



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 02:17 PM BST

PDB ID : 3RJR  
Title : Crystal Structure of pro-TGF beta 1  
Authors : Zhu, J.H.; Shi, M.L.; Springer, T.A.  
Deposited on : 2011-04-15  
Resolution : 3.05 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.

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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 : 2.13.1  
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) : 2.13.1

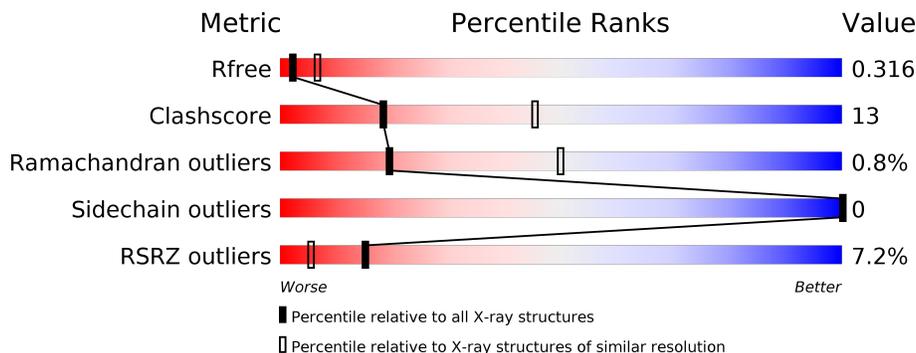
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.05 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	1754 (3.10-3.02)
Clashscore	141614	1864 (3.10-3.02)
Ramachandran outliers	138981	1794 (3.10-3.02)
Sidechain outliers	138945	1793 (3.10-3.02)
RSRZ outliers	127900	1713 (3.10-3.02)

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	363	 13% 65% 29% 6%
1	B	363	 6% 63% 27% 9%
1	C	363	 3% 65% 29% 6%
1	D	363	 5% 67% 27% 6%
2	E	2	 100%
2	F	2	 100%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 10955 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	340	2720	1728	477	498	17	0	0	0
1	B	330	2638	1675	465	481	17	0	0	0
1	C	343	2744	1743	481	503	17	0	0	0
1	D	342	2741	1742	480	502	17	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

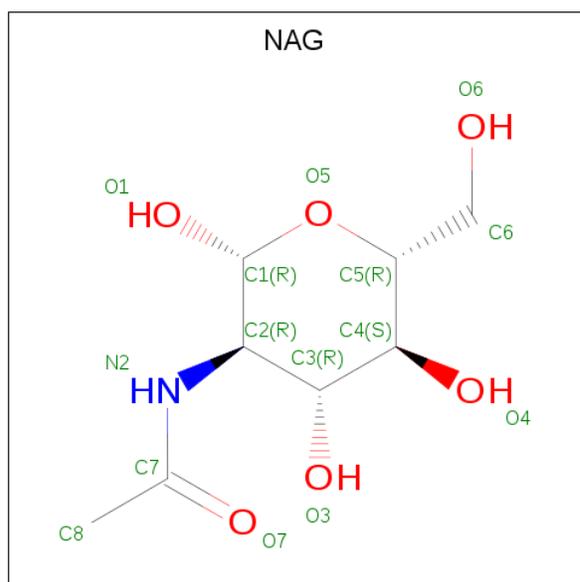
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P07200
A	0	PRO	-	expression tag	UNP P07200
A	4	SER	CYS	engineered mutation	UNP P07200
A	85	VAL	LEU	SEE REMARK 999	UNP P07200
A	147	GLN	ASN	engineered mutation	UNP P07200
B	-1	GLY	-	expression tag	UNP P07200
B	0	PRO	-	expression tag	UNP P07200
B	4	SER	CYS	engineered mutation	UNP P07200
B	85	VAL	LEU	SEE REMARK 999	UNP P07200
B	147	GLN	ASN	engineered mutation	UNP P07200
C	-1	GLY	-	expression tag	UNP P07200
C	0	PRO	-	expression tag	UNP P07200
C	4	SER	CYS	engineered mutation	UNP P07200
C	85	VAL	LEU	SEE REMARK 999	UNP P07200
C	147	GLN	ASN	engineered mutation	UNP P07200
D	-1	GLY	-	expression tag	UNP P07200
D	0	PRO	-	expression tag	UNP P07200
D	4	SER	CYS	engineered mutation	UNP P07200
D	85	VAL	LEU	SEE REMARK 999	UNP P07200
D	147	GLN	ASN	engineered mutation	UNP P07200

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



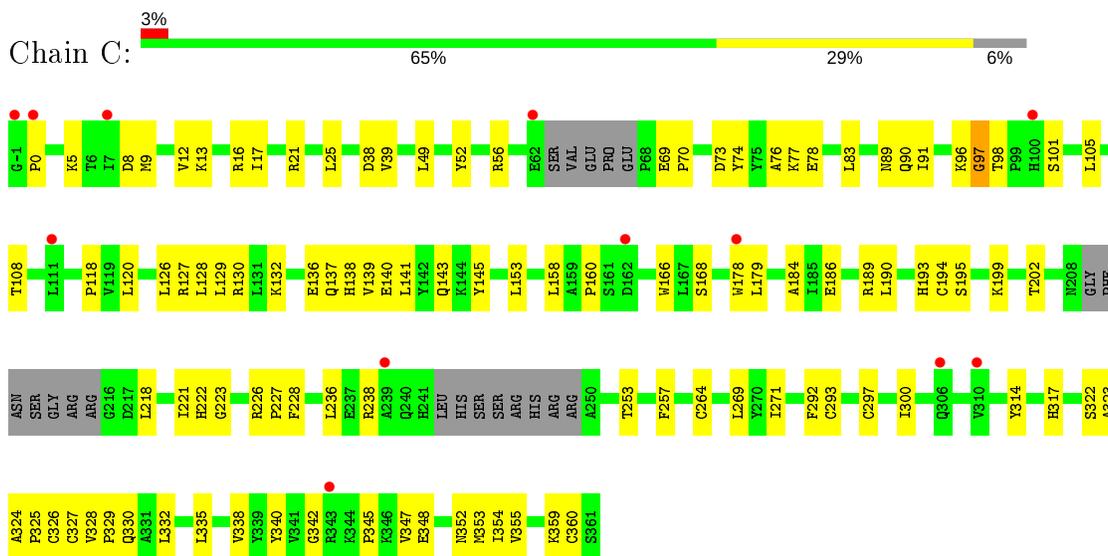
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	E	2	28	16	2	10	0	0	0
2	F	2	28	16	2	10	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).

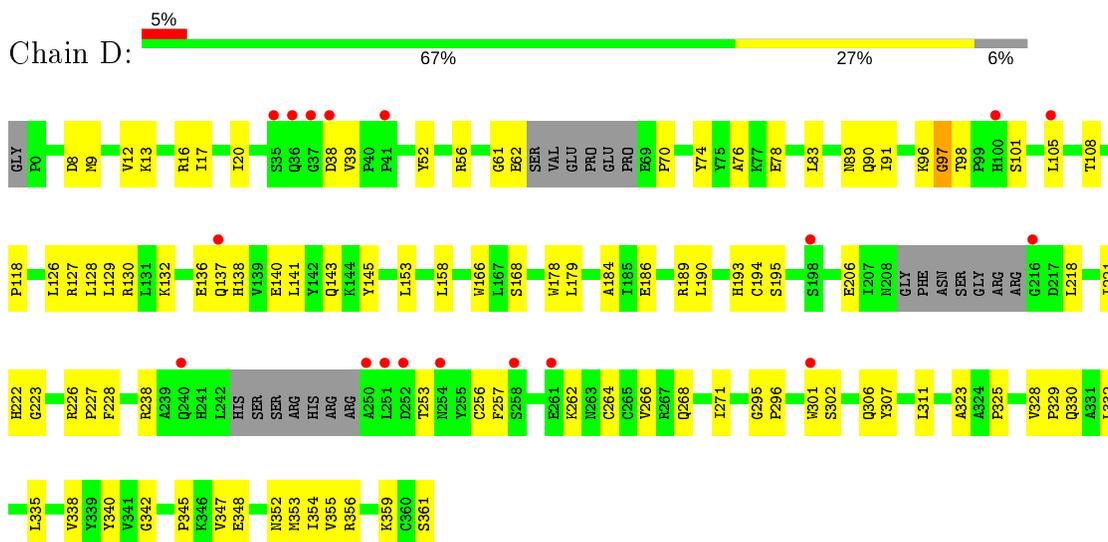


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	14	8	1	5	0	0
3	C	1	14	8	1	5	0	0
3	D	1	14	8	1	5	0	0
3	D	1	14	8	1	5	0	0

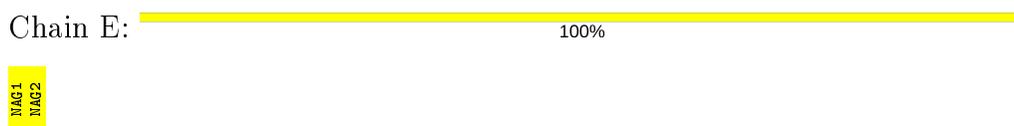




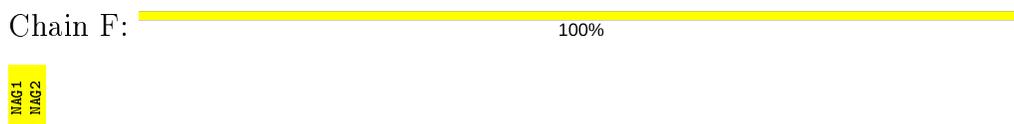
- Molecule 1: Transforming growth factor beta-1



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: 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 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.69Å 126.94Å 137.93Å 90.00° 96.72° 90.00°	Depositor
Resolution (Å)	46.55 – 3.05 46.55 – 3.05	Depositor EDS
% Data completeness (in resolution range)	98.8 (46.55-3.05) 98.9 (46.55-3.05)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.10 (at 3.06Å)	Xtrriage
Refinement program	PHENIX dev_276	Depositor
R, $R_{free}$	0.274 , 0.311 0.291 , 0.316	Depositor DCC
$R_{free}$ test set	1041 reflections (2.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	102.5	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 222.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	10955	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	214.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.00% 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: 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	0.20	0/2784	0.37	0/3773
1	B	0.20	0/2698	0.37	0/3654
1	C	0.20	0/2810	0.37	0/3810
1	D	0.20	0/2806	0.37	0/3804
All	All	0.20	0/11098	0.37	0/15041

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	2720	0	2706	85	0
1	B	2638	0	2635	79	0
1	C	2744	0	2730	79	0
1	D	2741	0	2730	71	0
2	E	28	0	25	1	0
2	F	28	0	25	3	0
3	A	14	0	13	0	0
3	C	14	0	13	0	0
3	D	28	0	26	0	0
All	All	10955	0	10903	290	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 290 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:D:91:ILE:CD1	1:D:105:LEU:HD12	1.52	1.39
1:A:91:ILE:CD1	1:A:105:LEU:HD12	1.51	1.38
1:B:91:ILE:CD1	1:B:105:LEU:HD12	1.52	1.37
1:C:91:ILE:CD1	1:C:105:LEU:HD12	1.56	1.36
1:D:91:ILE:HD12	1:D:105:LEU:CD1	1.79	1.12

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	332/363 (92%)	295 (89%)	35 (10%)	2 (1%)	25	55
1	B	320/363 (88%)	282 (88%)	36 (11%)	2 (1%)	25	55
1	C	335/363 (92%)	294 (88%)	38 (11%)	3 (1%)	17	47
1	D	334/363 (92%)	294 (88%)	36 (11%)	4 (1%)	13	40
All	All	1321/1452 (91%)	1165 (88%)	145 (11%)	11 (1%)	19	50

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	70	PRO
1	A	97	GLY
1	B	97	GLY
1	C	97	GLY
1	D	97	GLY

### 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	302/323 (94%)	302 (100%)	0	100	100
1	B	293/323 (91%)	293 (100%)	0	100	100
1	C	305/323 (94%)	305 (100%)	0	100	100
1	D	305/323 (94%)	305 (100%)	0	100	100
All	All	1205/1292 (93%)	1205 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	C	155	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	NAG	E	1	1,2	14,14,15	0.59	0	17,19,21	0.83	0
2	NAG	E	2	2	14,14,15	0.55	0	17,19,21	0.60	0
2	NAG	F	1	1,2	14,14,15	0.52	0	17,19,21	0.73	0
2	NAG	F	2	2	14,14,15	0.52	0	17,19,21	0.68	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	NAG	E	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	0/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

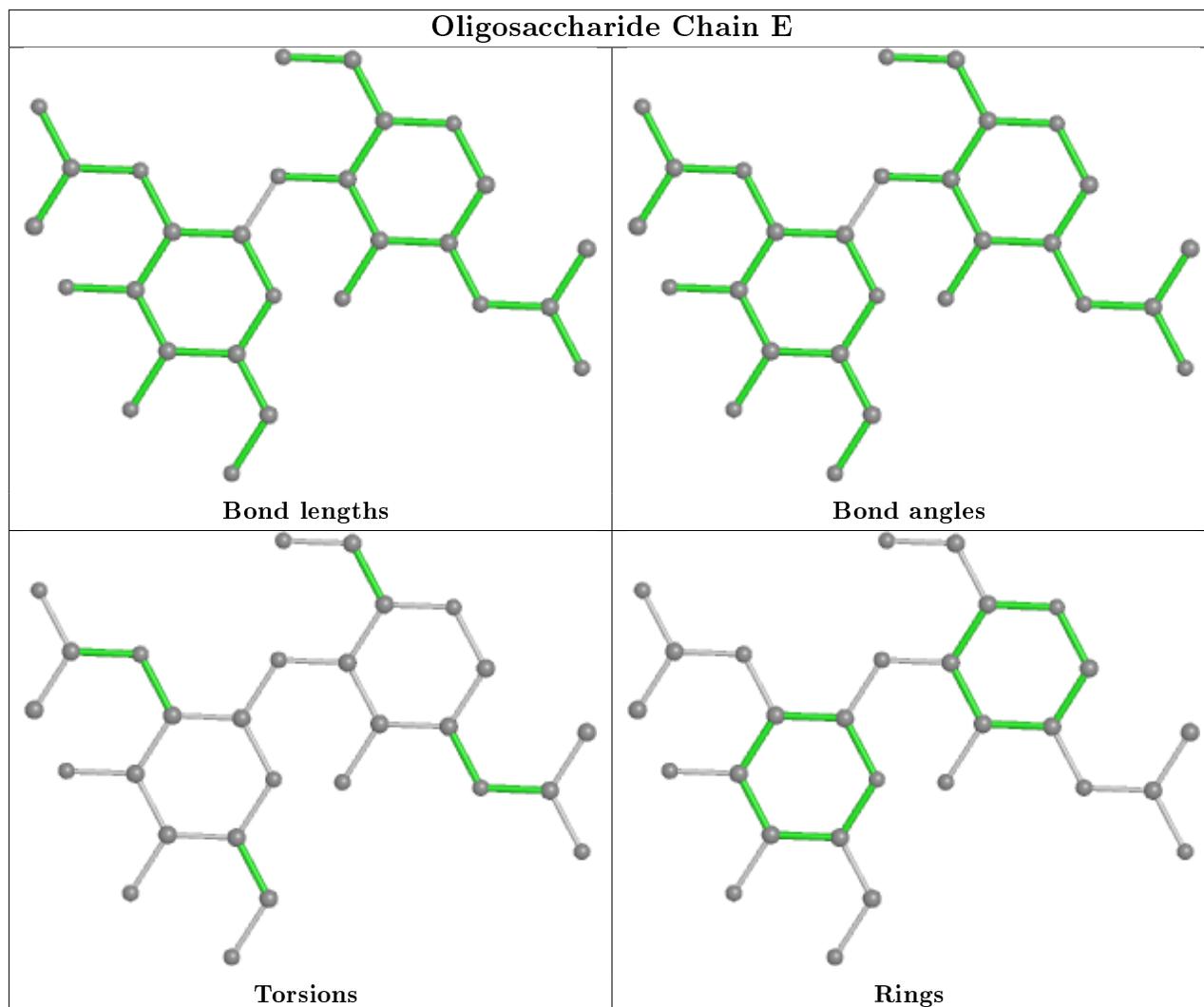
Mol	Chain	Res	Type	Atoms
2	F	1	NAG	C8-C7-N2-C2
2	F	1	NAG	O7-C7-N2-C2

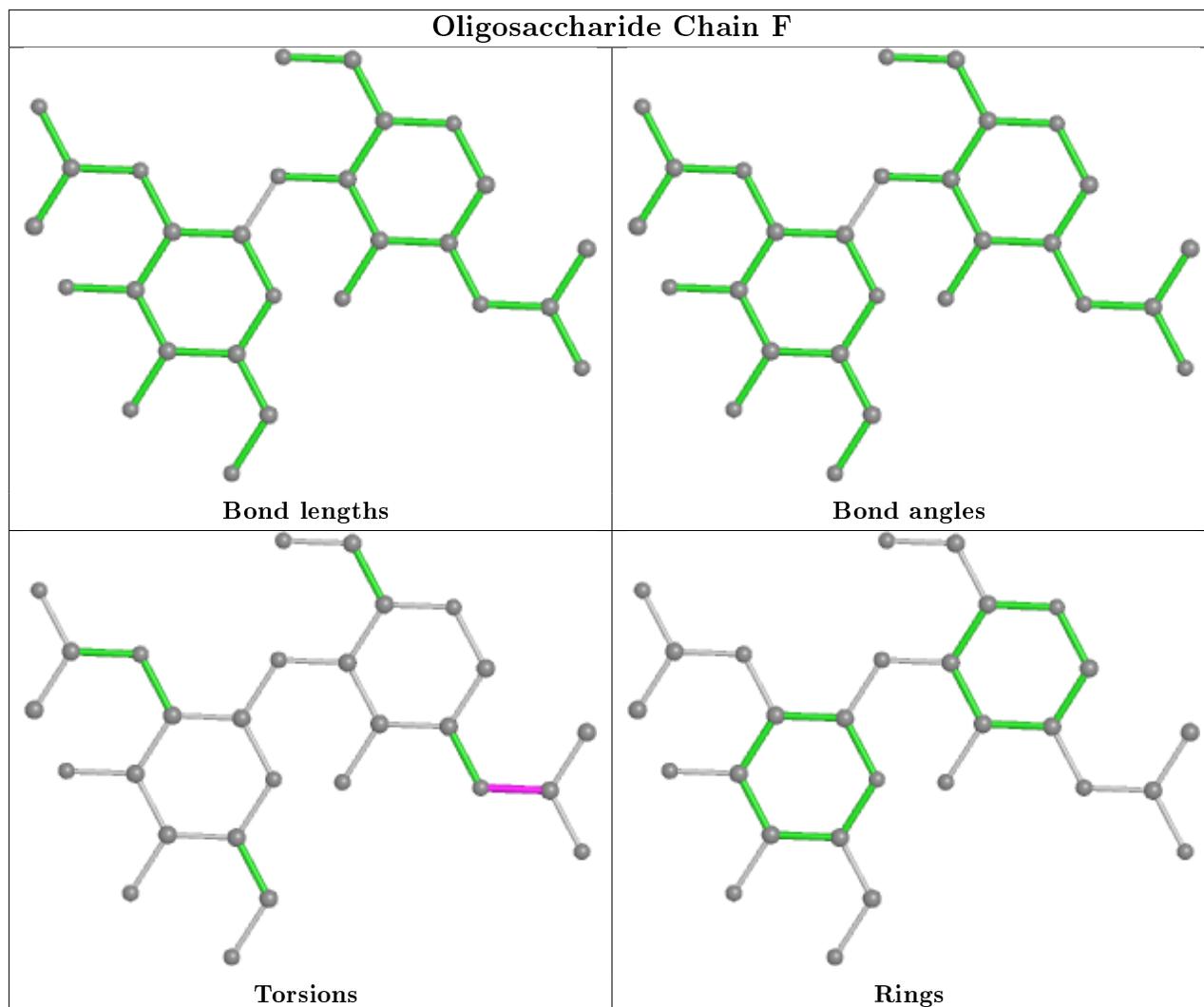
There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	NAG	1	0
2	E	2	NAG	1	0
2	F	2	NAG	2	0
2	F	1	NAG	3	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](#)

4 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	$\# Z  > 2$
3	NAG	A	3053	1	14,14,15	0.55	0	17,19,21	0.63	0
3	NAG	D	3053	1	14,14,15	0.51	0	17,19,21	0.70	0
3	NAG	D	3107	1	14,14,15	0.55	0	17,19,21	0.69	0
3	NAG	C	3107	1	14,14,15	0.53	0	17,19,21	0.67	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
3	NAG	A	3053	1	-	0/6/23/26	0/1/1/1
3	NAG	D	3053	1	-	2/6/23/26	0/1/1/1
3	NAG	D	3107	1	-	0/6/23/26	0/1/1/1
3	NAG	C	3107	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	3107	NAG	C8-C7-N2-C2
3	C	3107	NAG	O7-C7-N2-C2
3	D	3053	NAG	C4-C5-C6-O6
3	D	3053	NAG	O5-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, 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	340/363 (93%)	0.52	48 (14%) 2 1	102, 217, 358, 468	0
1	B	330/363 (90%)	0.29	20 (6%) 21 8	84, 203, 339, 433	0
1	C	343/363 (94%)	0.23	12 (3%) 44 22	74, 188, 326, 423	0
1	D	342/363 (94%)	0.39	18 (5%) 26 11	94, 194, 348, 467	0
All	All	1355/1452 (93%)	0.36	98 (7%) 15 5	74, 201, 349, 468	0

The worst 5 of 98 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	250	ALA	11.8
1	D	251	LEU	7.2
1	D	252	ASP	7.0
1	C	306	GLN	6.0
1	A	310	VAL	5.8

### 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.

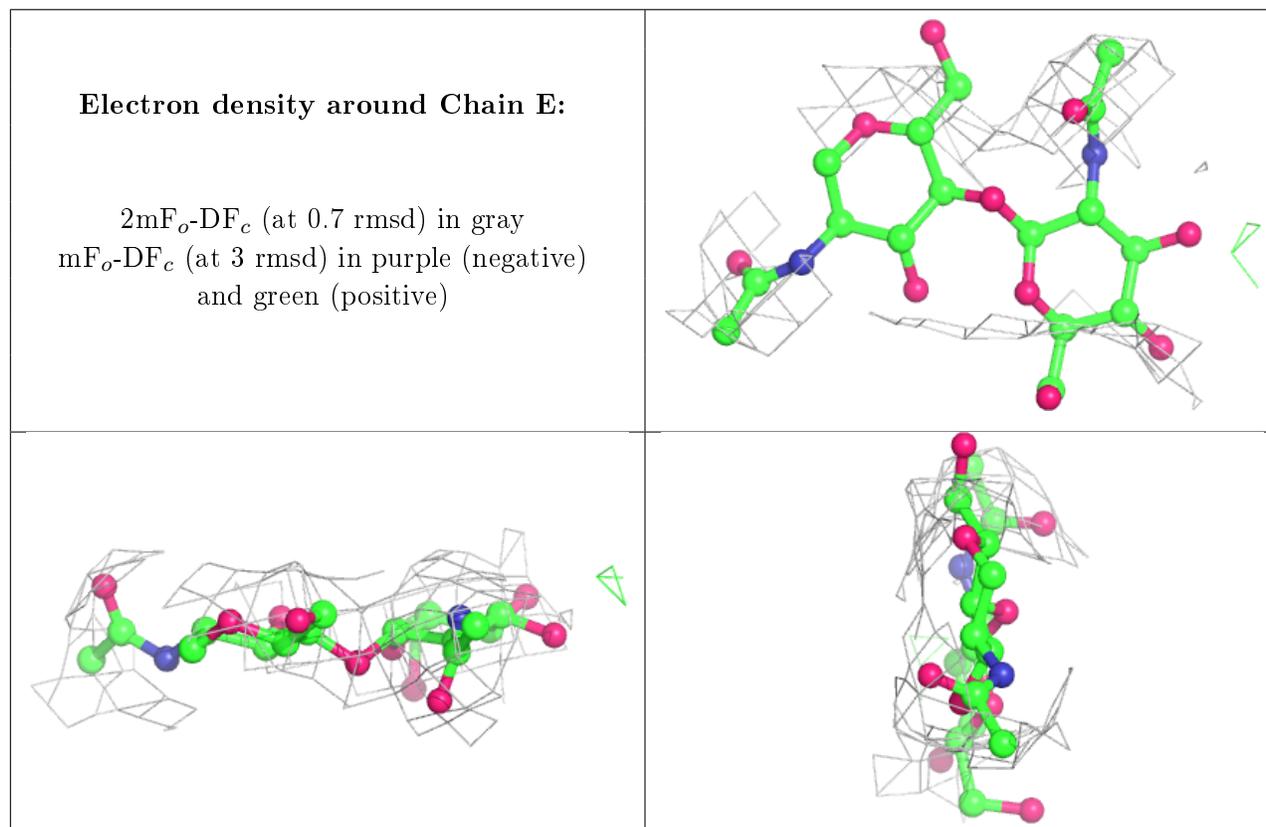
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q < 0.9
2	NAG	E	2	14/15	0.64	0.20	136,290,333,337	0
2	NAG	F	1	14/15	0.89	0.17	96,196,283,318	0

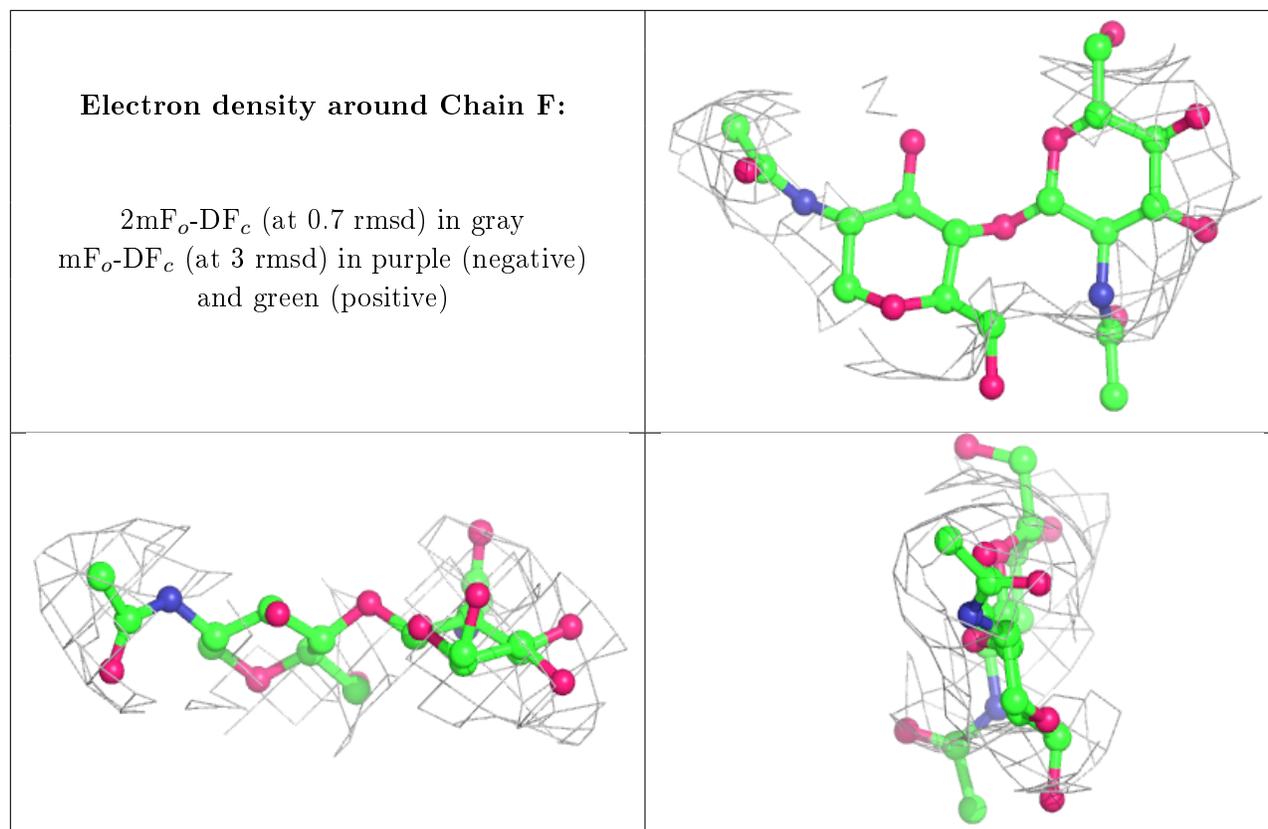
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	F	2	14/15	0.90	0.28	241,302,378,404	0
2	NAG	E	1	14/15	0.92	0.14	141,232,277,312	0

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
3	NAG	A	3053	14/15	0.56	0.27	140,268,304,307	0
3	NAG	D	3107	14/15	0.69	0.38	223,281,316,317	0
3	NAG	C	3107	14/15	0.81	0.25	196,269,311,322	0
3	NAG	D	3053	14/15	0.90	0.12	137,228,254,267	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.