



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:27 PM GMT

PDB ID : 4EYH  
Title : Human DNA polymerase iota incorporating dCTP opposite N-(deoxyguanosine-8-yl)-1-aminopyrene lesion  
Authors : Kirouac, K.; Ling, H.  
Deposited on : 2012-05-01  
Resolution : 2.90 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

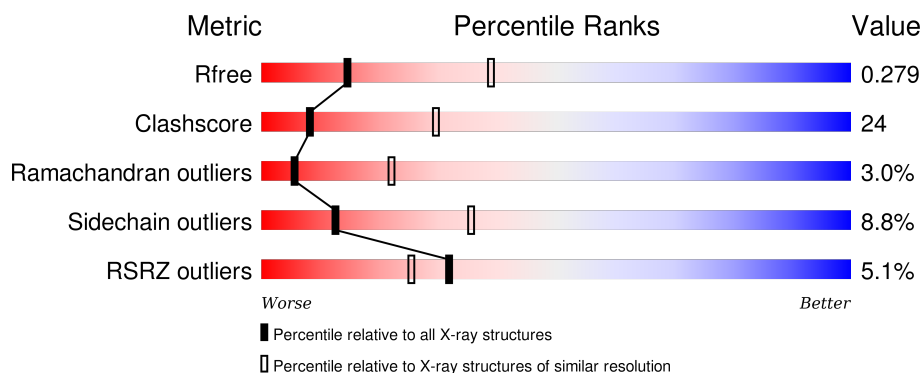
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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	420	<div> <div>5%</div> <div>53%</div> <div>31%</div> <div>6%</div> <div>10%</div> </div>
2	T	8	<div> <div>13%</div> <div>75%</div> <div>13%</div> </div>
3	P	7	<div> <div>29%</div> <div>57%</div> <div>14%</div> </div>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3238 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 iota.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	377	Total	C	N	O	S	0	1	0
			2853	1802	494	535	22			

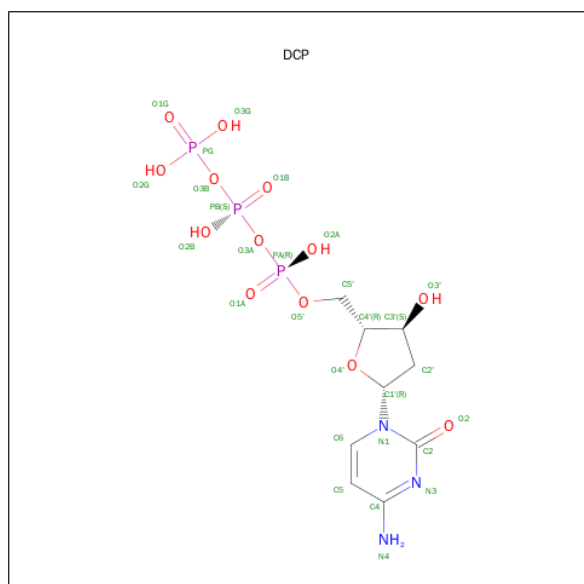
- Molecule 2 is a DNA chain called DNA template.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	8	Total	C	N	O	P	0	0	0
			183	94	31	50	8			

- Molecule 3 is a DNA chain called DNA primer.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	7	Total	C	N	O	P	0	0	0
			143	67	29	40	7			

- Molecule 4 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP) (formula:  $C_9H_{16}N_3O_{13}P_3$ ).



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

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	3	Total	Mg	0	0
			3	3		

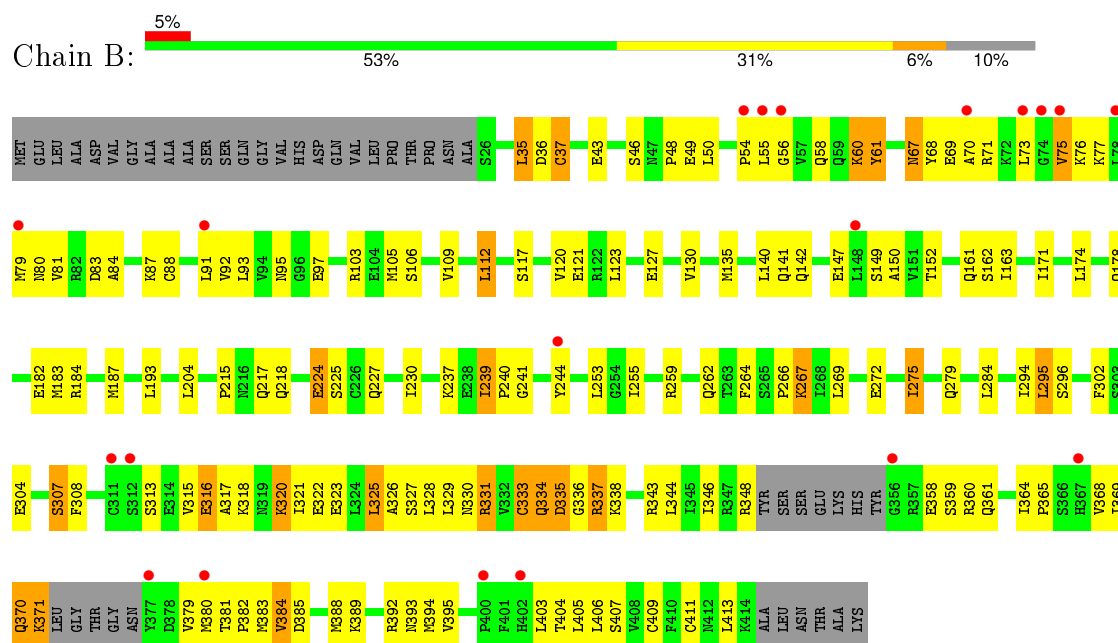
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	25	Total	O	0	0
			25	25		
6	T	2	Total	O	0	0
			2	2		
6	P	1	Total	O	0	0
			1	1		

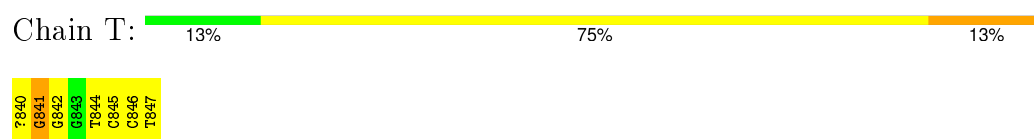
### 3 Residue-property plots [i](#)

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 iota



#### • Molecule 2: DNA template



#### • Molecule 3: DNA primer



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.05Å 98.05Å 194.65Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.09 – 2.90 32.09 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.5 (32.09-2.90) 97.6 (32.09-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.88 (at 2.90Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, $R_{free}$	0.239 , 0.281 0.236 , 0.279	Depositor DCC
$R_{free}$ test set	1008 reflections (8.70%)	DCC
Wilson B-factor (Å <sup>2</sup> )	74.6	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 53.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 12593 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3238	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% 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, DG8, 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	0.37	0/2896	0.53	0/3925
2	T	0.92	0/160	1.65	3/245 (1.2%)
3	P	0.63	0/160	1.27	1/244 (0.4%)
All	All	0.43	0/3216	0.70	4/4414 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	872	DC	O4'-C4'-C3'	-7.65	101.41	106.00
2	T	841	DG	O4'-C1'-N9	7.20	113.04	108.00
2	T	841	DG	C3'-C2'-C1'	-5.15	96.33	102.50
2	T	841	DG	N3-C4-C5	5.02	131.11	128.60

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	2853	0	2818	132	0
2	T	183	0	101	14	0
3	P	143	0	78	10	0
4	B	28	0	12	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	3	0	0	0	0
6	B	25	0	0	1	0
6	P	1	0	0	0	0
6	T	2	0	0	1	0
All	All	3238	0	3009	152	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 24.

All (152) 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:B:267:LYS:H	1:B:267:LYS:HD2	1.17	1.04
1:B:267:LYS:H	1:B:267:LYS:CD	1.91	0.81
1:B:95:ASN:HD21	1:B:97:GLU:HB2	1.46	0.81
1:B:67:ASN:ND2	1:B:70:ALA:H	1.78	0.80
1:B:267:LYS:N	1:B:267:LYS:HD2	1.98	0.78
1:B:325:LEU:HD11	1:B:383:MET:HB3	1.68	0.76
2:T:840:DG8:H17	2:T:840:DG8:N7	2.01	0.75
1:B:343:ARG:HH21	1:B:361:GLN:NE2	1.86	0.74
1:B:61:TYR:HD2	1:B:61:TYR:H	1.35	0.74
4:B:501:DCP:H5'2	3:P:873:DC:H2''	1.70	0.74
1:B:227:GLN:OE1	1:B:230:ILE:HD11	1.89	0.71
1:B:88:CYS:SG	1:B:91:LEU:HB2	2.30	0.71
2:T:841:DG:H2'	2:T:841:DG:OP2	1.89	0.71
1:B:112:LEU:O	1:B:112:LEU:HD12	1.93	0.68
1:B:361:GLN:HG2	3:P:867:DA:OP2	1.95	0.66
1:B:329:LEU:O	1:B:333:CYS:HB2	1.96	0.66
1:B:48:PRO:C	1:B:50:LEU:H	1.99	0.65
1:B:343:ARG:HH21	1:B:361:GLN:HE22	1.42	0.65
1:B:308:PHE:HE2	1:B:403:LEU:O	1.81	0.64
1:B:55:LEU:HD12	1:B:56:GLY:N	2.13	0.63
1:B:79:MET:HG2	1:B:80:ASN:N	2.13	0.63
1:B:275:ILE:HD11	1:B:279:GLN:OE1	1.98	0.62
1:B:105:MET:O	1:B:109:VAL:HG23	1.99	0.62
1:B:55:LEU:HD12	1:B:56:GLY:H	1.65	0.61
1:B:346:ILE:HG22	1:B:406:LEU:CD2	2.30	0.61
1:B:325:LEU:HD11	1:B:383:MET:CB	2.31	0.60
1:B:385:ASP:O	1:B:389:LYS:HG3	2.02	0.60
1:B:123:LEU:O	1:B:127:GLU:HB2	2.01	0.59
1:B:161:GLN:HE22	1:B:224:GLU:CG	2.16	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:67:ASN:ND2	1:B:69:GLU:HB3	2.18	0.59
1:B:48:PRO:O	1:B:50:LEU:N	2.34	0.59
1:B:50:LEU:HD13	1:B:55:LEU:HD22	1.84	0.59
1:B:58:GLN:HE21	1:B:81:VAL:HG21	1.68	0.59
1:B:343:ARG:HG3	1:B:409:CYS:HB3	1.86	0.58
1:B:95:ASN:ND2	1:B:97:GLU:H	2.02	0.58
1:B:371:LYS:N	1:B:371:LYS:HD2	2.19	0.57
1:B:67:ASN:HD21	1:B:70:ALA:H	1.52	0.57
1:B:255:ILE:HD11	1:B:264:PHE:CD1	2.39	0.57
1:B:346:ILE:HG22	1:B:406:LEU:HD23	1.86	0.56
1:B:346:ILE:HD11	1:B:394:MET:HG2	1.85	0.56
1:B:121:GLU:HB2	1:B:294:ILE:O	2.05	0.56
1:B:313:SER:HB3	1:B:316:GLU:OE2	2.04	0.56
1:B:239:ILE:CD1	1:B:284:LEU:HB3	2.35	0.56
1:B:95:ASN:HD21	1:B:97:GLU:CB	2.17	0.56
1:B:71:ARG:HH21	1:B:77:LYS:HG3	1.70	0.56
1:B:237:LYS:O	1:B:237:LYS:HG2	2.07	0.55
1:B:411:CYS:HA	1:B:413:LEU:HD11	1.89	0.55
1:B:140:LEU:C	1:B:142:GLN:H	2.09	0.54
2:T:840:DG8:H22	2:T:840:DG8:O5'	2.06	0.54
1:B:384:VAL:O	1:B:388:MET:HG2	2.07	0.54
1:B:381:THR:N	1:B:382:PRO:HD2	2.23	0.54
1:B:316:GLU:O	1:B:320:LYS:HD3	2.08	0.54
1:B:87:LYS:CB	6:B:615:HOH:O	2.55	0.54
1:B:120:VAL:HG22	1:B:130:VAL:HG22	1.89	0.54
1:B:73:LEU:HD23	1:B:73:LEU:N	2.22	0.53
1:B:117:SER:HB2	1:B:135:MET:CE	2.39	0.53
1:B:411:CYS:HA	1:B:413:LEU:CD1	2.39	0.53
1:B:241:GLY:O	3:P:871:DC:H5''	2.08	0.53
1:B:67:ASN:HD22	1:B:69:GLU:N	2.06	0.52
1:B:392:ARG:O	1:B:395:VAL:O	2.27	0.52
1:B:161:GLN:HE22	1:B:224:GLU:HG2	1.74	0.52
1:B:317:ALA:O	1:B:321:ILE:HG13	2.10	0.52
3:P:872:DC:C2'	3:P:873:DC:H5'	2.40	0.52
1:B:61:TYR:O	1:B:81:VAL:HG23	2.11	0.51
1:B:215:PRO:O	1:B:217:GLN:HG3	2.09	0.51
3:P:867:DA:H2''	3:P:868:DG:OP2	2.10	0.51
1:B:364:ILE:HG22	1:B:368:VAL:HB	1.91	0.51
1:B:103:ARG:HA	1:B:106:SER:HB3	1.92	0.51
1:B:313:SER:HB3	1:B:316:GLU:CG	2.40	0.51
1:B:343:ARG:CG	1:B:409:CYS:HB3	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:307:SER:HB3	1:B:405:LEU:HD12	1.93	0.51
1:B:239:ILE:HD11	1:B:284:LEU:HB3	1.93	0.51
1:B:308:PHE:CE2	1:B:403:LEU:O	2.64	0.51
1:B:346:ILE:O	1:B:346:ILE:HG13	2.10	0.51
1:B:237:LYS:HE2	1:B:244:TYR:N	2.26	0.51
1:B:68:TYR:CZ	1:B:215:PRO:HB3	2.46	0.50
1:B:330:ASN:O	1:B:333:CYS:HB3	2.12	0.50
1:B:413:LEU:N	1:B:413:LEU:HD12	2.26	0.50
3:P:871:DC:H2'	3:P:872:DC:C6	2.46	0.50
1:B:405:LEU:HD23	1:B:406:LEU:N	2.26	0.50
2:T:844:DT:H2'	2:T:845:DC:C6	2.46	0.50
1:B:50:LEU:HD21	1:B:92:VAL:HG11	1.94	0.49
2:T:840:DG8:C26	2:T:840:DG8:N7	2.75	0.49
1:B:348:ARG:HD2	1:B:358:GLU:OE1	2.12	0.49
4:B:501:DCP:HN41	2:T:840:DG8:C6	2.26	0.49
1:B:67:ASN:ND2	1:B:70:ALA:N	2.55	0.49
1:B:43:GLU:HA	1:B:43:GLU:OE2	2.12	0.49
1:B:67:ASN:HD21	1:B:70:ALA:N	2.11	0.49
1:B:365:PRO:HB2	1:B:368:VAL:HG23	1.95	0.49
1:B:253:LEU:HD11	1:B:272:GLU:HG2	1.95	0.48
3:P:871:DC:H2'	3:P:872:DC:H6	1.78	0.48
2:T:846:DC:H2''	2:T:847:DT:O5'	2.14	0.48
1:B:315:VAL:O	1:B:318:LYS:HB3	2.12	0.48
4:B:501:DCP:C4	2:T:840:DG8:H10	2.27	0.48
1:B:161:GLN:NE2	1:B:224:GLU:HG3	2.28	0.48
1:B:295:LEU:HD12	1:B:296:SER:N	2.29	0.48
1:B:359:SER:O	1:B:360:ARG:HD2	2.14	0.48
1:B:183:MET:O	1:B:187:MET:HG3	2.13	0.47
4:B:501:DCP:N3	2:T:840:DG8:N1	2.56	0.47
4:B:501:DCP:C2	2:T:840:DG8:H11	2.28	0.47
1:B:178:GLN:O	1:B:182:GLU:HG3	2.15	0.47
1:B:150:ALA:O	1:B:152:THR:HG23	2.15	0.46
1:B:266:PRO:HG2	1:B:267:LYS:HZ3	1.81	0.46
1:B:304:GLU:HG3	1:B:328:LEU:HG	1.97	0.46
1:B:48:PRO:C	1:B:50:LEU:N	2.66	0.46
1:B:255:ILE:HD11	1:B:264:PHE:CG	2.50	0.46
1:B:103:ARG:HA	1:B:106:SER:CB	2.45	0.46
1:B:35:LEU:HD11	1:B:193:LEU:HD13	1.96	0.46
1:B:334:GLN:O	1:B:336:GLY:N	2.49	0.45
1:B:321:ILE:O	1:B:325:LEU:HB2	2.17	0.45
1:B:307:SER:HA	1:B:405:LEU:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:371:LYS:N	1:B:371:LYS:CD	2.79	0.45
1:B:88:CYS:O	1:B:88:CYS:SG	2.74	0.45
1:B:259:ARG:HA	1:B:262:GLN:HB2	1.98	0.45
1:B:36:ASP:O	1:B:37:CYS:C	2.55	0.45
1:B:344:LEU:HD12	1:B:407:SER:O	2.17	0.45
1:B:275:ILE:O	1:B:279:GLN:HG3	2.17	0.44
1:B:380:MET:O	1:B:384:VAL:HG13	2.18	0.44
1:B:75:VAL:HG12	1:B:76:LYS:N	2.32	0.44
1:B:370:GLN:C	1:B:371:LYS:HD2	2.37	0.44
1:B:239:ILE:HD12	1:B:284:LEU:HB3	1.99	0.44
1:B:140:LEU:C	1:B:142:GLN:N	2.71	0.44
1:B:55:LEU:HB3	1:B:67:ASN:OD1	2.18	0.43
1:B:123:LEU:HD11	3:P:872:DC:H2''	2.00	0.43
1:B:360:ARG:HG3	3:P:867:DA:OP1	2.18	0.43
1:B:379:VAL:O	1:B:382:PRO:HG2	2.18	0.43
1:B:171:ILE:HD13	1:B:171:ILE:HA	1.79	0.43
1:B:147:GLU:H	1:B:147:GLU:HG2	1.64	0.43
3:P:872:DC:H2''	3:P:873:DC:H5'	2.01	0.43
1:B:92:VAL:HG12	1:B:93:LEU:N	2.33	0.43
1:B:163:ILE:HD13	1:B:174:LEU:HD11	2.01	0.42
1:B:147:GLU:O	1:B:150:ALA:HB3	2.19	0.42
1:B:61:TYR:N	1:B:61:TYR:CD2	2.71	0.42
2:T:845:DC:H2''	2:T:846:DC:C6	2.54	0.42
1:B:338:LYS:O	1:B:413:LEU:HA	2.20	0.42
1:B:302:PHE:HE2	1:B:413:LEU:HD21	1.84	0.42
1:B:60:LYS:HB3	1:B:61:TYR:HD2	1.84	0.42
1:B:266:PRO:O	1:B:269:LEU:N	2.51	0.42
1:B:318:LYS:O	1:B:322:GLU:HG3	2.20	0.42
1:B:334:GLN:O	1:B:335:ASP:C	2.57	0.41
1:B:368:VAL:O	1:B:370:GLN:N	2.53	0.41
1:B:323:GLU:O	1:B:326:ALA:HB3	2.21	0.41
1:B:411:CYS:C	1:B:413:LEU:HD12	2.40	0.41
2:T:842:DG:H4'	2:T:842:DG:OP1	2.21	0.41
1:B:54:PRO:CA	1:B:70:ALA:HB2	2.50	0.41
1:B:239:ILE:HA	1:B:240:PRO:HD3	1.95	0.41
1:B:50:LEU:CD2	1:B:92:VAL:HG11	2.51	0.41
1:B:333:CYS:O	1:B:334:GLN:O	2.40	0.41
1:B:302:PHE:HD1	1:B:331:ARG:CZ	2.34	0.41
2:T:842:DG:H1'	6:T:901:HOH:O	2.20	0.41
1:B:184:ARG:HE	1:B:218:GLN:HE21	1.69	0.41
4:B:501:DCP:HN41	2:T:840:DG8:H10	1.70	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	B	372/420 (89%)	327 (88%)	34 (9%)	11 (3%)	5 22

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	334	GLN
1	B	335	ASP
1	B	337	ARG
1	B	37	CYS
1	B	49	GLU
1	B	333	CYS
1	B	369	ILE
1	B	370	GLN
1	B	75	VAL
1	B	84	ALA
1	B	141	GLN

### 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	B	309/376 (82%)	282 (91%)	27 (9%)	13 36

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	35	LEU
1	B	46	SER
1	B	60	LYS
1	B	61	TYR
1	B	67	ASN
1	B	83	ASP
1	B	112	LEU
1	B	149	SER
1	B	162	SER
1	B	204	LEU
1	B	224	GLU
1	B	225	SER
1	B	239	ILE
1	B	267	LYS
1	B	275	ILE
1	B	295	LEU
1	B	307	SER
1	B	316	GLU
1	B	320	LYS
1	B	325	LEU
1	B	327	SER
1	B	331	ARG
1	B	337	ARG
1	B	371	LYS
1	B	384	VAL
1	B	393	ASN
1	B	404	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	58	GLN
1	B	67	ASN
1	B	95	ASN
1	B	161	GLN
1	B	218	GLN
1	B	231	HIS
1	B	256	ASN
1	B	361	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	DG8	T	840	-	36,45,46	2.37	4 (11%)	51,68,71	2.16	9 (17%)

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	DG8	T	840	-	-	0/5/25/26	0/7/7/7

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	T	840	DG8	C6-N1	3.09	1.38	1.33
2	T	840	DG8	C25-N24	4.07	1.49	1.39
2	T	840	DG8	C2-N2	4.82	1.43	1.34
2	T	840	DG8	C8-N24	11.05	1.49	1.35

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	840	DG8	C2'-C1'-N9	-8.85	106.96	115.83
2	T	840	DG8	C25-N24-C8	-5.40	117.58	128.84
2	T	840	DG8	N3-C2-N1	-5.21	119.50	127.44
2	T	840	DG8	C5-C6-N1	-2.78	119.78	123.59
2	T	840	DG8	C1'-N9-C4	-2.44	123.58	127.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	840	DG8	C6-C5-C4	-2.40	118.03	120.90
2	T	840	DG8	N2-C2-N1	2.69	121.65	117.20
2	T	840	DG8	C6-N1-C2	3.34	120.57	115.94
2	T	840	DG8	O4'-C1'-N9	6.27	113.52	108.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	T	840	DG8	8	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 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	DCP	B	501	5	21,29,29	0.82	0	33,45,45	1.34	5 (15%)

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	DCP	B	501	5	-	0/18/34/34	0/2/2/2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
4	B	501	DCP	C5-C4-N3	-2.49	118.66	121.80
4	B	501	DCP	O2B-PB-O3B	2.14	114.80	105.09
4	B	501	DCP	O2B-PB-O3A	2.18	114.97	105.09
4	B	501	DCP	N4-C4-N3	2.20	120.51	116.50
4	B	501	DCP	C2-N3-C4	3.72	120.86	115.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	501	DCP	6	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	377/420 (89%)	0.16	20 (5%)	30 23	51, 82, 127, 143	0
2	T	7/8 (87%)	-0.09	0	100 100	77, 85, 95, 113	0
3	P	7/7 (100%)	-0.44	0	100 100	76, 78, 82, 90	0
All	All	391/435 (89%)	0.14	20 (5%)	32 25	51, 82, 126, 143	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	54	PRO	5.2
1	B	73	LEU	4.9
1	B	78	LEU	4.5
1	B	400	PRO	3.7
1	B	91	LEU	3.4
1	B	74	GLY	3.4
1	B	312	SER	3.2
1	B	402	HIS	3.1
1	B	79	MET	3.0
1	B	148	LEU	3.0
1	B	377	TYR	2.8
1	B	244	TYR	2.8
1	B	367	HIS	2.8
1	B	75	VAL	2.7
1	B	70	ALA	2.6
1	B	56	GLY	2.5
1	B	55	LEU	2.3
1	B	311	CYS	2.3
1	B	356	GLY	2.3
1	B	380	MET	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	DG8	T	840	39/40	0.60	0.28	-	105,124,148,152	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	MG	B	502	1/1	0.91	0.20	0.65	76,76,76,76	0
4	DCP	B	501	28/28	0.91	0.16	-0.64	89,106,133,161	0
5	MG	B	503	1/1	0.82	0.11	-1.48	58,58,58,58	0
5	MG	B	504	1/1	0.52	0.50	-	109,109,109,109	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.