



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:48 AM GMT

PDB ID : 2UVV
Title : CRYSTAL STRUCTURES OF MUTANT DPO4 DNA POLYMERASES
WITH 8-OXOG CONTAINING DNA TEMPLATE-PRIMER CONSTRUCTS
Authors : Irimia, A.; Egli, M.
Deposited on : 2007-03-14
Resolution : 2.20 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

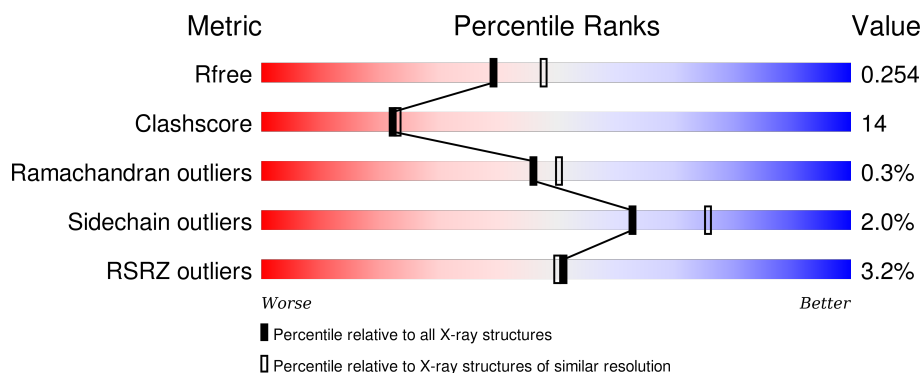
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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 ≥ 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>3%</div> <div>70%</div> <div>25%</div> <div>• •</div> </div>
2	P	14	<div> <div>7%</div> <div>50%</div> <div>50%</div> </div>
3	T	18	<div> <div>56%</div> <div>28%</div> <div>17%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3590 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	1	1
			2762	1770	475	510	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	332	GLU	ARG	ENGINEERED MUTATION	UNP Q97W02

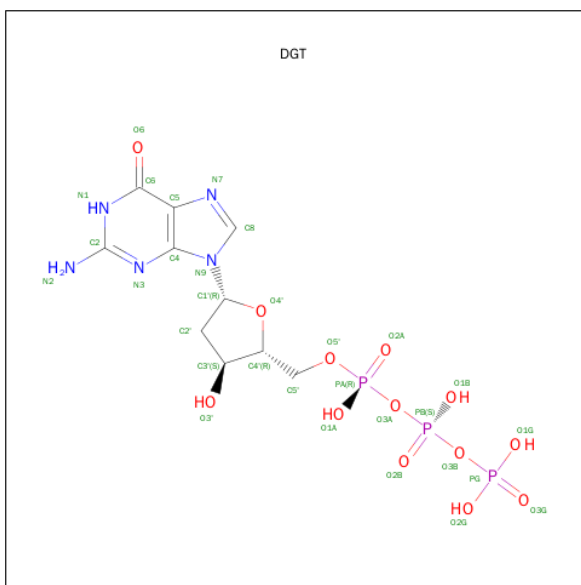
- Molecule 2 is a DNA chain called 5'-D(*GP*GP*GP*GP*GP*AP*AP*GP*GP*AP*TP*TP*CP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	14	Total	C	N	O	P	0	0	0
			292	138	60	81	13			

- Molecule 3 is a DNA chain called 5'-D(*TP*CP*AP*CP*8OGP*GP*AP*AP*TP*CP*CP*TP*TP*CP*CP*CP*CP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	15	Total	C	N	O	P	0	1	0
			320	151	53	100	16			

- Molecule 4 is 2'-DEOXYGUANOSINE-5'-TRIPHOSPHATE (three-letter code: DGT) (formula: C₁₀H₁₆N₅O₁₃P₃).



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

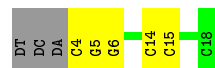
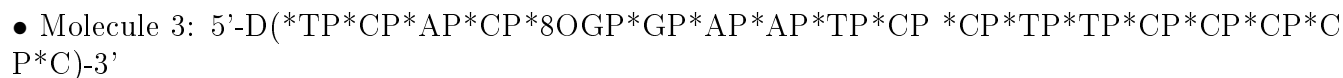
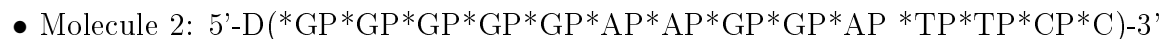
- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	143	Total O 143 143	0	0
6	P	21	Total O 21 21	0	0
6	T	18	Total O 18 18	0	0

- Molecule 1: DNA POLYMERASE IV



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	95.78 Å 103.72 Å 53.03 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.32 – 2.20 29.32 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.32-2.20) 99.8 (29.32-2.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.86 (at 2.20 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.228 , 0.257 0.227 , 0.254	Depositor DCC
R_{free} test set	1345 reflections (5.15%)	DCC
Wilson B-factor (Å ²)	38.0	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 55.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 27479 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3590	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.09% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 8OG, 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	0.39	0/2801	0.62	0/3762
2	P	0.48	0/329	0.86	0/508
3	T	0.82	2/327 (0.6%)	0.97	0/491
All	All	0.46	2/3457 (0.1%)	0.69	0/4761

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	T	4[A]	DC	OP3-P	-7.30	1.52	1.61
3	T	4[B]	DC	OP3-P	-7.30	1.52	1.61

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	2762	0	2900	83	0
2	P	292	0	158	8	0
3	T	320	0	180	5	0
4	A	31	0	12	1	0
5	A	3	0	0	0	0
6	A	143	0	0	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	P	21	0	0	1	0
6	T	18	0	0	1	0
All	All	3590	0	3250	92	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 14.

All (92) 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:302:PHE:HB2	6:A:2129:HOH:O	1.27	1.31
1:A:1:MET:HE2	6:A:2113:HOH:O	1.33	1.22
2:P:14:DC:H42	3:T:5:8OG:H1	1.13	0.97
1:A:24:LYS:HE3	6:A:2024:HOH:O	1.71	0.90
1:A:242:ARG:HB2	1:A:279:ARG:HH12	1.37	0.88
1:A:316:VAL:O	1:A:320:GLN:HG3	1.83	0.78
1:A:242:ARG:HD3	6:A:2119:HOH:O	1.83	0.76
1:A:153:ILE:O	1:A:157:MET:HG3	1.84	0.76
1:A:144:ILE:HB	1:A:165:VAL:HG22	1.71	0.72
1:A:102:ALA:HB3	1:A:106:GLU:HG3	1.72	0.72
1:A:36:ARG:HG2	6:A:2137:HOH:O	1.91	0.71
1:A:197:LEU:HD22	1:A:212:LYS:HE3	1.73	0.70
1:A:258:LEU:HG	1:A:262:LYS:HD2	1.73	0.69
2:P:14:DC:N4	3:T:5:8OG:H1	1.90	0.69
1:A:146:LYS:HD2	6:A:2109:HOH:O	1.91	0.69
1:A:12:TYR:OH	1:A:78:LYS:HE2	1.93	0.69
1:A:189:ILE:HG22	1:A:193:LYS:HE3	1.75	0.68
2:P:10:DA:H2''	2:P:11:DT:H5'	1.77	0.67
1:A:242:ARG:HB2	1:A:279:ARG:NH1	2.12	0.65
1:A:321:LYS:O	1:A:325:GLU:HG3	1.97	0.64
1:A:256:ARG:NH1	1:A:256:ARG:HB3	2.15	0.62
1:A:158:ALA:HB2	1:A:164:LYS:HB2	1.82	0.61
1:A:134:GLU:OE2	1:A:135:LYS:NZ	2.29	0.61
1:A:100:GLU:HB2	1:A:237:ILE:HG23	1.83	0.60
2:P:10:DA:H2''	2:P:11:DT:C5'	2.33	0.59
1:A:247[B]:ARG:HH12	1:A:275:LYS:HZ2	1.51	0.59
1:A:210:PHE:CE2	1:A:214:LYS:HD2	2.39	0.58
3:T:14:DC:H2''	3:T:15:DC:H5'	1.85	0.58
1:A:242:ARG:HG2	6:T:2011:HOH:O	2.03	0.58
1:A:219:GLU:OE1	6:A:2103:HOH:O	2.17	0.57
1:A:326:ASP:OD2	1:A:328:ARG:HB2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:302:PHE:HZ	1:A:314:GLU:HG2	1.70	0.56
1:A:247[B]:ARG:HH22	1:A:275:LYS:HD2	1.70	0.56
1:A:96:SER:HB3	1:A:109:LEU:HD22	1.86	0.56
2:P:2:DG:N7	6:P:2004:HOH:O	2.33	0.53
1:A:247[B]:ARG:NH2	1:A:275:LYS:HD2	2.23	0.53
1:A:256:ARG:HG2	1:A:329:LYS:HA	1.92	0.52
1:A:192:GLU:O	1:A:196:LYS:HG3	2.10	0.52
1:A:242:ARG:HH11	1:A:245:ILE:HD11	1.75	0.51
1:A:331:ARG:NH2	6:A:2138:HOH:O	2.41	0.51
1:A:117:ASP:OD1	1:A:120:GLU:HG3	2.10	0.51
1:A:248:ILE:HG22	3:T:6:DG:OP2	2.11	0.50
1:A:331:ARG:HG2	1:A:332:GLU:HG3	1.94	0.50
1:A:312:TYR:O	1:A:316:VAL:HG23	2.13	0.49
1:A:98:LYS:HB2	1:A:110:ASP:HB3	1.93	0.49
1:A:201:LYS:HB2	1:A:203:VAL:HG12	1.93	0.49
1:A:242:ARG:HH11	1:A:245:ILE:CD1	2.25	0.49
1:A:100:GLU:CB	1:A:237:ILE:HG23	2.41	0.49
1:A:302:PHE:N	1:A:302:PHE:CD1	2.80	0.49
2:P:4:DG:H2''	2:P:5:DG:H5''	1.95	0.49
1:A:242:ARG:HD2	1:A:245:ILE:HD11	1.95	0.48
1:A:258:LEU:HG	1:A:262:LYS:CD	2.44	0.48
2:P:5:DG:H2''	2:P:6:DA:C8	2.49	0.48
1:A:331:ARG:HG3	1:A:331:ARG:HH11	1.78	0.48
1:A:9:ASP:O	1:A:10:TYR:C	2.52	0.47
1:A:242:ARG:CD	6:A:2119:HOH:O	2.53	0.47
1:A:171:VAL:O	1:A:175:ILE:HG13	2.15	0.47
1:A:295:ILE:HD12	1:A:295:ILE:N	2.30	0.47
1:A:262:LYS:N	1:A:263:PRO:HD2	2.30	0.46
1:A:199:ILE:HG23	1:A:204:ASP:HB2	1.95	0.46
1:A:309:GLU:H	1:A:309:GLU:CD	2.19	0.46
1:A:20:ASN:C	1:A:20:ASN:HD22	2.18	0.46
1:A:247[B]:ARG:HH22	1:A:275:LYS:NZ	2.14	0.46
1:A:189:ILE:CG2	1:A:193:LYS:HE3	2.42	0.46
1:A:321:LYS:HA	1:A:324:GLU:HG2	1.98	0.45
1:A:173:ARG:HG2	1:A:173:ARG:HH11	1.81	0.45
1:A:242:ARG:CB	1:A:279:ARG:HH12	2.18	0.45
1:A:289:VAL:HG22	1:A:295:ILE:HG13	1.98	0.44
1:A:254:ASN:ND2	1:A:291:GLU:HB3	2.33	0.44
2:P:4:DG:C2'	2:P:5:DG:H5''	2.48	0.44
1:A:12:TYR:CE2	4:A:1000:DGT:H2'	2.53	0.44
1:A:290:THR:OG1	1:A:294:ASP:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:GLN:O	1:A:18:VAL:HG23	2.17	0.43
1:A:237:ILE:N	1:A:237:ILE:HD12	2.33	0.43
1:A:289:VAL:HG11	1:A:332:GLU:OE1	2.18	0.43
1:A:197:LEU:HD11	1:A:216:MET:HG2	2.01	0.42
1:A:166:ILE:HG22	1:A:171:VAL:HG23	2.02	0.42
1:A:159:LYS:HE2	6:A:2008:HOH:O	2.20	0.42
1:A:178:LEU:HD22	1:A:182:ASP:HB2	2.01	0.42
1:A:242:ARG:HD2	1:A:279:ARG:NH1	2.35	0.42
1:A:247[B]:ARG:NH1	1:A:275:LYS:HZ2	2.15	0.42
1:A:8:PHE:N	1:A:8:PHE:CD1	2.88	0.42
1:A:246:GLY:O	1:A:247[B]:ARG:HG2	2.19	0.41
1:A:250:THR:OG1	3:T:5:8OG:OP3	2.37	0.41
1:A:221:LYS:HE2	1:A:221:LYS:HB2	1.94	0.41
1:A:63:GLU:HA	1:A:63:GLU:OE2	2.20	0.41
1:A:82:GLN:HG3	6:A:2065:HOH:O	2.21	0.41
1:A:95:TYR:HD2	1:A:124:LEU:HD11	1.86	0.41
1:A:108:TYR:CD2	1:A:148:LYS:HG2	2.56	0.41
1:A:174:LEU:HA	1:A:174:LEU:HD23	1.92	0.41
1:A:152:LYS:NZ	6:A:2089:HOH:O	2.53	0.40
1:A:247[B]:ARG:HH22	1:A:275:LYS:CD	2.34	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	342/358 (96%)	330 (96%)	11 (3%)	1 (0%)	46 50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
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	302/315 (96%)	296 (98%)	6 (2%)	63 76

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	178	LEU
1	A	213	LEU
1	A	277	ASP
1	A	294	ASP
1	A	302	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	285	HIS
1	A	320	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	$\# Z > 2$
3	8OG	T	5	3,2	16,25,26	1.34	2 (12%)	21,37,40	2.25	7 (33%)

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	8OG	T	5	3,2	-	0/3/21/22	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	T	5	8OG	C2-N1	3.01	1.40	1.35
3	T	5	8OG	C6-N1	4.07	1.40	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	T	5	8OG	N3-C2-N1	-4.86	120.04	127.44
3	T	5	8OG	C5-C6-N1	-3.49	118.82	123.59
3	T	5	8OG	C3'-C2'-C1'	-2.80	95.67	102.40
3	T	5	8OG	C4-C5-N7	-2.10	107.70	109.55
3	T	5	8OG	O4'-C1'-C2'	-2.06	102.16	106.27
3	T	5	8OG	C6-N1-C2	2.48	119.38	115.94
3	T	5	8OG	O4'-C1'-N9	5.68	113.02	108.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	T	5	8OG	3	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	DGT	A	1000	5	25,33,33	1.29	2 (8%)	35,52,52	1.77	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	1000	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	1000	DGT	C2-N1	2.89	1.40	1.35
4	A	1000	DGT	C6-N1	3.99	1.40	1.33

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1000	DGT	N3-C2-N1	-5.02	119.79	127.44
4	A	1000	DGT	C5-C6-N1	-3.42	118.91	123.59
4	A	1000	DGT	O3A-PA-O5'	-3.25	94.33	102.94
4	A	1000	DGT	O5'-PA-O2A	-3.03	97.87	109.62
4	A	1000	DGT	O1A-PA-O5'	-2.70	94.83	108.46
4	A	1000	DGT	C4-C5-N7	-2.55	107.13	109.48
4	A	1000	DGT	PB-O3B-PG	-2.29	125.00	132.67

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	A	1000	DGT	O1A-PA-O3A	2.26	115.36	105.09
4	A	1000	DGT	C6-N1-C2	2.48	119.39	115.94

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	A	1000	DGT	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 [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, 95th 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 ²)	Q<0.9
1	A	343/358 (95%)	0.14	11 (3%) 51 50	17, 36, 58, 74	36 (10%)
2	P	14/14 (100%)	0.47	1 (7%) 19 18	32, 41, 62, 68	0
3	T	14/18 (77%)	0.14	0 100 100	31, 46, 56, 57	0
All	All	371/390 (95%)	0.15	12 (3%) 51 50	17, 37, 58, 74	36 (9%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	342	GLU	3.5
1	A	287	VAL	3.4
1	A	335	VAL	2.9
2	P	4	DG	2.5
1	A	327	GLU	2.4
1	A	116	ARG	2.4
1	A	241	VAL	2.2
1	A	318	LEU	2.2
1	A	334	GLY	2.1
1	A	36	ARG	2.1
1	A	322	ILE	2.1
1	A	277	ASP	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, 95th 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(\AA^2)	Q<0.9
3	8OG	T	5	23/24	0.85	0.14	-	40,44,47,49	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, 95th 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(\AA^2)	Q<0.9
5	CA	A	3000	1/1	0.97	0.19	0.57	40,40,40,40	0
4	DGT	A	1000	31/31	0.96	0.12	-0.39	18,25,29,31	0
5	CA	A	3001	1/1	0.98	0.12	-1.08	23,23,23,23	0
5	CA	A	3002	1/1	0.95	0.07	-2.79	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.