



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 12:27 PM GMT

PDB ID : 3RAX  
Title : Dpo4 extension ternary complex with 3'-terminal primer T base opposite the 1-methylguanine (M1G) lesion  
Authors : Rechkoblit, O.; Patel, D.J.  
Deposited on : 2011-03-28  
Resolution : 1.89 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

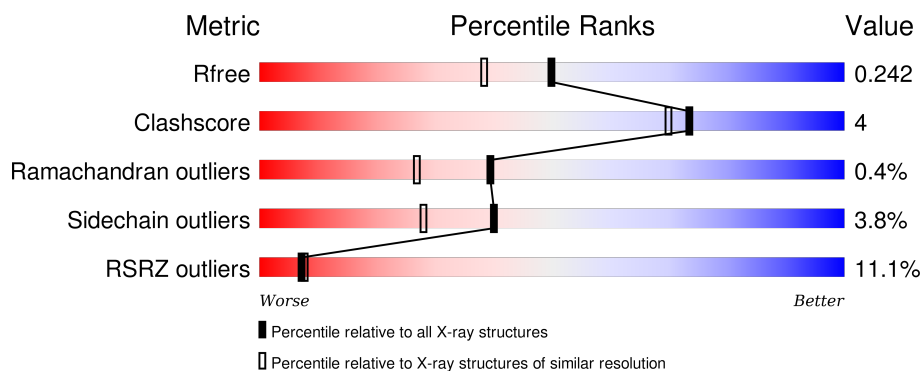
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.89 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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	A	341	<div> <div>9%</div> <div>89%</div> <div>11%</div> </div>
1	B	341	<div> <div>13%</div> <div>91%</div> <div>8%</div> </div>
2	D	13	<div> <div>54%</div> <div>46%</div> </div>
2	H	13	<div> <div>8%</div> <div>69%</div> <div>31%</div> </div>
3	E	20	<div> <div>10%</div> <div>65%</div> <div>20%</div> <div>5%</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
3	J	20	 A horizontal bar chart showing the quality of chain J. The bar is divided into four segments: a red segment on the left labeled '15%', a green segment labeled '60%', a yellow segment labeled '25%', and a grey segment on the right labeled '15%'.

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7302 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	341	Total	C	N	O	S	0	0	0
			2740	1757	472	505	6			
1	B	341	Total	C	N	O	S	0	0	0
			2740	1757	472	505	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	EXPRESSION TAG	UNP Q97W02
B	1001	GLY	-	EXPRESSION TAG	UNP Q97W02

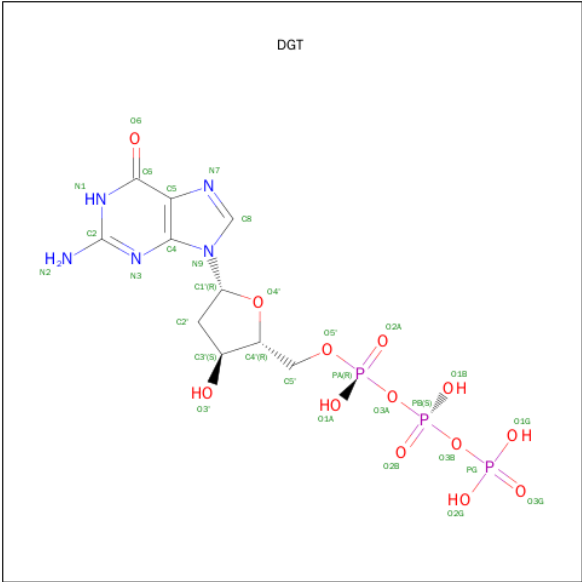
- Molecule 2 is a DNA chain called DNA (5'-D(\*GP\*TP\*TP\*GP\*GP\*AP\*TP\*GP\*GP\*TP\*AP\*GP\*(2DT))-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	13	Total	C	N	O	P	0	0	0
			270	130	50	78	12			
2	H	13	Total	C	N	O	P	0	0	0
			270	130	50	78	12			

- Molecule 3 is a DNA chain called DNA (5'-D(\*CP\*CP\*TP\*AP\*AP\*CP\*(MG1)P\*CP\*TP\*AP\*CP\*CP\*AP\*TP\*CP\*CP\*AP\*AP\*CP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	18	Total	C	N	O	P	0	0	0
			358	173	65	103	17			
3	J	17	Total	C	N	O	P	0	0	0
			338	163	63	96	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		
4	B	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	B	3	Total	Ca	0	0
			3	3		
5	A	3	Total	Ca	0	0
			3	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	259	Total	O	0	0
			259	259		
6	D	24	Total	O	0	0
			24	24		
6	E	22	Total	O	0	0
			22	22		
6	B	170	Total	O	0	0
			170	170		
6	H	22	Total	O	0	0
			22	22		

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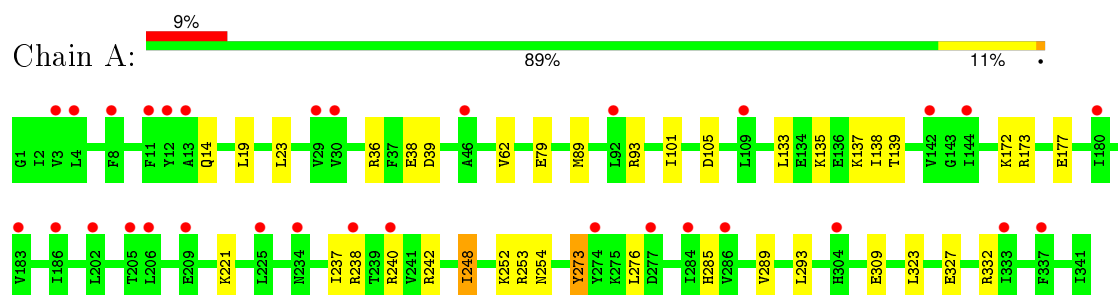
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	J	21	Total	O	0	0
			21	21		

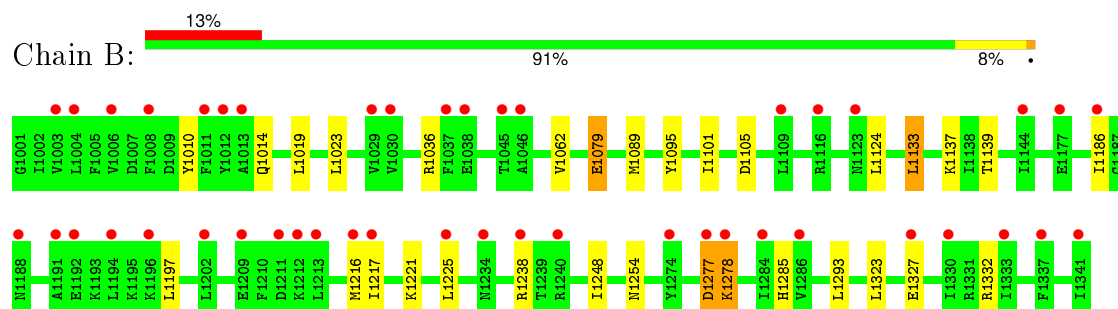
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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 polymerase IV



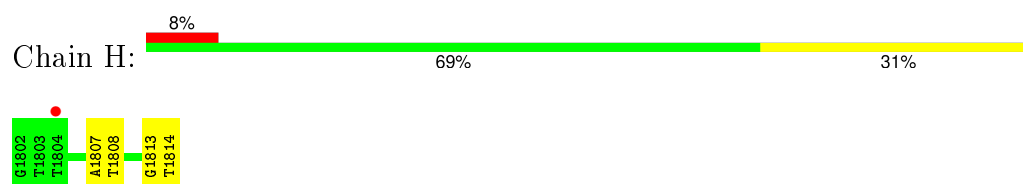
- Molecule 1: DNA polymerase IV



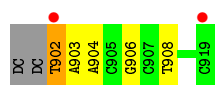
- Molecule 2: DNA (5'-D(\*GP\*TP\*TP\*GP\*GP\*AP\*TP\*GP\*GP\*TP\*AP\*GP\*(2DT))-3')



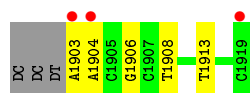
- Molecule 2: DNA (5'-D(\*GP\*TP\*TP\*GP\*GP\*AP\*TP\*GP\*GP\*TP\*AP\*GP\*(2DT))-3')



- Molecule 3: DNA (5'-D(\*CP\*CP\*TP\*AP\*AP\*CP\*(MG1)P\*CP\*TP\*AP\*CP\*CP\*AP\*TP\*CP\*CP\*AP\*AP\*CP\*C)-3')



- Molecule 3: DNA (5'-D(\*CP\*CP\*TP\*AP\*AP\*CP\*(MG1)P\*CP\*TP\*AP\*CP\*CP\*AP\*TP\*CP\*CP\*AP\*AP\*CP\*C)-3')





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.88Å 61.65Å 92.68Å 98.50° 103.82° 93.29°	Depositor
Resolution (Å)	20.00 – 1.89 19.98 – 1.89	Depositor EDS
% Data completeness (in resolution range)	95.8 (20.00-1.89) 90.8 (19.98-1.89)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.18 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.197 , 0.230 0.214 , 0.242	Depositor DCC
$R_{free}$ test set	4290 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.6	Xtriage
Anisotropy	0.340	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 43.7	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 85541 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7302	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.09% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 2DT, CA, MG1, 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	0.44	0/2779	0.60	0/3731
1	B	0.37	0/2779	0.55	0/3731
2	D	0.76	0/282	1.42	6/436 (1.4%)
2	H	0.65	0/282	1.29	3/436 (0.7%)
3	E	0.75	0/373	1.37	5/568 (0.9%)
3	J	0.66	0/351	1.24	2/534 (0.4%)
All	All	0.48	0/6846	0.80	16/9436 (0.2%)

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	902	DT	O4'-C4'-C3'	7.39	110.43	106.00
3	E	902	DT	P-O3'-C3'	7.02	128.13	119.70
2	H	1813	DG	O4'-C1'-N9	6.87	112.81	108.00
3	E	902	DT	C5'-C4'-O4'	6.61	121.85	109.30
3	J	1913	DT	P-O3'-C3'	6.30	127.26	119.70

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	2740	0	2883	28	0
1	B	2740	0	2880	20	0
2	D	270	0	150	4	0
2	H	270	0	150	3	0
3	E	358	0	205	10	0
3	J	338	0	193	4	0
4	A	31	0	12	0	0
4	B	31	0	12	0	0
5	A	3	0	0	0	0
5	B	3	0	0	0	0
6	A	259	0	0	8	0
6	B	170	0	0	3	0
6	D	24	0	0	0	0
6	E	22	0	0	1	0
6	H	22	0	0	0	0
6	J	21	0	0	2	0
All	All	7302	0	6485	54	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 4.

The worst 5 of 54 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)
6:A:567:HOH:O	2:D:814:2DT:H3'2	1.02	1.18
6:B:107:HOH:O	2:H:1814:2DT:H3'2	1.56	1.05
1:B:1014:GLN:HE22	1:B:1139:THR:H	1.11	0.95
1:A:101:ILE:O	1:A:240:ARG:HG3	1.71	0.89
1:A:14:GLN:HE22	1:A:139:THR:H	1.20	0.87

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	339/341 (99%)	332 (98%)	7 (2%)	0	100	100
1	B	339/341 (99%)	332 (98%)	4 (1%)	3 (1%)	21	9
All	All	678/682 (99%)	664 (98%)	11 (2%)	3 (0%)	39	27

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1277	ASP
1	B	1010	TYR
1	B	1278	LYS

### 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	299/299 (100%)	284 (95%)	15 (5%)	30	18
1	B	299/299 (100%)	291 (97%)	8 (3%)	52	43
All	All	598/598 (100%)	575 (96%)	23 (4%)	40	28

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	253	ARG
1	A	309	GLU
1	B	1323	LEU
1	A	273	TYR
1	A	323	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	285	HIS
1	B	1014	GLN

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Mol	Chain	Res	Type
1	B	1285	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	2DT	D	814	3,2	11,20,21	1.50	2 (18%)	12,28,31	5.29	4 (33%)
3	MG1	E	906	3,2	16,25,26	1.03	1 (6%)	20,37,40	1.04	1 (5%)
2	2DT	H	1814	3,2	11,20,21	1.56	2 (18%)	12,28,31	4.77	3 (25%)
3	MG1	J	1906	3,2	16,25,26	0.81	1 (6%)	20,37,40	1.17	3 (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
2	2DT	D	814	3,2	-	0/3/18/19	0/2/2/2
3	MG1	E	906	3,2	-	0/3/21/22	0/3/3/3
2	2DT	H	1814	3,2	-	0/3/18/19	0/2/2/2
3	MG1	J	1906	3,2	-	0/3/21/22	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	906	MG1	C6-N1	-3.55	1.33	1.38
3	J	1906	MG1	C6-N1	-2.43	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	814	2DT	C4-N3	3.14	1.38	1.33
2	D	814	2DT	C6-N1	3.19	1.39	1.35
2	H	1814	2DT	C6-N1	3.21	1.39	1.35

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	814	2DT	C5-C4-N3	-9.36	114.71	125.14
2	H	1814	2DT	C5-C4-N3	-8.55	115.62	125.14
3	J	1906	MG1	C1'-N9-C4	-2.52	122.89	127.16
3	J	1906	MG1	C4-C5-N7	-2.21	107.44	109.48
3	E	906	MG1	C4-C5-N7	-2.13	107.52	109.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	814	2DT	4	0
3	E	906	MG1	3	0
2	H	1814	2DT	3	0
3	J	1906	MG1	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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	414	5	25,33,33	1.15	1 (4%)	35,52,52	3.12	14 (40%)
4	DGT	B	1414	5	25,33,33	1.07	1 (4%)	35,52,52	3.30	13 (37%)

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	414	5	-	0/18/34/34	0/3/3/3
4	DGT	B	1414	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	B	1414	DGT	C6-N1	3.92	1.40	1.33
4	A	414	DGT	C6-N1	4.36	1.41	1.33

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1414	DGT	C5-C6-N1	-8.72	111.66	123.59
4	A	414	DGT	C5-C6-N1	-8.33	112.20	123.59
4	B	1414	DGT	O2G-PG-O3G	-7.75	85.62	110.58
4	B	1414	DGT	O1G-PG-O3G	-6.27	90.41	110.58
4	A	414	DGT	O2G-PG-O3G	-6.05	91.10	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<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	341/341 (100%)	0.57	31 (9%) 11 13	20, 35, 52, 61	0
1	B	341/341 (100%)	0.81	45 (13%) 4 5	29, 44, 73, 92	0
2	D	12/13 (92%)	0.02	0 100 100	32, 40, 84, 89	0
2	H	12/13 (92%)	0.18	1 (8%) 14 15	41, 46, 94, 96	0
3	E	17/20 (85%)	0.26	2 (11%) 6 6	34, 47, 89, 92	0
3	J	16/20 (80%)	0.61	3 (18%) 2 2	37, 63, 90, 98	0
All	All	739/748 (98%)	0.66	82 (11%) 7 8	20, 41, 73, 98	0

The worst 5 of 82 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1225	LEU	5.1
1	B	1209	GLU	4.7
1	B	1217	ILE	4.7
1	B	1037	PHE	4.4
1	A	225	LEU	4.3

### 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	2DT	D	814	19/20	0.81	0.43	-	50,66,73,73	0
3	MG1	J	1906	23/24	0.97	0.08	-	35,39,43,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	2DT	H	1814	19/20	0.76	0.46	-	62,73,80,80	0
3	MG1	E	906	23/24	0.95	0.10	-	33,36,38,41	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( $\text{\AA}^2$ )	Q<0.9
4	DGT	A	414	31/31	0.98	0.13	-0.35	21,24,27,29	0
4	DGT	B	1414	31/31	0.97	0.12	-0.58	28,30,36,42	0
5	CA	A	416	1/1	0.99	0.10	-1.19	18,18,18,18	0
5	CA	B	1417	1/1	0.97	0.07	-1.57	42,42,42,42	0
5	CA	A	417	1/1	1.00	0.03	-1.84	36,36,36,36	0
5	CA	B	1416	1/1	0.98	0.07	-2.37	26,26,26,26	0
5	CA	B	1415	1/1	0.98	0.03	-	29,29,29,29	0
5	CA	A	415	1/1	1.00	0.05	-	20,20,20,20	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.