



## wwPDB EM Validation Summary Report ⓘ

Jun 2, 2026 – 12:14 AM JST

PDB ID : 24NA / pdb\_000024na  
EMDB ID : EMD-69681  
Title : DRT4 homoheptamer with dGTP  
Authors : Wang, L.; Li, J.  
Deposited on : 2026-03-11  
Resolution : 2.80 Å(reported)

This is a wwPDB EM 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

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : **FAILED**  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : **NOT EXECUTED**  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

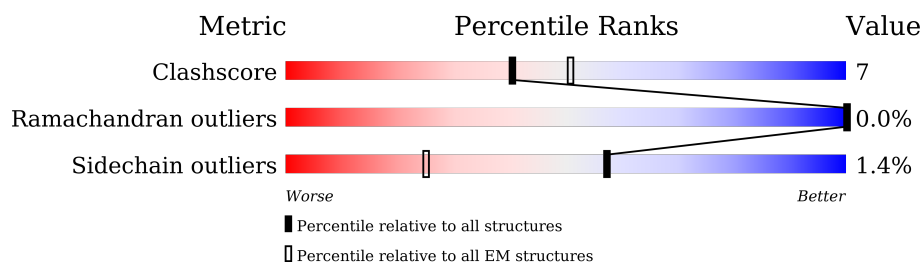
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.80 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)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	540	76% 19% • 5%
1	B	540	76% 19% 5%
1	C	540	79% 15% • 5%
1	D	540	80% 15% 5%
1	E	540	79% 15% 5%
1	F	540	77% 18% 5%

## 2 Entry composition [i](#)

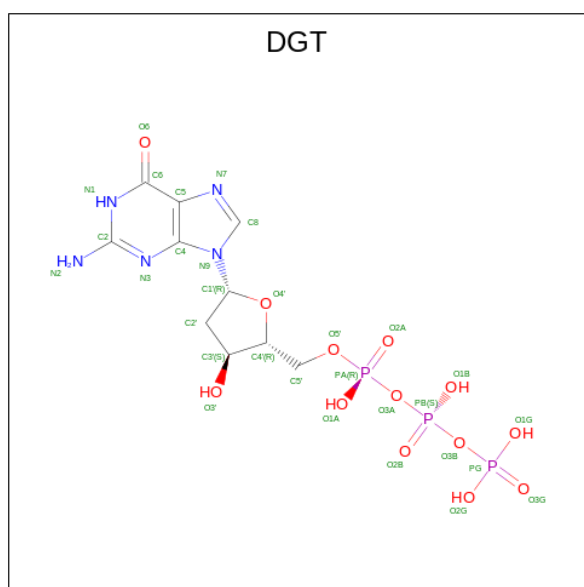
There are 3 unique types of molecules in this entry. The entry contains 25524 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Reverse transcriptase domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	515	Total	C	N	O	S	0	0
			4221	2695	701	802	23		
1	B	515	Total	C	N	O	S	0	0
			4221	2695	701	802	23		
1	C	515	Total	C	N	O	S	0	0
			4221	2695	701	802	23		
1	D	515	Total	C	N	O	S	0	0
			4221	2695	701	802	23		
1	E	515	Total	C	N	O	S	0	0
			4221	2695	701	802	23		
1	F	515	Total	C	N	O	S	0	0
			4221	2695	701	802	23		

- Molecule 2 is 2'-DEOXYGUANOSINE-5'-TRIPHOSPHATE (CCD ID: DGT) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	E	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	F	1	Total	C	N	O	P	0
			31	10	5	13	3	

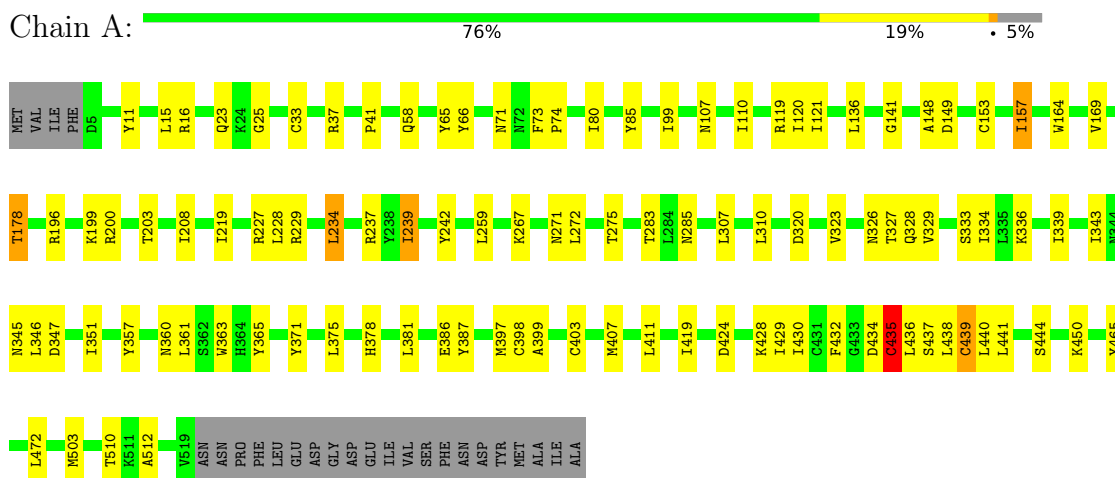
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Mg	0
			2	2	
3	B	2	Total	Mg	0
			2	2	
3	C	2	Total	Mg	0
			2	2	
3	D	2	Total	Mg	0
			2	2	
3	E	2	Total	Mg	0
			2	2	
3	F	2	Total	Mg	0
			2	2	

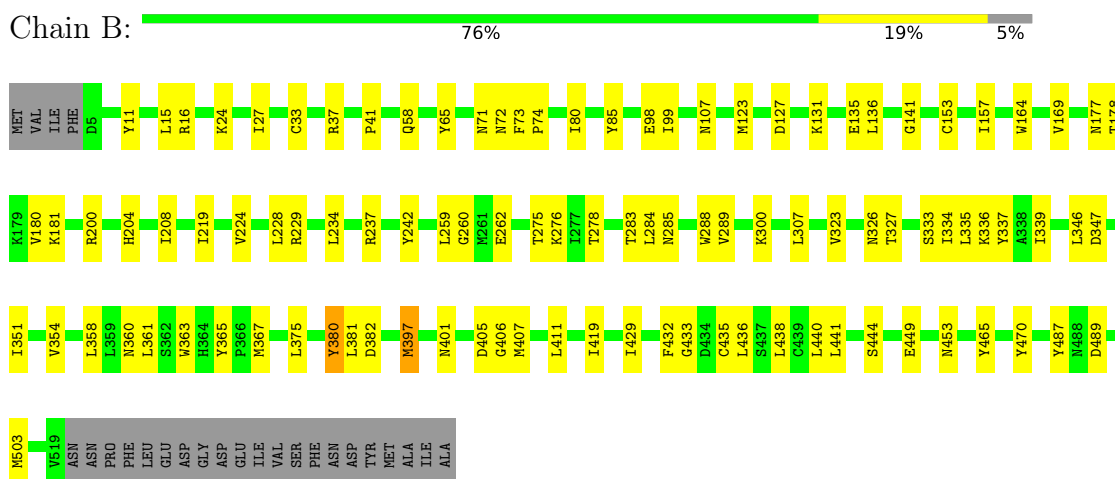
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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. 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. 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.

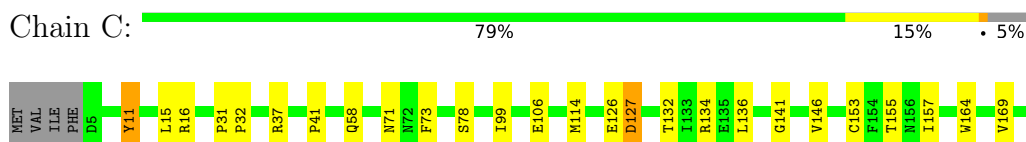
- Molecule 1: Reverse transcriptase domain-containing protein

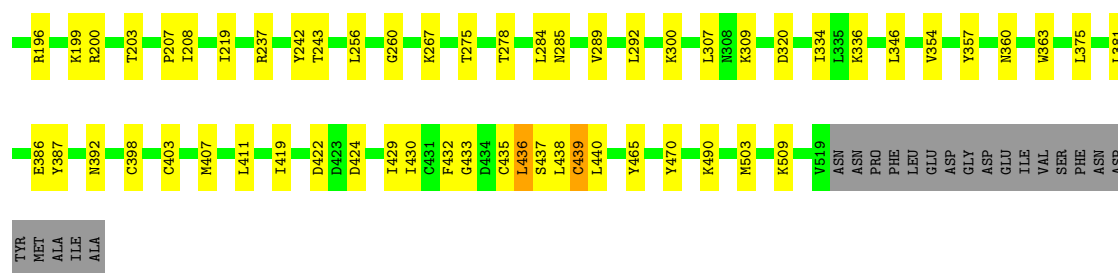


- Molecule 1: Reverse transcriptase domain-containing protein



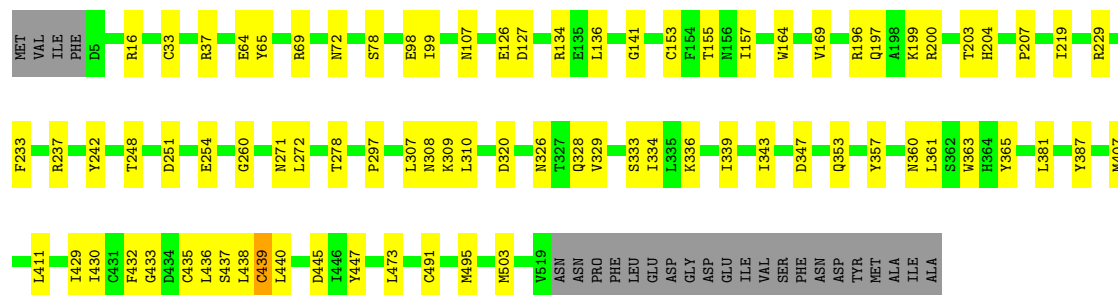
- Molecule 1: Reverse transcriptase domain-containing protein





- Molecule 1: Reverse transcriptase domain-containing protein

Chain D: 80% 15% 5%



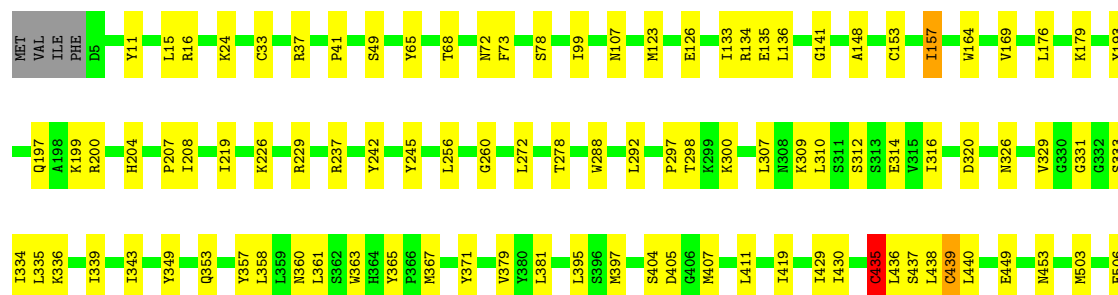
- Molecule 1: Reverse transcriptase domain-containing protein

Chain E: 79% 15% 5%



- Molecule 1: Reverse transcriptase domain-containing protein

Chain F: 77% 18% 5%



V519
ASN
ASN
PRO
PHE
LEU
GLU
ASP
GLY
ASP
GLU
ILE
VAL
SER
PHE
ASN
ASP
TYR
MET
ALA
ILE
ALA

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51326	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DGT, 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	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.12	0/4322	0.37	2/5851 (0.0%)
1	B	0.12	0/4322	0.28	0/5851
1	C	0.14	0/4322	0.33	1/5851 (0.0%)
1	D	0.12	0/4322	0.31	1/5851 (0.0%)
1	E	0.11	0/4322	0.35	2/5851 (0.0%)
1	F	0.12	0/4322	0.37	2/5851 (0.0%)
All	All	0.12	0/25932	0.34	8/35106 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	E	0	1
1	F	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	439	CYS	CA-CB-SG	10.16	137.78	114.40
1	E	439	CYS	CA-CB-SG	9.92	137.21	114.40
1	A	439	CYS	CA-CB-SG	9.66	136.62	114.40
1	C	439	CYS	CA-CB-SG	8.84	134.73	114.40
1	A	435	CYS	CA-CB-SG	7.89	132.56	114.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	435	CYS	Peptide
1	E	435	CYS	Peptide
1	F	435	CYS	Peptide

## 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	4221	0	4102	75	0
1	B	4221	0	4104	67	0
1	C	4221	0	4102	57	0
1	D	4221	0	4102	54	0
1	E	4221	0	4104	62	0
1	F	4221	0	4102	68	0
2	A	31	0	12	2	0
2	B	31	0	12	1	0
2	C	31	0	12	2	0
2	D	31	0	12	2	0
2	E	31	0	12	2	0
2	F	31	0	12	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
All	All	25524	0	24688	351	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 7.

The worst 5 of 351 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:C:275:THR:HG22	1:F:72:ASN:HD22	1.49	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:ILE:HA	1:A:438:LEU:HD21	1.69	0.74
1:B:435:CYS:O	1:B:438:LEU:N	2.19	0.74
1:E:326:ASN:HA	1:E:334:ILE:HD12	1.71	0.73
1:A:398:CYS:HB3	1:A:403:CYS:H	1.53	0.73

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 PDB entries followed by that with respect to all EM entries.

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	513/540 (95%)	501 (98%)	11 (2%)	1 (0%)	43	72
1	B	513/540 (95%)	507 (99%)	6 (1%)	0	100	100
1	C	513/540 (95%)	502 (98%)	11 (2%)	0	100	100
1	D	513/540 (95%)	498 (97%)	15 (3%)	0	100	100
1	E	513/540 (95%)	498 (97%)	15 (3%)	0	100	100
1	F	513/540 (95%)	499 (97%)	14 (3%)	0	100	100
All	All	3078/3240 (95%)	3005 (98%)	72 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	239	ILE

### 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 PDB entries followed by that with respect to all EM entries.

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	472/494 (96%)	467 (99%)	5 (1%)	65	87
1	B	472/494 (96%)	464 (98%)	8 (2%)	53	83
1	C	472/494 (96%)	464 (98%)	8 (2%)	53	83
1	D	472/494 (96%)	468 (99%)	4 (1%)	73	90
1	E	472/494 (96%)	468 (99%)	4 (1%)	73	90
1	F	472/494 (96%)	460 (98%)	12 (2%)	42	76
All	All	2832/2964 (96%)	2791 (99%)	41 (1%)	57	85

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	234	LEU
1	F	314	GLU
1	F	11	TYR
1	F	226	LYS
1	F	367	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	95	ASN
1	F	328	GLN
1	D	507	ASN
1	F	257	HIS
1	D	364	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

Of 18 ligands modelled in this entry, 12 are monoatomic - leaving 6 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	$\# Z  > 2$
2	DGT	B	601	3	29,33,33	0.51	0	44,52,52	0.56	0
2	DGT	F	601	3	29,33,33	0.51	0	44,52,52	0.55	0
2	DGT	D	601	3	29,33,33	0.50	0	44,52,52	0.55	0
2	DGT	A	601	3	29,33,33	0.50	0	44,52,52	0.55	0
2	DGT	E	601	3	29,33,33	0.50	0	44,52,52	0.56	0
2	DGT	C	601	3	29,33,33	0.50	0	44,52,52	0.55	0

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	DGT	B	601	3	-	3/22/34/34	0/3/3/3
2	DGT	F	601	3	-	1/22/34/34	0/3/3/3
2	DGT	D	601	3	-	5/22/34/34	0/3/3/3
2	DGT	A	601	3	-	1/22/34/34	0/3/3/3
2	DGT	E	601	3	-	4/22/34/34	0/3/3/3
2	DGT	C	601	3	-	6/22/34/34	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

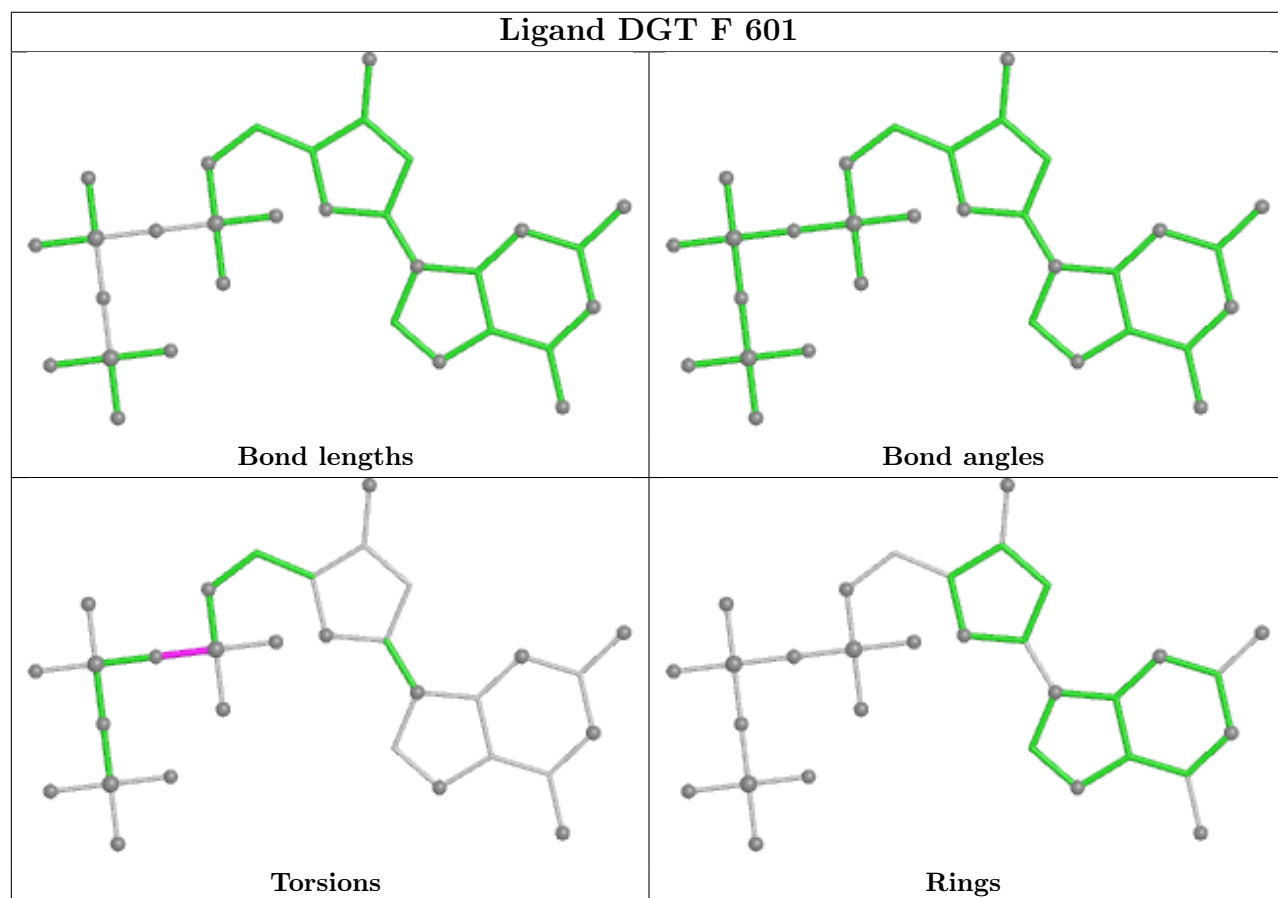
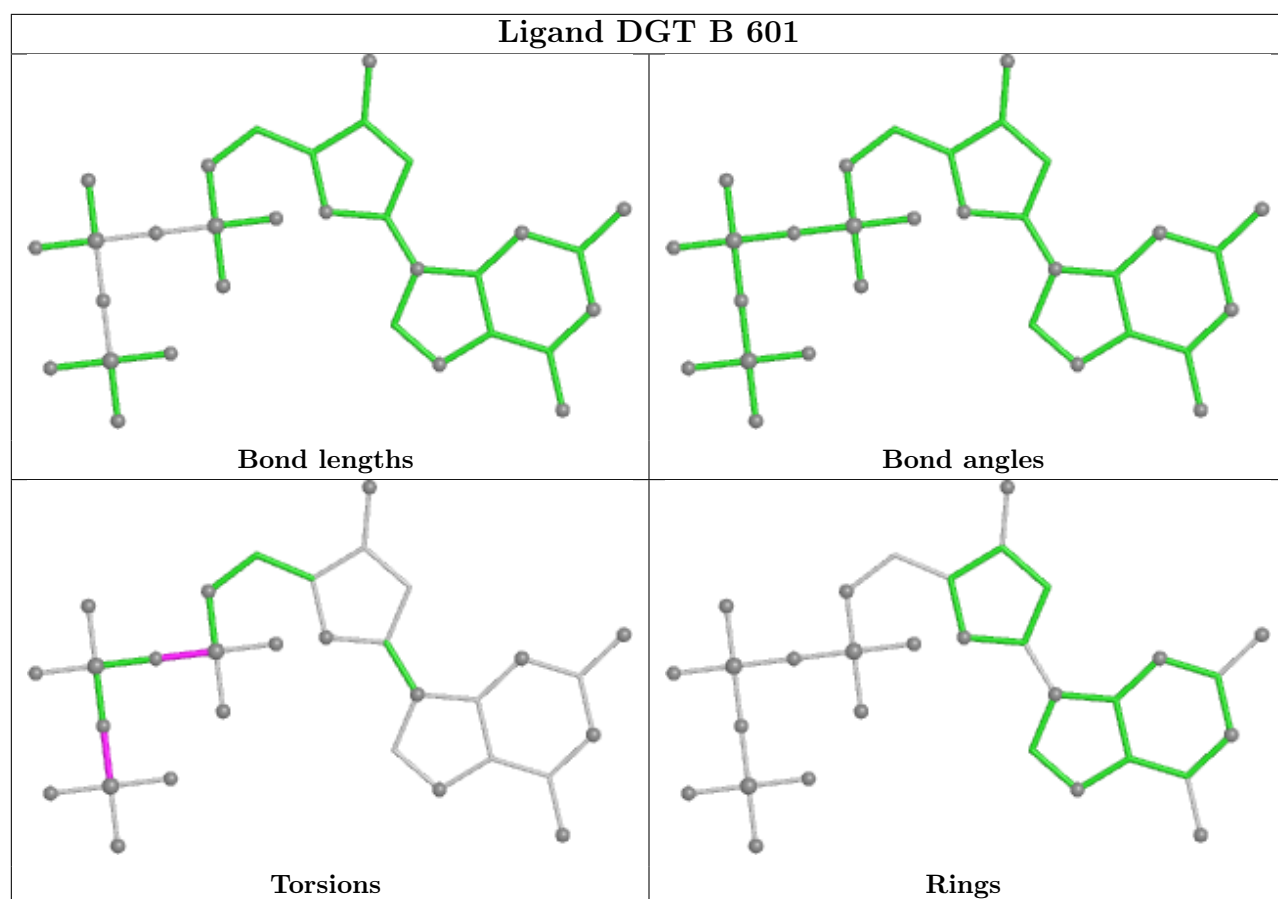
Mol	Chain	Res	Type	Atoms
2	A	601	DGT	PB-O3A-PA-O5'
2	B	601	DGT	PB-O3B-PG-O1G
2	B	601	DGT	PB-O3A-PA-O5'
2	C	601	DGT	PB-O3B-PG-O2G
2	C	601	DGT	O4'-C4'-C5'-O5'

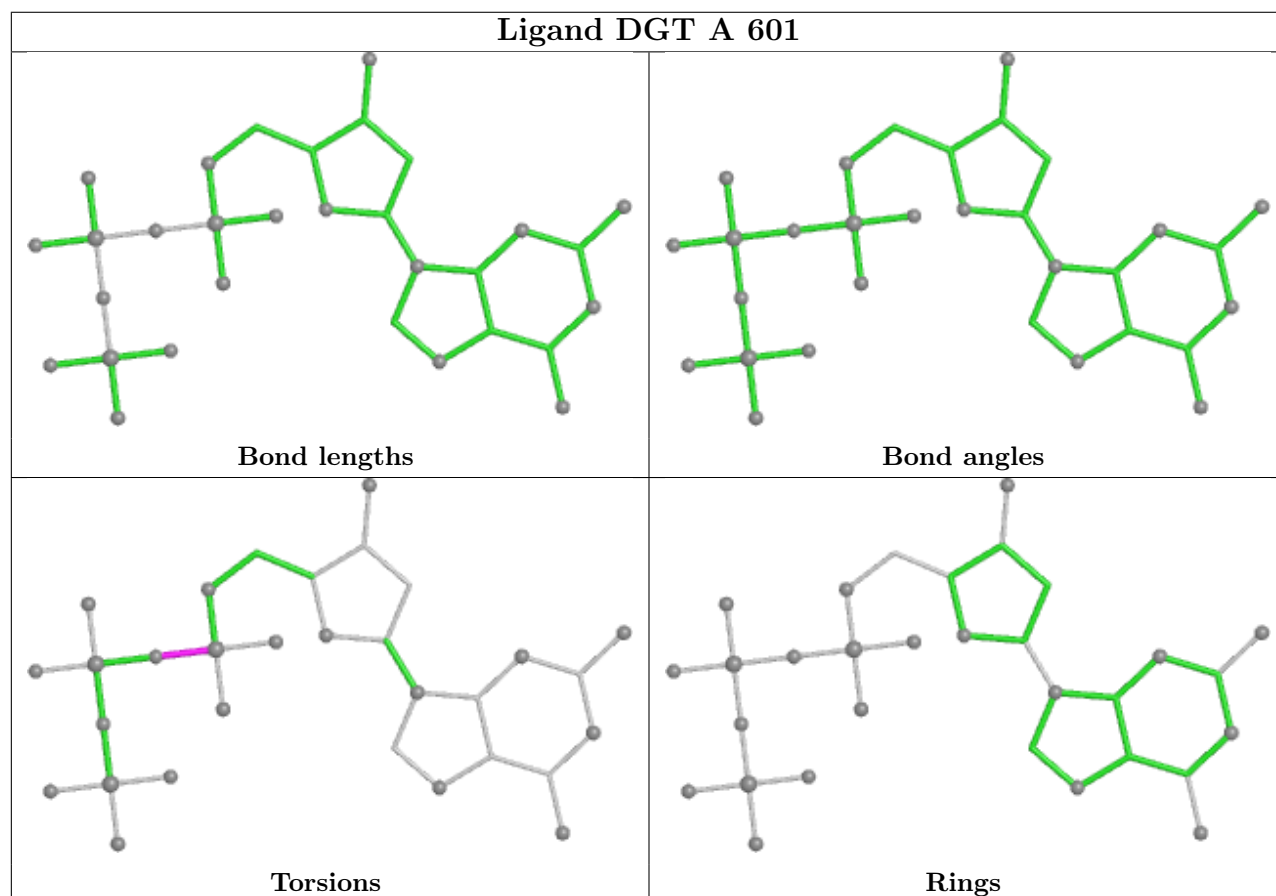
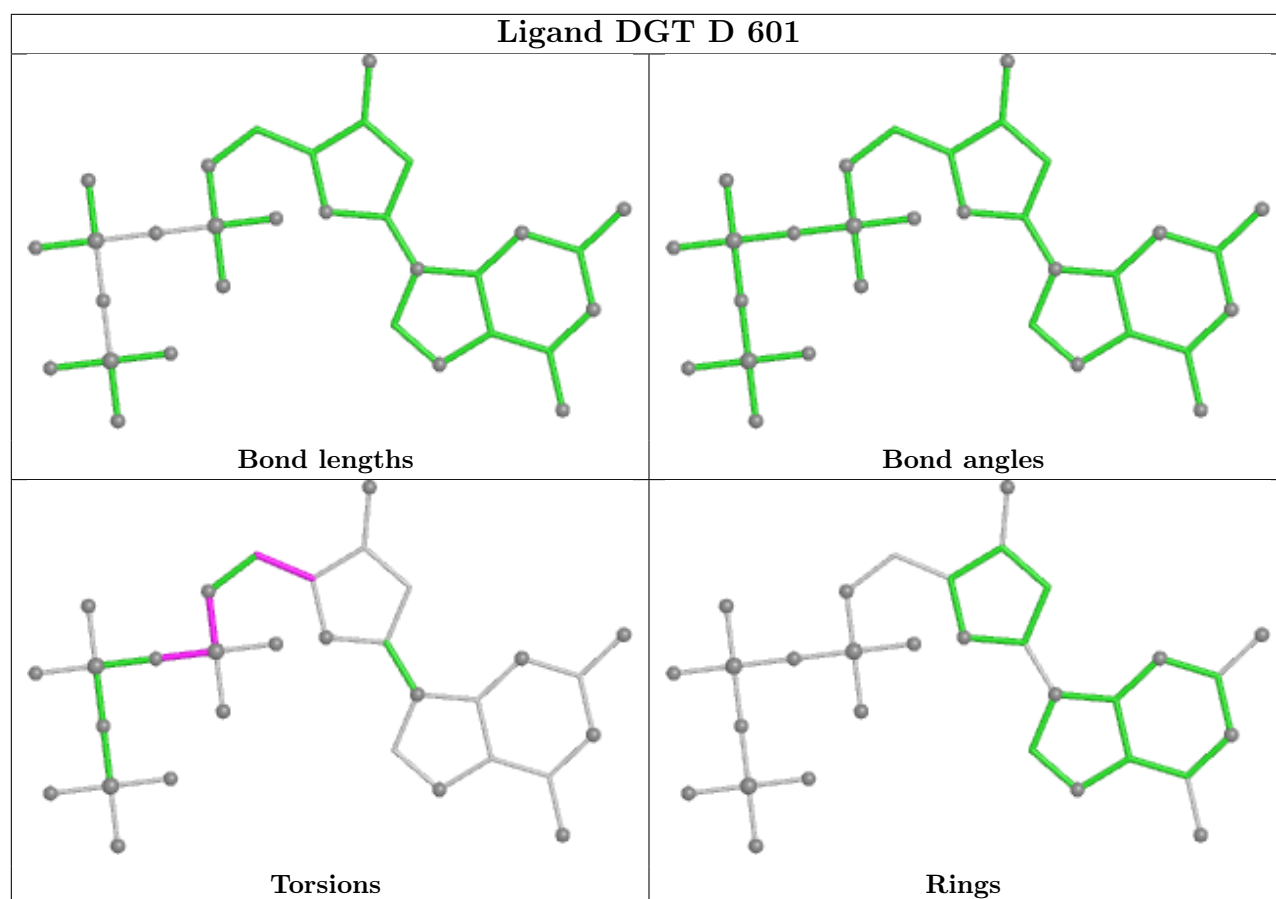
There are no ring outliers.

6 monomers are involved in 10 short contacts:

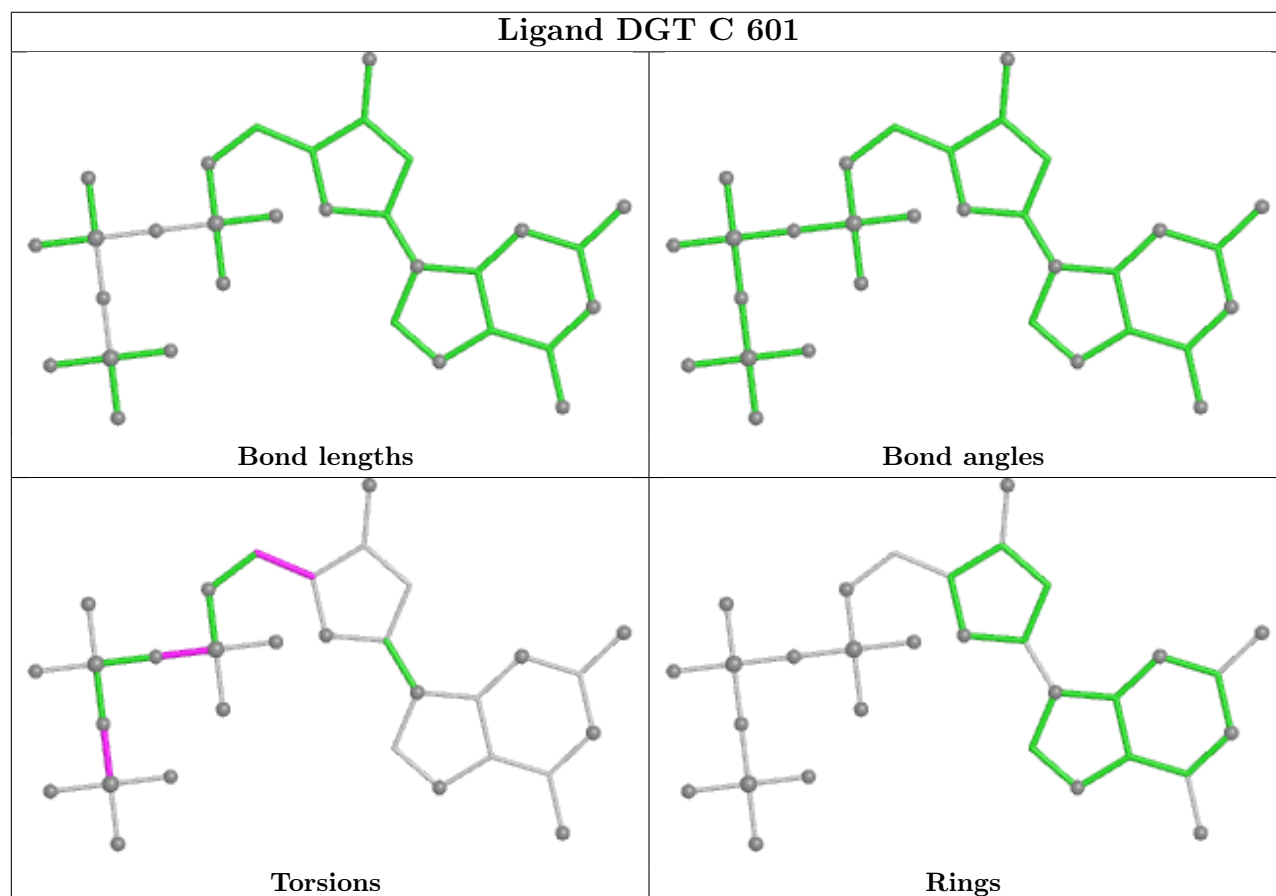
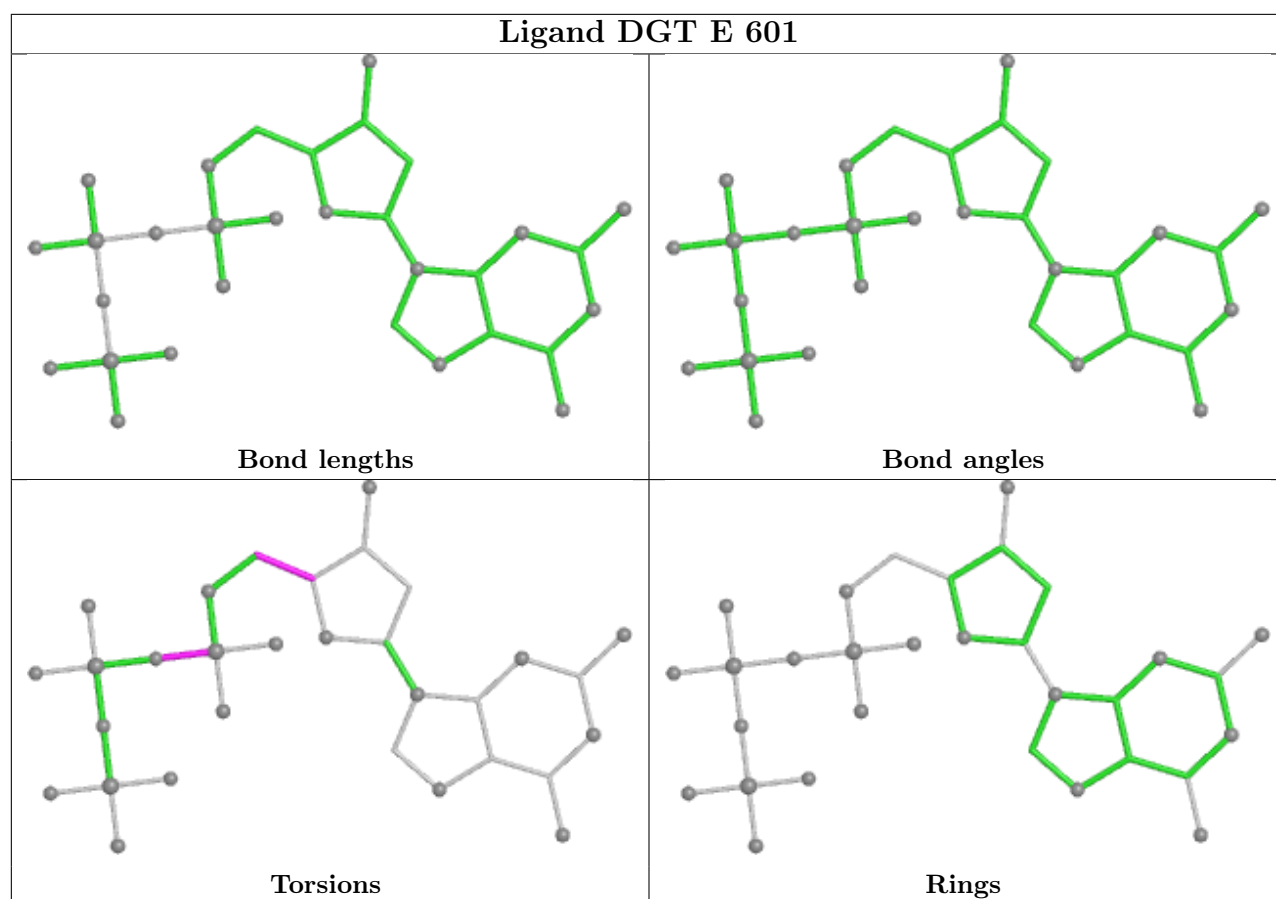
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	DGT	1	0
2	F	601	DGT	1	0
2	D	601	DGT	2	0
2	A	601	DGT	2	0
2	E	601	DGT	2	0
2	C	601	DGT	2	0

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 than 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.