



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 03:44 PM UTC

PDB ID : 6UDO / pdb_00006udo
EMDB ID : EMD-20741
Title : Human IMPDH2 treated with ATP, IMP, and 20 mM GTP. Fully compressed filament segment reconstruction.
Authors : Johnson, M.C.; Kollman, J.M.
Deposited on : 2019-09-19
Resolution : 3.21 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

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>.

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

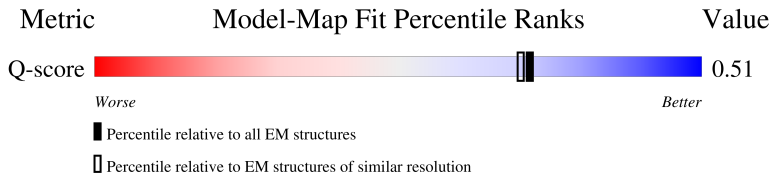
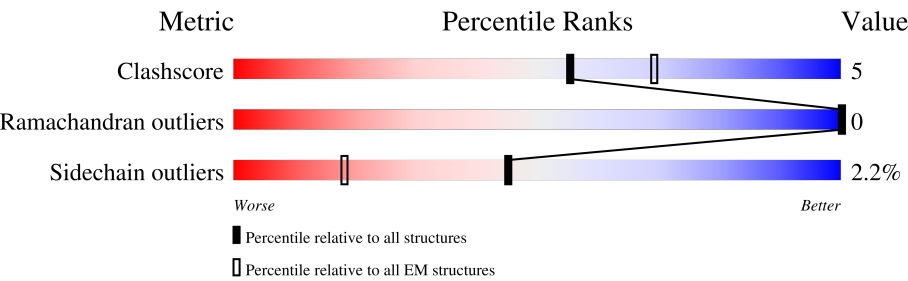
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.21 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.



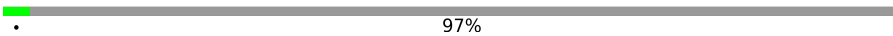
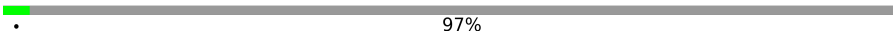
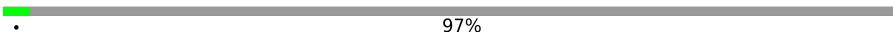
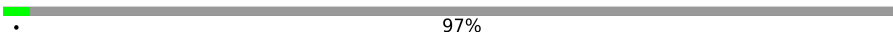
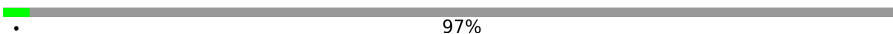
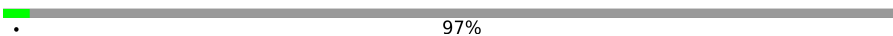
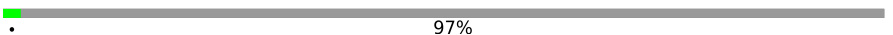
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14613 (2.71 - 3.71)

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 ≥ 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	519	80%13%6%
1	B	519	80%13%6%
1	C	519	81%13%6%
1	D	519	80%14%6%

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Mol	Chain	Length	Quality of chain
1	E	519	 80%13% • 6%
1	F	519	 79%14% • 6%
1	G	519	 81%13% • 6%
1	H	519	 80%14% • 6%
1	I	519	 97%
1	J	519	 97%
1	K	519	 97%
1	L	519	 97%
1	M	519	 97%
1	N	519	 97%
1	O	519	 97%
1	P	519	 97%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 31392 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 Inosine-5'-monophosphate dehydrogenase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	487	Total	C	N	O	S	0	0
			3704	2337	639	707	21		
1	B	487	Total	C	N	O	S	0	0
			3704	2337	639	707	21		
1	C	487	Total	C	N	O	S	0	0
			3704	2337	639	707	21		
1	D	487	Total	C	N	O	S	0	0
			3704	2337	639	707	21		
1	E	487	Total	C	N	O	S	0	0
			3704	2337	639	707	21		
1	F	487	Total	C	N	O	S	0	0
			3704	2337	639	707	21		
1	G	487	Total	C	N	O	S	0	0
			3704	2337	639	707	21		
1	H	487	Total	C	N	O	S	0	0
			3704	2337	639	707	21		
1	I	14	Total	C	N	O	S	0	0
			102	66	14	21	1		
1	J	14	Total	C	N	O	S	0	0
			102	66	14	21	1		
1	K	14	Total	C	N	O	S	0	0
			102	66	14	21	1		
1	L	14	Total	C	N	O	S	0	0
			102	66	14	21	1		
1	M	14	Total	C	N	O	S	0	0
			102	66	14	21	1		
1	N	14	Total	C	N	O	S	0	0
			102	66	14	21	1		
1	O	14	Total	C	N	O	S	0	0
			102	66	14	21	1		
1	P	14	Total	C	N	O	S	0	0
			102	66	14	21	1		

There are 80 discrepancies between the modelled and reference sequences:

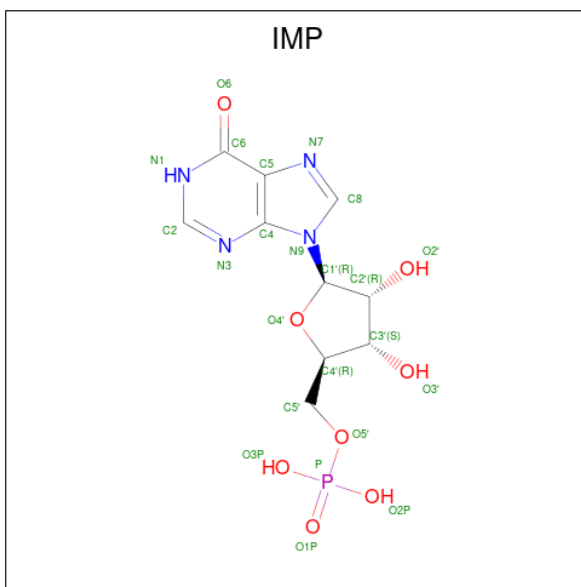
Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	SER	-	expression tag	UNP P12268
A	-3	GLU	-	expression tag	UNP P12268
A	-2	PHE	-	expression tag	UNP P12268
A	-1	GLU	-	expression tag	UNP P12268
A	0	LEU	-	expression tag	UNP P12268
B	-4	SER	-	expression tag	UNP P12268
B	-3	GLU	-	expression tag	UNP P12268
B	-2	PHE	-	expression tag	UNP P12268
B	-1	GLU	-	expression tag	UNP P12268
B	0	LEU	-	expression tag	UNP P12268
C	-4	SER	-	expression tag	UNP P12268
C	-3	GLU	-	expression tag	UNP P12268
C	-2	PHE	-	expression tag	UNP P12268
C	-1	GLU	-	expression tag	UNP P12268
C	0	LEU	-	expression tag	UNP P12268
D	-4	SER	-	expression tag	UNP P12268
D	-3	GLU	-	expression tag	UNP P12268
D	-2	PHE	-	expression tag	UNP P12268
D	-1	GLU	-	expression tag	UNP P12268
D	0	LEU	-	expression tag	UNP P12268
E	-4	SER	-	expression tag	UNP P12268
E	-3	GLU	-	expression tag	UNP P12268
E	-2	PHE	-	expression tag	UNP P12268
E	-1	GLU	-	expression tag	UNP P12268
E	0	LEU	-	expression tag	UNP P12268
F	-4	SER	-	expression tag	UNP P12268
F	-3	GLU	-	expression tag	UNP P12268
F	-2	PHE	-	expression tag	UNP P12268
F	-1	GLU	-	expression tag	UNP P12268
F	0	LEU	-	expression tag	UNP P12268
G	-4	SER	-	expression tag	UNP P12268
G	-3	GLU	-	expression tag	UNP P12268
G	-2	PHE	-	expression tag	UNP P12268
G	-1	GLU	-	expression tag	UNP P12268
G	0	LEU	-	expression tag	UNP P12268
H	-4	SER	-	expression tag	UNP P12268
H	-3	GLU	-	expression tag	UNP P12268
H	-2	PHE	-	expression tag	UNP P12268
H	-1	GLU	-	expression tag	UNP P12268
H	0	LEU	-	expression tag	UNP P12268
I	-4	SER	-	expression tag	UNP P12268
I	-3	GLU	-	expression tag	UNP P12268
I	-2	PHE	-	expression tag	UNP P12268

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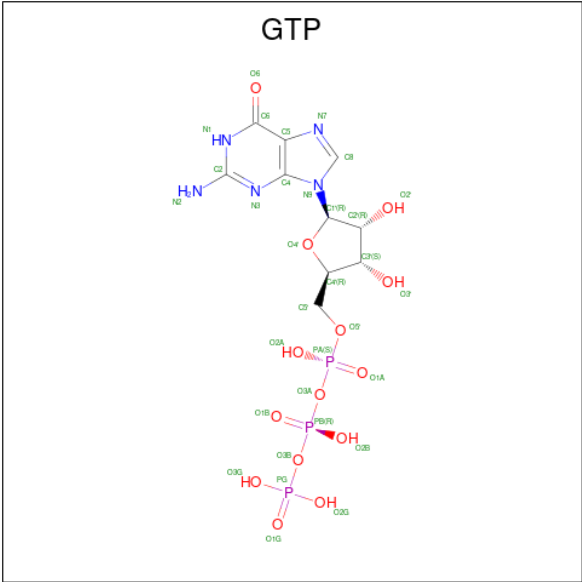
Chain	Residue	Modelled	Actual	Comment	Reference
I	-1	GLU	-	expression tag	UNP P12268
I	0	LEU	-	expression tag	UNP P12268
J	-4	SER	-	expression tag	UNP P12268
J	-3	GLU	-	expression tag	UNP P12268
J	-2	PHE	-	expression tag	UNP P12268
J	-1	GLU	-	expression tag	UNP P12268
J	0	LEU	-	expression tag	UNP P12268
K	-4	SER	-	expression tag	UNP P12268
K	-3	GLU	-	expression tag	UNP P12268
K	-2	PHE	-	expression tag	UNP P12268
K	-1	GLU	-	expression tag	UNP P12268
K	0	LEU	-	expression tag	UNP P12268
L	-4	SER	-	expression tag	UNP P12268
L	-3	GLU	-	expression tag	UNP P12268
L	-2	PHE	-	expression tag	UNP P12268
L	-1	GLU	-	expression tag	UNP P12268
L	0	LEU	-	expression tag	UNP P12268
M	-4	SER	-	expression tag	UNP P12268
M	-3	GLU	-	expression tag	UNP P12268
M	-2	PHE	-	expression tag	UNP P12268
M	-1	GLU	-	expression tag	UNP P12268
M	0	LEU	-	expression tag	UNP P12268
N	-4	SER	-	expression tag	UNP P12268
N	-3	GLU	-	expression tag	UNP P12268
N	-2	PHE	-	expression tag	UNP P12268
N	-1	GLU	-	expression tag	UNP P12268
N	0	LEU	-	expression tag	UNP P12268
O	-4	SER	-	expression tag	UNP P12268
O	-3	GLU	-	expression tag	UNP P12268
O	-2	PHE	-	expression tag	UNP P12268
O	-1	GLU	-	expression tag	UNP P12268
O	0	LEU	-	expression tag	UNP P12268
P	-4	SER	-	expression tag	UNP P12268
P	-3	GLU	-	expression tag	UNP P12268
P	-2	PHE	-	expression tag	UNP P12268
P	-1	GLU	-	expression tag	UNP P12268
P	0	LEU	-	expression tag	UNP P12268

- Molecule 2 is INOSINIC ACID (CCD ID: IMP) (formula: $C_{10}H_{13}N_4O_8P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			23	10	4	8	1	
2	B	1	Total	C	N	O	P	0
			23	10	4	8	1	
2	C	1	Total	C	N	O	P	0
			23	10	4	8	1	
2	D	1	Total	C	N	O	P	0
			23	10	4	8	1	
2	E	1	Total	C	N	O	P	0
			23	10	4	8	1	
2	F	1	Total	C	N	O	P	0
			23	10	4	8	1	
2	G	1	Total	C	N	O	P	0
			23	10	4	8	1	
2	H	1	Total	C	N	O	P	0
			23	10	4	8	1	

- Molecule 3 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



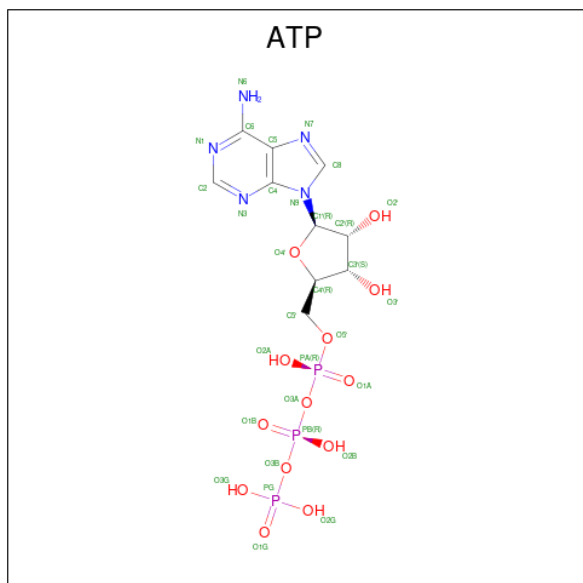
Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	A	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	B	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	B	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	C	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	C	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	D	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	D	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	E	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	E	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	F	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	F	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	G	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	G	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms					AltConf
3	H	1	Total	C	N	O	P	0
			32	10	5	14	3	
3	H	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



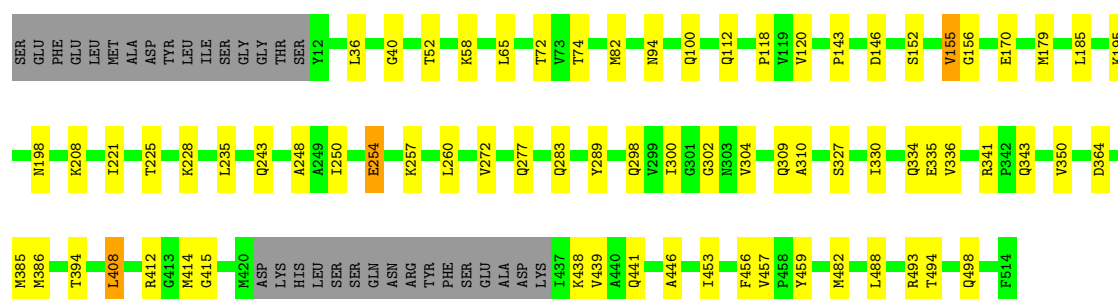
Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	E	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	F	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	G	1	Total	C	N	O	P	0
			31	10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

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 and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

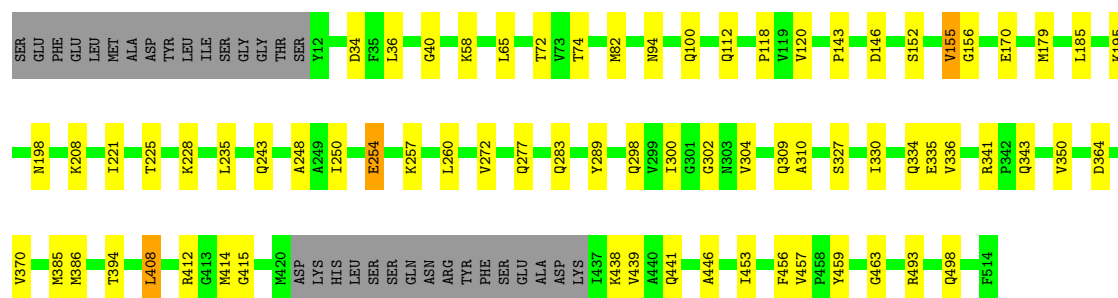
- Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

Chain A: 



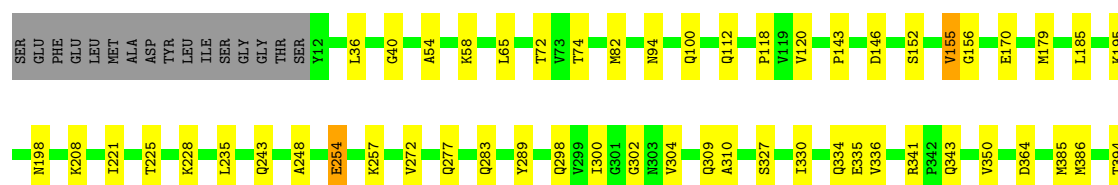
- Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

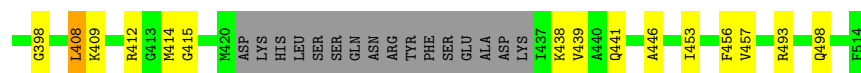
Chain B: 



- Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

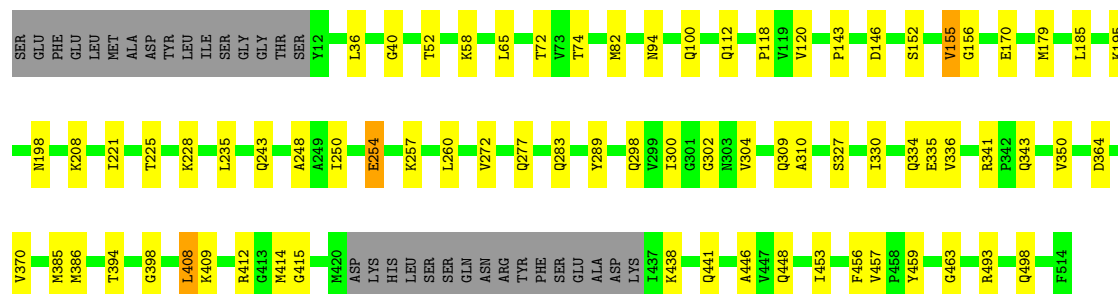
Chain C: 





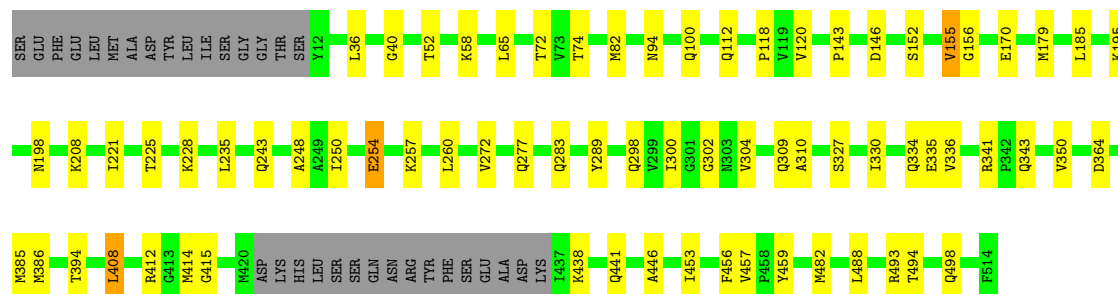
• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

Chain D: 80% 14% • 6%



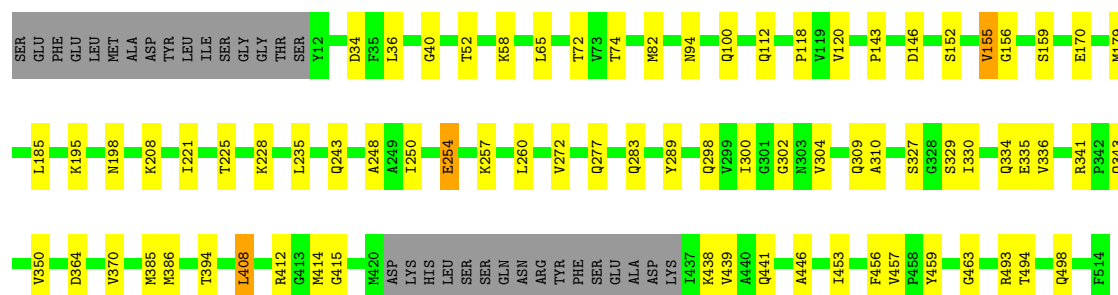
• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

Chain E: 80% 13% • 6%



• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

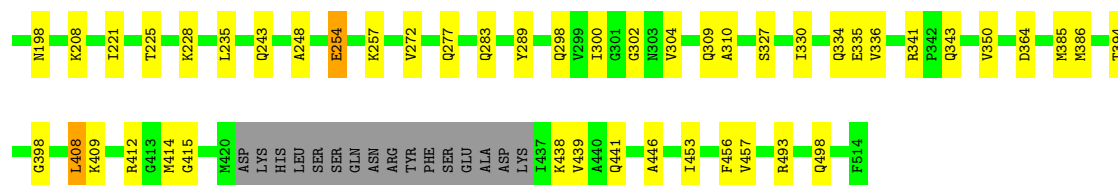
Chain F: 79% 14% • 6%



• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

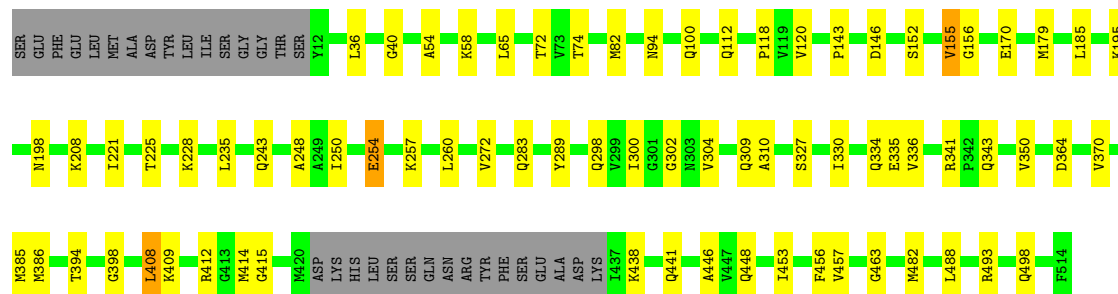
Chain G: 81% 13% • 6%





• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

Chain H: 80% 14% 6%



• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

Chain I: 97% 1% 2%



• Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

Chain J: 97% 1% 2%

97%

ser	gly	ser	gly	thr	val	leu	leu	asp	leu	ser
glu	glu	glu	ile	ala	glu	cys	val	arg	val	glu
leu	asn	asn	glu	ala	ala	ala	ala	arg	ser	leu
lys	lys	arg	asn	glu	glu	ala	pro	asp	pro	met
phe	phe	tyr	val	ala	ile	ile	ala	val	asp	m1
glu	glu	phe	gly	lys	lys	thr	gly	phe	thr	
lys	lys	ser	his	asn	thr	thr	ile	glu	thr	
glu	glu	glu	ile	leu	glu	his	thr	ala	val	
thr	thr	ala	ala	ile	ile	glu	glu	thr	thr	
ser	ser	asp	lys	asp	asp	asp	lys	ala	glu	
ser	ser	lys	ala	ala	asp	asp	glu	ala	ala	
ala	ile	ile	leu	gly	gly	lys	ala	his	gly	
glu	glu	val	ala	val	val	tyr	asn	gly	met	
val	val	val	leu	asp	arg	arg	leu	pro	ala	
glu	glu	ala	gly	ala	leu	leu	ile	cys	thr	
gly	gly	glu	ala	leu	arg	leu	glu	ile	met	
val	val	val	thr	thr	val	leu	arg	pro	ala	
his	his	ser	val	gly	gly	ala	ser	ile	leu	
ser	ser	gly	met	met	met	glu	lys	phe	ala	
leu	leu	ala	met	gly	glu	ala	lys	cys	thr	
leu	his	glu	gly	ser	val	asp	gly	thr	lys	
ser	ser	glu	ser	leu	asp	val	lys	arg	lys	
tyr	tyr	asn	leu	thr	thr	thr	ile	arg	pro	
glu	lys	glu	ala	leu	val	val	pro	met	val	
arg	arg	ser	ala	ile	ile	val	val	thr	thr	
leu	leu	ile	thr	thr	leu	leu	leu	ile	leu	
phe	his	his	thr	thr	asn	asn	val	ser	phe	
	lys	lys	thr	thr	glu	glu	ala	ser	glu	
	phe	lys	glu	ala	ser	ser	asp	leu	asn	
	val	val	ala	val	thr	thr	thr	thr	thr	
	pro	pro	pro	leu	glu	glu	leu	ile	pro	
	tyr	tyr	tyr	glu	cys	asn	val	ser	phe	
	leu	leu	glu	tyr	gly	ser	ala	ser	glu	
	ile	ile	phe	phe	arg	ile	ile	arg	ala	
	ala	gly	ser	ser	pro	phe	ala	ile	asn	
	ile	ile	asp	asp	ala	ile	arg	thr	asp	
	glu	glu	thr	thr	ala	met	asp	phe	lys	
	his	ser	arg	arg	val	ile	leu	leu	val	
	cys	cys	lys	tyr	tyr	lys	lys	glu	asp	
	glu	glu	lys	lys	lys	tyr	lys	glu	lys	
	asn	asn	val	val	ile	ile	asn	glu	tyr	
	ile	ile	tyr	ser	lys	lys	arg	his	glu	
	gly	gly	arg	thr	asp	asp	asp	asp	glu	
	ala	ala	gly	tyr	tyr	lys	tyr	cys	thr	
	lys	lys	met	ala	val	glu	asp	thr	thr	
	thr	thr	thr	thr	thr	thr	thr	thr	thr	
	glu	glu	thr	thr	thr	thr	thr	thr	thr	
	asn	asn	thr	thr	thr	thr	thr	thr	thr	
	glu	glu	thr	thr	thr	thr	thr	thr	thr	
	thr	thr	thr	thr	thr	thr	thr	thr	thr	
	thr	thr	thr	thr	thr	thr	thr	thr	thr	
	thr	thr	thr	thr	thr	thr	thr	thr	thr	
	thr	thr	thr	thr	thr	thr	thr	thr	thr	
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	thr	thr	thr	thr	thr	thr	thr	thr	thr	
	thr	thr	thr	thr	thr	thr	thr	thr	thr	
	thr	thr	thr	thr	thr	thr	thr	thr	thr	
	thr	thr	thr	thr	thr	thr	thr	thr	thr	
	thr	thr	thr	thr	thr	thr	thr	thr	thr	
	thr	thr	thr	thr	thr	thr	thr	thr	thr	
	thr	thr	thr	thr	thr	thr	thr	thr	thr	
	thr	thr	thr	thr	thr	thr	thr	thr	thr	
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	thr	thr	thr	thr	thr	thr	thr	thr	thr	
	thr	thr	thr	thr	thr	thr	thr			

Chain M:

97%

VAL	GLY	THR	VAL	LEU	LEU	ASP	LEU	ASP	LEU	SER
THR	GLY	THR	VAL	CYS	VAL	ARG	VAL	ARG	VAL	GLU
ALA	ILE	ALA	GLY	GLY	VAL	VAL	VAL	VAL	SER	PHE
ALA	GLN	ALA	ALA	ALA	ALA	PRO	ASP	ASP	SER	GLU
ALA	VAL	ALA	ILE	ILE	ILE	GLY	PHE	PHE	MET	M1
LYS	GLY	ASN	THR	THR	THR	ILE	GLU	GLU	THR	L5
ASN	HIS	ILE	HIS	HIS	ALA	ALA	ALA	ALA	VAL	P14
GLY	ILE	ILE	GLU	GLU	GLU	LYS	LYS	ARG	ASP	ASP
VAL	LYS	ASP	ASP	ASP	ASP	GLU	GLY	HIS	GLY	GLY
ALA	ALA	ALA	LYS	LYS	LYS	ALA	HIS	ASP	ALA	ASP
LEU	LEU	GLY	TYR	ASN	ASN	ASN	GLY	GLY	GLY	LEU
VAL	VAL	VAL	VAL	TYR	ARG	ASP	PHE	PHE	MET	THR
ALA	GLY	ALA	ALA	LEU	LEU	ILE	CYS	CYS	ILE	ALA
ALA	GLY	ALA	ILE	ASP	ASP	GLY	GLY	GLY	ILE	GLN
GLN	ALA	LEU	LEU	LEU	LEU	ILE	ILE	ILE	MET	LEU
GLY	SER	ARG	VAL	LEU	ARG	PRO	PRO	PRO	ALA	LEU
VAL	THR	VAL	VAL	LEU	SER	ILE	ALA	ILE	ALA	PHE
VAL	VAL	VAL	GLY	ALA	ALA	ARG	ASP	GLY	LEU	THR
GLY	VAL	MET	MET	GLN	GLN	LYS	THR	THR	THR	ALA
GLY	MET	GLY	GLY	ALA	ALA	LYS	ASP	ASP	GLY	CYS
VAL	GLY	SER	SER	VAL	GLY	GLY	THR	THR	ILE	GLY
GLN	SER	GLY	GLY	VAL	VAL	LYS	GLY	ARG	GLY	ASP
GLN	LEU	SER	SER	ASP	ASP	LEU	ARG	GLY	GLY	GLY
LYS	LEU	THR	THR	ASP	ASP	GLU	LEU	ASN	ASN	ASP
PHE	ALA	ALA	VAL	SER	SER	ASP	VAL	CYS	PHE	PHE
VAL	PRO	LEU	LEU	GLN	GLN	GLU	ILE	PRO	THR	LEU
PRO	GLY	ALA	ALA	GLY	GLY	LEU	ILE	ILE	GLU	ILE
TYR	GLU	CYS	GLY	ASN	ASN	VAL	SER	PHE	PHE	PRO
LEU	TYR	GLY	THR	SER	SER	ALA	SER	GLN	GLN	TYR
ILE	PHE	ARG	ARG	ILE	ILE	ILE	ARG	ARG	ALA	GLY
ALA	PHE	GLN	PRO	PHE	ILE	ILE	ASP	ASP	ASN	ILE
ILE	ILE	ASP	ALA	ILE	ILE	ARG	VAL	VAL	ASP	ASP
GLN	GLY	THR	ALA	ASN	THR	PHE	PHE	ARG	LYS	THR
HIS	ILE	ALA	VAL	MET	ASP	LEU	LEU	LYS	VAL	ALA
SER	ARG	VAL	VAL	ILE	ILE	GLY	GLY	VAL	VAL	ASP
CYS	LEU	THR	THR	LYS	LYS	GLU	GLY	GLY	GLN	GLN
GLN	ARG	LYS	LYS	TYR	TYR	GLU	GLU	GLU	LYS	VAL
ASP	ILE	VAL	VAL	ILE	ILE	ASN	GLU	GLU	TYR	ASP
ILE	TYR	SER	SER	LYS	LYS	ARG	HIS	HIS	GLU	LEU
GLY	ARG	GLU	GLU	ASP	ASP	ASP	ASP	ASP	GLN	THR
ALA	GLY	TYR	TYR	LYS	LYS	CYS	CYS	CYS	GLY	SER
LYS	MET	ALA	ALA	TYR	PRO	PHE	PHE	PHE	ILE	ALA
SER	GLY	ARG	ARG	PRO	PRO	LEU	LEU	LEU	THR	LYS
LEU	SER	ARG	PHE	ASN	ASN	ASN	ASN	ASN	THR	LYS
THR	LEU	PHE	GLY	GLN	GLN	ILE	ASP	ASP	ASP	LYS
GLN	ASP	GLY	GLY	VAL	VAL	ILE	ILE	ILE	PRO	LYS
VAL	ALA	VAL	VAL	VAL	VAL	MET	MET	MET	VAL	ILE
ARG	MET	PRO	PRO	ILE	ILE	THR	THR	THR	VAL	THR
ALA	ASP	VAL	VAL	GLY	GLY	LYS	LYS	ARG	LEU	LEU
MET	MET	ILE	ILE	GLY	GLY	GLY	ARG	GLY	SER	LYS
MET	THR	THR	THR	ASN	ASN	ASN	GLU	GLU	THR	THR
THR	ILE	ASP	ASP	GLN	GLN	THR	THR	THR	PRO	PRO
ASN	THR	THR	THR	VAL	VAL	ASP	ASP	ASP	LYS	LYS

[illegible]

- Molecule 1: Inosine-5'-monophosphate dehydrogenase 2

Chain P: 97%

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D4	Depositor
Number of particles used	31392	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	100	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	138.716	Depositor
Minimum map value	-88.945	Depositor
Average map value	0.058	Depositor
Map value standard deviation	3.698	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	330.6, 330.6, 330.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8265, 0.8265, 0.8265	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IMP, GTP, ATP

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	0.32	0/3760	0.63	5/5070 (0.1%)
1	B	0.32	0/3760	0.63	5/5070 (0.1%)
1	C	0.32	0/3760	0.63	5/5070 (0.1%)
1	D	0.32	0/3760	0.63	5/5070 (0.1%)
1	E	0.32	0/3760	0.63	5/5070 (0.1%)
1	F	0.32	0/3760	0.63	5/5070 (0.1%)
1	G	0.32	0/3760	0.63	5/5070 (0.1%)
1	H	0.32	0/3760	0.63	5/5070 (0.1%)
1	I	0.28	0/104	0.75	0/141
1	J	0.28	0/104	0.75	0/141
1	K	0.28	0/104	0.75	0/141
1	L	0.28	0/104	0.75	0/141
1	M	0.28	0/104	0.75	0/141
1	N	0.28	0/104	0.75	0/141
1	O	0.28	0/104	0.75	0/141
1	P	0.28	0/104	0.75	0/141
All	All	0.32	0/30912	0.63	40/41688 (0.1%)

There are no bond length outliers.

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	254	GLU	CB-CG-CD	5.92	122.67	112.60
1	G	254	GLU	CB-CG-CD	5.92	122.67	112.60
1	D	254	GLU	CB-CG-CD	5.92	122.66	112.60
1	B	254	GLU	CB-CG-CD	5.92	122.66	112.60
1	E	254	GLU	CB-CG-CD	5.91	122.65	112.60

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	3704	0	3760	43	0
1	B	3704	0	3760	42	0
1	C	3704	0	3760	40	0
1	D	3704	0	3760	43	0
1	E	3704	0	3760	42	0
1	F	3704	0	3760	46	0
1	G	3704	0	3760	40	0
1	H	3704	0	3760	42	0
1	I	102	0	99	1	0
1	J	102	0	99	0	0
1	K	102	0	99	1	0
1	L	102	0	99	1	0
1	M	102	0	99	1	0
1	N	102	0	99	1	0
1	O	102	0	99	2	0
1	P	102	0	99	1	0
2	A	23	0	11	1	0
2	B	23	0	11	1	0
2	C	23	0	11	1	0
2	D	23	0	11	1	0
2	E	23	0	11	1	0
2	F	23	0	11	2	0
2	G	23	0	11	1	0
2	H	23	0	11	1	0
3	A	64	0	23	3	0
3	B	64	0	23	4	0
3	C	64	0	23	3	0
3	D	64	0	23	3	0
3	E	64	0	23	3	0
3	F	64	0	23	4	0
3	G	64	0	23	3	0
3	H	64	0	23	3	0
4	A	31	0	12	1	0
4	B	31	0	12	1	0
4	C	31	0	12	1	0
4	D	31	0	12	1	0
4	E	31	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	31	0	12	2	0
4	G	31	0	12	1	0
4	H	31	0	12	1	0
All	All	31392	0	31240	310	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 5.

The worst 5 of 310 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:ASN:HB2	1:A:414:MET:HE1	1.77	0.66
1:E:94:ASN:HB2	1:E:414:MET:HE1	1.77	0.66
1:B:94:ASN:HB2	1:B:414:MET:HE1	1.77	0.66
1:F:94:ASN:HB2	1:F:414:MET:HE1	1.77	0.66
1:H:94:ASN:HB2	1:H:414:MET:HE1	1.77	0.66

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	483/519 (93%)	459 (95%)	24 (5%)	0	100	100
1	B	483/519 (93%)	459 (95%)	24 (5%)	0	100	100
1	C	483/519 (93%)	459 (95%)	24 (5%)	0	100	100
1	D	483/519 (93%)	459 (95%)	24 (5%)	0	100	100
1	E	483/519 (93%)	459 (95%)	24 (5%)	0	100	100
1	F	483/519 (93%)	459 (95%)	24 (5%)	0	100	100
1	G	483/519 (93%)	459 (95%)	24 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	483/519 (93%)	459 (95%)	24 (5%)	0	100	100
1	I	12/519 (2%)	7 (58%)	5 (42%)	0	100	100
1	J	12/519 (2%)	7 (58%)	5 (42%)	0	100	100
1	K	12/519 (2%)	7 (58%)	5 (42%)	0	100	100
1	L	12/519 (2%)	7 (58%)	5 (42%)	0	100	100
1	M	12/519 (2%)	7 (58%)	5 (42%)	0	100	100
1	N	12/519 (2%)	7 (58%)	5 (42%)	0	100	100
1	O	12/519 (2%)	7 (58%)	5 (42%)	0	100	100
1	P	12/519 (2%)	7 (58%)	5 (42%)	0	100	100
All	All	3960/8304 (48%)	3728 (94%)	232 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	397/425 (93%)	388 (98%)	9 (2%)	44	68
1	B	397/425 (93%)	388 (98%)	9 (2%)	44	68
1	C	397/425 (93%)	388 (98%)	9 (2%)	44	68
1	D	397/425 (93%)	388 (98%)	9 (2%)	44	68
1	E	397/425 (93%)	388 (98%)	9 (2%)	44	68
1	F	397/425 (93%)	388 (98%)	9 (2%)	44	68
1	G	397/425 (93%)	388 (98%)	9 (2%)	44	68
1	H	397/425 (93%)	388 (98%)	9 (2%)	44	68
1	I	11/425 (3%)	11 (100%)	0	100	100
1	J	11/425 (3%)	11 (100%)	0	100	100
1	K	11/425 (3%)	11 (100%)	0	100	100
1	L	11/425 (3%)	11 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	11/425 (3%)	11 (100%)	0	100	100
1	N	11/425 (3%)	11 (100%)	0	100	100
1	O	11/425 (3%)	11 (100%)	0	100	100
1	P	11/425 (3%)	11 (100%)	0	100	100
All	All	3264/6800 (48%)	3192 (98%)	72 (2%)	45	69

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	228	LYS
1	H	438	LYS
1	G	254	GLU
1	H	225	THR
1	C	330	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	253	HIS
1	H	498	GLN
1	F	253	HIS
1	H	454	HIS
1	H	253	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

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
3	GTP	F	603	-	33,34,34	3.91	18 (54%)	50,54,54	1.65	11 (22%)
3	GTP	F	602	-	33,34,34	3.90	19 (57%)	50,54,54	1.82	11 (22%)
2	IMP	E	601	-	25,25,25	2.75	7 (28%)	37,38,38	2.16	8 (21%)
3	GTP	H	603	-	33,34,34	3.92	19 (57%)	50,54,54	1.65	11 (22%)
3	GTP	C	602	-	33,34,34	3.91	19 (57%)	50,54,54	1.82	11 (22%)
2	IMP	G	601	-	25,25,25	2.75	7 (28%)	37,38,38	2.17	8 (21%)
3	GTP	B	602	-	33,34,34	3.90	19 (57%)	50,54,54	1.82	11 (22%)
4	ATP	A	604	-	32,33,33	1.36	5 (15%)	48,52,52	1.74	9 (18%)
3	GTP	E	603	-	33,34,34	3.91	18 (54%)	50,54,54	1.64	11 (22%)
3	GTP	H	602	-	33,34,34	3.91	19 (57%)	50,54,54	1.82	11 (22%)
2	IMP	D	601	-	25,25,25	2.76	7 (28%)	37,38,38	2.19	9 (24%)
3	GTP	G	602	-	33,34,34	3.91	19 (57%)	50,54,54	1.82	11 (22%)
3	GTP	A	603	-	33,34,34	3.92	18 (54%)	50,54,54	1.65	11 (22%)
3	GTP	E	602	-	33,34,34	3.90	19 (57%)	50,54,54	1.81	11 (22%)
4	ATP	G	604	-	32,33,33	1.36	5 (15%)	48,52,52	1.74	9 (18%)
2	IMP	B	601	-	25,25,25	2.75	7 (28%)	37,38,38	2.19	9 (24%)
3	GTP	C	603	-	33,34,34	3.91	18 (54%)	50,54,54	1.64	11 (22%)
4	ATP	B	604	-	32,33,33	1.36	5 (15%)	48,52,52	1.73	9 (18%)
2	IMP	A	601	-	25,25,25	2.75	7 (28%)	37,38,38	2.19	9 (24%)
4	ATP	F	604	-	32,33,33	1.37	5 (15%)	48,52,52	1.73	9 (18%)
3	GTP	B	603	-	33,34,34	3.91	18 (54%)	50,54,54	1.64	11 (22%)
2	IMP	C	601	-	25,25,25	2.76	7 (28%)	37,38,38	2.18	9 (24%)
3	GTP	D	602	-	33,34,34	3.90	19 (57%)	50,54,54	1.82	11 (22%)
4	ATP	E	604	-	32,33,33	1.36	5 (15%)	48,52,52	1.73	9 (18%)
2	IMP	F	601	-	25,25,25	2.76	7 (28%)	37,38,38	2.16	8 (21%)
3	GTP	A	602	-	33,34,34	3.90	19 (57%)	50,54,54	1.82	11 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	ATP	D	604	-	32,33,33	1.37	5 (15%)	48,52,52	1.74	9 (18%)
4	ATP	C	604	-	32,33,33	1.36	5 (15%)	48,52,52	1.73	9 (18%)
3	GTP	G	603	-	33,34,34	3.92	18 (54%)	50,54,54	1.64	11 (22%)
2	IMP	H	601	-	25,25,25	2.75	7 (28%)	37,38,38	2.16	8 (21%)
4	ATP	H	604	-	32,33,33	1.36	5 (15%)	48,52,52	1.74	9 (18%)
3	GTP	D	603	-	33,34,34	3.91	18 (54%)	50,54,54	1.64	11 (22%)

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
3	GTP	F	603	-	-	4/22/38/38	0/3/3/3
3	GTP	F	602	-	-	8/22/38/38	0/3/3/3
2	IMP	E	601	-	-	5/10/26/26	0/3/3/3
3	GTP	H	603	-	-	4/22/38/38	0/3/3/3
3	GTP	C	602	-	-	8/22/38/38	0/3/3/3
2	IMP	G	601	-	-	5/10/26/26	0/3/3/3
3	GTP	B	602	-	-	8/22/38/38	0/3/3/3
4	ATP	A	604	-	-	7/22/38/38	0/3/3/3
3	GTP	E	603	-	-	4/22/38/38	0/3/3/3
3	GTP	H	602	-	-	8/22/38/38	0/3/3/3
2	IMP	D	601	-	-	5/10/26/26	0/3/3/3
3	GTP	G	602	-	-	8/22/38/38	0/3/3/3
3	GTP	A	603	-	-	4/22/38/38	0/3/3/3
3	GTP	E	602	-	-	8/22/38/38	0/3/3/3
4	ATP	G	604	-	-	7/22/38/38	0/3/3/3
2	IMP	B	601	-	-	5/10/26/26	0/3/3/3
3	GTP	C	603	-	-	4/22/38/38	0/3/3/3
4	ATP	B	604	-	-	7/22/38/38	0/3/3/3
2	IMP	A	601	-	-	5/10/26/26	0/3/3/3
4	ATP	F	604	-	-	7/22/38/38	0/3/3/3
3	GTP	B	603	-	-	4/22/38/38	0/3/3/3
2	IMP	C	601	-	-	5/10/26/26	0/3/3/3
3	GTP	D	602	-	-	8/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ATP	E	604	-	-	7/22/38/38	0/3/3/3
2	IMP	F	601	-	-	5/10/26/26	0/3/3/3
3	GTP	A	602	-	-	8/22/38/38	0/3/3/3
4	ATP	D	604	-	-	7/22/38/38	0/3/3/3
4	ATP	C	604	-	-	7/22/38/38	0/3/3/3
3	GTP	G	603	-	-	4/22/38/38	0/3/3/3
2	IMP	H	601	-	-	5/10/26/26	0/3/3/3
4	ATP	H	604	-	-	7/22/38/38	0/3/3/3
3	GTP	D	603	-	-	4/22/38/38	0/3/3/3

The worst 5 of 393 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	603	GTP	C2'-C3'	-11.01	1.23	1.53
3	G	603	GTP	C2'-C3'	-11.01	1.23	1.53
3	C	603	GTP	C2'-C3'	-11.01	1.23	1.53
3	A	603	GTP	C2'-C3'	-11.00	1.23	1.53
3	D	603	GTP	C2'-C3'	-11.00	1.23	1.53

The worst 5 of 316 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	601	IMP	C5-C6-N1	6.71	120.43	110.78
2	A	601	IMP	C5-C6-N1	6.69	120.40	110.78
2	B	601	IMP	C5-C6-N1	6.69	120.40	110.78
2	E	601	IMP	C5-C6-N1	6.67	120.36	110.78
2	D	601	IMP	C5-C6-N1	6.65	120.34	110.78

There are no chirality outliers.

5 of 192 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	IMP	C5'-O5'-P-O1P
2	A	601	IMP	C5'-O5'-P-O2P
2	A	601	IMP	C5'-O5'-P-O3P
2	B	601	IMP	C5'-O5'-P-O1P
2	B	601	IMP	C5'-O5'-P-O2P

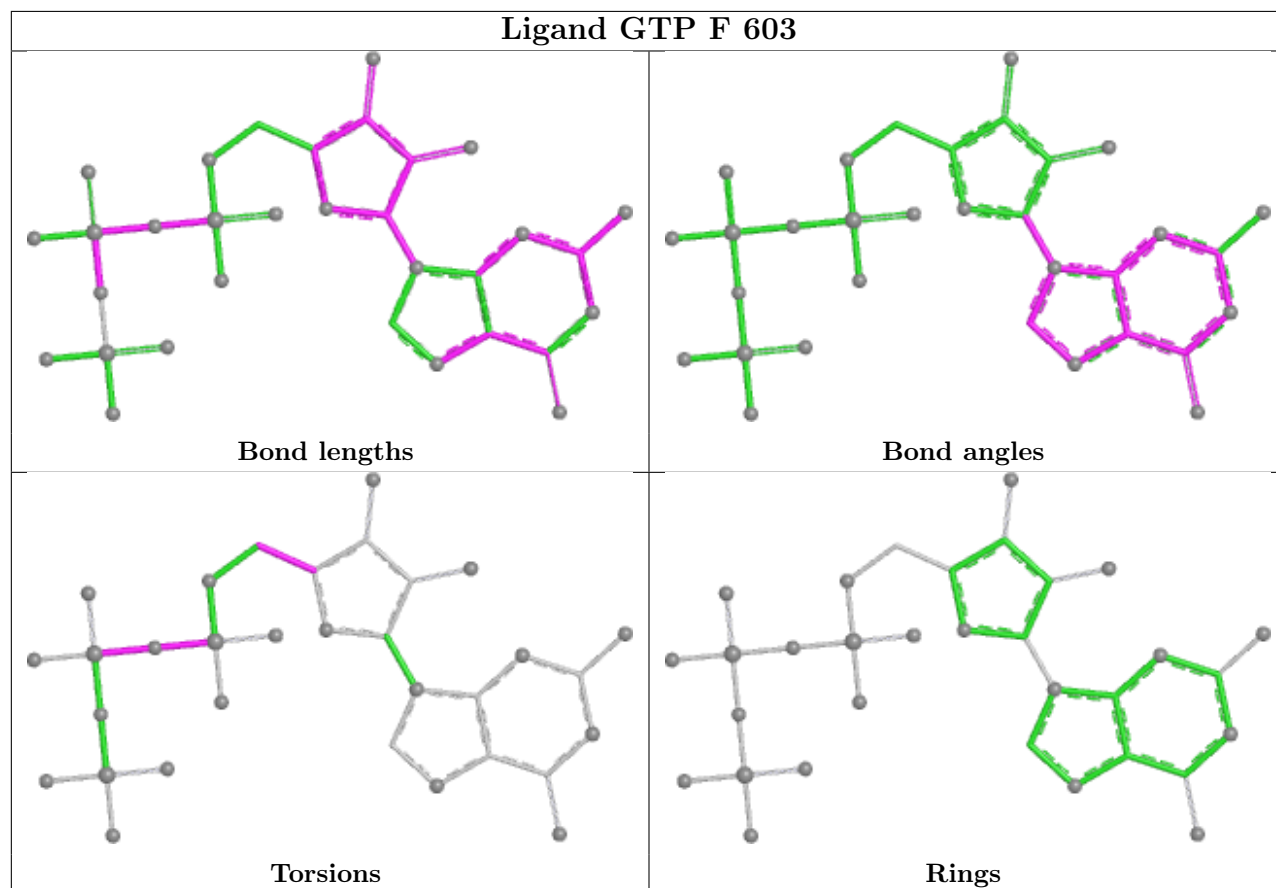
There are no ring outliers.

32 monomers are involved in 44 short contacts:

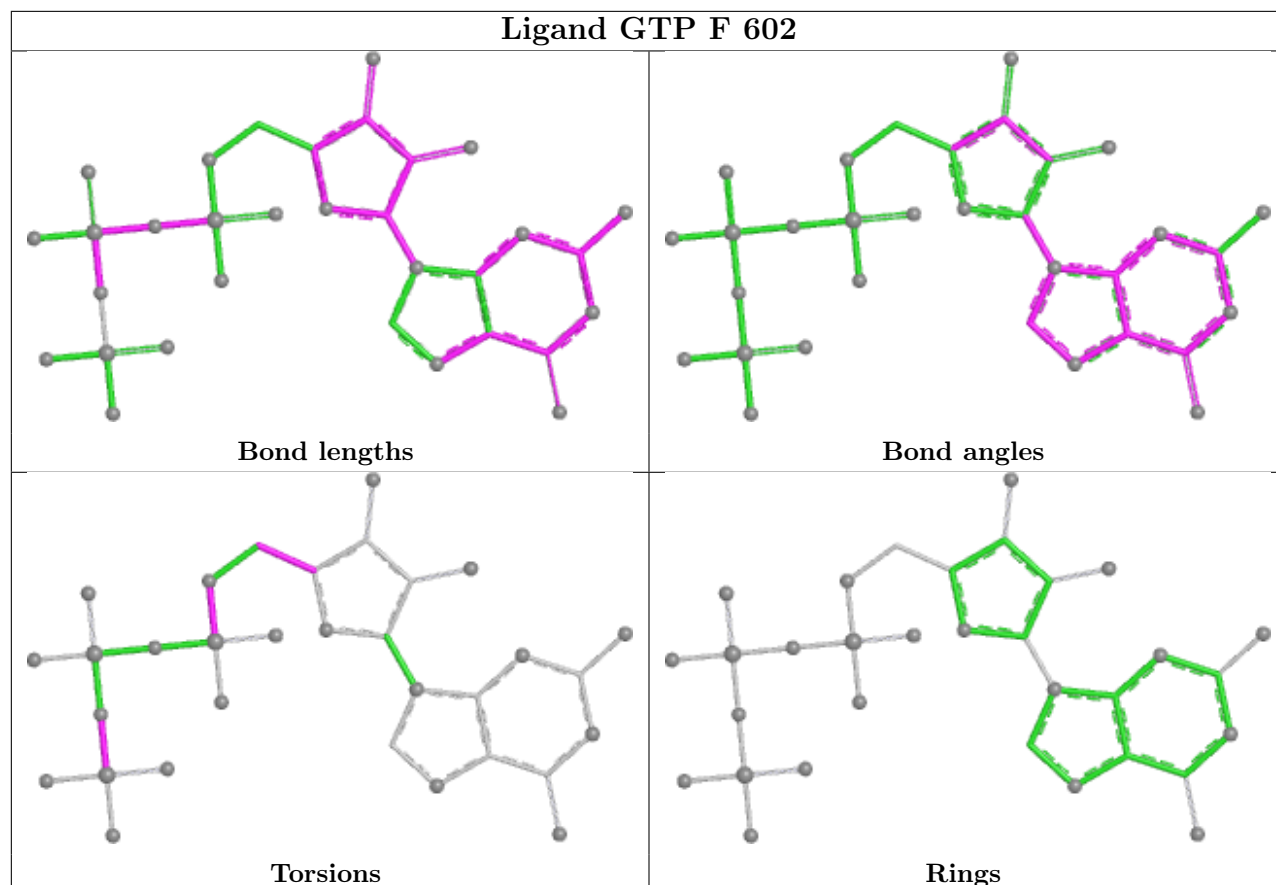
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	603	GTP	3	0
3	F	602	GTP	1	0
2	E	601	IMP	1	0
3	H	603	GTP	2	0
3	C	602	GTP	1	0
2	G	601	IMP	1	0
3	B	602	GTP	1	0
4	A	604	ATP	1	0
3	E	603	GTP	2	0
3	H	602	GTP	1	0
2	D	601	IMP	1	0
3	G	602	GTP	1	0
3	A	603	GTP	2	0
3	E	602	GTP	1	0
4	G	604	ATP	1	0
2	B	601	IMP	1	0
3	C	603	GTP	2	0
4	B	604	ATP	1	0
2	A	601	IMP	1	0
4	F	604	ATP	2	0
3	B	603	GTP	3	0
2	C	601	IMP	1	0
3	D	602	GTP	1	0
4	E	604	ATP	1	0
2	F	601	IMP	2	0
3	A	602	GTP	1	0
4	D	604	ATP	1	0
4	C	604	ATP	1	0
3	G	603	GTP	2	0
2	H	601	IMP	1	0
4	H	604	ATP	1	0
3	D	603	GTP	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

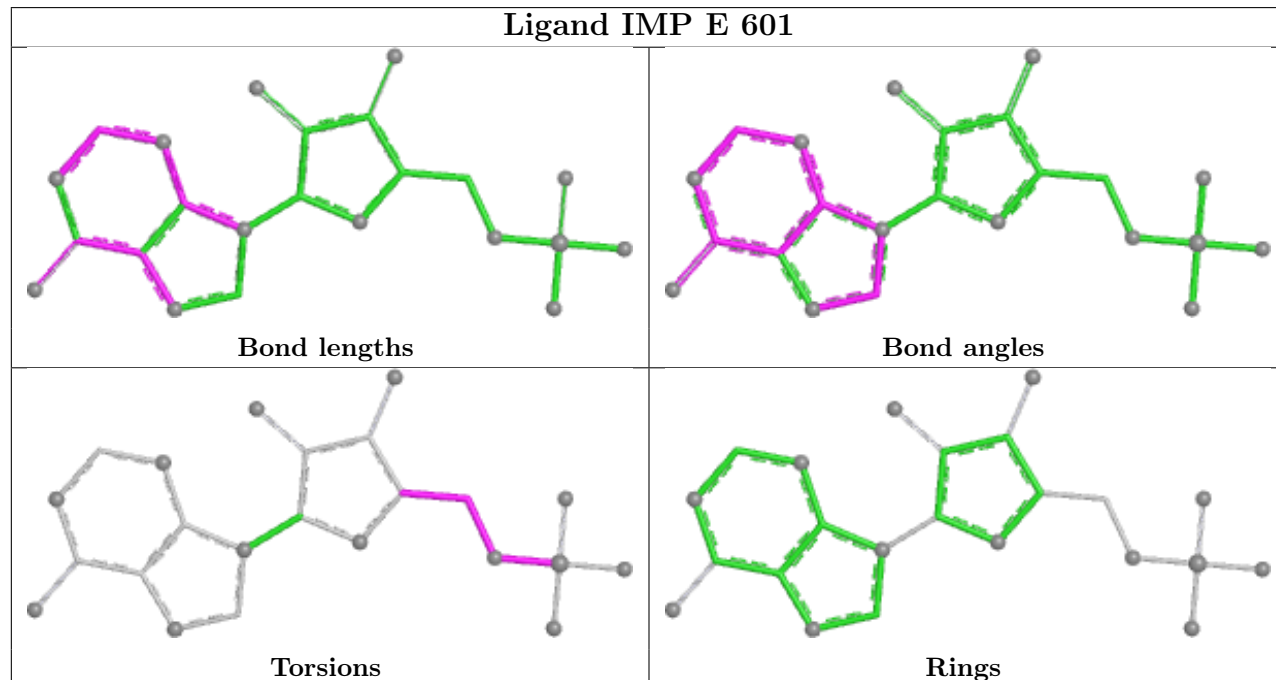
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

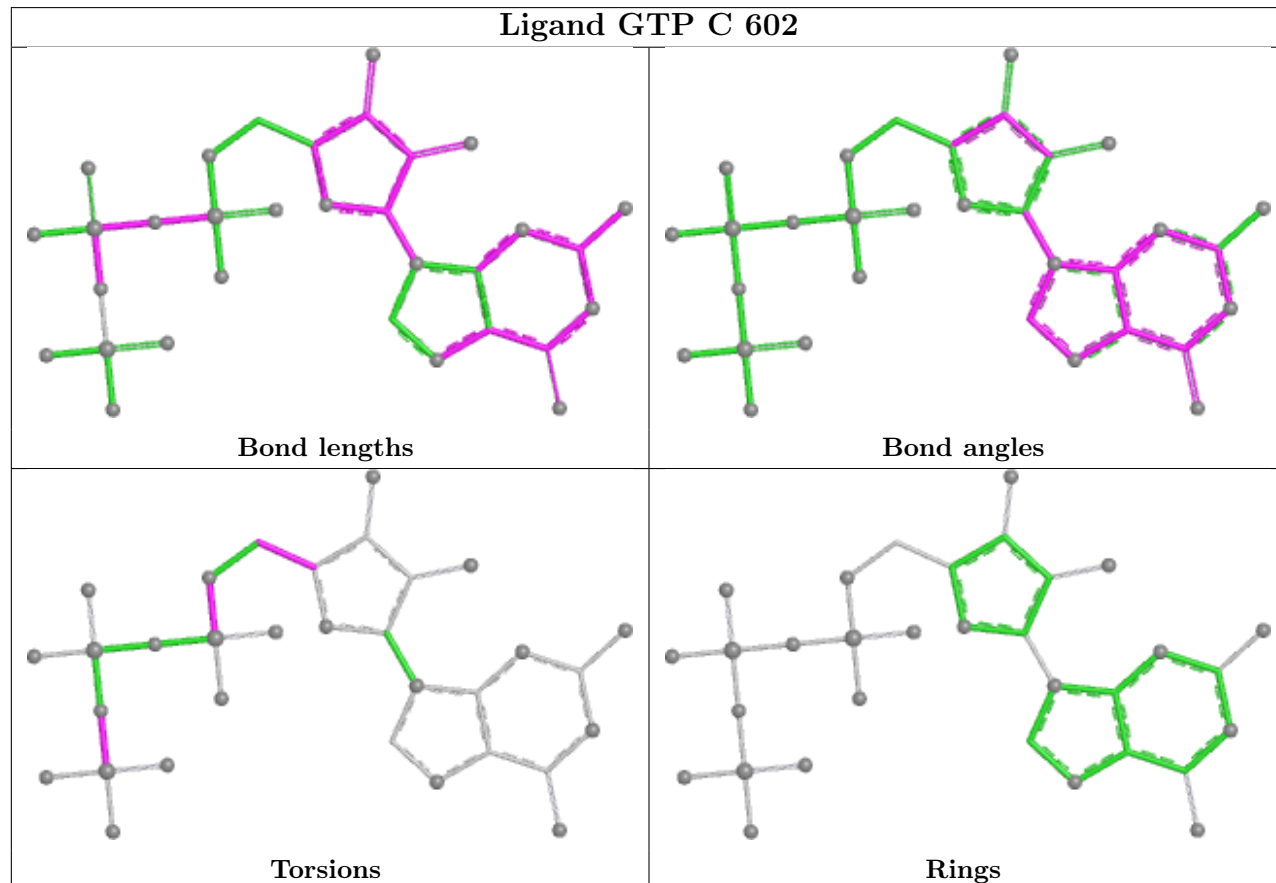
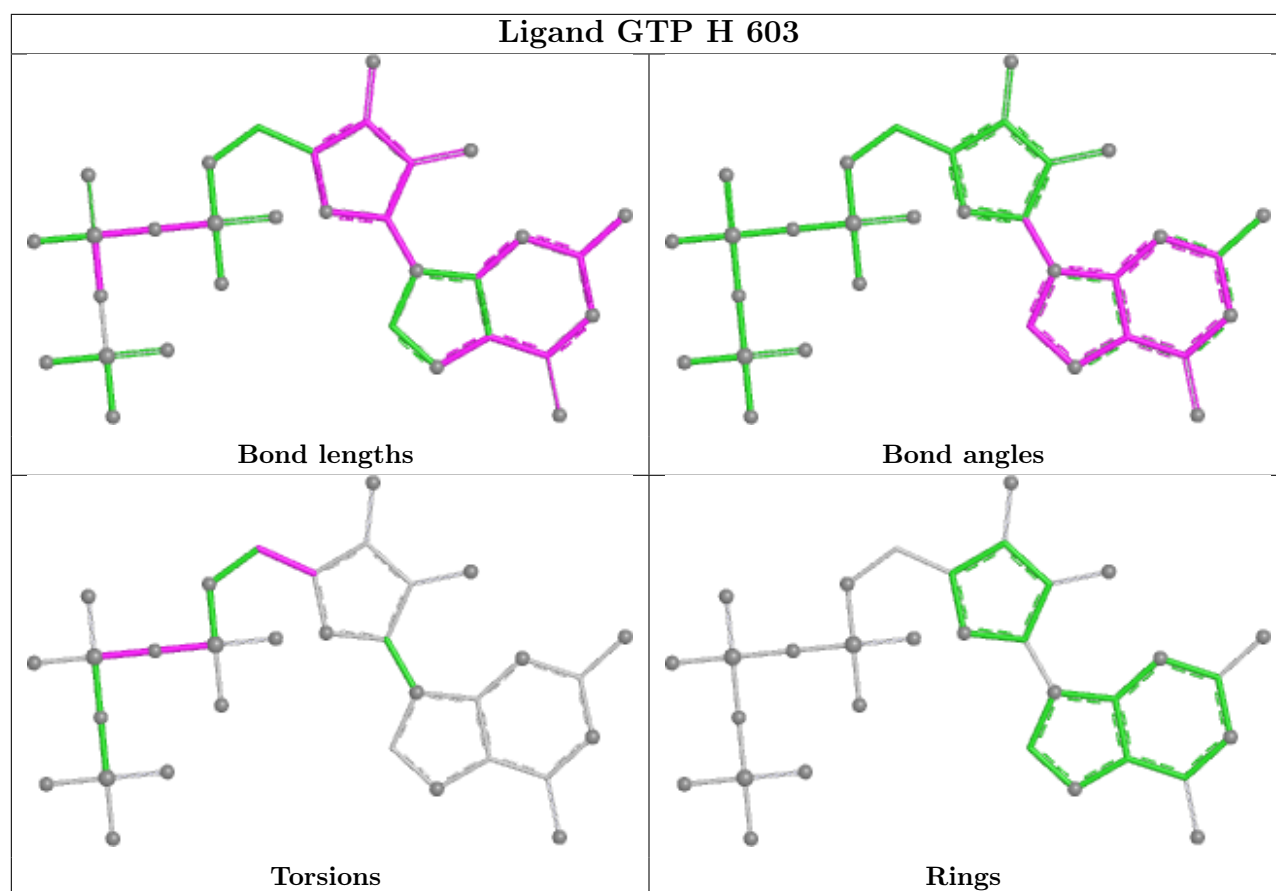


Ligand GTP F 602

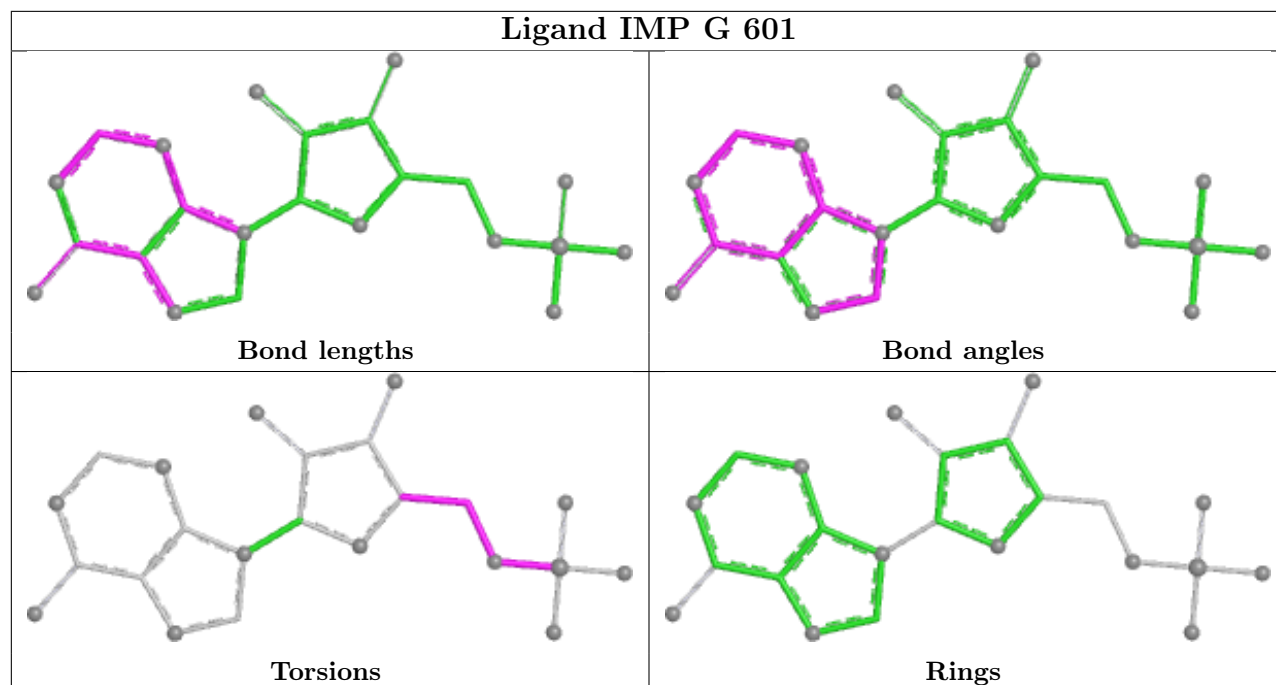


Ligand IMP E 601

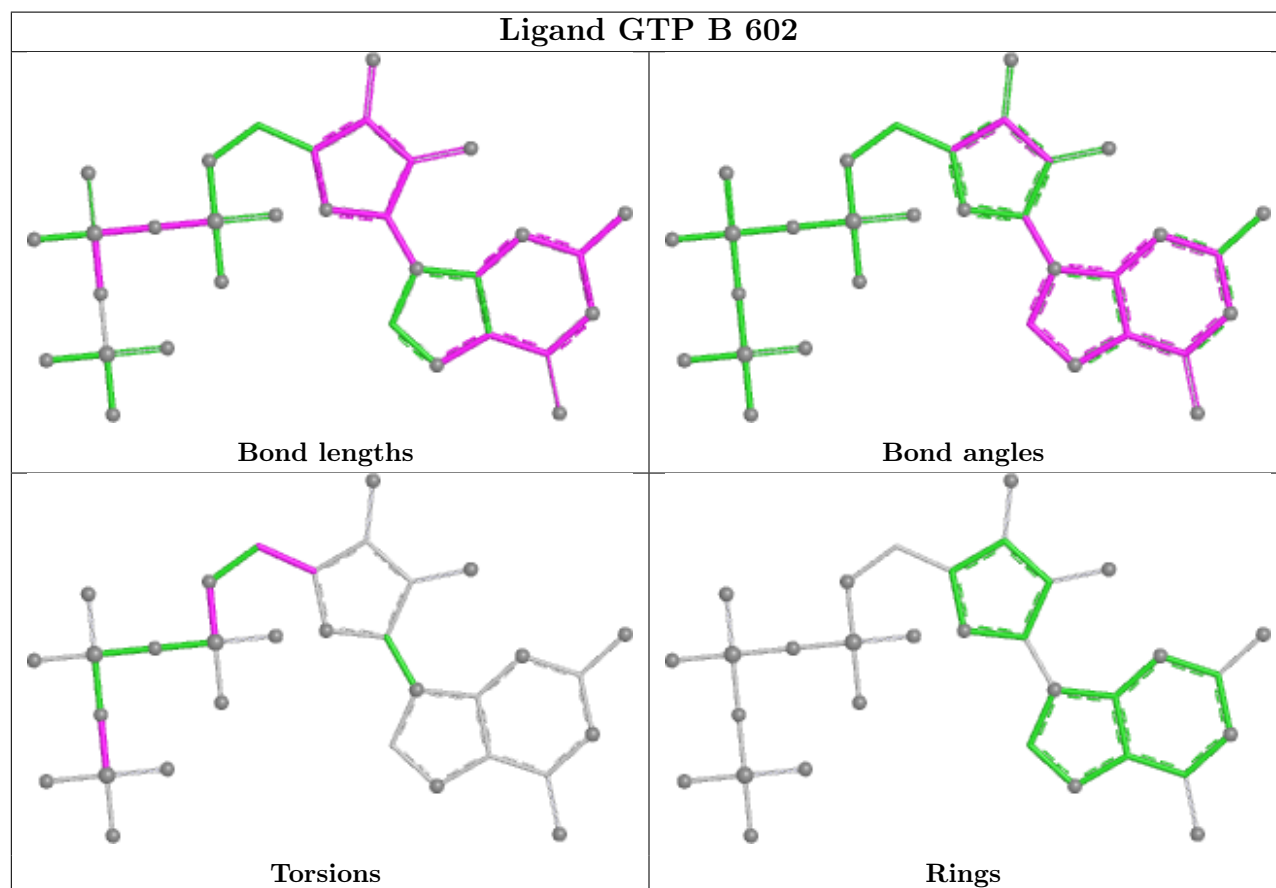


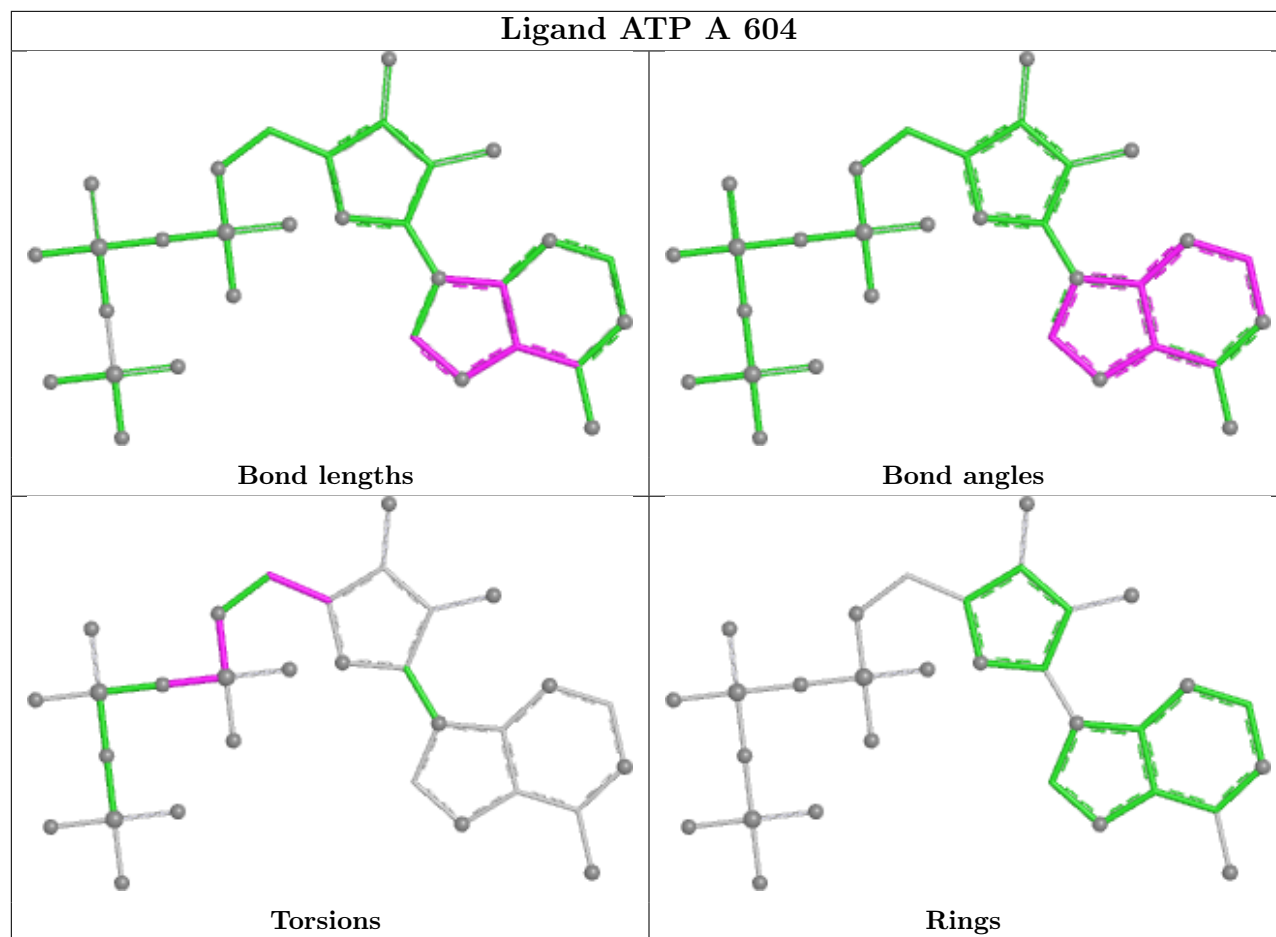


Ligand IMP G 601

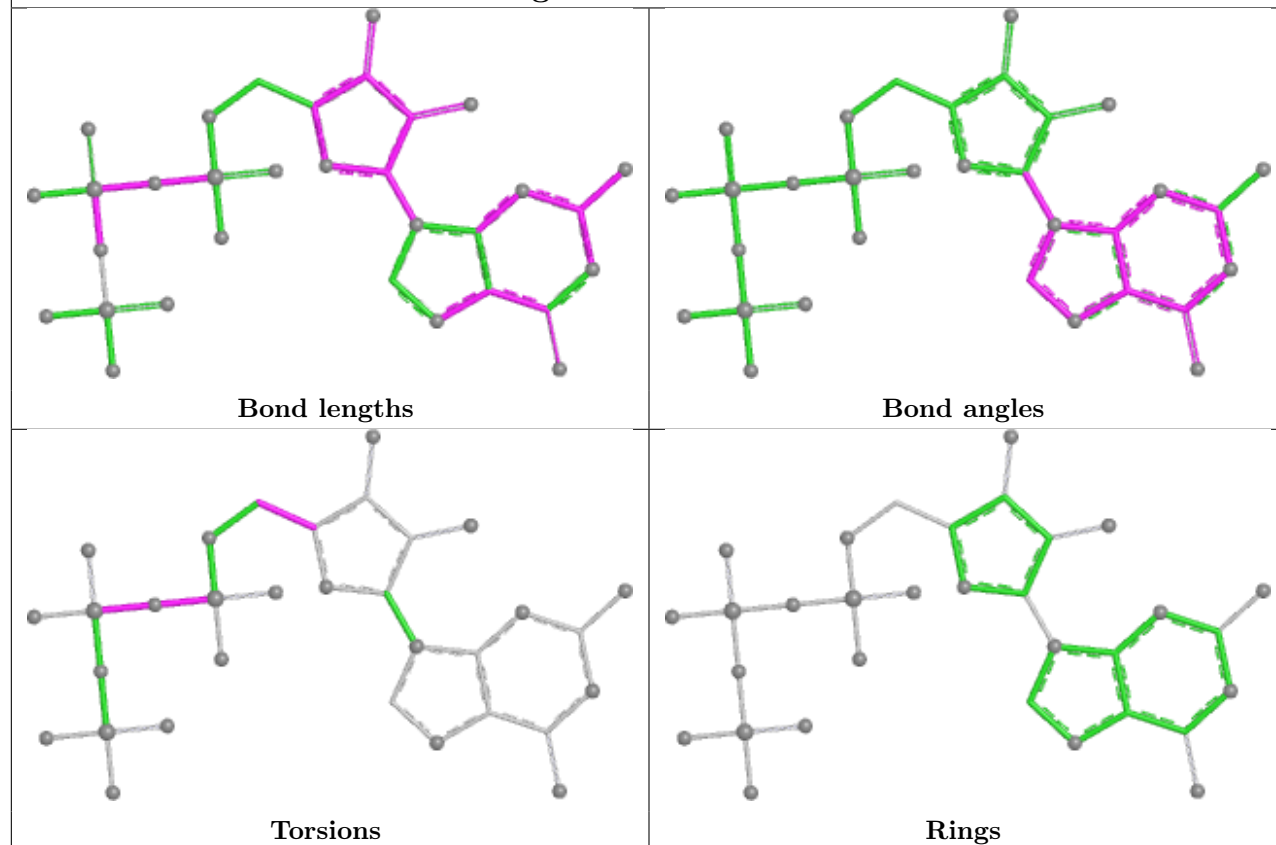


Ligand GTP B 602

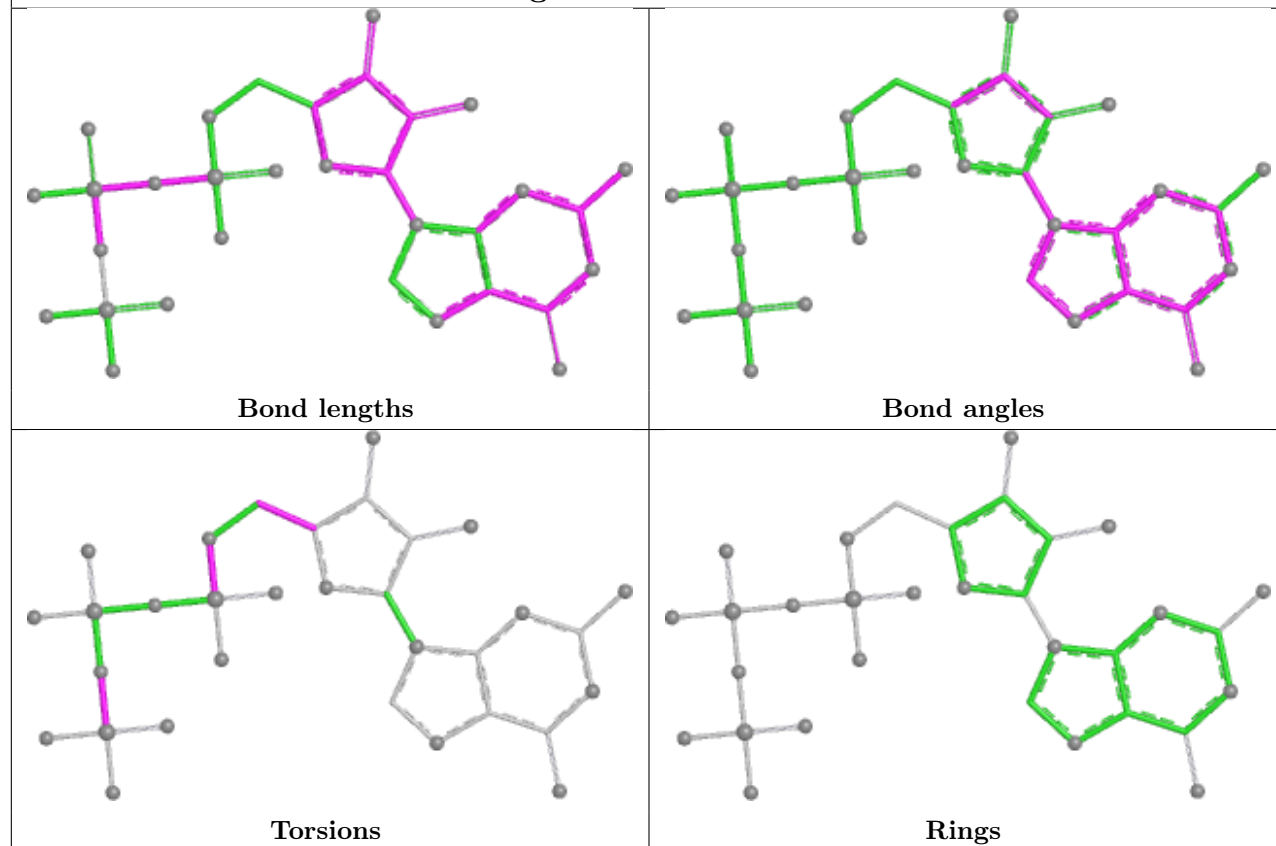




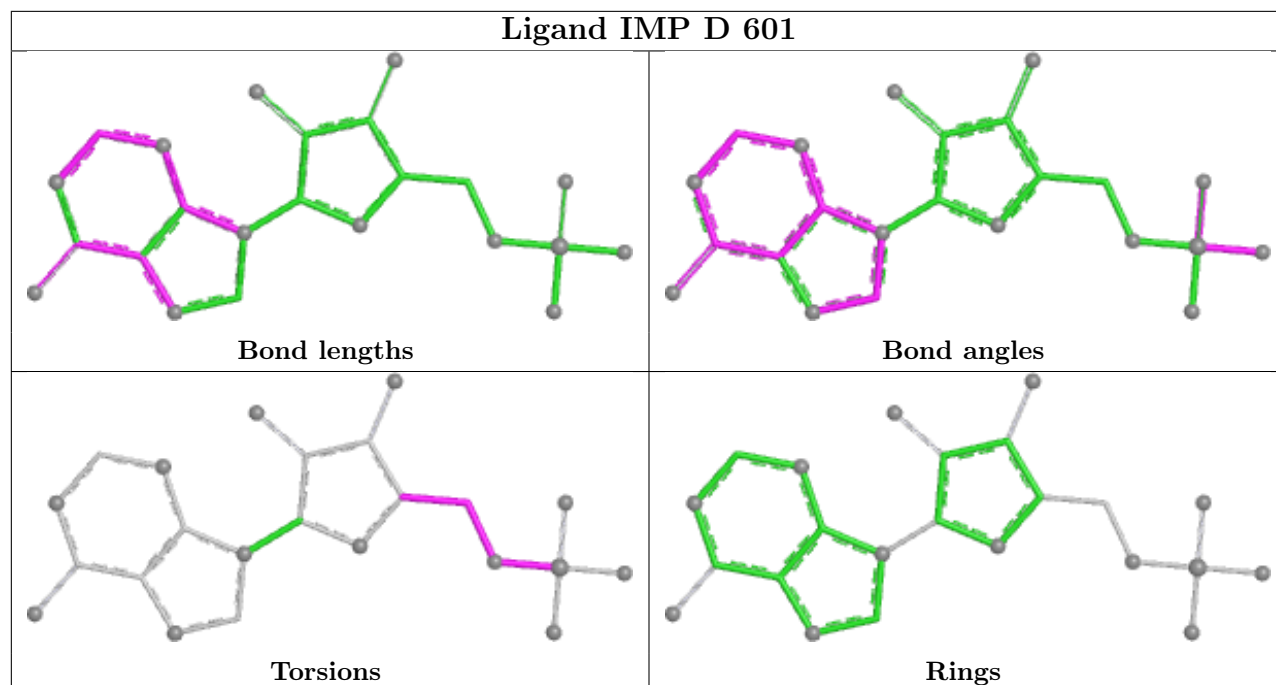
Ligand GTP E 603



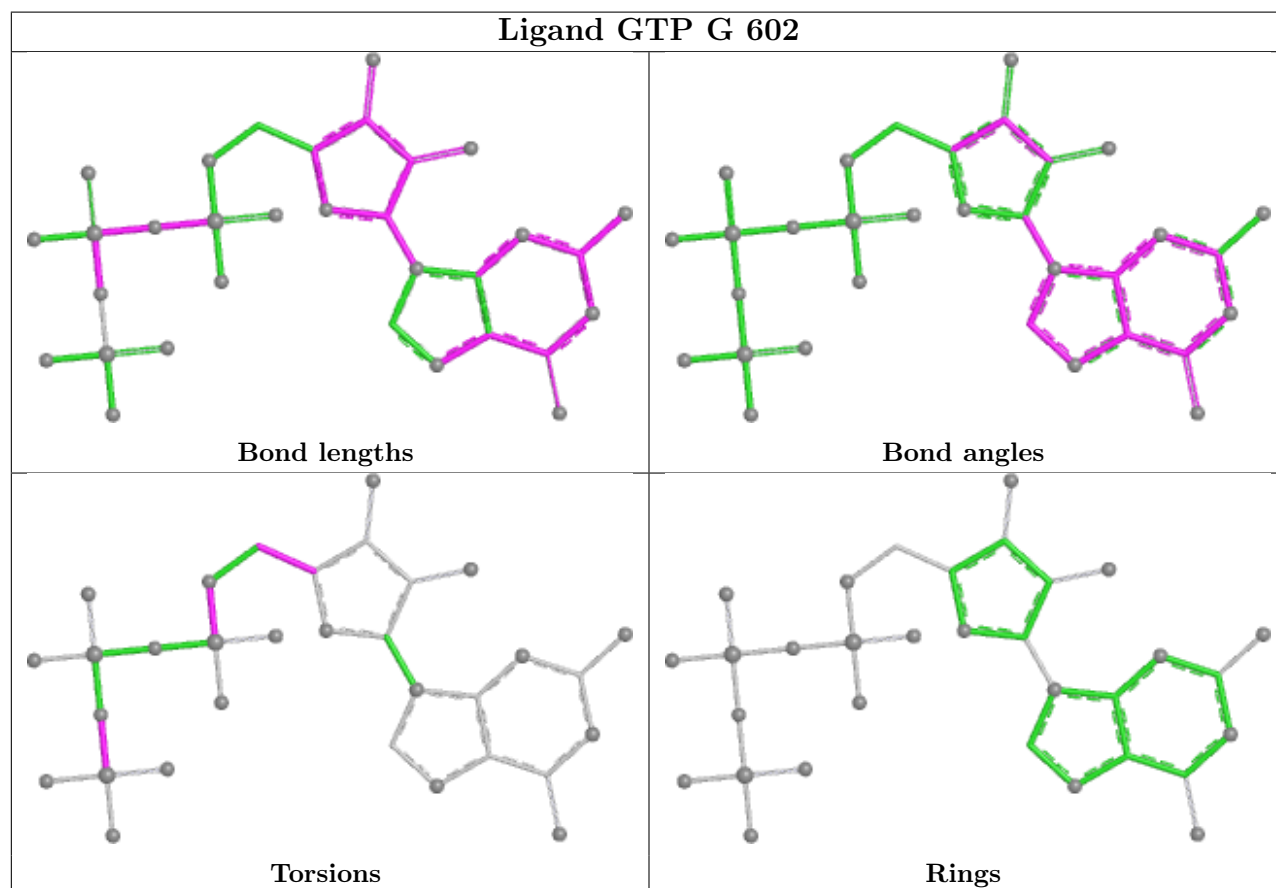
Ligand GTP H 602



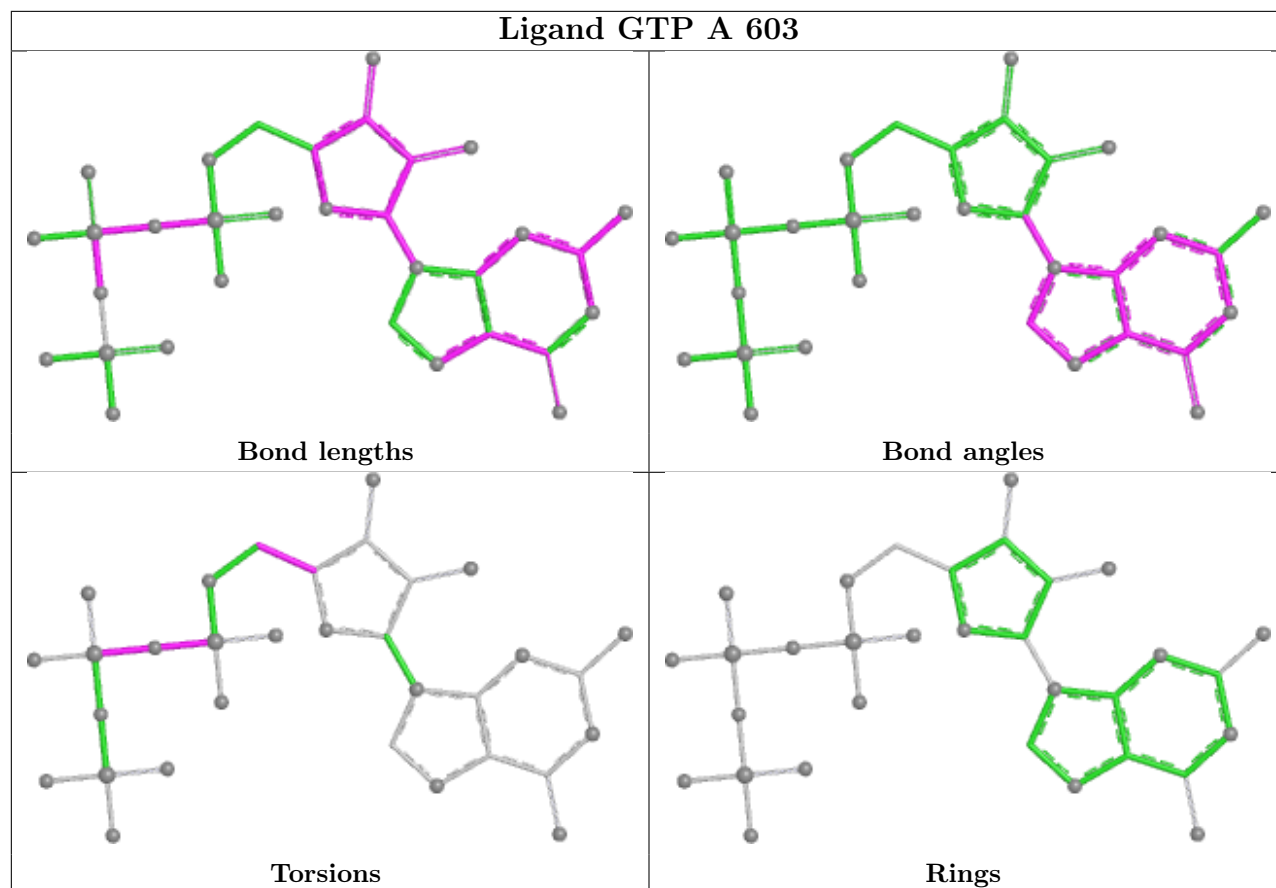
Ligand IMP D 601



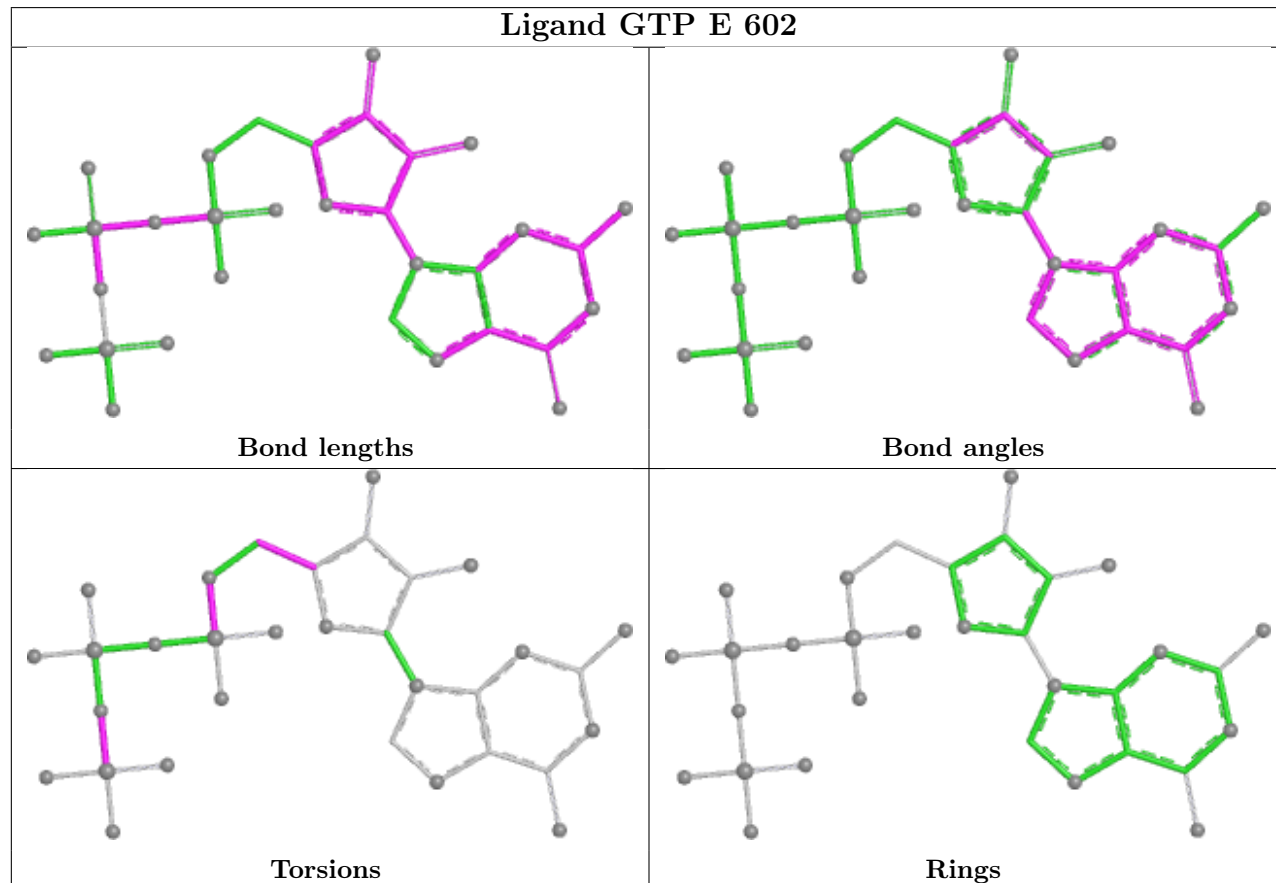
Ligand GTP G 602

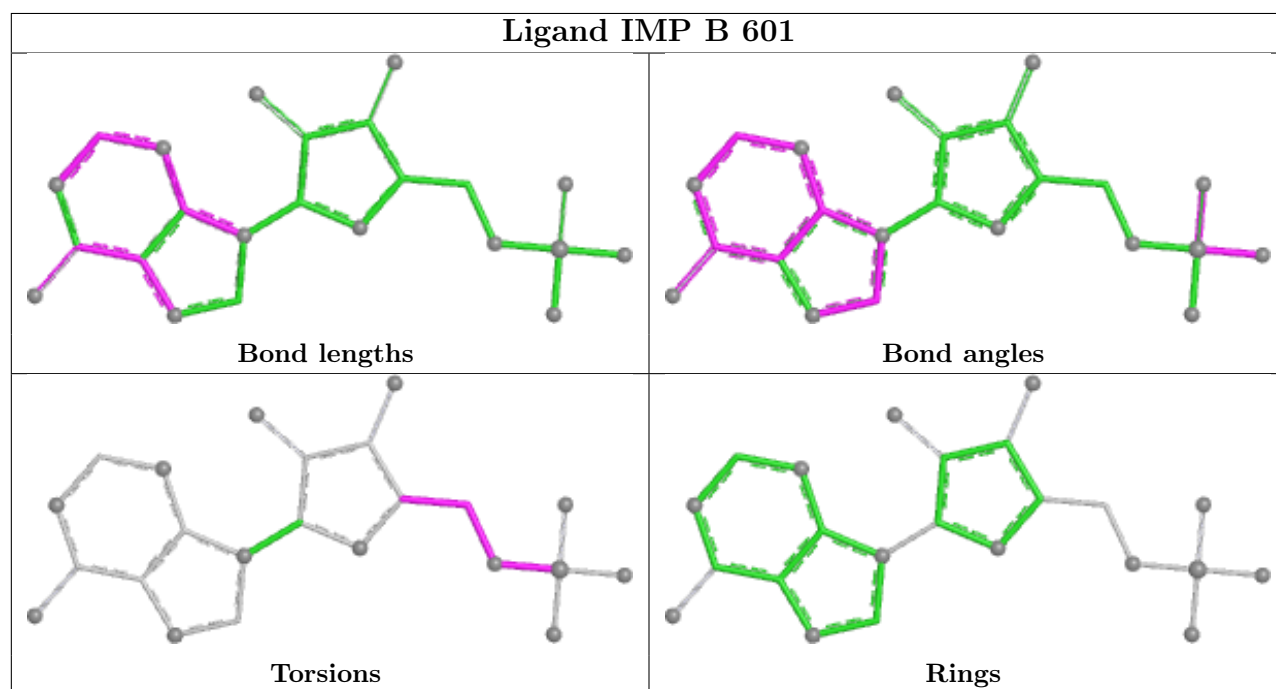
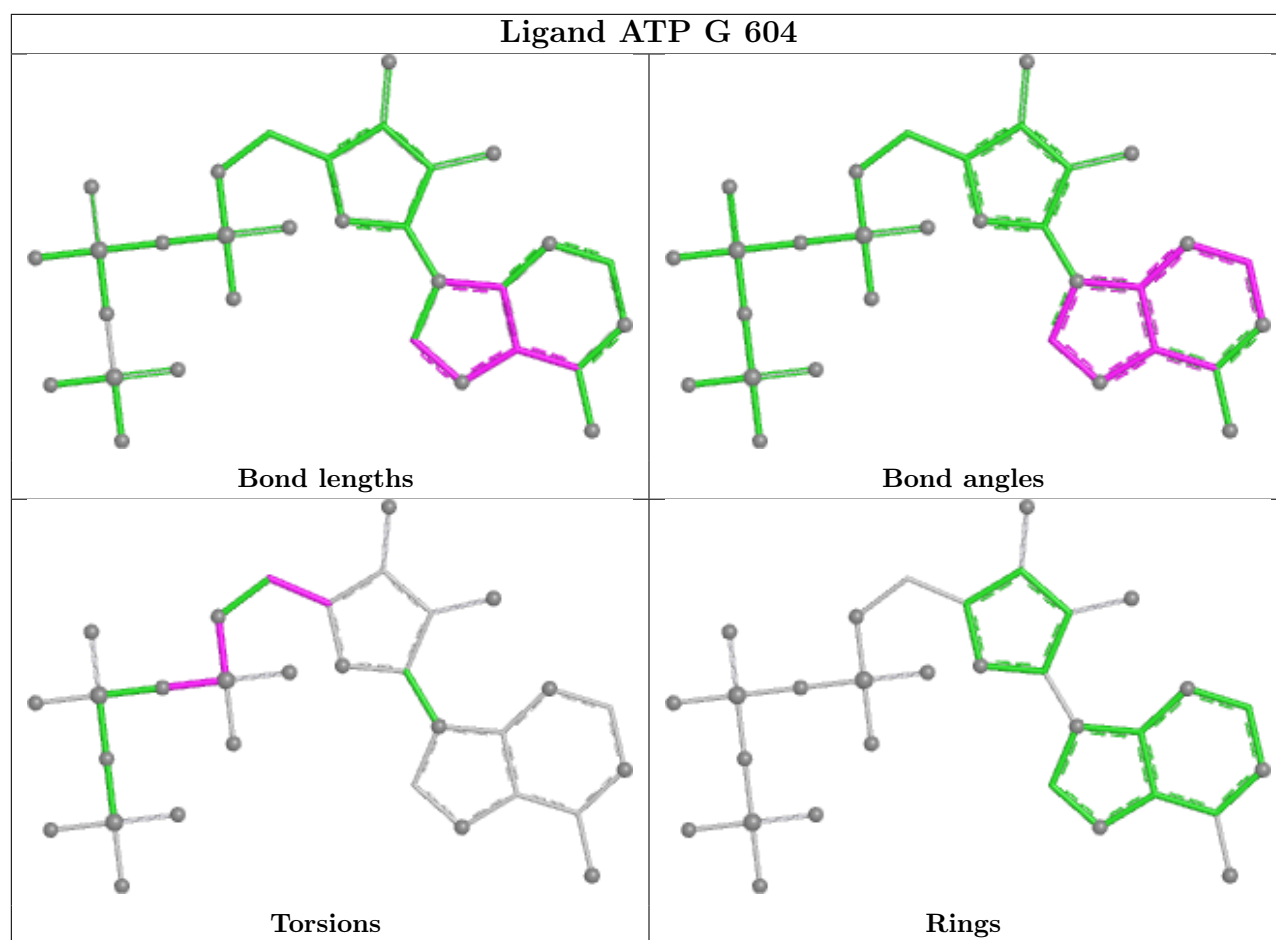


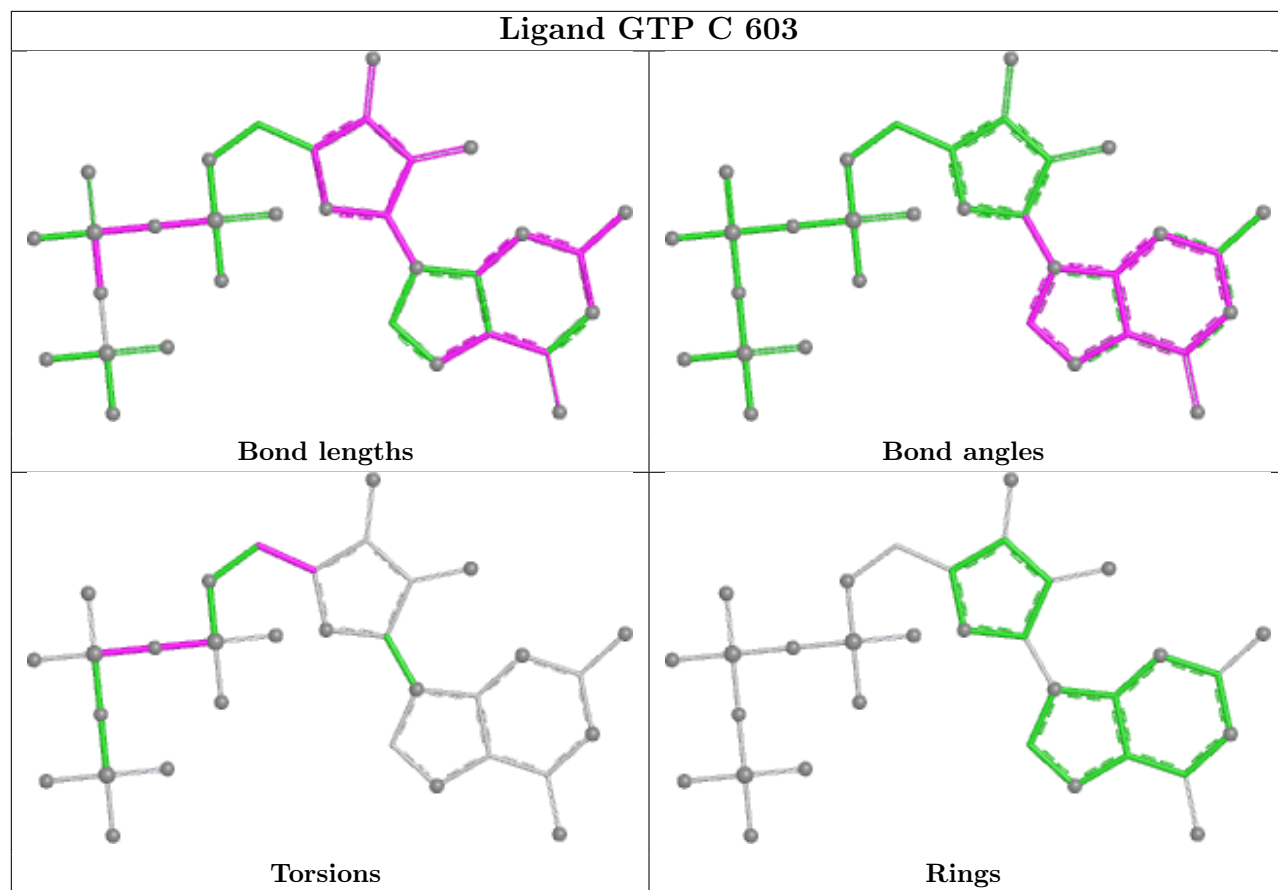
Ligand GTP A 603



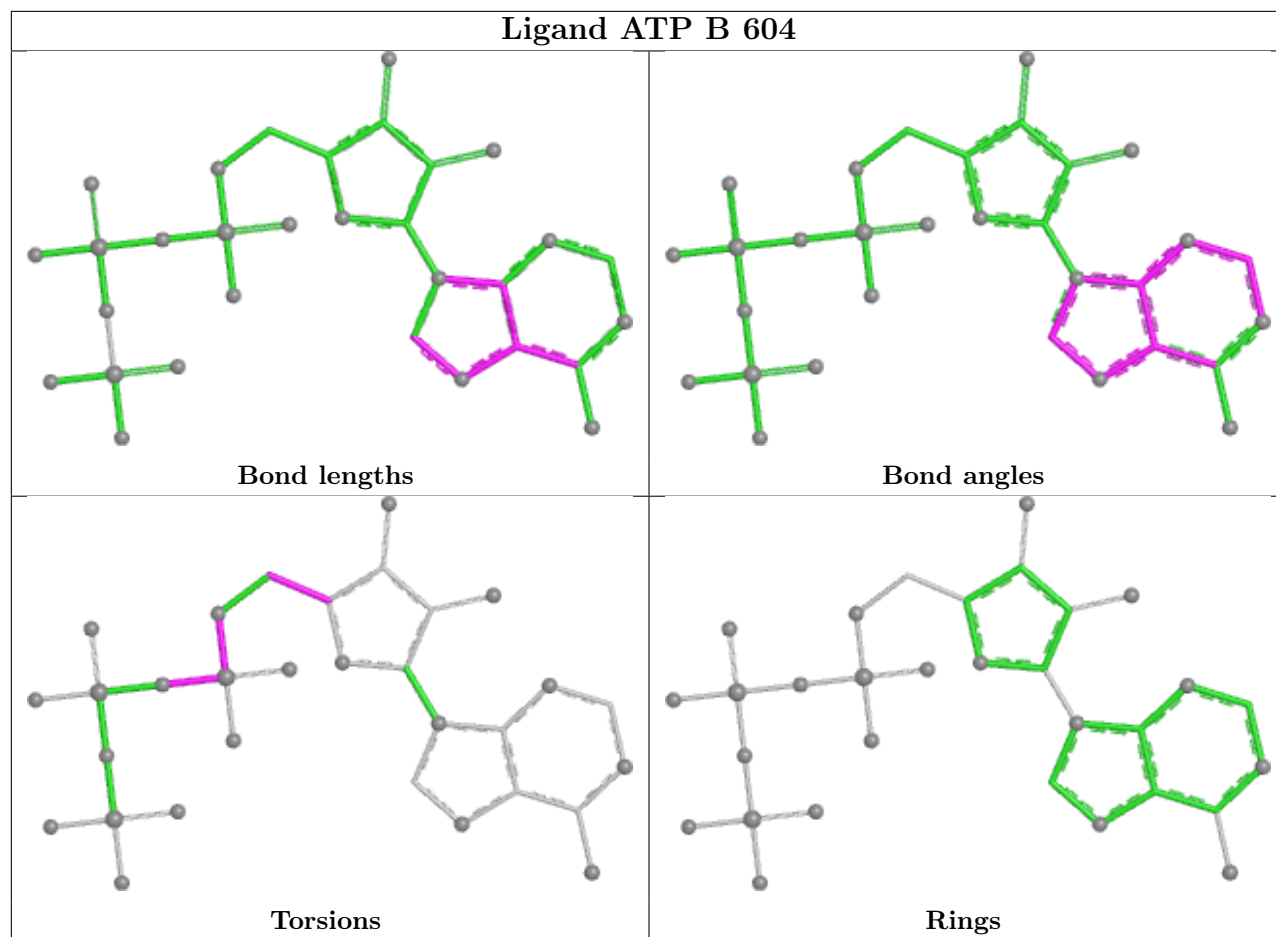
Ligand GTP E 602



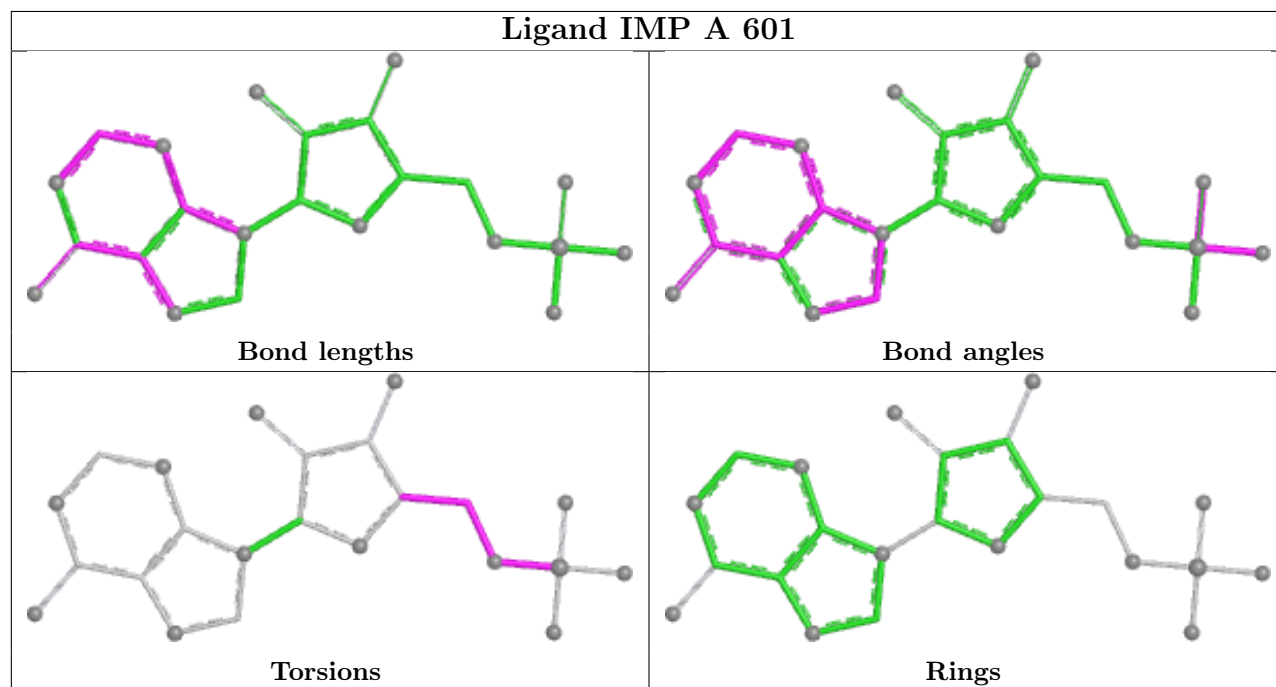




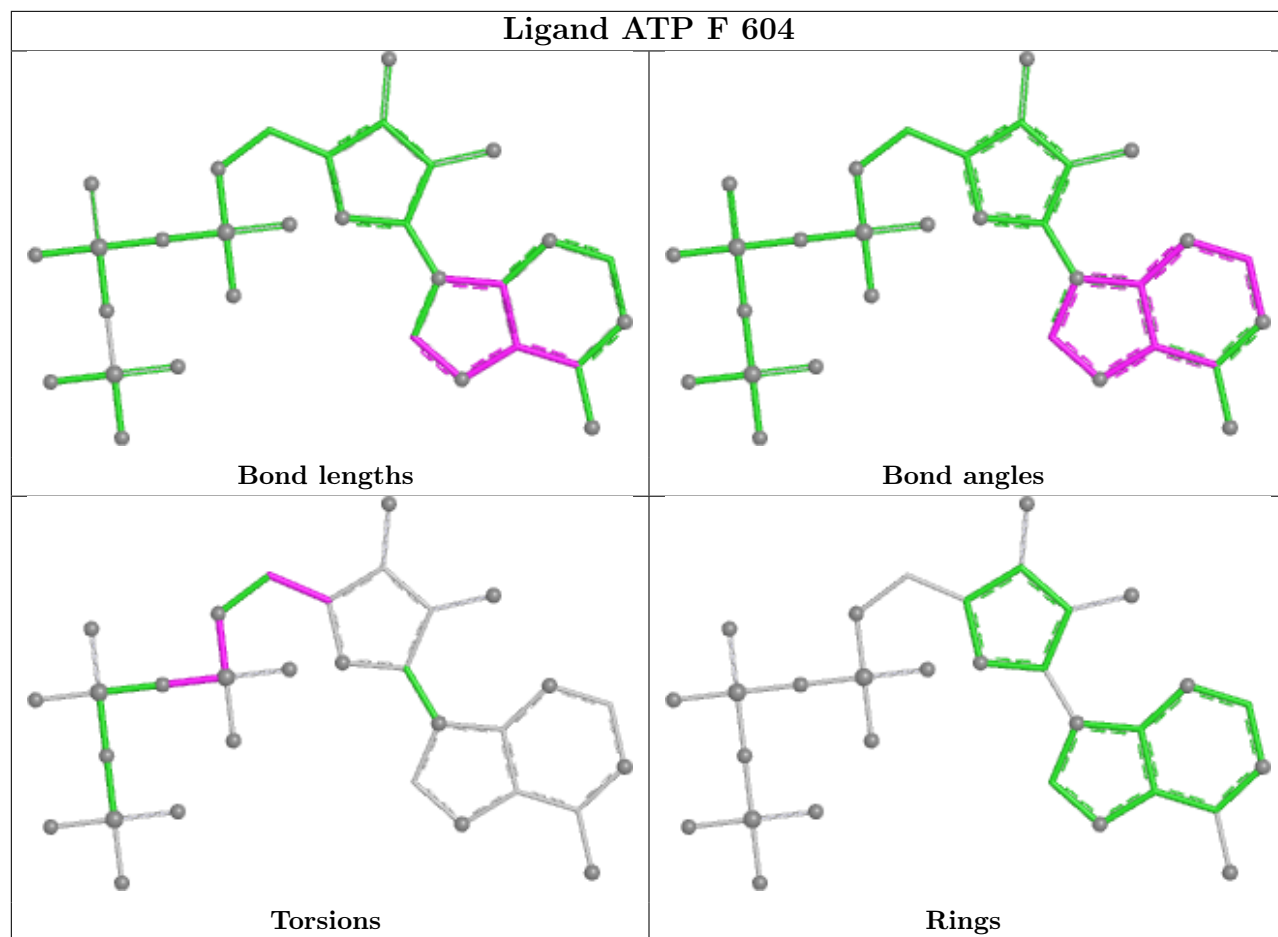
Ligand ATP B 604

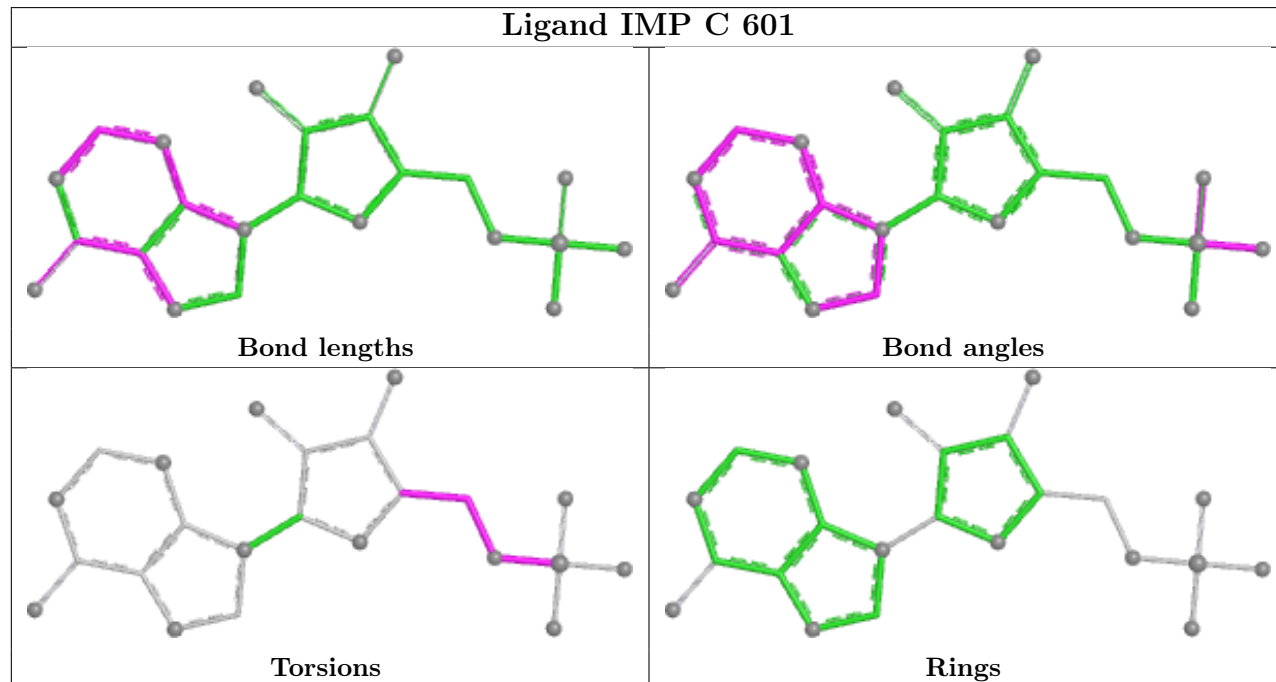
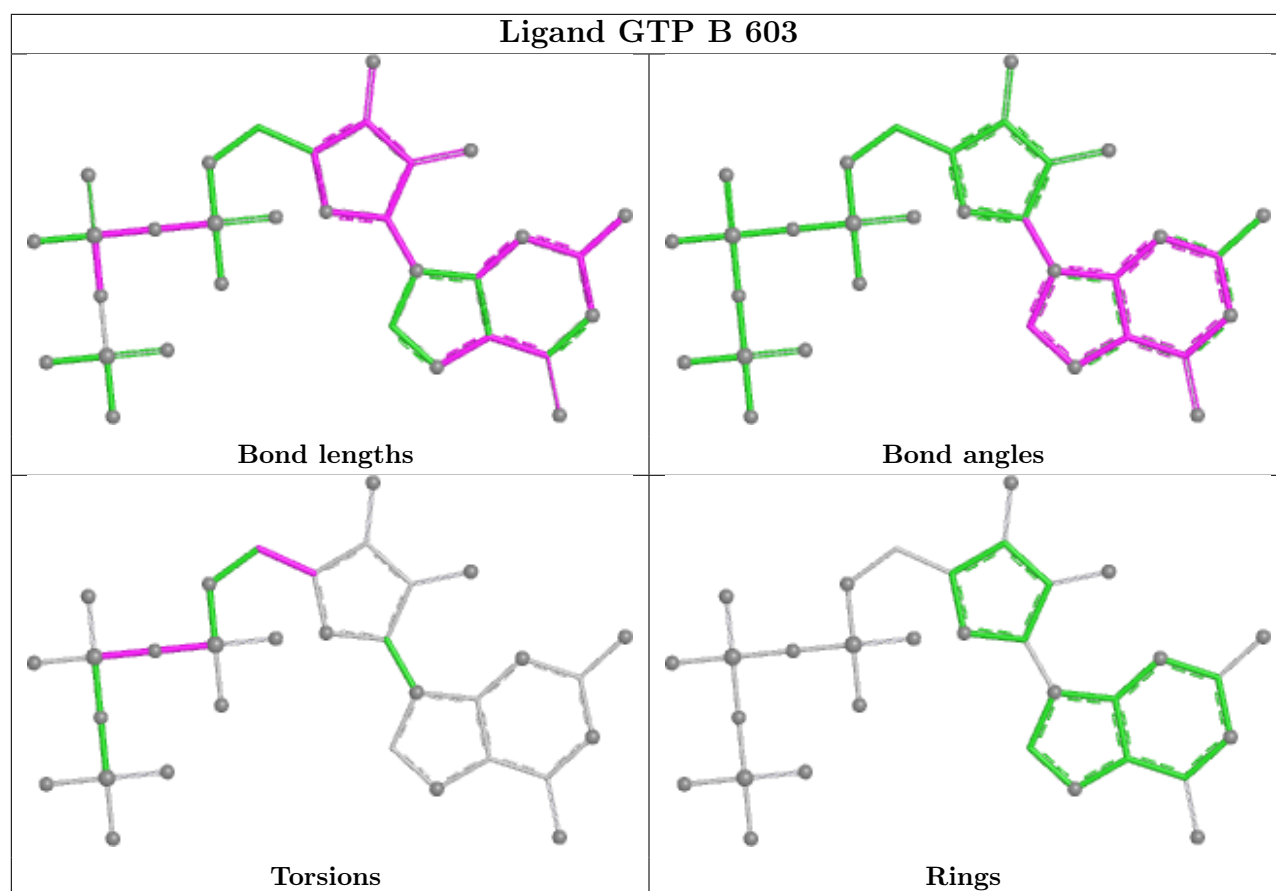


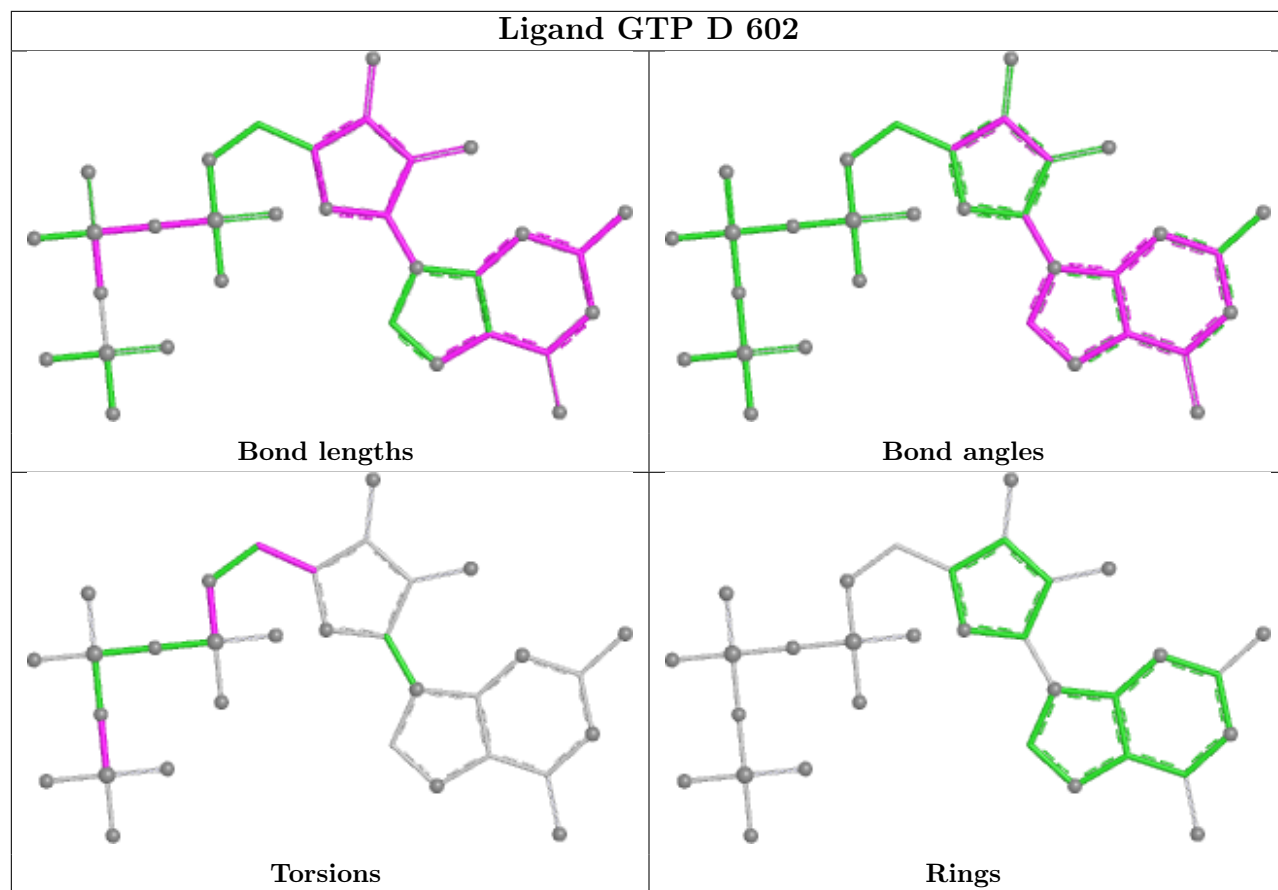
Ligand IMP A 601



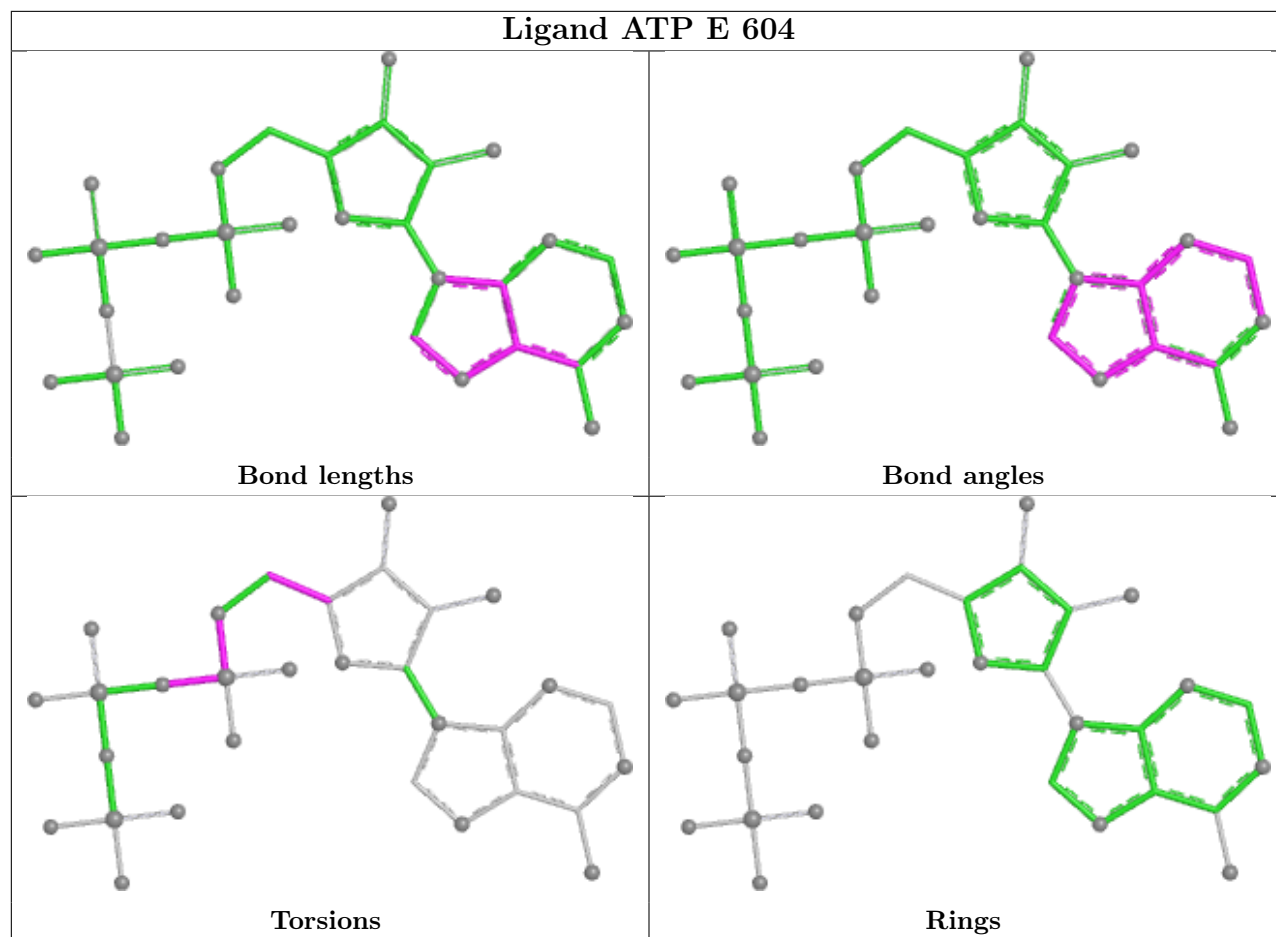
Ligand ATP F 604



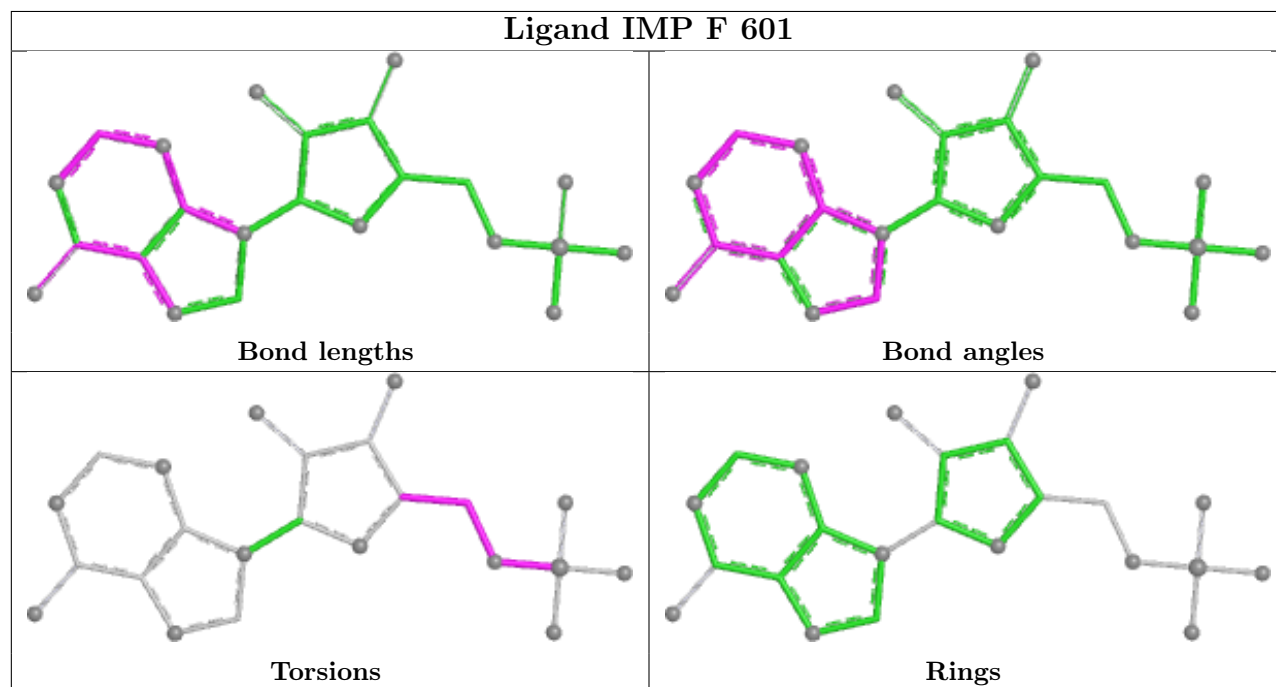


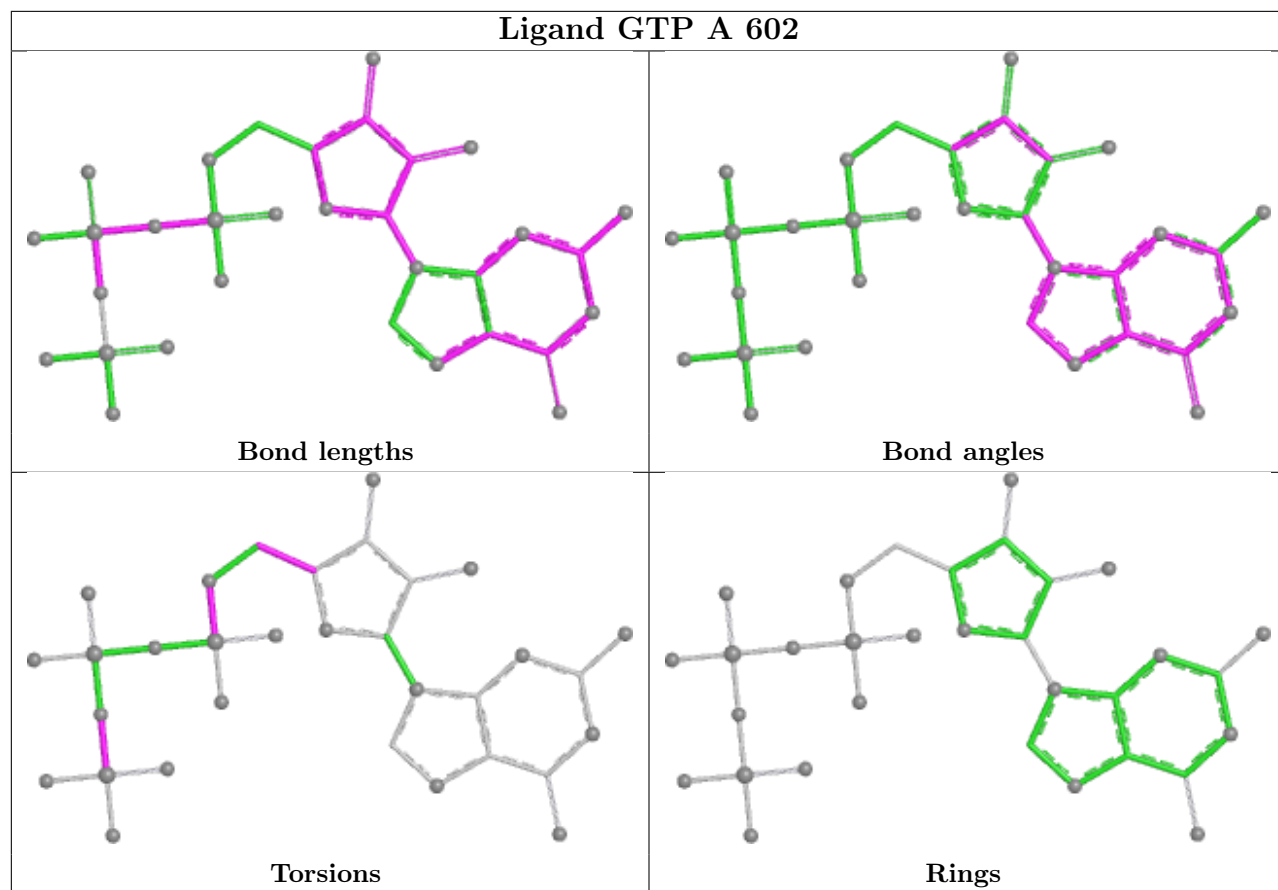


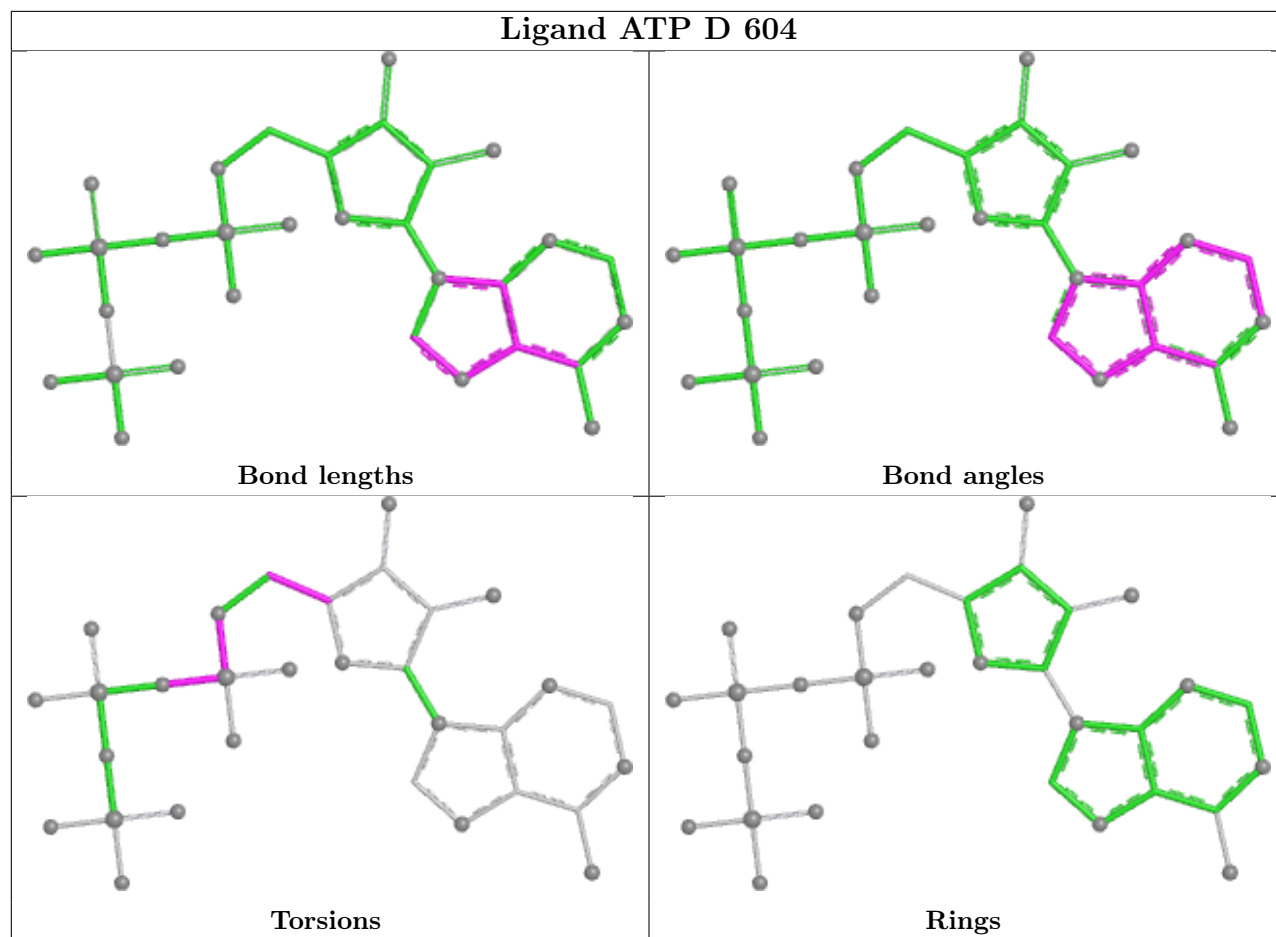
Ligand ATP E 604

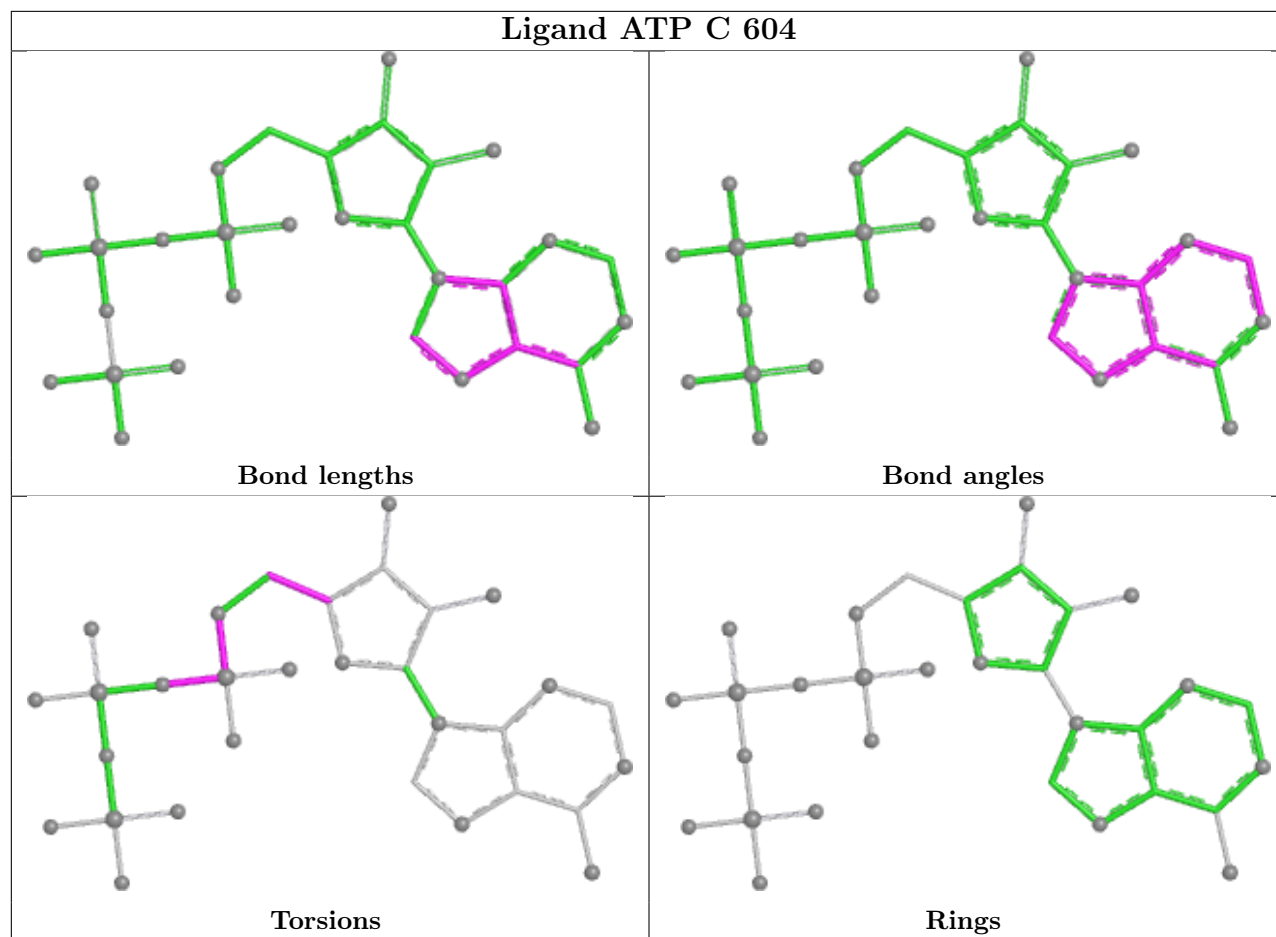


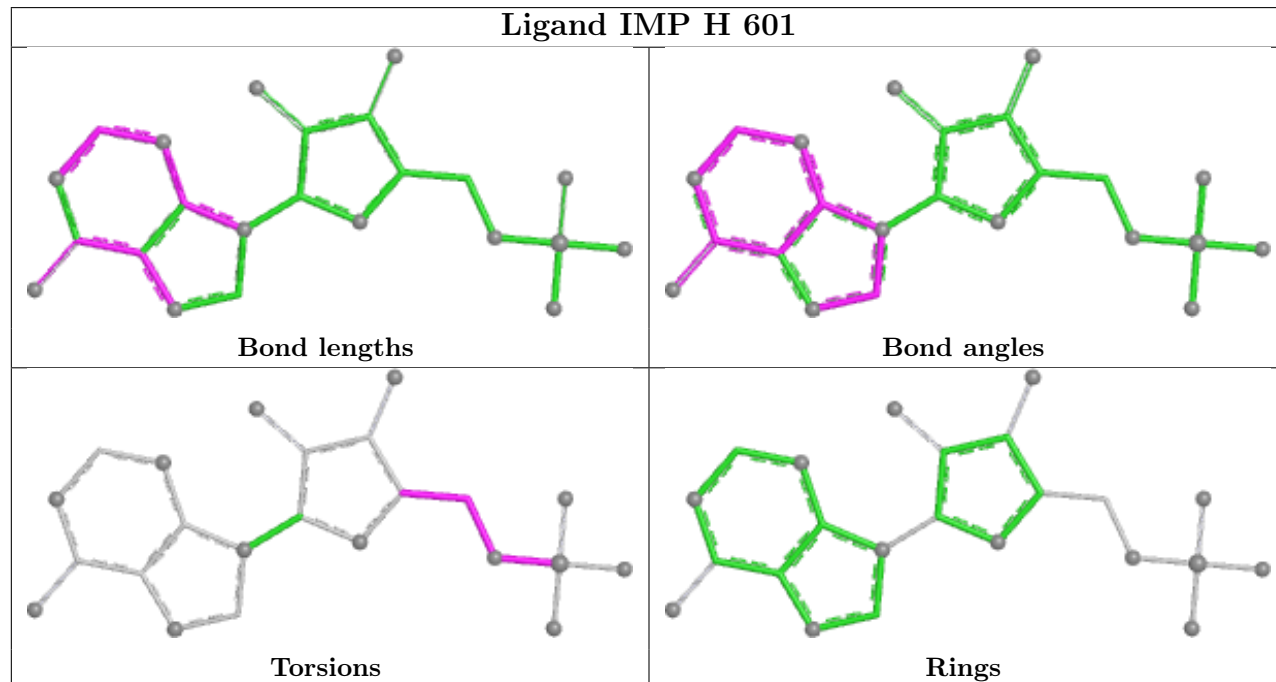
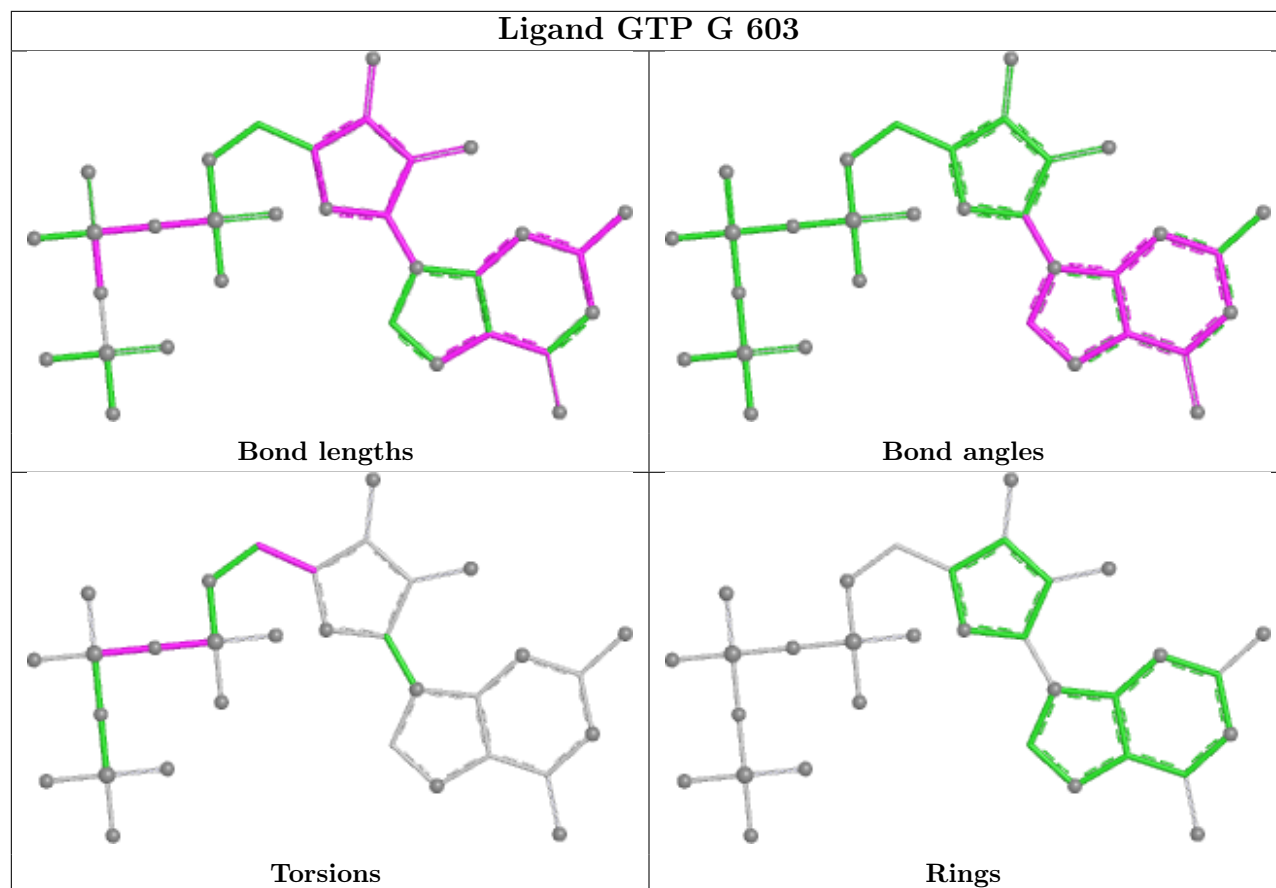
Ligand IMP F 601

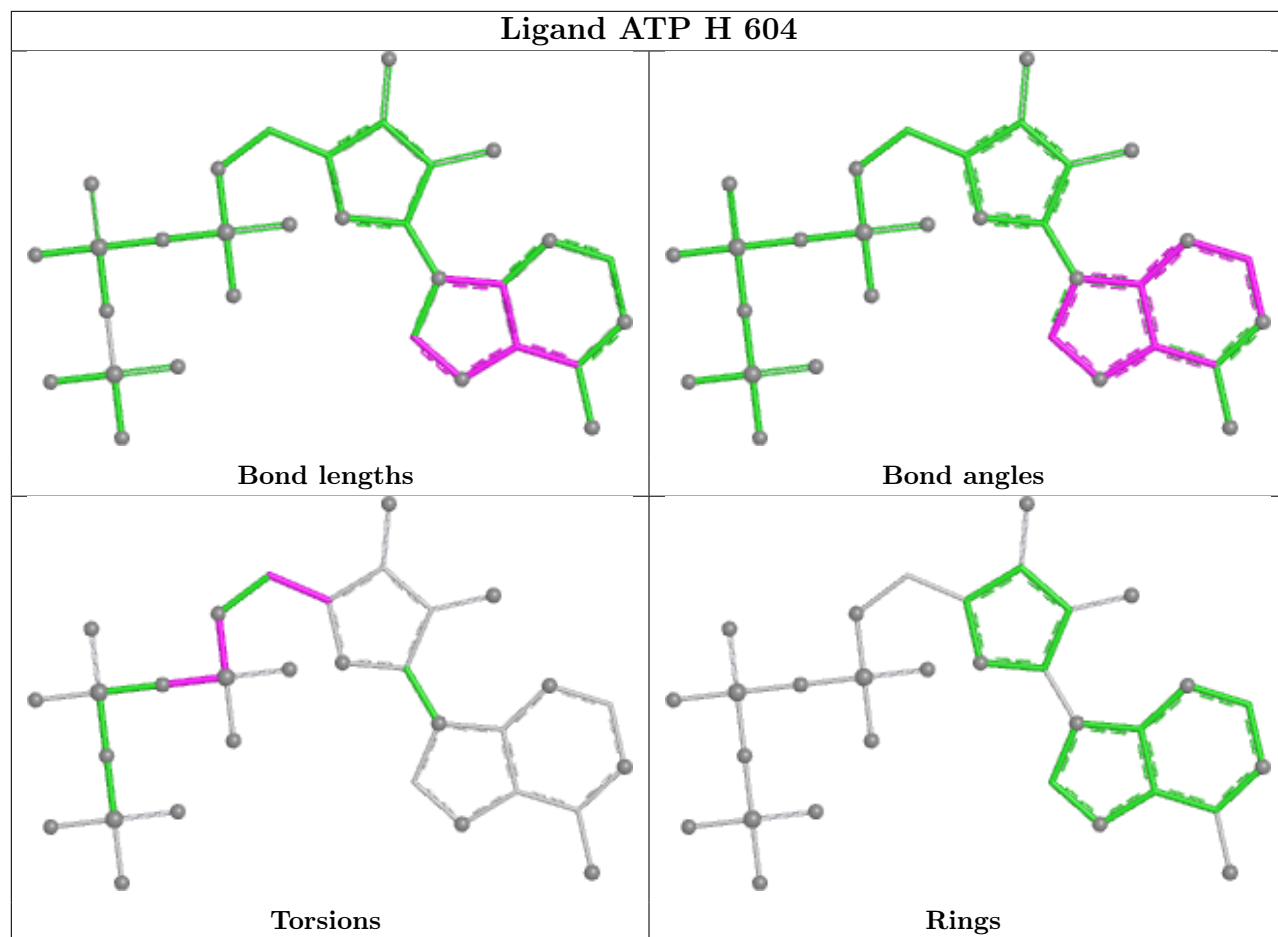


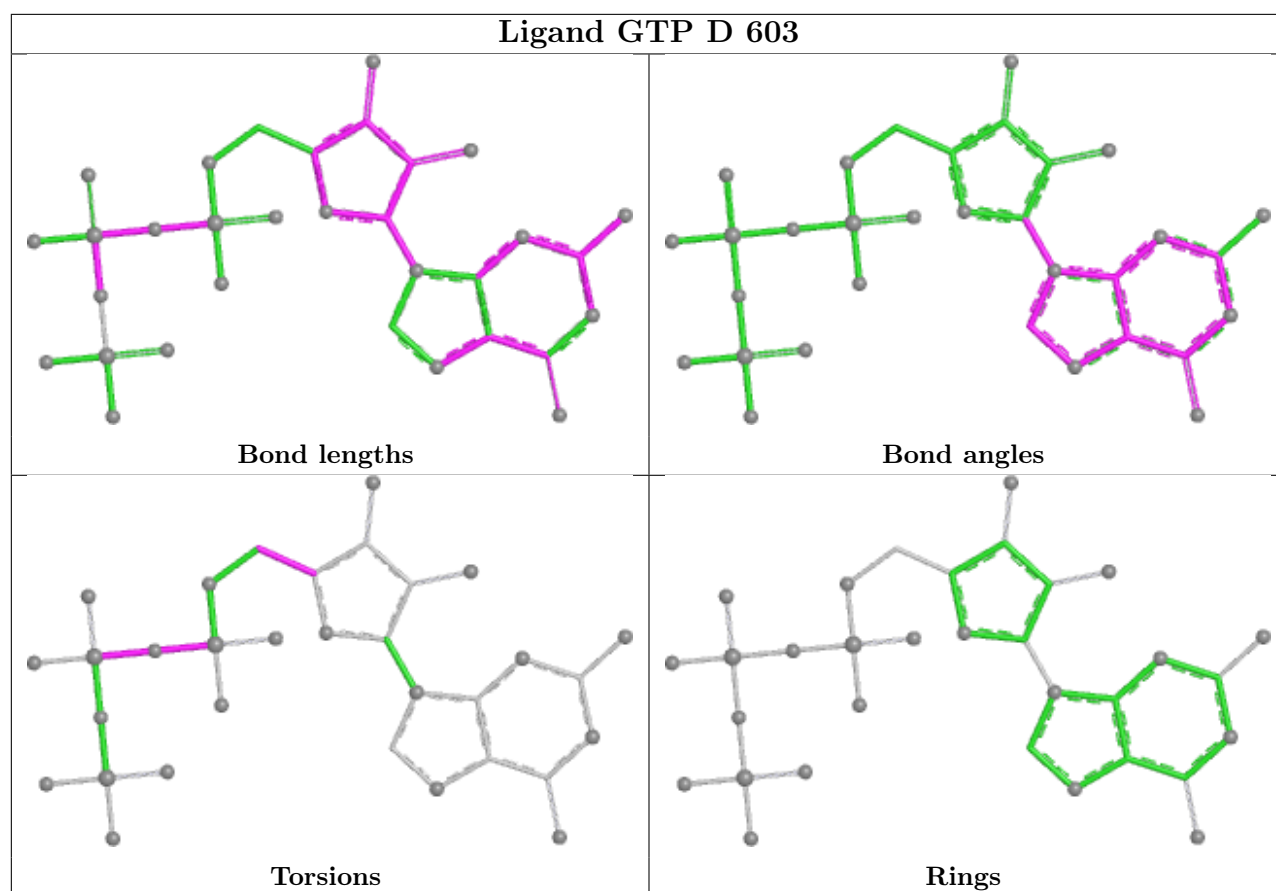












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

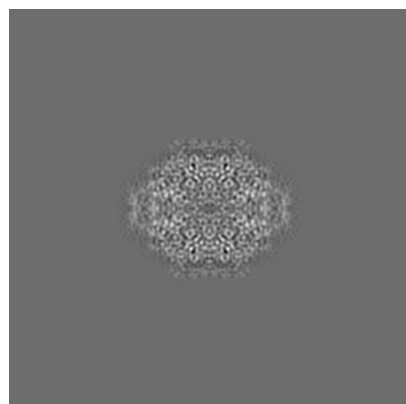
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20741. These allow visual inspection of the internal detail of the map and identification of artifacts.

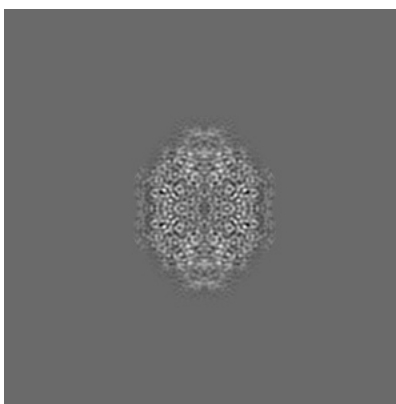
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

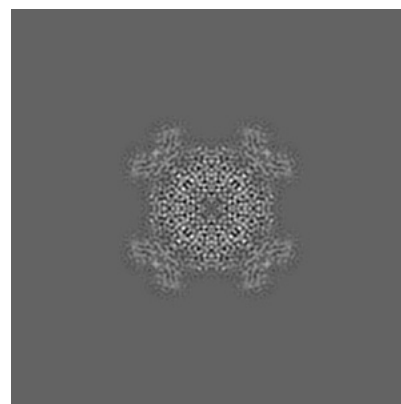
6.1.1 Primary map



X

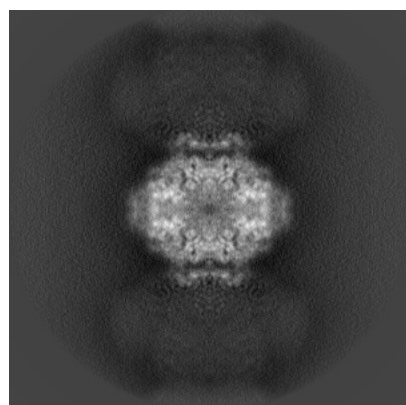


Y

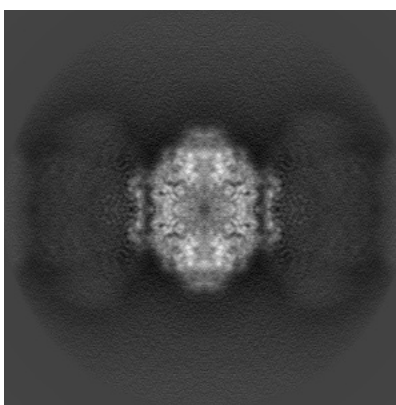


Z

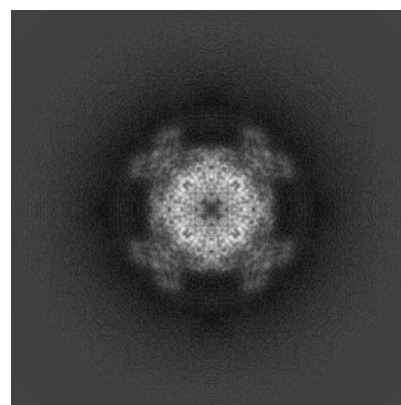
6.1.2 Raw map



X



Y

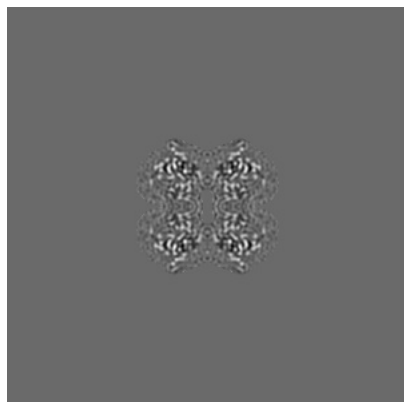


Z

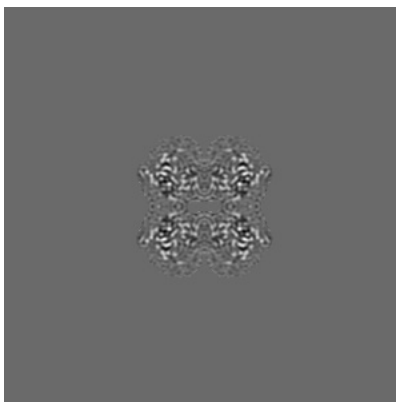
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

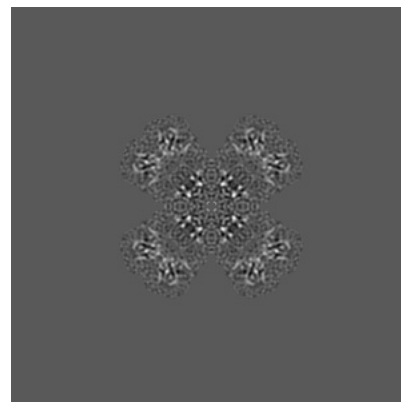
6.2.1 Primary map



X Index: 200

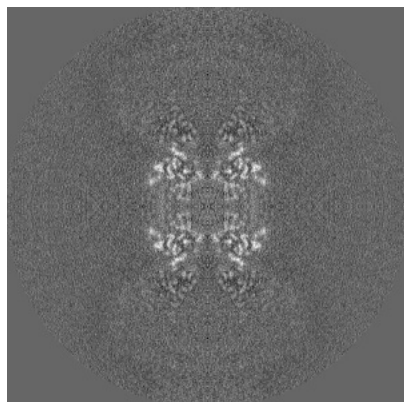


Y Index: 200

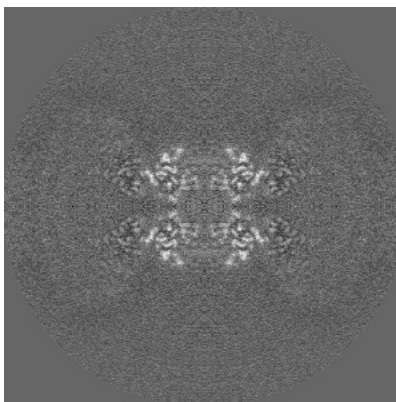


Z Index: 200

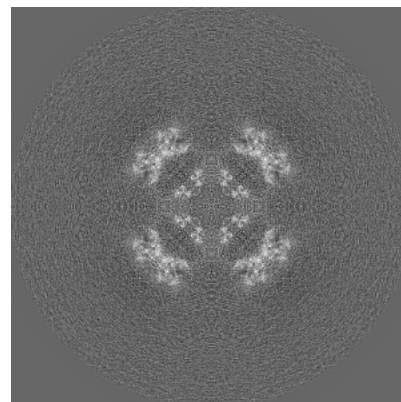
6.2.2 Raw map



X Index: 200



Y Index: 200

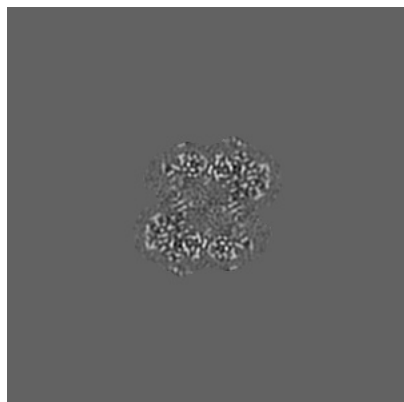


Z Index: 200

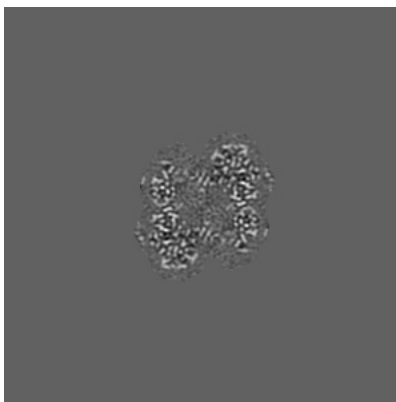
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

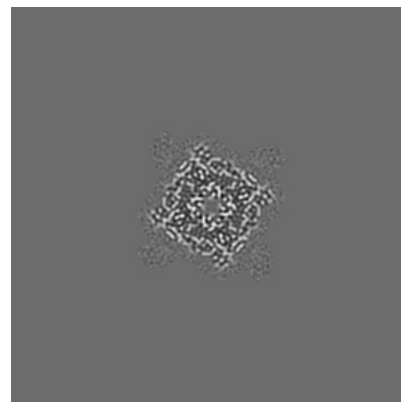
6.3.1 Primary map



X Index: 188

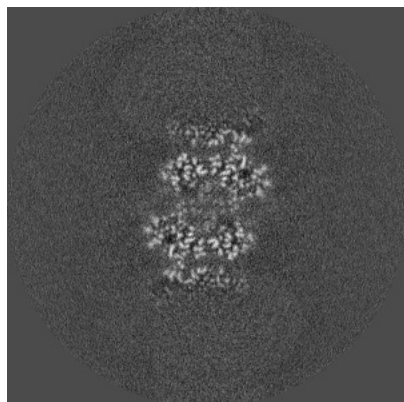


Y Index: 212

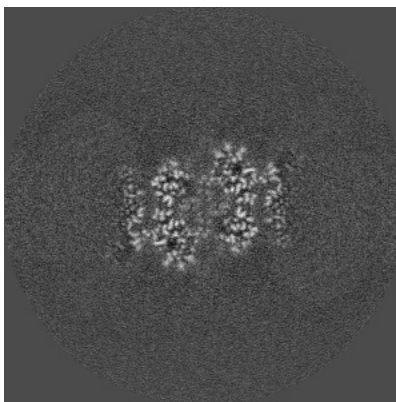


Z Index: 235

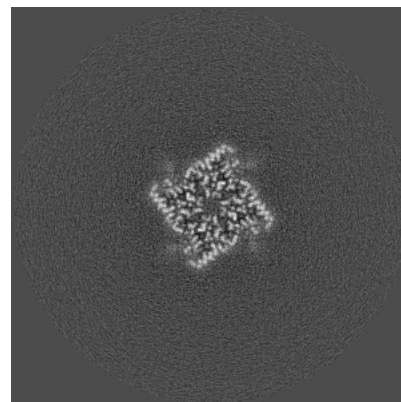
6.3.2 Raw map



X Index: 181



Y Index: 219

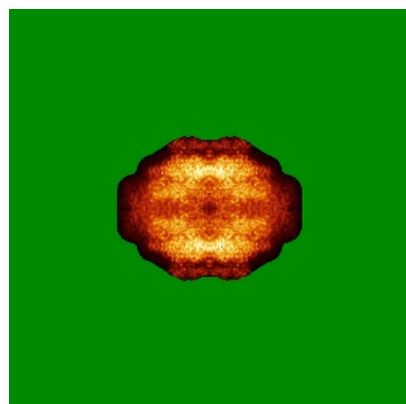


Z Index: 161

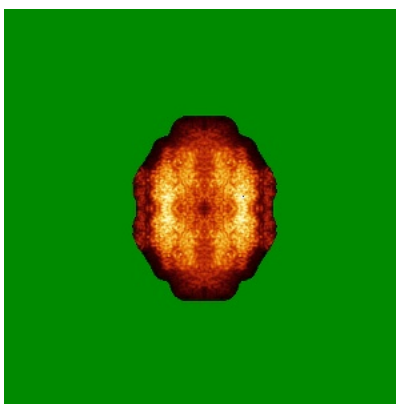
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

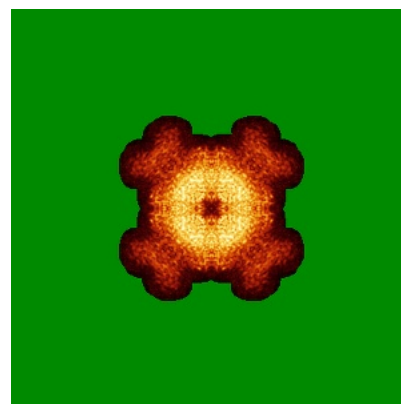
6.4.1 Primary map



X

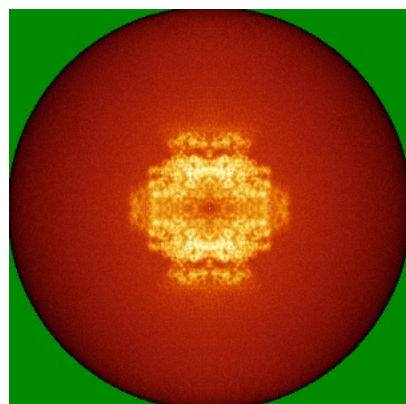


Y

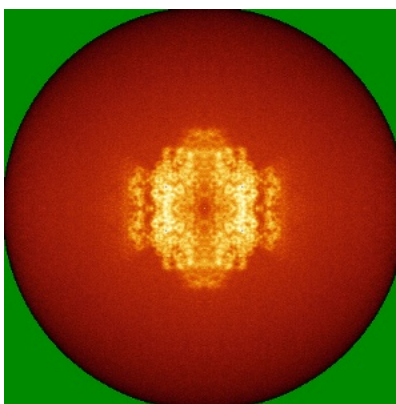


Z

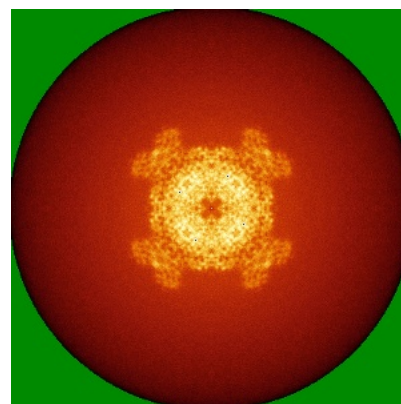
6.4.2 Raw map



X



Y

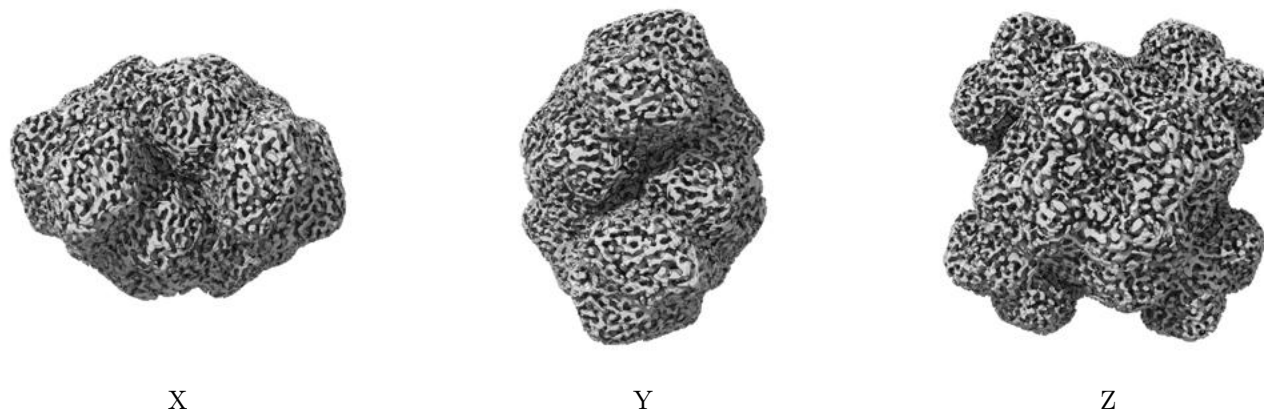


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

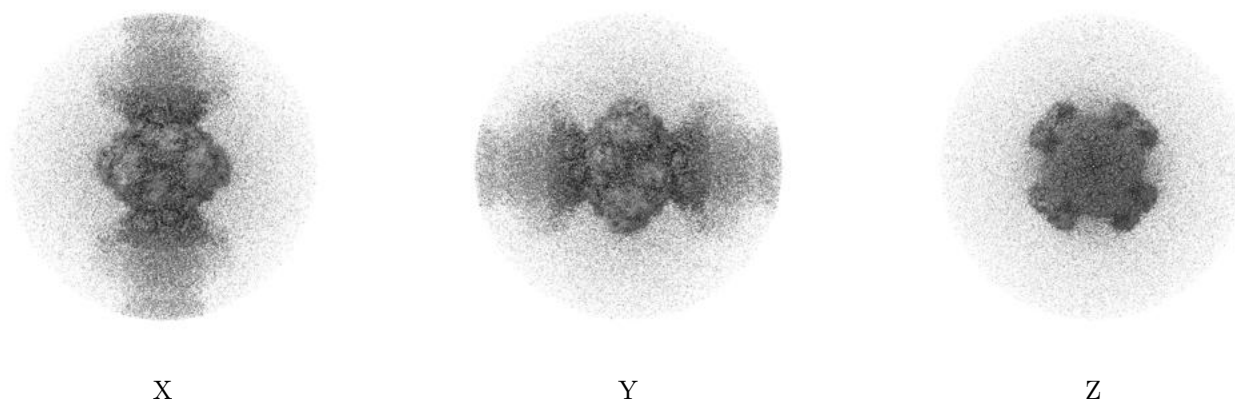
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

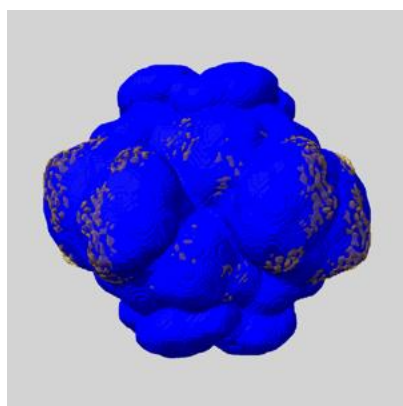
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

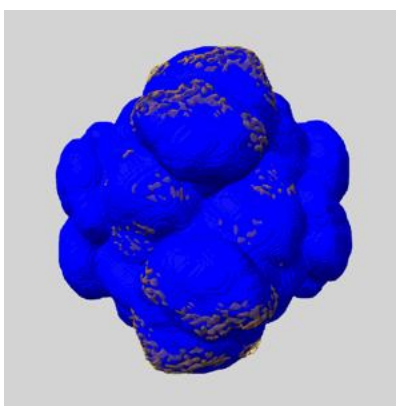
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

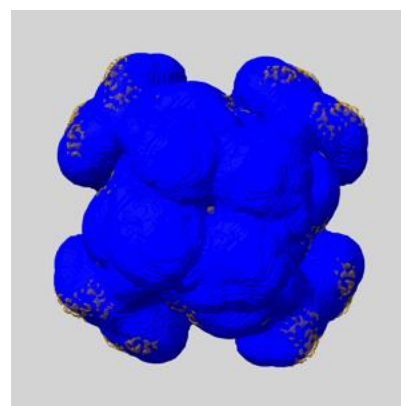
6.6.1 emd_20741_msk_1.map [i](#)



X



Y

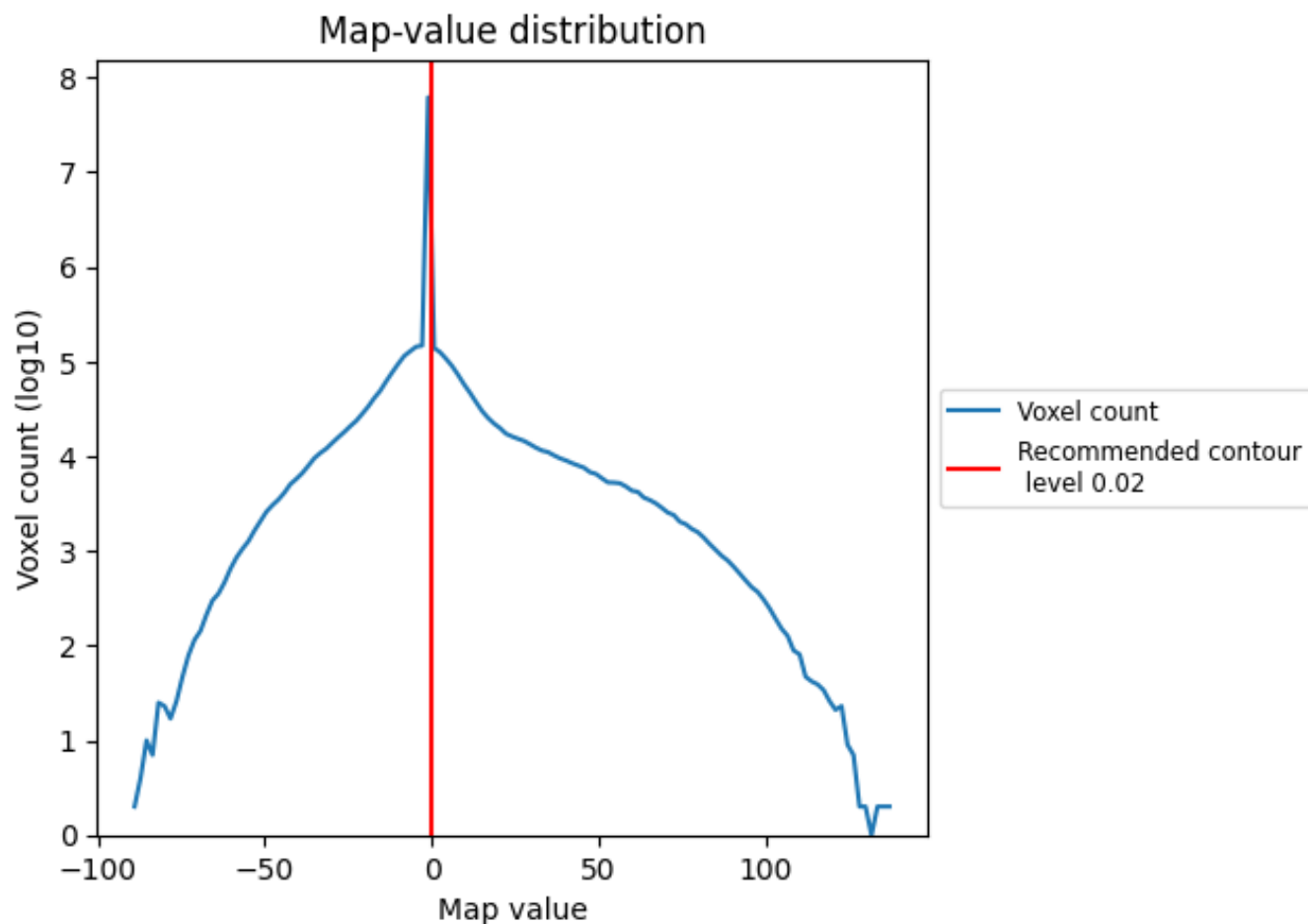


Z

7 Map analysis [i](#)

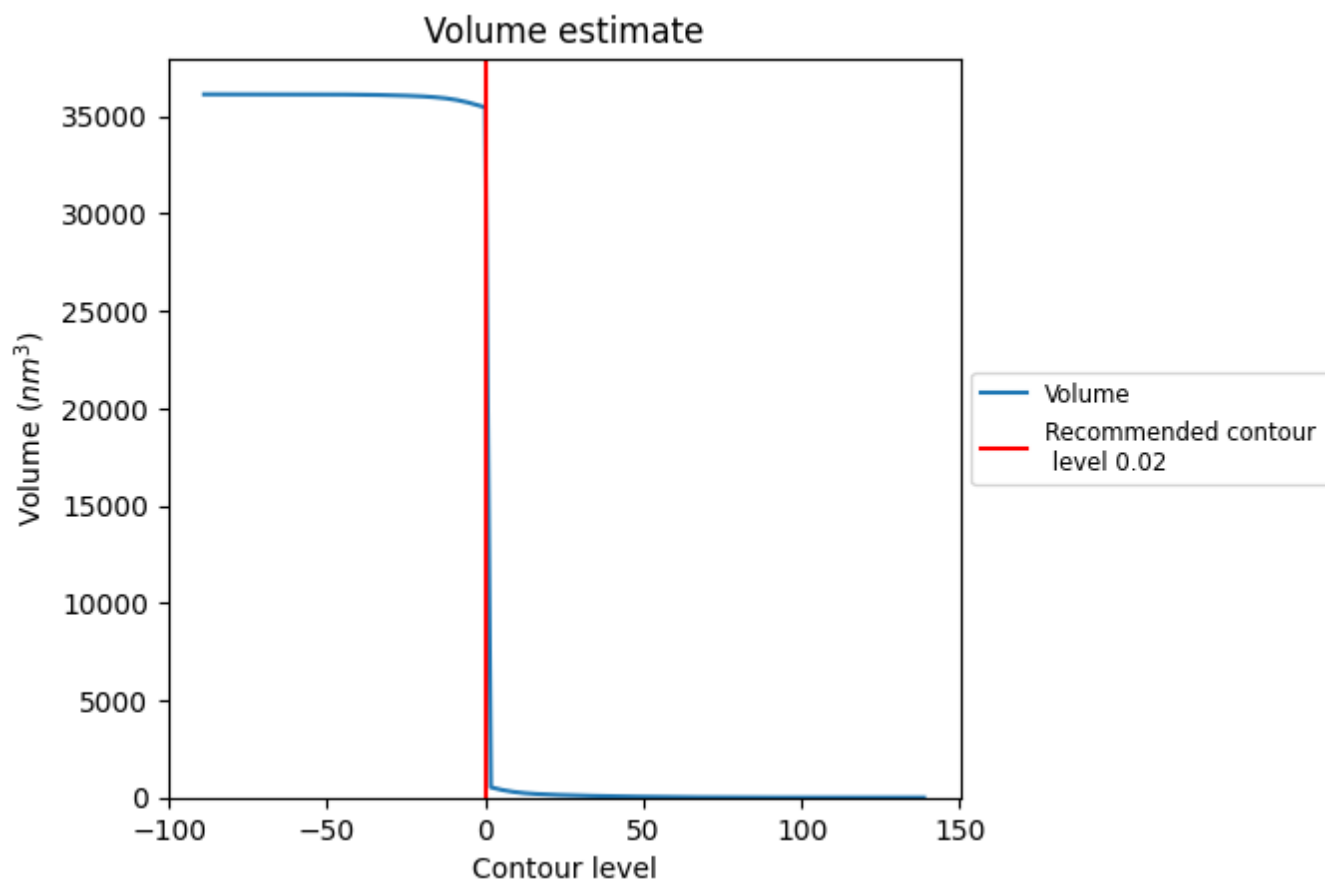
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

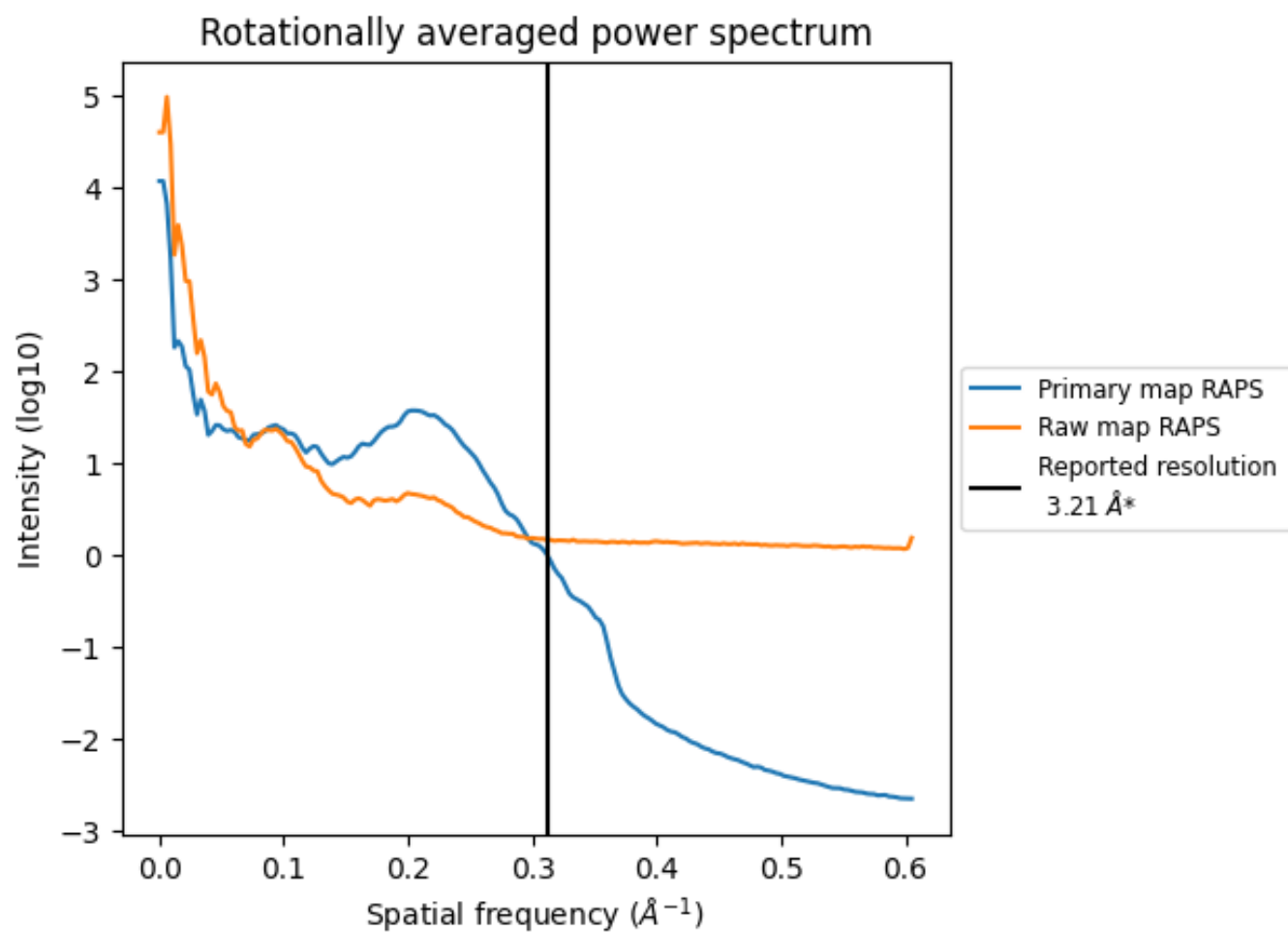
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 34772 nm³; this corresponds to an approximate mass of 31411 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

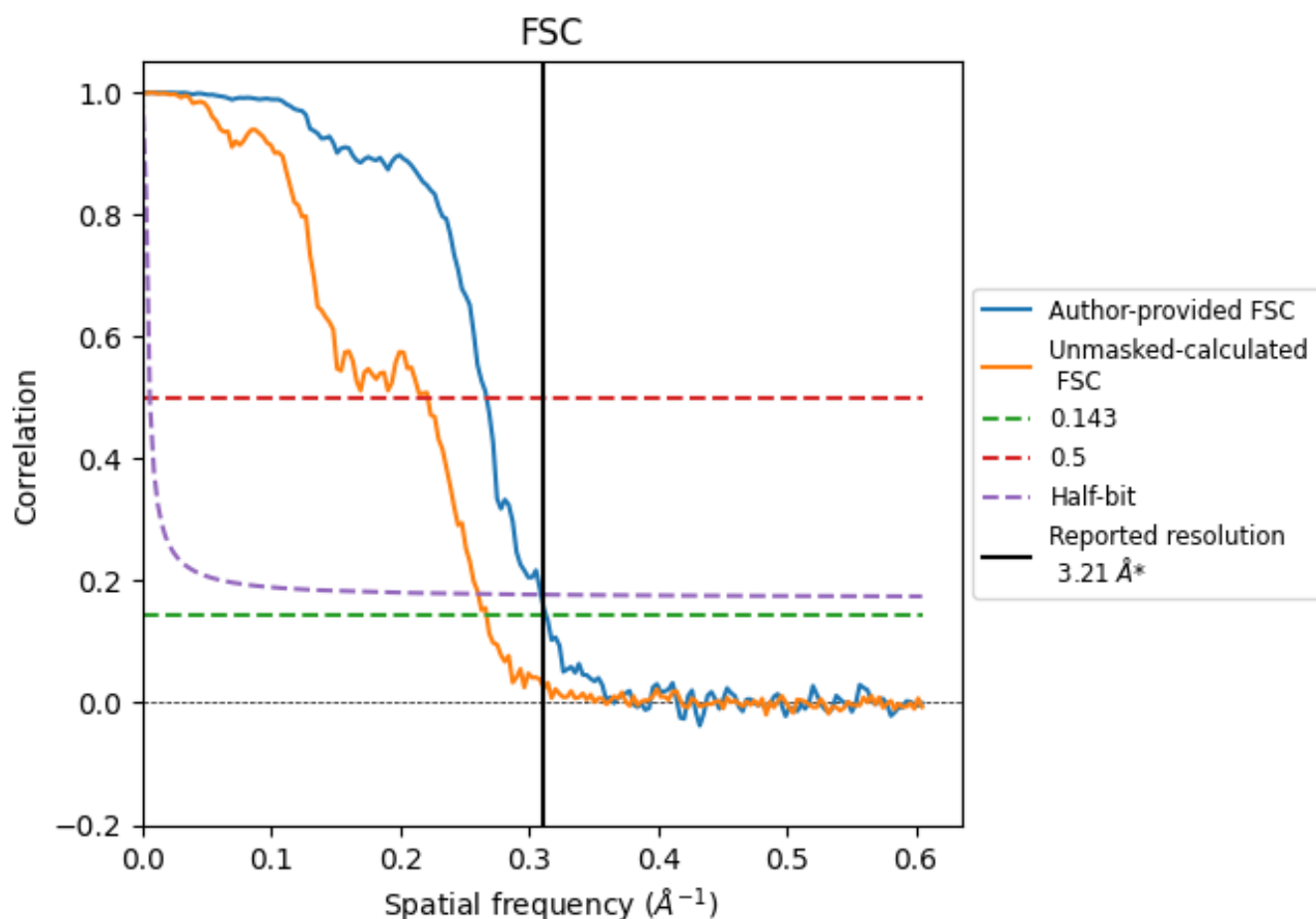


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

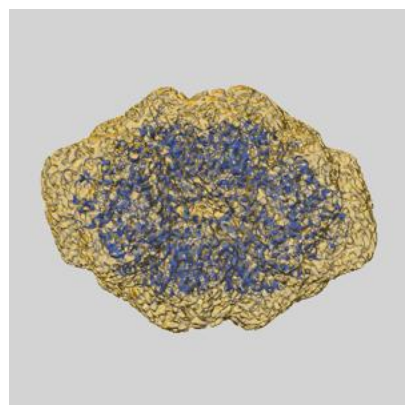
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.21	-	-
Author-provided FSC curve	3.19	3.74	3.23
Unmasked-calculated*	3.74	4.51	3.84

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.74 differs from the reported value 3.21 by more than 10 %

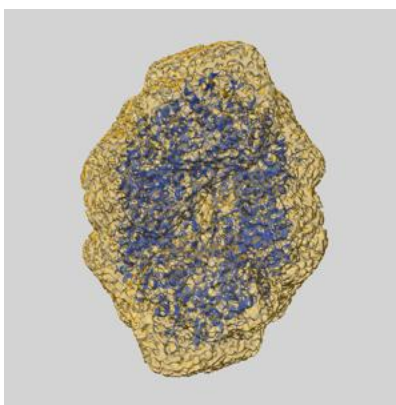
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20741 and PDB model 6UDO. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

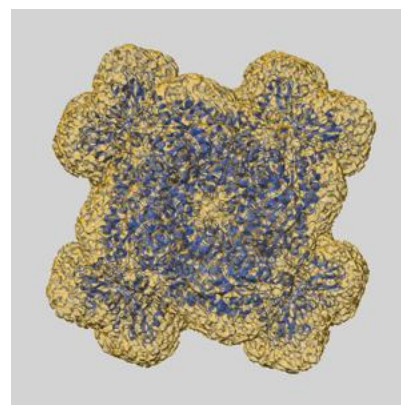
9.1 Map-model overlay [i](#)



X



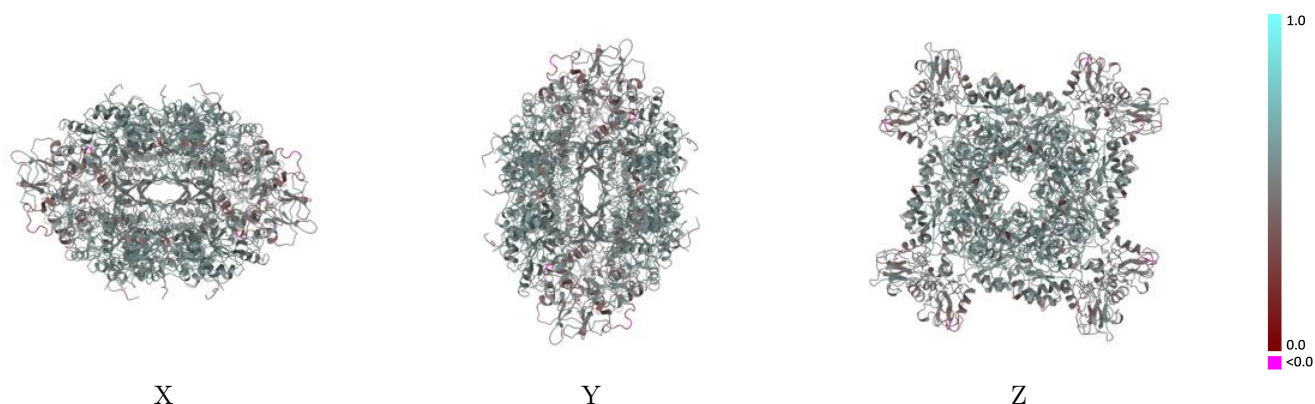
Y



Z

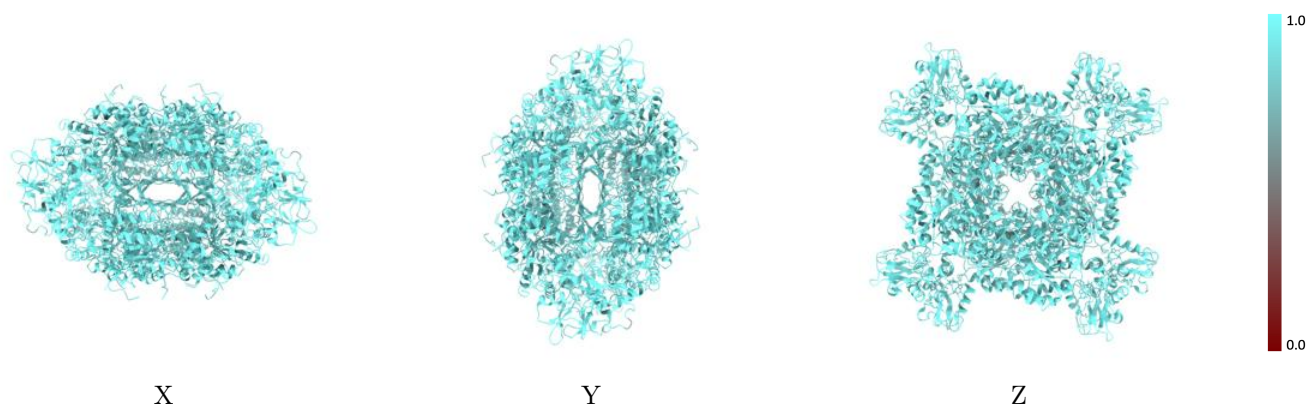
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



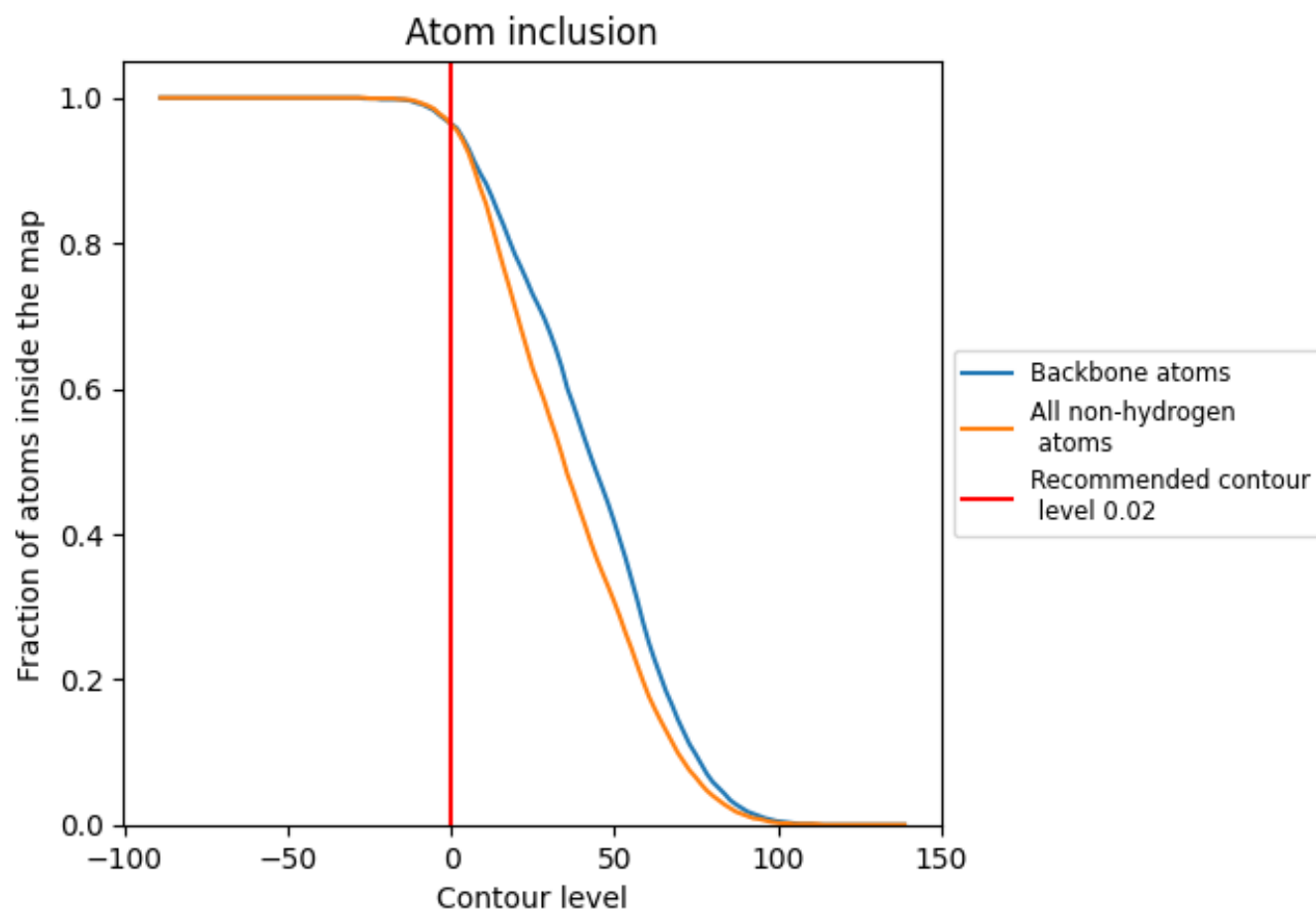
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9630	0.5100
A	0.9640	0.5120
B	0.9630	0.5120
C	0.9640	0.5110
D	0.9630	0.5110
E	0.9630	0.5110
F	0.9630	0.5120
G	0.9640	0.5120
H	0.9630	0.5120
I	0.9500	0.4760
J	0.9300	0.4570
K	0.9500	0.4660
L	0.9400	0.4650
M	0.9500	0.4730
N	0.9400	0.4780
O	0.9500	0.4660
P	0.9500	0.4790

