



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 12:36 am GMT

PDB ID : 3RB0  
Title : Dpo4 extension ternary complex with 3'-terminal primer G base opposite the 1-methylguanine (M1G) lesion  
Authors : Rechkoblit, O.; Patel, D.J.  
Deposited on : 2011-03-28  
Resolution : 3.23 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

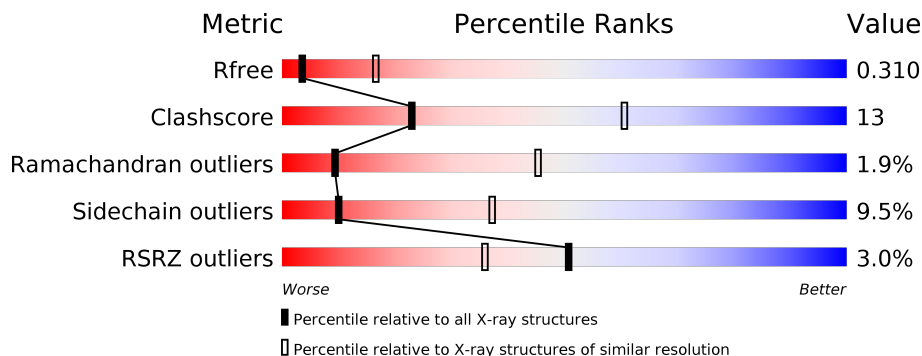
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.23 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))
$R_{free}$	100719	1036 (3.24-3.20)
Clashscore	112137	1161 (3.24-3.20)
Ramachandran outliers	110173	1140 (3.24-3.20)
Sidechain outliers	110143	1139 (3.24-3.20)
RSRZ outliers	101464	1040 (3.24-3.20)

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  $\geq 3$ , 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>70%</div> <div>27%</div> <div>•</div> </div>
1	B	341	<div> <div>4%</div> <div>61%</div> <div>35%</div> <div>• •</div> </div>
2	D	13	<div> <div>46%</div> <div>38%</div> <div>15%</div> </div>
2	H	13	<div> <div>23%</div> <div>46%</div> <div>38%</div> <div>8%</div> <div>8%</div> </div>
3	E	20	<div> <div>10%</div> <div>65%</div> <div>15%</div> <div>15%</div> <div>5%</div> </div>
3	J	20	<div> <div>25%</div> <div>30%</div> <div>45%</div> <div>25%</div> </div>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6759 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
			2739	1757	472	504	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\*(DDG))-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	13	Total	C	N	O	P	0	0	0
			271	129	53	77	12			
2	H	12	Total	C	N	O	P	0	0	0
			233	110	43	69	11			

- Molecule 3 is a DNA chain called DNA (5'-D(\*C\*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	19	Total	C	N	O	P	0	0	0
			377	182	68	109	18			
3	J	15	Total	C	N	O	P	0	0	0
			300	145	57	84	14			

- 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 31	C 10	N 5	O 13	P 3	0	0
4	B	1	Total 31	C 10	N 5	O 13	P 3	0	0

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

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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	9	Total O 9 9	0	0
6	D	4	Total O 4 4	0	0
6	E	4	Total O 4 4	0	0
6	B	8	Total O 8 8	0	0
6	H	4	Total O 4 4	0	0

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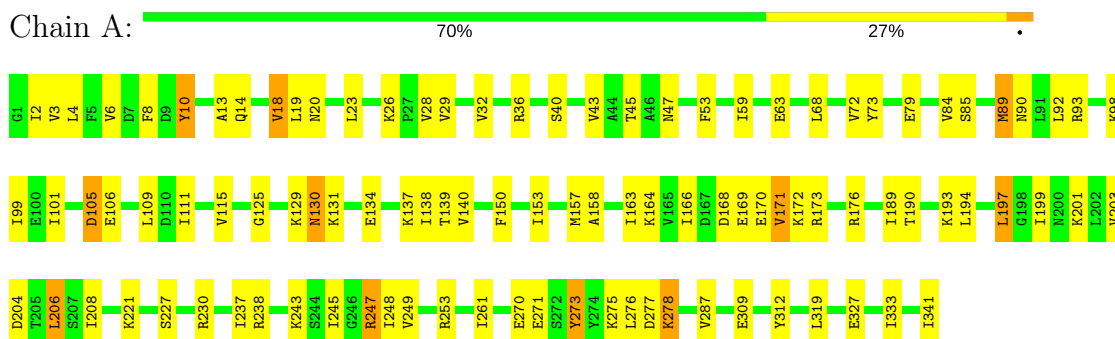
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	J	2	Total	O	0	0
			2	2		

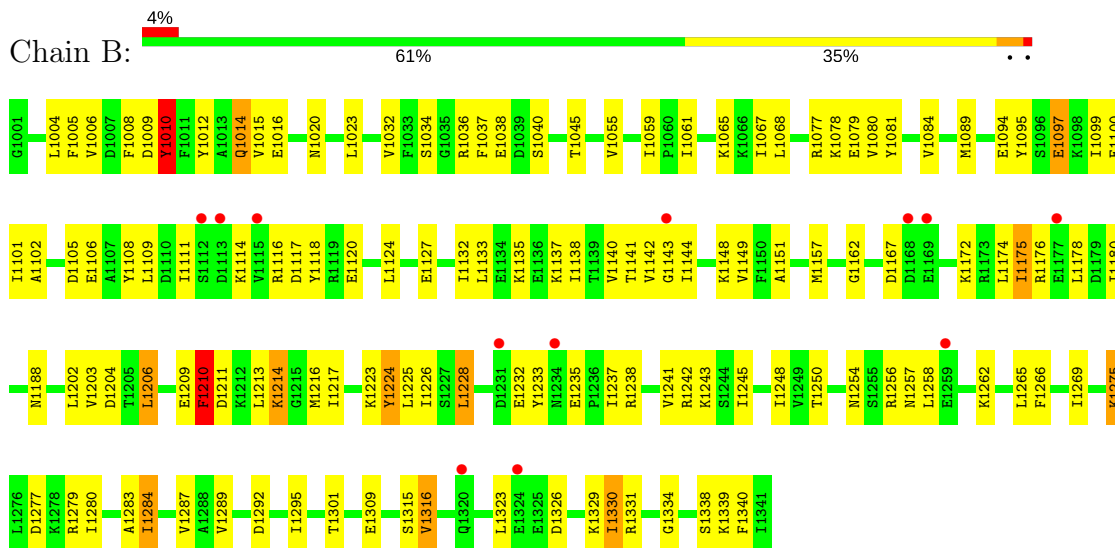
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

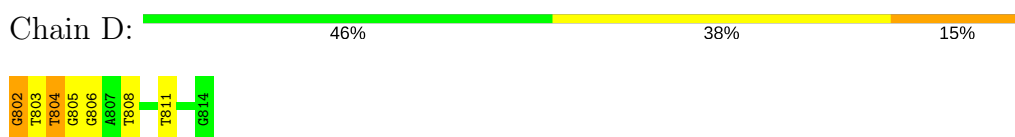
#### • Molecule 1: DNA polymerase IV



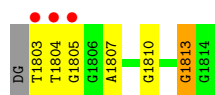
#### • Molecule 1: DNA polymerase IV



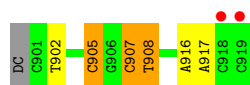
#### • Molecule 2: DNA (5'-D(\*GP\*TP\*TP\*GP\*GP\*AP\*TP\*GP\*GP\*TP\*AP\*GP\*(DDG))-3')



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



• Molecule 3: DNA (5'-D(\*C\*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(\*C\*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 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.42Å 110.36Å 102.27Å 90.00° 101.28° 90.00°	Depositor
Resolution (Å)	20.00 – 3.23 19.99 – 3.22	Depositor EDS
% Data completeness (in resolution range)	95.8 (20.00-3.23) 95.7 (19.99-3.22)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.47 (at 3.22Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.223 , 0.294 0.229 , 0.310	Depositor DCC
$R_{free}$ test set	893 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	80.1	Xtriage
Anisotropy	0.518	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 82.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6759	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	108.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.52% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: CA, DDG, 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	0.51	0/2778	0.64	0/3731
1	B	0.39	0/2779	0.55	0/3731
2	D	0.92	0/282	1.87	9/436 (2.1%)
2	H	0.72	0/257	1.46	4/397 (1.0%)
3	E	0.89	0/394	1.63	8/600 (1.3%)
3	J	0.75	0/309	1.62	8/470 (1.7%)
All	All	0.54	0/6799	0.91	29/9365 (0.3%)

There are no bond length outliers.

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	917	DA	O4'-C1'-C2'	-8.88	98.80	105.90
2	D	802	DG	O4'-C4'-C3'	-8.72	100.77	106.00
3	E	917	DA	O4'-C1'-N9	8.55	113.98	108.00
2	D	802	DG	C4'-C3'-C2'	-8.22	95.70	103.10
2	D	804	DT	O4'-C4'-C3'	-7.64	101.42	106.00

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	2739	0	2883	76	0
1	B	2740	0	2880	81	0
2	D	271	0	144	3	0
2	H	233	0	126	3	0
3	E	377	0	216	3	0
3	J	300	0	171	7	0
4	A	31	0	12	2	0
4	B	31	0	12	0	0
5	A	3	0	0	0	0
5	B	3	0	0	0	0
6	A	9	0	0	0	0
6	B	8	0	0	0	0
6	D	4	0	0	0	0
6	E	4	0	0	0	0
6	H	4	0	0	0	0
6	J	2	0	0	0	0
All	All	6759	0	6444	167	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 13.

The worst 5 of 167 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:23:LEU:HD11	1:A:72:VAL:HG11	1.53	0.91
1:B:1014:GLN:HE22	1:B:1138:ILE:HA	1.40	0.86
1:B:1132:ILE:HD13	1:B:1140:VAL:HG11	1.64	0.80
1:A:4:LEU:HB2	1:A:111:ILE:HD13	1.61	0.80
1:A:150:PHE:HA	1:A:153:ILE:HD12	1.64	0.79

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	A	339/341 (99%)	304 (90%)	32 (9%)	3 (1%)	20	63
1	B	339/341 (99%)	279 (82%)	50 (15%)	10 (3%)	5	33
All	All	678/682 (99%)	583 (86%)	82 (12%)	13 (2%)	9	45

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1277	ASP
1	B	1010	TYR
1	B	1210	PHE
1	B	1339	LYS
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	299/299 (100%)	276 (92%)	23 (8%)	15	50
1	B	299/299 (100%)	265 (89%)	34 (11%)	7	29
All	All	598/598 (100%)	541 (90%)	57 (10%)	10	37

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1020	ASN
1	B	1094	GLU
1	B	1292	ASP
1	B	1023	LEU
1	B	1038	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1014	GLN

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Mol	Chain	Res	Type
1	B	1304	HIS
1	B	1188	ASN
1	A	130	ASN
1	B	1257	ASN

### 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	DDG	D	814	2,5	14,21,24	1.45	1 (7%)	14,29,36	3.04	5 (35%)
3	MG1	E	906	3	17,25,26	1.17	2 (11%)	19,37,40	1.54	3 (15%)
2	DDG	H	1814	2	0,3,24	0.00	-	0,3,36	0.00	-
3	MG1	J	1906	3	17,25,26	0.76	0	19,37,40	2.03	5 (26%)

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	DDG	D	814	2,5	-	1/6/11/19	0/2/2/3
3	MG1	E	906	3	-	0/3/21/22	0/3/3/3
2	DDG	H	1814	2	-	0/0/0/19	0/0/0/3
3	MG1	J	1906	3	-	0/3/21/22	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	906	MG1	C6-N1	-3.14	1.33	1.38
3	E	906	MG1	O5'-C5'	-2.38	1.41	1.44
2	D	814	DDG	C6-N1	4.13	1.40	1.33

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	814	DDG	C5-C6-N1	-7.96	112.15	123.48
3	J	1906	MG1	C4-C5-N7	-2.58	106.92	109.41
2	D	814	DDG	N3-C2-N1	-2.50	123.80	127.46
3	E	906	MG1	C4-C5-N7	-2.48	107.02	109.41
2	D	814	DDG	C2-N3-C4	-2.21	112.58	115.16

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	814	DDG	C4'-O4'-C1'-C2'

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	J	1906	MG1	3	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	26,33,33	1.03	2 (7%)	28,52,52	3.28	9 (32%)
4	DGT	B	1414	5	26,33,33	1.03	1 (3%)	28,52,52	3.15	9 (32%)

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 (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	414	DGT	C8-N7	-2.41	1.30	1.34
4	A	414	DGT	C6-N1	3.12	1.38	1.33
4	B	1414	DGT	C6-N1	3.96	1.40	1.33

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	414	DGT	C5-C6-N1	-8.03	112.05	123.48
4	B	1414	DGT	C5-C6-N1	-7.77	112.43	123.48
4	A	414	DGT	O2G-PG-O3G	-7.39	81.57	110.50
4	A	414	DGT	O1G-PG-O3G	-7.01	83.07	110.50
4	B	1414	DGT	O1G-PG-O3G	-6.88	83.59	110.50

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	414	DGT	2	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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%)	-0.30	0 <span>100</span> <span>100</span>	55, 78, 110, 137	0
1	B	341/341 (100%)	0.13	12 (3%) <span>44</span> <span>30</span>	91, 128, 169, 187	0
2	D	12/13 (92%)	0.07	0 <span>100</span> <span>100</span>	69, 87, 144, 155	0
2	H	11/13 (84%)	1.13	3 (27%) <span>1</span> <span>1</span>	116, 143, 193, 240	0
3	E	18/20 (90%)	0.35	2 (11%) <span>6</span> <span>4</span>	61, 86, 152, 178	0
3	J	14/20 (70%)	1.17	5 (35%) <span>0</span> <span>0</span>	103, 146, 218, 266	0
All	All	737/748 (98%)	-0.03	22 (2%) <span>51</span> <span>36</span>	55, 102, 164, 266	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	1803	DT	4.4
1	B	1143	GLY	4.3
3	E	919	DC	4.2
1	B	1169	GLU	4.0
1	B	1113	ASP	3.8

### 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
3	MG1	E	906	23/24	0.95	0.15	-	64,68,70,71	0
3	MG1	J	1906	23/24	0.81	0.22	-	124,129,156,158	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	DDG	H	1814	4/22	0.83	0.38	-	130,130,131,132	0
2	DDG	D	814	20/22	0.85	0.26	-	101,125,136,140	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	0.95	0.20	-0.35	60,66,70,83	0
4	DGT	B	1414	31/31	0.92	0.18	-1.20	133,136,144,146	0
5	CA	B	1417	1/1	0.86	0.12	-1.69	73,73,73,73	0
5	CA	A	416	1/1	0.97	0.11	-1.86	46,46,46,46	0
5	CA	A	417	1/1	0.98	0.05	-2.50	99,99,99,99	0
5	CA	B	1416	1/1	0.98	0.03	-3.20	61,61,61,61	0
5	CA	B	1415	1/1	0.79	0.15	-	73,73,73,73	0
5	CA	A	415	1/1	0.90	0.06	-	48,48,48,48	0

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

There are no such residues in this entry.