

# Full wwPDB X-ray Structure Validation Report (i)

May 13, 2020 – 09:25 am BST

PDB ID : 6DTA

Title : Bacteriophage N4 RNA polymerase II elongation complex 2

Authors: Molodtsov, V.; Murakami, K.S.

Deposited on : 2018-06-15

Resolution : 2.69 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

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

Mol Probity : 4.02b-467

Mogul : 1.8.5 (274361), CSD as 541 be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.11

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0158

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

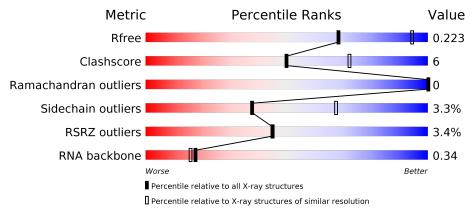
Validation Pipeline (wwPDB-VP) : 2.11

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$ 

The reported resolution of this entry is 2.69 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)
RNA backbone	3102	1159 (3.00-2.40)

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 respectively. 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 <=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	269	3%		80%	12%	6 • 7%				
2	В	404	2%		86%		12% •				
3	С	48	10%	13%	77%						
4	D	8		25% 25%	50%	13%	13%				



# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5692 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 RNAP1.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace
1	Λ	250	Total	С	N	О	S	0	0	0
1	A	250	2023	1287	348	375	13	U	U	0

• Molecule 2 is a protein called RNAP2.

Mol	Chain	Residues		Atoms					AltConf	Trace
2	R	404	Total	С	N	О	S	0	0	0
	ע	404	3250	2070	542	617	21		0	

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

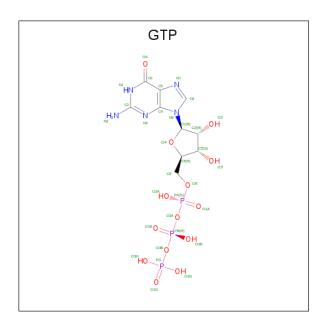
Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace
3	С	11	Total 221	C 105	N 45	O 60	P 11	0	0	0

• Molecule 4 is a RNA chain called RNA (5'-R(\*UP\*UP\*GP\*GP\*UP\*GP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	7	Total	С	N	О	Р	0	0	0
4		4	149	67	26	50	6	0	U	U

• Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).





Mol	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf	
5	R	1	Total	С	N	О	Р	0	0
0	ט	1	32	10	5	14	3	U	0

• Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	В	1	Total Mg 1 1	0	0
6	D	2	$\begin{array}{cc} \text{Total} & \text{Mg} \\ 2 & 2 \end{array}$	0	0

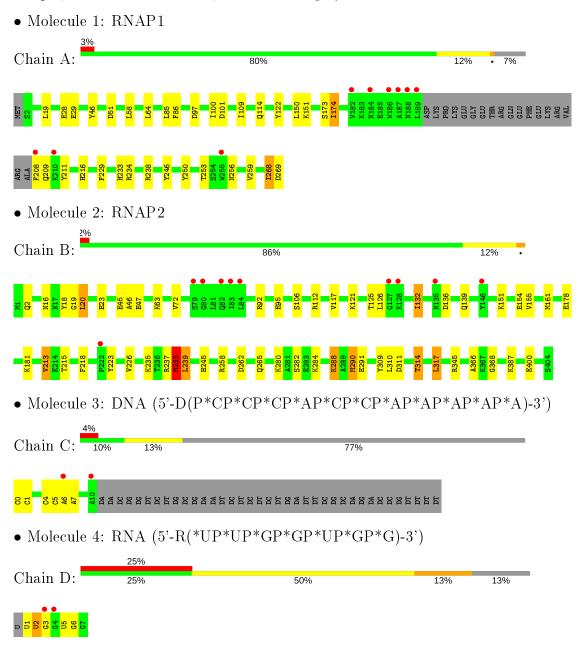
• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	8	Total O 8 8	0	0
7	В	5	Total O 5 5	0	0
7	С	1	Total O 1 1	0	0



# 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.





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 4	Depositor
Cell constants	$175.05 ext{Å}$ $175.05 ext{Å}$ $76.60 ext{Å}$	Domositon
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	29.92 - 2.69	Depositor
Resolution (A)	29.92 - 2.69	EDS
% Data completeness	97.9 (29.92-2.69)	Depositor
(in resolution range)	97.9 (29.92-2.69)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.83 (at 2.68Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
D D.	0.191 , 0.223	Depositor
$R, R_{free}$	0.191 , $0.223$	DCC
$R_{free}$ test set	1993 reflections (6.32%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	79.4	Xtriage
Anisotropy	0.119	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.30,55.4	EDS
L-test for twinning <sup>2</sup>	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.022 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5692	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.51% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $< L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: GTP, MG

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		
MIOI	Chain	RMSZ	# Z >5	RMSZ	# Z  > 5	
1	A	0.51	0/2071	0.75	0/2797	
2	В	0.50	0/3317	0.76	4/4489 (0.1%)	
3	С	0.95	0/248	0.95	0/378	
4	D	0.68	0/166	1.38	$2/258 \ (0.8\%)$	
All	All	0.54	0/5802	0.80	6/7922 (0.1%)	

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\mathbf{Ideal}(^o)$
2	В	317	LEU	CA-CB-CG	9.25	136.58	115.30
2	В	238	MET	CA-CB-CG	7.55	126.14	113.30
4	D	1	U	C2-N1-C1'	6.03	124.93	117.70
2	В	239	LEU	CB-CG-CD2	-5.49	101.67	111.00
2	В	258	ARG	NE-CZ-NH1	-5.49	117.56	120.30
4	D	2	U	C2-N1-C1'	5.27	124.03	117.70

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	2023	0	1941	21	0	



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Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
2	В	3250	0	3203	35	0
3	С	221	0	122	12	0
4	D	149	0	76	1	0
5	В	32	0	12	1	0
6	В	1	0	0	0	0
6	D	2	0	0	0	0
7	A	8	0	0	0	0
7	В	5	0	0	0	0
7	С	1	0	0	0	0
All	All	5692	0	5354	63	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 6.

All (63) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A 4 a ma 1	A 4 a ros 2	Interatomic	Clash
Atom-1	Atom-2	${ m distance} \; ({ m \AA})$	overlap (Å)
2:B:290:MET:HG2	2:B:317:LEU:HD21	1.65	0.76
2:B:366:ALA:O	2:B:387:LYS:HE2	1.95	0.66
2:B:309:TYR:O	2:B:314:THR:HG21	1.96	0.65
2:B:310:LEU:HA	2:B:314:THR:CG2	2.27	0.65
3:C:4:DC:H2'	3:C:5:DC:C6	2.38	0.58
2:B:310:LEU:HA	2:B:314:THR:HG21	1.86	0.58
2:B:238:MET:HB2	3:C:1:DC:H5"	1.86	0.58
2:B:290:MET:SD	2:B:317:LEU:HD11	2.45	0.56
1:A:208:PHE:CG	1:A:209:GLN:N	2.73	0.56
1:A:211:TYR:HE1	1:A:246:TYR:CE1	2.24	0.56
2:B:235:LYS:HE3	2:B:237:ARG:HE	1.70	0.56
2:B:2:GLN:HG2	2:B:400:GLU:OE2	2.05	0.56
1:A:28:GLU:HG2	1:A:46:TYR:OH	2.06	0.55
2:B:72:VAL:O	2:B:345:ARG:HA	2.07	0.55
1:A:19:LEU:HD21	1:A:58:LEU:HD11	1.89	0.55
2:B:282:SER:OG	2:B:284:LYS:HG2	2.07	0.55
1:A:97:ASP:OD1	1:A:100:ILE:HG12	2.07	0.54
2:B:95:GLU:O	2:B:112:ARG:HD3	2.08	0.53
2:B:310:LEU:HA	2:B:314:THR:HG22	1.91	0.53
3:C:5:DC:H2'	3:C:6:DA:C8	2.43	0.52
3:C:4:DC:H2'	3:C:5:DC:H6	1.73	0.52
5:B:1001:GTP:N3	5:B:1001:GTP:H2'	2.24	0.52
4:D:5:U:H2'	4:D:6:G:C8	2.46	0.51
3:C:6:DA:H8	3:C:6:DA:OP2	1.94	0.51



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Communa from pred		Interatomic	Clash
Atom-1	Atom-2	${\rm distance} \; (\mathring{\rm A})$	$overlap( ext{\AA})$
2:B:20:LEU:HB3	2:B:23:GLU:HG3	1.94	0.50
2:B:121:LYS:O	2:B:125:THR:HG23	2.12	0.49
1:A:151:LYS:HE3	3:C:4:DC:OP2	2.12	0.49
2:B:132:ILE:HD13	2:B:161:MET:HE2	1.94	0.48
3:C:6:DA:H2'	3:C:7:DA:C8	2.49	0.48
2:B:178:GLU:O	2:B:181:LYS:HB3	2.13	0.48
1:A:268:ILE:O	1:A:269:ASP:HB2	2.14	0.47
2:B:16:ASN:O	2:B:19:GLY:HA3	2.14	0.47
2:B:288:LYS:HE3	2:B:291:GLU:OE1	2.14	0.47
1:A:122:TYR:CE1	3:C:5:DC:H5'	2.49	0.47
2:B:213:VAL:HB	2:B:226:VAL:HG22	1.96	0.46
1:A:174:ILE:HD12	1:A:259:VAL:HG12	1.97	0.46
1:A:253:THR:OG1	1:A:256:ASN:HB2	2.15	0.46
3:C:5:DC:H2"	3:C:6:DA:H5'	1.97	0.46
3:C:6:DA:OP2	3:C:6:DA:H3'	2.16	0.45
2:B:237:ARG:HH11	3:C:0:DC:H5'	1.81	0.45
2:B:117:VAL:O	2:B:121:LYS:HG2	2.17	0.45
1:A:211:TYR:HE1	1:A:246:TYR:HE1	1.64	0.45
3:C:6:DA:H2"	3:C:7:DA:O4'	2.17	0.44
1:A:174:ILE:HD12	1:A:259:VAL:CG1	2.48	0.44
1:A:233:HIS:NE2	1:A:250:TYR:OH	2.48	0.44
1:A:86:PHE:HB2	2:B:218:PHE:CE2	2.53	0.44
2:B:262:ASP:HB3	2:B:265:GLN:HB3	2.01	0.43
2:B:280:LYS:O	2:B:311:ASP:HB2	2.19	0.43
1:A:150:LEU:HD23	1:A:234:ARG:CZ	2.49	0.43
2:B:136:ASP:HB3	2:B:155:VAL:HG13	2.01	0.43
2:B:18:TYR:O	2:B:47:GLU:N	2.44	0.43
2:B:18:TYR:O	2:B:46:ALA:HA	2.19	0.43
2:B:151:LYS:NZ	2:B:154:GLU:OE2	2.48	0.42
2:B:238:MET:SD	2:B:239:LEU:HD23	2.60	0.42
1:A:268:ILE:HG22	1:A:269:ASP:O	2.20	0.42
2:B:368:GLY:O	2:B:387:LYS:NZ	2.34	0.42
2:B:235:LYS:CE	2:B:237:ARG:HE	2.32	0.41
1:A:173:SER:HA	1:A:229:PHE:CE2	2.55	0.41
1:A:64:LEU:HD23	2:B:223:TYR:CD1	2.56	0.41
2:B:18:TYR:OH	2:B:45:GLU:OE1	2.35	0.40
1:A:238:ARG:NH1	2:B:245:HIS:ND1	2.69	0.40
1:A:85:LEU:HA	1:A:85:LEU:HD23	1.91	0.40
1:A:109:ILE:HD11	1:A:114:GLN:OE1	2.21	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	${f Analysed}$	Favoured	Allowed	Outliers	Perce	entiles
1	A	$246/269 \; (91\%)$	238 (97%)	8 (3%)	0	100	100
2	В	402/404 (100%)	390 (97%)	12 (3%)	0	100	100
All	All	648/673 (96%)	628 (97%)	20 (3%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	A	$218/243 \ (90\%)$	212 (97%)	6 (3%)	43 73		
2	В	350/351 (100%)	337 (96%)	13 (4%)	34 63		
All	All	568/594 (96%)	549 (97%)	19 (3%)	38 67		

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	GLU
1	A	51	ASP
1	A	101	ASP
1	A	174	ILE
1	A	216	HIS
1	A	268	ILE
2	В	20	LEU
2	В	63	LYS



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Mol	Chain	Res	Type
2	В	92	ARG
2	В	106	SER
2	В	126	LEU
2	В	132	ILE
2	В	139	GLN
2	В	213	VAL
2	В	215	THR
2	В	238	MET
2	В	288	LYS
2	В	290	MET
2	В	314	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	$\mathbf{Type}$	
2	В	180	ASN	

#### 5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	D	6/8 (75%)	2 (33%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	D	2	U
4	D	3	G

There are no RNA pucker outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 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 Lin			Link	Bond lengths			Bond angles		
MIOI	Type	Chain	III   nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	GTP	В	1001	-	26,34,34	1.08	2 (7%)	33,54,54	2.08	8 (24%)

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	$\mathbf{Type}$	Chain	Res	Link	Chirals	Torsions	Rings
5	GTP	В	1001	-	-	8/18/38/38	0/3/3/3

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}( ext{\AA})$
5	В	1001	GTP	C6-N1	3.78	1.39	1.33
5	В	1001	GTP	C2-N1	2.68	1.40	1.35

#### All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\mathbf{Ideal}(^{o})$
5	В	1001	GTP	N3-C2-N1	-6.13	119.04	127.22
5	В	1001	GTP	C2-N3-C4	5.01	121.08	115.36
5	В	1001	GTP	N2-C2-N1	4.00	123.48	117.25
5	В	1001	GTP	C3'-C2'-C1'	3.45	106.17	100.98
5	В	1001	GTP	C5-C6-N1	-3.39	118.80	123.43
5	В	1001	GTP	C6-N1-C2	3.18	120.98	115.93
5	В	1001	GTP	PB-O3B-PG	-2.96	122.66	132.83
5	В	1001	GTP	PA-O3A-PB	-2.43	124.48	132.83

There are no chirality outliers.

All (8) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
5	В	1001	GTP	PB-O3B-PG-O2G
5	В	1001	GTP	PB-O3B-PG-O3G
5	В	1001	GTP	C5'-O5'-PA-O3A
5	В	1001	GTP	C5'-O5'-PA-O1A
5	В	1001	GTP	C5'-O5'-PA-O2A
5	В	1001	GTP	C3'-C4'-C5'-O5'
5	В	1001	GTP	O4'-C4'-C5'-O5'
5	В	1001	GTP	PB-O3B-PG-O1G

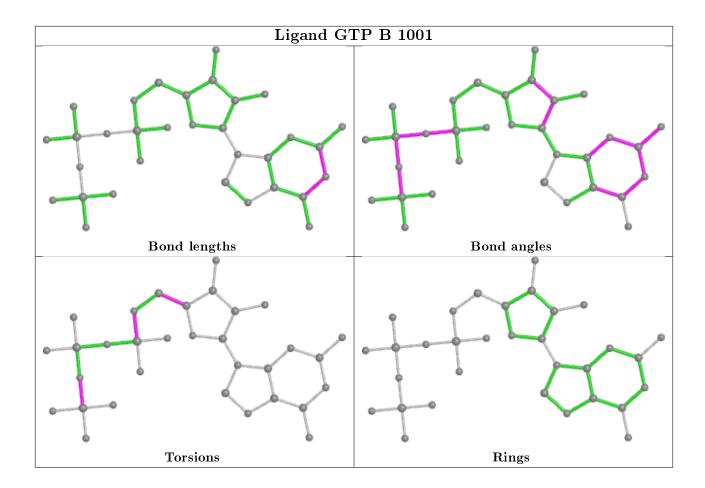
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	В	1001	GTP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





# 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,  $95^{th}$  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 $>$	$\#\mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q<0.9
1	A	$250/269 \; (92\%)$	0.06	9 (3%) 42 42	53, 92, 156, 208	0
2	В	404/404 (100%)	0.02	10 (2%) 57 59	52, 88, 134, 187	0
3	С	11/48 (22%)	0.70	2 (18%) 1 1	106, 130, 220, 230	0
4	D	7/8 (87%)	1.71	2 (28%) 0 0	135, 151, 200, 202	0
All	All	672/729 (92%)	0.06	23 (3%) 45 45	52, 91, 151, 230	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	3	G	6.1
1	A	187	ALA	4.7
2	В	128	LYS	4.5
1	A	186	TRP	4.3
1	A	255	TRP	4.0
1	A	189	LEU	3.3
2	В	127	GLY	3.2
1	A	184	ASN	3.2
1	A	188	ASN	3.2
1	A	210	LYS	3.1
3	С	10	DA	2.6
1	A	208	PHE	2.6
3	С	6	DA	2.5
2	В	83	ILE	2.5
4	D	4	G	2.4
2	В	84	LEU	2.4
2	В	222	PRO	2.3
2	В	80	GLY	2.3
2	В	146	TYR	2.2
2	В	135	ASN	2.2
2	В	82	GLN	2.2



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Mol	Chain	Res	Type	RSRZ
1	A	182	VAL	2.1
2	В	79	SER	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

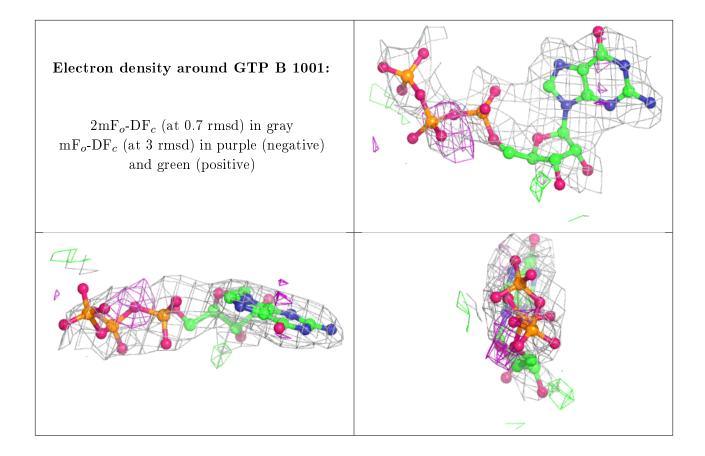
### 6.4 Ligands (i)

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. The B-factors column lists the minimum, median,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
5	GTP	В	1001	32/32	0.74	0.28	92,165,236,238	0
6	MG	D	102	1/1	0.83	0.39	102,102,102,102	0
6	MG	В	1002	1/1	0.92	0.82	94,94,94,94	0
6	MG	D	101	1/1	0.94	0.36	101,101,101,101	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





### 6.5 Other polymers (i)

There are no such residues in this entry.

