



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:56 AM GMT

PDB ID : 2JEG  
Title : THE MOLECULAR BASIS OF SELECTIVITY OF NUCLEOSIDE  
TRIPHOSPHATE INCORPORATION OPPOSITE O6-BENZYLGUANINE  
BY SULFOLOBUS SOLFATARICUS DNA POLYMERASE IV: STEADY-  
STATE AND PRE-STEADY-STATE KINETICS AND X-RAY CRYSTAL-  
LOGRAPHY OF CORRECT AND INCORRECT PAIRING  
Authors : Eoff, R.L.; Angel, K.C.; Kosekov, I.D.; Egli, M.; Guengerich, F.P.  
Deposited on : 2007-01-17  
Resolution : 2.38 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

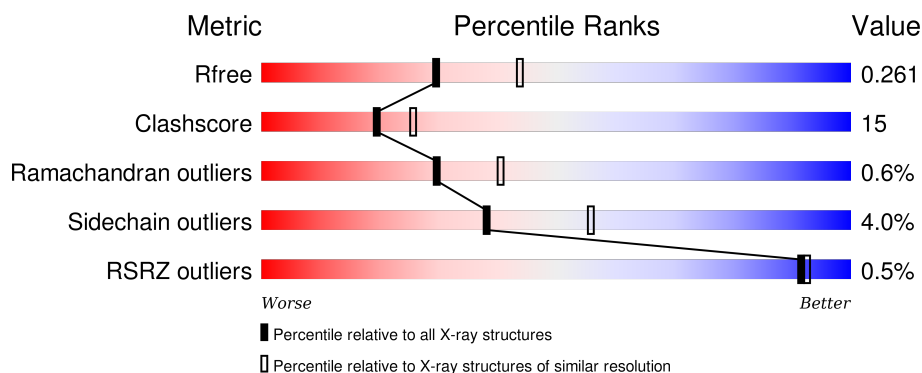
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.38 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	4019 (2.40-2.36)
Clashscore	102246	4595 (2.40-2.36)
Ramachandran outliers	100387	4520 (2.40-2.36)
Sidechain outliers	100360	4522 (2.40-2.36)
RSRZ outliers	91569	4034 (2.40-2.36)

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	A	358	<div> <div style="width: 74%;"></div> <div style="width: 20%;"></div> <div style="width: 6%;"></div> <div style="width: 6%;"></div> </div>
2	P	14	<div> <div style="width: 14%;"></div> <div style="width: 64%;"></div> <div style="width: 14%;"></div> <div style="width: 7%;"></div> </div>
3	T	18	<div> <div style="width: 6%;"></div> <div style="width: 6%;"></div> <div style="width: 50%;"></div> <div style="width: 39%;"></div> <div style="width: 6%;"></div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3559 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 DNA POLYMERASE IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	S	0	3	1
			2787	1784	488	508	7			

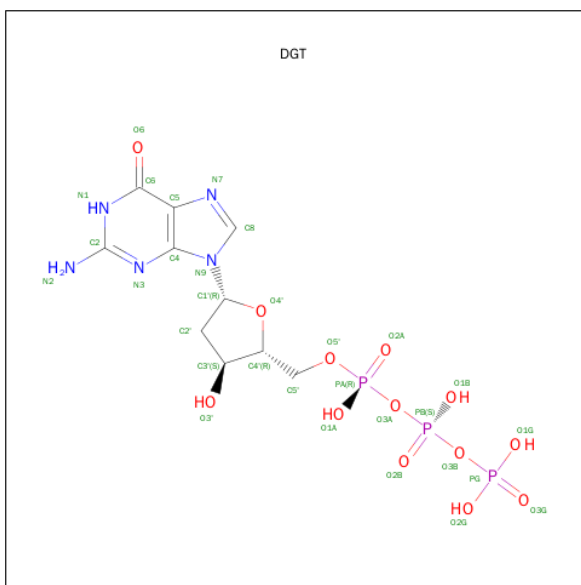
- Molecule 2 is a DNA chain called 5'-D(\*GP\*GP\*GP\*GP\*GP\*AP\*AP\*GP\*GP\*AP\*TP\*TP\*CP\*DOC)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	14	Total	C	N	O	P	0	0	0
			291	138	60	80	13			

- Molecule 3 is a DNA chain called 5'-D(\*TP\*CP\*AP\*C BZGP\*GP\*AP\*AP\*TP\*CP \*CP\*TP\*TP\*CP\*CP\*CP\*CP\*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	17	Total	C	N	O	P	0	0	0
			342	168	58	100	16			

- Molecule 4 is 2'-DEOXYGUANOSINE-5'-TRIPHOSPHATE (three-letter code: DGT) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	P	1	Total Ca 1 1	0	0
5	A	3	Total Ca 3 3	0	0

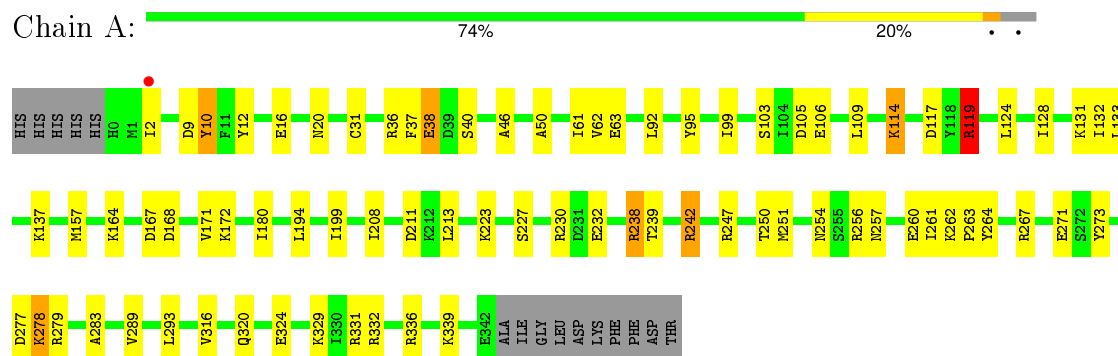
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	94	Total O 94 94	0	0
6	P	7	Total O 7 7	0	0
6	T	3	Total O 3 3	0	0

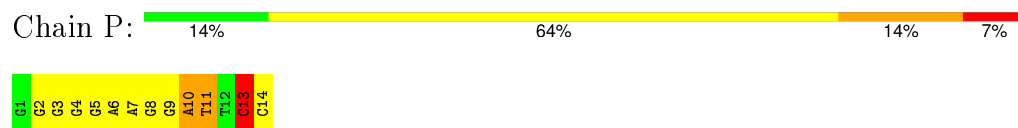
### 3 Residue-property plots

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 ( $RSRZ > 2$ ). 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.

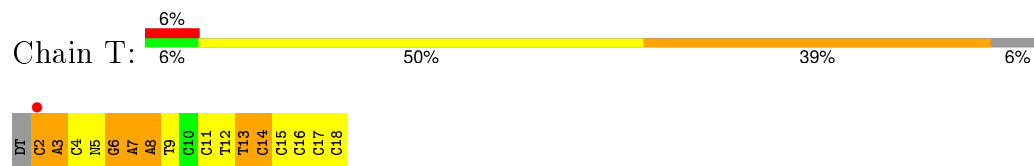
#### • Molecule 1: DNA POLYMERASE IV



#### • Molecule 2: 5'-D(\*GP\*GP\*GP\*GP\*GP\*AP\*AP\*GP\*GP\*AP \*TP\*TP\*CP\*DOC)-3'



#### • Molecule 3: 5'-D(\*TP\*CP\*AP\*C BZGP\*GP\*AP\*AP\*TP\*CP \*CP\*TP\*TP\*CP\*CP\*CP\*CP\*C)-3'



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.10Å 103.17Å 52.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.55 – 2.38 46.88 – 2.38	Depositor EDS
% Data completeness (in resolution range)	98.7 (46.55-2.38) 98.8 (46.88-2.38)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.34 (at 2.37Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.226 , 0.263 0.222 , 0.261	Depositor DCC
$R_{free}$ test set	1007 reflections (5.08%)	DCC
Wilson B-factor (Å <sup>2</sup> )	48.8	Xtriage
Anisotropy	0.373	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 40.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 20833 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3559	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% 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: BZG, DOC, CA, DGT

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	0.40	0/2827	0.96	8/3795 (0.2%)
2	P	0.66	0/308	1.11	9/476 (1.9%)
3	T	0.60	0/347	1.11	14/528 (2.7%)
All	All	0.45	0/3482	0.99	31/4799 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	P	0	1
3	T	2	0
All	All	2	2

There are no bond length outliers.

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	119[A]	ARG	NE-CZ-NH2	-24.53	108.03	120.30
1	A	119[B]	ARG	NE-CZ-NH2	-24.53	108.03	120.30
1	A	119[A]	ARG	NE-CZ-NH1	18.36	129.48	120.30
1	A	119[B]	ARG	NE-CZ-NH1	18.36	129.48	120.30
1	A	119[A]	ARG	NH1-CZ-NH2	-8.43	110.13	119.40
1	A	119[B]	ARG	NH1-CZ-NH2	-8.43	110.13	119.40
3	T	17	DC	OP1-P-OP2	-6.29	110.16	119.60
2	P	3	DG	P-O5'-C5'	-6.22	110.95	120.90
3	T	18	DC	OP1-P-OP2	-5.93	110.71	119.60
2	P	9	DG	OP1-P-OP2	-5.81	110.89	119.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	T	3	DA	OP1-P-OP2	-5.80	110.90	119.60
2	P	13	DC	OP1-P-OP2	-5.59	111.22	119.60
2	P	2	DG	OP1-P-OP2	-5.56	111.26	119.60
3	T	12	DT	OP1-P-OP2	-5.46	111.41	119.60
2	P	7	DA	OP1-P-OP2	-5.44	111.44	119.60
2	P	10	DA	OP1-P-OP2	-5.44	111.44	119.60
1	A	119[A]	ARG	CG-CD-NE	5.39	123.12	111.80
1	A	119[B]	ARG	CG-CD-NE	5.39	123.12	111.80
2	P	11	DT	OP1-P-OP2	-5.38	111.54	119.60
3	T	9	DT	OP1-P-OP2	-5.37	111.54	119.60
3	T	4	DC	OP1-P-OP2	-5.32	111.63	119.60
2	P	4	DG	OP1-P-OP2	-5.29	111.66	119.60
3	T	6	DG	OP1-P-OP2	-5.28	111.68	119.60
3	T	14	DC	OP1-P-OP2	-5.23	111.75	119.60
3	T	11	DC	OP1-P-OP2	-5.23	111.75	119.60
3	T	15	DC	OP1-P-OP2	-5.15	111.88	119.60
3	T	16	DC	OP1-P-OP2	-5.15	111.88	119.60
3	T	13	DT	OP1-P-OP2	-5.12	111.92	119.60
3	T	7	DA	OP1-P-OP2	-5.04	112.04	119.60
3	T	8	DA	OP1-P-OP2	-5.04	112.04	119.60
2	P	8	DG	OP1-P-OP2	-5.03	112.06	119.60

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	T	2	DC	C4',C3'

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	119[A]	ARG	Sidechain
2	P	13	DC	Sidechain

## 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	A	2787	0	2932	83	0
2	P	291	0	158	9	0
3	T	342	0	197	20	0
4	A	31	0	12	4	0
5	A	3	0	0	0	0
5	P	1	0	0	0	0
6	A	94	0	0	2	0
6	P	7	0	0	0	0
6	T	3	0	0	3	0
All	All	3559	0	3299	100	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 15.

All (100) 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:273:TYR:HE1	6:A:2082:HOH:O	1.56	0.88
3:T:13:DT:H2"	3:T:14:DC:H5"	1.57	0.87
3:T:3:DA:H1'	6:T:2001:HOH:O	1.75	0.85
2:P:10:DA:H2"	2:P:11:DT:H5'	1.66	0.78
1:A:289:VAL:HB	1:A:332[B]:ARG:HB2	1.67	0.76
1:A:257:ASN:HD22	1:A:260:GLU:H	1.30	0.75
1:A:289:VAL:HB	1:A:332[A]:ARG:HB2	1.69	0.74
1:A:331:ARG:NH2	3:T:3:DA:H4'	2.02	0.74
3:T:5:BZG:HWC1	3:T:5:BZG:NN	2.02	0.74
1:A:277:ASP:HB3	1:A:278:LYS:NZ	2.02	0.73
1:A:250:THR:HA	1:A:332[A]:ARG:HG2	1.69	0.73
3:T:13:DT:C2'	3:T:14:DC:H5"	2.19	0.72
3:T:13:DT:H2"	3:T:14:DC:C5'	2.22	0.69
1:A:238:ARG:HH11	1:A:238:ARG:HA	1.59	0.68
1:A:289:VAL:HG11	1:A:332[A]:ARG:HH21	1.57	0.68
1:A:331:ARG:HH22	3:T:3:DA:H4'	1.58	0.68
1:A:37:PHE:HD1	6:A:2019:HOH:O	1.76	0.67
2:P:13:DC:H4'	2:P:14:DOC:H5'	1.76	0.67
1:A:119[A]:ARG:HG2	1:A:119[A]:ARG:HH11	1.60	0.66
3:T:3:DA:C1'	6:T:2001:HOH:O	2.37	0.65
1:A:103:SER:HB3	2:P:14:DOC:H2"	1.80	0.64
1:A:257:ASN:HD22	1:A:260:GLU:N	1.94	0.64
1:A:267:ARG:O	1:A:271:GLU:HG2	1.99	0.63
2:P:13:DC:C4'	2:P:14:DOC:OP1	2.47	0.63
1:A:114:LYS:NZ	1:A:114:LYS:HB2	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:ARG:HB3	1:A:256:ARG:NH1	2.15	0.61
1:A:256:ARG:HG2	1:A:329:LYS:HA	1.83	0.60
1:A:124:LEU:O	1:A:128:ILE:HG13	2.00	0.60
1:A:277:ASP:HB3	1:A:278:LYS:HZ3	1.67	0.60
1:A:316:VAL:O	1:A:320:GLN:HG3	2.05	0.57
1:A:238:ARG:NH1	1:A:239:THR:H	2.02	0.57
1:A:257:ASN:ND2	1:A:260:GLU:H	2.02	0.56
1:A:95:TYR:HD2	1:A:124:LEU:HD11	1.71	0.56
1:A:247:ARG:HD2	3:T:6:DG:OP1	2.06	0.55
1:A:331:ARG:HH22	3:T:3:DA:C4'	2.19	0.55
1:A:278:LYS:H	1:A:278:LYS:CE	2.20	0.54
3:T:3:DA:N3	3:T:3:DA:H2'	2.22	0.54
1:A:278:LYS:H	1:A:278:LYS:HE2	1.73	0.54
1:A:12:TYR:CD2	4:A:1344:DGT:H2'	2.42	0.54
1:A:95:TYR:CD2	1:A:124:LEU:HD11	2.44	0.53
1:A:10:TYR:HA	4:A:1344:DGT:PB	2.48	0.53
1:A:157:MET:CE	1:A:164:LYS:HE2	2.38	0.53
1:A:242:ARG:HH12	3:T:8:DA:P	2.31	0.53
2:P:13:DC:H4'	2:P:14:DOC:OP1	2.09	0.52
1:A:31:CYS:HB3	1:A:61:ILE:CD1	2.39	0.52
1:A:180:ILE:HG12	1:A:194:LEU:HD13	1.91	0.52
1:A:99:ILE:HG13	1:A:109:LEU:HD23	1.92	0.52
1:A:62:VAL:HG11	3:T:3:DA:N7	2.25	0.51
1:A:278:LYS:N	1:A:278:LYS:HE2	2.26	0.50
1:A:230:ARG:O	1:A:232:GLU:HG3	2.12	0.50
1:A:277:ASP:HB3	1:A:278:LYS:HZ1	1.75	0.50
1:A:242:ARG:HH11	1:A:242:ARG:HG3	1.77	0.49
1:A:293:LEU:HD22	1:A:293:LEU:N	2.27	0.49
1:A:2:ILE:N	1:A:2:ILE:HD12	2.27	0.49
1:A:278:LYS:HE2	1:A:279:ARG:N	2.27	0.49
1:A:36:ARG:NH2	1:A:254:ASN:OD1	2.46	0.48
1:A:257:ASN:ND2	1:A:260:GLU:HB2	2.28	0.48
1:A:40:SER:HA	6:T:2001:HOH:O	2.13	0.48
1:A:251:MET:HA	1:A:264:TYR:CE1	2.49	0.48
1:A:257:ASN:HD22	1:A:260:GLU:HB2	1.78	0.47
1:A:336[A]:ARG:NH1	3:T:6:DG:H2''	2.29	0.47
1:A:12:TYR:CG	4:A:1344:DGT:H2'	2.49	0.47
1:A:103:SER:OG	1:A:106:GLU:HG2	2.16	0.46
2:P:5:DG:H2''	2:P:6:DA:H8	1.80	0.46
1:A:277:ASP:CB	1:A:278:LYS:HZ3	2.28	0.46
1:A:242:ARG:NH1	3:T:8:DA:OP1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:257:ASN:ND2	1:A:260:GLU:N	2.61	0.45
1:A:12:TYR:CE2	4:A:1344:DGT:H2'	2.51	0.45
1:A:31:CYS:HB3	1:A:61:ILE:HD11	1.99	0.45
1:A:168:ASP:O	1:A:172:LYS:HG2	2.16	0.45
1:A:62:VAL:HG13	1:A:63:GLU:N	2.31	0.45
1:A:16:GLU:OE1	1:A:16:GLU:HA	2.16	0.45
1:A:167:ASP:O	1:A:171:VAL:HG23	2.17	0.45
1:A:331:ARG:HH22	3:T:3:DA:C5'	2.30	0.44
1:A:242:ARG:HH12	3:T:7:DA:C3'	2.30	0.44
1:A:256:ARG:CG	1:A:329:LYS:HA	2.48	0.43
1:A:283:ALA:HB2	1:A:339:LYS:HD2	2.00	0.43
1:A:262:LYS:HB2	1:A:263:PRO:HD3	2.00	0.43
1:A:256:ARG:HB3	1:A:256:ARG:HH11	1.83	0.42
1:A:114:LYS:HZ2	1:A:114:LYS:HB2	1.84	0.42
1:A:46:ALA:HB1	1:A:50:ALA:HB3	2.02	0.42
2:P:5:DG:H2''	2:P:6:DA:O5'	2.19	0.42
1:A:92:LEU:HD21	1:A:132:ILE:HD11	2.02	0.42
1:A:133:LEU:O	1:A:137:LYS:HA	2.19	0.42
1:A:199:ILE:HD11	1:A:208:ILE:HG13	2.02	0.42
1:A:99:ILE:HG13	1:A:109:LEU:CD2	2.50	0.41
1:A:9:ASP:O	1:A:10:TYR:C	2.58	0.41
1:A:336[A]:ARG:HH12	3:T:6:DG:H2''	1.85	0.41
1:A:36:ARG:NH1	1:A:331:ARG:NE	2.68	0.41
1:A:251:MET:SD	1:A:261:ILE:HG12	2.61	0.41
1:A:223:LYS:O	1:A:227:SER:HB2	2.21	0.41
1:A:37:PHE:O	1:A:38:GLU:C	2.58	0.41
1:A:230:ARG:HB3	1:A:232:GLU:OE2	2.20	0.41
1:A:238:ARG:HG3	1:A:239:THR:N	2.36	0.41
2:P:5:DG:H2''	2:P:6:DA:C8	2.56	0.41
1:A:289:VAL:HG21	1:A:332[B]:ARG:HD3	2.03	0.41
3:T:2:DC:O2	3:T:2:DC:C2'	2.70	0.40
2:P:10:DA:C2'	2:P:11:DT:H5'	2.42	0.40
3:T:5:BZG:CW	3:T:5:BZG:NN	2.78	0.40
1:A:278:LYS:HE3	1:A:279:ARG:HG3	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	344/358 (96%)	331 (96%)	11 (3%)	2 (1%)	30	40

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	38	GLU
1	A	10	TYR

### 5.3.2 Protein sidechains

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	304/315 (96%)	291 (96%)	13 (4%)	35	52

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	105	ASP
1	A	114	LYS
1	A	117	ASP
1	A	119[A]	ARG
1	A	119[B]	ARG
1	A	131	LYS
1	A	211	ASP
1	A	213	LEU

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Mol	Chain	Res	Type
1	A	238	ARG
1	A	242	ARG
1	A	278	LYS
1	A	324	GLU

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	20	ASN
1	A	257	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	DOC	P	14	2	11,19,20	1.38	2 (18%)	14,26,29	2.86	7 (50%)
3	BZG	T	5	3	24,32,33	1.21	1 (4%)	30,45,48	2.00	9 (30%)

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	DOC	P	14	2	-	0/3/18/19	0/2/2/2
3	BZG	T	5	3	-	2/8/26/27	0/4/4/4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	T	5	BZG	CW-CE	-4.74	1.39	1.50
2	P	14	DOC	O4'-C4'	2.67	1.50	1.44
2	P	14	DOC	C6-N1	3.07	1.40	1.35

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	14	DOC	O4'-C4'-C5'	-5.82	100.95	109.54
2	P	14	DOC	C2'-C1'-N1	-5.06	102.24	112.49
3	T	5	BZG	NG-CH-NJ	-4.39	120.76	127.44
3	T	5	BZG	C4'-OS'-CT'	-3.89	99.64	109.47
3	T	5	BZG	CW-OL-CK	-3.02	113.59	117.52
3	T	5	BZG	CM-CK-NJ	-2.65	119.14	123.81
3	T	5	BZG	CF-CM-NN	-2.56	107.13	109.48
2	P	14	DOC	N4-C4-N3	2.18	120.48	116.50
2	P	14	DOC	O4'-C1'-N1	2.64	112.28	107.72
3	T	5	BZG	OS'-CT'-NE	2.72	112.42	107.72
2	P	14	DOC	C2'-C3'-C4'	2.82	108.08	102.59
3	T	5	BZG	OL-CW-CE	2.90	117.92	109.21
2	P	14	DOC	C3'-C2'-C1'	3.03	106.09	102.71
3	T	5	BZG	CH-NJ-CK	3.73	121.16	116.03
2	P	14	DOC	C2-N3-C4	4.02	121.29	115.61
3	T	5	BZG	OL-CK-CM	4.54	122.17	115.07

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	T	5	BZG	CW-OL-CK-NJ
3	T	5	BZG	CW-OL-CK-CM

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	14	DOC	4	0
3	T	5	BZG	2	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	$\# Z  > 2$
4	DGT	A	1344	5	25,33,33	1.29	2 (8%)	35,52,52	1.67	9 (25%)

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	DGT	A	1344	5	-	0/18/34/34	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1344	DGT	C2-N1	3.15	1.41	1.35
4	A	1344	DGT	C6-N1	3.72	1.40	1.33

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1344	DGT	N3-C2-N1	-5.14	119.62	127.44
4	A	1344	DGT	C5-C6-N1	-3.42	118.92	123.59
4	A	1344	DGT	PA-O3A-PB	-2.52	125.65	132.73
4	A	1344	DGT	C2'-C3'-C4'	-2.19	98.23	102.77
4	A	1344	DGT	C4-C5-N7	-2.13	107.52	109.48
4	A	1344	DGT	PB-O3B-PG	-2.12	125.54	132.67
4	A	1344	DGT	O1B-PB-O2B	2.14	124.14	112.53

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Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
4	A	1344	DGT	C6-N1-C2	2.62	119.57	115.94
4	A	1344	DGT	O1B-PB-O3B	3.05	118.94	105.09

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1344	DGT	4	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 [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	343/358 (95%)	0.25	1 (0%) 94 95	28, 44, 62, 72	11 (3%)
2	P	13/14 (92%)	0.12	0 100 100	37, 44, 68, 71	0
3	T	16/18 (88%)	0.48	1 (6%) 23 27	45, 54, 107, 129	0
All	All	372/390 (95%)	0.25	2 (0%) 91 92	28, 45, 63, 129	11 (2%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	T	2	DC	3.4
1	A	2	ILE	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [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
2	DOC	P	14	18/19	0.86	0.40	-	60,75,78,79	0
3	BZG	T	5	29/30	0.94	0.18	-	45,48,60,62	0

### 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
5	CA	A	1347	1/1	0.97	0.18	0.96	52,52,52,52	0
4	DGT	A	1344	31/31	0.98	0.13	-0.77	27,31,34,35	0
5	CA	A	1346	1/1	0.97	0.12	-1.71	37,37,37,37	0
5	CA	A	1345	1/1	0.91	0.13	-	51,51,51,51	0
5	CA	P	1015	1/1	0.96	0.07	-	62,62,62,62	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.