



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 05:43 AM UTC

PDB ID : 7LU5 / pdb\_00007lu5  
Title : SAMHD1(113-626) H206R D207N R366H  
Authors : Temple, J.T.; Bowen, N.E.  
Deposited on : 2021-02-20  
Resolution : 3.57 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

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

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:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

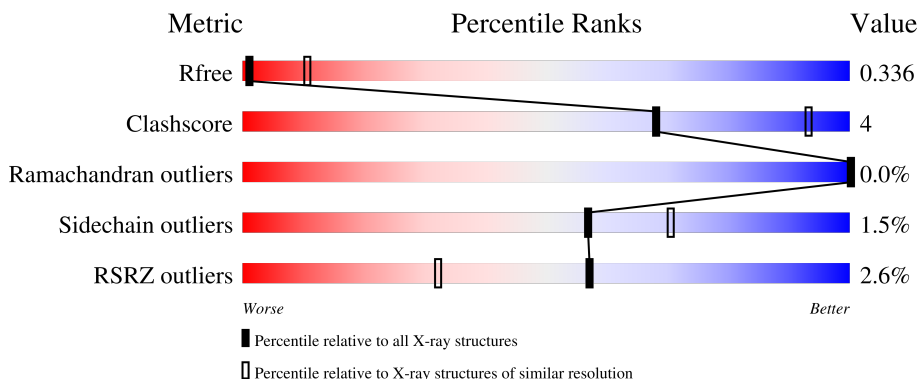
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.57 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))
$R_{free}$	180053	1521 (3.66-3.50)
Clashscore	190562	1595 (3.66-3.50)
Ramachandran outliers	187476	1551 (3.66-3.50)
Sidechain outliers	187428	1551 (3.66-3.50)
RSRZ outliers	180081	1520 (3.66-3.50)

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 of the lower 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  $\leq 5\%$ . 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	535	 3% 81% 9% 10%
1	B	535	 4% 81% 9% 10%
1	C	535	 3% 81% 8% 10%
1	D	535	 2% 83% 7% 10%
1	E	535	 2% 81% 9% 10%

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Mol	Chain	Length	Quality of chain
1	F	535	<p>2% 81% 8% • 10%</p>
1	G	535	<p>3% 81% 8% • 10%</p>
1	H	535	<p>2% 82% 7% • 10%</p>
1	I	535	<p>3% 81% 8% • 10%</p>
1	J	535	<p>2% 80% 9% • 10%</p>
1	K	535	<p>1% 81% 8% • 10%</p>
1	L	535	<p>1% 81% 8% 10%</p>
1	M	535	<p>1% 81% 8% 10%</p>
1	N	535	<p>1% 81% 8% • 10%</p>
1	O	535	<p>2% 81% 9% • 10%</p>
1	P	535	<p>3% 82% 7% • 10%</p>

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 63936 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 Deoxynucleoside triphosphate triphosphohydrolase SAMHD1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	481	3932	2517	684	711	20	0	0	0
1	B	481	3932	2517	684	711	20	0	0	0
1	C	481	3932	2517	684	711	20	0	0	0
1	D	481	3940	2521	686	713	20	0	1	0
1	E	481	3932	2517	684	711	20	0	0	0
1	F	481	3932	2517	684	711	20	0	0	0
1	G	481	3932	2517	684	711	20	0	0	0
1	H	481	3940	2521	686	713	20	0	1	0
1	I	481	3932	2517	684	711	20	0	0	0
1	J	481	3932	2517	684	711	20	0	0	0
1	K	481	3932	2517	684	711	20	0	0	0
1	L	481	3940	2521	686	713	20	0	1	0
1	M	481	3932	2517	684	711	20	0	0	0
1	N	481	3932	2517	684	711	20	0	0	0
1	O	481	3932	2517	684	711	20	0	0	0
1	P	481	3940	2521	686	713	20	0	1	0

There are 384 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	92	MET	-	initiating methionine	UNP Q9Y3Z3
A	93	GLY	-	expression tag	UNP Q9Y3Z3
A	94	SER	-	expression tag	UNP Q9Y3Z3
A	95	SER	-	expression tag	UNP Q9Y3Z3
A	96	HIS	-	expression tag	UNP Q9Y3Z3
A	97	HIS	-	expression tag	UNP Q9Y3Z3
A	98	HIS	-	expression tag	UNP Q9Y3Z3
A	99	HIS	-	expression tag	UNP Q9Y3Z3
A	100	HIS	-	expression tag	UNP Q9Y3Z3
A	101	HIS	-	expression tag	UNP Q9Y3Z3
A	102	SER	-	expression tag	UNP Q9Y3Z3
A	103	SER	-	expression tag	UNP Q9Y3Z3
A	104	GLY	-	expression tag	UNP Q9Y3Z3
A	105	LEU	-	expression tag	UNP Q9Y3Z3
A	106	VAL	-	expression tag	UNP Q9Y3Z3
A	107	PRO	-	expression tag	UNP Q9Y3Z3
A	108	ARG	-	expression tag	UNP Q9Y3Z3
A	109	GLY	-	expression tag	UNP Q9Y3Z3
A	110	SER	-	expression tag	UNP Q9Y3Z3
A	111	HIS	-	expression tag	UNP Q9Y3Z3
A	112	MET	-	expression tag	UNP Q9Y3Z3
A	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
A	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
A	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
B	92	MET	-	initiating methionine	UNP Q9Y3Z3
B	93	GLY	-	expression tag	UNP Q9Y3Z3
B	94	SER	-	expression tag	UNP Q9Y3Z3
B	95	SER	-	expression tag	UNP Q9Y3Z3
B	96	HIS	-	expression tag	UNP Q9Y3Z3
B	97	HIS	-	expression tag	UNP Q9Y3Z3
B	98	HIS	-	expression tag	UNP Q9Y3Z3
B	99	HIS	-	expression tag	UNP Q9Y3Z3
B	100	HIS	-	expression tag	UNP Q9Y3Z3
B	101	HIS	-	expression tag	UNP Q9Y3Z3
B	102	SER	-	expression tag	UNP Q9Y3Z3
B	103	SER	-	expression tag	UNP Q9Y3Z3
B	104	GLY	-	expression tag	UNP Q9Y3Z3
B	105	LEU	-	expression tag	UNP Q9Y3Z3
B	106	VAL	-	expression tag	UNP Q9Y3Z3
B	107	PRO	-	expression tag	UNP Q9Y3Z3
B	108	ARG	-	expression tag	UNP Q9Y3Z3
B	109	GLY	-	expression tag	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	110	SER	-	expression tag	UNP Q9Y3Z3
B	111	HIS	-	expression tag	UNP Q9Y3Z3
B	112	MET	-	expression tag	UNP Q9Y3Z3
B	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
B	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
B	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
C	92	MET	-	initiating methionine	UNP Q9Y3Z3
C	93	GLY	-	expression tag	UNP Q9Y3Z3
C	94	SER	-	expression tag	UNP Q9Y3Z3
C	95	SER	-	expression tag	UNP Q9Y3Z3
C	96	HIS	-	expression tag	UNP Q9Y3Z3
C	97	HIS	-	expression tag	UNP Q9Y3Z3
C	98	HIS	-	expression tag	UNP Q9Y3Z3
C	99	HIS	-	expression tag	UNP Q9Y3Z3
C	100	HIS	-	expression tag	UNP Q9Y3Z3
C	101	HIS	-	expression tag	UNP Q9Y3Z3
C	102	SER	-	expression tag	UNP Q9Y3Z3
C	103	SER	-	expression tag	UNP Q9Y3Z3
C	104	GLY	-	expression tag	UNP Q9Y3Z3
C	105	LEU	-	expression tag	UNP Q9Y3Z3
C	106	VAL	-	expression tag	UNP Q9Y3Z3
C	107	PRO	-	expression tag	UNP Q9Y3Z3
C	108	ARG	-	expression tag	UNP Q9Y3Z3
C	109	GLY	-	expression tag	UNP Q9Y3Z3
C	110	SER	-	expression tag	UNP Q9Y3Z3
C	111	HIS	-	expression tag	UNP Q9Y3Z3
C	112	MET	-	expression tag	UNP Q9Y3Z3
C	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
C	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
C	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
D	92	MET	-	initiating methionine	UNP Q9Y3Z3
D	93	GLY	-	expression tag	UNP Q9Y3Z3
D	94	SER	-	expression tag	UNP Q9Y3Z3
D	95	SER	-	expression tag	UNP Q9Y3Z3
D	96	HIS	-	expression tag	UNP Q9Y3Z3
D	97	HIS	-	expression tag	UNP Q9Y3Z3
D	98	HIS	-	expression tag	UNP Q9Y3Z3
D	99	HIS	-	expression tag	UNP Q9Y3Z3
D	100	HIS	-	expression tag	UNP Q9Y3Z3
D	101	HIS	-	expression tag	UNP Q9Y3Z3
D	102	SER	-	expression tag	UNP Q9Y3Z3
D	103	SER	-	expression tag	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
D	104	GLY	-	expression tag	UNP Q9Y3Z3
D	105	LEU	-	expression tag	UNP Q9Y3Z3
D	106	VAL	-	expression tag	UNP Q9Y3Z3
D	107	PRO	-	expression tag	UNP Q9Y3Z3
D	108	ARG	-	expression tag	UNP Q9Y3Z3
D	109	GLY	-	expression tag	UNP Q9Y3Z3
D	110	SER	-	expression tag	UNP Q9Y3Z3
D	111	HIS	-	expression tag	UNP Q9Y3Z3
D	112	MET	-	expression tag	UNP Q9Y3Z3
D	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
D	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
D	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
E	92	MET	-	initiating methionine	UNP Q9Y3Z3
E	93	GLY	-	expression tag	UNP Q9Y3Z3
E	94	SER	-	expression tag	UNP Q9Y3Z3
E	95	SER	-	expression tag	UNP Q9Y3Z3
E	96	HIS	-	expression tag	UNP Q9Y3Z3
E	97	HIS	-	expression tag	UNP Q9Y3Z3
E	98	HIS	-	expression tag	UNP Q9Y3Z3
E	99	HIS	-	expression tag	UNP Q9Y3Z3
E	100	HIS	-	expression tag	UNP Q9Y3Z3
E	101	HIS	-	expression tag	UNP Q9Y3Z3
E	102	SER	-	expression tag	UNP Q9Y3Z3
E	103	SER	-	expression tag	UNP Q9Y3Z3
E	104	GLY	-	expression tag	UNP Q9Y3Z3
E	105	LEU	-	expression tag	UNP Q9Y3Z3
E	106	VAL	-	expression tag	UNP Q9Y3Z3
E	107	PRO	-	expression tag	UNP Q9Y3Z3
E	108	ARG	-	expression tag	UNP Q9Y3Z3
E	109	GLY	-	expression tag	UNP Q9Y3Z3
E	110	SER	-	expression tag	UNP Q9Y3Z3
E	111	HIS	-	expression tag	UNP Q9Y3Z3
E	112	MET	-	expression tag	UNP Q9Y3Z3
E	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
E	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
E	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
F	92	MET	-	initiating methionine	UNP Q9Y3Z3
F	93	GLY	-	expression tag	UNP Q9Y3Z3
F	94	SER	-	expression tag	UNP Q9Y3Z3
F	95	SER	-	expression tag	UNP Q9Y3Z3
F	96	HIS	-	expression tag	UNP Q9Y3Z3
F	97	HIS	-	expression tag	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
F	98	HIS	-	expression tag	UNP Q9Y3Z3
F	99	HIS	-	expression tag	UNP Q9Y3Z3
F	100	HIS	-	expression tag	UNP Q9Y3Z3
F	101	HIS	-	expression tag	UNP Q9Y3Z3
F	102	SER	-	expression tag	UNP Q9Y3Z3
F	103	SER	-	expression tag	UNP Q9Y3Z3
F	104	GLY	-	expression tag	UNP Q9Y3Z3
F	105	LEU	-	expression tag	UNP Q9Y3Z3
F	106	VAL	-	expression tag	UNP Q9Y3Z3
F	107	PRO	-	expression tag	UNP Q9Y3Z3
F	108	ARG	-	expression tag	UNP Q9Y3Z3
F	109	GLY	-	expression tag	UNP Q9Y3Z3
F	110	SER	-	expression tag	UNP Q9Y3Z3
F	111	HIS	-	expression tag	UNP Q9Y3Z3
F	112	MET	-	expression tag	UNP Q9Y3Z3
F	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
F	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
F	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
G	92	MET	-	initiating methionine	UNP Q9Y3Z3
G	93	GLY	-	expression tag	UNP Q9Y3Z3
G	94	SER	-	expression tag	UNP Q9Y3Z3
G	95	SER	-	expression tag	UNP Q9Y3Z3
G	96	HIS	-	expression tag	UNP Q9Y3Z3
G	97	HIS	-	expression tag	UNP Q9Y3Z3
G	98	HIS	-	expression tag	UNP Q9Y3Z3
G	99	HIS	-	expression tag	UNP Q9Y3Z3
G	100	HIS	-	expression tag	UNP Q9Y3Z3
G	101	HIS	-	expression tag	UNP Q9Y3Z3
G	102	SER	-	expression tag	UNP Q9Y3Z3
G	103	SER	-	expression tag	UNP Q9Y3Z3
G	104	GLY	-	expression tag	UNP Q9Y3Z3
G	105	LEU	-	expression tag	UNP Q9Y3Z3
G	106	VAL	-	expression tag	UNP Q9Y3Z3
G	107	PRO	-	expression tag	UNP Q9Y3Z3
G	108	ARG	-	expression tag	UNP Q9Y3Z3
G	109	GLY	-	expression tag	UNP Q9Y3Z3
G	110	SER	-	expression tag	UNP Q9Y3Z3
G	111	HIS	-	expression tag	UNP Q9Y3Z3
G	112	MET	-	expression tag	UNP Q9Y3Z3
G	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
G	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
G	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
H	92	MET	-	initiating methionine	UNP Q9Y3Z3
H	93	GLY	-	expression tag	UNP Q9Y3Z3
H	94	SER	-	expression tag	UNP Q9Y3Z3
H	95	SER	-	expression tag	UNP Q9Y3Z3
H	96	HIS	-	expression tag	UNP Q9Y3Z3
H	97	HIS	-	expression tag	UNP Q9Y3Z3
H	98	HIS	-	expression tag	UNP Q9Y3Z3
H	99	HIS	-	expression tag	UNP Q9Y3Z3
H	100	HIS	-	expression tag	UNP Q9Y3Z3
H	101	HIS	-	expression tag	UNP Q9Y3Z3
H	102	SER	-	expression tag	UNP Q9Y3Z3
H	103	SER	-	expression tag	UNP Q9Y3Z3
H	104	GLY	-	expression tag	UNP Q9Y3Z3
H	105	LEU	-	expression tag	UNP Q9Y3Z3
H	106	VAL	-	expression tag	UNP Q9Y3Z3
H	107	PRO	-	expression tag	UNP Q9Y3Z3
H	108	ARG	-	expression tag	UNP Q9Y3Z3
H	109	GLY	-	expression tag	UNP Q9Y3Z3
H	110	SER	-	expression tag	UNP Q9Y3Z3
H	111	HIS	-	expression tag	UNP Q9Y3Z3
H	112	MET	-	expression tag	UNP Q9Y3Z3
H	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
H	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
H	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
I	92	MET	-	initiating methionine	UNP Q9Y3Z3
I	93	GLY	-	expression tag	UNP Q9Y3Z3
I	94	SER	-	expression tag	UNP Q9Y3Z3
I	95	SER	-	expression tag	UNP Q9Y3Z3
I	96	HIS	-	expression tag	UNP Q9Y3Z3
I	97	HIS	-	expression tag	UNP Q9Y3Z3
I	98	HIS	-	expression tag	UNP Q9Y3Z3
I	99	HIS	-	expression tag	UNP Q9Y3Z3
I	100	HIS	-	expression tag	UNP Q9Y3Z3
I	101	HIS	-	expression tag	UNP Q9Y3Z3
I	102	SER	-	expression tag	UNP Q9Y3Z3
I	103	SER	-	expression tag	UNP Q9Y3Z3
I	104	GLY	-	expression tag	UNP Q9Y3Z3
I	105	LEU	-	expression tag	UNP Q9Y3Z3
I	106	VAL	-	expression tag	UNP Q9Y3Z3
I	107	PRO	-	expression tag	UNP Q9Y3Z3
I	108	ARG	-	expression tag	UNP Q9Y3Z3
I	109	GLY	-	expression tag	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
I	110	SER	-	expression tag	UNP Q9Y3Z3
I	111	HIS	-	expression tag	UNP Q9Y3Z3
I	112	MET	-	expression tag	UNP Q9Y3Z3
I	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
I	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
I	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
J	92	MET	-	initiating methionine	UNP Q9Y3Z3
J	93	GLY	-	expression tag	UNP Q9Y3Z3
J	94	SER	-	expression tag	UNP Q9Y3Z3
J	95	SER	-	expression tag	UNP Q9Y3Z3
J	96	HIS	-	expression tag	UNP Q9Y3Z3
J	97	HIS	-	expression tag	UNP Q9Y3Z3
J	98	HIS	-	expression tag	UNP Q9Y3Z3
J	99	HIS	-	expression tag	UNP Q9Y3Z3
J	100	HIS	-	expression tag	UNP Q9Y3Z3
J	101	HIS	-	expression tag	UNP Q9Y3Z3
J	102	SER	-	expression tag	UNP Q9Y3Z3
J	103	SER	-	expression tag	UNP Q9Y3Z3
J	104	GLY	-	expression tag	UNP Q9Y3Z3
J	105	LEU	-	expression tag	UNP Q9Y3Z3
J	106	VAL	-	expression tag	UNP Q9Y3Z3
J	107	PRO	-	expression tag	UNP Q9Y3Z3
J	108	ARG	-	expression tag	UNP Q9Y3Z3
J	109	GLY	-	expression tag	UNP Q9Y3Z3
J	110	SER	-	expression tag	UNP Q9Y3Z3
J	111	HIS	-	expression tag	UNP Q9Y3Z3
J	112	MET	-	expression tag	UNP Q9Y3Z3
J	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
J	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
J	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
K	92	MET	-	initiating methionine	UNP Q9Y3Z3
K	93	GLY	-	expression tag	UNP Q9Y3Z3
K	94	SER	-	expression tag	UNP Q9Y3Z3
K	95	SER	-	expression tag	UNP Q9Y3Z3
K	96	HIS	-	expression tag	UNP Q9Y3Z3
K	97	HIS	-	expression tag	UNP Q9Y3Z3
K	98	HIS	-	expression tag	UNP Q9Y3Z3
K	99	HIS	-	expression tag	UNP Q9Y3Z3
K	100	HIS	-	expression tag	UNP Q9Y3Z3
K	101	HIS	-	expression tag	UNP Q9Y3Z3
K	102	SER	-	expression tag	UNP Q9Y3Z3
K	103	SER	-	expression tag	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
K	104	GLY	-	expression tag	UNP Q9Y3Z3
K	105	LEU	-	expression tag	UNP Q9Y3Z3
K	106	VAL	-	expression tag	UNP Q9Y3Z3
K	107	PRO	-	expression tag	UNP Q9Y3Z3
K	108	ARG	-	expression tag	UNP Q9Y3Z3
K	109	GLY	-	expression tag	UNP Q9Y3Z3
K	110	SER	-	expression tag	UNP Q9Y3Z3
K	111	HIS	-	expression tag	UNP Q9Y3Z3
K	112	MET	-	expression tag	UNP Q9Y3Z3
K	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
K	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
K	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
L	92	MET	-	initiating methionine	UNP Q9Y3Z3
L	93	GLY	-	expression tag	UNP Q9Y3Z3
L	94	SER	-	expression tag	UNP Q9Y3Z3
L	95	SER	-	expression tag	UNP Q9Y3Z3
L	96	HIS	-	expression tag	UNP Q9Y3Z3
L	97	HIS	-	expression tag	UNP Q9Y3Z3
L	98	HIS	-	expression tag	UNP Q9Y3Z3
L	99	HIS	-	expression tag	UNP Q9Y3Z3
L	100	HIS	-	expression tag	UNP Q9Y3Z3
L	101	HIS	-	expression tag	UNP Q9Y3Z3
L	102	SER	-	expression tag	UNP Q9Y3Z3
L	103	SER	-	expression tag	UNP Q9Y3Z3
L	104	GLY	-	expression tag	UNP Q9Y3Z3
L	105	LEU	-	expression tag	UNP Q9Y3Z3
L	106	VAL	-	expression tag	UNP Q9Y3Z3
L	107	PRO	-	expression tag	UNP Q9Y3Z3
L	108	ARG	-	expression tag	UNP Q9Y3Z3
L	109	GLY	-	expression tag	UNP Q9Y3Z3
L	110	SER	-	expression tag	UNP Q9Y3Z3
L	111	HIS	-	expression tag	UNP Q9Y3Z3
L	112	MET	-	expression tag	UNP Q9Y3Z3
L	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
L	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
L	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
M	92	MET	-	initiating methionine	UNP Q9Y3Z3
M	93	GLY	-	expression tag	UNP Q9Y3Z3
M	94	SER	-	expression tag	UNP Q9Y3Z3
M	95	SER	-	expression tag	UNP Q9Y3Z3
M	96	HIS	-	expression tag	UNP Q9Y3Z3
M	97	HIS	-	expression tag	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
M	98	HIS	-	expression tag	UNP Q9Y3Z3
M	99	HIS	-	expression tag	UNP Q9Y3Z3
M	100	HIS	-	expression tag	UNP Q9Y3Z3
M	101	HIS	-	expression tag	UNP Q9Y3Z3
M	102	SER	-	expression tag	UNP Q9Y3Z3
M	103	SER	-	expression tag	UNP Q9Y3Z3
M	104	GLY	-	expression tag	UNP Q9Y3Z3
M	105	LEU	-	expression tag	UNP Q9Y3Z3
M	106	VAL	-	expression tag	UNP Q9Y3Z3
M	107	PRO	-	expression tag	UNP Q9Y3Z3
M	108	ARG	-	expression tag	UNP Q9Y3Z3
M	109	GLY	-	expression tag	UNP Q9Y3Z3
M	110	SER	-	expression tag	UNP Q9Y3Z3
M	111	HIS	-	expression tag	UNP Q9Y3Z3
M	112	MET	-	expression tag	UNP Q9Y3Z3
M	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
M	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
M	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
N	92	MET	-	initiating methionine	UNP Q9Y3Z3
N	93	GLY	-	expression tag	UNP Q9Y3Z3
N	94	SER	-	expression tag	UNP Q9Y3Z3
N	95	SER	-	expression tag	UNP Q9Y3Z3
N	96	HIS	-	expression tag	UNP Q9Y3Z3
N	97	HIS	-	expression tag	UNP Q9Y3Z3
N	98	HIS	-	expression tag	UNP Q9Y3Z3
N	99	HIS	-	expression tag	UNP Q9Y3Z3
N	100	HIS	-	expression tag	UNP Q9Y3Z3
N	101	HIS	-	expression tag	UNP Q9Y3Z3
N	102	SER	-	expression tag	UNP Q9Y3Z3
N	103	SER	-	expression tag	UNP Q9Y3Z3
N	104	GLY	-	expression tag	UNP Q9Y3Z3
N	105	LEU	-	expression tag	UNP Q9Y3Z3
N	106	VAL	-	expression tag	UNP Q9Y3Z3
N	107	PRO	-	expression tag	UNP Q9Y3Z3
N	108	ARG	-	expression tag	UNP Q9Y3Z3
N	109	GLY	-	expression tag	UNP Q9Y3Z3
N	110	SER	-	expression tag	UNP Q9Y3Z3
N	111	HIS	-	expression tag	UNP Q9Y3Z3
N	112	MET	-	expression tag	UNP Q9Y3Z3
N	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
N	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
N	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3

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Chain	Residue	Modelled	Actual	Comment	Reference
O	92	MET	-	initiating methionine	UNP Q9Y3Z3
O	93	GLY	-	expression tag	UNP Q9Y3Z3
O	94	SER	-	expression tag	UNP Q9Y3Z3
O	95	SER	-	expression tag	UNP Q9Y3Z3
O	96	HIS	-	expression tag	UNP Q9Y3Z3
O	97	HIS	-	expression tag	UNP Q9Y3Z3
O	98	HIS	-	expression tag	UNP Q9Y3Z3
O	99	HIS	-	expression tag	UNP Q9Y3Z3
O	100	HIS	-	expression tag	UNP Q9Y3Z3
O	101	HIS	-	expression tag	UNP Q9Y3Z3
O	102	SER	-	expression tag	UNP Q9Y3Z3
O	103	SER	-	expression tag	UNP Q9Y3Z3
O	104	GLY	-	expression tag	UNP Q9Y3Z3
O	105	LEU	-	expression tag	UNP Q9Y3Z3
O	106	VAL	-	expression tag	UNP Q9Y3Z3
O	107	PRO	-	expression tag	UNP Q9Y3Z3
O	108	ARG	-	expression tag	UNP Q9Y3Z3
O	109	GLY	-	expression tag	UNP Q9Y3Z3
O	110	SER	-	expression tag	UNP Q9Y3Z3
O	111	HIS	-	expression tag	UNP Q9Y3Z3
O	112	MET	-	expression tag	UNP Q9Y3Z3
O	206	ARG	HIS	engineered mutation	UNP Q9Y3Z3
O	207	ASN	ASP	engineered mutation	UNP Q9Y3Z3
O	366	HIS	ARG	engineered mutation	UNP Q9Y3Z3
P	92	MET	-	initiating methionine	UNP Q9Y3Z3
P	93	GLY	-	expression tag	UNP Q9Y3Z3
P	94	SER	-	expression tag	UNP Q9Y3Z3
P	95	SER	-	expression tag	UNP Q9Y3Z3
P	96	HIS	-	expression tag	UNP Q9Y3Z3
P	97	HIS	-	expression tag	UNP Q9Y3Z3
P	98	HIS	-	expression tag	UNP Q9Y3Z3
P	99	HIS	-	expression tag	UNP Q9Y3Z3
P	100	HIS	-	expression tag	UNP Q9Y3Z3
P	101	HIS	-	expression tag	UNP Q9Y3Z3
P	102	SER	-	expression tag	UNP Q9Y3Z3
P	103	SER	-	expression tag	UNP Q9Y3Z3
P	104	GLY	-	expression tag	UNP Q9Y3Z3
P	105	LEU	-	expression tag	UNP Q9Y3Z3
P	106	VAL	-	expression tag	UNP Q9Y3Z3
P	107	PRO	-	expression tag	UNP Q9Y3Z3
P	108	ARG	-	expression tag	UNP Q9Y3Z3
P	109	GLY	-	expression tag	UNP Q9Y3Z3

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	G	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	G	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	H	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	I	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	I	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	J	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	J	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	J	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	K	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	K	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	L	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	M	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	M	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	N	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	O	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	O	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

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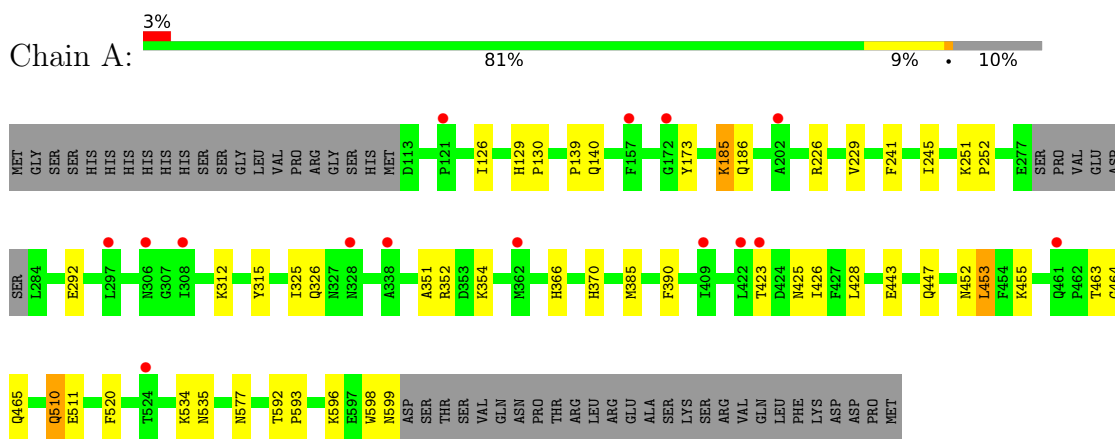
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>					<b>ZeroOcc</b>	<b>AltConf</b>
2	O	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	P	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	P	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

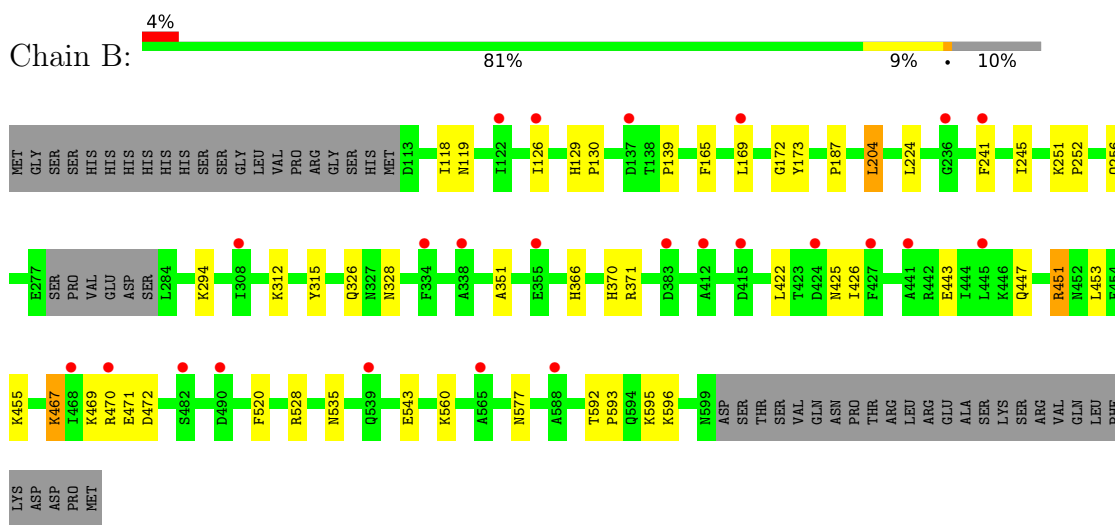
### 3 Residue-property plots [i](#)

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 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.

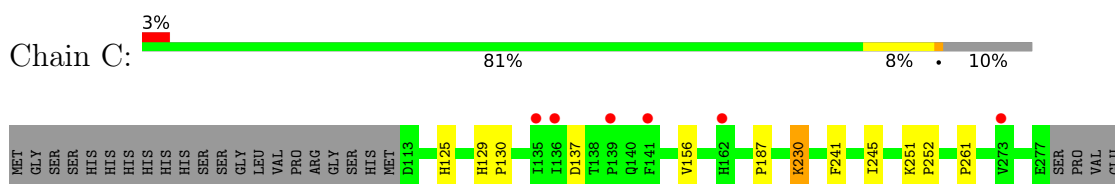
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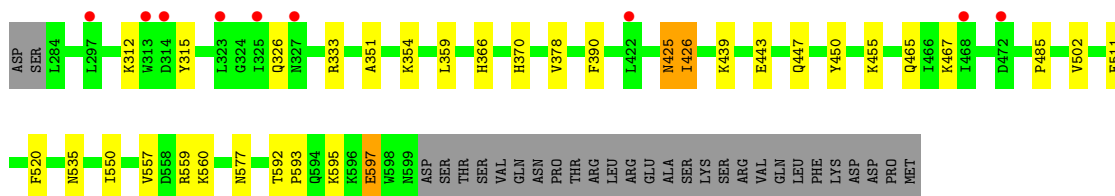


- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

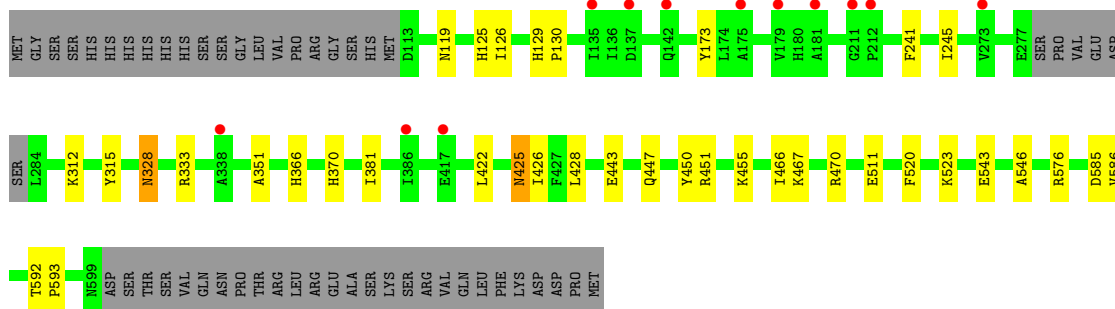
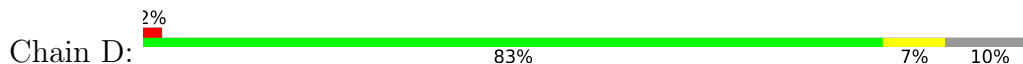


- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

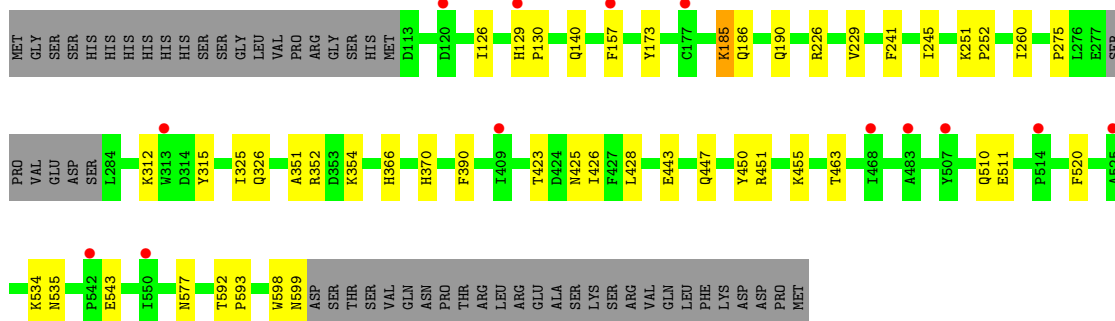
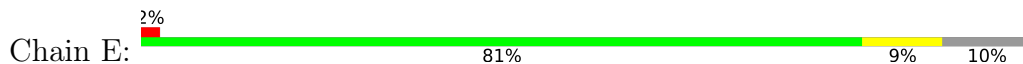




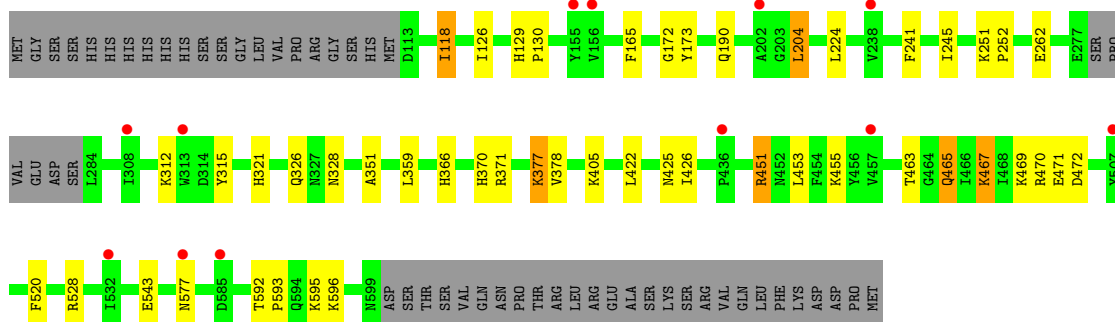
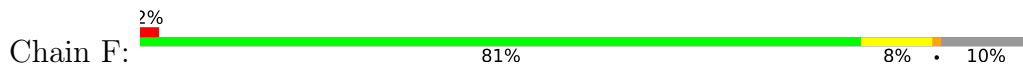
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



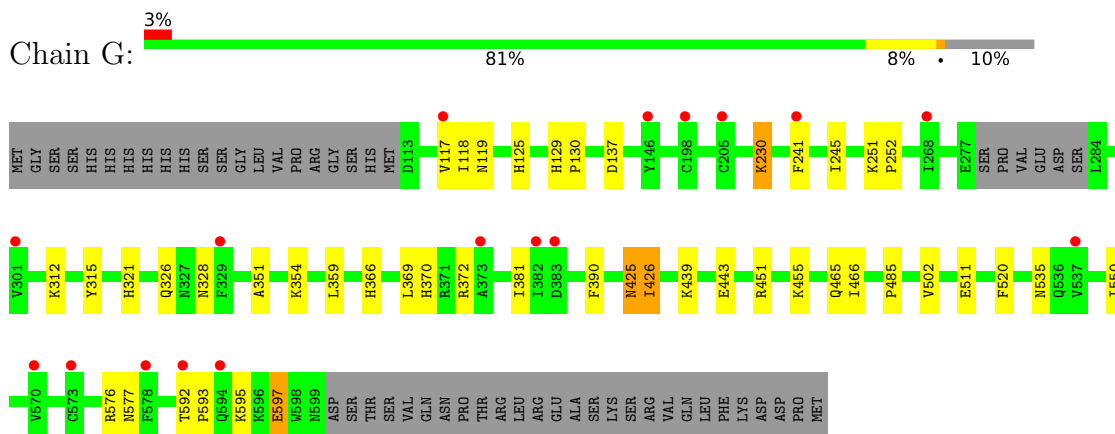
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



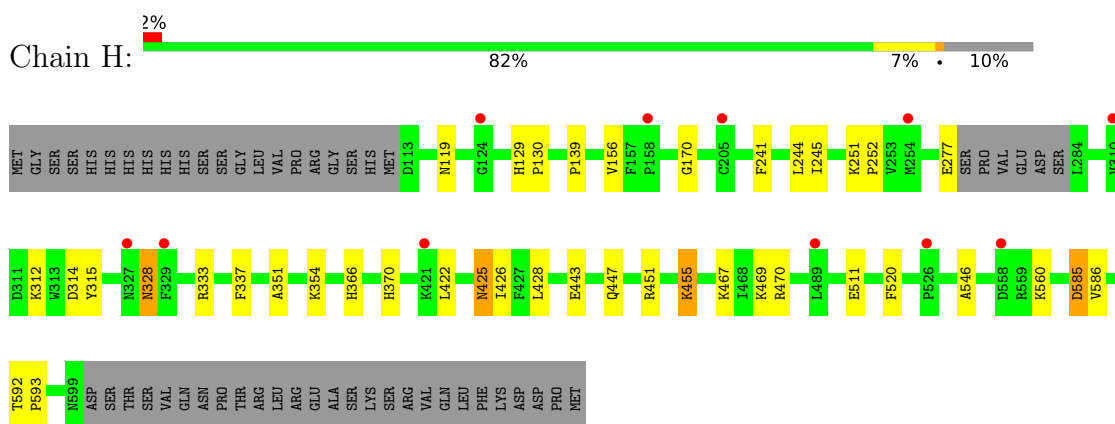
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



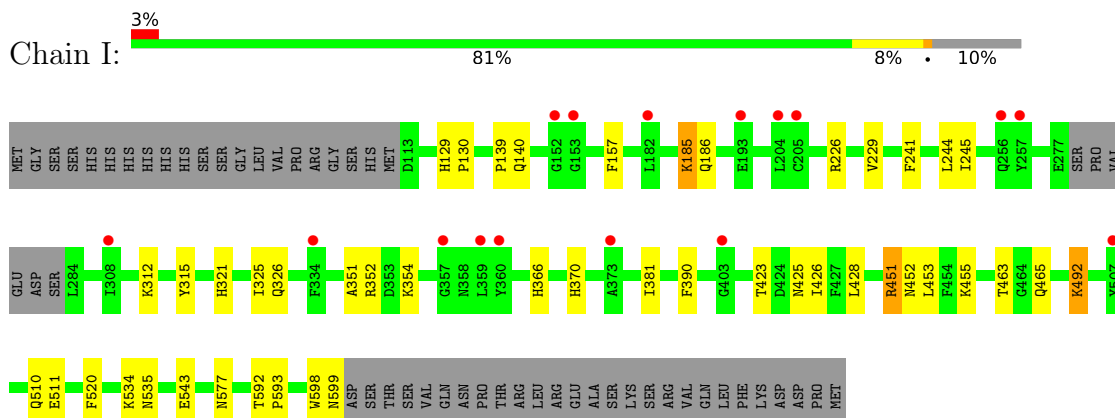
- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



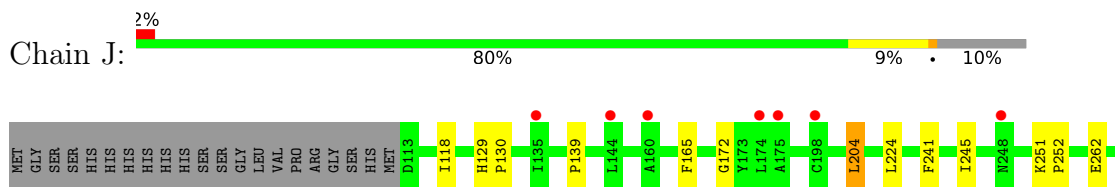
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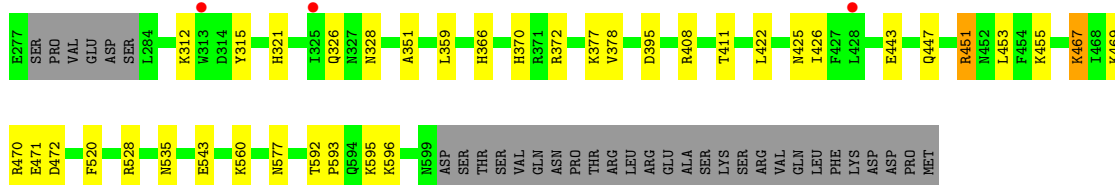


- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

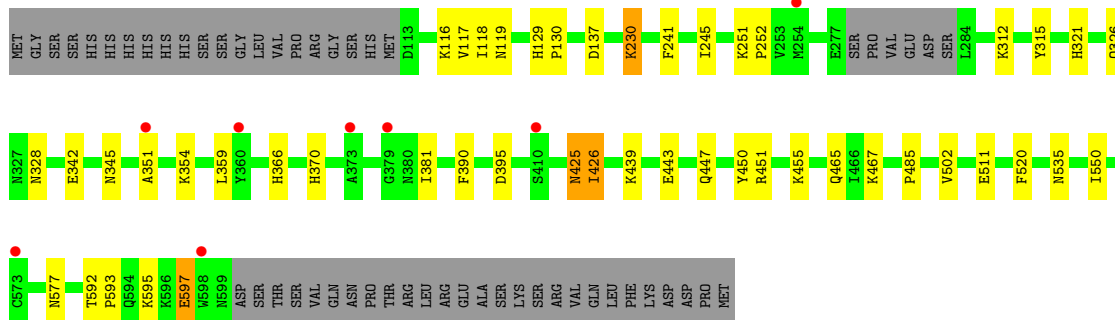
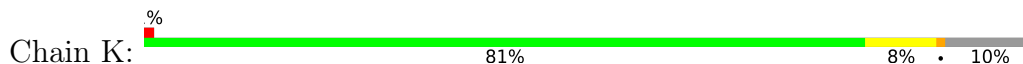


- Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1

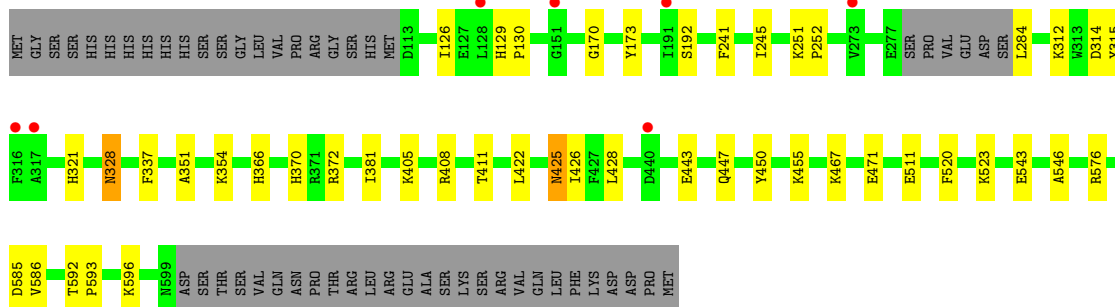
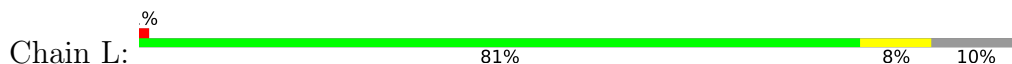




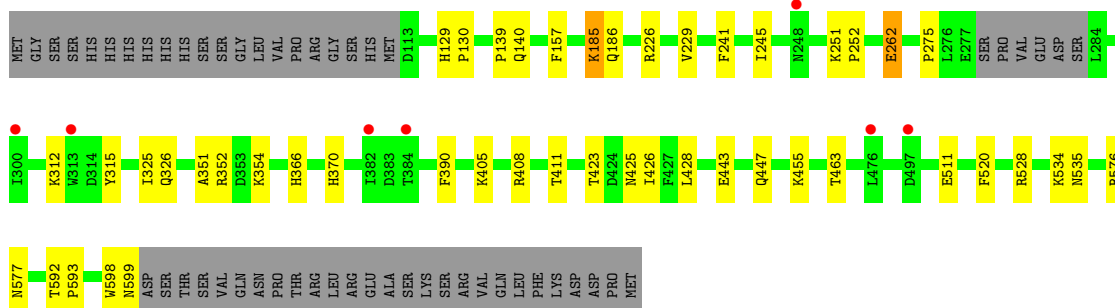
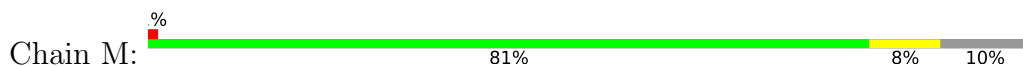
● Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



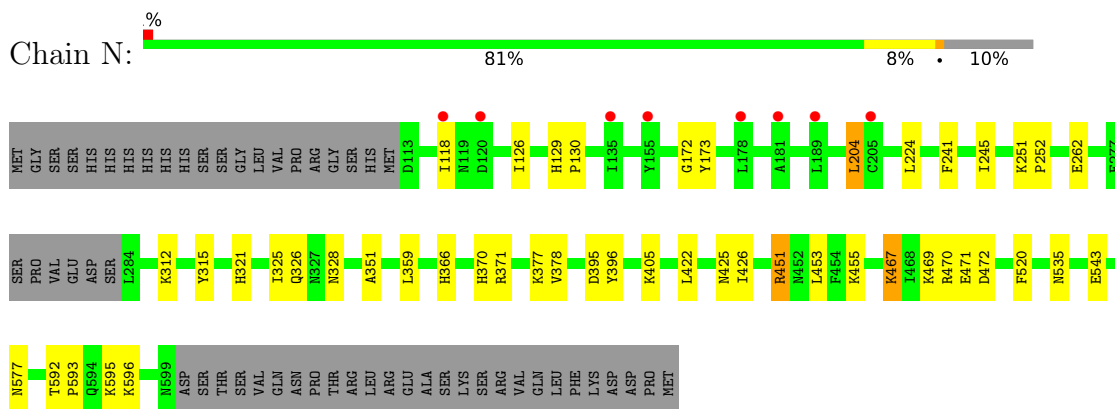
● Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



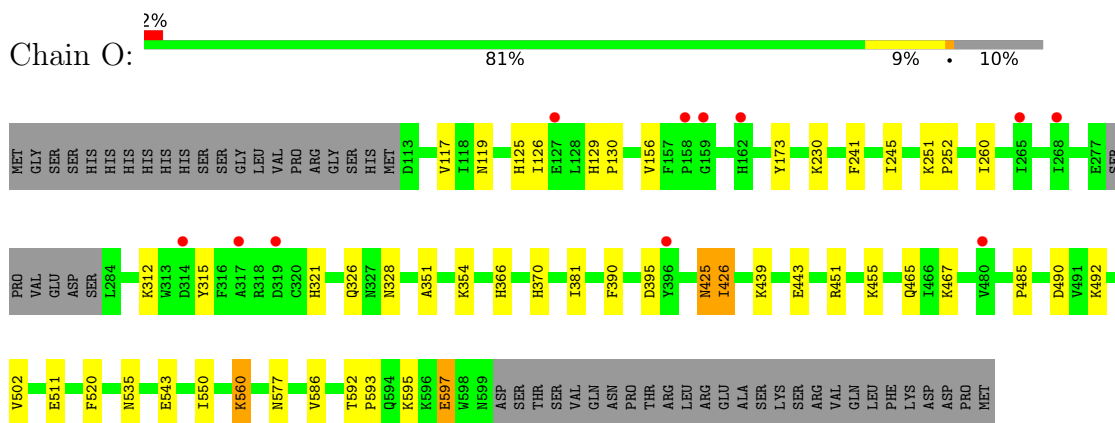
● Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



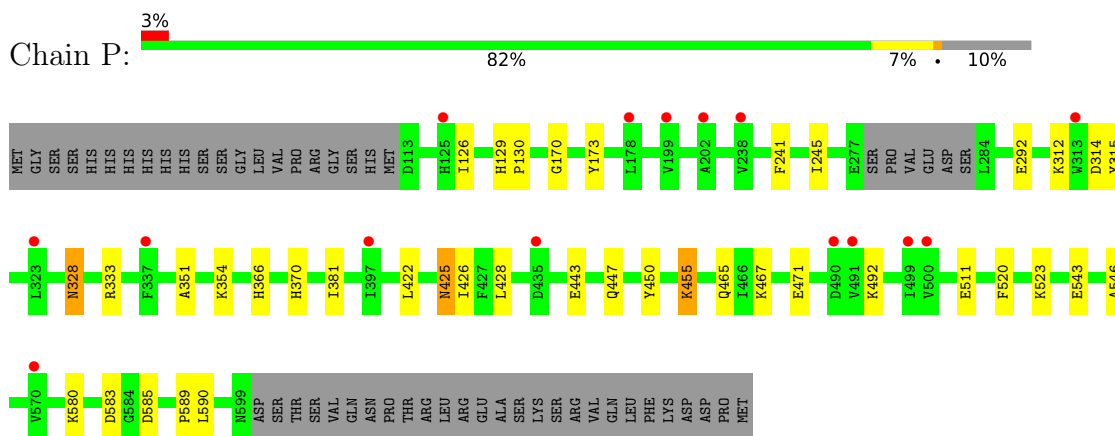
● Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



• Molecule 1: Deoxynucleoside triphosphate triphosphohydrolase SAMHD1



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.73Å 573.48Å 100.50Å 90.00° 114.72° 90.00°	Depositor
Resolution (Å)	49.27 – 3.57 49.27 – 3.57	Depositor EDS
% Data completeness (in resolution range)	83.9 (49.27-3.57) 91.6 (49.27-3.57)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.20 (at 3.57Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.236 , 0.274 0.298 , 0.336	Depositor DCC
$R_{free}$ test set	4552 reflections (4.50%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	159.8	Xtriage
Anisotropy	0.126	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 129.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.036 for h,-k,-h-l	Xtriage
Reported twinning fraction	0.598 for H, K, L 0.402 for -H, -K, H+L	Depositor
Outliers	0 of 92616 reflections	Xtriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	63936	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	188.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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: 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	0.89	0/4025	1.25	8/5434 (0.1%)
1	B	0.89	2/4025 (0.0%)	1.24	6/5434 (0.1%)
1	C	0.88	1/4025 (0.0%)	1.24	4/5434 (0.1%)
1	D	0.87	0/4033	1.22	2/5445 (0.0%)
1	E	0.88	1/4025 (0.0%)	1.24	5/5434 (0.1%)
1	F	0.89	2/4025 (0.0%)	1.25	7/5434 (0.1%)
1	G	0.87	0/4025	1.23	4/5434 (0.1%)
1	H	0.87	0/4033	1.21	2/5445 (0.0%)
1	I	0.89	1/4025 (0.0%)	1.25	8/5434 (0.1%)
1	J	0.89	1/4025 (0.0%)	1.24	5/5434 (0.1%)
1	K	0.87	0/4025	1.23	4/5434 (0.1%)
1	L	0.87	0/4033	1.21	1/5445 (0.0%)
1	M	0.89	2/4025 (0.0%)	1.24	6/5434 (0.1%)
1	N	0.90	2/4025 (0.0%)	1.24	5/5434 (0.1%)
1	O	0.87	0/4025	1.23	4/5434 (0.1%)
1	P	0.88	0/4033	1.21	1/5445 (0.0%)
All	All	0.88	12/64432 (0.0%)	1.23	72/86988 (0.1%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	261	PRO	N-CD	7.44	1.58	1.47
1	F	328	ASN	C-O	6.91	1.32	1.23
1	I	510	GLN	C-N	-6.51	1.23	1.33
1	N	328	ASN	C-O	6.33	1.32	1.23
1	J	328	ASN	C-O	6.21	1.31	1.23

The worst 5 of 72 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	485	PRO	N-CA-C	10.05	128.38	113.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	485	PRO	N-CA-C	9.95	128.23	113.81
1	G	485	PRO	N-CA-C	9.88	128.14	113.81
1	K	485	PRO	N-CA-C	9.86	128.11	113.81
1	C	559	ARG	N-CA-C	-8.51	102.08	111.36

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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	3932	0	3915	30	2
1	B	3932	0	3915	43	0
1	C	3932	0	3915	35	0
1	D	3940	0	3920	26	2
1	E	3932	0	3915	31	0
1	F	3932	0	3915	36	14
1	G	3932	0	3915	37	14
1	H	3940	0	3920	31	0
1	I	3932	0	3915	30	6
1	J	3932	0	3915	34	6
1	K	3932	0	3915	40	2
1	L	3940	0	3920	32	3
1	M	3932	0	3915	29	5
1	N	3932	0	3915	31	3
1	O	3932	0	3915	38	5
1	P	3940	0	3920	26	6
2	A	93	0	36	5	0
2	B	62	0	24	2	0
2	C	62	0	24	8	0
2	D	31	0	12	1	0
2	E	93	0	36	3	0
2	F	62	0	24	6	0
2	G	62	0	24	4	0
2	H	31	0	12	7	0
2	I	62	0	24	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	93	0	36	12	0
2	K	62	0	24	4	0
2	L	31	0	12	2	0
2	M	62	0	24	1	0
2	N	31	0	12	0	0
2	O	93	0	36	4	0
2	P	62	0	24	6	0
All	All	63936	0	63044	455	34

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 455 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:J:543:GLU:HG3	1:L:543:GLU:HG3	1.72	0.70
1:N:543:GLU:HG3	1:P:543:GLU:HG3	1.73	0.70
1:N:377:LYS:NZ	2:P:701:DGT:O1G	2.25	0.69
2:D:701:DGT:H5'A	2:D:701:DGT:H8	1.74	0.69
1:J:118:ILE:HG12	2:K:701:DGT:H2'	1.75	0.68

The worst 5 of 34 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:492:LYS:CE	1:J:395:ASP:OD1[1_454]	1.17	1.03
1:F:465:GLN:OE1	1:G:576:ARG:O[1_455]	1.19	1.01
1:F:465:GLN:OE1	1:G:576:ARG:C[1_455]	1.22	0.98
1:F:465:GLN:CD	1:G:576:ARG:C[1_455]	1.31	0.89
1:F:465:GLN:CD	1:G:576:ARG:O[1_455]	1.34	0.86

## 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	477/535 (89%)	469 (98%)	8 (2%)	0	100	100
1	B	477/535 (89%)	469 (98%)	8 (2%)	0	100	100
1	C	477/535 (89%)	470 (98%)	7 (2%)	0	100	100
1	D	478/535 (89%)	471 (98%)	7 (2%)	0	100	100
1	E	477/535 (89%)	468 (98%)	9 (2%)	0	100	100
1	F	477/535 (89%)	469 (98%)	8 (2%)	0	100	100
1	G	477/535 (89%)	470 (98%)	7 (2%)	0	100	100
1	H	478/535 (89%)	470 (98%)	8 (2%)	0	100	100
1	I	477/535 (89%)	466 (98%)	11 (2%)	0	100	100
1	J	477/535 (89%)	469 (98%)	8 (2%)	0	100	100
1	K	477/535 (89%)	470 (98%)	7 (2%)	0	100	100
1	L	478/535 (89%)	471 (98%)	7 (2%)	0	100	100
1	M	477/535 (89%)	468 (98%)	9 (2%)	0	100	100
1	N	477/535 (89%)	468 (98%)	9 (2%)	0	100	100
1	O	477/535 (89%)	470 (98%)	7 (2%)	0	100	100
1	P	478/535 (89%)	470 (98%)	7 (2%)	1 (0%)	43	72
All	All	7636/8560 (89%)	7508 (98%)	127 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	P	589	PRO

### 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	427/477 (90%)	420 (98%)	7 (2%)	55	69
1	B	427/477 (90%)	423 (99%)	4 (1%)	70	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	427/477 (90%)	420 (98%)	7 (2%)	55	69
1	D	428/477 (90%)	422 (99%)	6 (1%)	59	71
1	E	427/477 (90%)	420 (98%)	7 (2%)	55	69
1	F	427/477 (90%)	420 (98%)	7 (2%)	55	69
1	G	427/477 (90%)	421 (99%)	6 (1%)	59	71
1	H	428/477 (90%)	421 (98%)	7 (2%)	55	69
1	I	427/477 (90%)	420 (98%)	7 (2%)	55	69
1	J	427/477 (90%)	422 (99%)	5 (1%)	63	73
1	K	427/477 (90%)	420 (98%)	7 (2%)	55	69
1	L	428/477 (90%)	422 (99%)	6 (1%)	59	71
1	M	427/477 (90%)	423 (99%)	4 (1%)	70	76
1	N	427/477 (90%)	422 (99%)	5 (1%)	63	73
1	O	427/477 (90%)	418 (98%)	9 (2%)	47	65
1	P	428/477 (90%)	419 (98%)	9 (2%)	47	65
All	All	6836/7632 (90%)	6733 (98%)	103 (2%)	57	70

5 of 103 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	577	ASN
1	L	455	LYS
1	P	580	LYS
1	J	377	LYS
1	K	354	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 229 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	149	GLN
1	P	326	GLN
1	J	539	GLN
1	P	248	ASN
1	N	425	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

32 ligands 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	DGT	P	702	-	32,33,33	0.51	0	48,52,52	0.58	0
2	DGT	B	701	-	32,33,33	0.59	0	48,52,52	0.67	0
2	DGT	I	702	-	32,33,33	0.54	0	48,52,52	0.58	0
2	DGT	O	703	-	32,33,33	0.56	0	48,52,52	0.60	0
2	DGT	E	703	-	32,33,33	0.52	0	48,52,52	0.70	0
2	DGT	F	701	-	32,33,33	0.71	1 (3%)	48,52,52	0.58	0
2	DGT	J	703	-	32,33,33	0.74	1 (3%)	48,52,52	0.56	0
2	DGT	L	701	-	32,33,33	0.56	0	48,52,52	0.57	0
2	DGT	N	701	-	32,33,33	0.79	1 (3%)	48,52,52	0.54	0
2	DGT	H	701	-	32,33,33	0.62	0	48,52,52	0.68	0
2	DGT	K	701	-	32,33,33	0.51	0	48,52,52	0.59	0
2	DGT	G	702	-	32,33,33	0.59	0	48,52,52	0.69	0
2	DGT	E	701	-	32,33,33	0.50	0	48,52,52	0.69	0
2	DGT	D	701	-	32,33,33	0.60	0	48,52,52	0.55	0
2	DGT	C	701	-	32,33,33	0.50	0	48,52,52	0.60	0
2	DGT	J	702	-	32,33,33	0.57	0	48,52,52	0.69	0
2	DGT	A	703	-	32,33,33	0.52	0	48,52,52	0.80	2 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	DGT	P	701	-	32,33,33	0.64	0	48,52,52	0.69	0
2	DGT	I	701	-	32,33,33	0.49	0	48,52,52	0.69	0
2	DGT	F	702	-	32,33,33	0.45	0	48,52,52	0.61	0
2	DGT	M	701	-	32,33,33	0.54	0	48,52,52	0.67	0
2	DGT	A	701	-	32,33,33	0.55	0	48,52,52	0.70	0
2	DGT	K	702	-	32,33,33	0.53	0	48,52,52	0.59	0
2	DGT	E	702	-	32,33,33	0.53	0	48,52,52	0.59	0
2	DGT	A	702	-	32,33,33	0.55	0	48,52,52	0.56	0
2	DGT	C	702	-	32,33,33	0.52	0	48,52,52	0.55	0
2	DGT	B	702	-	32,33,33	0.73	0	48,52,52	0.57	0
2	DGT	M	702	-	32,33,33	0.57	0	48,52,52	0.58	0
2	DGT	O	701	-	32,33,33	0.59	0	48,52,52	0.67	0
2	DGT	G	701	-	32,33,33	0.56	0	48,52,52	0.67	0
2	DGT	J	701	-	32,33,33	0.59	0	48,52,52	0.68	0
2	DGT	O	702	-	32,33,33	0.46	0	48,52,52	0.61	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	P	702	-	-	5/22/34/34	0/3/3/3
2	DGT	B	701	-	-	8/22/34/34	0/3/3/3
2	DGT	I	702	-	-	6/22/34/34	0/3/3/3
2	DGT	O	703	-	-	4/22/34/34	0/3/3/3
2	DGT	E	703	-	-	7/22/34/34	0/3/3/3
2	DGT	F	701	-	-	5/22/34/34	0/3/3/3
2	DGT	J	703	-	-	5/22/34/34	0/3/3/3
2	DGT	L	701	-	-	7/22/34/34	0/3/3/3
2	DGT	N	701	-	-	5/22/34/34	0/3/3/3
2	DGT	H	701	-	-	7/22/34/34	0/3/3/3
2	DGT	K	701	-	-	2/22/34/34	0/3/3/3
2	DGT	G	702	-	-	3/22/34/34	0/3/3/3
2	DGT	E	701	-	-	6/22/34/34	0/3/3/3
2	DGT	D	701	-	-	6/22/34/34	0/3/3/3
2	DGT	C	701	-	-	2/22/34/34	0/3/3/3
2	DGT	J	702	-	-	8/22/34/34	0/3/3/3
2	DGT	A	703	-	-	6/22/34/34	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DGT	P	701	-	-	7/22/34/34	0/3/3/3
2	DGT	I	701	-	-	6/22/34/34	0/3/3/3
2	DGT	F	702	-	-	2/22/34/34	0/3/3/3
2	DGT	M	701	-	-	6/22/34/34	0/3/3/3
2	DGT	A	701	-	-	6/22/34/34	0/3/3/3
2	DGT	K	702	-	-	4/22/34/34	0/3/3/3
2	DGT	E	702	-	-	5/22/34/34	0/3/3/3
2	DGT	A	702	-	-	4/22/34/34	0/3/3/3
2	DGT	C	702	-	-	5/22/34/34	0/3/3/3
2	DGT	B	702	-	-	6/22/34/34	0/3/3/3
2	DGT	M	702	-	-	5/22/34/34	0/3/3/3
2	DGT	O	701	-	-	8/22/34/34	0/3/3/3
2	DGT	G	701	-	-	8/22/34/34	0/3/3/3
2	DGT	J	701	-	-	7/22/34/34	0/3/3/3
2	DGT	O	702	-	-	2/22/34/34	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	703	DGT	PA-O3A	2.32	1.62	1.59
2	N	701	DGT	PA-O3A	2.28	1.62	1.59
2	F	701	DGT	PA-O3A	2.02	1.61	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	703	DGT	C1'-N9-C8	-2.55	122.20	127.91
2	A	703	DGT	C1'-N9-C4	2.43	132.06	125.50

There are no chirality outliers.

5 of 173 torsion outliers are listed below:

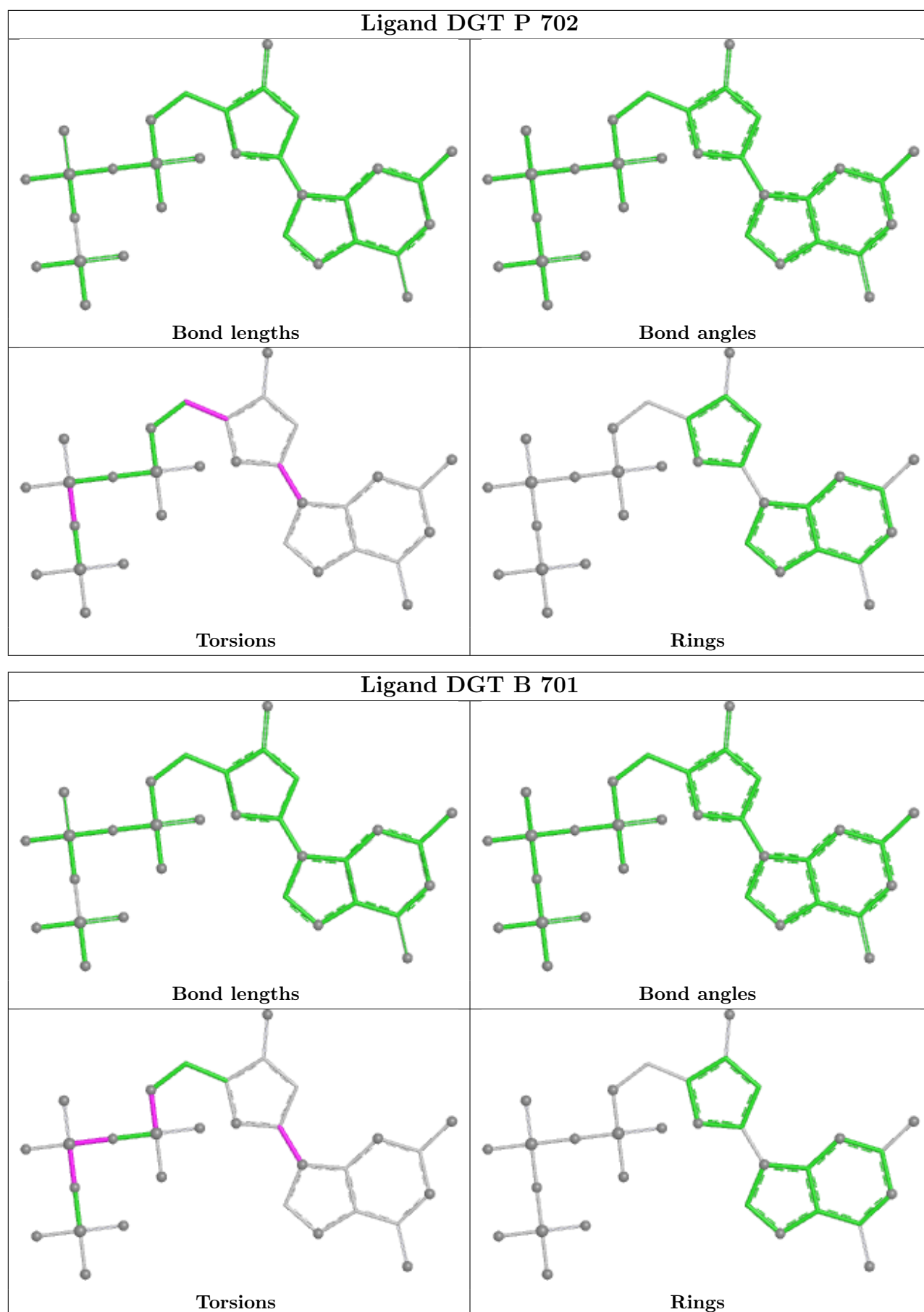
Mol	Chain	Res	Type	Atoms
2	A	701	DGT	C5'-O5'-PA-O3A
2	A	701	DGT	C5'-O5'-PA-O2A
2	A	702	DGT	PB-O3B-PG-O1G
2	A	703	DGT	O4'-C1'-N9-C8
2	A	703	DGT	O4'-C1'-N9-C4

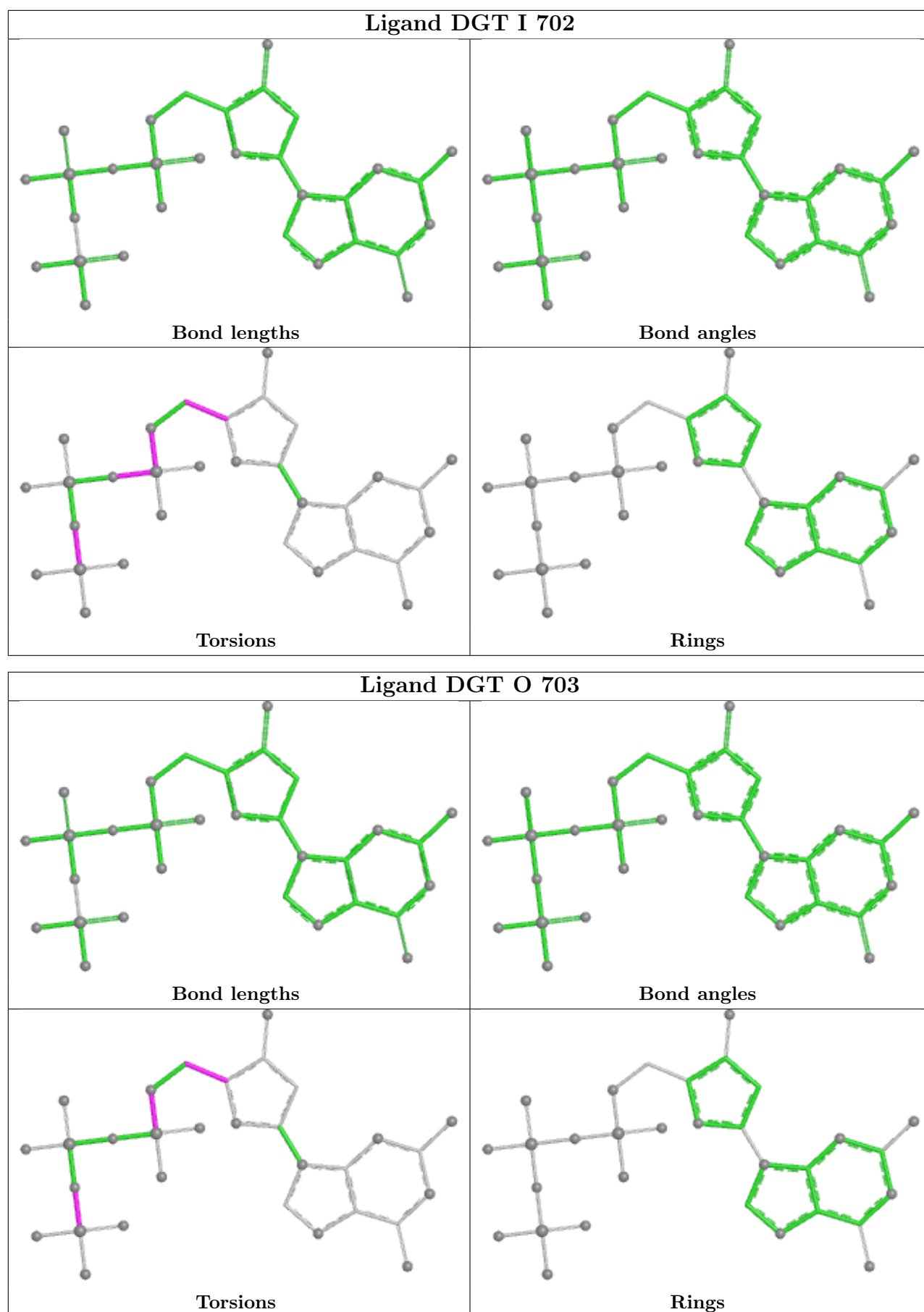
There are no ring outliers.

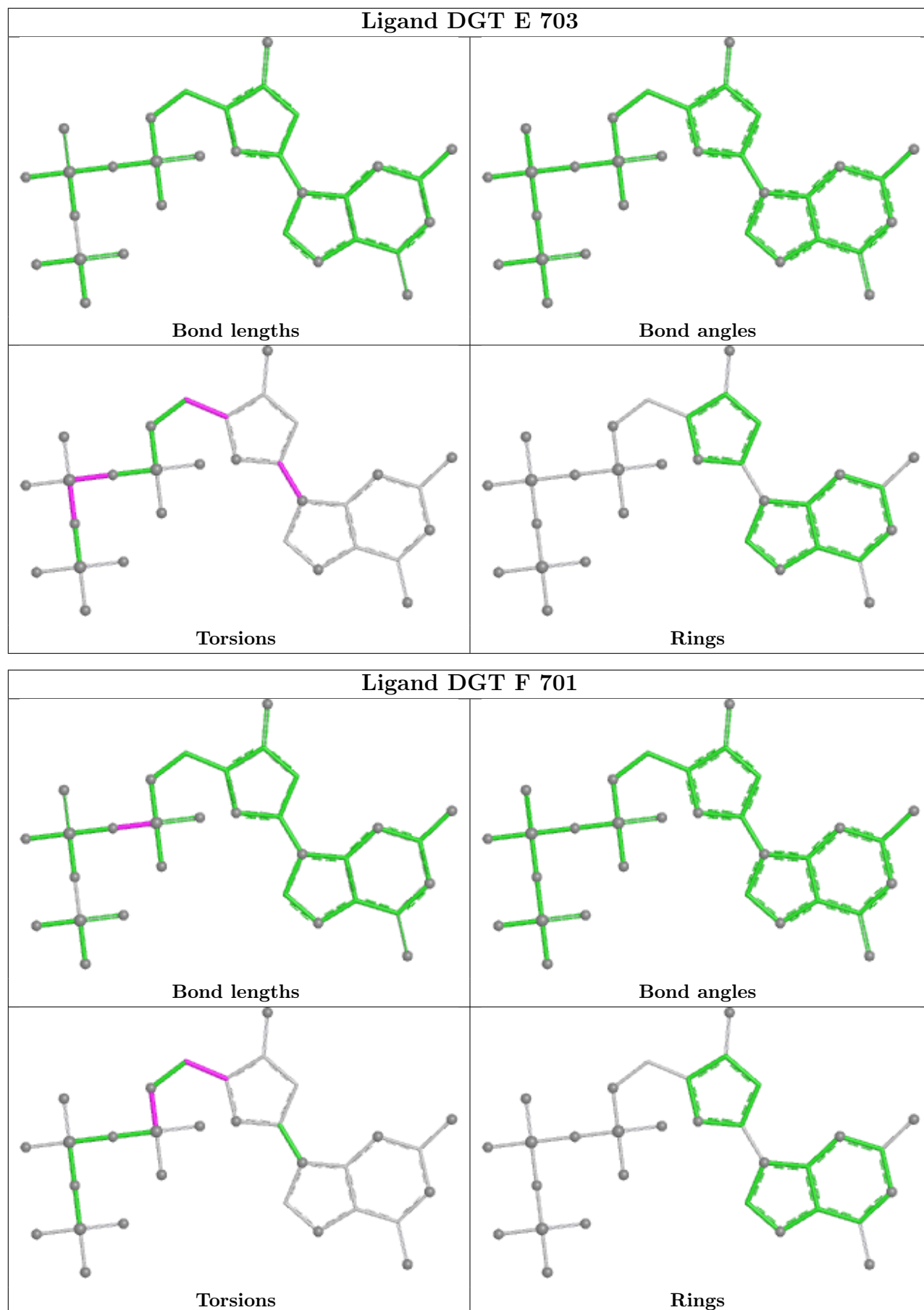
23 monomers are involved in 61 short contacts:

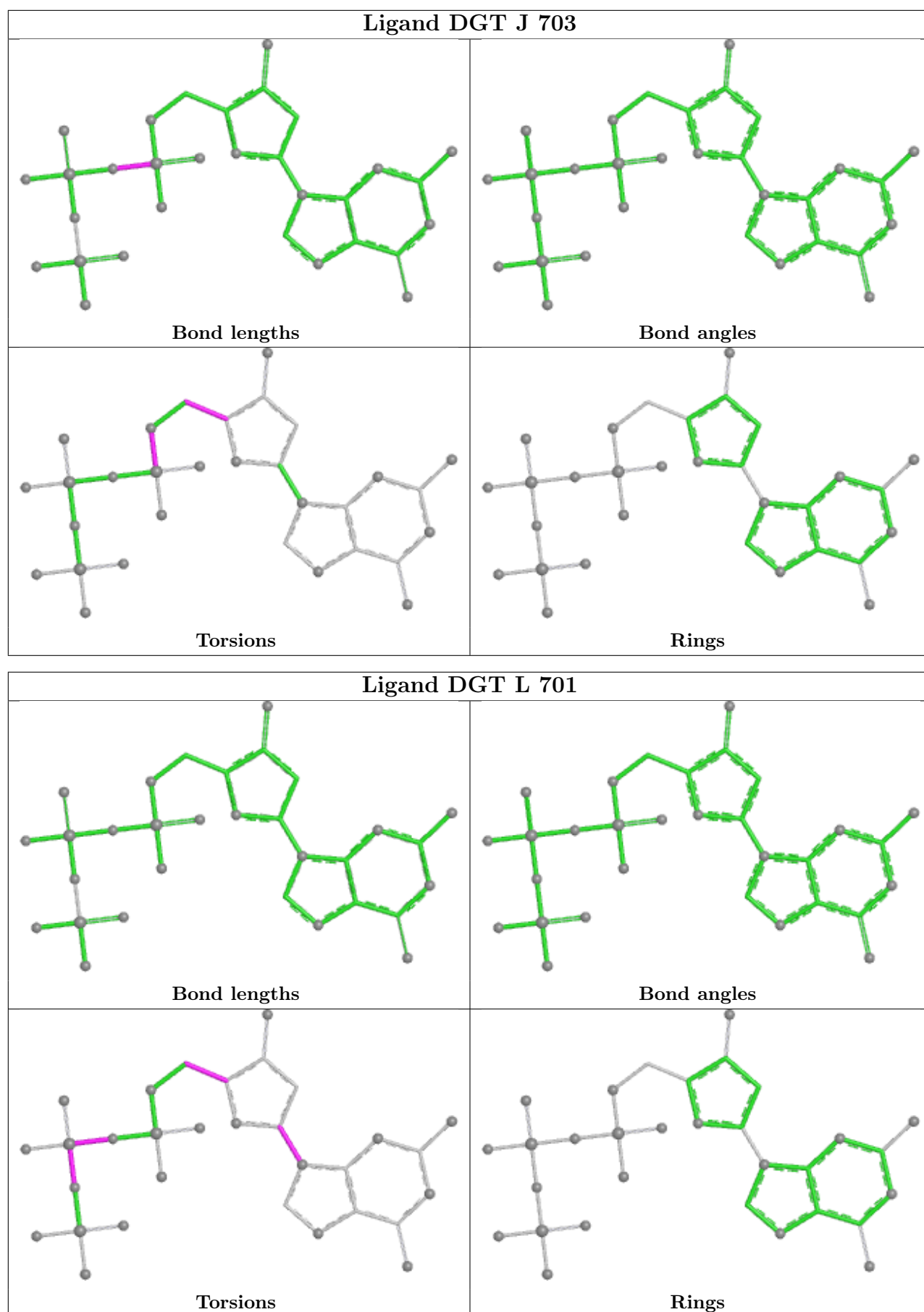
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	DGT	2	0
2	O	703	DGT	1	0
2	F	701	DGT	2	0
2	J	703	DGT	1	0
2	L	701	DGT	2	0
2	H	701	DGT	7	0
2	K	701	DGT	3	0
2	G	702	DGT	3	0
2	E	701	DGT	1	0
2	D	701	DGT	1	0
2	C	701	DGT	4	0
2	J	702	DGT	3	0
2	A	703	DGT	1	0
2	P	701	DGT	6	0
2	F	702	DGT	4	0
2	K	702	DGT	1	0
2	E	702	DGT	2	0
2	A	702	DGT	4	0
2	C	702	DGT	4	0
2	M	702	DGT	1	0
2	G	701	DGT	1	0
2	J	701	DGT	8	0
2	O	702	DGT	3	0

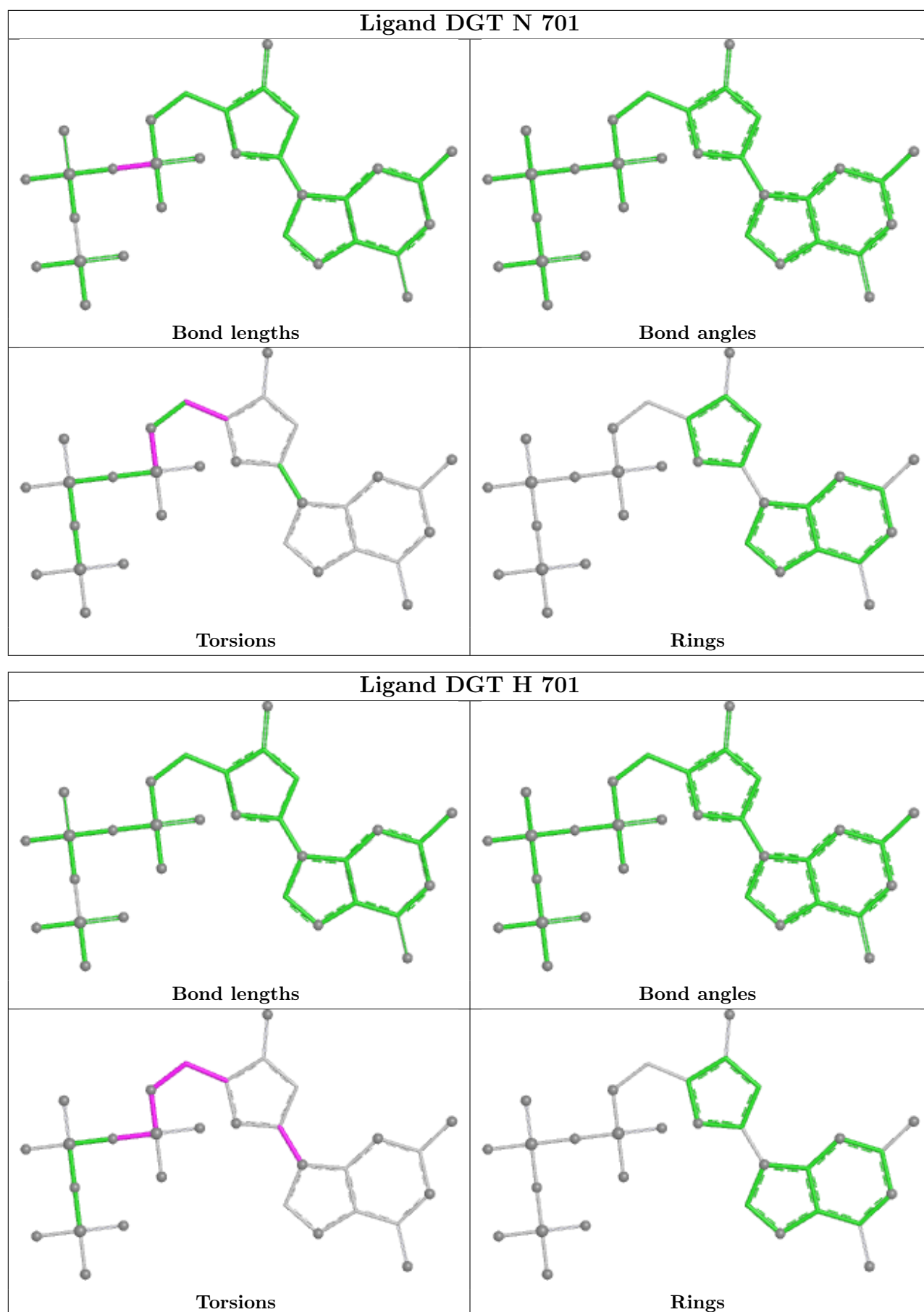
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

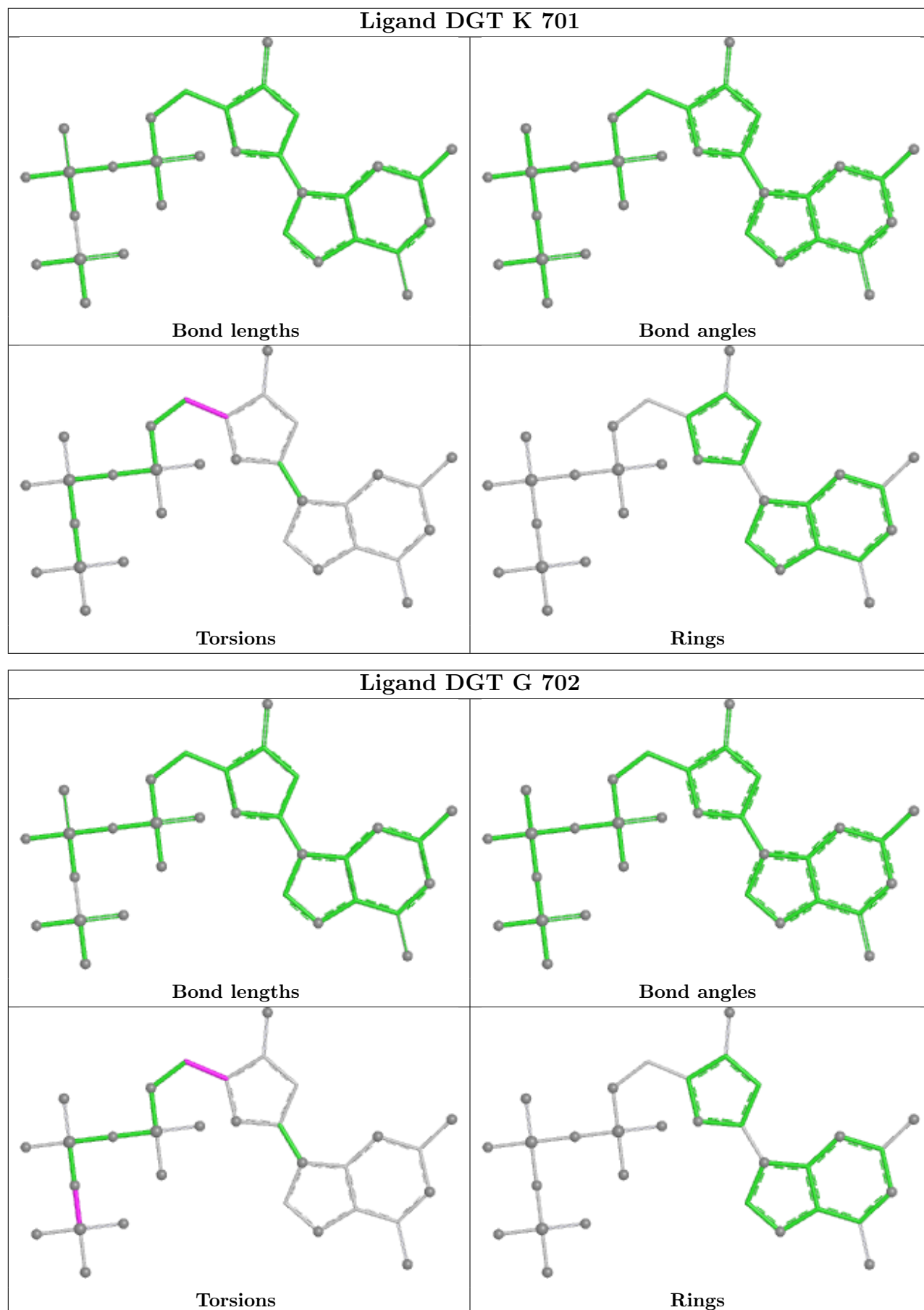


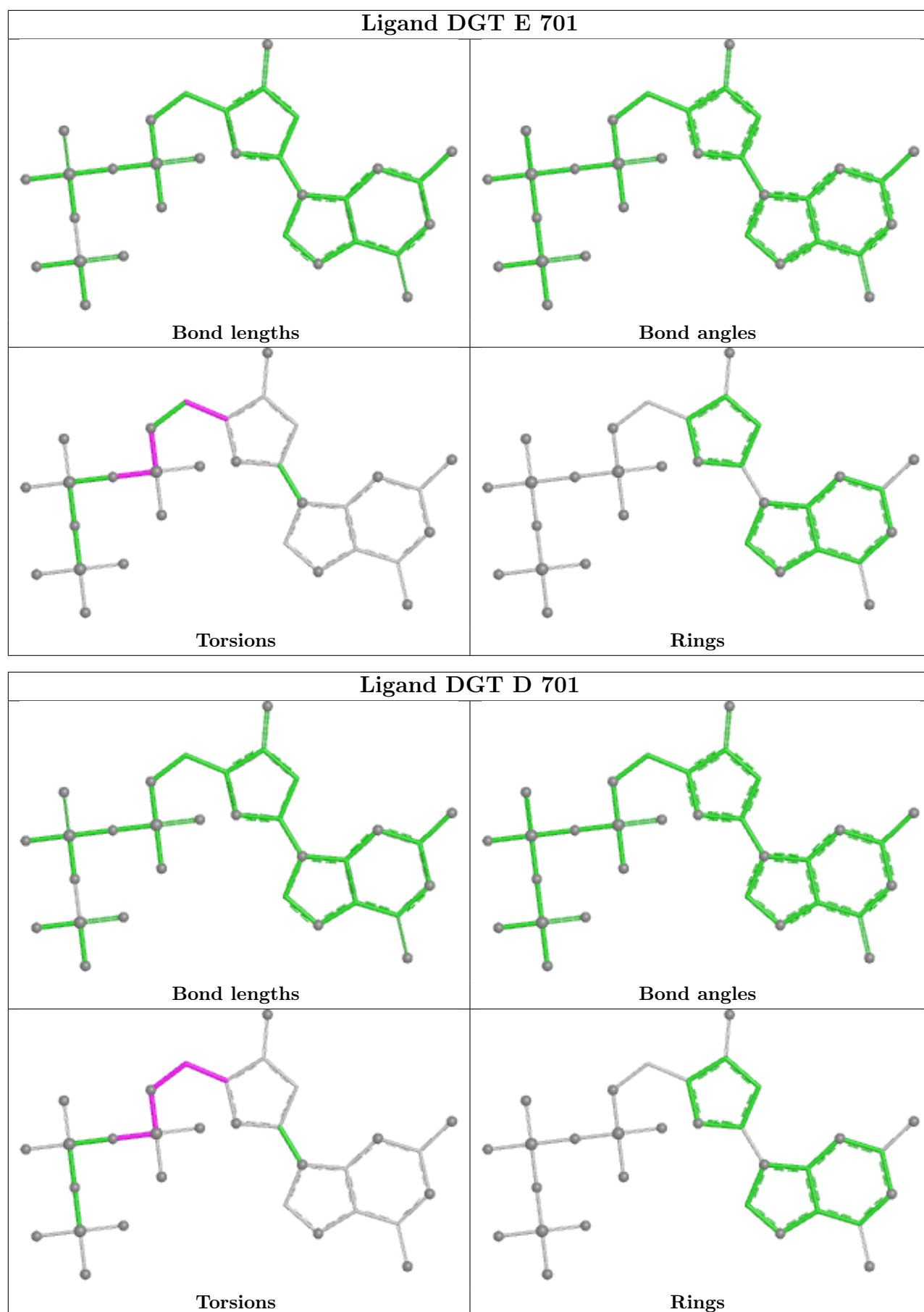


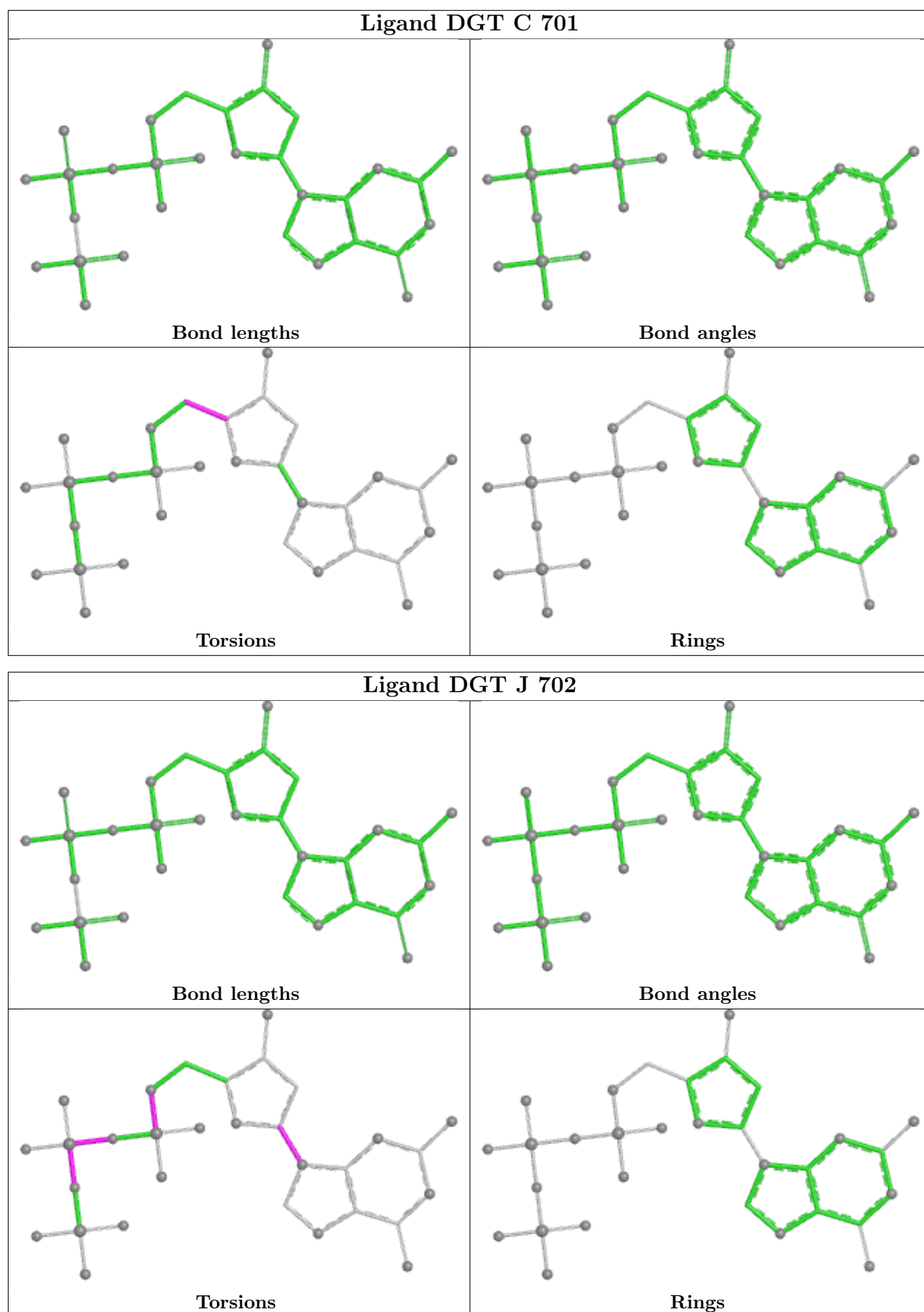


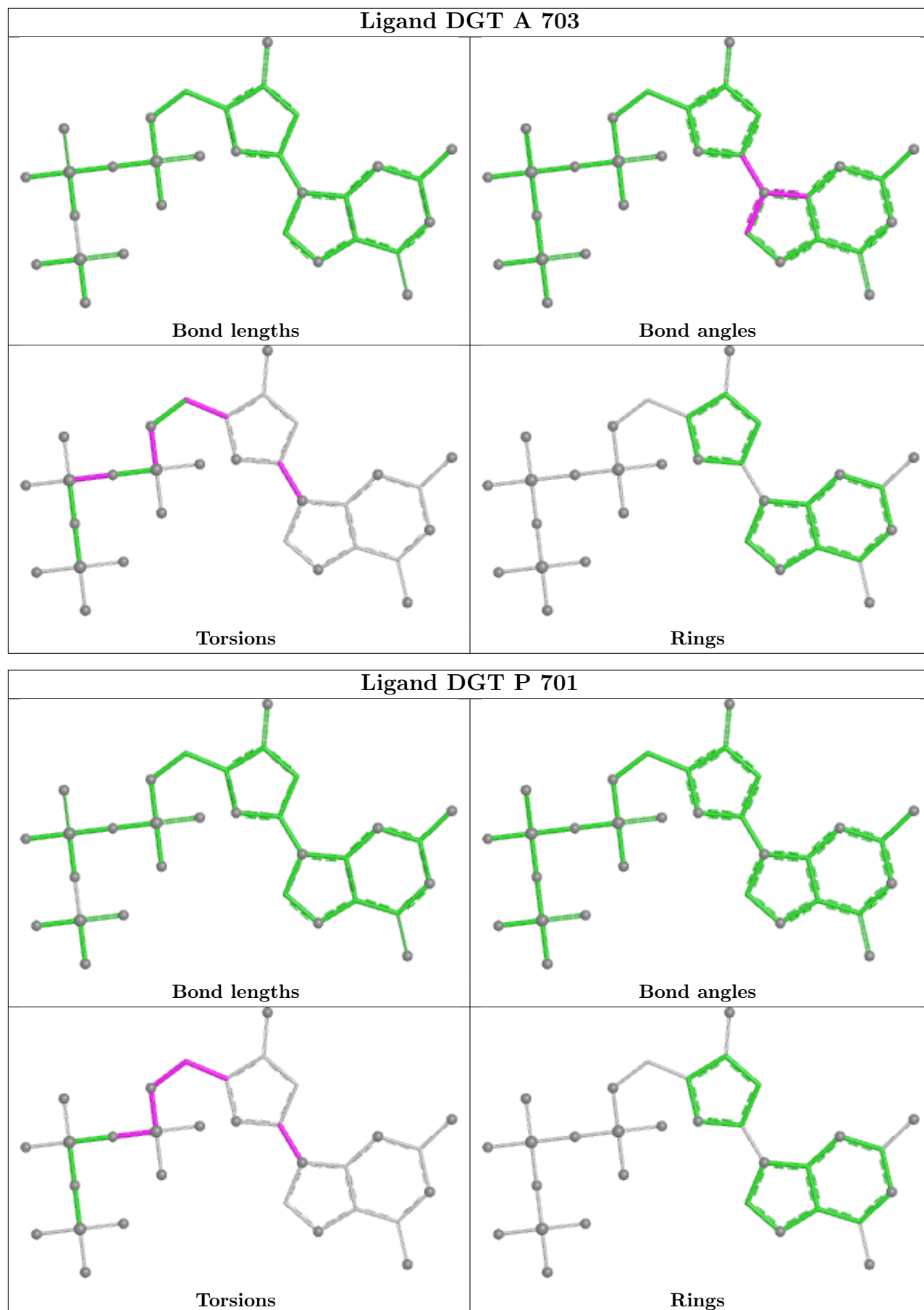


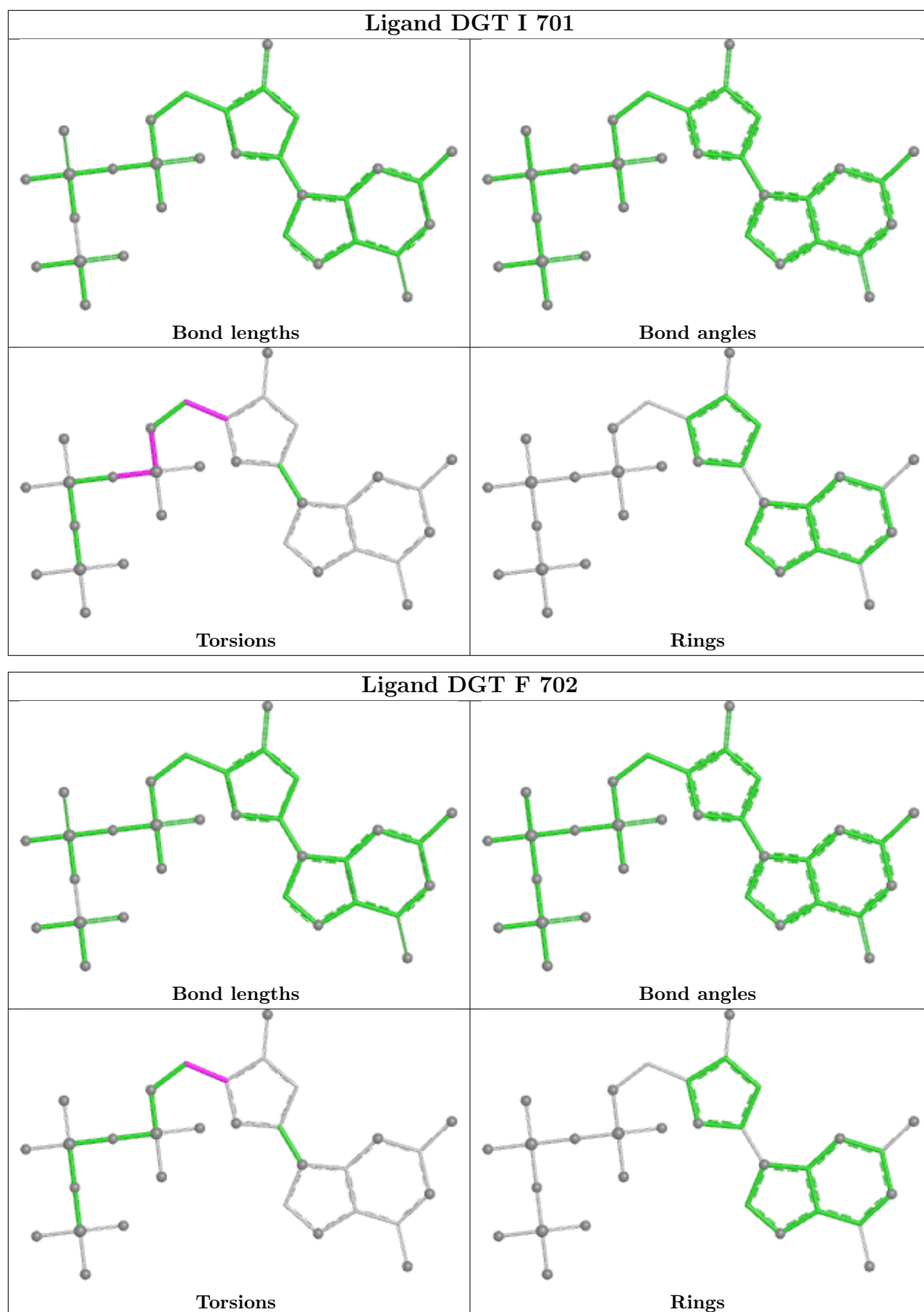


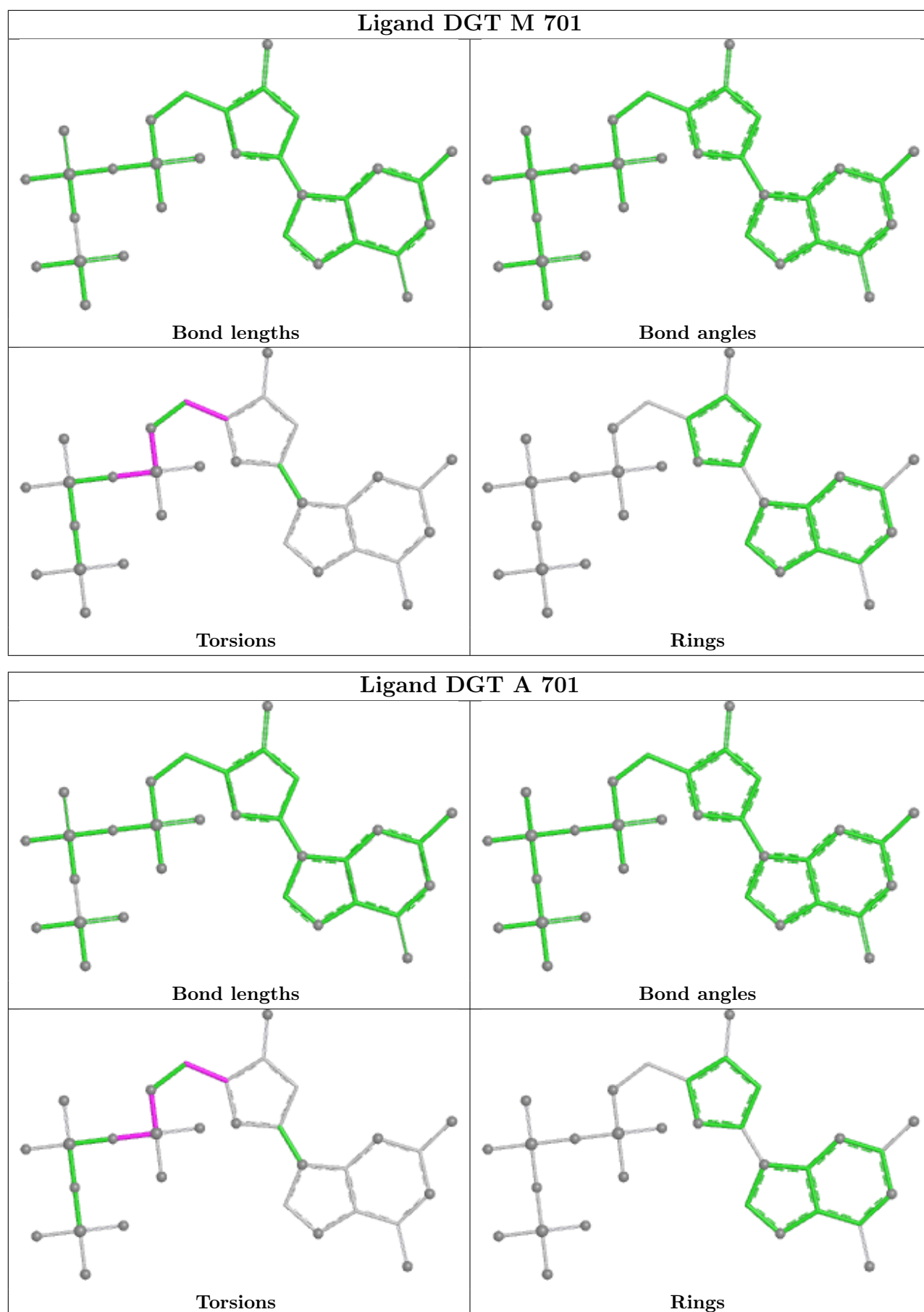


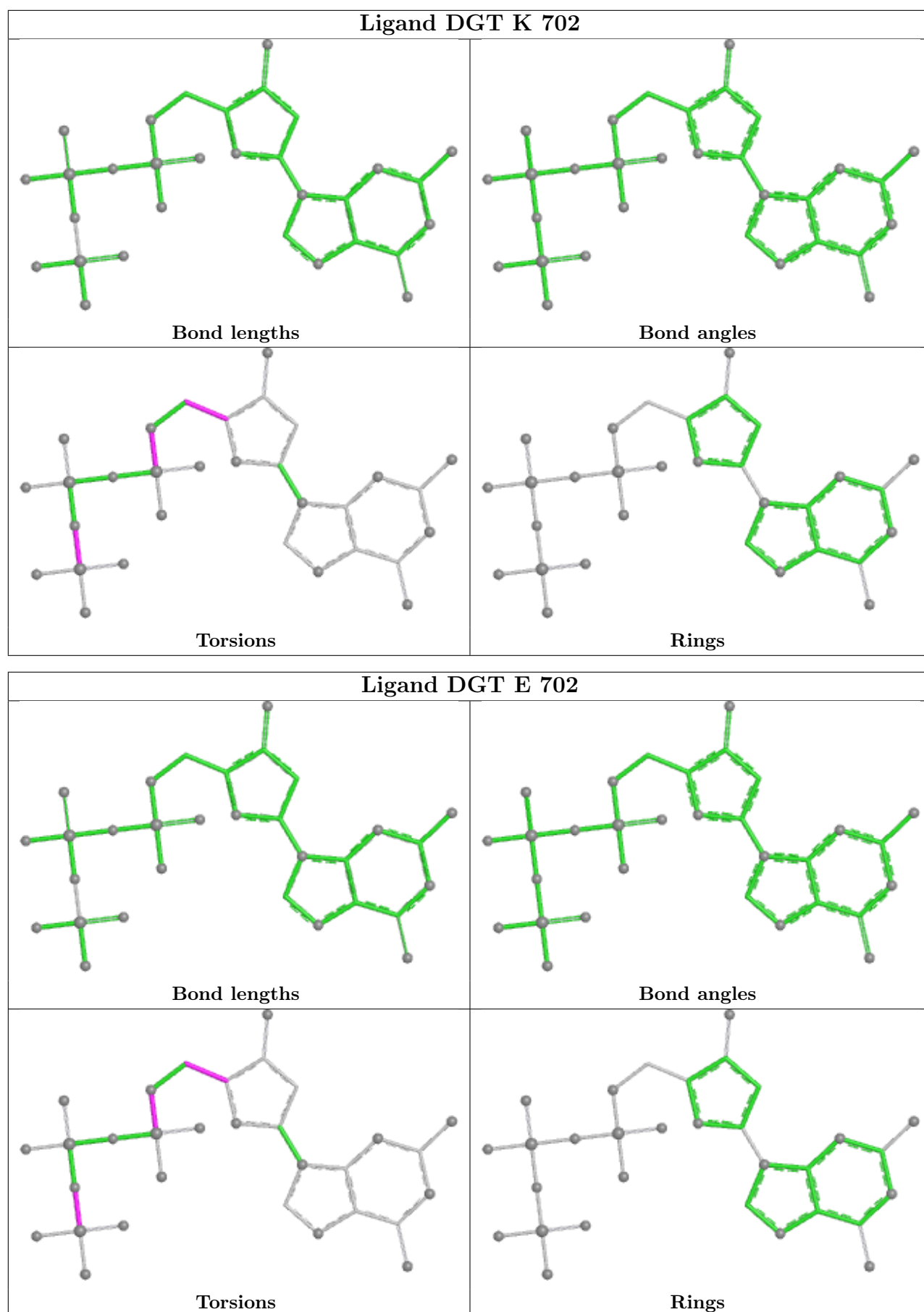


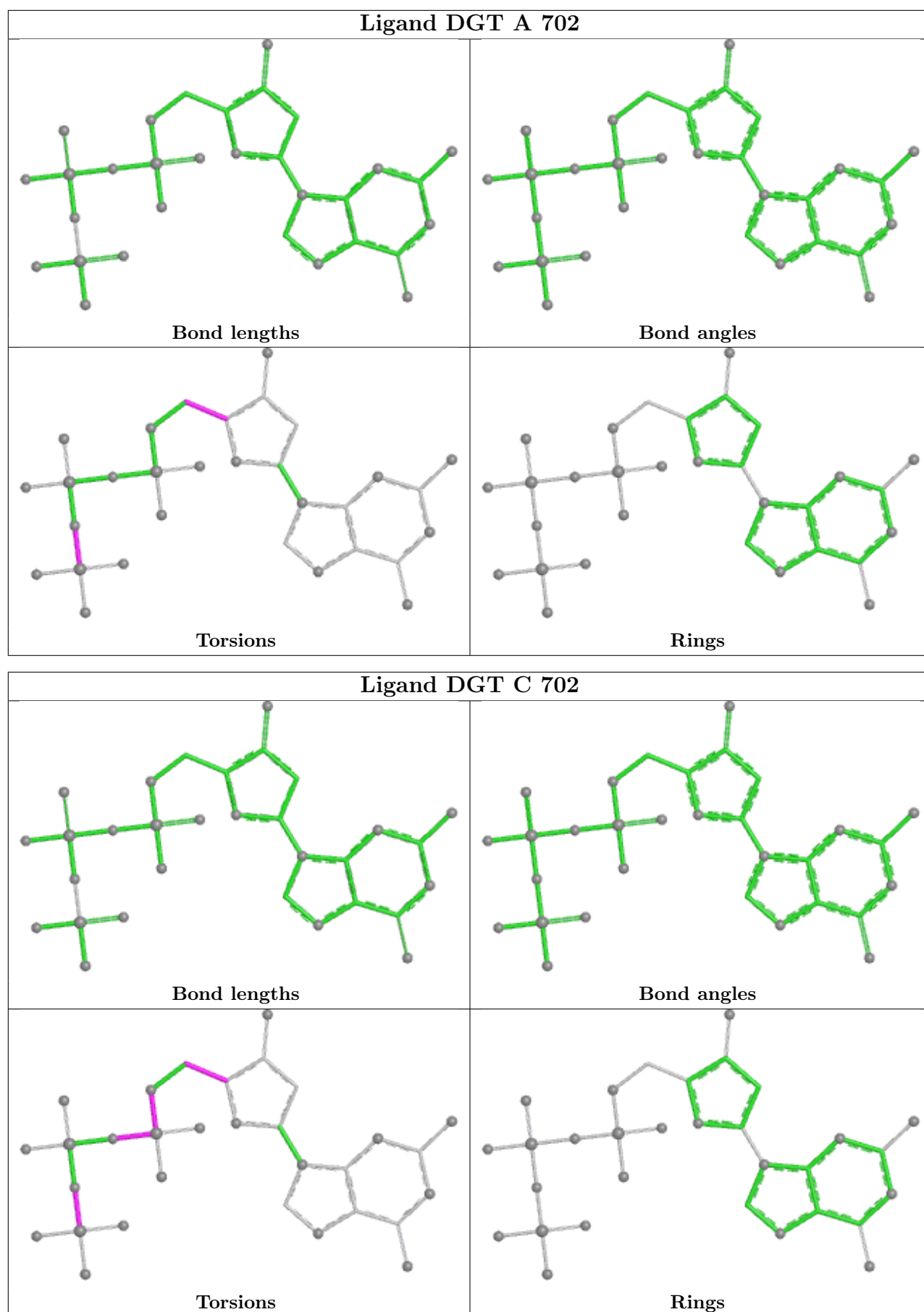


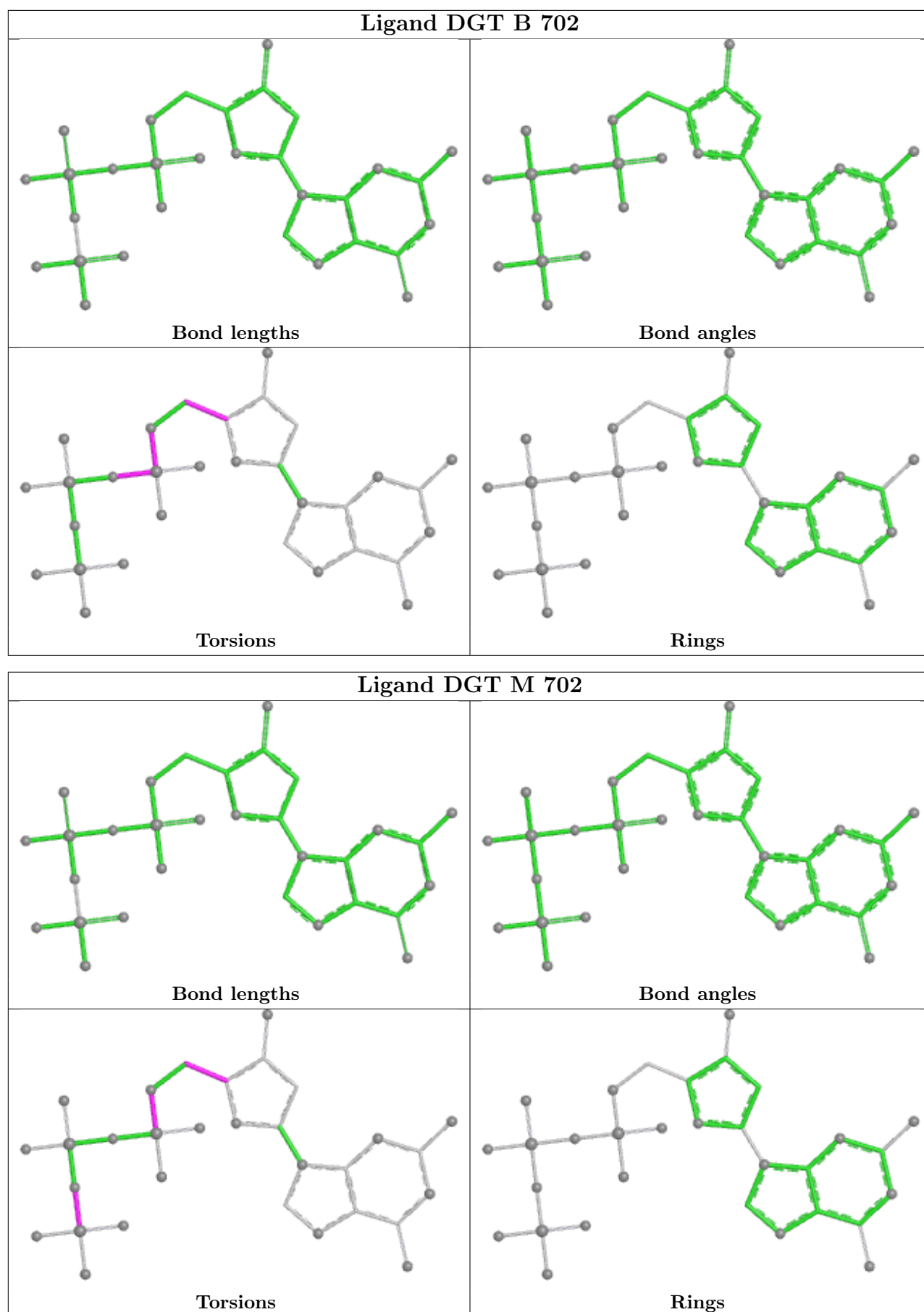


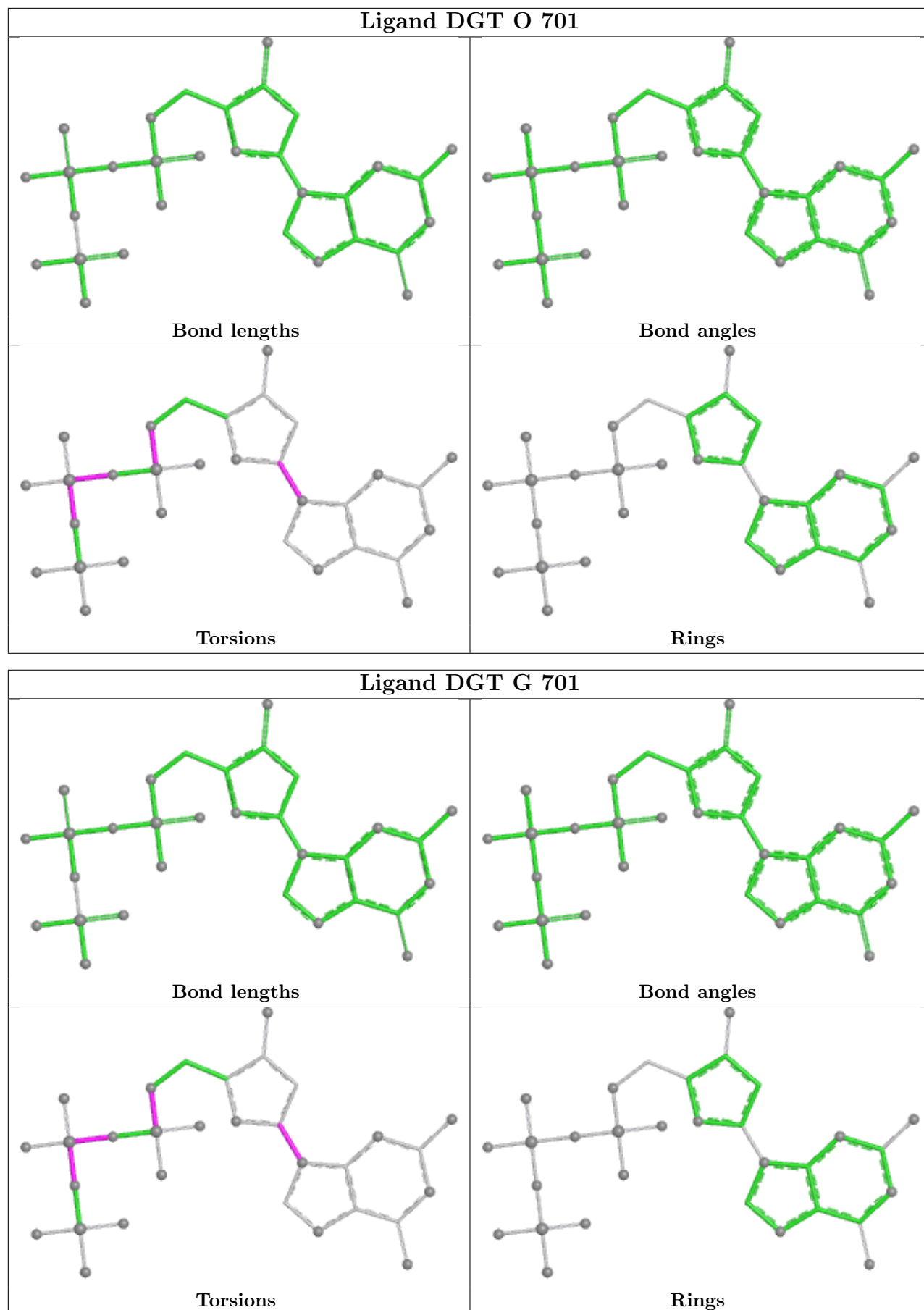


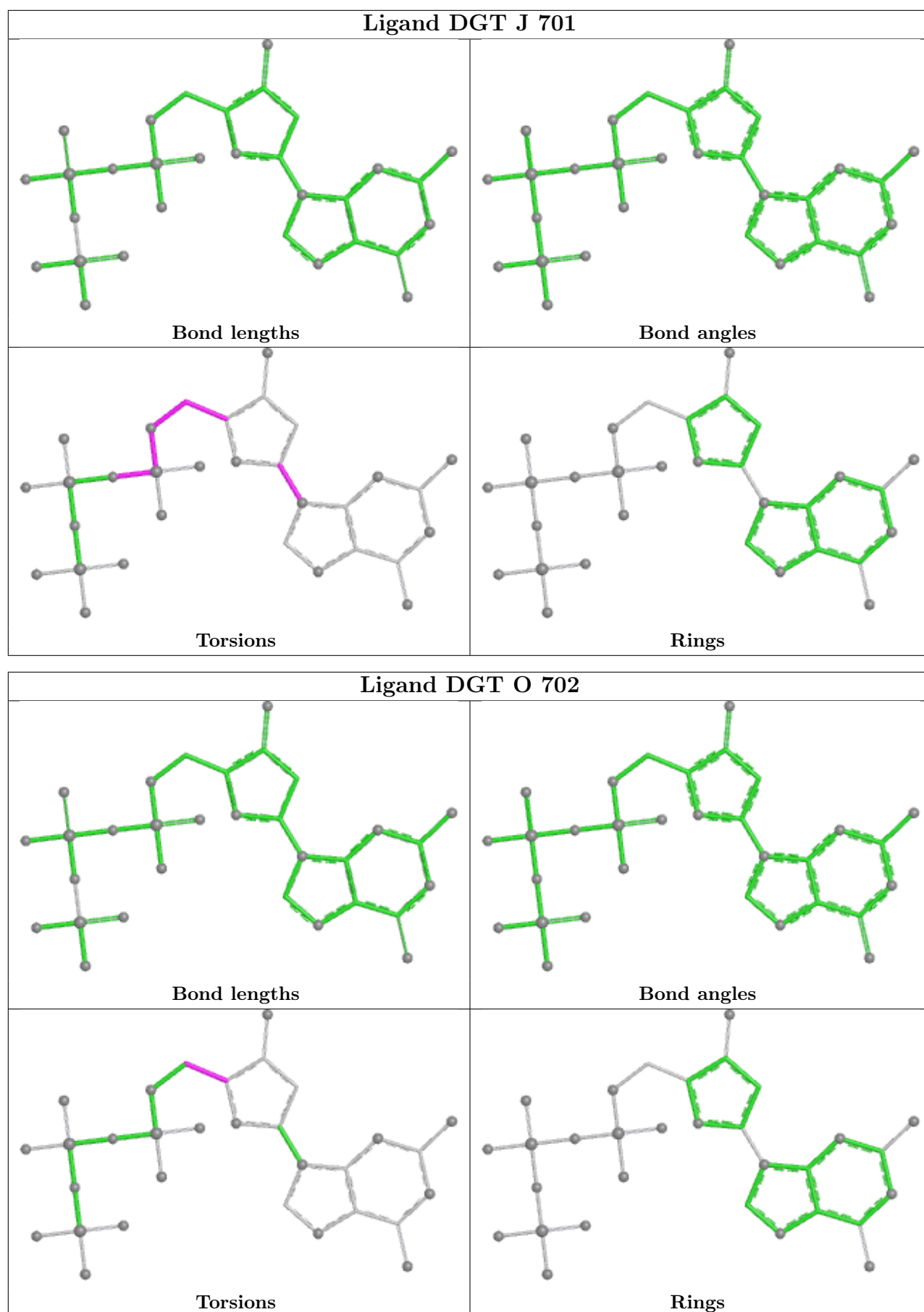












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 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	481/535 (89%)	0.10	15 (3%)	51 28	111, 176, 242, 304	0
1	B	481/535 (89%)	0.17	24 (4%)	34 19	101, 176, 237, 298	0
1	C	481/535 (89%)	0.19	15 (3%)	51 28	102, 179, 235, 265	0
1	D	481/535 (89%)	0.09	12 (2%)	58 33	82, 176, 239, 287	1 (0%)
1	E	481/535 (89%)	0.10	13 (2%)	56 31	87, 164, 223, 258	0
1	F	481/535 (89%)	0.08	12 (2%)	58 33	103, 182, 247, 317	0
1	G	481/535 (89%)	0.16	17 (3%)	47 26	108, 181, 254, 313	0
1	H	481/535 (89%)	0.06	11 (2%)	61 34	61, 178, 243, 303	1 (0%)
1	I	481/535 (89%)	0.16	16 (3%)	49 27	102, 187, 245, 283	0
1	J	481/535 (89%)	0.10	10 (2%)	63 36	120, 189, 262, 339	0
1	K	481/535 (89%)	0.07	8 (1%)	69 40	119, 193, 269, 307	0
1	L	481/535 (89%)	0.01	7 (1%)	72 44	75, 191, 275, 324	1 (0%)
1	M	481/535 (89%)	0.17	7 (1%)	72 44	128, 206, 278, 317	0
1	N	481/535 (89%)	0.01	8 (1%)	69 40	100, 185, 248, 270	0
1	O	481/535 (89%)	0.05	11 (2%)	61 34	116, 189, 270, 318	0
1	P	481/535 (89%)	0.10	15 (3%)	51 28	108, 193, 257, 341	1 (0%)
All	All	7696/8560 (89%)	0.10	201 (2%)	57 32	61, 184, 256, 341	4 (0%)

The worst 5 of 201 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	313	TRP	6.8
1	C	313	TRP	6.4
1	C	135	ILE	5.8
1	J	428	LEU	5.1
1	A	306	ASN	4.9

## 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 oligosaccharides 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<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.

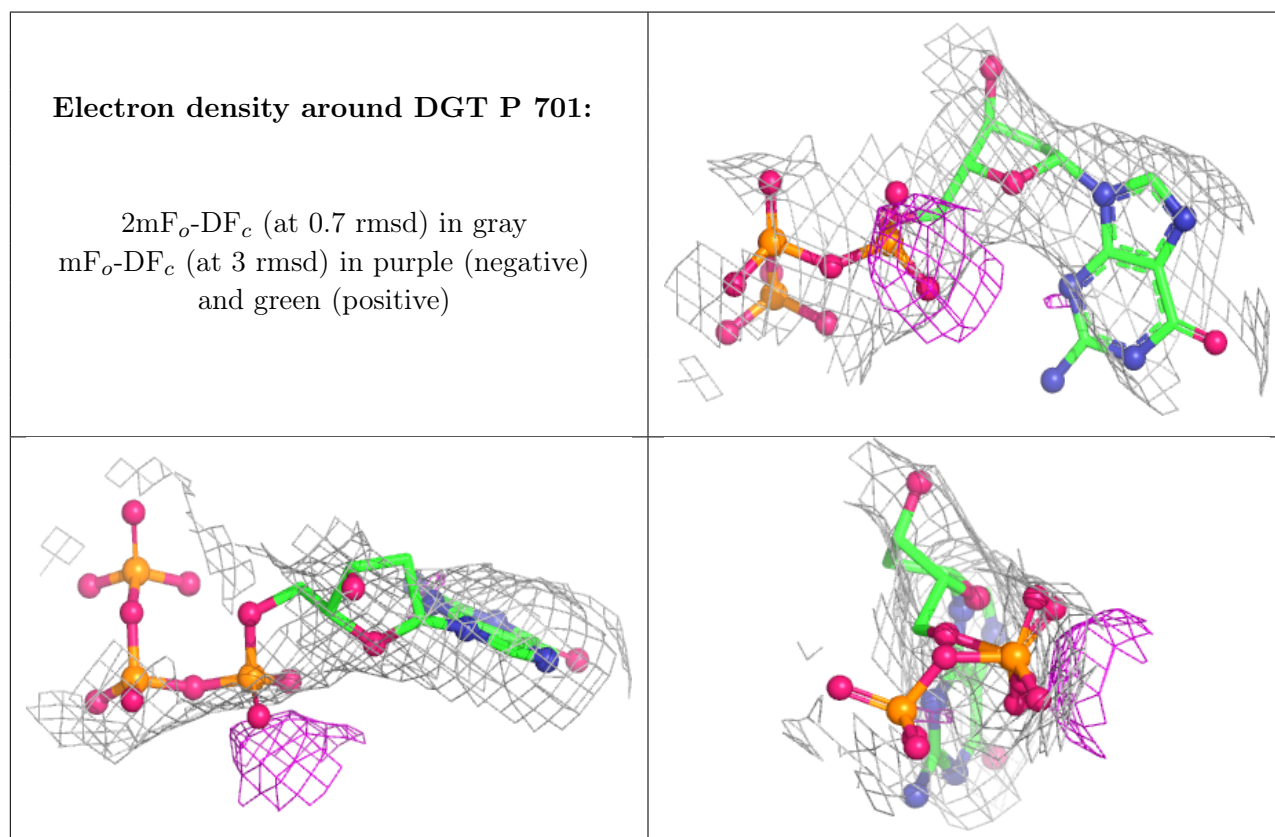
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	DGT	P	701	31/31	0.70	0.12	108,163,260,277	0
2	DGT	F	701	31/31	0.71	0.12	115,163,258,286	0
2	DGT	J	701	31/31	0.72	0.11	158,196,236,251	0
2	DGT	J	703	31/31	0.77	0.10	148,179,222,224	0
2	DGT	B	702	31/31	0.79	0.12	123,161,221,241	0
2	DGT	I	701	31/31	0.80	0.10	119,176,216,232	0
2	DGT	K	701	31/31	0.80	0.11	146,190,210,214	0
2	DGT	G	701	31/31	0.80	0.10	114,167,193,203	0
2	DGT	E	702	31/31	0.81	0.09	104,152,183,186	0
2	DGT	M	702	31/31	0.81	0.09	111,145,210,237	0
2	DGT	A	703	31/31	0.81	0.16	118,158,255,262	0
2	DGT	C	702	31/31	0.82	0.10	105,162,186,208	0
2	DGT	F	702	31/31	0.84	0.10	120,163,193,201	0
2	DGT	M	701	31/31	0.84	0.08	77,162,195,234	0
2	DGT	N	701	31/31	0.85	0.08	121,182,200,207	0
2	DGT	A	701	31/31	0.85	0.10	79,136,185,195	0
2	DGT	D	701	31/31	0.86	0.08	111,173,229,241	0
2	DGT	O	703	31/31	0.86	0.09	101,149,199,203	0
2	DGT	J	702	31/31	0.86	0.10	109,172,198,208	0
2	DGT	L	701	31/31	0.87	0.12	139,192,250,256	0
2	DGT	C	701	31/31	0.87	0.09	84,132,159,171	0
2	DGT	K	702	31/31	0.87	0.08	106,157,197,225	0
2	DGT	A	702	31/31	0.88	0.09	78,102,159,161	0
2	DGT	O	701	31/31	0.88	0.08	104,155,198,238	0
2	DGT	O	702	31/31	0.90	0.09	103,170,202,219	0
2	DGT	H	701	31/31	0.90	0.09	106,142,204,224	0
2	DGT	G	702	31/31	0.90	0.08	92,119,161,175	0

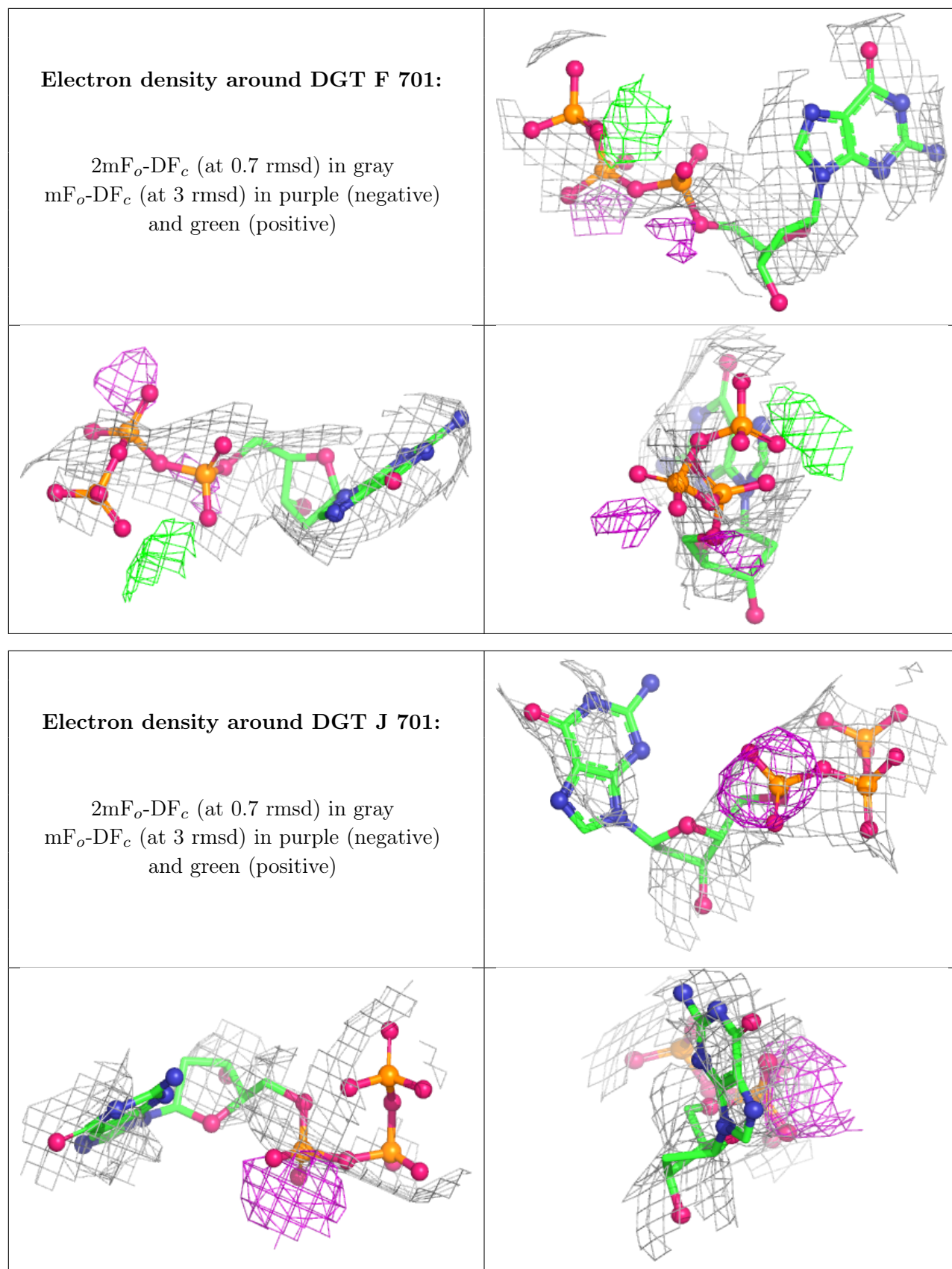
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	DGT	E	701	31/31	0.91	0.10	155,194,231,249	0
2	DGT	P	702	31/31	0.91	0.11	122,171,232,248	0
2	DGT	I	702	31/31	0.92	0.07	123,168,202,210	0
2	DGT	E	703	31/31	0.93	0.09	97,159,257,259	0
2	DGT	B	701	31/31	0.94	0.07	101,133,155,171	0

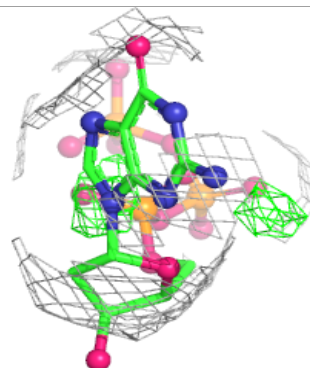
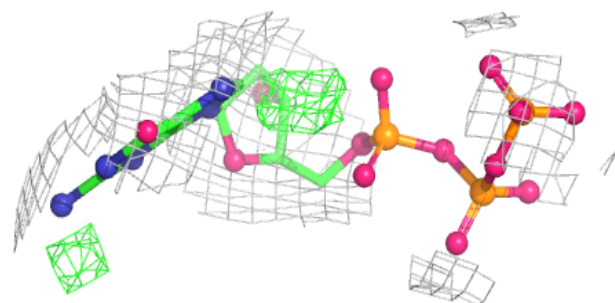
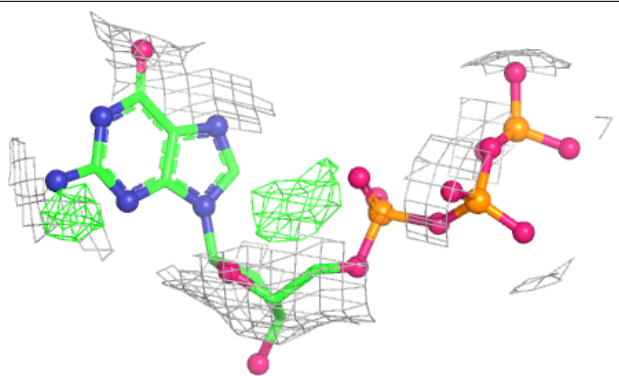
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



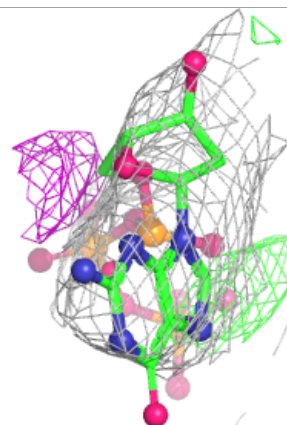
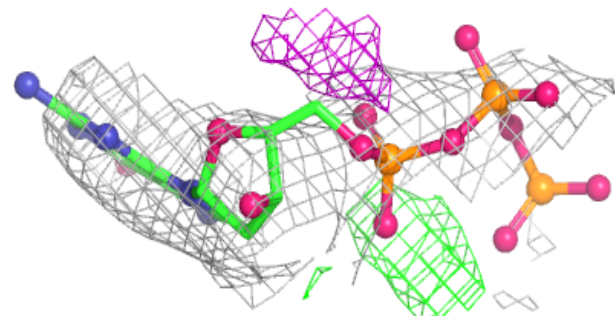
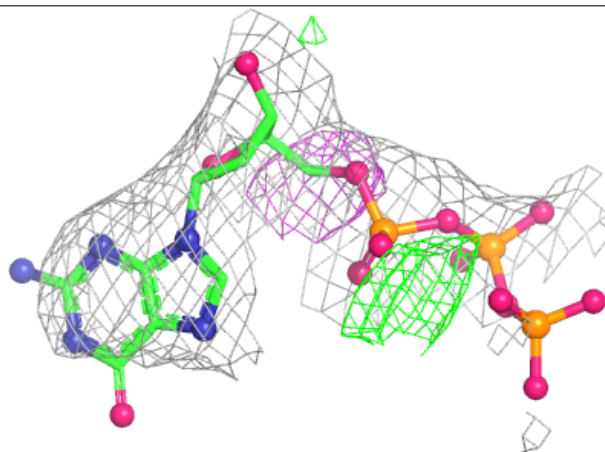


**Electron density around DGT J 703:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

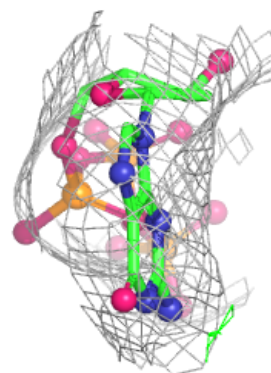
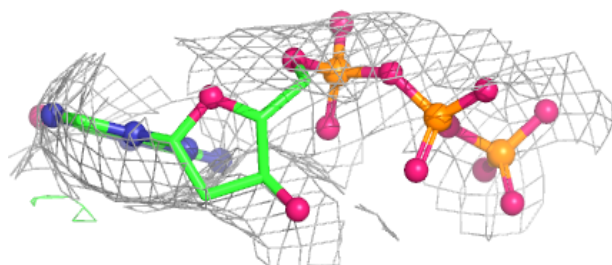
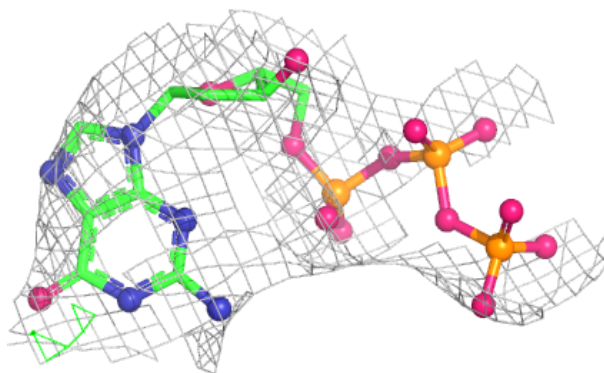
**Electron density around DGT B 702:**

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 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

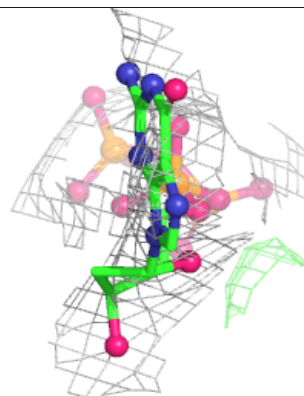
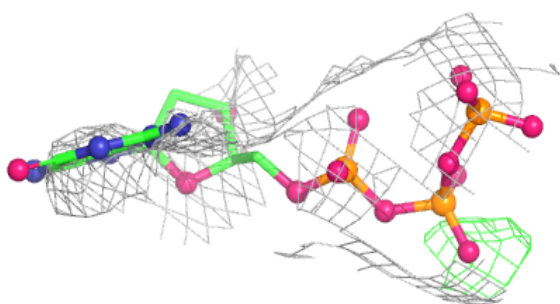
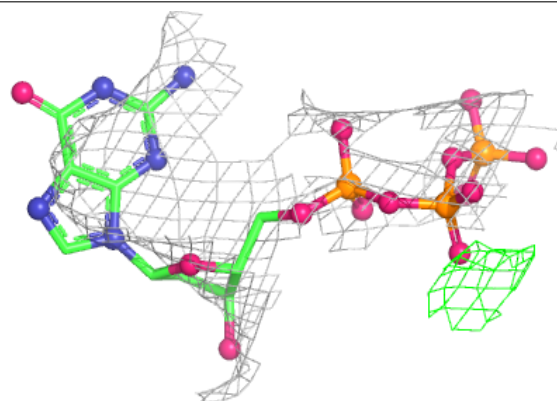


**Electron density around DGT I 701:**

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and green (positive)

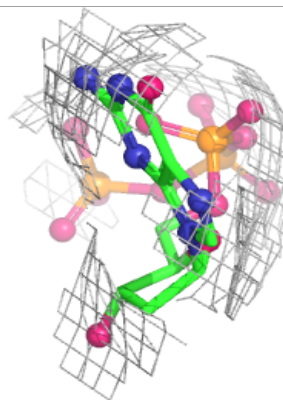
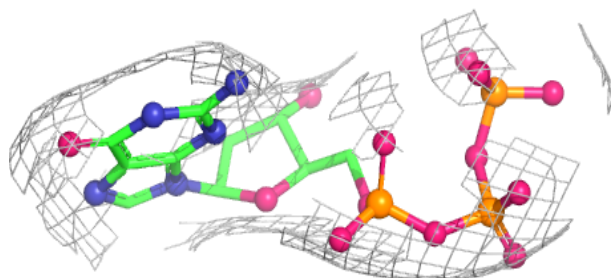
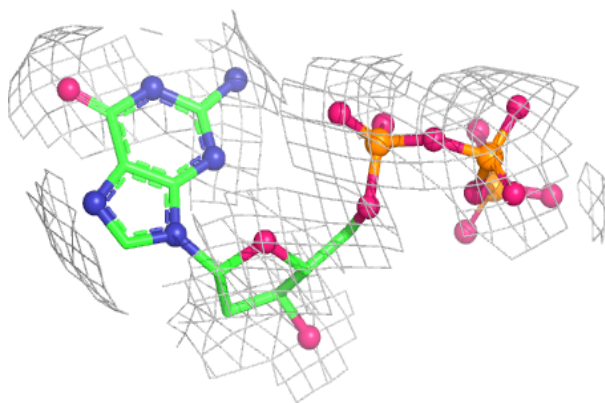
**Electron density around DGT K 701:**

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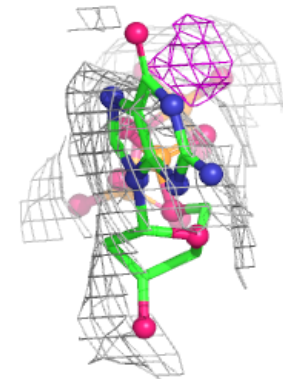
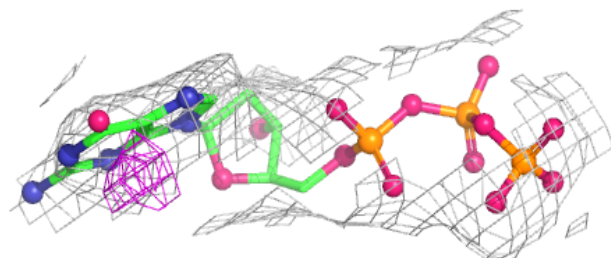
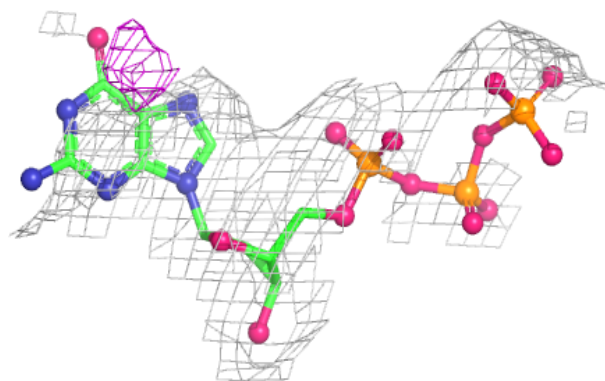


**Electron density around DGT G 701:**

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and green (positive)

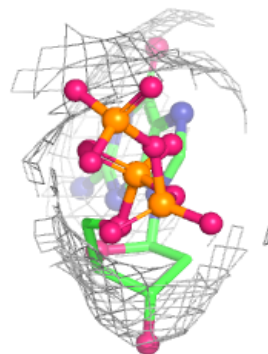
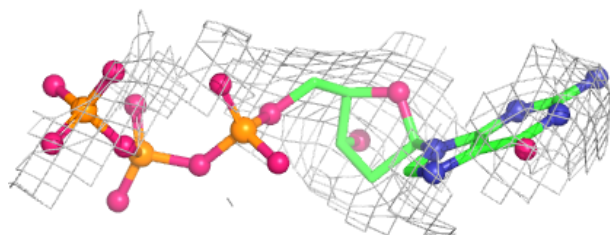
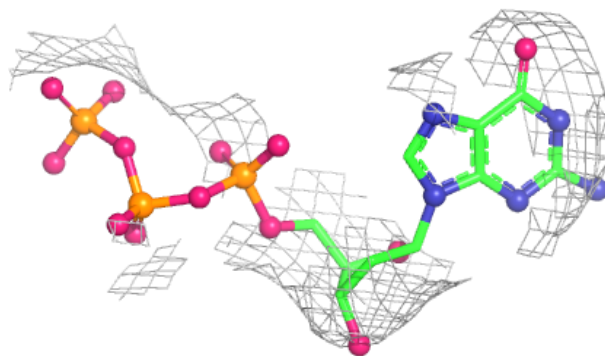
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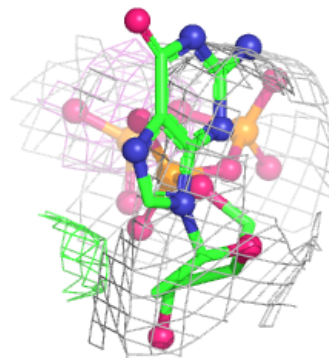
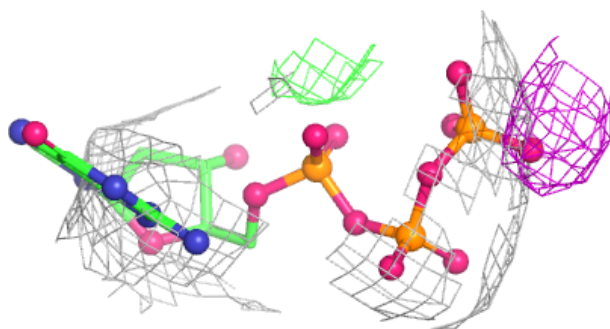
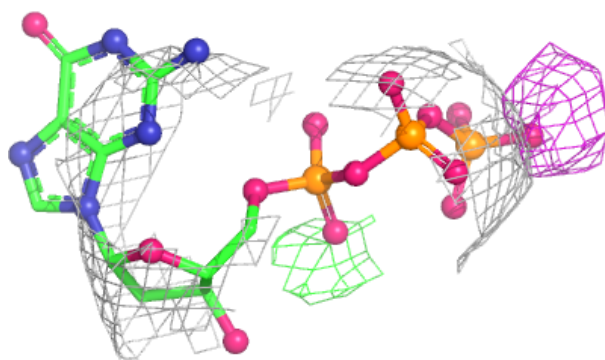


**Electron density around DGT M 702:**

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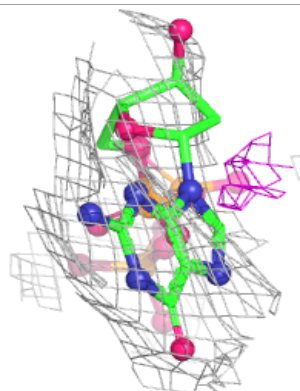
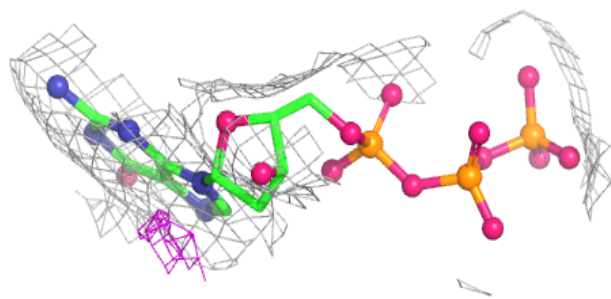
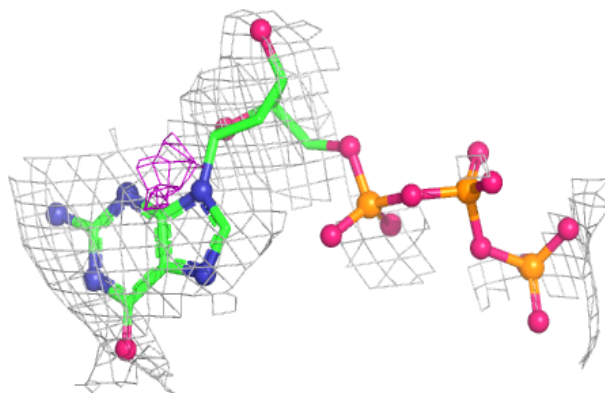
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and green (positive)

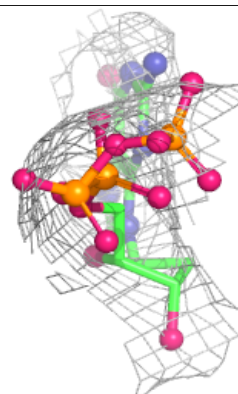
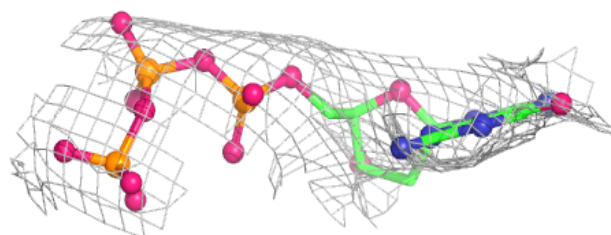
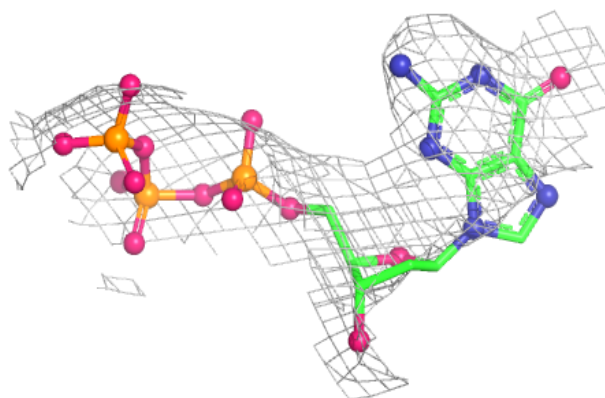


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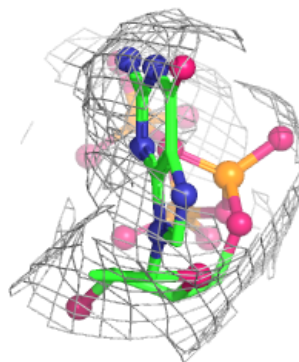
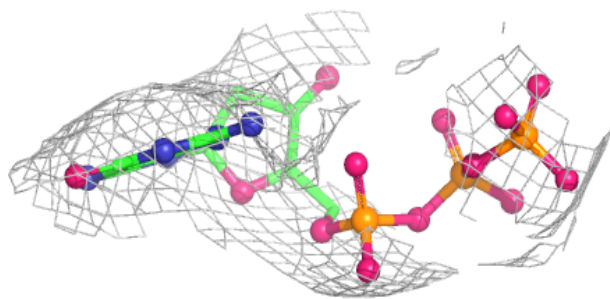
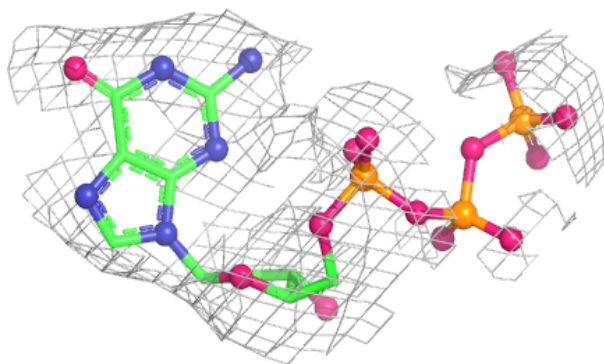
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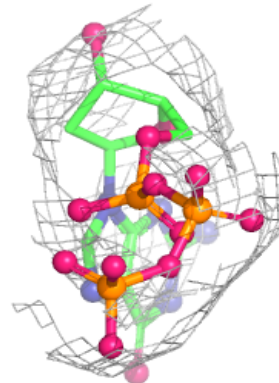
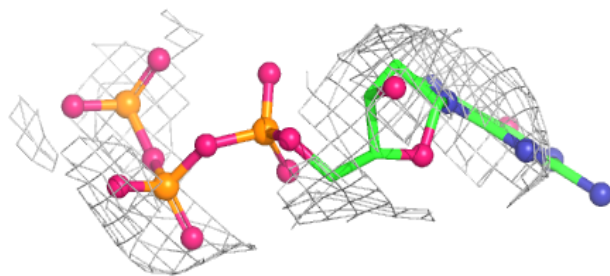
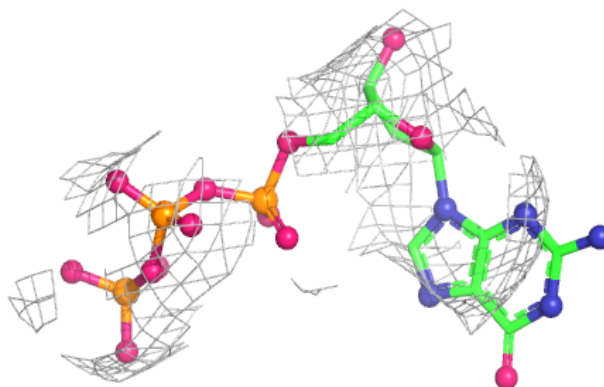


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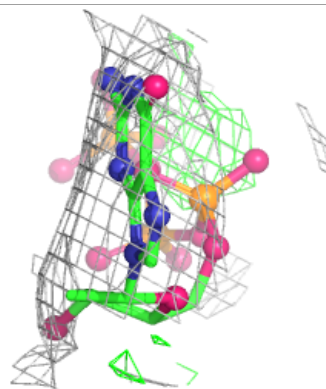
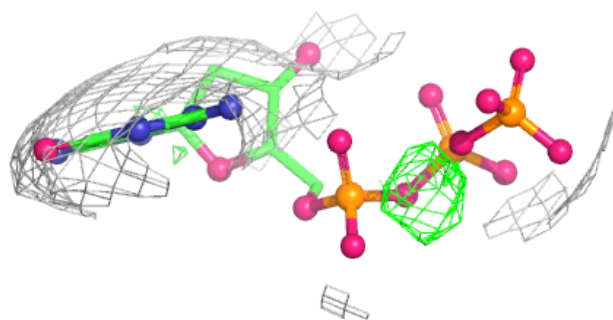
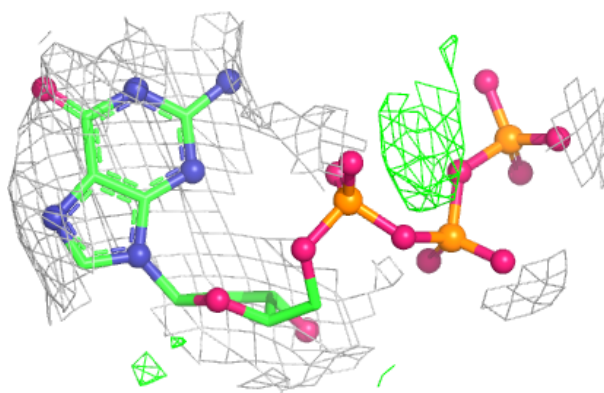
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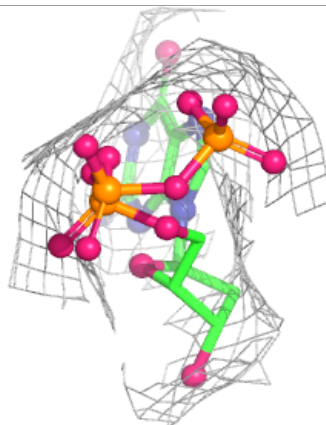
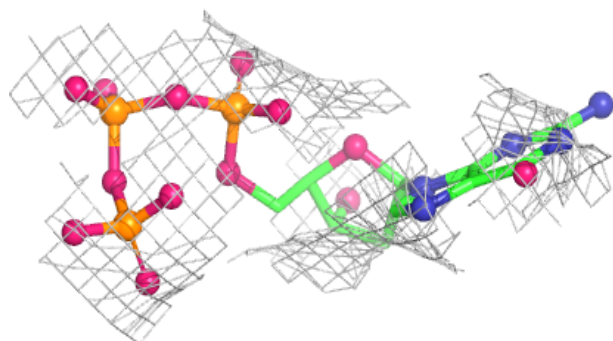
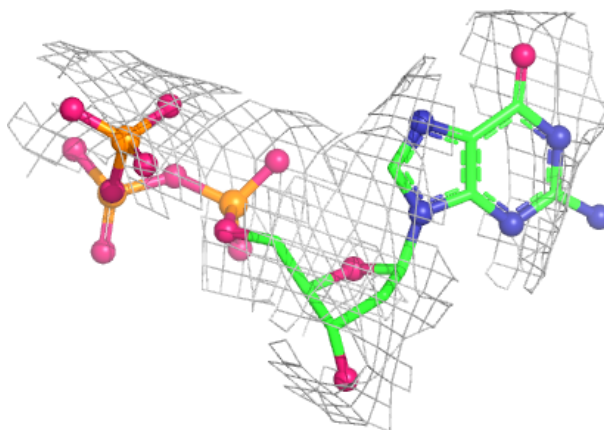


**Electron density around DGT A 701:**

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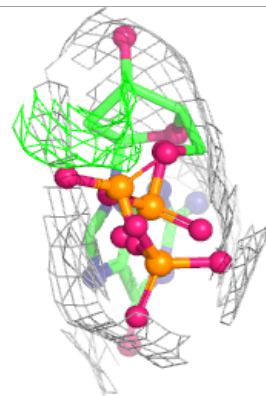
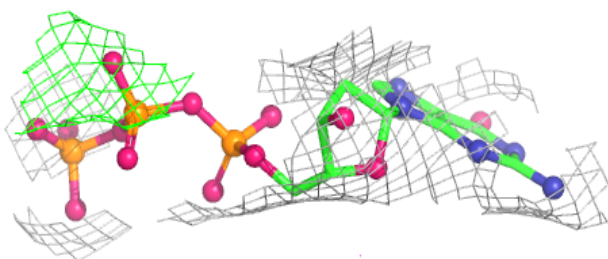
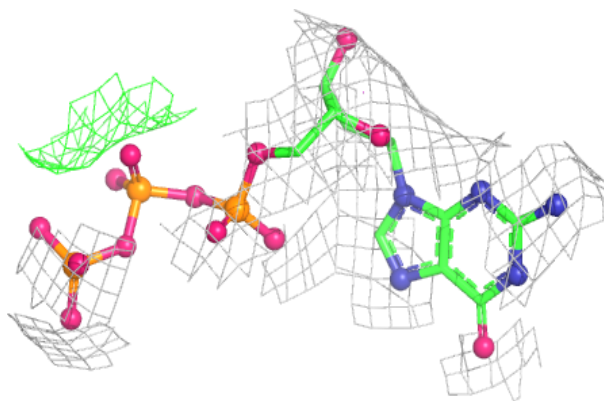
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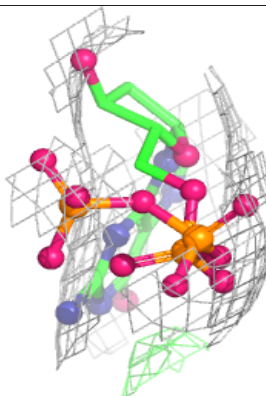
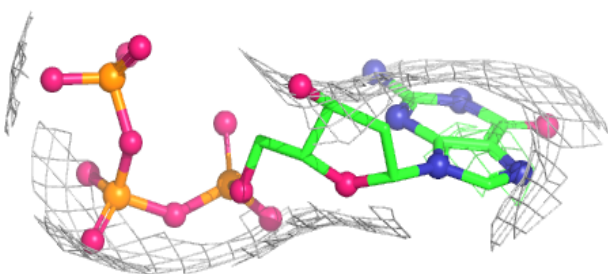
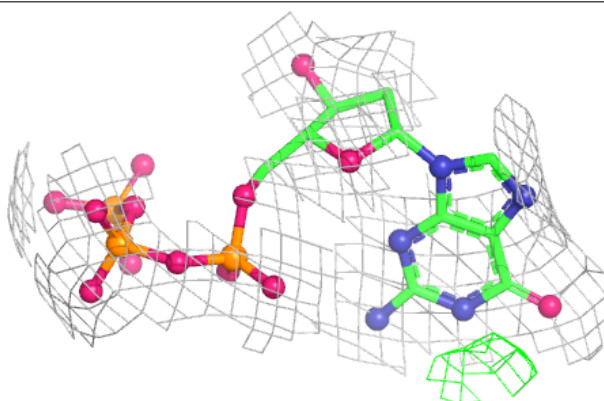


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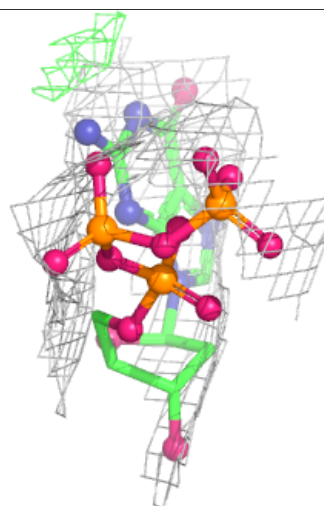
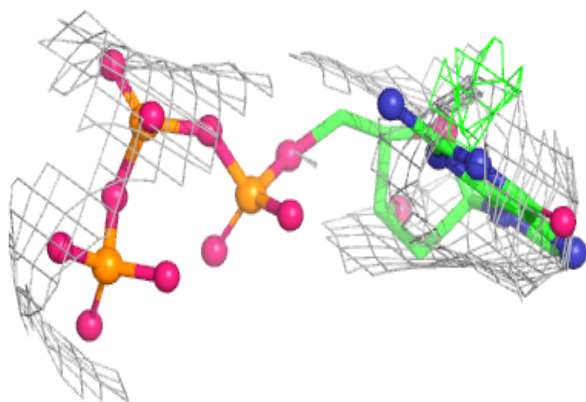
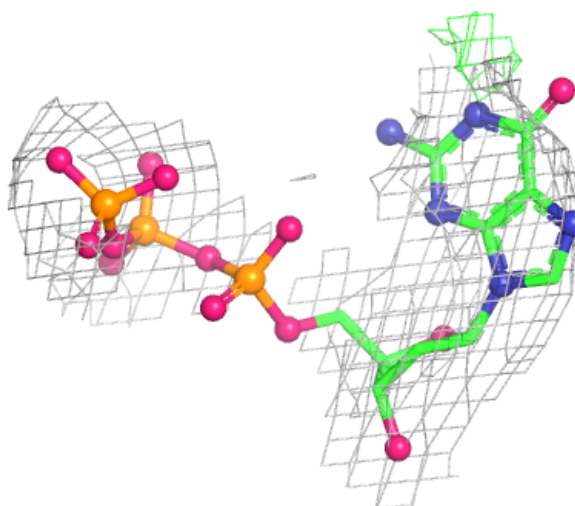
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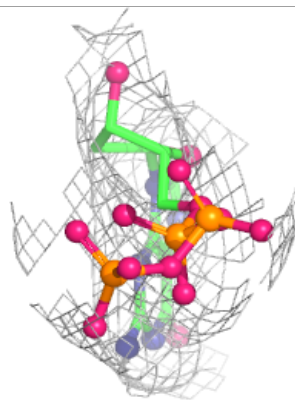
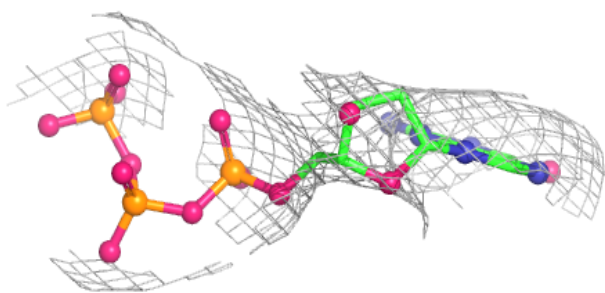
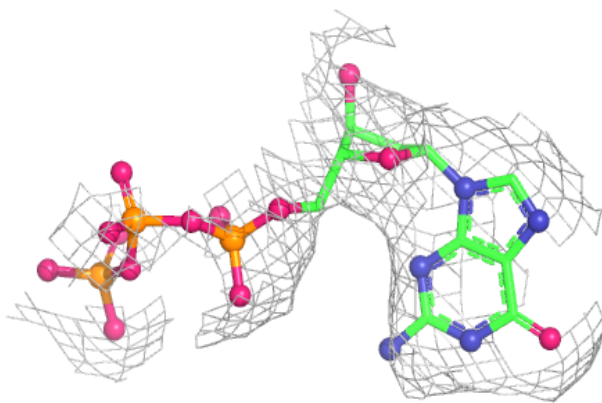
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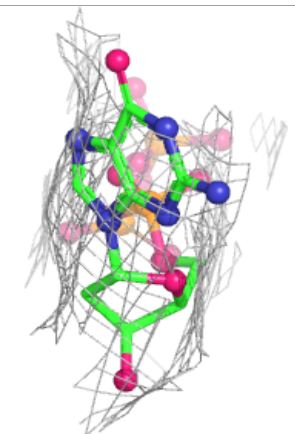
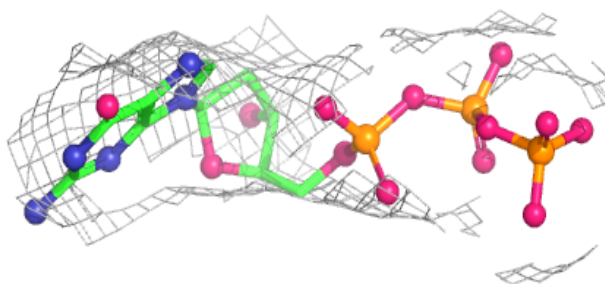
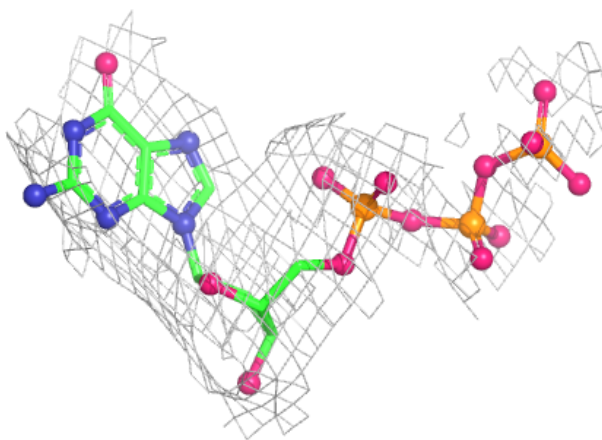


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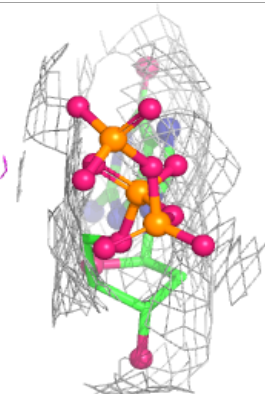
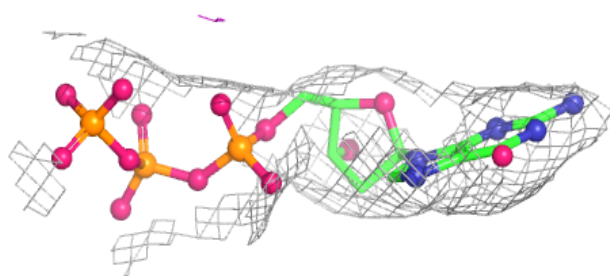
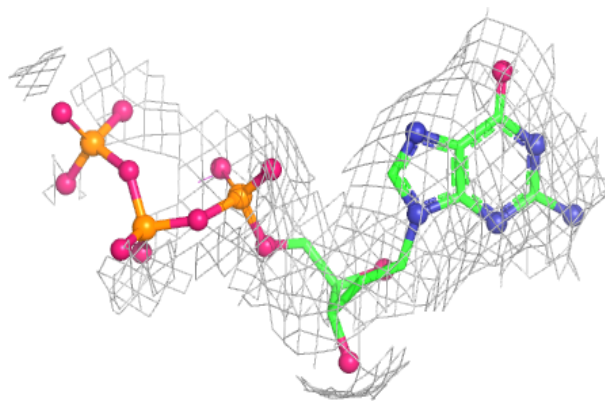
**Electron density around DGT K 702:**

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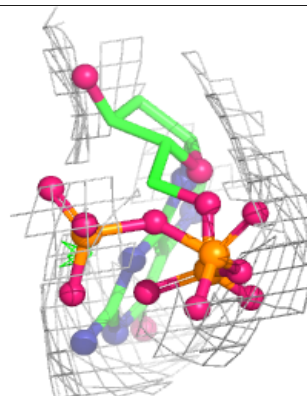
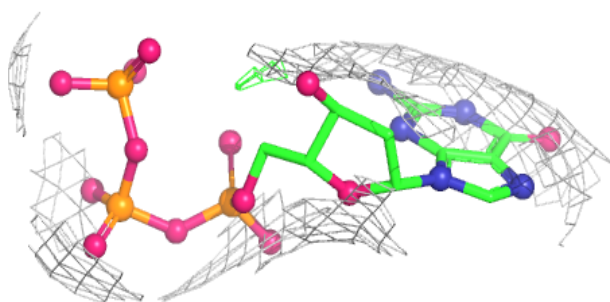
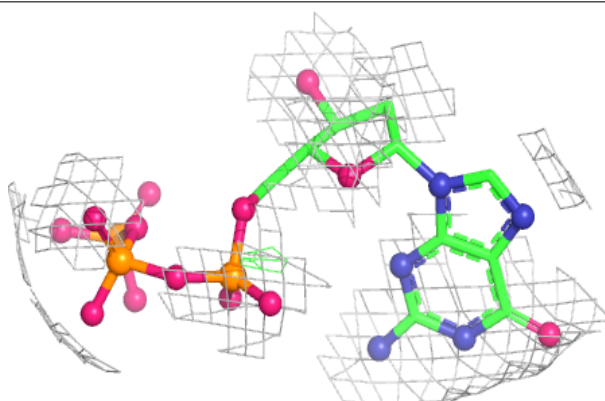


**Electron density around DGT A 702:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

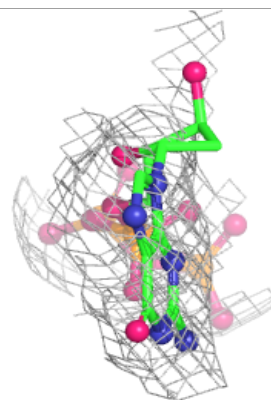
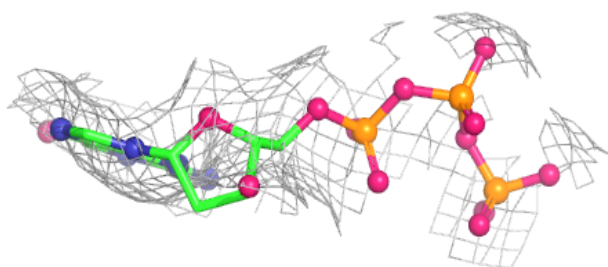
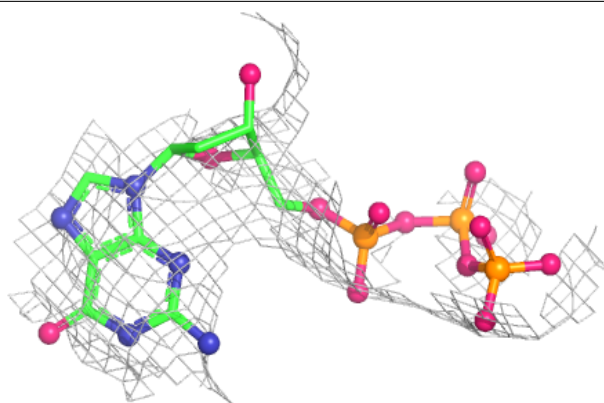
**Electron density around DGT O 701:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

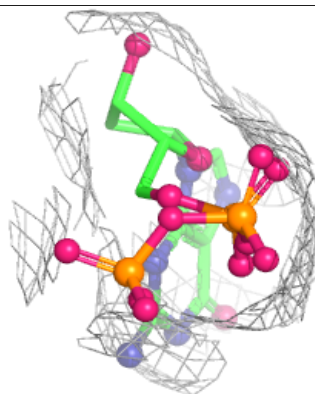
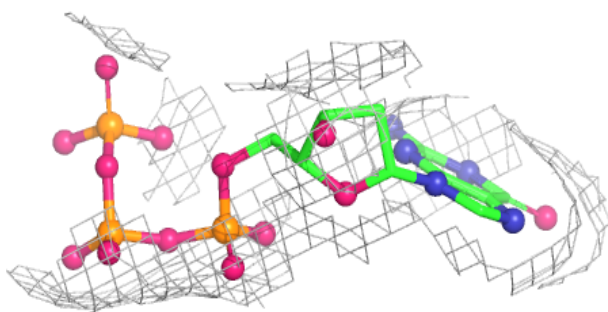
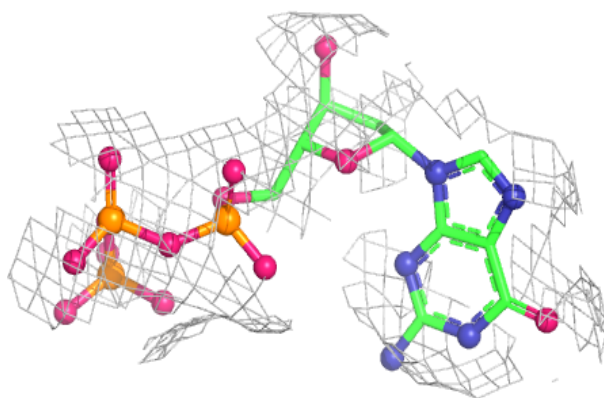


**Electron density around DGT O 702:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

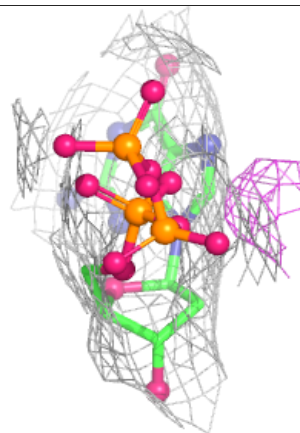
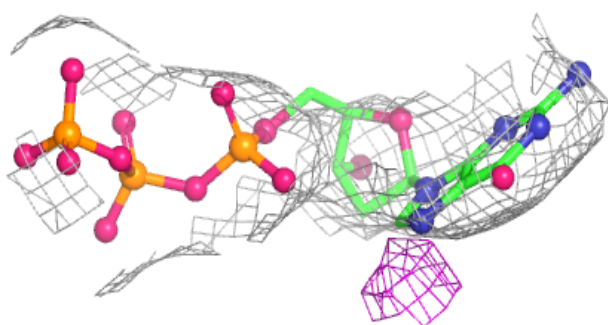
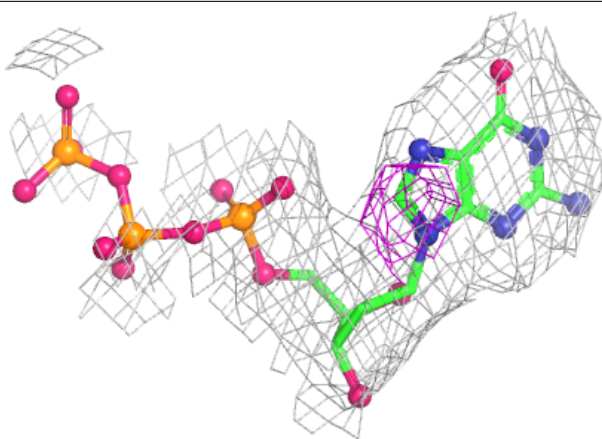
**Electron density around DGT H 701:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

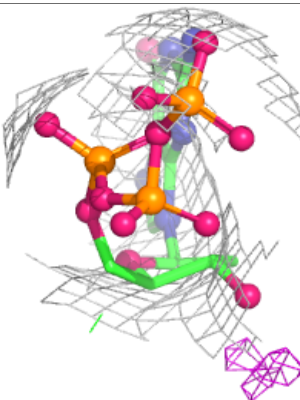
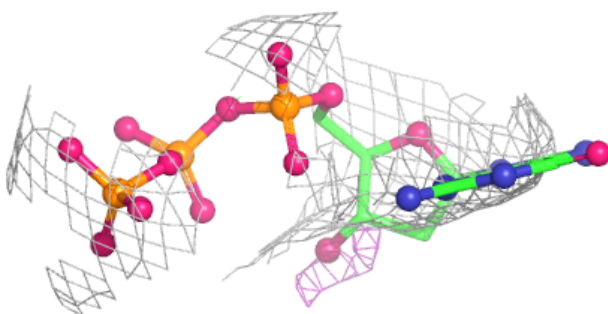
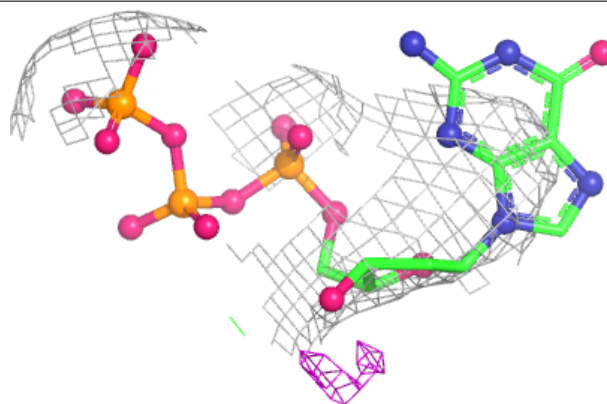


**Electron density around DGT G 702:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

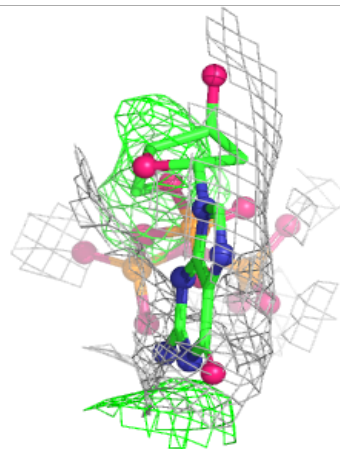
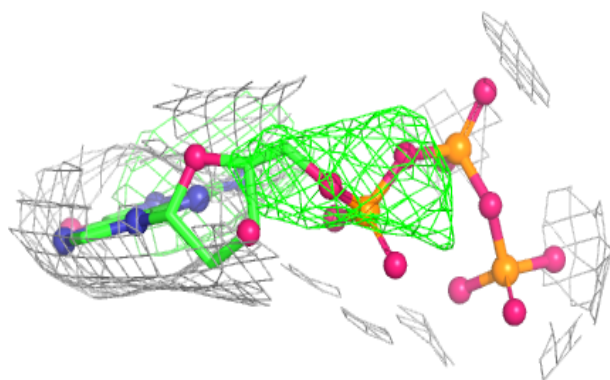
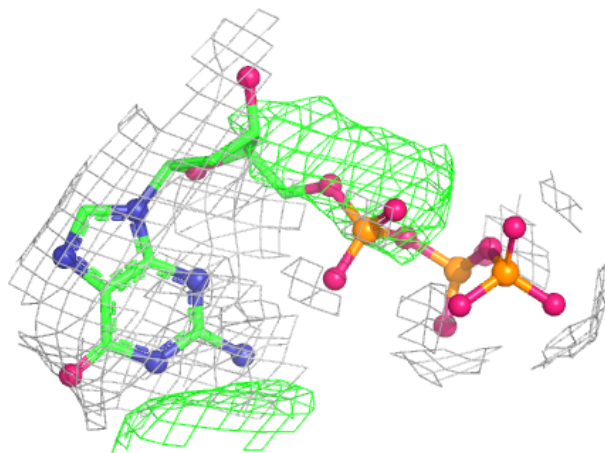
**Electron density around DGT E 701:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



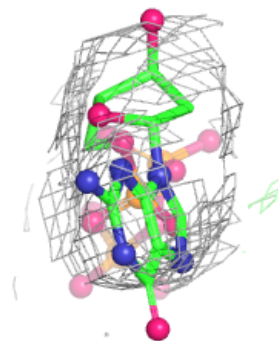
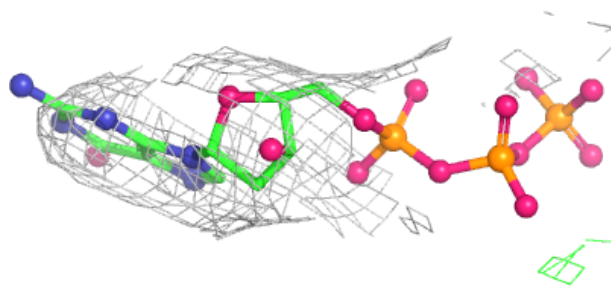
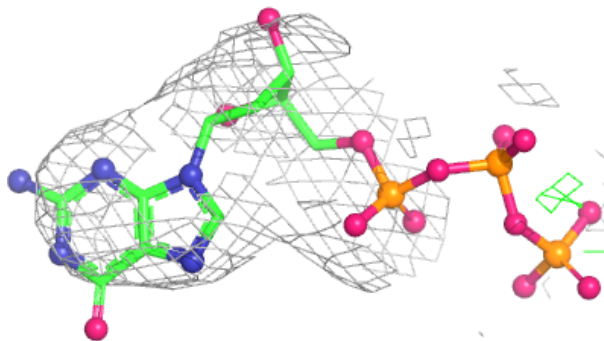
**Electron density around DGT P 702:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



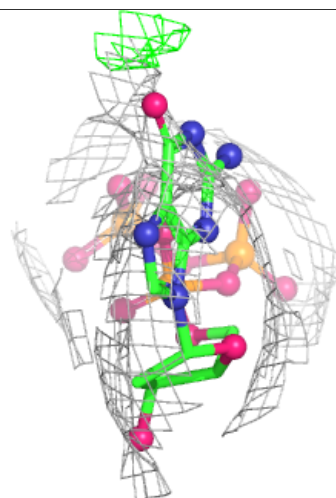
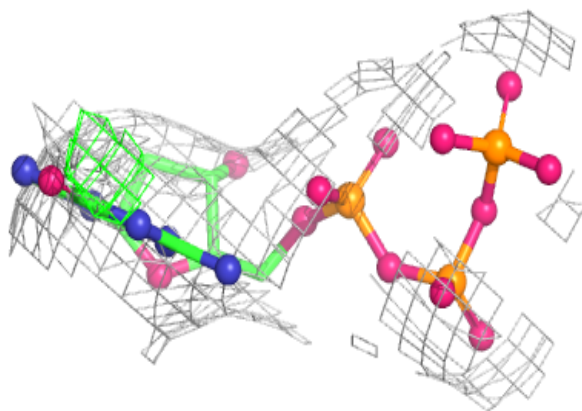
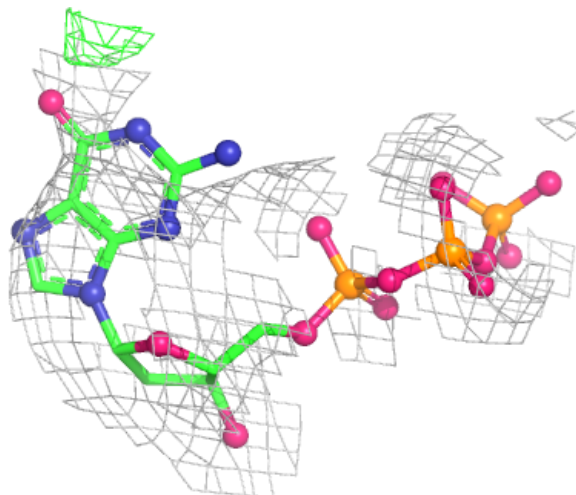
**Electron density around DGT I 702:**

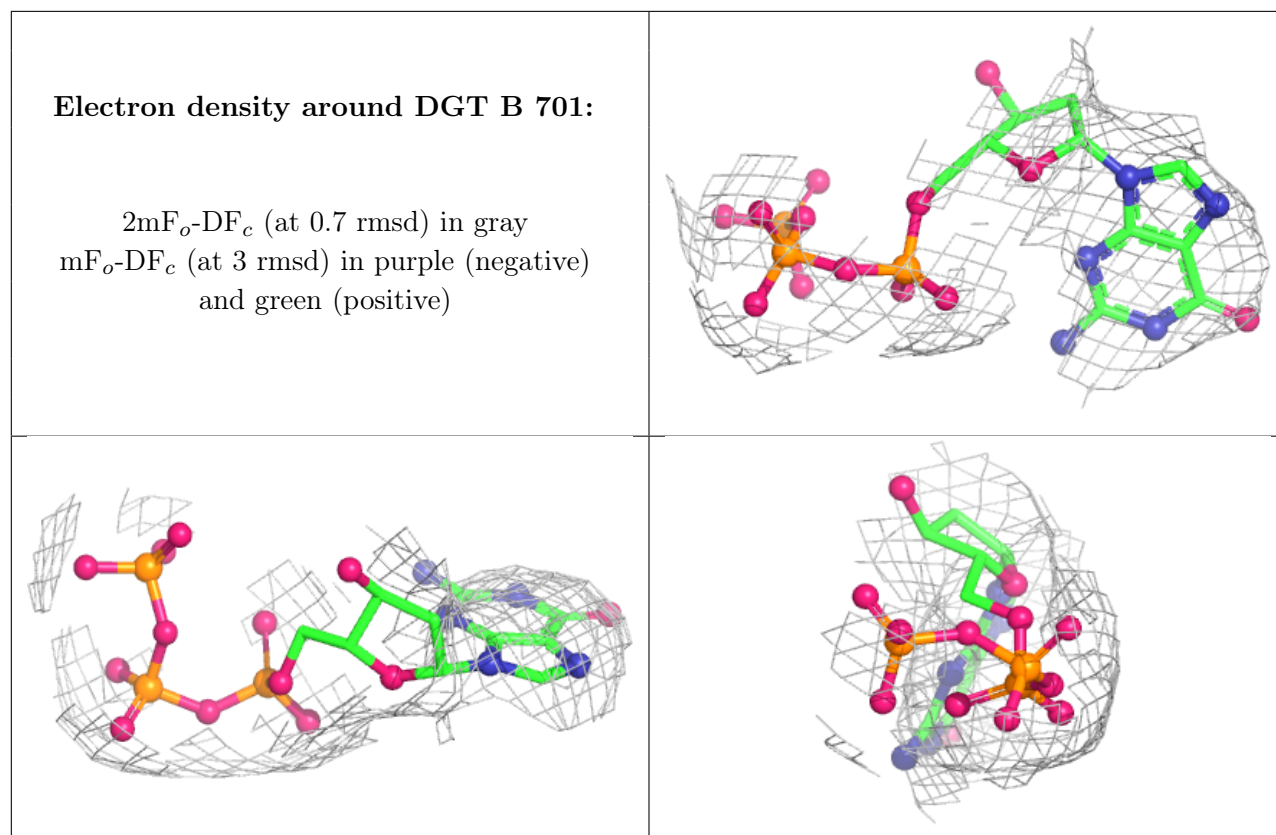
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around DGT E 703:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.