



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:07 PM GMT

PDB ID : 1NKE  
Title : A BACILLUS DNA POLYMERASE I PRODUCT COMPLEX BOUND TO  
A CYTOSINE-THYMINE MISMATCH AFTER A SINGLE ROUND OF  
PRIMER EXTENSION, FOLLOWING INCORPORATION OF DCTP.  
Authors : Johnson, S.J.; Beese, L.S.  
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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

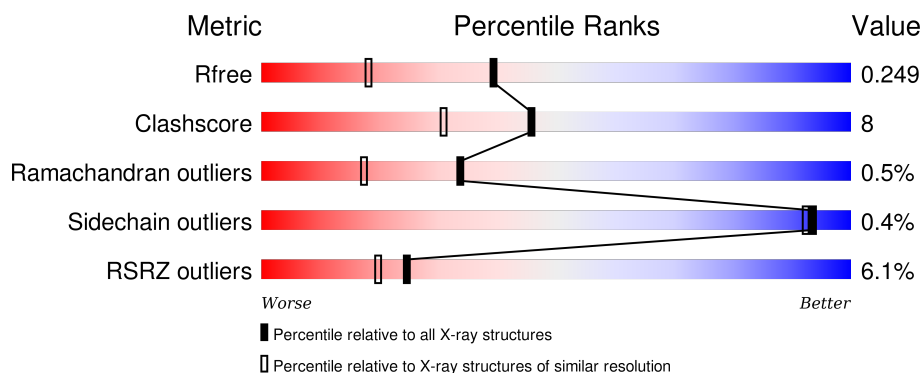
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	11	<div> <div>9%</div> <div>55%</div> <div>45%</div> </div>
2	C	16	<div> <div>25%</div> <div>19%</div> <div>56%</div> <div>25%</div> </div>
3	A	580	<div> <div>6%</div> <div>87%</div> <div>13%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SUC	A	902	-	-	-	X
7	DCP	A	2	-	-	-	X

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 5692 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	B	11	Total	C	N	O	P	0	0	0
			220	105	42	63	10			

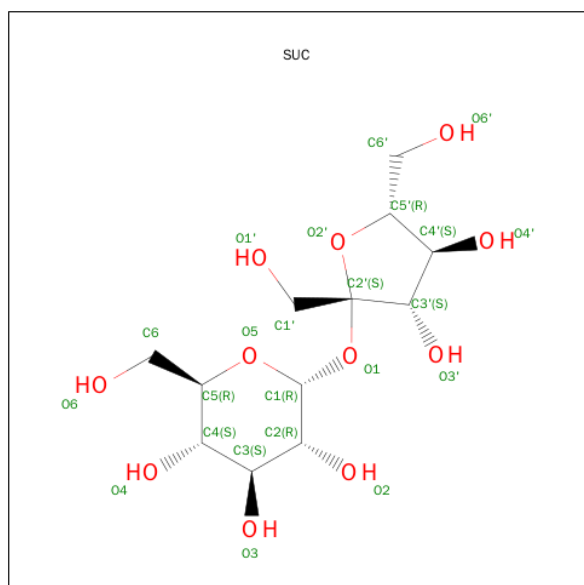
- Molecule 2 is a DNA chain called DNA TEMPLATE STRAND.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	12	Total	C	N	O	P	0	0	0
			244	117	45	71	11			

- Molecule 3 is a protein called DNA POLYMERASE I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	580	Total	C	N	O	S	0	4	0
			4687	2976	815	879	17			

- Molecule 4 is SUGAR (SUCROSE) (three-letter code: SUC) (formula: C<sub>12</sub>H<sub>22</sub>O<sub>11</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			23	12	11		
4	A	1	Total	C	O	0	0
			23	12	11		

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

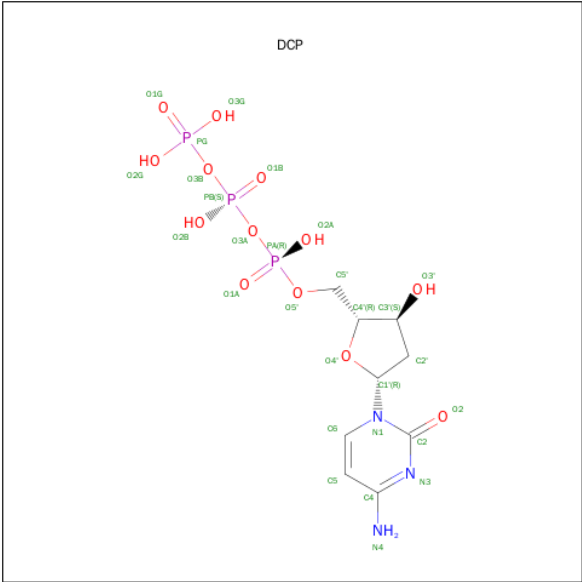


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		

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

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

- Molecule 7 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP) (formula: C<sub>9</sub>H<sub>16</sub>N<sub>3</sub>O<sub>13</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	P	0	0
			28	9	3	13	3		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	404	Total	O	0	0
			404	404		
8	B	9	Total	O	0	0
			9	9		
8	C	28	Total	O	0	0
			28	28		

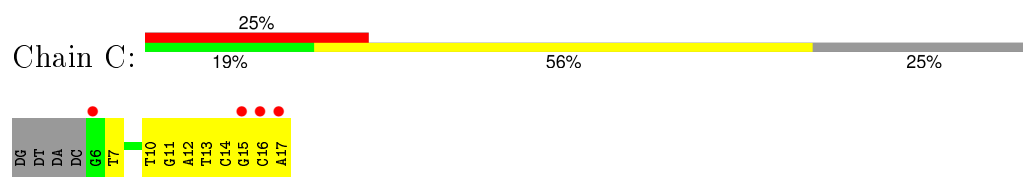
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ( $\text{RSRZ} > 2$ ). 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.

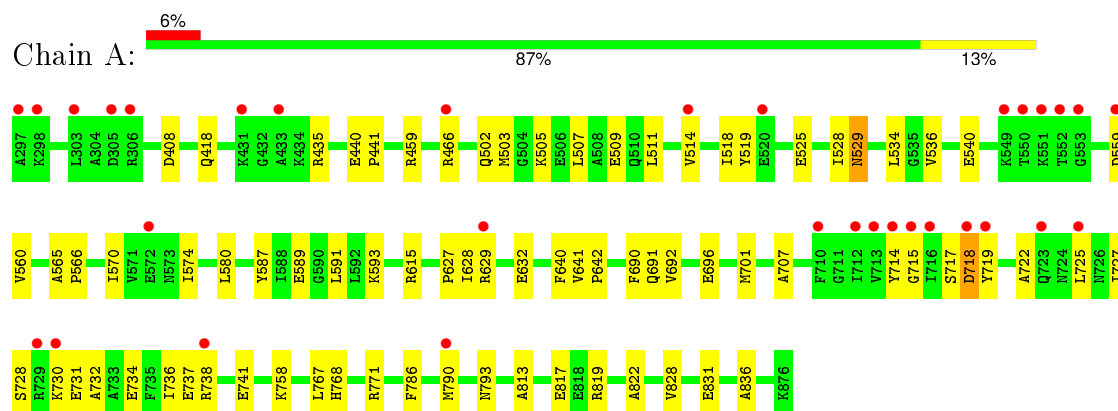
#### • Molecule 1: DNA PRIMER STRAND



#### • Molecule 2: DNA TEMPLATE STRAND



#### • Molecule 3: DNA POLYMERASE I



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.29 Å 94.32 Å 105.69 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.07 – 1.80 43.07 – 1.80	Depositor EDS
% Data completeness (in resolution range)	88.5 (43.07-1.80) 93.8 (43.07-1.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.21 (at 1.79 Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.216 , 0.248 0.218 , 0.249	Depositor DCC
$R_{free}$ test set	3709 reflections (5.09%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.1	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 47.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 77224 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5692	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.83% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, SUC, SO4, DCP

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	0.28	0/246	0.75	0/377
2	C	0.36	0/273	0.76	0/420
3	A	0.32	0/4771	0.56	0/6447
All	All	0.32	0/5290	0.58	0/7244

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

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	220	0	124	7	0
2	C	244	0	137	9	0
3	A	4687	0	4725	64	0
4	A	46	0	44	1	0
5	A	25	0	0	0	0
6	A	1	0	0	0	0
7	A	28	0	12	2	0
8	A	404	0	0	6	0
8	B	9	0	0	0	0
8	C	28	0	0	0	0
All	All	5692	0	5042	79	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.

All (79) 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:528:ILE:HG13	8:A:3250:HOH:O	1.76	0.85
3:A:771:ARG:NH2	3:A:790:MET:HE3	2.03	0.73
3:A:730:LYS:O	3:A:734:GLU:HG3	1.88	0.71
1:B:22:DA:H2''	1:B:23:DT:H5'	1.73	0.69
1:B:22:DA:H2''	1:B:23:DT:C5'	2.22	0.68
3:A:771:ARG:HH21	3:A:790:MET:HE3	1.59	0.68
1:B:28:DC:OP2	3:A:629:ARG:HD3	1.96	0.66
3:A:632:GLU:CD	3:A:632:GLU:H	2.01	0.64
3:A:518:ILE:HD13	3:A:574:ILE:HD13	1.81	0.62
3:A:519:TYR:CD1	3:A:525:GLU:HA	2.34	0.62
3:A:731:GLU:HA	3:A:734:GLU:OE1	2.01	0.61
3:A:466:ARG:HG3	3:A:466:ARG:HH11	1.66	0.60
3:A:813:ALA:O	3:A:817:GLU:HG3	2.01	0.60
3:A:503:MET:O	3:A:507:LEU:HD13	2.01	0.59
3:A:435:ARG:HG2	3:A:435:ARG:HH11	1.67	0.59
3:A:738:ARG:HH11	3:A:738:ARG:HA	1.67	0.59
2:C:16:DC:H2'	2:C:17:DA:C8	2.38	0.59
3:A:691:GLN:HG3	3:A:738:ARG:HH21	1.69	0.58
3:A:502:GLN:O	3:A:505:LYS:HG2	2.03	0.57
3:A:758:LYS:NZ	3:A:758:LYS:HB2	2.19	0.57
3:A:737:GLU:O	3:A:741:GLU:HG3	2.05	0.55
2:C:12:DA:H2''	2:C:13:DT:C5'	2.37	0.55
3:A:615[B]:ARG:HG3	3:A:615[B]:ARG:HH11	1.72	0.55
3:A:559:ASP:OD1	3:A:560:VAL:HG23	2.06	0.55
3:A:819:ARG:HG2	8:A:3091:HOH:O	2.06	0.54
3:A:570:ILE:O	3:A:574:ILE:HG12	2.08	0.53
1:B:25:DA:H2''	1:B:26:DG:H5'	1.91	0.53
2:C:12:DA:H4'	3:A:529:ASN:OD1	2.09	0.52
3:A:408:ASP:HB2	4:A:901:SUC:H1'1	1.92	0.52
2:C:16:DC:H2''	2:C:17:DA:H5'	1.93	0.51
3:A:591:LEU:HD21	3:A:640:PHE:CZ	2.45	0.50
2:C:7:DT:OP1	3:A:790:MET:HG2	2.11	0.50
2:C:12:DA:H1'	2:C:13:DT:H5''	1.93	0.50
3:A:738:ARG:CA	3:A:738:ARG:HH11	2.24	0.50
3:A:536:VAL:O	3:A:540:GLU:HB2	2.12	0.49
3:A:822:ALA:CB	3:A:836:ALA:HB2	2.41	0.49
3:A:690:PHE:CD2	3:A:701:MET:HE3	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:771:ARG:NH2	3:A:790:MET:CE	2.73	0.49
3:A:435:ARG:HG2	3:A:435:ARG:NH1	2.28	0.49
3:A:728:SER:OG	3:A:731:GLU:HG3	2.13	0.48
3:A:717:SER:C	3:A:719:TYR:H	2.17	0.48
7:A:2:DCP:O2B	7:A:2:DCP:O2A	2.32	0.48
3:A:505:LYS:O	3:A:509:GLU:HG3	2.14	0.47
1:B:28:DC:H2''	8:A:3337:HOH:O	2.14	0.47
3:A:466:ARG:HG3	3:A:466:ARG:NH1	2.28	0.47
3:A:714:TYR:HA	3:A:793:ASN:ND2	2.30	0.46
3:A:691:GLN:CG	3:A:738:ARG:HH21	2.28	0.46
3:A:519:TYR:CG	3:A:525:GLU:HG2	2.51	0.46
2:C:10:DT:H2'	2:C:11:DG:C8	2.51	0.45
2:C:14:DC:H2'	2:C:15:DG:C8	2.50	0.45
3:A:587:TYR:CE2	3:A:627:PRO:HD3	2.52	0.45
2:C:12:DA:H2''	2:C:13:DT:H5'	1.97	0.45
3:A:722:ALA:HA	3:A:727:ILE:HG13	1.98	0.45
7:A:2:DCP:O5'	7:A:2:DCP:H6	2.17	0.45
3:A:718:ASP:C	8:A:3243:HOH:O	2.55	0.45
3:A:732:ALA:O	3:A:736:ILE:HG13	2.18	0.44
3:A:692:VAL:HB	3:A:696:GLU:HB2	1.99	0.44
3:A:615[B]:ARG:NH1	8:A:3195:HOH:O	2.51	0.43
3:A:828:VAL:HG12	3:A:828:VAL:O	2.19	0.43
3:A:502:GLN:OE1	3:A:505:LYS:HD2	2.19	0.42
3:A:767:LEU:O	3:A:768:HIS:HB2	2.19	0.42
3:A:828:VAL:HB	3:A:831:GLU:HG2	2.01	0.42
3:A:589:GLU:O	3:A:593:LYS:HG3	2.18	0.42
3:A:459:ARG:HD3	3:A:459:ARG:O	2.19	0.42
1:B:25:DA:H2''	1:B:26:DG:C5'	2.50	0.42
3:A:707:ALA:CB	3:A:725:LEU:HD21	2.50	0.42
3:A:418:GLN:HA	8:A:3213:HOH:O	2.19	0.42
3:A:738:ARG:NH1	3:A:738:ARG:HB3	2.34	0.42
1:B:22:DA:H2''	1:B:23:DT:H5''	1.97	0.41
3:A:565:ALA:HB3	3:A:566:PRO:HD3	2.03	0.41
3:A:771:ARG:CZ	3:A:790:MET:CE	2.98	0.41
3:A:722:ALA:HA	3:A:727:ILE:CG1	2.51	0.41
3:A:514:VAL:O	3:A:518:ILE:HG13	2.21	0.41
3:A:440:GLU:HB3	3:A:441:PRO:HD3	2.03	0.41
3:A:722:ALA:HB1	3:A:727:ILE:O	2.21	0.41
3:A:511:LEU:HD21	3:A:580:LEU:HB2	2.02	0.40
3:A:786:PHE:CE2	3:A:790:MET:SD	3.14	0.40
3:A:758:LYS:NZ	3:A:758:LYS:CB	2.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:641:VAL:HB	3:A:642:PRO:CD	2.52	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	582/580 (100%)	559 (96%)	20 (3%)	3 (0%)	34 17

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	715	GLY
3	A	628	ILE
3	A	718	ASP

### 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	499/496 (101%)	497 (100%)	2 (0%)	93 92

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

Mol	Chain	Res	Type
3	A	529	ASN
3	A	534	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 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	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
7	DCP	A	2	-	21,29,29	1.65	3 (14%)	33,45,45	1.47	6 (18%)
4	SUC	A	901	-	24,24,24	1.54	3 (12%)	36,36,36	0.91	2 (5%)
4	SUC	A	902	-	24,24,24	1.55	3 (12%)	36,36,36	0.92	1 (2%)
5	SO4	A	910	-	4,4,4	0.22	0	6,6,6	0.08	0
5	SO4	A	911	-	4,4,4	0.21	0	6,6,6	0.07	0
5	SO4	A	912	-	4,4,4	0.18	0	6,6,6	0.10	0
5	SO4	A	913	-	4,4,4	0.22	0	6,6,6	0.08	0
5	SO4	A	914	-	4,4,4	0.23	0	6,6,6	0.08	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
7	DCP	A	2	-	-	0/18/34/34	0/2/2/2
4	SUC	A	901	-	-	0/12/51/51	0/2/2/2
4	SUC	A	902	-	-	0/12/51/51	0/2/2/2
5	SO4	A	910	-	-	0/0/0/0	0/0/0/0
5	SO4	A	911	-	-	0/0/0/0	0/0/0/0
5	SO4	A	912	-	-	0/0/0/0	0/0/0/0
5	SO4	A	913	-	-	0/0/0/0	0/0/0/0
5	SO4	A	914	-	-	0/0/0/0	0/0/0/0

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	902	SUC	C4-C5	2.33	1.58	1.53
4	A	901	SUC	C4-C5	2.40	1.58	1.53
4	A	902	SUC	O5-C1	2.45	1.48	1.41
4	A	901	SUC	O5-C1	2.54	1.48	1.41
7	A	2	DCP	O4'-C1'	2.66	1.48	1.42
7	A	2	DCP	C4-N3	3.37	1.41	1.35
7	A	2	DCP	C6-N1	4.69	1.42	1.35
4	A	902	SUC	C3-C2	5.40	1.66	1.52
4	A	901	SUC	C3-C2	5.51	1.66	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	2	DCP	PB-O3A-PA	-3.39	123.22	132.73
7	A	2	DCP	PB-O3B-PG	-3.38	121.34	132.67
4	A	901	SUC	C1-C2-C3	-2.07	105.89	109.97
4	A	901	SUC	C1-O5-C5	2.08	117.78	113.75
4	A	902	SUC	C1-O5-C5	2.13	117.88	113.75
7	A	2	DCP	O2B-PB-O1B	2.28	124.86	112.53
7	A	2	DCP	O2G-PG-O1G	2.41	118.32	110.58
7	A	2	DCP	O2B-PB-O3B	2.83	117.91	105.09
7	A	2	DCP	C2-N3-C4	3.39	120.40	115.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	2	DCP	2	0
4	A	901	SUC	1	0

## 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	B	11/11 (100%)	0.57	1 (9%) 11 9	29, 36, 59, 61	0
2	C	12/16 (75%)	1.35	4 (33%) 0 0	28, 35, 71, 76	0
3	A	580/580 (100%)	0.41	32 (5%) 29 23	13, 24, 47, 58	0
All	All	603/607 (99%)	0.43	37 (6%) 25 20	13, 24, 47, 76	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	719	TYR	7.8
2	C	17	DA	5.7
3	A	729	ARG	5.3
3	A	297	ALA	5.2
3	A	433	ALA	4.2
3	A	559	ASP	4.2
3	A	716	ILE	4.1
3	A	710	PHE	4.1
3	A	306	ARG	3.8
2	C	16	DC	3.8
3	A	552	THR	3.7
3	A	305	ASP	3.5
3	A	551	LYS	3.5
3	A	550	THR	3.4
3	A	713	VAL	3.4
3	A	714	TYR	3.4
3	A	303	LEU	3.4
3	A	718	ASP	3.1
3	A	431	LYS	3.1
2	C	15	DG	3.1
3	A	723	GLN	3.0
3	A	553	GLY	3.0
3	A	520	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	19	DG	2.9
3	A	549	LYS	2.8
3	A	730	LYS	2.7
3	A	629	ARG	2.7
3	A	298	LYS	2.6
3	A	514	VAL	2.6
3	A	738	ARG	2.4
3	A	712	ILE	2.3
3	A	725	LEU	2.3
2	C	6	DG	2.2
3	A	790	MET	2.2
3	A	715	GLY	2.2
3	A	466	ARG	2.1
3	A	572	GLU	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](#)

There are no carbohydrates in this entry.

## 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
7	DCP	A	2	28/28	0.47	0.39	4.50	43,50,62,62	0
4	SUC	A	902	23/23	0.80	0.29	3.07	47,47,48,49	0
4	SUC	A	901	23/23	0.85	0.14	0.32	28,30,31,32	0
5	SO4	A	912	5/5	0.92	0.14	0.07	46,46,47,47	0
5	SO4	A	913	5/5	0.80	0.24	-	92,92,92,92	0
5	SO4	A	911	5/5	0.90	0.13	-	72,72,72,73	0
6	MG	A	920	1/1	0.97	0.10	-	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	SO4	A	910	5/5	0.94	0.09	-	62,62,62,62	0
5	SO4	A	914	5/5	0.64	0.53	-	100,100,100,100	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.