

# Full wwPDB X-ray Structure Validation Report (i)

#### Aug 8, 2023 – 12:29 AM EDT

PDB ID : 1NKC

Title : A BACILLUS DNA POLYMERASE I PRODUCT COMPLEX BOUND TO A

> GUANINE-THYMINE MISMATCH AFTER FIVE ROUNDS OF PRIMER EXTENSION, FOLLOWING INCORPORATION OF DCTP, DGTP, DTTP,

AND DATP.

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Deposited on 2003-01-02

Resolution 1.80 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 A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

> The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity 4.02b-467

> 1.8.5 (274361), CSD as541be (2020) Mogul

Xtriage (Phenix) 1.13

EDS 2.35

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)

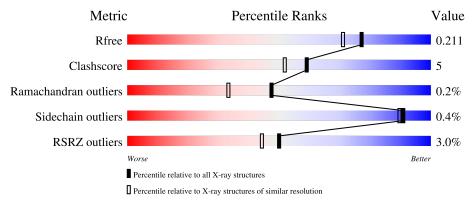
Validation Pipeline (wwPDB-VP) : 2.35

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	Similar resolution
Metric	$(\#  ext{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	В	15	67%	33%				
2	С	15	87%	13%				
3	A	580	88%	12%				
4	D	2	50%	50%				



## 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5912 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 DNA chain called DNA PRIMER STRAND.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	В	15	Total	C 145	N 50	O 87	P	0	0	0
			305	145	59	87	14			

• Molecule 2 is a DNA chain called DNA TEMPLATE STRAND.

Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf	Trace
9	С	15	Total	С	N	О	Р	0	0	0
		15	305	146	55	90	14	0		U

• Molecule 3 is a protein called DNA POLYMERASE I.

Mol	Chain	Residues		Atoms			ZeroOcc	AltConf	Trace	
3	A	580	Total 4650	C 2956	N 807	O 870	S 17	0	0	0

• Molecule 4 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace	
4	D	2	Total 23	C 12	O 11	0	0	0

• Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0

 $\bullet$  Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Mg 1 1	0	0

• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	В	32	Total O 32 32	0	0
7	С	49	Total O 49 49	0	0
7	A	532	Total O 532 532	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: DNA PRIMER STRAND





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	87.80Å 93.49Å 105.47Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.76 - 1.80	Depositor
Resolution (A)	26.76 - 1.80	EDS
% Data completeness	75.1 (26.76-1.80)	Depositor
(in resolution range)	76.5 (26.76-1.80)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.04	Depositor
$< I/\sigma(I) > 1$	4.50 (at 1.80Å)	Xtriage
Refinement program	CNS	Depositor
D D.	0.186 , 0.218	Depositor
$R, R_{free}$	0.180 , 0.211	DCC
$R_{free}$ test set	3090 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.5	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.40, 53.5	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.49, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5912	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.11% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: FRU, GLC, SO4, MG

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		
IVIOI		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	В	0.30	0/342	0.77	1/526~(0.2%)	
2	С	0.35	0/341	0.70	0/525	
3	A	0.30	0/4734	0.56	0/6398	
All	All	0.30	0/5417	0.59	$1/7449 \ (0.0\%)$	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$Ideal(^{o})$
1	В	12	DC	C1'-O4'-C4'	-5.64	104.46	110.10

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	В	305	0	169	5	0
2	С	305	0	171	2	0
3	A	4650	0	4698	43	0
4	D	23	0	21	1	0
5	A	15	0	0	0	0
6	A	1	0	0	0	0
7	A	532	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	В	32	0	0	0	0
7	С	49	0	0	0	0
All	All	5912	0	5059	49	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 5.

All (49) 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:738:ARG:HA	3:A:738:ARG:HH11	1.56	0.71
3:A:408:ASP:HB2	4:D:2:FRU:H11	1.75	0.69
1:B:6:DT:H2"	1:B:7:DC:C5'	2.25	0.66
3:A:737:GLU:O	3:A:741:GLU:HG3	1.96	0.66
1:B:6:DT:H2"	1:B:7:DC:H5'	1.78	0.65
3:A:534:LEU:HD11	3:A:574:ILE:HD13	1.79	0.65
3:A:579:GLN:HB2	7:A:2988:HOH:O	1.98	0.64
3:A:690:PHE:CD2	3:A:701:MET:HE2	2.35	0.61
3:A:813:ALA:O	3:A:817:GLU:HG3	2.04	0.58
2:C:35:DT:OP1	3:A:532:LYS:HE3	2.04	0.57
3:A:728:SER:OG	3:A:731:GLU:HG3	2.05	0.57
3:A:738:ARG:HH11	3:A:738:ARG:CA	2.18	0.56
3:A:589:GLU:O	3:A:593:LYS:HG3	2.04	0.56
3:A:532:LYS:O	3:A:536:VAL:HG23	2.06	0.56
3:A:459:ARG:HB3	3:A:460:PRO:HD3	1.87	0.55
3:A:334:GLY:HA2	3:A:348:PRO:HD3	1.89	0.54
3:A:693:SER:OG	3:A:696:GLU:HG3	2.08	0.54
3:A:530:SER:HB3	3:A:533:GLN:HB2	1.90	0.53
3:A:692:VAL:HB	3:A:696:GLU:HB2	1.92	0.52
3:A:485:LEU:O	3:A:489:GLU:HG3	2.10	0.52
3:A:784:ARG:O	3:A:788:GLU:HG3	2.11	0.51
3:A:760:LYS:HE3	7:A:3033:HOH:O	2.13	0.49
3:A:591:LEU:HD21	3:A:640:PHE:CZ	2.48	0.49
3:A:426:GLU:HG3	7:A:2025:HOH:O	2.12	0.49
3:A:876:LYS:HE2	7:A:3175:HOH:O	2.13	0.47
1:B:6:DT:H2'	1:B:7:DC:C6	2.49	0.47
2:C:35:DT:H2"	2:C:36:DG:C8	2.49	0.47
3:A:822:ALA:CB	3:A:836:ALA:HB2	2.45	0.46
3:A:565:ALA:HB3	3:A:566:PRO:HD3	1.97	0.46
3:A:848:VAL:HB	3:A:849:PRO:HD3	1.98	0.45
3:A:610:LEU:HD23	3:A:610:LEU:C	2.38	0.44

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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}({ m \AA})$	overlap (Å)
1:B:3:DC:H2"	1:B:4:DG:C8	2.52	0.44
3:A:584:GLN:O	3:A:589:GLU:HG3	2.18	0.44
3:A:587:TYR:CE1	3:A:627:PRO:HD3	2.53	0.43
3:A:730:LYS:O	3:A:734:GLU:HG3	2.18	0.43
3:A:691:GLN:HG3	3:A:738:ARG:NH2	2.33	0.43
3:A:700:ASN:O	3:A:704:GLN:HG3	2.19	0.43
3:A:664:HIS:ND1	3:A:859:ARG:HG3	2.34	0.43
3:A:416:MET:HE3	7:A:2385:HOH:O	2.19	0.42
3:A:716:ILE:HG13	3:A:717:SER:N	2.34	0.42
3:A:510:GLN:O	3:A:514:VAL:HG23	2.20	0.42
3:A:794:THR:HB	3:A:795:PRO:HD3	2.02	0.42
3:A:677:ARG:HB2	3:A:679:LEU:HG	2.02	0.42
1:B:6:DT:H2"	1:B:7:DC:O5'	2.20	0.41
3:A:738:ARG:HB3	3:A:738:ARG:NH1	2.36	0.41
3:A:607:ASN:HB3	3:A:617:SER:OG	2.20	0.40
3:A:453:ALA:O	3:A:457:LEU:HG	2.21	0.40
3:A:828:VAL:HB	3:A:831:GLU:HG2	2.02	0.40
3:A:718:ASP:OD1	3:A:719:TYR:N	2.55	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	
3	A	578/580 (100%)	564 (98%)	13 (2%)	1 (0%)	47 33	

#### All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	628	ILE



#### 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		
3	A	495/496 (100%)	493 (100%)	2 (0%)	91	89	

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	303	LEU
3	A	844	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	782	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)

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	Trunc	Chain	Res	Dog Link	Bo	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2	
4	GLC	D	1	4	11,11,12	3.38	4 (36%)	15,15,17	1.60	2 (13%)	
4	FRU	D	2	4	11,12,12	1.50	2 (18%)	10,18,18	0.76	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
4	GLC	D	1	4	-	0/2/19/22	0/1/1/1
4	FRU	D	2	4	-	0/5/24/24	0/1/1/1

#### All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
4	D	1	GLC	C2-C3	9.94	1.67	1.52
4	D	2	FRU	O2-C2	4.09	1.47	1.40
4	D	1	GLC	O5-C1	2.72	1.48	1.43
4	D	1	GLC	O5-C5	2.61	1.48	1.43
4	D	1	GLC	C4-C5	2.48	1.58	1.53
4	D	2	FRU	C1-C2	2.25	1.55	1.52

#### All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\mathrm{Ideal}(^{o})$
4	D	1	GLC	C1-O5-C5	4.16	117.82	112.19
4	D	1	GLC	C1-C2-C3	-3.10	105.85	109.67

There are no chirality outliers.

There are no torsion outliers.

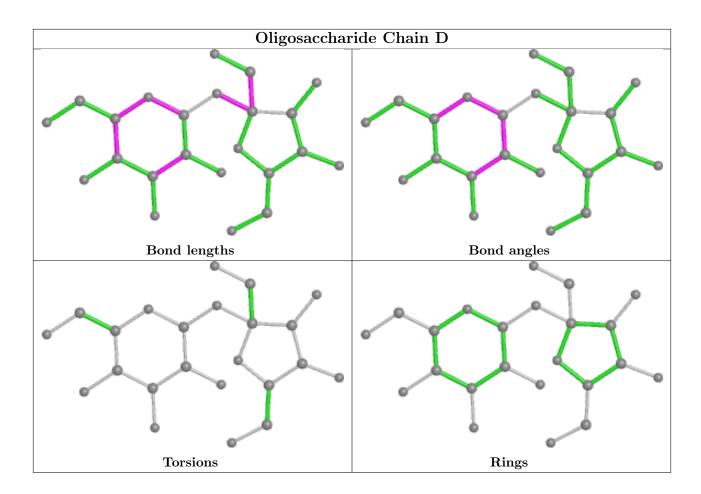
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	2	FRU	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 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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	Type Chain		Res	Link	Bond lengths			Bond angles		
	туре	Chain	nes	tes Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	SO4	A	910	-	4,4,4	0.27	0	6,6,6	0.04	0
5	SO4	A	912	-	4,4,4	0.24	0	6,6,6	0.09	0
5	SO4	A	911	-	4,4,4	0.26	0	6,6,6	0.06	0

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,  $95^{th}$  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>	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	В	15/15 (100%)	0.08	0 100 100	13, 32, 40, 43	0
2	С	15/15 (100%)	0.03	0 100 100	12, 23, 45, 51	0
3	A	580/580 (100%)	0.02	18 (3%) 49 43	7, 16, 34, 52	0
All	All	610/610 (100%)	0.03	18 (2%) 50 44	7, 16, 36, 52	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	719	TYR	7.6
3	A	552	THR	4.9
3	A	551	LYS	4.4
3	A	729	ARG	3.7
3	A	297	ALA	3.4
3	A	433	ALA	3.1
3	A	549	LYS	3.1
3	A	434	LYS	3.0
3	A	466	ARG	2.8
3	A	723	GLN	2.5
3	A	319	VAL	2.4
3	A	550	THR	2.4
3	A	629	ARG	2.3
3	A	406	GLY	2.2
3	A	779	ARG	2.1
3	A	876	LYS	2.1
3	A	726	ASN	2.1
3	A	553	GLY	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.

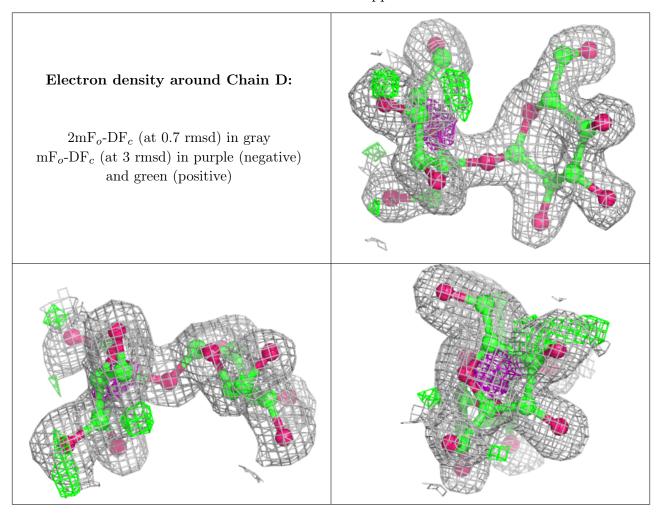


### 6.3 Carbohydrates (i)

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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
4	FRU	D	2	12/12	0.73	0.20	22,27,28,28	0
4	GLC	D	1	11/12	0.90	0.14	28,29,30,31	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	$\operatorname{Res}$	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
5	SO4	A	911	5/5	0.81	0.19	79,80,80,80	0
5	SO4	A	910	5/5	0.94	0.17	58,58,58,58	0
5	SO4	A	912	5/5	0.96	0.12	38,38,39,40	0
6	MG	A	920	1/1	0.99	0.05	25,25,25,25	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

