	2.32	0.44
1:B:255:TRP:HB2	1:B:257:VAL:HG22	2.00	0.43
1:A:251:VAL:HG13	1:A:255:TRP:NE1	2.34	0.43
1:A:134:LEU:O	1:A:154:VAL:HG23	2.19	0.43
1:A:221:LEU:HD22	1:A:242:TYR:CE2	2.54	0.43
1:B:431:PRO:HD2	1:B:434:LEU:HD12	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:290:PHE:CE2	2:C:2:FUC:H62	2.54	0.42
1:B:139:TYR:CE1	1:B:207:LYS:HE2	2.55	0.42
1:B:137:THR:HG21	1:B:140:THR:HG22	2.02	0.42
1:B:35:TRP:CZ3	1:B:153:LEU:HD13	2.55	0.42
1:B:442:LEU:HD11	1:B:444:LEU:HD11	2.01	0.41
1:A:175:GLY:HA3	1:A:225:MET:O	2.19	0.41
1:A:16:ARG:NH2	1:B:260:TRP:O	2.50	0.41
1:B:251:VAL:HG13	1:B:255:TRP:NE1	2.36	0.41
1:B:73:ARG:HB2	1:B:184:PRO:HB3	2.02	0.40
1:B:95:LYS:O	1:B:99:LEU:HD13	2.21	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	429/449 (96%)	405 (94%)	23 (5%)	1 (0%)	47	64
1	B	428/449 (95%)	408 (95%)	19 (4%)	1 (0%)	47	64
All	All	857/898 (95%)	813 (95%)	42 (5%)	2 (0%)	47	64

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	148	GLY
1	B	405	ALA

### 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	375/388 (97%)	356 (95%)	19 (5%)	24	37
1	B	375/388 (97%)	362 (96%)	13 (4%)	36	52
All	All	750/776 (97%)	718 (96%)	32 (4%)	29	44

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	ARG
1	A	32	PHE
1	A	56	ASP
1	A	66	GLU
1	A	113	LEU
1	A	134	LEU
1	A	176	LEU
1	A	215	LEU
1	A	221	LEU
1	A	222	TRP
1	A	228	PRO
1	A	251	VAL
1	A	266	GLU
1	A	322	LEU
1	A	344	LEU
1	A	346	GLU
1	A	379	LYS
1	A	402	ASN
1	A	407	THR
1	B	32	PHE
1	B	66	GLU
1	B	113	LEU
1	B	176	LEU
1	B	215	LEU
1	B	221	LEU
1	B	222	TRP
1	B	266	GLU
1	B	311	LEU
1	B	322	LEU
1	B	339	GLU
1	B	344	LEU
1	B	407	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	402	ASN
1	B	108	GLN
1	B	208	GLN
1	B	402	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](#)

4 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	$\# Z  > 2$
2	FUY	C	1	2	12,13,13	0.61	0	17,18,18	2.56	5 (29%)
2	FUC	C	2	2	10,10,11	0.25	0	14,14,16	0.84	0
2	FUY	D	1	2	12,13,13	0.61	0	17,18,18	2.13	5 (29%)
2	FUC	D	2	2	10,10,11	0.34	0	14,14,16	1.03	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
2	FUY	C	1	2	-	0/2/23/23	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FUC	C	2	2	-	-	0/1/1/1
2	FUY	D	1	2	-	1/2/23/23	0/1/1/1
2	FUC	D	2	2	-	-	0/1/1/1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	FUY	O5-C1-C2	-6.39	105.72	111.27
2	C	1	FUY	C3-C2-C1	-5.89	105.13	110.29
2	D	1	FUY	C3-C2-C1	-5.30	105.65	110.29
2	D	1	FUY	O5-C1-C2	-4.68	107.20	111.27
2	C	1	FUY	O2-C2-C1	2.85	114.12	110.06
2	C	1	FUY	C1-N1-N2	2.54	119.10	113.65
2	D	1	FUY	O2-C2-C1	2.53	113.67	110.06
2	C	1	FUY	C3-C4-C5	2.40	113.51	109.77
2	D	1	FUY	C3-C4-C5	2.30	113.35	109.77
2	D	1	FUY	C1-N1-N2	2.19	118.35	113.65

There are no chirality outliers.

All (1) torsion outliers are listed below:

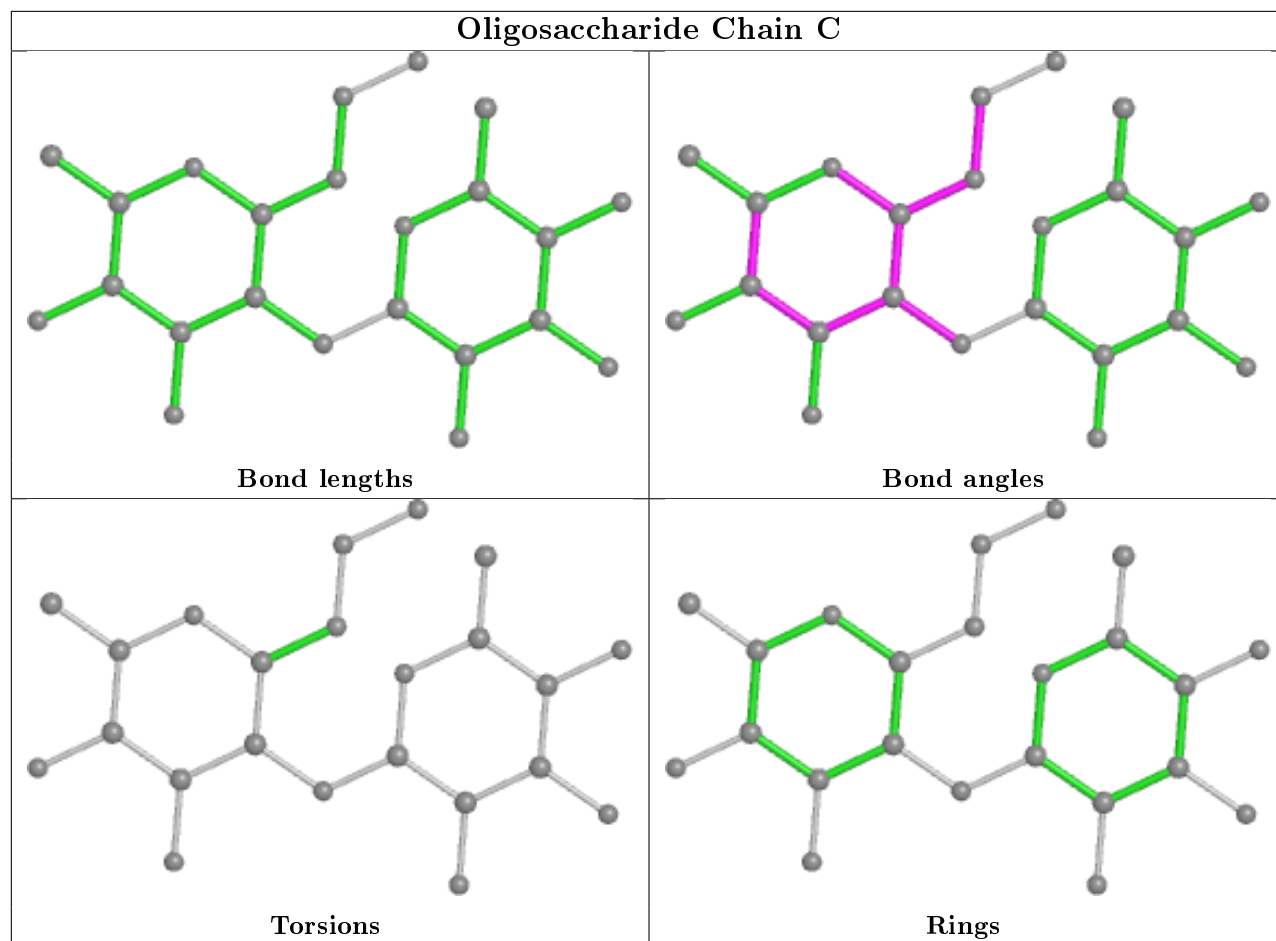
Mol	Chain	Res	Type	Atoms
2	D	1	FUY	O5-C1-N1-N2

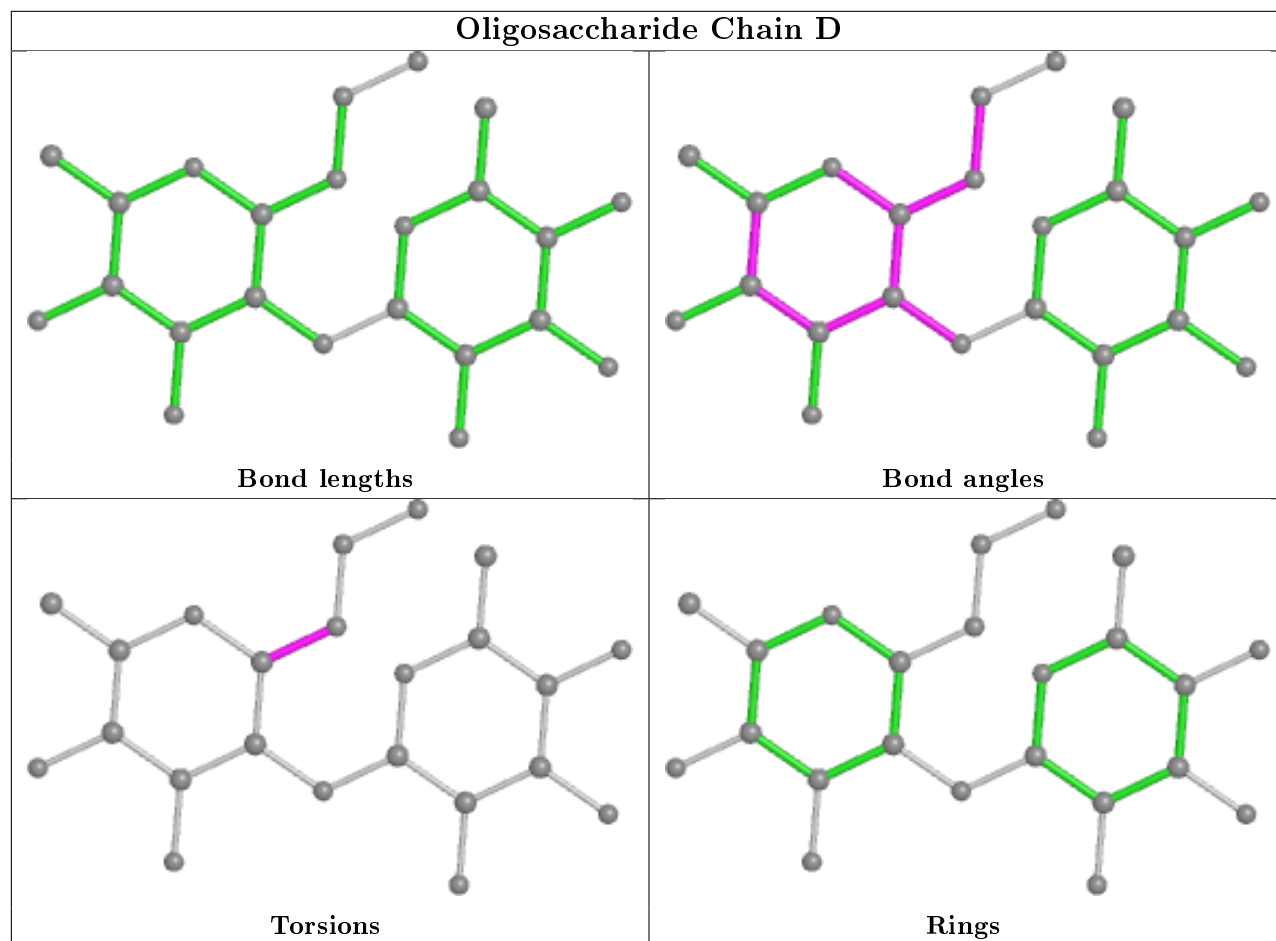
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	FUC	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 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	435/449 (96%)	0.16	21 (4%) 30 27	26, 47, 90, 115	0
1	B	434/449 (96%)	0.26	17 (3%) 39 35	30, 50, 95, 112	0
All	All	869/898 (96%)	0.21	38 (4%) 34 31	26, 48, 93, 115	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	267	TYR	5.2
1	A	404	SER	4.8
1	A	54	PRO	4.4
1	A	267	TYR	4.3
1	A	392	THR	4.2
1	A	405	ALA	3.8
1	B	5	LYS	3.6
1	B	56	ASP	3.5
1	A	55	MET	3.4
1	A	53	VAL	3.3
1	B	428	ILE	3.0
1	A	56	ASP	2.9
1	B	404	SER	2.8
1	A	403	LEU	2.8
1	B	407	THR	2.7
1	A	397	VAL	2.7
1	B	171	TYR	2.7
1	A	48	GLY	2.6
1	A	381	ASN	2.6
1	B	426	LEU	2.6
1	B	381	ASN	2.6
1	B	397	VAL	2.5
1	A	290	PHE	2.5
1	A	34	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	266	GLU	2.3
1	B	414	GLY	2.3
1	B	7	ARG	2.3
1	B	187	TYR	2.2
1	B	81	GLU	2.2
1	A	326	GLY	2.2
1	B	76	GLU	2.2
1	A	49	GLU	2.1
1	B	128	HIS	2.1
1	A	32	PHE	2.1
1	A	125	THR	2.0
1	A	325	VAL	2.0
1	A	291	GLY	2.0
1	B	420	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, 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.

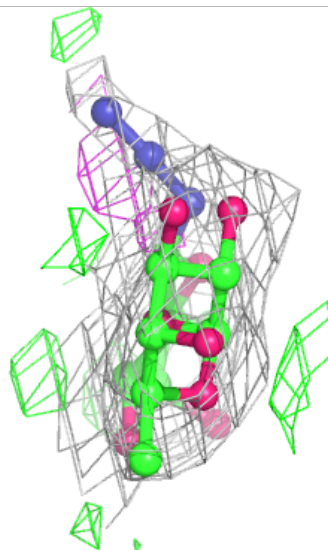
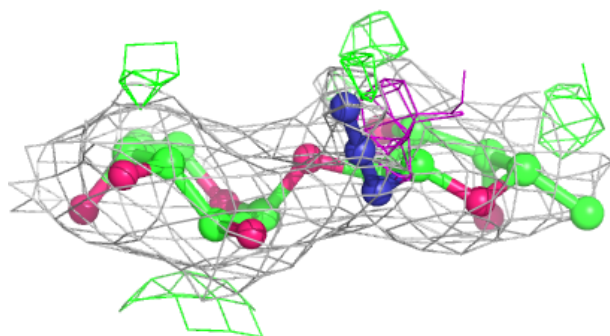
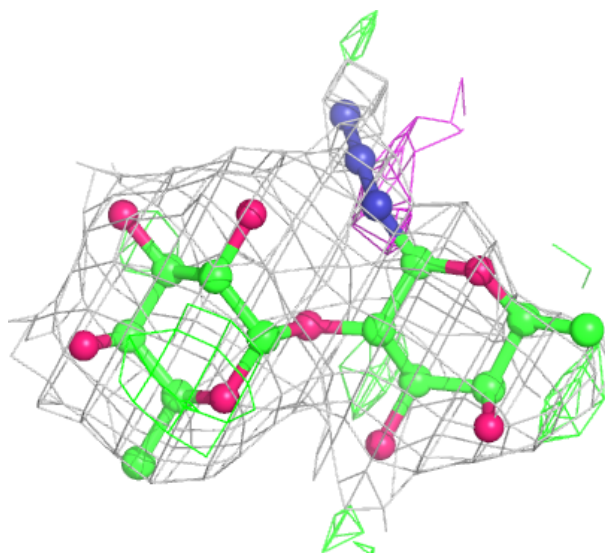
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	FUY	C	1	13/13	0.75	0.24	58,64,65,65	0
2	FUY	D	1	13/13	0.78	0.26	58,64,66,66	0
2	FUC	C	2	10/11	0.94	0.32	51,51,53,54	0
2	FUC	D	2	10/11	0.95	0.34	54,54,55,56	0

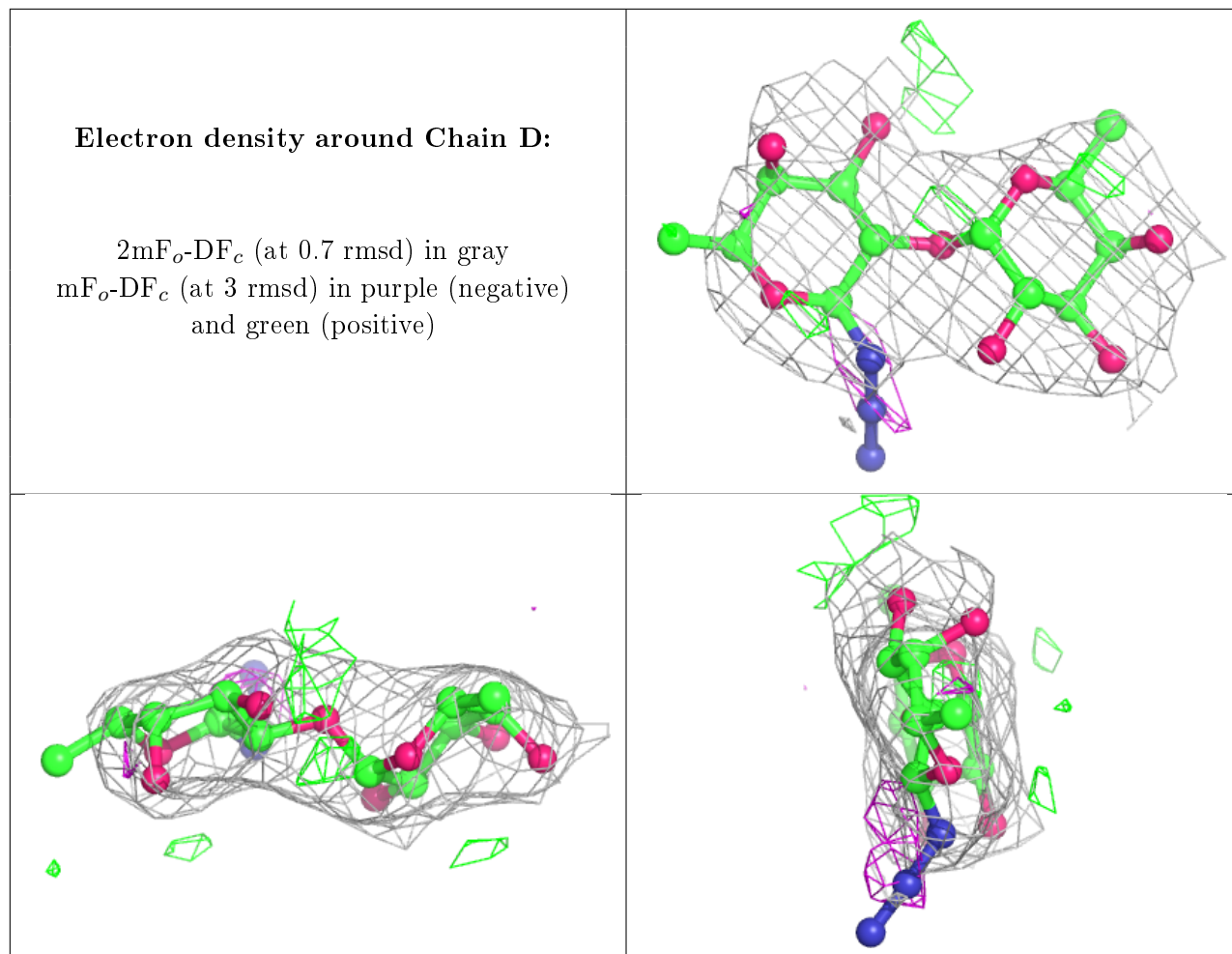
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



**Electron density around Chain C:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.