



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 24, 2026 – 01:55 AM UTC

PDB ID : 4EIL / pdb_00004eil
Title : Crystal Structure of the loop truncated Toxoplasma gondii TS-DHFR
Authors : Sharma, H.
Deposited on : 2012-04-05
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ 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:

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

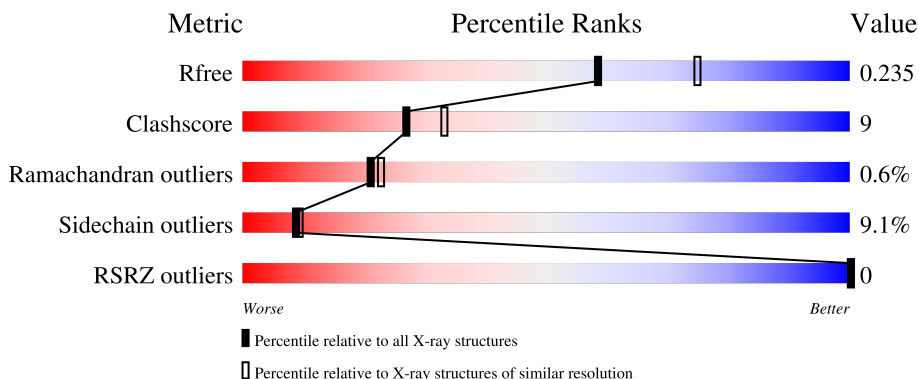
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	566	 69% 18% 10%
1	B	566	 66% 18% 13%
1	C	566	 69% 18% 10%
1	D	566	 64% 19% 13%
1	E	566	 72% 16% 10%

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Mol	Chain	Length	Quality of chain
1	F	566	
1	G	566	
1	H	566	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UMP	B	701	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 35087 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 Bifunctional dihydrofolate reductase-thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	510	4096	2618	718	735	25	0	2	0
1	B	491	3948	2531	682	710	25	0	1	0
1	C	510	4096	2618	718	735	25	0	2	0
1	D	491	3948	2531	682	710	25	0	1	0
1	E	510	4096	2618	718	735	25	0	2	0
1	F	491	3948	2531	682	710	25	0	1	0
1	G	510	4096	2618	718	735	25	0	2	0
1	H	491	3948	2531	682	710	25	0	1	0

There are 352 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ARG	deletion	UNP Q07422
A	?	-	LEU	deletion	UNP Q07422
A	?	-	ASN	deletion	UNP Q07422
A	?	-	GLY	deletion	UNP Q07422
A	?	-	TRP	deletion	UNP Q07422
A	?	-	LEU	deletion	UNP Q07422
A	?	-	PRO	deletion	UNP Q07422
A	?	-	ARG	deletion	UNP Q07422
A	?	-	LYS	deletion	UNP Q07422
A	?	-	PHE	deletion	UNP Q07422
A	?	-	ALA	deletion	UNP Q07422
A	?	-	LYS	deletion	UNP Q07422
A	?	-	THR	deletion	UNP Q07422

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLY	deletion	UNP Q07422
A	?	-	ASP	deletion	UNP Q07422
A	?	-	SER	deletion	UNP Q07422
A	?	-	GLY	deletion	UNP Q07422
A	?	-	LEU	deletion	UNP Q07422
A	?	-	PRO	deletion	UNP Q07422
A	?	-	SER	deletion	UNP Q07422
A	?	-	PRO	deletion	UNP Q07422
A	?	-	SER	deletion	UNP Q07422
A	?	-	VAL	deletion	UNP Q07422
A	?	-	GLY	deletion	UNP Q07422
A	?	-	LYS	deletion	UNP Q07422
A	?	-	GLN	deletion	UNP Q07422
A	?	-	ALA	deletion	UNP Q07422
A	?	-	ALA	deletion	UNP Q07422
A	?	-	ALA	deletion	UNP Q07422
A	?	-	PRO	deletion	UNP Q07422
A	?	-	ALA	deletion	UNP Q07422
A	?	-	GLU	deletion	UNP Q07422
A	?	-	SER	deletion	UNP Q07422
A	?	-	VAL	deletion	UNP Q07422
A	?	-	PHE	deletion	UNP Q07422
A	?	-	VAL	deletion	UNP Q07422
A	?	-	PRO	deletion	UNP Q07422
A	?	-	PHE	deletion	UNP Q07422
A	?	-	CYS	deletion	UNP Q07422
A	?	-	PRO	deletion	UNP Q07422
A	?	-	GLU	deletion	UNP Q07422
A	?	-	LEU	deletion	UNP Q07422
A	?	-	GLY	deletion	UNP Q07422
A	?	-	ARG	deletion	UNP Q07422
B	?	-	ARG	deletion	UNP Q07422
B	?	-	LEU	deletion	UNP Q07422
B	?	-	ASN	deletion	UNP Q07422
B	?	-	GLY	deletion	UNP Q07422
B	?	-	TRP	deletion	UNP Q07422
B	?	-	LEU	deletion	UNP Q07422
B	?	-	PRO	deletion	UNP Q07422
B	?	-	ARG	deletion	UNP Q07422
B	?	-	LYS	deletion	UNP Q07422
B	?	-	PHE	deletion	UNP Q07422
B	?	-	ALA	deletion	UNP Q07422

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	LYS	deletion	UNP Q07422
B	?	-	THR	deletion	UNP Q07422
B	?	-	GLY	deletion	UNP Q07422
B	?	-	ASP	deletion	UNP Q07422
B	?	-	SER	deletion	UNP Q07422
B	?	-	GLY	deletion	UNP Q07422
B	?	-	LEU	deletion	UNP Q07422
B	?	-	PRO	deletion	UNP Q07422
B	?	-	SER	deletion	UNP Q07422
B	?	-	PRO	deletion	UNP Q07422
B	?	-	SER	deletion	UNP Q07422
B	?	-	VAL	deletion	UNP Q07422
B	?	-	GLY	deletion	UNP Q07422
B	?	-	LYS	deletion	UNP Q07422
B	?	-	GLN	deletion	UNP Q07422
B	?	-	ALA	deletion	UNP Q07422
B	?	-	ALA	deletion	UNP Q07422
B	?	-	ALA	deletion	UNP Q07422
B	?	-	PRO	deletion	UNP Q07422
B	?	-	ALA	deletion	UNP Q07422
B	?	-	GLU	deletion	UNP Q07422
B	?	-	SER	deletion	UNP Q07422
B	?	-	VAL	deletion	UNP Q07422
B	?	-	PHE	deletion	UNP Q07422
B	?	-	VAL	deletion	UNP Q07422
B	?	-	PRO	deletion	UNP Q07422
B	?	-	PHE	deletion	UNP Q07422
B	?	-	CYS	deletion	UNP Q07422
B	?	-	PRO	deletion	UNP Q07422
B	?	-	GLU	deletion	UNP Q07422
B	?	-	LEU	deletion	UNP Q07422
B	?	-	GLY	deletion	UNP Q07422
B	?	-	ARG	deletion	UNP Q07422
C	?	-	ARG	deletion	UNP Q07422
C	?	-	LEU	deletion	UNP Q07422
C	?	-	ASN	deletion	UNP Q07422
C	?	-	GLY	deletion	UNP Q07422
C	?	-	TRP	deletion	UNP Q07422
C	?	-	LEU	deletion	UNP Q07422
C	?	-	PRO	deletion	UNP Q07422
C	?	-	ARG	deletion	UNP Q07422
C	?	-	LYS	deletion	UNP Q07422

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	PHE	deletion	UNP Q07422
C	?	-	ALA	deletion	UNP Q07422
C	?	-	LYS	deletion	UNP Q07422
C	?	-	THR	deletion	UNP Q07422
C	?	-	GLY	deletion	UNP Q07422
C	?	-	ASP	deletion	UNP Q07422
C	?	-	SER	deletion	UNP Q07422
C	?	-	GLY	deletion	UNP Q07422
C	?	-	LEU	deletion	UNP Q07422
C	?	-	PRO	deletion	UNP Q07422
C	?	-	SER	deletion	UNP Q07422
C	?	-	PRO	deletion	UNP Q07422
C	?	-	SER	deletion	UNP Q07422
C	?	-	VAL	deletion	UNP Q07422
C	?	-	GLY	deletion	UNP Q07422
C	?	-	LYS	deletion	UNP Q07422
C	?	-	GLN	deletion	UNP Q07422
C	?	-	ALA	deletion	UNP Q07422
C	?	-	ALA	deletion	UNP Q07422
C	?	-	ALA	deletion	UNP Q07422
C	?	-	PRO	deletion	UNP Q07422
C	?	-	ALA	deletion	UNP Q07422
C	?	-	GLU	deletion	UNP Q07422
C	?	-	SER	deletion	UNP Q07422
C	?	-	VAL	deletion	UNP Q07422
C	?	-	PHE	deletion	UNP Q07422
C	?	-	VAL	deletion	UNP Q07422
C	?	-	PRO	deletion	UNP Q07422
C	?	-	PHE	deletion	UNP Q07422
C	?	-	CYS	deletion	UNP Q07422
C	?	-	PRO	deletion	UNP Q07422
C	?	-	GLU	deletion	UNP Q07422
C	?	-	LEU	deletion	UNP Q07422
C	?	-	GLY	deletion	UNP Q07422
C	?	-	ARG	deletion	UNP Q07422
D	?	-	ARG	deletion	UNP Q07422
D	?	-	LEU	deletion	UNP Q07422
D	?	-	ASN	deletion	UNP Q07422
D	?	-	GLY	deletion	UNP Q07422
D	?	-	TRP	deletion	UNP Q07422
D	?	-	LEU	deletion	UNP Q07422
D	?	-	PRO	deletion	UNP Q07422

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Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	ARG	deletion	UNP Q07422
D	?	-	LYS	deletion	UNP Q07422
D	?	-	PHE	deletion	UNP Q07422
D	?	-	ALA	deletion	UNP Q07422
D	?	-	LYS	deletion	UNP Q07422
D	?	-	THR	deletion	UNP Q07422
D	?	-	GLY	deletion	UNP Q07422
D	?	-	ASP	deletion	UNP Q07422
D	?	-	SER	deletion	UNP Q07422
D	?	-	GLY	deletion	UNP Q07422
D	?	-	LEU	deletion	UNP Q07422
D	?	-	PRO	deletion	UNP Q07422
D	?	-	SER	deletion	UNP Q07422
D	?	-	PRO	deletion	UNP Q07422
D	?	-	SER	deletion	UNP Q07422
D	?	-	VAL	deletion	UNP Q07422
D	?	-	GLY	deletion	UNP Q07422
D	?	-	LYS	deletion	UNP Q07422
D	?	-	GLN	deletion	UNP Q07422
D	?	-	ALA	deletion	UNP Q07422
D	?	-	ALA	deletion	UNP Q07422
D	?	-	ALA	deletion	UNP Q07422
D	?	-	PRO	deletion	UNP Q07422
D	?	-	ALA	deletion	UNP Q07422
D	?	-	GLU	deletion	UNP Q07422
D	?	-	SER	deletion	UNP Q07422
D	?	-	VAL	deletion	UNP Q07422
D	?	-	PHE	deletion	UNP Q07422
D	?	-	VAL	deletion	UNP Q07422
D	?	-	PRO	deletion	UNP Q07422
D	?	-	PHE	deletion	UNP Q07422
D	?	-	CYS	deletion	UNP Q07422
D	?	-	PRO	deletion	UNP Q07422
D	?	-	GLU	deletion	UNP Q07422
D	?	-	LEU	deletion	UNP Q07422
D	?	-	GLY	deletion	UNP Q07422
D	?	-	ARG	deletion	UNP Q07422
E	?	-	ARG	deletion	UNP Q07422
E	?	-	LEU	deletion	UNP Q07422
E	?	-	ASN	deletion	UNP Q07422
E	?	-	GLY	deletion	UNP Q07422
E	?	-	TRP	deletion	UNP Q07422

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Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	LEU	deletion	UNP Q07422
E	?	-	PRO	deletion	UNP Q07422
E	?	-	ARG	deletion	UNP Q07422
E	?	-	LYS	deletion	UNP Q07422
E	?	-	PHE	deletion	UNP Q07422
E	?	-	ALA	deletion	UNP Q07422
E	?	-	LYS	deletion	UNP Q07422
E	?	-	THR	deletion	UNP Q07422
E	?	-	GLY	deletion	UNP Q07422
E	?	-	ASP	deletion	UNP Q07422
E	?	-	SER	deletion	UNP Q07422
E	?	-	GLY	deletion	UNP Q07422
E	?	-	LEU	deletion	UNP Q07422
E	?	-	PRO	deletion	UNP Q07422
E	?	-	SER	deletion	UNP Q07422
E	?	-	PRO	deletion	UNP Q07422
E	?	-	SER	deletion	UNP Q07422
E	?	-	VAL	deletion	UNP Q07422
E	?	-	GLY	deletion	UNP Q07422
E	?	-	LYS	deletion	UNP Q07422
E	?	-	GLN	deletion	UNP Q07422
E	?	-	ALA	deletion	UNP Q07422
E	?	-	ALA	deletion	UNP Q07422
E	?	-	ALA	deletion	UNP Q07422
E	?	-	PRO	deletion	UNP Q07422
E	?	-	ALA	deletion	UNP Q07422
E	?	-	GLU	deletion	UNP Q07422
E	?	-	SER	deletion	UNP Q07422
E	?	-	VAL	deletion	UNP Q07422
E	?	-	PHE	deletion	UNP Q07422
E	?	-	VAL	deletion	UNP Q07422
E	?	-	PRO	deletion	UNP Q07422
E	?	-	PHE	deletion	UNP Q07422
E	?	-	CYS	deletion	UNP Q07422
E	?	-	PRO	deletion	UNP Q07422
E	?	-	GLU	deletion	UNP Q07422
E	?	-	LEU	deletion	UNP Q07422
E	?	-	GLY	deletion	UNP Q07422
E	?	-	ARG	deletion	UNP Q07422
F	?	-	ARG	deletion	UNP Q07422
F	?	-	LEU	deletion	UNP Q07422
F	?	-	ASN	deletion	UNP Q07422

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Chain	Residue	Modelled	Actual	Comment	Reference
F	?	-	GLY	deletion	UNP Q07422
F	?	-	TRP	deletion	UNP Q07422
F	?	-	LEU	deletion	UNP Q07422
F	?	-	PRO	deletion	UNP Q07422
F	?	-	ARG	deletion	UNP Q07422
F	?	-	LYS	deletion	UNP Q07422
F	?	-	PHE	deletion	UNP Q07422
F	?	-	ALA	deletion	UNP Q07422
F	?	-	LYS	deletion	UNP Q07422
F	?	-	THR	deletion	UNP Q07422
F	?	-	GLY	deletion	UNP Q07422
F	?	-	ASP	deletion	UNP Q07422
F	?	-	SER	deletion	UNP Q07422
F	?	-	GLY	deletion	UNP Q07422
F	?	-	LEU	deletion	UNP Q07422
F	?	-	PRO	deletion	UNP Q07422
F	?	-	SER	deletion	UNP Q07422
F	?	-	PRO	deletion	UNP Q07422
F	?	-	SER	deletion	UNP Q07422
F	?	-	VAL	deletion	UNP Q07422
F	?	-	GLY	deletion	UNP Q07422
F	?	-	LYS	deletion	UNP Q07422
F	?	-	GLN	deletion	UNP Q07422
F	?	-	ALA	deletion	UNP Q07422
F	?	-	ALA	deletion	UNP Q07422
F	?	-	ALA	deletion	UNP Q07422
F	?	-	PRO	deletion	UNP Q07422
F	?	-	ALA	deletion	UNP Q07422
F	?	-	GLU	deletion	UNP Q07422
F	?	-	SER	deletion	UNP Q07422
F	?	-	VAL	deletion	UNP Q07422
F	?	-	PHE	deletion	UNP Q07422
F	?	-	VAL	deletion	UNP Q07422
F	?	-	PRO	deletion	UNP Q07422
F	?	-	PHE	deletion	UNP Q07422
F	?	-	CYS	deletion	UNP Q07422
F	?	-	PRO	deletion	UNP Q07422
F	?	-	GLU	deletion	UNP Q07422
F	?	-	LEU	deletion	UNP Q07422
F	?	-	GLY	deletion	UNP Q07422
F	?	-	ARG	deletion	UNP Q07422
G	?	-	ARG	deletion	UNP Q07422

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Chain	Residue	Modelled	Actual	Comment	Reference
G	?	-	LEU	deletion	UNP Q07422
G	?	-	ASN	deletion	UNP Q07422
G	?	-	GLY	deletion	UNP Q07422
G	?	-	TRP	deletion	UNP Q07422
G	?	-	LEU	deletion	UNP Q07422
G	?	-	PRO	deletion	UNP Q07422
G	?	-	ARG	deletion	UNP Q07422
G	?	-	LYS	deletion	UNP Q07422
G	?	-	PHE	deletion	UNP Q07422
G	?	-	ALA	deletion	UNP Q07422
G	?	-	LYS	deletion	UNP Q07422
G	?	-	THR	deletion	UNP Q07422
G	?	-	GLY	deletion	UNP Q07422
G	?	-	ASP	deletion	UNP Q07422
G	?	-	SER	deletion	UNP Q07422
G	?	-	GLY	deletion	UNP Q07422
G	?	-	LEU	deletion	UNP Q07422
G	?	-	PRO	deletion	UNP Q07422
G	?	-	SER	deletion	UNP Q07422
G	?	-	PRO	deletion	UNP Q07422
G	?	-	SER	deletion	UNP Q07422
G	?	-	VAL	deletion	UNP Q07422
G	?	-	GLY	deletion	UNP Q07422
G	?	-	LYS	deletion	UNP Q07422
G	?	-	GLN	deletion	UNP Q07422
G	?	-	ALA	deletion	UNP Q07422
G	?	-	ALA	deletion	UNP Q07422
G	?	-	ALA	deletion	UNP Q07422
G	?	-	PRO	deletion	UNP Q07422
G	?	-	ALA	deletion	UNP Q07422
G	?	-	GLU	deletion	UNP Q07422
G	?	-	SER	deletion	UNP Q07422
G	?	-	VAL	deletion	UNP Q07422
G	?	-	PHE	deletion	UNP Q07422
G	?	-	VAL	deletion	UNP Q07422
G	?	-	PRO	deletion	UNP Q07422
G	?	-	PHE	deletion	UNP Q07422
G	?	-	CYS	deletion	UNP Q07422
G	?	-	PRO	deletion	UNP Q07422
G	?	-	GLU	deletion	UNP Q07422
G	?	-	LEU	deletion	UNP Q07422
G	?	-	GLY	deletion	UNP Q07422

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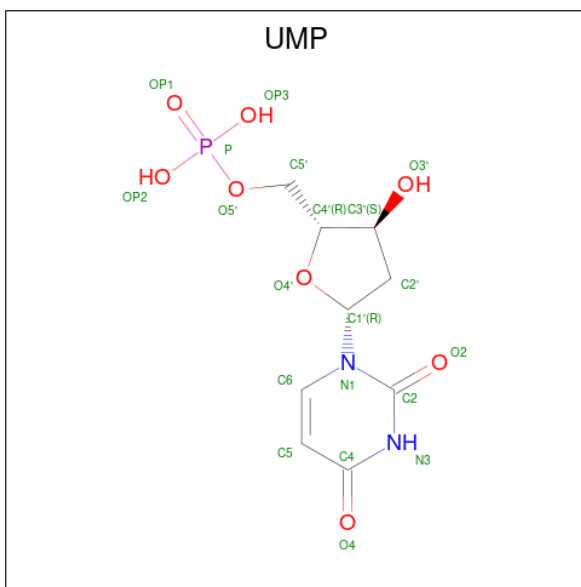
Chain	Residue	Modelled	Actual	Comment	Reference
G	?	-	ARG	deletion	UNP Q07422
H	?	-	ARG	deletion	UNP Q07422
H	?	-	LEU	deletion	UNP Q07422
H	?	-	ASN	deletion	UNP Q07422
H	?	-	GLY	deletion	UNP Q07422
H	?	-	TRP	deletion	UNP Q07422
H	?	-	LEU	deletion	UNP Q07422
H	?	-	PRO	deletion	UNP Q07422
H	?	-	ARG	deletion	UNP Q07422
H	?	-	LYS	deletion	UNP Q07422
H	?	-	PHE	deletion	UNP Q07422
H	?	-	ALA	deletion	UNP Q07422
H	?	-	LYS	deletion	UNP Q07422
H	?	-	THR	deletion	UNP Q07422
H	?	-	GLY	deletion	UNP Q07422
H	?	-	ASP	deletion	UNP Q07422
H	?	-	SER	deletion	UNP Q07422
H	?	-	GLY	deletion	UNP Q07422
H	?	-	LEU	deletion	UNP Q07422
H	?	-	PRO	deletion	UNP Q07422
H	?	-	SER	deletion	UNP Q07422
H	?	-	PRO	deletion	UNP Q07422
H	?	-	SER	deletion	UNP Q07422
H	?	-	VAL	deletion	UNP Q07422
H	?	-	GLY	deletion	UNP Q07422
H	?	-	LYS	deletion	UNP Q07422
H	?	-	GLN	deletion	UNP Q07422
H	?	-	ALA	deletion	UNP Q07422
H	?	-	ALA	deletion	UNP Q07422
H	?	-	ALA	deletion	UNP Q07422
H	?	-	PRO	deletion	UNP Q07422
H	?	-	ALA	deletion	UNP Q07422
H	?	-	GLU	deletion	UNP Q07422
H	?	-	SER	deletion	UNP Q07422
H	?	-	VAL	deletion	UNP Q07422
H	?	-	PHE	deletion	UNP Q07422
H	?	-	VAL	deletion	UNP Q07422
H	?	-	PRO	deletion	UNP Q07422
H	?	-	PHE	deletion	UNP Q07422
H	?	-	CYS	deletion	UNP Q07422
H	?	-	PRO	deletion	UNP Q07422
H	?	-	GLU	deletion	UNP Q07422

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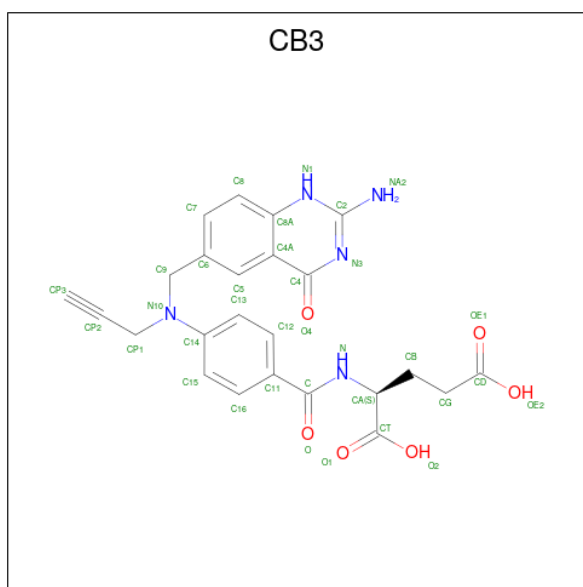
Chain	Residue	Modelled	Actual	Comment	Reference
H	?	-	LEU	deletion	UNP Q07422
H	?	-	GLY	deletion	UNP Q07422
H	?	-	ARG	deletion	UNP Q07422

- Molecule 2 is 2'-DEOXYURIDINE 5'-MONOPHOSPHATE (CCD ID: UMP) (formula: C₉H₁₃N₂O₈P).



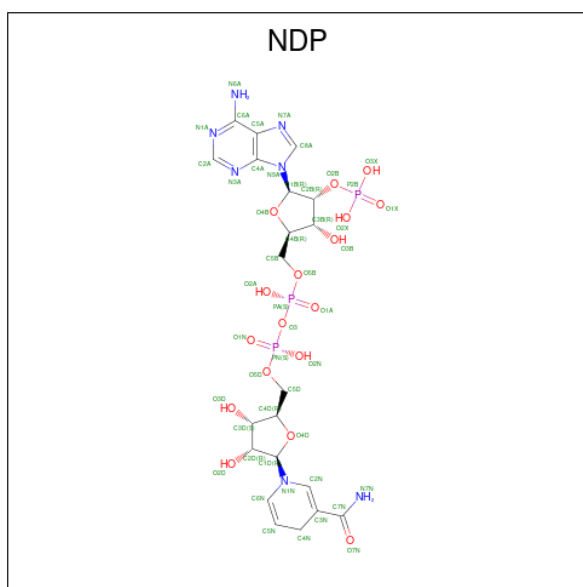
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	B	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	C	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	D	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	E	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	F	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	G	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
2	H	1	Total	C	N	O	P	0	0
			20	9	2	8	1		

- Molecule 3 is 10-PROPARGYL-5,8-DIDEAZAFOLIC ACID (CCD ID: CB3) (formula: C₂₄H₂₃N₅O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	35	24	5	6	0	0
3	B	1	35	24	5	6	0	0
3	C	1	35	24	5	6	0	0
3	D	1	35	24	5	6	0	0
3	E	1	35	24	5	6	0	0
3	F	1	35	24	5	6	0	0
3	G	1	35	24	5	6	0	0
3	H	1	35	24	5	6	0	0

- Molecule 4 is FOLIC ACID (CCD ID: FOL) (formula: C₁₉H₁₉N₇O₆).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
5	B	1	Total 48	C 21	N 7	O 17	P 3	0	0
5	C	1	Total 48	C 21	N 7	O 17	P 3	0	0
5	D	1	Total 48	C 21	N 7	O 17	P 3	0	0
5	E	1	Total 48	C 21	N 7	O 17	P 3	0	0
5	F	1	Total 48	C 21	N 7	O 17	P 3	0	0
5	G	1	Total 48	C 21	N 7	O 17	P 3	0	0
5	H	1	Total 48	C 21	N 7	O 17	P 3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	248	Total 248	O 248	0	0
6	B	229	Total 229	O 229	0	0
6	C	224	Total 224	O 224	0	0
6	D	232	Total 232	O 232	0	0

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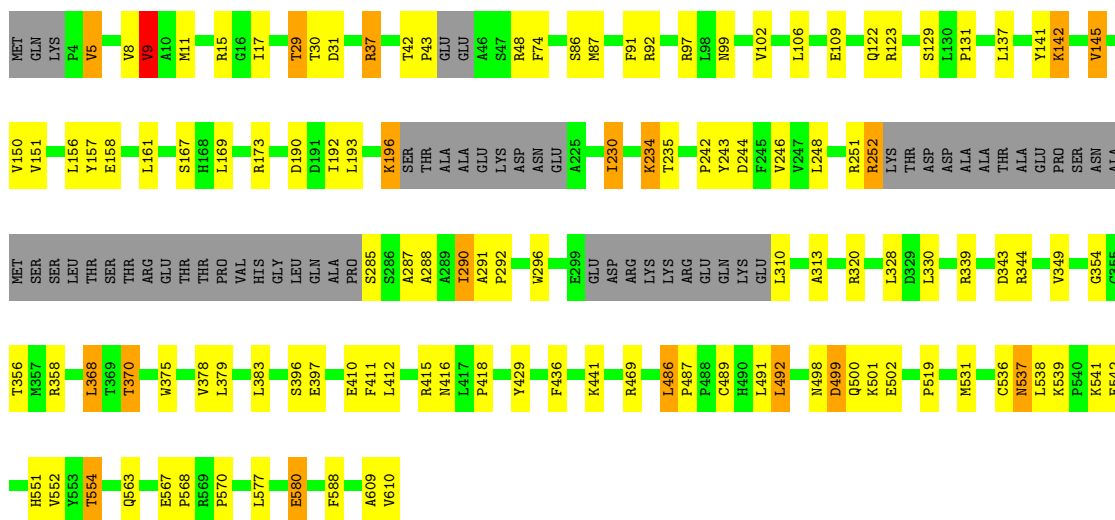
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	220	Total 220	O 220	0	0
6	F	242	Total 242	O 242	0	0
6	G	221	Total 221	O 221	0	0
6	H	215	Total 215	O 215	0	0

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.

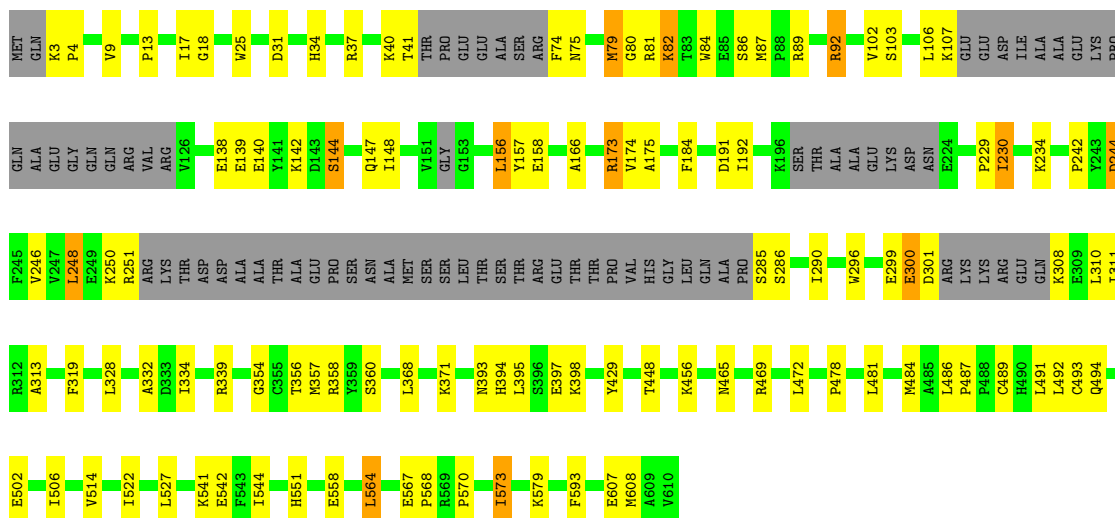
- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

Chain A: 



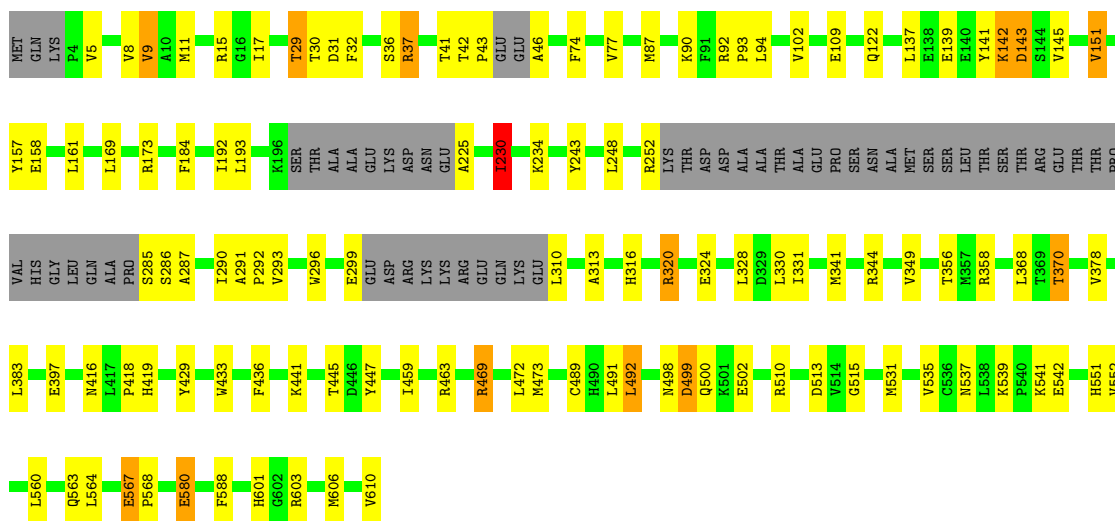
- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

Chain B: 



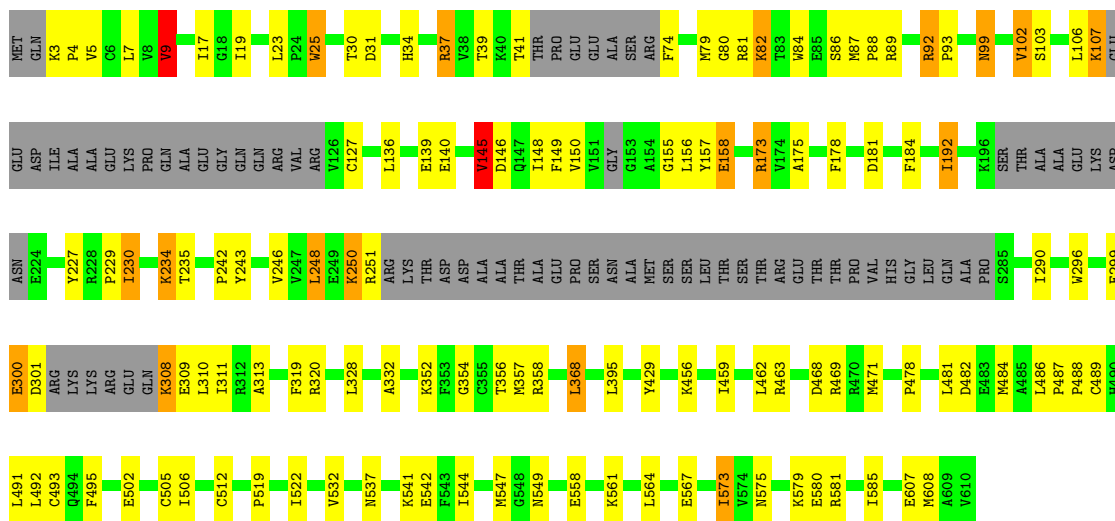
- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

Chain C:  69% 18% 10%



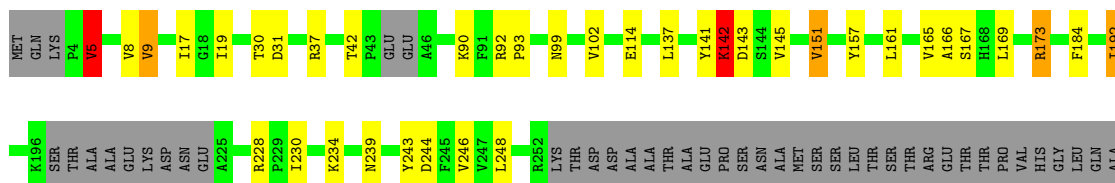
- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

Chain D:  64% 19% 13%



- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

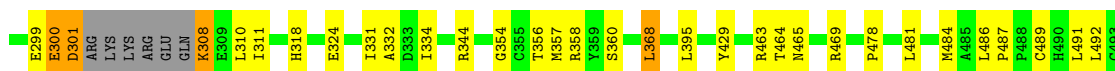
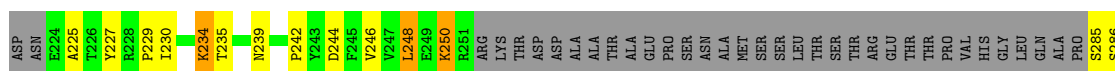
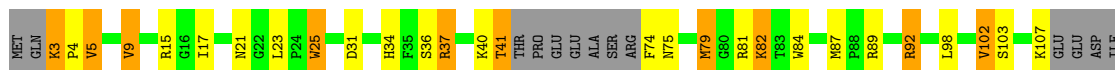
Chain E:  72% 16% 10%





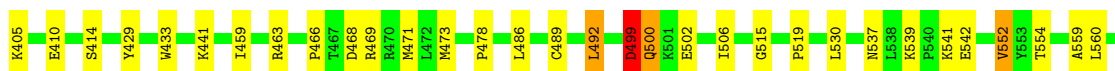
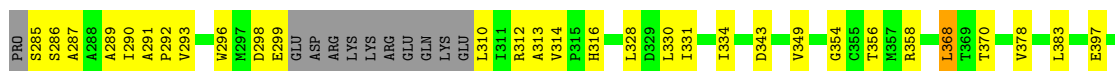
- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

Chain F: 65% 17% 13%



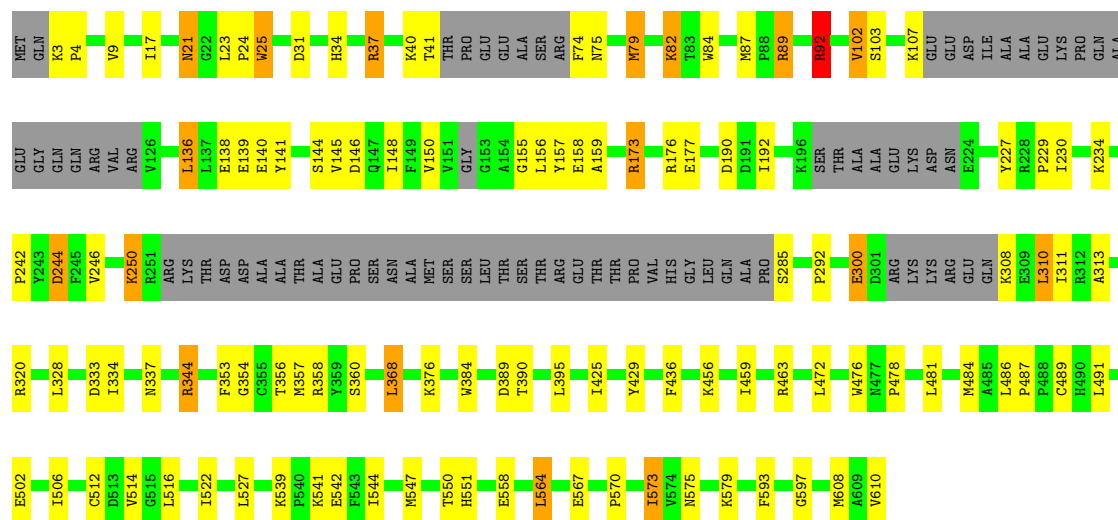
- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

Chain G: 71% 17% 10%



- Molecule 1: Bifunctional dihydrofolate reductase-thymidylate synthase

Chain H: 66% 17% 13%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	53.79Å 144.40Å 177.60Å 90.01° 89.93° 90.38°	Depositor
Resolution (Å)	48.40 – 2.20 48.40 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.2 (48.40-2.20) 95.6 (48.40-2.20)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 2.20Å)	Xtrriage
Refinement program	PHENIX 1.8.2_1309, REFMAC 5.6.0117	Depositor
R, R_{free}	0.183 , 0.233 0.184 , 0.235	Depositor DCC
R_{free} test set	13380 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	41.1	Xtrriage
Anisotropy	0.155	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 29.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.417 for h,-k,-l 0.410 for -h,k,-l 0.447 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	35087	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: CB3, NDP, UMP, FOL

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	0.43	0/4196	0.84	8/5683 (0.1%)
1	B	0.42	0/4043	0.84	3/5473 (0.1%)
1	C	0.44	0/4196	0.85	4/5683 (0.1%)
1	D	0.43	0/4043	0.84	4/5473 (0.1%)
1	E	0.43	0/4196	0.82	3/5683 (0.1%)
1	F	0.42	0/4043	0.82	4/5473 (0.1%)
1	G	0.44	0/4196	0.80	0/5683
1	H	0.42	0/4043	0.83	2/5473 (0.0%)
All	All	0.43	0/32956	0.83	28/44624 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	92	ARG	CA-C-N	-7.25	111.37	120.79
1	B	92	ARG	C-N-CA	-7.25	111.37	120.79
1	C	230	ILE	N-CA-C	-6.43	106.98	113.47
1	A	9	VAL	CB-CA-C	-6.28	99.88	111.18
1	D	9	VAL	CB-CA-C	-5.96	99.75	110.48
1	A	291	ALA	CA-C-N	-5.96	112.39	119.84
1	A	291	ALA	C-N-CA	-5.96	112.39	119.84
1	D	92	ARG	CA-C-N	-5.86	112.51	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	92	ARG	C-N-CA	-5.86	112.51	119.84
1	B	106	LEU	N-CA-C	5.84	118.28	109.41
1	F	92	ARG	CA-C-N	-5.69	112.72	119.84
1	F	92	ARG	C-N-CA	-5.69	112.72	119.84
1	E	142	LYS	N-CA-C	-5.67	102.64	110.35
1	A	142	LYS	N-CA-C	-5.52	103.24	110.53
1	A	230	ILE	N-CA-C	-5.40	107.86	113.10
1	F	9	VAL	CB-CA-C	-5.40	101.46	111.18
1	H	92	ARG	CA-C-N	-5.36	113.83	120.79
1	H	92	ARG	C-N-CA	-5.36	113.83	120.79
1	E	5	VAL	N-CA-C	5.35	117.02	108.89
1	C	498	ASN	CA-C-N	5.32	128.15	120.38
1	C	498	ASN	C-N-CA	5.32	128.15	120.38
1	E	9	VAL	CB-CA-C	-5.18	101.86	111.18
1	A	499	ASP	N-CA-C	5.13	117.54	111.33
1	C	9	VAL	CB-CA-C	-5.13	101.95	111.18
1	D	106	LEU	N-CA-C	5.11	116.49	109.29
1	A	498	ASN	CA-C-N	5.10	127.36	120.38
1	A	498	ASN	C-N-CA	5.10	127.36	120.38
1	F	189	GLY	N-CA-C	-5.07	108.01	114.85

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	609	ALA	Peptide

5.2 Too-close contacts [\(i\)](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4096	0	4058	89	0
1	B	3948	0	3910	79	0
1	C	4096	0	4058	70	0
1	D	3948	0	3910	83	0
1	E	4096	0	4058	61	0
1	F	3948	0	3910	87	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	4096	0	4058	62	0
1	H	3948	0	3910	81	0
2	A	20	0	11	3	0
2	B	20	0	11	7	0
2	C	20	0	11	4	0
2	D	20	0	11	4	0
2	E	20	0	11	3	0
2	F	20	0	11	4	0
2	G	20	0	11	2	0
2	H	20	0	11	5	0
3	A	35	0	21	2	0
3	B	35	0	21	4	0
3	C	35	0	21	4	0
3	D	35	0	21	4	0
3	E	35	0	21	1	0
3	F	35	0	21	3	0
3	G	35	0	21	1	0
3	H	35	0	21	4	0
4	A	32	0	17	4	0
4	B	32	0	17	2	0
4	C	32	0	17	5	0
4	D	32	0	17	2	0
4	E	32	0	17	4	0
4	F	32	0	17	3	0
4	G	32	0	17	4	0
4	H	32	0	17	2	0
5	A	48	0	24	3	0
5	B	48	0	25	7	0
5	C	48	0	24	5	0
5	D	48	0	24	7	0
5	E	48	0	24	4	0
5	F	48	0	25	8	0
5	G	48	0	24	3	0
5	H	48	0	25	8	0
6	A	248	0	0	28	0
6	B	229	0	0	11	0
6	C	224	0	0	10	0
6	D	232	0	0	21	0
6	E	220	0	0	16	0
6	F	242	0	0	28	0
6	G	221	0	0	14	0
6	H	215	0	0	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	35087	0	32459	603	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 9.

All (603) 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:F:481:LEU:HA	1:F:484:MET:HE2	1.52	0.91
1:B:481:LEU:HA	1:B:484:MET:HE2	1.52	0.90
1:G:287:ALA:HA	1:G:290:ILE:HD12	1.54	0.89
1:H:481:LEU:HA	1:H:484:MET:HE2	1.53	0.89
1:D:481:LEU:HA	1:D:484:MET:HE2	1.56	0.86
1:G:370:THR:HG23	1:G:563:GLN:HE21	1.41	0.82
1:F:484:MET:SD	6:F:872:HOH:O	2.38	0.82
1:G:499:ASP:HB3	1:G:500:GLN:HG2	1.62	0.81
1:B:484:MET:SD	6:B:842:HOH:O	2.42	0.77
1:D:484:MET:SD	6:D:844:HOH:O	2.43	0.76
1:C:328:LEU:HD21	1:C:370:THR:HG21	1.66	0.76
1:E:358:ARG:NH2	1:F:354:GLY:O	2.20	0.75
1:D:558:GLU:HA	6:D:968:HOH:O	1.87	0.75
1:A:328:LEU:HD21	1:A:370:THR:HG21	1.67	0.74
1:F:234:LYS:HB3	6:F:948:HOH:O	1.88	0.73
1:A:287:ALA:HA	1:A:290:ILE:HD12	1.70	0.72
1:H:344:ARG:NH2	1:H:610:VAL:O	2.23	0.72
1:B:244:ASP:HB2	1:B:570:PRO:HG3	1.71	0.71
1:D:495:PHE:HB2	6:D:920:HOH:O	1.90	0.71
1:E:354:GLY:O	1:F:358:ARG:NH2	2.24	0.71
1:E:328:LEU:HD21	1:E:370:THR:HG21	1.73	0.70
6:E:886:HOH:O	1:F:494:GLN:HB3	1.90	0.70
1:D:505:CYS:SG	6:D:990:HOH:O	2.49	0.70
1:A:538:LEU:HA	6:A:954:HOH:O	1.91	0.70
1:D:192:ILE:HD12	1:D:248:LEU:HD11	1.72	0.69
1:E:313:ALA:O	1:E:320:ARG:NH2	2.23	0.69
1:D:505:CYS:SG	6:D:1015:HOH:O	2.50	0.69
1:A:296:TRP:HB3	1:B:37:ARG:HG3	1.75	0.68
1:G:328:LEU:HD21	1:G:370:THR:HG21	1.76	0.68
1:A:102:VAL:O	5:A:704:NDP:H1B	1.94	0.68
1:E:499:ASP:HB3	1:E:500:GLN:HG2	1.76	0.68
1:E:287:ALA:HA	1:E:290:ILE:HD12	1.76	0.67
1:H:141:TYR:O	1:H:145:VAL:HG12	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:536:CYS:SG	6:A:950:HOH:O	2.51	0.67
1:B:82:LYS:HD3	5:B:704:NDP:H51A	1.75	0.67
1:A:537:ASN:O	6:A:954:HOH:O	2.12	0.67
1:A:313:ALA:O	1:A:320:ARG:NH2	2.19	0.66
1:F:244:ASP:HB2	1:F:570:PRO:HG3	1.77	0.66
1:A:501:LYS:HB3	6:A:954:HOH:O	1.96	0.66
1:F:532:VAL:HA	6:F:930:HOH:O	1.95	0.66
1:C:102:VAL:O	5:C:704:NDP:H1B	1.96	0.66
1:A:343:ASP:OD1	1:B:469:ARG:NH1	2.29	0.66
1:E:102:VAL:O	5:E:704:NDP:H1B	1.96	0.66
1:A:491:LEU:HD11	1:B:492:LEU:HD11	1.78	0.65
1:A:42:THR:HG22	1:A:43:PRO:HD2	1.78	0.65
1:C:568:PRO:HA	6:C:883:HOH:O	1.96	0.65
1:C:358:ARG:NH2	1:D:354:GLY:O	2.30	0.65
1:G:370:THR:CG2	1:G:563:GLN:HE21	2.10	0.65
1:A:344:ARG:NH2	6:A:862:HOH:O	2.28	0.65
1:G:9:VAL:HG12	1:G:157:TYR:CZ	2.31	0.65
1:D:234:LYS:HB3	6:D:935:HOH:O	1.97	0.65
1:H:176:ARG:HG3	6:H:975:HOH:O	1.96	0.65
1:H:102:VAL:O	5:H:704:NDP:H1B	1.97	0.65
1:H:313:ALA:O	1:H:320:ARG:NH1	2.30	0.64
1:H:244:ASP:HB2	1:H:570:PRO:HG3	1.79	0.64
1:G:17:ILE:O	5:G:704:NDP:H2N	1.98	0.64
1:G:17:ILE:HD13	6:G:981:HOH:O	1.96	0.64
1:A:368:LEU:HD23	1:A:519:PRO:HB3	1.78	0.63
1:C:225:ALA:HA	1:C:252:ARG:HA	1.80	0.63
1:H:82:LYS:HD3	5:H:704:NDP:H51A	1.80	0.63
1:H:313:ALA:HB2	1:H:564:LEU:HD13	1.78	0.63
1:F:585:ILE:HD13	6:F:930:HOH:O	1.97	0.63
1:G:102:VAL:O	5:G:704:NDP:H1B	1.99	0.63
1:B:313:ALA:HB2	1:B:564:LEU:HD13	1.80	0.62
1:A:469:ARG:NH1	2:B:701:UMP:OP3	2.31	0.62
1:A:554:THR:N	6:A:927:HOH:O	2.31	0.62
1:A:141:TYR:HB3	1:A:145:VAL:HG13	1.82	0.62
1:F:465:ASN:N	6:F:855:HOH:O	2.31	0.62
1:D:478:PRO:HA	1:D:481:LEU:HG	1.81	0.62
1:G:42:THR:HG22	1:G:43:PRO:HD2	1.81	0.62
1:B:568:PRO:HA	6:B:925:HOH:O	1.99	0.62
1:D:17:ILE:O	5:D:704:NDP:H2N	2.00	0.62
1:A:570:PRO:HB2	6:A:999:HOH:O	1.99	0.61
1:B:393:ASN:HB2	6:B:946:HOH:O	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:239:ASN:HB2	6:G:979:HOH:O	2.00	0.61
1:G:468:ASP:HB3	1:G:471:MET:HE2	1.83	0.61
1:E:508:TYR:OH	6:E:886:HOH:O	2.10	0.61
1:F:311:ILE:HD11	1:F:332:ALA:HA	1.83	0.61
1:A:173:ARG:HD3	1:A:244:ASP:OD1	2.01	0.60
1:B:465:ASN:N	6:B:843:HOH:O	2.34	0.60
1:E:17:ILE:O	5:E:704:NDP:H2N	2.01	0.60
1:C:143:ASP:HB3	6:C:865:HOH:O	2.00	0.60
1:F:357:MET:HE1	1:F:522:ILE:HD11	1.84	0.60
1:H:3:LYS:N	6:H:853:HOH:O	2.35	0.60
4:F:703:FOL:C7	5:F:704:NDP:H42N	2.32	0.59
1:B:568:PRO:HG3	6:B:972:HOH:O	2.03	0.59
1:E:406:ASN:ND2	6:E:871:HOH:O	2.35	0.59
1:H:40:LYS:HA	1:H:75:ASN:HD22	1.67	0.59
4:D:703:FOL:C7	5:D:704:NDP:H42N	2.33	0.58
1:E:296:TRP:HB3	1:F:37:ARG:HG3	1.86	0.58
1:F:579:LYS:H	1:F:579:LYS:HE2	1.68	0.58
1:F:368:LEU:HD23	6:F:1029:HOH:O	2.03	0.58
1:A:29:THR:HG22	6:A:851:HOH:O	2.04	0.57
1:C:17:ILE:O	5:C:704:NDP:H2N	2.03	0.57
1:A:48:ARG:NH1	6:A:937:HOH:O	2.32	0.57
1:A:501:LYS:HE3	6:A:954:HOH:O	2.04	0.57
1:A:568:PRO:HA	6:A:912:HOH:O	2.05	0.57
1:C:368:LEU:HD22	1:C:368:LEU:H	1.69	0.57
1:G:29:THR:HG22	6:G:845:HOH:O	2.05	0.57
1:H:9:VAL:HG12	1:H:157:TYR:CZ	2.39	0.57
1:F:84:TRP:CE2	1:F:92:ARG:HD2	2.39	0.57
1:B:17:ILE:O	5:B:704:NDP:H2N	2.05	0.57
1:C:469:ARG:HD3	1:D:549:ASN:CG	2.30	0.57
1:E:239:ASN:HB2	6:E:866:HOH:O	2.04	0.57
1:F:84:TRP:HB3	6:F:894:HOH:O	2.04	0.57
1:H:155:GLY:O	1:H:159:ALA:N	2.32	0.57
1:A:169:LEU:HD12	1:A:248:LEU:HD12	1.86	0.56
1:B:192:ILE:HD11	1:B:229:PRO:HD3	1.87	0.56
1:D:561:LYS:HB2	6:D:968:HOH:O	2.05	0.56
1:F:82:LYS:HD3	5:F:704:NDP:H51A	1.88	0.56
1:A:411:PHE:HB3	6:A:1012:HOH:O	2.05	0.56
1:C:313:ALA:O	1:C:320:ARG:NH2	2.23	0.56
1:G:298:ASP:OD1	1:G:299:GLU:N	2.38	0.56
1:B:608:MET:HE2	3:B:702:CB3:H16	1.87	0.56
1:H:79:MET:HE2	1:H:84:TRP:HA	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:573:ILE:HD11	1:D:575:ASN:OD1	2.05	0.56
1:H:31:ASP:OD2	4:H:703:FOL:N3	2.39	0.56
1:D:175:ALA:HB3	1:D:242:PRO:HG2	1.88	0.56
1:F:15:ARG:NH2	1:F:184:PHE:O	2.35	0.56
1:F:506:ILE:HG12	1:F:544:ILE:HB	1.88	0.55
4:A:703:FOL:C7	5:A:704:NDP:H42N	2.36	0.55
1:C:31:ASP:OD2	4:C:703:FOL:N3	2.39	0.55
1:D:84:TRP:CZ2	1:D:92:ARG:HD2	2.41	0.55
1:H:310:LEU:N	6:H:979:HOH:O	2.38	0.55
1:D:506:ILE:HG12	1:D:544:ILE:HB	1.88	0.55
1:E:416:ASN:C	1:E:418:PRO:HD3	2.32	0.55
1:B:9:VAL:HG12	1:B:157:TYR:CZ	2.42	0.55
1:D:561:LYS:HD3	6:D:968:HOH:O	2.06	0.55
1:D:537:ASN:HB3	6:D:807:HOH:O	2.06	0.55
1:A:285:SER:HA	1:A:288:ALA:HB3	1.88	0.55
1:B:74:PHE:N	1:B:144:SER:O	2.40	0.55
1:D:93:PRO:HA	6:D:884:HOH:O	2.06	0.55
1:F:607:GLU:CD	1:F:607:GLU:H	2.14	0.55
1:G:354:GLY:O	1:H:358:ARG:NH2	2.39	0.55
1:H:17:ILE:O	5:H:704:NDP:H2N	2.07	0.55
1:H:597:GLY:HA3	6:H:975:HOH:O	2.05	0.55
1:G:5:VAL:HG21	1:G:150:VAL:HG23	1.89	0.55
1:F:176:ARG:HG3	6:F:952:HOH:O	2.06	0.55
1:H:357:MET:HE1	1:H:522:ILE:HD11	1.88	0.55
1:A:551:HIS:NE2	2:A:701:UMP:O3'	2.31	0.55
1:G:492:LEU:HD11	1:H:491:LEU:HD11	1.89	0.55
1:G:9:VAL:HG11	1:G:184:PHE:CE1	2.42	0.54
1:H:368:LEU:HD23	6:H:1004:HOH:O	2.06	0.54
1:A:290:ILE:HG21	1:B:319:PHE:CD2	2.42	0.54
1:F:3:LYS:HG3	6:F:810:HOH:O	2.07	0.54
1:B:3:LYS:N	1:B:4:PRO:HD3	2.21	0.54
1:A:354:GLY:O	1:B:358:ARG:NH2	2.39	0.54
1:B:13:PRO:HD3	1:B:174:VAL:O	2.07	0.54
1:C:499:ASP:HB3	1:C:500:GLN:HG2	1.88	0.54
1:B:102:VAL:HG21	1:B:156:LEU:HD11	1.89	0.54
1:B:173:ARG:HD2	1:B:246:VAL:HG13	1.88	0.54
1:F:597:GLY:HA3	6:F:952:HOH:O	2.06	0.54
1:D:313:ALA:O	1:D:320:ARG:NH1	2.40	0.54
1:C:169:LEU:HD12	1:C:248:LEU:HD12	1.90	0.54
1:F:79:MET:HE2	1:F:84:TRP:HA	1.89	0.54
1:H:551:HIS:NE2	2:H:701:UMP:O3'	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:5:VAL:HG13	1:F:148:ILE:HG12	1.90	0.53
1:C:515:GLY:O	1:C:606:MET:HE1	2.07	0.53
1:C:601:HIS:ND1	6:C:894:HOH:O	2.33	0.53
1:D:192:ILE:CD1	1:D:246:VAL:HG21	2.37	0.53
1:G:370:THR:HG23	1:G:563:GLN:NE2	2.19	0.53
1:G:368:LEU:HD23	1:G:519:PRO:HB3	1.89	0.53
5:C:704:NDP:N6A	6:C:886:HOH:O	2.34	0.53
1:F:484:MET:CE	1:F:487:PRO:HA	2.39	0.53
1:G:285:SER:HB2	1:G:289:ALA:HB2	1.90	0.53
1:A:339:ARG:HB2	6:B:994:HOH:O	2.08	0.53
1:G:358:ARG:NH2	1:H:354:GLY:O	2.40	0.53
1:A:190:ASP:OD1	1:A:196:LYS:HE3	2.09	0.53
1:A:358:ARG:HD3	1:A:542:GLU:OE1	2.09	0.53
1:D:155:GLY:HA2	1:D:158:GLU:CD	2.34	0.53
1:G:107:LYS:HB2	1:G:109:GLU:HG2	1.91	0.52
1:G:109:GLU:CD	1:G:109:GLU:H	2.16	0.52
1:A:11:MET:HG2	1:A:15:ARG:HA	1.91	0.52
1:C:87:MET:HE2	1:C:92:ARG:HB3	1.91	0.52
1:D:585:ILE:HD13	6:D:914:HOH:O	2.08	0.52
1:E:298:ASP:OD1	1:E:299:GLU:N	2.39	0.52
6:E:886:HOH:O	1:F:506:ILE:HB	2.09	0.52
1:H:155:GLY:N	6:H:973:HOH:O	2.30	0.52
1:A:412:LEU:HG	6:A:1012:HOH:O	2.09	0.52
1:B:40:LYS:HA	1:B:75:ASN:HD22	1.73	0.52
1:H:376:LYS:NZ	6:H:884:HOH:O	2.41	0.52
1:A:230:ILE:HG23	1:B:290:ILE:HD11	1.91	0.52
1:B:551:HIS:NE2	2:B:701:UMP:O3'	2.34	0.52
1:H:344:ARG:O	1:H:344:ARG:HG2	2.10	0.52
1:A:296:TRP:CZ2	1:B:34:HIS:HB2	2.45	0.52
1:H:74:PHE:O	1:H:145:VAL:HA	2.10	0.52
1:H:484:MET:CE	1:H:487:PRO:HA	2.39	0.52
1:E:9:VAL:HG12	1:E:157:TYR:CZ	2.45	0.52
1:F:324:GLU:HA	6:F:914:HOH:O	2.08	0.52
1:H:242:PRO:HG3	1:H:573:ILE:HG23	1.91	0.52
1:E:167:SER:HB3	6:E:997:HOH:O	2.10	0.52
1:F:31:ASP:OD2	4:F:703:FOL:N3	2.42	0.52
1:H:4:PRO:HA	6:H:820:HOH:O	2.09	0.52
1:D:82:LYS:HD3	5:D:704:NDP:H51A	1.92	0.52
1:E:291:ALA:N	1:E:292:PRO:HD2	2.25	0.52
1:E:368:LEU:HD22	6:E:1007:HOH:O	2.10	0.52
1:H:192:ILE:HD11	1:H:229:PRO:HD3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:TRP:CB	1:B:37:ARG:HG3	2.38	0.52
1:B:102:VAL:O	5:B:704:NDP:H1B	2.10	0.52
1:C:141:TYR:HB3	1:C:145:VAL:HG13	1.92	0.52
1:D:368:LEU:HD23	1:D:519:PRO:HB3	1.92	0.52
1:F:535:VAL:HA	6:F:957:HOH:O	2.09	0.52
1:G:405:LYS:NZ	6:G:933:HOH:O	2.42	0.52
1:D:102:VAL:O	5:D:704:NDP:H1B	2.09	0.51
1:D:84:TRP:CE2	1:D:92:ARG:HD2	2.45	0.51
2:A:701:UMP:H1'	3:A:702:CB3:N3	2.26	0.51
1:E:358:ARG:HD3	1:E:542:GLU:OE1	2.10	0.51
4:E:703:FOL:C7	5:E:704:NDP:H42N	2.40	0.51
1:F:21:ASN:HA	5:F:704:NDP:H3D	1.93	0.51
1:E:9:VAL:HG11	1:E:184:PHE:CE1	2.45	0.51
1:E:486:LEU:HD23	1:E:487:PRO:HD2	1.93	0.51
1:G:252:ARG:NH2	6:G:952:HOH:O	2.43	0.51
1:F:129:SER:HA	6:F:844:HOH:O	2.10	0.51
1:A:17:ILE:O	5:A:704:NDP:H2N	2.10	0.51
1:C:296:TRP:CZ2	1:D:34:HIS:HB2	2.46	0.51
1:F:103:SER:OG	5:F:704:NDP:O1X	2.29	0.51
1:H:333:ASP:OD1	1:H:337:ASN:ND2	2.40	0.51
1:H:506:ILE:HG12	1:H:544:ILE:HB	1.92	0.51
4:G:703:FOL:H15	6:G:867:HOH:O	2.11	0.50
1:A:31:ASP:OD2	4:A:703:FOL:N3	2.44	0.50
1:F:150:VAL:HG13	1:F:156:LEU:HD23	1.93	0.50
1:H:136:LEU:HB3	6:H:905:HOH:O	2.11	0.50
1:B:31:ASP:OD2	4:B:703:FOL:N3	2.44	0.50
1:B:484:MET:CE	1:B:487:PRO:HA	2.41	0.50
4:G:703:FOL:C7	5:G:704:NDP:H42N	2.41	0.50
1:C:29:THR:HG22	6:C:957:HOH:O	2.11	0.50
1:F:17:ILE:O	5:F:704:NDP:H2N	2.11	0.50
1:F:464:THR:N	6:F:855:HOH:O	2.44	0.50
1:D:512:CYS:SG	1:D:547:MET:HB3	2.52	0.50
1:G:173:ARG:HD2	1:G:246:VAL:HG13	1.92	0.50
3:A:702:CB3:HB1	6:A:899:HOH:O	2.11	0.50
1:B:175:ALA:HB3	1:B:242:PRO:HG2	1.92	0.50
2:B:701:UMP:H1'	3:B:702:CB3:N3	2.27	0.50
1:G:31:ASP:OD2	4:G:703:FOL:N3	2.44	0.50
2:F:701:UMP:H1'	3:F:702:CB3:N3	2.27	0.50
1:G:358:ARG:HD3	1:G:542:GLU:OE1	2.11	0.50
1:C:9:VAL:HG12	1:C:157:TYR:CZ	2.47	0.50
1:B:9:VAL:HG11	1:B:184:PHE:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:19:ILE:HB	6:E:967:HOH:O	2.12	0.49
1:F:344:ARG:NH2	1:F:610:VAL:O	2.46	0.49
1:G:515:GLY:O	1:G:606:MET:HE1	2.12	0.49
1:H:300:GLU:O	1:H:300:GLU:HG2	2.12	0.49
1:B:358:ARG:HD3	1:B:542:GLU:OE1	2.12	0.49
1:D:234:LYS:HG2	1:D:235:THR:N	2.27	0.49
1:B:484:MET:HE1	1:B:487:PRO:HA	1.95	0.49
1:D:39:THR:HA	1:D:149:PHE:CE2	2.47	0.49
1:E:5:VAL:HG12	1:E:166:ALA:HA	1.94	0.49
1:E:165:VAL:HG21	6:E:986:HOH:O	2.11	0.49
1:G:368:LEU:HD22	6:G:802:HOH:O	2.11	0.49
2:H:701:UMP:H1'	3:H:702:CB3:N3	2.28	0.49
1:A:436:PHE:CE1	1:B:478:PRO:HD2	2.48	0.49
1:G:478:PRO:HD2	1:H:436:PHE:CE1	2.47	0.49
1:H:484:MET:HE3	1:H:487:PRO:HA	1.94	0.49
1:A:358:ARG:NH2	1:B:354:GLY:O	2.46	0.48
1:A:416:ASN:C	1:A:418:PRO:HD3	2.38	0.48
2:D:701:UMP:H1'	3:D:702:CB3:N3	2.28	0.48
1:D:103:SER:OG	5:D:704:NDP:O1X	2.30	0.48
1:E:492:LEU:HD11	1:F:491:LEU:HD11	1.95	0.48
1:A:368:LEU:HD22	6:A:1041:HOH:O	2.12	0.48
1:E:169:LEU:HD12	1:E:248:LEU:HD12	1.95	0.48
1:E:230:ILE:HB	6:E:953:HOH:O	2.13	0.48
4:C:703:FOL:C7	5:C:704:NDP:H42N	2.42	0.48
1:D:9:VAL:HG13	1:D:157:TYR:CZ	2.49	0.48
1:E:141:TYR:HB3	1:E:145:VAL:HG13	1.96	0.48
5:H:704:NDP:C3B	5:H:704:NDP:C8A	2.91	0.48
1:D:357:MET:HE1	1:D:522:ILE:HD11	1.96	0.48
1:E:334:ILE:HG21	1:E:552:VAL:HG13	1.96	0.48
1:G:316:HIS:HB2	6:G:922:HOH:O	2.13	0.48
1:A:492:LEU:HD11	1:B:491:LEU:HD11	1.94	0.48
1:B:394:HIS:CD2	6:B:946:HOH:O	2.66	0.48
1:A:235:THR:HG23	6:A:999:HOH:O	2.13	0.48
1:D:469:ARG:HD3	6:D:815:HOH:O	2.13	0.48
1:D:484:MET:CE	1:D:487:PRO:HA	2.44	0.48
1:G:296:TRP:CZ2	1:H:34:HIS:HB2	2.49	0.48
1:H:84:TRP:CE2	1:H:92:ARG:HD2	2.47	0.48
1:H:502:GLU:HB3	1:H:541:LYS:HB2	1.96	0.48
1:E:296:TRP:CZ2	1:F:34:HIS:HB2	2.49	0.48
1:A:469:ARG:NH1	2:B:701:UMP:P	2.87	0.48
1:B:81:ARG:HE	5:B:704:NDP:P2B	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:502:GLU:HB3	1:E:541:LYS:HB2	1.96	0.48
1:D:468:ASP:O	1:D:471:MET:HE2	2.13	0.47
1:F:300:GLU:HA	1:F:301:ASP:HA	1.66	0.47
1:D:173:ARG:HD2	1:D:246:VAL:HG13	1.95	0.47
1:G:173:ARG:HD3	1:G:244:ASP:OD1	2.14	0.47
1:H:608:MET:HE2	3:H:702:CB3:H16	1.95	0.47
1:A:415:ARG:HB2	6:A:940:HOH:O	2.13	0.47
1:A:491:LEU:HD11	1:B:492:LEU:CD1	2.43	0.47
1:C:296:TRP:HB3	1:D:37:ARG:HG2	1.97	0.47
1:D:300:GLU:HA	1:D:301:ASP:HA	1.66	0.47
4:E:703:FOL:H15	6:E:895:HOH:O	2.13	0.47
1:H:476:TRP:HB2	1:H:491:LEU:HD13	1.96	0.47
1:A:86:SER:HB3	6:A:920:HOH:O	2.14	0.47
1:D:488:PRO:HD2	6:D:895:HOH:O	2.13	0.47
1:F:74:PHE:N	1:F:144:SER:O	2.47	0.47
1:H:3:LYS:HG3	6:H:863:HOH:O	2.13	0.47
1:C:416:ASN:C	1:C:418:PRO:HD3	2.39	0.47
1:E:230:ILE:HD13	1:F:286:SER:HB2	1.94	0.47
1:D:74:PHE:O	1:D:145:VAL:HA	2.13	0.47
1:D:493:CYS:HB2	6:D:1015:HOH:O	2.13	0.47
1:A:173:ARG:HD2	1:A:246:VAL:HG13	1.96	0.47
1:E:334:ILE:HD11	1:E:550:THR:HG22	1.96	0.47
1:F:175:ALA:HB3	1:F:242:PRO:HG2	1.96	0.47
1:G:291:ALA:N	1:G:292:PRO:HD2	2.28	0.47
1:H:138:GLU:HA	6:H:821:HOH:O	2.15	0.47
1:C:9:VAL:HG11	1:C:184:PHE:CE1	2.50	0.47
1:C:151:VAL:HG13	4:C:703:FOL:H7	1.97	0.47
1:C:515:GLY:C	1:C:606:MET:HE1	2.39	0.47
1:D:84:TRP:HA	6:D:901:HOH:O	2.14	0.47
5:D:704:NDP:C8A	5:D:704:NDP:C3B	2.93	0.47
1:F:173:ARG:HD2	1:F:246:VAL:HG13	1.96	0.47
1:H:539:LYS:HD3	6:H:972:HOH:O	2.15	0.47
1:B:229:PRO:HA	1:B:248:LEU:HD12	1.97	0.47
1:C:287:ALA:HA	1:C:290:ILE:HD13	1.96	0.47
1:A:290:ILE:C	1:A:292:PRO:HD2	2.40	0.46
1:B:368:LEU:H	1:B:368:LEU:HD22	1.80	0.46
2:E:701:UMP:H1'	3:E:702:CB3:N3	2.30	0.46
1:G:26:PRO:HG2	6:G:979:HOH:O	2.15	0.46
1:D:608:MET:HE2	3:D:702:CB3:H16	1.97	0.46
1:F:25:TRP:HB3	1:F:178:PHE:CE2	2.51	0.46
1:F:155:GLY:HA2	1:F:158:GLU:CD	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:433:TRP:CE2	1:C:473:MET:HE3	2.50	0.46
1:D:19:ILE:HA	1:D:181:ASP:OD1	2.15	0.46
1:A:577:LEU:HA	6:A:952:HOH:O	2.15	0.46
1:B:166:ALA:O	1:B:250:LYS:HE2	2.15	0.46
1:C:492:LEU:HD11	1:D:491:LEU:HD11	1.98	0.46
1:A:158:GLU:HG3	6:A:926:HOH:O	2.14	0.46
1:E:173:ARG:HD3	1:E:244:ASP:OD1	2.15	0.46
1:G:492:LEU:CD1	1:H:491:LEU:HD11	2.46	0.46
1:H:489:CYS:SG	2:H:701:UMP:C6	3.09	0.46
1:A:151:VAL:HG13	4:A:703:FOL:H7	1.98	0.46
1:H:328:LEU:HD22	1:H:564:LEU:HD22	1.96	0.46
1:A:502:GLU:HB3	1:A:541:LYS:HB2	1.98	0.46
5:B:704:NDP:C8A	5:B:704:NDP:C3B	2.93	0.46
1:D:358:ARG:HD3	1:D:542:GLU:OE1	2.16	0.46
1:G:27[A]:HIS:O	6:G:845:HOH:O	2.15	0.46
1:H:478:PRO:HA	1:H:481:LEU:HG	1.98	0.46
1:A:42:THR:CG2	1:A:43:PRO:HD2	2.45	0.46
1:E:151:VAL:O	4:E:703:FOL:H7	2.16	0.46
1:E:531:MET:HE3	1:E:588:PHE:CD2	2.51	0.46
1:H:23:LEU:HD13	1:H:25:TRP:CZ3	2.51	0.46
1:E:368:LEU:HD23	1:E:519:PRO:HB3	1.97	0.46
1:A:499:ASP:HB3	1:A:500:GLN:HG2	1.97	0.45
1:E:9:VAL:CG1	1:E:157:TYR:CZ	3.00	0.45
1:E:31:ASP:OD2	4:E:703:FOL:N3	2.49	0.45
1:F:239:ASN:HB2	6:F:980:HOH:O	2.15	0.45
1:E:173:ARG:HD2	1:E:246:VAL:HG13	1.98	0.45
1:F:176:ARG:HD2	1:F:596:VAL:CG1	2.46	0.45
1:F:537:ASN:HB3	6:F:905:HOH:O	2.16	0.45
1:G:85:GLU:OE2	6:G:871:HOH:O	2.21	0.45
4:H:703:FOL:C7	5:H:704:NDP:H42N	2.46	0.45
1:C:324:GLU:OE1	1:C:370:THR:HB	2.16	0.45
1:D:532:VAL:HA	6:D:914:HOH:O	2.16	0.45
1:E:296:TRP:CB	1:F:37:ARG:HG3	2.46	0.45
2:G:701:UMP:H1'	3:G:702:CB3:N3	2.31	0.45
1:A:30:THR:HB	1:A:243:TYR:OH	2.16	0.45
1:A:290:ILE:HG21	1:B:319:PHE:CE2	2.52	0.45
1:B:4:PRO:HA	6:B:834:HOH:O	2.15	0.45
1:C:43:PRO:O	1:C:46:ALA:N	2.50	0.45
1:C:77:VAL:HG21	1:C:94:LEU:HD12	1.98	0.45
1:F:143:ASP:O	6:F:832:HOH:O	2.21	0.45
1:F:40:LYS:HA	1:F:75:ASN:HD22	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:5:VAL:HG23	1:G:148:ILE:HG22	1.98	0.45
1:G:469:ARG:HD3	2:H:701:UMP:OP1	2.17	0.45
1:B:138:GLU:O	1:B:142:LYS:HB2	2.17	0.45
1:F:4:PRO:HA	6:F:829:HOH:O	2.16	0.45
1:A:43:PRO:HD3	6:A:869:HOH:O	2.17	0.45
1:A:416:ASN:HB2	6:A:832:HOH:O	2.16	0.45
1:C:331:ILE:HD13	1:C:560:LEU:HD22	1.98	0.45
1:G:489:CYS:SG	2:G:701:UMP:C6	3.10	0.45
1:C:11:MET:SD	1:C:193:LEU:HD11	2.57	0.45
1:C:290:ILE:HD11	1:D:230:ILE:HG21	1.99	0.45
1:D:80:GLY:N	1:D:156:LEU:HD22	2.32	0.45
1:G:17:ILE:HG21	6:G:981:HOH:O	2.16	0.45
1:H:425:ILE:HG23	6:H:988:HOH:O	2.16	0.45
1:B:18:GLY:HA3	5:B:704:NDP:O3D	2.17	0.44
1:D:308:LYS:HE3	1:D:308:LYS:HA	1.99	0.44
1:A:9:VAL:CG1	1:A:157:TYR:CZ	3.00	0.44
1:B:242:PRO:HG3	1:B:573:ILE:HG23	1.98	0.44
1:D:482:ASP:OD2	6:D:967:HOH:O	2.21	0.44
1:F:368:LEU:HD22	6:F:1022:HOH:O	2.15	0.44
1:F:489:CYS:SG	2:F:701:UMP:C6	3.11	0.44
1:G:459:ILE:O	1:G:463:ARG:HG3	2.17	0.44
1:B:489:CYS:SG	2:B:701:UMP:C6	3.11	0.44
1:B:506:ILE:HG12	1:B:544:ILE:HB	1.98	0.44
4:B:703:FOL:C7	5:B:704:NDP:H42N	2.47	0.44
1:D:99:ASN:N	1:D:99:ASN:HD22	2.16	0.44
2:D:701:UMP:HI'	3:D:702:CB3:C4	2.47	0.44
1:F:74:PHE:O	1:F:145:VAL:HA	2.17	0.44
1:G:296:TRP:HB3	1:H:37:ARG:HG2	2.00	0.44
1:H:334:ILE:CD1	1:H:514:VAL:HG21	2.47	0.44
1:H:358:ARG:HD3	1:H:542:GLU:OE1	2.17	0.44
1:A:167:SER:HB3	6:A:830:HOH:O	2.17	0.44
1:A:375:TRP:CH2	1:A:379:LEU:HD22	2.52	0.44
1:C:459:ILE:O	1:C:463:ARG:HG3	2.17	0.44
1:D:368:LEU:HD22	6:D:834:HOH:O	2.16	0.44
1:G:9:VAL:HB	6:G:932:HOH:O	2.17	0.44
1:A:469:ARG:HH12	2:B:701:UMP:P	2.41	0.44
1:B:472:LEU:HG	1:B:494:GLN:HG3	1.99	0.44
1:F:502:GLU:HB3	1:F:541:LYS:HB2	2.00	0.44
1:G:142:LYS:HD3	1:G:142:LYS:HA	1.83	0.44
1:A:343:ASP:OD1	1:B:469:ARG:CZ	2.66	0.44
1:D:352:LYS:HD3	6:D:989:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:151:VAL:O	4:G:703:FOL:H7	2.18	0.44
1:H:173:ARG:HD2	1:H:246:VAL:HG13	1.98	0.44
1:H:334:ILE:HD11	1:H:550:THR:HG22	1.99	0.44
1:H:484:MET:HE3	1:H:484:MET:HB2	1.80	0.44
1:A:11:MET:SD	1:A:193:LEU:HD11	2.57	0.44
1:A:97:ARG:O	1:A:99:ASN:ND2	2.51	0.44
1:B:92:ARG:NH1	6:B:877:HOH:O	2.40	0.44
1:C:358:ARG:HD3	1:C:542:GLU:OE1	2.18	0.44
1:D:81:ARG:NE	5:D:704:NDP:O1X	2.38	0.44
1:E:192:ILE:HG23	1:E:567:GLU:HG3	1.99	0.44
3:H:702:CB3:C6	3:H:702:CB3:H15	2.47	0.44
1:C:9:VAL:CG1	1:C:157:TYR:CZ	3.01	0.44
1:F:142:LYS:HB3	6:F:841:HOH:O	2.18	0.44
1:F:242:PRO:HG2	6:F:952:HOH:O	2.17	0.44
1:F:534:HIS:HD2	6:F:909:HOH:O	2.00	0.44
1:H:227:TYR:CE2	1:H:250:LYS:HG3	2.52	0.44
1:A:91:PHE:HB2	6:A:992:HOH:O	2.18	0.43
1:A:489:CYS:SG	2:A:701:UMP:C6	3.11	0.43
1:B:80:GLY:N	1:B:156:LEU:HD22	2.33	0.43
1:B:484:MET:HE3	1:B:484:MET:HB2	1.73	0.43
2:B:701:UMP:H1'	3:B:702:CB3:C4	2.48	0.43
1:C:37:ARG:O	1:C:41:THR:HG23	2.18	0.43
1:F:192:ILE:HD11	1:F:229:PRO:HD3	2.00	0.43
1:F:484:MET:HE3	1:F:487:PRO:HA	1.99	0.43
3:F:702:CB3:C6	3:F:702:CB3:H15	2.48	0.43
1:G:466:PRO:O	1:G:471:MET:HE1	2.17	0.43
1:G:502:GLU:HB3	1:G:541:LYS:HB2	2.00	0.43
2:H:701:UMP:H1'	3:H:702:CB3:C4	2.48	0.43
1:A:242:PRO:HB2	6:A:999:HOH:O	2.17	0.43
1:A:580:GLU:H	1:A:580:GLU:CD	2.26	0.43
1:B:502:GLU:HB3	1:B:541:LYS:HB2	1.99	0.43
1:C:316:HIS:HB2	6:C:879:HOH:O	2.17	0.43
1:F:81:ARG:HA	6:F:894:HOH:O	2.18	0.43
1:G:433:TRP:CE2	1:G:473:MET:HE3	2.53	0.43
1:A:554:THR:HG23	6:A:927:HOH:O	2.17	0.43
1:E:333:ASP:OD1	1:E:337:ASN:ND2	2.48	0.43
6:G:916:HOH:O	1:H:344:ARG:HB2	2.18	0.43
1:H:516:LEU:HD22	6:H:886:HOH:O	2.19	0.43
1:B:328:LEU:HD22	1:B:564:LEU:HD22	2.00	0.43
1:D:311:ILE:HD11	1:D:332:ALA:HA	2.00	0.43
1:D:328:LEU:HD13	6:D:891:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:551:HIS:NE2	2:E:701:UMP:O3'	2.36	0.43
1:B:79:MET:HE1	1:B:87:MET:SD	2.58	0.43
1:D:502:GLU:HB3	1:D:541:LYS:HB2	2.00	0.43
1:G:559:ALA:HB1	1:G:604:ILE:HG21	1.99	0.43
1:H:512:CYS:SG	1:H:547:MET:HB3	2.58	0.43
1:B:191:ASP:HB2	6:B:856:HOH:O	2.19	0.43
1:C:252:ARG:NH2	6:C:976:HOH:O	2.43	0.43
1:E:291:ALA:O	1:E:295:ALA:N	2.43	0.43
1:F:9:VAL:CG1	1:F:157:TYR:CZ	3.02	0.43
1:F:234:LYS:HG2	1:F:235:THR:N	2.33	0.43
1:H:79:MET:HE1	1:H:87:MET:SD	2.58	0.43
1:A:87:MET:HE2	1:A:92:ARG:HB3	2.00	0.43
1:B:81:ARG:HD3	1:B:103:SER:OG	2.18	0.43
1:B:87:MET:HE2	1:B:87:MET:HB3	1.89	0.43
1:C:551:HIS:NE2	2:C:701:UMP:O3'	2.31	0.43
1:H:139:GLU:HB2	6:H:838:HOH:O	2.19	0.43
1:B:397[A]:GLU:OE2	1:B:398:LYS:HG3	2.19	0.43
1:D:3:LYS:N	1:D:4:PRO:HD3	2.33	0.43
1:D:459:ILE:O	1:D:463:ARG:HG3	2.19	0.43
1:F:79:MET:HE1	1:F:87:MET:SD	2.58	0.43
1:F:299:GLU:OE2	6:F:870:HOH:O	2.21	0.43
1:H:9:VAL:CG1	1:H:157:TYR:CZ	3.02	0.43
1:H:21:ASN:HA	5:H:704:NDP:H3D	2.00	0.43
1:B:311:ILE:HD11	1:B:332:ALA:HA	2.01	0.43
1:B:357:MET:HE1	1:B:522:ILE:HD11	2.00	0.43
1:D:156:LEU:HD12	1:D:156:LEU:HA	1.71	0.43
1:E:489:CYS:SG	2:E:701:UMP:C6	3.12	0.43
1:H:459:ILE:O	1:H:463:ARG:HG3	2.18	0.43
1:A:486:LEU:HD23	1:A:487:PRO:HD2	2.01	0.42
1:B:527:LEU:HD11	1:B:593:PHE:CE2	2.54	0.42
1:C:32:PHE:HE2	4:C:703:FOL:C11	2.32	0.42
3:C:702:CB3:C6	3:C:702:CB3:H15	2.49	0.42
1:D:31:ASP:OD2	4:D:703:FOL:N3	2.52	0.42
1:E:30:THR:HB	1:E:243:TYR:OH	2.19	0.42
1:F:551:HIS:NE2	2:F:701:UMP:O3'	2.40	0.42
1:A:290:ILE:HD11	1:B:230:ILE:HG21	2.01	0.42
1:C:230:ILE:HG23	1:D:290:ILE:HD11	2.01	0.42
2:C:701:UMP:H1'	3:C:702:CB3:N3	2.34	0.42
3:D:702:CB3:C6	3:D:702:CB3:H15	2.49	0.42
1:F:102:VAL:O	5:F:704:NDP:H1B	2.18	0.42
1:F:463:ARG:NH1	1:F:535:VAL:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:484:MET:HE1	1:F:487:PRO:HA	1.99	0.42
1:H:390:THR:C	6:H:988:HOH:O	2.61	0.42
1:A:234:LYS:HE3	6:A:874:HOH:O	2.19	0.42
1:A:436:PHE:CZ	1:B:478:PRO:HD2	2.54	0.42
1:C:158:GLU:HG3	6:C:902:HOH:O	2.19	0.42
1:C:436:PHE:CE1	1:D:478:PRO:HD2	2.55	0.42
1:C:513:ASP:OD2	3:C:702:CB3:N3	2.52	0.42
1:C:580:GLU:CD	1:C:580:GLU:H	2.27	0.42
1:D:192:ILE:HD11	1:D:246:VAL:HG21	2.00	0.42
1:E:331:ILE:HD13	1:E:560:LEU:HD22	2.01	0.42
1:A:129:SER:HB2	1:A:131:PRO:HD2	2.02	0.42
1:A:287:ALA:HA	1:A:290:ILE:CD1	2.47	0.42
6:A:911:HOH:O	1:G:113:ALA:HB2	2.20	0.42
1:C:74:PHE:O	1:C:145:VAL:HA	2.20	0.42
1:C:293:VAL:HA	1:C:296:TRP:CD1	2.54	0.42
1:D:7:LEU:HD22	1:D:150:VAL:HB	2.01	0.42
2:F:701:UMP:H1'	3:F:702:CB3:C4	2.48	0.42
1:A:230:ILE:HD13	1:B:286:SER:HB2	2.00	0.42
1:C:290:ILE:HG21	1:D:319:PHE:CD2	2.54	0.42
1:D:227:TYR:CZ	1:D:250:LYS:HG3	2.55	0.42
1:B:9:VAL:CG1	1:B:157:TYR:CZ	3.02	0.42
5:C:704:NDP:H52N	5:C:704:NDP:H2D	1.31	0.42
1:A:370:THR:HG23	1:A:563:GLN:CG	2.50	0.42
1:C:313:ALA:HB2	1:C:564:LEU:HD22	2.01	0.42
1:E:287:ALA:CA	1:E:290:ILE:HD12	2.47	0.42
1:D:23:LEU:HD13	1:D:25:TRP:CZ3	2.55	0.42
1:H:3:LYS:NZ	6:H:863:HOH:O	2.52	0.42
1:C:30:THR:HB	1:C:243:TYR:OH	2.20	0.42
1:C:603:ARG:NE	6:C:988:HOH:O	2.40	0.42
1:D:489:CYS:SG	2:D:701:UMP:C6	3.13	0.42
1:C:142:LYS:HD3	1:C:142:LYS:HA	1.77	0.42
1:A:99:ASN:HD22	1:A:99:ASN:N	2.17	0.41
1:B:80:GLY:HA2	1:B:102:VAL:HG23	2.01	0.41
1:C:502:GLU:HB3	1:C:541:LYS:HB2	2.02	0.41
1:D:30:THR:HB	1:D:243:TYR:OH	2.20	0.41
1:F:176:ARG:N	6:F:952:HOH:O	2.53	0.41
1:F:469:ARG:HD3	6:F:850:HOH:O	2.20	0.41
1:H:384:TRP:CD1	1:H:389:ASP:HB3	2.55	0.41
1:A:5:VAL:HG21	1:A:150:VAL:HG23	2.02	0.41
1:A:151:VAL:O	4:A:703:FOL:H7	2.19	0.41
1:C:344:ARG:NH1	6:C:963:HOH:O	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:532:VAL:HA	6:E:894:HOH:O	2.20	0.41
1:F:192:ILE:HD13	1:F:248:LEU:HD11	2.02	0.41
1:F:308:LYS:HE3	1:F:308:LYS:HA	2.02	0.41
1:G:169:LEU:HD12	1:G:248:LEU:HD12	2.01	0.41
1:G:293:VAL:HA	1:G:296:TRP:CD1	2.55	0.41
1:B:84:TRP:CE2	1:B:92:ARG:HD2	2.55	0.41
1:C:36:SER:HB2	4:C:703:FOL:HB2	2.03	0.41
1:D:9:VAL:HG11	1:D:184:PHE:CD1	2.55	0.41
1:F:334:ILE:CD1	1:F:514:VAL:HG21	2.50	0.41
1:F:516:LEU:HD22	6:F:966:HOH:O	2.20	0.41
1:G:334:ILE:HG21	1:G:552:VAL:HG13	2.02	0.41
1:H:292:PRO:HB2	6:H:935:HOH:O	2.20	0.41
1:C:291:ALA:N	1:C:292:PRO:HD2	2.35	0.41
1:C:469:ARG:NH1	2:D:701:UMP:OP3	2.52	0.41
1:D:107:LYS:O	1:D:107:LYS:NZ	2.50	0.41
4:F:703:FOL:C6	5:F:704:NDP:H42N	2.51	0.41
1:G:37:ARG:O	1:G:41:THR:HG23	2.21	0.41
1:C:296:TRP:CB	1:D:37:ARG:HG2	2.51	0.41
1:C:489:CYS:SG	2:C:701:UMP:C6	3.13	0.41
1:E:228:ARG:O	6:E:953:HOH:O	2.22	0.41
1:F:84:TRP:CZ2	1:F:92:ARG:HD2	2.56	0.41
1:F:225:ALA:HB3	6:F:892:HOH:O	2.18	0.41
1:H:23:LEU:HA	1:H:24:PRO:HD3	1.89	0.41
1:H:103:SER:OG	5:H:704:NDP:O1X	2.39	0.41
1:B:158:GLU:HG3	6:B:977:HOH:O	2.20	0.41
1:D:87:MET:HA	1:D:88:PRO:HD2	1.88	0.41
5:E:704:NDP:H52N	5:E:704:NDP:H2D	1.31	0.41
1:F:40:LYS:O	1:F:41:THR:HG23	2.21	0.41
1:G:30:THR:HB	1:G:243:TYR:OH	2.20	0.41
1:H:150:VAL:HG13	1:H:156:LEU:HD23	2.01	0.41
1:B:300:GLU:HA	1:B:301:ASP:HA	1.59	0.41
1:E:329:ASP:OD2	6:E:838:HOH:O	2.22	0.41
1:H:384:TRP:HZ2	6:H:988:HOH:O	2.03	0.41
1:A:37:ARG:HG2	1:B:296:TRP:HB3	2.02	0.41
1:A:251:ARG:O	1:A:252:ARG:HB3	2.21	0.41
1:C:370:THR:HG23	1:C:563:GLN:CG	2.51	0.41
1:C:445:THR:HB	1:C:447:TYR:CZ	2.56	0.41
1:C:11:MET:CG	1:C:15:ARG:HA	2.50	0.41
1:C:92:ARG:HA	1:C:93:PRO:C	2.45	0.41
1:C:491:LEU:HD21	1:C:510:ARG:HB3	2.03	0.41
1:C:531:MET:HE3	1:C:588:PHE:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:567:GLU:HA	1:C:568:PRO:HD3	1.93	0.41
1:E:491:LEU:HD11	1:F:492:LEU:HD11	2.03	0.41
1:F:478:PRO:HA	1:F:481:LEU:HG	2.02	0.41
1:G:13:PRO:HD3	1:G:174:VAL:O	2.21	0.41
1:H:527:LEU:HD11	1:H:593:PHE:CE1	2.56	0.41
3:B:702:CB3:C6	3:B:702:CB3:H15	2.50	0.41
1:C:341:MET:HE3	1:C:341:MET:HB3	1.92	0.41
1:E:114:GLU:HG3	6:E:876:HOH:O	2.21	0.41
1:C:37:ARG:HG2	1:D:296:TRP:HB3	2.03	0.40
1:E:142:LYS:O	1:E:143:ASP:CG	2.64	0.40
1:B:334:ILE:CD1	1:B:514:VAL:HG21	2.51	0.40
1:B:368:LEU:HD22	1:B:368:LEU:N	2.35	0.40
1:B:493:CYS:HA	1:B:506:ILE:O	2.21	0.40
2:C:701:UMP:H1'	3:C:702:CB3:C4	2.51	0.40
1:F:227:TYR:CZ	1:F:250:LYS:HG3	2.57	0.40
1:H:573:ILE:HD11	1:H:575:ASN:OD1	2.22	0.40
5:H:704:NDP:C8A	5:H:704:NDP:H3B	2.52	0.40
1:A:74:PHE:O	1:A:145:VAL:HA	2.21	0.40
1:B:79:MET:HE2	1:B:84:TRP:HA	2.04	0.40
1:D:462:LEU:HD21	6:D:920:HOH:O	2.20	0.40
1:D:484:MET:HE1	1:D:487:PRO:HA	2.02	0.40
1:E:92:ARG:HA	1:E:93:PRO:C	2.46	0.40
1:F:23:LEU:HD13	1:F:25:TRP:CZ3	2.56	0.40
1:H:141:TYR:HE2	6:H:905:HOH:O	2.04	0.40
1:H:242:PRO:HG2	6:H:975:HOH:O	2.20	0.40
1:E:99:ASN:HD22	1:E:99:ASN:N	2.19	0.40
1:E:313:ALA:O	1:E:314:VAL:C	2.65	0.40
1:E:320:ARG:HD3	6:E:838:HOH:O	2.21	0.40
1:E:469:ARG:HD3	1:F:511:SER:OG	2.21	0.40
1:E:492:LEU:CD1	1:F:491:LEU:HD11	2.51	0.40
5:F:704:NDP:C8A	5:F:704:NDP:C3B	2.99	0.40
1:G:506:ILE:HG13	1:H:353:PHE:CE2	2.56	0.40
1:A:531:MET:HE3	1:A:588:PHE:CD2	2.56	0.40
1:D:25:TRP:HB3	1:D:178:PHE:CE2	2.57	0.40
1:D:229:PRO:HA	1:D:248:LEU:HD12	2.03	0.40
1:G:331:ILE:HD13	1:G:560:LEU:HD22	2.03	0.40
1:H:89:ARG:HA	1:H:92:ARG:HG3	2.04	0.40

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 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	502/566 (89%)	487 (97%)	14 (3%)	1 (0%)	43	51
1	B	478/566 (84%)	456 (95%)	19 (4%)	3 (1%)	21	23
1	C	502/566 (89%)	488 (97%)	12 (2%)	2 (0%)	30	34
1	D	478/566 (84%)	449 (94%)	24 (5%)	5 (1%)	12	11
1	E	502/566 (89%)	489 (97%)	10 (2%)	3 (1%)	21	23
1	F	478/566 (84%)	454 (95%)	21 (4%)	3 (1%)	21	23
1	G	502/566 (89%)	488 (97%)	10 (2%)	4 (1%)	16	16
1	H	478/566 (84%)	456 (95%)	18 (4%)	4 (1%)	16	16
All	All	3920/4528 (87%)	3767 (96%)	128 (3%)	25 (1%)	21	23

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	429	TYR
1	B	429	TYR
1	C	286	SER
1	D	429	TYR
1	E	429	TYR
1	F	429	TYR
1	G	313	ALA
1	H	429	TYR
1	B	299	GLU
1	D	139	GLU
1	D	146	ASP
1	E	286	SER
1	G	286	SER
1	C	429	TYR
1	D	299	GLU
1	G	429	TYR
1	E	499	ASP

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Mol	Chain	Res	Type
1	F	139	GLU
1	G	499	ASP
1	H	144	SER
1	F	190	ASP
1	H	146	ASP
1	H	190	ASP
1	B	139	GLU
1	D	145	VAL

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	444/491 (90%)	404 (91%)	40 (9%)	9	9
1	B	431/491 (88%)	395 (92%)	36 (8%)	10	11
1	C	444/491 (90%)	402 (90%)	42 (10%)	8	8
1	D	431/491 (88%)	389 (90%)	42 (10%)	8	8
1	E	444/491 (90%)	408 (92%)	36 (8%)	11	12
1	F	431/491 (88%)	390 (90%)	41 (10%)	8	8
1	G	444/491 (90%)	402 (90%)	42 (10%)	8	8
1	H	431/491 (88%)	393 (91%)	38 (9%)	9	10
All	All	3500/3928 (89%)	3183 (91%)	317 (9%)	9	9

All (317) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	VAL
1	A	8	VAL
1	A	9	VAL
1	A	29	THR
1	A	37	ARG
1	A	106	LEU
1	A	109	GLU

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Mol	Chain	Res	Type
1	A	122	GLN
1	A	123	ARG
1	A	137	LEU
1	A	142	LYS
1	A	145	VAL
1	A	156	LEU
1	A	161	LEU
1	A	192	ILE
1	A	196	LYS
1	A	234	LYS
1	A	252	ARG
1	A	290	ILE
1	A	310	LEU
1	A	330	LEU
1	A	349	VAL
1	A	356	THR
1	A	368	LEU
1	A	370	THR
1	A	378	VAL
1	A	383	LEU
1	A	396	SER
1	A	397	GLU
1	A	410	GLU
1	A	441	LYS
1	A	486	LEU
1	A	492	LEU
1	A	537	ASN
1	A	539	LYS
1	A	552	VAL
1	A	554	THR
1	A	567	GLU
1	A	580	GLU
1	A	610	VAL
1	B	25	TRP
1	B	41	THR
1	B	79	MET
1	B	82	LYS
1	B	86	SER
1	B	89	ARG
1	B	107	LYS
1	B	140	GLU
1	B	144	SER

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Mol	Chain	Res	Type
1	B	147	GLN
1	B	148	ILE
1	B	156	LEU
1	B	173	ARG
1	B	230	ILE
1	B	234	LYS
1	B	244	ASP
1	B	248	LEU
1	B	251	ARG
1	B	285	SER
1	B	300	GLU
1	B	308	LYS
1	B	310	LEU
1	B	339	ARG
1	B	356	THR
1	B	360	SER
1	B	371	LYS
1	B	395	LEU
1	B	448	THR
1	B	456	LYS
1	B	486	LEU
1	B	558	GLU
1	B	564	LEU
1	B	567	GLU
1	B	573	ILE
1	B	579	LYS
1	B	607	GLU
1	C	5	VAL
1	C	8	VAL
1	C	29	THR
1	C	37	ARG
1	C	42	THR
1	C	90	LYS
1	C	109	GLU
1	C	122	GLN
1	C	137	LEU
1	C	139	GLU
1	C	142	LYS
1	C	143	ASP
1	C	151	VAL
1	C	161	LEU
1	C	173	ARG

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Mol	Chain	Res	Type
1	C	192	ILE
1	C	230	ILE
1	C	234	LYS
1	C	285	SER
1	C	299	GLU
1	C	310	LEU
1	C	320	ARG
1	C	330	LEU
1	C	349	VAL
1	C	356	THR
1	C	370	THR
1	C	378	VAL
1	C	383	LEU
1	C	397	GLU
1	C	419	HIS
1	C	441	LYS
1	C	469	ARG
1	C	472	LEU
1	C	492	LEU
1	C	499	ASP
1	C	535	VAL
1	C	537	ASN
1	C	539	LYS
1	C	552	VAL
1	C	567	GLU
1	C	580	GLU
1	C	610	VAL
1	D	5	VAL
1	D	9	VAL
1	D	25	TRP
1	D	37	ARG
1	D	41	THR
1	D	79	MET
1	D	82	LYS
1	D	86	SER
1	D	89	ARG
1	D	99	ASN
1	D	102	VAL
1	D	107	LYS
1	D	127	CYS
1	D	136	LEU
1	D	140	GLU

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Mol	Chain	Res	Type
1	D	145	VAL
1	D	148	ILE
1	D	158	GLU
1	D	173	ARG
1	D	192	ILE
1	D	230	ILE
1	D	234	LYS
1	D	248	LEU
1	D	250	LYS
1	D	251	ARG
1	D	300	GLU
1	D	308	LYS
1	D	309	GLU
1	D	310	LEU
1	D	356	THR
1	D	368	LEU
1	D	395	LEU
1	D	456	LYS
1	D	486	LEU
1	D	492	LEU
1	D	564	LEU
1	D	567	GLU
1	D	573	ILE
1	D	579	LYS
1	D	580	GLU
1	D	581	ARG
1	D	607	GLU
1	E	5	VAL
1	E	8	VAL
1	E	37	ARG
1	E	42	THR
1	E	90	LYS
1	E	137	LEU
1	E	142	LYS
1	E	151	VAL
1	E	161	LEU
1	E	173	ARG
1	E	192	ILE
1	E	234	LYS
1	E	310	LEU
1	E	311	ILE
1	E	320	ARG

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Mol	Chain	Res	Type
1	E	330	LEU
1	E	343	ASP
1	E	349	VAL
1	E	356	THR
1	E	368	LEU
1	E	370	THR
1	E	378	VAL
1	E	383	LEU
1	E	396	SER
1	E	397	GLU
1	E	414	SER
1	E	415	ARG
1	E	486	LEU
1	E	500	GLN
1	E	530	LEU
1	E	539	LYS
1	E	552	VAL
1	E	554	THR
1	E	567	GLU
1	E	580	GLU
1	E	610	VAL
1	F	3	LYS
1	F	5	VAL
1	F	25	TRP
1	F	36	SER
1	F	37	ARG
1	F	41	THR
1	F	79	MET
1	F	82	LYS
1	F	89	ARG
1	F	98	LEU
1	F	102	VAL
1	F	107	LYS
1	F	127	CYS
1	F	140	GLU
1	F	148	ILE
1	F	156	LEU
1	F	158	GLU
1	F	173	ARG
1	F	230	ILE
1	F	234	LYS
1	F	248	LEU

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Mol	Chain	Res	Type
1	F	250	LYS
1	F	285	SER
1	F	300	GLU
1	F	301	ASP
1	F	308	LYS
1	F	310	LEU
1	F	318	HIS
1	F	331	ILE
1	F	356	THR
1	F	360	SER
1	F	368	LEU
1	F	395	LEU
1	F	486	LEU
1	F	500	GLN
1	F	564	LEU
1	F	567	GLU
1	F	573	ILE
1	F	579	LYS
1	F	605	GLN
1	F	607	GLU
1	G	8	VAL
1	G	29	THR
1	G	37	ARG
1	G	42	THR
1	G	107	LYS
1	G	109	GLU
1	G	122	GLN
1	G	123	ARG
1	G	137	LEU
1	G	142	LYS
1	G	143	ASP
1	G	151	VAL
1	G	161	LEU
1	G	173	ARG
1	G	192	ILE
1	G	234	LYS
1	G	310	LEU
1	G	312	ARG
1	G	314	VAL
1	G	330	LEU
1	G	343	ASP
1	G	349	VAL

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Mol	Chain	Res	Type
1	G	356	THR
1	G	368	LEU
1	G	378	VAL
1	G	383	LEU
1	G	397	GLU
1	G	410	GLU
1	G	414	SER
1	G	441	LYS
1	G	486	LEU
1	G	492	LEU
1	G	499	ASP
1	G	500	GLN
1	G	530	LEU
1	G	537	ASN
1	G	539	LYS
1	G	552	VAL
1	G	554	THR
1	G	567	GLU
1	G	580	GLU
1	G	610	VAL
1	H	21	ASN
1	H	25	TRP
1	H	37	ARG
1	H	41	THR
1	H	79	MET
1	H	82	LYS
1	H	89	ARG
1	H	92	ARG
1	H	102	VAL
1	H	107	LYS
1	H	136	LEU
1	H	140	GLU
1	H	148	ILE
1	H	158	GLU
1	H	173	ARG
1	H	177	GLU
1	H	230	ILE
1	H	234	LYS
1	H	244	ASP
1	H	250	LYS
1	H	285	SER
1	H	300	GLU

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Mol	Chain	Res	Type
1	H	308	LYS
1	H	310	LEU
1	H	311	ILE
1	H	344	ARG
1	H	356	THR
1	H	360	SER
1	H	368	LEU
1	H	395	LEU
1	H	456	LYS
1	H	472	LEU
1	H	486	LEU
1	H	558	GLU
1	H	564	LEU
1	H	567	GLU
1	H	573	ILE
1	H	579	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	239	ASN
1	A	435	HIS
1	A	575	ASN
1	C	147	GLN
1	C	239	ASN
1	C	435	HIS
1	C	450	GLN
1	C	575	ASN
1	D	534	HIS
1	E	444	HIS
1	E	450	GLN
1	E	575	ASN
1	F	444	HIS
1	G	363	GLN
1	G	435	HIS
1	G	563	GLN
1	G	575	ASN
1	H	444	HIS
1	H	537	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
3	CB3	H	702	-	37,37,37	1.87	8 (21%)	50,51,51	1.32	6 (12%)
2	UMP	H	701	-	21,21,21	1.24	4 (19%)	30,31,31	5.28	15 (50%)
3	CB3	C	702	-	37,37,37	1.86	7 (18%)	50,51,51	1.27	5 (10%)
4	FOL	B	703	-	34,34,34	1.88	6 (17%)	43,47,47	1.30	7 (16%)
4	FOL	E	703	-	34,34,34	1.92	8 (23%)	43,47,47	2.33	12 (27%)
2	UMP	B	701	-	21,21,21	1.26	4 (19%)	30,31,31	5.29	15 (50%)
2	UMP	A	701	-	21,21,21	1.30	4 (19%)	30,31,31	5.26	16 (53%)
2	UMP	E	701	-	21,21,21	1.29	4 (19%)	30,31,31	5.31	16 (53%)
5	NDP	F	704	-	51,52,52	2.24	17 (33%)	71,80,80	4.07	26 (36%)
2	UMP	C	701	-	21,21,21	1.30	4 (19%)	30,31,31	5.31	15 (50%)
4	FOL	F	703	-	34,34,34	1.85	6 (17%)	43,47,47	1.55	6 (13%)
5	NDP	D	704	-	51,52,52	2.38	19 (37%)	71,80,80	3.70	27 (38%)
5	NDP	G	704	-	51,52,52	2.40	18 (35%)	71,80,80	3.79	28 (39%)
5	NDP	E	704	-	51,52,52	2.36	18 (35%)	71,80,80	3.75	30 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	FOL	C	703	-	34,34,34	1.92	8 (23%)	43,47,47	2.42	11 (25%)
5	NDP	A	704	-	51,52,52	2.37	15 (29%)	71,80,80	3.76	27 (38%)
5	NDP	C	704	-	51,52,52	2.38	16 (31%)	71,80,80	3.79	28 (39%)
3	CB3	A	702	-	37,37,37	1.95	7 (18%)	50,51,51	1.64	8 (16%)
2	UMP	F	701	-	21,21,21	1.23	3 (14%)	30,31,31	5.28	15 (50%)
5	NDP	H	704	-	51,52,52	2.27	18 (35%)	71,80,80	3.84	26 (36%)
5	NDP	B	704	-	51,52,52	2.22	17 (33%)	71,80,80	3.93	26 (36%)
4	FOL	D	703	-	34,34,34	1.94	7 (20%)	43,47,47	1.52	5 (11%)
3	CB3	B	702	-	37,37,37	1.85	7 (18%)	50,51,51	1.45	7 (14%)
3	CB3	D	702	-	37,37,37	1.76	7 (18%)	50,51,51	1.55	10 (20%)
4	FOL	G	703	-	34,34,34	1.90	7 (20%)	43,47,47	2.31	11 (25%)
3	CB3	F	702	-	37,37,37	1.78	6 (16%)	50,51,51	1.46	8 (16%)
2	UMP	G	701	-	21,21,21	1.29	4 (19%)	30,31,31	5.25	16 (53%)
4	FOL	A	703	-	34,34,34	1.87	7 (20%)	43,47,47	1.55	7 (16%)
4	FOL	H	703	-	34,34,34	1.87	6 (17%)	43,47,47	1.53	6 (13%)
3	CB3	G	702	-	37,37,37	2.03	8 (21%)	50,51,51	1.83	11 (22%)
2	UMP	D	701	-	21,21,21	1.24	4 (19%)	30,31,31	5.27	16 (53%)
3	CB3	E	702	-	37,37,37	1.89	8 (21%)	50,51,51	1.32	6 (12%)

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	CB3	H	702	-	-	3/27/28/28	0/3/3/3
2	UMP	H	701	-	-	4/10/22/22	0/2/2/2
3	CB3	C	702	-	-	7/27/28/28	0/3/3/3
4	FOL	B	703	-	-	6/22/22/22	0/3/3/3
4	FOL	E	703	-	-	2/22/22/22	0/3/3/3
2	UMP	B	701	-	-	2/10/22/22	0/2/2/2
2	UMP	A	701	-	-	6/10/22/22	0/2/2/2
2	UMP	E	701	-	-	5/10/22/22	0/2/2/2
5	NDP	F	704	-	-	7/34/77/77	0/5/5/5
2	UMP	C	701	-	-	5/10/22/22	0/2/2/2
4	FOL	F	703	-	-	2/22/22/22	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NDP	D	704	-	-	10/34/77/77	0/5/5/5
5	NDP	G	704	-	-	8/34/77/77	0/5/5/5
5	NDP	E	704	-	-	10/34/77/77	0/5/5/5
4	FOL	C	703	-	-	1/22/22/22	0/3/3/3
5	NDP	A	704	-	-	9/34/77/77	0/5/5/5
5	NDP	C	704	-	-	10/34/77/77	0/5/5/5
3	CB3	A	702	-	-	4/27/28/28	0/3/3/3
2	UMP	F	701	-	-	4/10/22/22	0/2/2/2
5	NDP	H	704	-	-	6/34/77/77	0/5/5/5
5	NDP	B	704	-	-	7/34/77/77	0/5/5/5
4	FOL	D	703	-	-	2/22/22/22	0/3/3/3
3	CB3	B	702	-	-	5/27/28/28	0/3/3/3
3	CB3	D	702	-	-	3/27/28/28	0/3/3/3
4	FOL	G	703	-	-	2/22/22/22	0/3/3/3
3	CB3	F	702	-	-	3/27/28/28	0/3/3/3
2	UMP	G	701	-	-	6/10/22/22	0/2/2/2
4	FOL	A	703	-	-	0/22/22/22	0/3/3/3
4	FOL	H	703	-	-	2/22/22/22	0/3/3/3
3	CB3	G	702	-	-	5/27/28/28	0/3/3/3
2	UMP	D	701	-	-	3/10/22/22	0/2/2/2
3	CB3	E	702	-	-	9/27/28/28	0/3/3/3

All (282) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	704	NDP	C4N-C3N	-5.93	1.38	1.50
5	F	704	NDP	C4N-C3N	-5.92	1.38	1.50
3	A	702	CB3	C9-C6	-5.88	1.40	1.51
5	G	704	NDP	C4N-C3N	-5.78	1.39	1.50
5	C	704	NDP	C4N-C3N	-5.77	1.39	1.50
5	A	704	NDP	C4N-C3N	-5.76	1.39	1.50
5	B	704	NDP	C3B-C2B	5.76	1.65	1.53
5	A	704	NDP	C3B-C2B	5.75	1.65	1.53
5	E	704	NDP	C4N-C3N	-5.71	1.39	1.50
5	B	704	NDP	C4N-C3N	-5.69	1.39	1.50
5	C	704	NDP	C3B-C2B	5.68	1.65	1.53
4	G	703	FOL	C4A-C4	-5.68	1.36	1.47
5	G	704	NDP	C3B-C2B	5.67	1.65	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	704	NDP	C4N-C3N	-5.62	1.39	1.50
5	F	704	NDP	C3B-C2B	5.61	1.65	1.53
4	E	703	FOL	C4A-C4	-5.52	1.36	1.47
4	D	703	FOL	C4A-C4	-5.49	1.36	1.47
4	A	703	FOL	C4A-C4	-5.49	1.36	1.47
3	G	702	CB3	C9-C6	-5.49	1.41	1.51
4	C	703	FOL	C4A-C4	-5.47	1.37	1.47
3	E	702	CB3	C9-C6	-5.44	1.41	1.51
5	E	704	NDP	C3B-C2B	5.43	1.64	1.53
4	H	703	FOL	C4A-C4	-5.37	1.37	1.47
3	B	702	CB3	C9-C6	-5.34	1.41	1.51
5	D	704	NDP	C3B-C2B	5.31	1.64	1.53
5	H	704	NDP	C3B-C2B	5.30	1.64	1.53
3	C	702	CB3	C4A-C4	-5.29	1.39	1.48
3	E	702	CB3	C4A-C4	-5.28	1.39	1.48
3	G	702	CB3	C4A-C4	-5.27	1.39	1.48
3	H	702	CB3	C9-C6	-5.26	1.41	1.51
4	F	703	FOL	C4A-C4	-5.20	1.37	1.47
4	B	703	FOL	C4A-C4	-5.17	1.37	1.47
3	A	702	CB3	C4A-C4	-5.10	1.39	1.48
3	H	702	CB3	C4A-C4	-5.09	1.39	1.48
5	G	704	NDP	O4D-C1D	5.05	1.53	1.42
3	C	702	CB3	C9-C6	-5.03	1.42	1.51
3	A	702	CB3	C11-C	-4.98	1.39	1.50
4	D	703	FOL	C9-C6	-4.90	1.40	1.50
4	B	703	FOL	C9-C6	-4.90	1.40	1.50
3	F	702	CB3	C4A-C4	-4.88	1.39	1.48
3	B	702	CB3	C4A-C4	-4.88	1.39	1.48
3	D	702	CB3	C4A-C4	-4.87	1.39	1.48
5	D	704	NDP	O4D-C1D	4.84	1.53	1.42
3	D	702	CB3	C9-C6	-4.84	1.42	1.51
5	C	704	NDP	O4D-C1D	4.83	1.53	1.42
3	C	702	CB3	C11-C	-4.81	1.39	1.50
5	E	704	NDP	O4D-C1D	4.79	1.53	1.42
3	F	702	CB3	C9-C6	-4.66	1.43	1.51
3	G	702	CB3	C11-C	-4.65	1.40	1.50
4	A	703	FOL	C11-C	-4.64	1.40	1.50
5	A	704	NDP	C2D-C1D	-4.56	1.39	1.53
4	F	703	FOL	C9-C6	-4.54	1.41	1.50
4	H	703	FOL	C9-C6	-4.51	1.41	1.50
3	E	702	CB3	C11-C	-4.49	1.40	1.50
3	F	702	CB3	C11-C	-4.48	1.40	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	703	FOL	C11-C	-4.47	1.40	1.50
5	A	704	NDP	C3B-C4B	-4.46	1.41	1.53
5	E	704	NDP	C3B-C4B	-4.43	1.41	1.53
4	H	703	FOL	C11-C	-4.42	1.40	1.50
3	H	702	CB3	C11-C	-4.40	1.40	1.50
5	C	704	NDP	C3B-C4B	-4.40	1.41	1.53
5	G	704	NDP	C3B-C4B	-4.37	1.41	1.53
3	D	702	CB3	C11-C	-4.34	1.40	1.50
4	E	703	FOL	C9-C6	-4.30	1.41	1.50
4	F	703	FOL	C11-C	-4.29	1.40	1.50
5	C	704	NDP	C2D-C1D	-4.28	1.40	1.53
3	B	702	CB3	C11-C	-4.26	1.40	1.50
5	A	704	NDP	C7N-C3N	-4.26	1.39	1.48
5	A	704	NDP	O4D-C1D	4.24	1.51	1.42
4	C	703	FOL	C9-C6	-4.21	1.41	1.50
4	A	703	FOL	C9-C6	-4.19	1.41	1.50
4	G	703	FOL	C11-C	-4.16	1.41	1.50
5	H	704	NDP	PN-O3	4.13	1.64	1.59
5	C	704	NDP	C4N-C5N	-4.07	1.38	1.49
4	E	703	FOL	C11-C	-4.07	1.41	1.50
5	F	704	NDP	C7N-C3N	-4.07	1.40	1.48
5	D	704	NDP	C4N-C5N	-4.07	1.38	1.49
5	C	704	NDP	C7N-C3N	-4.06	1.40	1.48
5	G	704	NDP	C7N-C3N	-4.06	1.40	1.48
5	G	704	NDP	C4N-C5N	-4.05	1.38	1.49
4	G	703	FOL	C9-C6	-4.03	1.42	1.50
5	D	704	NDP	C2D-C3D	4.02	1.64	1.53
5	D	704	NDP	P2B-O2B	4.02	1.66	1.59
5	E	704	NDP	C4N-C5N	-4.01	1.38	1.49
5	H	704	NDP	P2B-O2B	4.00	1.66	1.59
5	A	704	NDP	C4N-C5N	-3.99	1.38	1.49
5	F	704	NDP	C3B-C4B	-3.99	1.42	1.53
5	C	704	NDP	P2B-O2B	3.97	1.66	1.59
5	H	704	NDP	C7N-C3N	-3.97	1.40	1.48
5	D	704	NDP	C7N-C3N	-3.96	1.40	1.48
5	B	704	NDP	P2B-O2B	3.95	1.66	1.59
5	E	704	NDP	C2D-C1D	-3.93	1.41	1.53
5	G	704	NDP	P2B-O2B	3.93	1.66	1.59
5	H	704	NDP	C3B-C4B	-3.92	1.43	1.53
4	D	703	FOL	C11-C	-3.90	1.41	1.50
5	E	704	NDP	C7N-C3N	-3.89	1.40	1.48
5	G	704	NDP	C2D-C1D	-3.89	1.41	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	704	NDP	P2B-O2B	3.88	1.66	1.59
5	B	704	NDP	C7N-C3N	-3.83	1.40	1.48
4	E	703	FOL	C7-N8	3.82	1.42	1.34
4	G	703	FOL	C7-N8	3.80	1.42	1.34
5	G	704	NDP	C5A-N7A	-3.79	1.32	1.39
5	A	704	NDP	P2B-O2B	3.78	1.66	1.59
4	C	703	FOL	C11-C	-3.75	1.42	1.50
5	A	704	NDP	C5A-N7A	-3.75	1.32	1.39
5	F	704	NDP	C4N-C5N	-3.75	1.39	1.49
5	C	704	NDP	C2D-C3D	3.74	1.63	1.53
5	G	704	NDP	C2D-C3D	3.73	1.63	1.53
5	E	704	NDP	C2D-C3D	3.71	1.63	1.53
4	C	703	FOL	C7-N8	3.69	1.41	1.34
5	B	704	NDP	C4N-C5N	-3.68	1.39	1.49
5	E	704	NDP	C5A-N7A	-3.68	1.32	1.39
5	H	704	NDP	C5A-N7A	-3.68	1.32	1.39
5	D	704	NDP	C2D-C1D	-3.67	1.41	1.53
5	H	704	NDP	C4N-C5N	-3.67	1.39	1.49
5	B	704	NDP	C5A-N7A	-3.66	1.32	1.39
3	G	702	CB3	CP2-CP3	-3.66	1.07	1.18
5	C	704	NDP	C5A-N7A	-3.64	1.32	1.39
5	F	704	NDP	C5A-N7A	-3.64	1.32	1.39
5	B	704	NDP	C3B-C4B	-3.63	1.43	1.53
5	D	704	NDP	C5A-N7A	-3.58	1.32	1.39
5	F	704	NDP	C2A-N3A	3.58	1.40	1.33
5	A	704	NDP	C2D-C3D	3.56	1.63	1.53
4	A	703	FOL	C7-N8	3.54	1.41	1.34
5	D	704	NDP	C3B-C4B	-3.51	1.44	1.53
4	D	703	FOL	C7-N8	3.43	1.41	1.34
5	E	704	NDP	P2B-O2B	3.40	1.65	1.59
5	B	704	NDP	C2A-N3A	3.40	1.40	1.33
5	B	704	NDP	C2A-N1A	3.37	1.39	1.33
5	H	704	NDP	C2A-N1A	3.37	1.39	1.33
5	H	704	NDP	O4D-C4D	3.33	1.52	1.45
5	D	704	NDP	C2A-N1A	3.31	1.39	1.33
4	H	703	FOL	C7-N8	3.28	1.41	1.34
4	F	703	FOL	C7-N8	3.25	1.41	1.34
5	F	704	NDP	C2A-N1A	3.21	1.39	1.33
5	B	704	NDP	O4D-C4D	3.19	1.52	1.45
4	B	703	FOL	C7-N8	3.16	1.40	1.34
5	C	704	NDP	C2A-N3A	3.16	1.39	1.33
5	A	704	NDP	C2A-N3A	3.12	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	704	NDP	C2A-N3A	3.10	1.39	1.33
3	A	702	CB3	C8A-N1	-3.10	1.34	1.39
3	C	702	CB3	C8A-N1	-3.08	1.34	1.39
5	D	704	NDP	C2A-N3A	3.05	1.39	1.33
5	A	704	NDP	C2A-N1A	3.04	1.39	1.33
3	E	702	CB3	C8A-N1	-3.04	1.34	1.39
3	H	702	CB3	C8A-N1	-3.04	1.34	1.39
5	E	704	NDP	C2A-N1A	3.03	1.39	1.33
3	B	702	CB3	C8A-N1	-3.01	1.34	1.39
3	G	702	CB3	C8A-N1	-3.00	1.34	1.39
5	G	704	NDP	C2A-N3A	2.97	1.39	1.33
5	E	704	NDP	C2A-N3A	2.96	1.39	1.33
5	F	704	NDP	PN-O3	2.95	1.62	1.59
5	G	704	NDP	C2A-N1A	2.94	1.39	1.33
4	C	703	FOL	CA-N	2.93	1.52	1.45
3	F	702	CB3	C8A-N1	-2.91	1.34	1.39
5	C	704	NDP	C2A-N1A	2.87	1.39	1.33
3	C	702	CB3	C2-N3	2.84	1.40	1.33
5	A	704	NDP	C5A-C6A	-2.84	1.33	1.41
2	C	701	UMP	O4'-C4'	2.83	1.51	1.45
5	H	704	NDP	C5A-C6A	-2.81	1.33	1.41
3	B	702	CB3	C2-N3	2.80	1.40	1.33
5	G	704	NDP	C5A-C6A	-2.79	1.33	1.41
4	B	703	FOL	C2-N3	2.79	1.39	1.33
5	D	704	NDP	C5A-C6A	-2.78	1.33	1.41
4	B	703	FOL	C8A-N1	-2.78	1.34	1.38
5	F	704	NDP	O4B-C4B	2.77	1.51	1.45
5	B	704	NDP	PN-O3	2.77	1.62	1.59
4	D	703	FOL	C2-N3	2.75	1.39	1.33
5	E	704	NDP	C5A-C6A	-2.75	1.33	1.41
5	B	704	NDP	C5A-C6A	-2.75	1.33	1.41
5	C	704	NDP	C5A-C6A	-2.75	1.33	1.41
3	D	702	CB3	C8A-N1	-2.72	1.35	1.39
4	D	703	FOL	C8A-N1	-2.70	1.34	1.38
3	A	702	CB3	C2-N3	2.70	1.39	1.33
3	F	702	CB3	C2-N3	2.69	1.39	1.33
4	A	703	FOL	C8A-N1	-2.69	1.34	1.38
4	G	703	FOL	C8A-N1	-2.67	1.34	1.38
2	A	701	UMP	O4'-C4'	2.67	1.50	1.45
2	G	701	UMP	O4'-C4'	2.67	1.50	1.45
5	H	704	NDP	PA-O5B	2.67	1.69	1.59
4	E	703	FOL	C8A-N1	-2.67	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	702	CB3	C2-N3	2.64	1.39	1.33
5	F	704	NDP	O4D-C4D	2.64	1.50	1.45
3	E	702	CB3	C2-N3	2.63	1.39	1.33
4	F	703	FOL	C2-N3	2.62	1.39	1.33
3	H	702	CB3	C2-N3	2.62	1.39	1.33
4	C	703	FOL	C2-N3	2.62	1.39	1.33
2	E	701	UMP	O4'-C4'	2.60	1.50	1.45
3	D	702	CB3	C2-N3	2.59	1.39	1.33
2	H	701	UMP	O4'-C4'	2.59	1.50	1.45
5	F	704	NDP	C5A-C6A	-2.58	1.33	1.41
3	G	702	CB3	CA-N	2.57	1.51	1.45
4	H	703	FOL	C2-N3	2.57	1.39	1.33
4	E	703	FOL	C2-N3	2.52	1.39	1.33
4	G	703	FOL	C2-N3	2.51	1.39	1.33
2	B	701	UMP	O4'-C4'	2.51	1.50	1.45
4	A	703	FOL	C2-N3	2.50	1.39	1.33
5	E	704	NDP	C5A-C4A	-2.49	1.34	1.39
4	F	703	FOL	C8A-N1	-2.49	1.34	1.38
4	H	703	FOL	C8A-N1	-2.49	1.34	1.38
5	D	704	NDP	PN-O5D	2.48	1.69	1.59
3	E	702	CB3	CP2-CP3	-2.48	1.10	1.18
5	G	704	NDP	C5A-C4A	-2.48	1.34	1.39
3	F	702	CB3	C9-N10	2.45	1.49	1.46
5	C	704	NDP	C5A-C4A	-2.45	1.34	1.39
4	C	703	FOL	C8A-N1	-2.44	1.35	1.38
2	F	701	UMP	O4'-C4'	2.43	1.50	1.45
4	C	703	FOL	CG-CD	2.43	1.56	1.50
2	E	701	UMP	C5-C4	-2.41	1.38	1.43
5	D	704	NDP	O4B-C4B	2.41	1.50	1.45
5	A	704	NDP	C5A-C4A	-2.40	1.34	1.39
5	B	704	NDP	O4B-C4B	2.39	1.50	1.45
3	A	702	CB3	CP2-CP3	-2.38	1.11	1.18
2	D	701	UMP	C5-C4	-2.37	1.38	1.43
3	E	702	CB3	C9-N10	2.36	1.49	1.46
5	B	704	NDP	C5A-C4A	-2.36	1.34	1.39
2	F	701	UMP	C5-C4	-2.34	1.38	1.43
5	D	704	NDP	C5A-C4A	-2.34	1.34	1.39
4	D	703	FOL	CA-N	2.32	1.50	1.45
3	B	702	CB3	CA-N	2.32	1.50	1.45
2	E	701	UMP	C2-N1	-2.31	1.34	1.38
3	G	702	CB3	C9-N10	2.29	1.49	1.46
2	B	701	UMP	C5-C4	-2.29	1.38	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	702	CB3	CP2-CP3	-2.28	1.11	1.18
2	D	701	UMP	O4'-C4'	2.27	1.50	1.45
5	H	704	NDP	C5A-C4A	-2.26	1.35	1.39
2	A	701	UMP	C5-C4	-2.26	1.38	1.43
2	C	701	UMP	C5-C4	-2.24	1.38	1.43
2	H	701	UMP	C5-C4	-2.24	1.38	1.43
5	H	704	NDP	C4A-N9A	-2.24	1.33	1.37
2	G	701	UMP	C5-C4	-2.23	1.38	1.43
2	A	701	UMP	P-OP2	-2.23	1.46	1.54
5	F	704	NDP	C5A-C4A	-2.23	1.35	1.39
4	E	703	FOL	CG-CD	2.22	1.55	1.50
3	E	702	CB3	CA-N	2.22	1.50	1.45
2	G	701	UMP	P-OP2	-2.21	1.46	1.54
2	C	701	UMP	C2-N1	-2.21	1.35	1.38
3	B	702	CB3	CP2-CP3	-2.20	1.11	1.18
5	E	704	NDP	C4A-N9A	-2.20	1.33	1.37
2	H	701	UMP	C2-N1	-2.19	1.35	1.38
3	C	702	CB3	C9-N10	2.18	1.49	1.46
2	A	701	UMP	C2-N1	-2.17	1.35	1.38
3	A	702	CB3	C9-N10	2.17	1.49	1.46
3	D	702	CB3	CA-N	2.15	1.50	1.45
5	E	704	NDP	PA-O5B	2.15	1.67	1.59
5	B	704	NDP	C6N-C5N	2.14	1.39	1.33
5	H	704	NDP	O2B-C2B	2.13	1.51	1.44
5	D	704	NDP	C2N-C3N	2.13	1.41	1.35
5	F	704	NDP	O2B-C2B	2.13	1.51	1.44
3	D	702	CB3	C9-N10	2.13	1.49	1.46
5	F	704	NDP	C6N-C5N	2.13	1.39	1.33
5	E	704	NDP	C2N-C3N	2.12	1.41	1.35
2	G	701	UMP	C2-N1	-2.11	1.35	1.38
2	D	701	UMP	P-OP2	-2.11	1.47	1.54
5	G	704	NDP	PA-O5B	2.11	1.67	1.59
2	B	701	UMP	C2-N1	-2.11	1.35	1.38
5	H	704	NDP	C2D-C3D	-2.10	1.47	1.53
2	E	701	UMP	P-OP2	-2.10	1.47	1.54
2	D	701	UMP	C2-N1	-2.10	1.35	1.38
5	H	704	NDP	C6N-C5N	2.10	1.39	1.33
2	C	701	UMP	P-OP2	-2.10	1.47	1.54
3	H	702	CB3	CA-CT	2.09	1.58	1.52
5	D	704	NDP	C4A-N9A	-2.09	1.33	1.37
5	G	704	NDP	C4A-N9A	-2.09	1.33	1.37
4	E	703	FOL	CA-N	2.08	1.50	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	702	CB3	CA-N	2.08	1.50	1.45
3	H	702	CB3	C9-N10	2.08	1.49	1.46
5	G	704	NDP	C2N-C3N	2.08	1.40	1.35
2	H	701	UMP	P-OP2	-2.08	1.47	1.54
5	D	704	NDP	O2B-C2B	2.07	1.51	1.44
5	C	704	NDP	C4A-N9A	-2.07	1.33	1.37
5	F	704	NDP	O4B-C1B	2.07	1.46	1.42
5	B	704	NDP	O2B-C2B	2.04	1.51	1.44
4	A	703	FOL	CG-CD	2.04	1.55	1.50
5	E	704	NDP	PN-O5D	2.03	1.67	1.59
5	B	704	NDP	C2D-C3D	-2.03	1.47	1.53
5	A	704	NDP	PA-O5B	2.03	1.67	1.59
4	G	703	FOL	CA-N	2.02	1.50	1.45
2	F	701	UMP	C2-N1	-2.02	1.35	1.38
2	B	701	UMP	P-OP2	-2.01	1.47	1.54
5	G	704	NDP	P2B-O2X	-2.01	1.47	1.54
5	C	704	NDP	P2B-O2X	-2.00	1.47	1.54

All (468) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	701	UMP	O4'-C1'-C2'	-21.17	66.69	106.25
2	F	701	UMP	O4'-C1'-C2'	-21.16	66.71	106.25
2	C	701	UMP	O4'-C1'-C2'	-21.14	66.74	106.25
2	H	701	UMP	O4'-C1'-C2'	-21.13	66.76	106.25
2	B	701	UMP	O4'-C1'-C2'	-21.11	66.80	106.25
2	D	701	UMP	O4'-C1'-C2'	-21.04	66.94	106.25
2	A	701	UMP	O4'-C1'-C2'	-20.85	67.28	106.25
2	G	701	UMP	O4'-C1'-C2'	-20.78	67.42	106.25
5	F	704	NDP	O4D-C1D-C2D	-15.69	73.04	106.62
5	B	704	NDP	O4D-C1D-C2D	-15.18	74.12	106.62
5	H	704	NDP	O4D-C1D-C2D	-15.01	74.48	106.62
5	F	704	NDP	C2B-C1B-N9A	-14.46	89.96	113.75
5	D	704	NDP	C2B-C1B-N9A	-14.35	90.13	113.75
5	B	704	NDP	C2B-C1B-N9A	-14.17	90.43	113.75
5	C	704	NDP	C2B-C1B-N9A	-12.85	92.61	113.75
5	H	704	NDP	C2B-C1B-N9A	-12.78	92.72	113.75
5	E	704	NDP	C2B-C1B-N9A	-12.64	92.96	113.75
5	G	704	NDP	C2B-C1B-N9A	-12.40	93.35	113.75
5	A	704	NDP	C2B-C1B-N9A	-11.86	94.23	113.75
2	E	701	UMP	O4'-C4'-C5'	-11.42	72.76	109.33
2	A	701	UMP	O4'-C4'-C5'	-11.33	73.03	109.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	701	UMP	O4'-C4'-C5'	-11.33	73.04	109.33
5	G	704	NDP	O4B-C1B-C2B	-11.33	87.08	106.59
2	H	701	UMP	O4'-C4'-C5'	-11.29	73.16	109.33
2	B	701	UMP	O4'-C4'-C5'	-11.29	73.18	109.33
5	A	704	NDP	O4B-C1B-C2B	-11.27	87.18	106.59
2	D	701	UMP	O4'-C4'-C5'	-11.27	73.25	109.33
2	F	701	UMP	O4'-C4'-C5'	-11.26	73.27	109.33
2	G	701	UMP	O4'-C4'-C5'	-11.25	73.29	109.33
5	H	704	NDP	O4B-C1B-C2B	-11.00	87.65	106.59
5	C	704	NDP	O4B-C1B-C2B	-10.82	87.97	106.59
5	E	704	NDP	O4B-C1B-C2B	-10.71	88.16	106.59
5	D	704	NDP	O4B-C1B-C2B	-10.71	88.16	106.59
5	B	704	NDP	O4B-C1B-C2B	-10.62	88.30	106.59
5	F	704	NDP	O4B-C1B-C2B	-10.36	88.76	106.59
5	F	704	NDP	O4D-C4D-C5D	-9.79	77.97	109.33
5	H	704	NDP	O4D-C4D-C3D	-9.44	86.42	105.15
5	H	704	NDP	O4D-C4D-C5D	-9.35	79.37	109.33
5	B	704	NDP	O4D-C4D-C5D	-9.34	79.42	109.33
2	B	701	UMP	O4'-C4'-C3'	-9.26	84.54	105.65
2	C	701	UMP	O4'-C4'-C3'	-9.25	84.55	105.65
5	B	704	NDP	O4D-C4D-C3D	-9.24	86.81	105.15
5	G	704	NDP	C5D-C4D-C3D	-9.19	82.12	115.21
2	E	701	UMP	O4'-C4'-C3'	-9.14	84.81	105.65
5	E	704	NDP	C5D-C4D-C3D	-9.14	82.32	115.21
2	F	701	UMP	O4'-C4'-C3'	-9.12	84.84	105.65
5	C	704	NDP	C5D-C4D-C3D	-9.12	82.39	115.21
2	H	701	UMP	O4'-C4'-C3'	-9.11	84.87	105.65
5	A	704	NDP	C5D-C4D-C3D	-9.08	82.53	115.21
2	G	701	UMP	O4'-C4'-C3'	-9.08	84.96	105.65
2	A	701	UMP	O4'-C4'-C3'	-9.04	85.05	105.65
2	D	701	UMP	O4'-C4'-C3'	-8.95	85.24	105.65
5	D	704	NDP	C5D-C4D-C3D	-8.95	83.00	115.21
5	F	704	NDP	O4D-C4D-C3D	-8.88	87.53	105.15
5	D	704	NDP	C2D-C1D-N1N	8.70	134.69	113.31
5	A	704	NDP	C2D-C1D-N1N	8.57	134.39	113.31
5	E	704	NDP	C2D-C1D-N1N	8.56	134.36	113.31
5	C	704	NDP	C2D-C1D-N1N	8.50	134.21	113.31
5	G	704	NDP	C2D-C1D-N1N	8.42	134.02	113.31
4	C	703	FOL	CB-CA-N	8.30	127.35	110.91
5	A	704	NDP	C3D-C2D-C1D	-7.56	87.16	101.46
5	C	704	NDP	C3D-C2D-C1D	-7.46	87.35	101.46
5	D	704	NDP	C3D-C2D-C1D	-7.45	87.38	101.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	704	NDP	C3D-C2D-C1D	-7.44	87.40	101.46
5	G	704	NDP	C3D-C2D-C1D	-7.33	87.59	101.46
4	E	703	FOL	CB-CA-N	7.31	125.39	110.91
5	B	704	NDP	C2B-C3B-C4B	-7.24	86.42	101.99
5	D	704	NDP	C2B-C3B-C4B	-7.20	86.52	101.99
4	G	703	FOL	CB-CA-N	7.07	124.91	110.91
5	C	704	NDP	O4D-C4D-C3D	-6.95	91.36	105.15
5	G	704	NDP	C2B-C3B-C4B	-6.93	87.09	101.99
5	C	704	NDP	C2B-C3B-C4B	-6.92	87.11	101.99
5	F	704	NDP	C2B-C3B-C4B	-6.88	87.19	101.99
5	A	704	NDP	O4D-C4D-C3D	-6.88	91.50	105.15
5	C	704	NDP	C1B-N9A-C8A	-6.81	111.98	127.09
5	E	704	NDP	O4D-C4D-C3D	-6.78	91.70	105.15
5	G	704	NDP	O4D-C4D-C3D	-6.76	91.73	105.15
5	A	704	NDP	C5B-C4B-C3B	6.76	139.53	115.21
5	A	704	NDP	C2B-C3B-C4B	-6.74	87.49	101.99
5	D	704	NDP	O4D-C4D-C3D	-6.74	91.77	105.15
5	G	704	NDP	C1D-N1N-C2N	6.68	132.15	121.14
5	F	704	NDP	C1B-N9A-C8A	-6.67	112.30	127.09
5	H	704	NDP	C5B-C4B-C3B	6.66	139.19	115.21
5	E	704	NDP	C5B-C4B-C3B	6.65	139.14	115.21
5	E	704	NDP	C2B-C3B-C4B	-6.63	87.75	101.99
5	C	704	NDP	C5B-C4B-C3B	6.62	139.05	115.21
5	H	704	NDP	C2B-C3B-C4B	-6.58	87.84	101.99
5	G	704	NDP	C5B-C4B-C3B	6.56	138.83	115.21
5	A	704	NDP	C1B-N9A-C8A	-6.44	112.79	127.09
5	E	704	NDP	C1D-N1N-C2N	6.44	131.75	121.14
5	F	704	NDP	N3A-C2A-N1A	-6.42	118.86	128.58
5	D	704	NDP	C5B-C4B-C3B	6.42	138.32	115.21
5	E	704	NDP	N3A-C2A-N1A	-6.40	118.89	128.58
5	B	704	NDP	C5B-C4B-C3B	6.39	138.22	115.21
5	C	704	NDP	N3A-C2A-N1A	-6.33	118.99	128.58
5	B	704	NDP	N3A-C2A-N1A	-6.28	119.07	128.58
5	F	704	NDP	C5B-C4B-C3B	6.26	137.73	115.21
5	H	704	NDP	N3A-C2A-N1A	-6.23	119.15	128.58
5	A	704	NDP	N3A-C2A-N1A	-6.17	119.24	128.58
5	D	704	NDP	N3A-C2A-N1A	-6.16	119.26	128.58
4	F	703	FOL	CB-CA-N	6.13	123.03	110.91
5	F	704	NDP	C4A-N9A-C1B	6.12	140.95	126.63
5	G	704	NDP	C1B-N9A-C8A	-6.10	113.55	127.09
4	C	703	FOL	CG-CB-CA	6.09	124.39	113.16
5	G	704	NDP	N3A-C2A-N1A	-6.09	119.36	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	704	NDP	C1D-N1N-C2N	5.99	131.00	121.14
5	C	704	NDP	C1D-N1N-C2N	5.81	130.71	121.14
5	G	704	NDP	C1D-N1N-C6N	-5.80	108.50	120.77
5	E	704	NDP	C1D-N1N-C6N	-5.80	108.51	120.77
3	G	702	CB3	CG-CB-CA	5.79	123.84	113.16
4	E	703	FOL	CG-CB-CA	5.78	123.81	113.16
5	E	704	NDP	C1B-N9A-C8A	-5.75	114.34	127.09
5	C	704	NDP	C4A-N9A-C1B	5.71	139.98	126.63
5	A	704	NDP	C1D-N1N-C6N	-5.55	109.03	120.77
5	C	704	NDP	C1D-N1N-C6N	-5.54	109.06	120.77
5	A	704	NDP	C4A-N9A-C1B	5.44	139.36	126.63
4	A	703	FOL	C7-C6-N5	-5.43	117.35	120.87
5	A	704	NDP	C1D-N1N-C2N	5.40	130.04	121.14
4	C	703	FOL	CB-CA-CT	-5.39	97.57	110.35
5	D	704	NDP	C1D-N1N-C6N	-5.32	109.53	120.77
4	G	703	FOL	C7-C6-N5	-5.31	117.42	120.87
5	F	704	NDP	C5A-C4A-N3A	-5.30	119.42	126.72
4	G	703	FOL	CG-CB-CA	5.29	122.92	113.16
5	G	704	NDP	C4A-N9A-C1B	5.13	138.62	126.63
2	F	701	UMP	O3'-C3'-C2'	5.04	128.41	110.88
4	C	703	FOL	C7-C6-N5	-5.00	117.63	120.87
2	H	701	UMP	O3'-C3'-C2'	4.99	128.21	110.88
5	A	704	NDP	C5A-C4A-N3A	-4.98	119.86	126.72
5	B	704	NDP	C5A-C4A-N3A	-4.97	119.87	126.72
5	G	704	NDP	C5A-C4A-N3A	-4.97	119.88	126.72
4	E	703	FOL	C7-C6-N5	-4.95	117.66	120.87
2	C	701	UMP	O3'-C3'-C2'	4.95	128.09	110.88
5	C	704	NDP	C5A-C4A-N3A	-4.91	119.95	126.72
2	G	701	UMP	O3'-C3'-C2'	4.90	127.91	110.88
2	B	701	UMP	O3'-C3'-C2'	4.88	127.84	110.88
2	E	701	UMP	O3'-C3'-C2'	4.88	127.84	110.88
2	G	701	UMP	C1'-N1-C2	4.88	127.20	117.66
2	D	701	UMP	O3'-C3'-C2'	4.88	127.83	110.88
4	D	703	FOL	CB-CA-N	4.88	120.56	110.91
5	H	704	NDP	C5D-C4D-C3D	4.86	132.70	115.21
2	A	701	UMP	C1'-N1-C2	4.86	127.16	117.66
3	G	702	CB3	CB-CG-CD	4.82	125.34	112.49
5	H	704	NDP	C3D-C2D-C1D	-4.81	92.37	101.46
3	A	702	CB3	CG-CB-CA	4.79	122.00	113.16
5	E	704	NDP	C5A-C4A-N3A	-4.79	120.12	126.72
2	D	701	UMP	C1'-N1-C2	4.78	127.01	117.66
4	G	703	FOL	CB-CA-CT	-4.78	99.01	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	704	NDP	C4A-N9A-C1B	4.74	137.71	126.63
5	B	704	NDP	C5D-C4D-C3D	4.67	132.01	115.21
2	C	701	UMP	C1'-N1-C2	4.64	126.73	117.66
2	B	701	UMP	C1'-N1-C2	4.63	126.72	117.66
2	A	701	UMP	O3'-C3'-C2'	4.63	126.97	110.88
5	F	704	NDP	C3D-C2D-C1D	-4.59	92.77	101.46
2	E	701	UMP	C4-N3-C2	-4.59	120.91	126.61
2	A	701	UMP	C1'-N1-C6	-4.59	112.50	121.53
5	D	704	NDP	C5A-C4A-N3A	-4.59	120.40	126.72
4	E	703	FOL	CB-CA-CT	-4.57	99.50	110.35
2	D	701	UMP	C4-N3-C2	-4.57	120.94	126.61
2	F	701	UMP	C4-N3-C2	-4.57	120.94	126.61
2	E	701	UMP	C2'-C1'-N1	-4.55	102.44	113.81
2	G	701	UMP	C1'-N1-C6	-4.51	112.67	121.53
5	H	704	NDP	C5A-C4A-N3A	-4.50	120.52	126.72
2	F	701	UMP	C1'-N1-C2	4.49	126.44	117.66
2	C	701	UMP	C2'-C1'-N1	-4.47	102.63	113.81
2	B	701	UMP	C4-N3-C2	-4.46	121.07	126.61
4	H	703	FOL	C6-C9-N10	4.46	122.92	113.13
2	H	701	UMP	C4-N3-C2	-4.45	121.08	126.61
2	A	701	UMP	C4-N3-C2	-4.45	121.09	126.61
4	G	703	FOL	C6-C9-N10	4.44	122.87	113.13
2	D	701	UMP	C1'-N1-C6	-4.43	112.81	121.53
2	C	701	UMP	C1'-N1-C6	-4.41	112.85	121.53
2	C	701	UMP	C4-N3-C2	-4.41	121.13	126.61
2	E	701	UMP	C1'-N1-C2	4.41	126.29	117.66
2	H	701	UMP	C1'-N1-C2	4.41	126.28	117.66
5	B	704	NDP	C3D-C2D-C1D	-4.40	93.13	101.46
2	B	701	UMP	C2'-C1'-N1	-4.40	102.81	113.81
2	H	701	UMP	C2'-C1'-N1	-4.39	102.83	113.81
2	F	701	UMP	C2'-C1'-N1	-4.36	102.90	113.81
4	H	703	FOL	C7-C6-N5	-4.34	118.05	120.87
2	G	701	UMP	C4-N3-C2	-4.33	121.23	126.61
3	C	702	CB3	CG-CB-CA	-4.28	105.26	113.16
2	D	701	UMP	C2'-C1'-N1	-4.28	103.12	113.81
2	A	701	UMP	C2'-C1'-N1	-4.27	103.13	113.81
2	E	701	UMP	C1'-N1-C6	-4.25	113.18	121.53
2	G	701	UMP	C2'-C1'-N1	-4.23	103.22	113.81
2	F	701	UMP	C1'-N1-C6	-4.23	113.21	121.53
2	B	701	UMP	C1'-N1-C6	-4.20	113.27	121.53
5	F	704	NDP	C5D-C4D-C3D	4.19	130.29	115.21
3	D	702	CB3	CA-N-C	4.19	131.61	121.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	702	CB3	CT-CA-N	4.16	120.22	110.57
5	G	704	NDP	O3B-C3B-C4B	-4.16	99.15	111.08
2	H	701	UMP	C1'-N1-C6	-4.12	113.43	121.53
3	B	702	CB3	CP1-N10-C9	-4.11	113.05	117.19
5	A	704	NDP	O3B-C3B-C4B	-4.09	99.34	111.08
5	A	704	NDP	C3N-C2N-N1N	-4.06	117.24	123.20
4	G	703	FOL	CB-CG-CD	-3.97	101.91	112.49
4	E	703	FOL	CB-CG-CD	-3.93	102.01	112.49
5	E	704	NDP	O3B-C3B-C4B	-3.91	99.85	111.08
4	E	703	FOL	C6-C9-N10	3.90	121.69	113.13
3	H	702	CB3	CP1-N10-C9	-3.86	113.30	117.19
5	B	704	NDP	C1B-N9A-C8A	-3.85	118.54	127.09
3	A	702	CB3	CB-CG-CD	3.79	122.59	112.49
2	H	701	UMP	C5-C4-N3	3.77	120.07	114.80
2	D	701	UMP	C5-C4-N3	3.73	120.03	114.80
2	F	701	UMP	C5-C4-N3	3.73	120.02	114.80
3	F	702	CB3	CA-N-C	3.72	130.49	121.56
2	E	701	UMP	C5-C4-N3	3.70	119.99	114.80
5	C	704	NDP	O3B-C3B-C4B	-3.68	100.52	111.08
3	D	702	CB3	CP1-N10-C9	-3.67	113.49	117.19
5	F	704	NDP	O5D-C5D-C4D	3.67	121.47	108.99
3	A	702	CB3	CP1-N10-C9	-3.66	113.50	117.19
3	G	702	CB3	CP1-N10-C9	-3.66	113.51	117.19
2	A	701	UMP	C5-C4-N3	3.65	119.91	114.80
4	E	703	FOL	N1-C8A-N8	3.63	121.81	116.38
2	C	701	UMP	C5-C4-N3	3.63	119.89	114.80
5	C	704	NDP	C3N-C2N-N1N	-3.63	117.88	123.20
4	F	703	FOL	C7-C6-N5	-3.62	118.52	120.87
5	G	704	NDP	O2D-C2D-C1D	-3.62	97.65	110.10
5	E	704	NDP	O2D-C2D-C1D	-3.62	97.65	110.10
2	B	701	UMP	C5-C4-N3	3.61	119.86	114.80
3	F	702	CB3	CB-CA-N	-3.61	103.76	110.91
5	G	704	NDP	C3B-C2B-C1B	3.60	109.71	102.81
2	G	701	UMP	C5-C4-N3	3.59	119.83	114.80
5	C	704	NDP	O2D-C2D-C1D	-3.54	97.92	110.10
4	G	703	FOL	N1-C8A-N8	3.52	121.64	116.38
3	E	702	CB3	CP1-N10-C9	-3.52	113.64	117.19
5	F	704	NDP	C5A-C4A-N9A	3.49	109.62	105.81
5	E	704	NDP	C5A-C4A-N9A	3.49	109.62	105.81
3	H	702	CB3	CB-CA-CT	3.49	118.62	110.35
5	D	704	NDP	C3B-C2B-C1B	3.46	109.43	102.81
4	A	703	FOL	C6-C9-N10	3.46	120.72	113.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	704	NDP	C3B-C2B-C1B	3.44	109.40	102.81
4	C	703	FOL	N1-C8A-N8	3.44	121.51	116.38
5	G	704	NDP	C5A-C4A-N9A	3.42	109.54	105.81
4	H	703	FOL	C9-C6-N5	3.42	123.02	116.56
5	B	704	NDP	C6A-C5A-C4A	3.38	121.79	117.18
5	B	704	NDP	C4A-N9A-C1B	3.37	134.51	126.63
5	E	704	NDP	C3N-C2N-N1N	-3.37	118.26	123.20
5	F	704	NDP	C2A-N3A-C4A	3.36	120.05	111.83
2	B	701	UMP	N3-C2-N1	3.35	119.25	114.89
5	C	704	NDP	C5A-C4A-N9A	3.33	109.44	105.81
5	A	704	NDP	O2D-C2D-C1D	-3.32	98.68	110.10
5	H	704	NDP	C3B-C2B-C1B	3.31	109.14	102.81
4	C	703	FOL	C6-C9-N10	3.29	120.36	113.13
5	A	704	NDP	C3B-C2B-C1B	3.29	109.11	102.81
2	H	701	UMP	N3-C2-N1	3.29	119.17	114.89
5	G	704	NDP	C3N-C2N-N1N	-3.28	118.39	123.20
4	A	703	FOL	N1-C8A-N8	3.28	121.28	116.38
3	A	702	CB3	CB-CA-CT	3.27	118.12	110.35
2	E	701	UMP	O4-C4-C5	-3.26	119.54	125.16
2	A	701	UMP	N3-C2-N1	3.26	119.13	114.89
2	C	701	UMP	N3-C2-N1	3.26	119.13	114.89
4	D	703	FOL	N1-C8A-N8	3.26	121.24	116.38
5	B	704	NDP	C3B-C2B-C1B	3.25	109.03	102.81
5	H	704	NDP	C5A-C4A-N9A	3.25	109.35	105.81
3	F	702	CB3	CP2-CP1-N10	-3.25	110.45	113.45
5	A	704	NDP	C5A-C4A-N9A	3.24	109.35	105.81
2	D	701	UMP	N3-C2-N1	3.24	119.11	114.89
5	E	704	NDP	C2A-N3A-C4A	3.23	119.72	111.83
5	E	704	NDP	C3B-C2B-C1B	3.22	108.97	102.81
3	D	702	CB3	CB-CA-N	-3.22	104.53	110.91
5	F	704	NDP	C6A-C5A-C4A	3.22	121.58	117.18
5	C	704	NDP	C3B-C2B-C1B	3.21	108.95	102.81
5	A	704	NDP	O2D-C2D-C3D	-3.21	101.53	111.82
5	C	704	NDP	C2A-N3A-C4A	3.21	119.66	111.83
2	F	701	UMP	N3-C2-N1	3.20	119.06	114.89
5	D	704	NDP	C3N-C2N-N1N	-3.20	118.50	123.20
5	A	704	NDP	C6A-C5A-C4A	3.20	121.55	117.18
2	A	701	UMP	OP2-P-O5'	-3.19	98.36	106.67
2	E	701	UMP	N3-C2-N1	3.18	119.03	114.89
5	H	704	NDP	O5D-C5D-C4D	3.17	119.78	108.99
2	G	701	UMP	O4-C4-C5	-3.16	119.71	125.16
3	A	702	CB3	CP2-CP1-N10	-3.16	110.54	113.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	702	CB3	CP2-CP1-N10	-3.15	110.54	113.45
5	B	704	NDP	O5D-C5D-C4D	3.15	119.71	108.99
5	D	704	NDP	O2D-C2D-C1D	-3.14	99.28	110.10
5	G	704	NDP	C2A-N3A-C4A	3.14	119.51	111.83
5	B	704	NDP	C2A-N3A-C4A	3.14	119.50	111.83
3	G	702	CB3	CB-CA-CT	3.13	117.79	110.35
5	A	704	NDP	C2A-N3A-C4A	3.13	119.48	111.83
5	G	704	NDP	C6A-C5A-C4A	3.13	121.45	117.18
2	G	701	UMP	N3-C2-N1	3.12	118.96	114.89
5	D	704	NDP	C5A-C4A-N9A	3.09	109.18	105.81
2	E	701	UMP	OP2-P-O5'	-3.09	98.60	106.67
5	D	704	NDP	C1B-N9A-C8A	-3.09	120.24	127.09
4	A	703	FOL	C9-C6-N5	3.09	122.39	116.56
5	D	704	NDP	C6A-C5A-C4A	3.08	121.38	117.18
2	F	701	UMP	O4-C4-C5	-3.07	119.86	125.16
4	G	703	FOL	C9-C6-N5	3.05	122.32	116.56
2	D	701	UMP	O4-C4-C5	-3.04	119.92	125.16
5	A	704	NDP	C4B-O4B-C1B	3.04	116.17	109.47
5	E	704	NDP	O2D-C2D-C3D	-3.04	102.09	111.82
5	D	704	NDP	O2B-C2B-C1B	3.03	120.70	110.05
3	D	702	CB3	CT-CA-N	3.03	117.59	110.57
2	C	701	UMP	OP2-P-O5'	-3.02	98.78	106.67
5	H	704	NDP	C6A-C5A-C4A	3.02	121.30	117.18
5	H	704	NDP	O2B-C2B-C1B	3.02	120.66	110.05
3	F	702	CB3	CP1-N10-C9	-3.01	114.15	117.19
5	B	704	NDP	C5A-C4A-N9A	3.01	109.09	105.81
2	A	701	UMP	O4-C4-C5	-3.01	119.97	125.16
2	G	701	UMP	OP2-P-O5'	-3.01	98.82	106.67
3	A	702	CB3	C9-N10-C14	3.01	125.94	120.72
3	C	702	CB3	CP1-N10-C9	-3.01	114.16	117.19
5	D	704	NDP	C2A-N3A-C4A	3.00	119.15	111.83
5	G	704	NDP	O2D-C2D-C3D	-3.00	102.21	111.82
5	C	704	NDP	O2D-C2D-C3D	-2.99	102.25	111.82
2	H	701	UMP	O3'-C3'-C4'	2.98	121.38	110.07
5	H	704	NDP	C2A-N3A-C4A	2.98	119.11	111.83
2	C	701	UMP	O4-C4-C5	-2.95	120.07	125.16
5	C	704	NDP	C6A-C5A-C4A	2.93	121.17	117.18
5	H	704	NDP	C4B-O4B-C1B	2.93	115.93	109.47
5	F	704	NDP	O3B-C3B-C4B	-2.91	102.72	111.08
2	F	701	UMP	O3'-C3'-C4'	2.91	121.10	110.07
2	B	701	UMP	O4-C4-C5	-2.91	120.14	125.16
3	B	702	CB3	CP2-CP1-N10	-2.89	110.78	113.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	703	FOL	N1-C8A-N8	2.89	120.70	116.38
3	G	702	CB3	OE1-CD-CG	-2.88	113.94	123.09
3	H	702	CB3	CP2-CP1-N10	-2.88	110.79	113.45
5	G	704	NDP	C4B-O4B-C1B	2.87	115.80	109.47
2	B	701	UMP	O3'-C3'-C4'	2.87	120.93	110.07
3	C	702	CB3	CP2-CP1-N10	-2.85	110.82	113.45
2	E	701	UMP	O3'-C3'-C4'	2.84	120.85	110.07
5	H	704	NDP	PN-O5D-C5D	-2.84	105.06	121.35
4	C	703	FOL	CB-CG-CD	-2.84	104.92	112.49
5	E	704	NDP	C6A-C5A-C4A	2.83	121.05	117.18
4	F	703	FOL	N1-C8A-N8	2.83	120.61	116.38
3	G	702	CB3	CT-CA-N	2.83	117.14	110.57
3	G	702	CB3	C9-N10-C14	2.82	125.61	120.72
5	F	704	NDP	PN-O5D-C5D	-2.81	105.22	121.35
2	C	701	UMP	O3'-C3'-C4'	2.80	120.67	110.07
2	H	701	UMP	O4-C4-C5	-2.78	120.36	125.16
3	D	702	CB3	CP2-CP1-N10	-2.78	110.88	113.45
5	D	704	NDP	C2D-C3D-C4D	2.77	107.97	102.61
4	F	703	FOL	C9-C6-N5	2.77	121.80	116.56
5	H	704	NDP	O5B-C5B-C4B	2.77	118.41	108.99
5	B	704	NDP	C5A-C6A-N6A	-2.75	116.49	123.29
4	B	703	FOL	CB-CA-N	2.74	116.33	110.91
4	B	703	FOL	C7-C6-N5	-2.73	119.10	120.87
4	C	703	FOL	C9-C6-N5	2.71	121.69	116.56
2	D	701	UMP	O3'-C3'-C4'	2.71	120.34	110.07
5	H	704	NDP	O3B-C3B-C4B	-2.70	103.31	111.08
3	D	702	CB3	C11-C-N	-2.70	112.03	117.04
3	E	702	CB3	CB-CA-CT	2.69	116.74	110.35
5	B	704	NDP	O5B-C5B-C4B	2.69	118.15	108.99
2	G	701	UMP	O3'-C3'-C4'	2.67	120.20	110.07
3	A	702	CB3	OE1-CD-CG	-2.66	114.64	123.09
3	E	702	CB3	C9-N10-C14	2.65	125.32	120.72
5	A	704	NDP	C5A-C6A-N6A	-2.65	116.72	123.29
5	C	704	NDP	C4B-O4B-C1B	2.65	115.31	109.47
3	B	702	CB3	C9-N10-C14	2.65	125.31	120.72
4	D	703	FOL	C6-C7-N8	-2.64	120.61	123.14
5	E	704	NDP	C5A-C6A-N6A	-2.63	116.77	123.29
4	H	703	FOL	CB-CA-N	-2.63	105.70	110.91
5	D	704	NDP	C4A-N9A-C1B	2.62	132.77	126.63
5	D	704	NDP	C5A-C6A-N6A	-2.61	116.82	123.29
2	B	701	UMP	C3'-C2'-C1'	-2.61	96.21	102.60
5	G	704	NDP	C2D-C3D-C4D	2.60	107.64	102.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	704	NDP	C4B-O4B-C1B	2.60	115.21	109.47
5	D	704	NDP	O5B-C5B-C4B	2.60	117.85	108.99
5	B	704	NDP	PN-O5D-C5D	-2.60	106.47	121.35
3	E	702	CB3	CP2-CP1-N10	-2.59	111.06	113.45
5	F	704	NDP	C5A-C6A-N6A	-2.59	116.87	123.29
5	H	704	NDP	C5A-C6A-N6A	-2.59	116.88	123.29
5	F	704	NDP	O5B-C5B-C4B	2.59	117.80	108.99
3	H	702	CB3	C9-N10-C14	2.58	125.20	120.72
2	F	701	UMP	C3'-C2'-C1'	-2.58	96.28	102.60
3	E	702	CB3	OE1-CD-CG	-2.56	114.98	123.09
4	D	703	FOL	C7-C6-N5	-2.56	119.21	120.87
5	E	704	NDP	C2D-C3D-C4D	2.55	107.53	102.61
5	G	704	NDP	C5A-C6A-N6A	-2.55	116.98	123.29
2	A	701	UMP	O3'-C3'-C4'	2.55	119.72	110.07
5	C	704	NDP	C2D-C3D-C4D	2.53	107.51	102.61
5	C	704	NDP	C5A-C6A-N6A	-2.53	117.02	123.29
3	H	702	CB3	CT-CA-N	2.53	116.43	110.57
4	B	703	FOL	CB-CG-CD	-2.53	105.75	112.49
2	H	701	UMP	C3'-C2'-C1'	-2.52	96.42	102.60
3	C	702	CB3	CB-CA-N	2.52	115.90	110.91
5	F	704	NDP	O2B-C2B-C1B	2.52	118.91	110.05
4	A	703	FOL	CG-CB-CA	-2.51	108.53	113.16
5	F	704	NDP	C2D-C1D-N1N	-2.50	107.15	113.31
4	B	703	FOL	N1-C8A-N8	2.50	120.11	116.38
4	B	703	FOL	OE1-CD-CG	-2.48	115.22	123.09
3	F	702	CB3	C9-N10-C14	2.47	125.01	120.72
5	B	704	NDP	C4B-O4B-C1B	2.47	114.92	109.47
5	B	704	NDP	O3B-C3B-C4B	-2.47	103.99	111.08
5	D	704	NDP	C4B-O4B-C1B	2.47	114.92	109.47
3	D	702	CB3	C9-N10-C14	2.46	124.98	120.72
5	B	704	NDP	O2B-C2B-C1B	2.44	118.63	110.05
5	D	704	NDP	O2D-C2D-C3D	-2.43	104.02	111.82
5	A	704	NDP	O5B-C5B-C4B	2.42	117.25	108.99
3	G	702	CB3	O-C-C11	-2.42	116.10	120.90
4	C	703	FOL	O1-CT-CA	-2.42	114.45	122.26
3	B	702	CB3	C4A-C8A-N1	2.42	121.35	119.46
4	C	703	FOL	CA-N-C	2.41	127.35	121.56
2	E	701	UMP	C3'-C2'-C1'	-2.38	96.77	102.60
4	E	703	FOL	C9-C6-N5	2.38	121.05	116.56
4	B	703	FOL	C6-C7-N8	-2.38	120.86	123.14
2	H	701	UMP	OP2-P-O5'	-2.36	100.51	106.67
5	F	704	NDP	C4A-N9A-C8A	-2.36	103.26	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	704	NDP	C2D-C3D-C4D	2.35	107.14	102.61
2	D	701	UMP	C3'-C2'-C1'	-2.34	96.86	102.60
3	F	702	CB3	CG-CB-CA	2.34	117.47	113.16
4	F	703	FOL	C6-C9-N10	2.33	118.25	113.13
5	D	704	NDP	O3B-C3B-C4B	-2.33	104.39	111.08
3	C	702	CB3	C9-N10-C14	2.32	124.75	120.72
4	B	703	FOL	C9-C6-N5	2.31	120.93	116.56
2	F	701	UMP	OP2-P-O5'	-2.31	100.65	106.67
5	E	704	NDP	O5B-C5B-C4B	2.29	116.79	108.99
2	A	701	UMP	OP3-P-OP2	2.28	116.36	107.80
2	E	701	UMP	OP3-P-OP2	2.28	116.35	107.80
3	D	702	CB3	O-C-N	2.28	126.80	122.47
2	G	701	UMP	OP3-P-OP2	2.28	116.33	107.80
4	E	703	FOL	C4-C4A-N5	-2.26	114.98	118.55
2	G	701	UMP	C3'-C2'-C1'	-2.26	97.07	102.60
5	A	704	NDP	C4A-N9A-C8A	-2.25	103.37	105.74
2	C	701	UMP	OP3-P-OP2	2.25	116.25	107.80
4	F	703	FOL	CB-CA-CT	-2.25	105.01	110.35
2	C	701	UMP	C3'-C2'-C1'	-2.24	97.11	102.60
3	F	702	CB3	CT-CA-N	2.24	115.76	110.57
3	G	702	CB3	OE2-CD-CG	2.24	121.06	114.00
4	G	703	FOL	C4-C4A-N5	-2.22	115.05	118.55
5	F	704	NDP	C4B-O4B-C1B	2.22	114.36	109.47
3	H	702	CB3	CB-CA-N	-2.21	106.53	110.91
5	E	704	NDP	O3B-C3B-C2B	-2.21	105.00	111.19
2	A	701	UMP	C2'-C3'-C4'	-2.20	98.33	102.80
3	F	702	CB3	C11-C-N	-2.19	112.98	117.04
4	E	703	FOL	NA2-C2-N1	2.19	121.37	116.77
5	G	704	NDP	O5B-C5B-C4B	2.18	116.43	108.99
2	H	701	UMP	O2-C2-N3	-2.18	117.46	121.49
4	A	703	FOL	CB-CA-CT	-2.17	105.21	110.35
5	E	704	NDP	O2B-P2B-O1X	-2.17	101.62	109.33
5	H	704	NDP	C1B-N9A-C8A	-2.16	122.30	127.09
4	H	703	FOL	OE1-CD-CG	-2.15	116.27	123.09
5	C	704	NDP	O5B-C5B-C4B	2.15	116.31	108.99
2	B	701	UMP	OP3-P-OP2	2.15	115.86	107.80
2	D	701	UMP	C2'-C3'-C4'	-2.14	98.46	102.80
5	H	704	NDP	O3B-C3B-C2B	-2.14	105.20	111.19
4	G	703	FOL	O1-CT-CA	-2.14	115.36	122.26
4	A	703	FOL	NA2-C2-N1	2.13	121.25	116.77
5	E	704	NDP	O5D-C5D-C4D	-2.13	101.75	108.99
5	G	704	NDP	O2B-P2B-O1X	-2.12	101.76	109.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	704	NDP	C4A-N9A-C8A	-2.11	103.53	105.74
3	B	702	CB3	CG-CB-CA	2.10	117.04	113.16
5	B	704	NDP	N3A-C4A-N9A	2.10	130.74	127.17
4	G	703	FOL	NA2-C2-N1	2.10	121.19	116.77
4	C	703	FOL	NA2-C2-N1	2.10	121.19	116.77
3	D	702	CB3	CG-CB-CA	2.09	117.02	113.16
5	C	704	NDP	C4A-N9A-C8A	-2.09	103.55	105.74
4	E	703	FOL	C16-C15-C14	2.08	122.70	120.30
3	A	702	CB3	CB-CA-N	2.08	115.02	110.91
2	A	701	UMP	C3'-C2'-C1'	-2.07	97.54	102.60
2	E	701	UMP	C2'-C3'-C4'	-2.06	98.62	102.80
2	F	701	UMP	OP3-P-OP2	2.06	115.51	107.80
4	E	703	FOL	C9-N10-C14	2.05	128.45	121.87
4	D	703	FOL	OE1-CD-CG	-2.05	116.60	123.09
2	B	701	UMP	O2-C2-N3	-2.04	117.73	121.49
3	D	702	CB3	NA2-C2-N1	2.03	121.05	116.77
3	G	702	CB3	O1-CT-CA	-2.03	115.70	122.26
5	C	704	NDP	O5D-C5D-C4D	-2.03	102.08	108.99
5	H	704	NDP	C2D-C1D-N1N	-2.03	108.31	113.31
2	G	701	UMP	C2'-C3'-C4'	-2.02	98.69	102.80
2	D	701	UMP	O2-C2-N3	-2.02	117.77	121.49
5	H	704	NDP	O2D-C2D-C3D	-2.02	105.36	111.82
3	E	702	CB3	O1-CT-CA	-2.01	115.76	122.26
2	D	701	UMP	OP2-P-O5'	-2.01	101.42	106.67
3	B	702	CB3	CB-CG-CD	-2.01	107.14	112.49
5	B	704	NDP	O3-PN-O1N	2.01	116.74	110.70
5	E	704	NDP	C4A-N9A-C8A	-2.00	103.64	105.74

There are no chirality outliers.

All (158) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	UMP	C5'-O5'-P-OP2
2	A	701	UMP	C5'-O5'-P-OP3
2	B	701	UMP	C5'-O5'-P-OP3
2	C	701	UMP	C5'-O5'-P-OP1
2	C	701	UMP	C5'-O5'-P-OP2
2	C	701	UMP	C5'-O5'-P-OP3
2	E	701	UMP	C5'-O5'-P-OP2
2	E	701	UMP	C5'-O5'-P-OP3
2	F	701	UMP	C5'-O5'-P-OP2
2	F	701	UMP	C5'-O5'-P-OP3

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Mol	Chain	Res	Type	Atoms
2	G	701	UMP	C5'-O5'-P-OP1
2	G	701	UMP	C5'-O5'-P-OP2
2	G	701	UMP	C5'-O5'-P-OP3
2	H	701	UMP	C5'-O5'-P-OP2
2	H	701	UMP	C5'-O5'-P-OP3
5	A	704	NDP	O4B-C4B-C5B-O5B
5	A	704	NDP	C5D-O5D-PN-O2N
5	B	704	NDP	O4D-C1D-N1N-C2N
5	C	704	NDP	O4B-C4B-C5B-O5B
5	C	704	NDP	C5D-O5D-PN-O2N
5	D	704	NDP	O4B-C4B-C5B-O5B
5	D	704	NDP	C5D-O5D-PN-O2N
5	E	704	NDP	O4B-C4B-C5B-O5B
5	E	704	NDP	C5D-O5D-PN-O2N
5	F	704	NDP	O4B-C4B-C5B-O5B
5	F	704	NDP	O4D-C1D-N1N-C2N
5	G	704	NDP	O4B-C4B-C5B-O5B
5	G	704	NDP	C5D-O5D-PN-O2N
5	H	704	NDP	O4B-C4B-C5B-O5B
5	H	704	NDP	O4D-C1D-N1N-C2N
3	A	702	CB3	CB-CA-N-C
3	G	702	CB3	CB-CA-N-C
3	D	702	CB3	CT-CA-N-C
3	F	702	CB3	CT-CA-N-C
5	B	704	NDP	O4B-C4B-C5B-O5B
5	B	704	NDP	C3D-C4D-C5D-O5D
5	F	704	NDP	C3D-C4D-C5D-O5D
5	H	704	NDP	C3D-C4D-C5D-O5D
2	A	701	UMP	C3'-C4'-C5'-O5'
2	B	701	UMP	C3'-C4'-C5'-O5'
2	C	701	UMP	C3'-C4'-C5'-O5'
2	E	701	UMP	C3'-C4'-C5'-O5'
2	F	701	UMP	C3'-C4'-C5'-O5'
2	G	701	UMP	C3'-C4'-C5'-O5'
2	H	701	UMP	C3'-C4'-C5'-O5'
3	E	702	CB3	CB-CA-N-C
3	C	702	CB3	N-CA-CT-O1
2	D	701	UMP	C3'-C4'-C5'-O5'
3	A	702	CB3	CT-CA-N-C
3	C	702	CB3	N-CA-CT-O2
3	E	702	CB3	N-CA-CT-O1
3	E	702	CB3	N-CA-CT-O2

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Mol	Chain	Res	Type	Atoms
3	G	702	CB3	N-CA-CT-O1
3	G	702	CB3	CT-CA-N-C
3	E	702	CB3	CA-CB-CG-CD
3	G	702	CB3	CT-CA-CB-CG
2	A	701	UMP	C5'-O5'-P-OP1
3	G	702	CB3	N-CA-CT-O2
5	A	704	NDP	C2D-C1D-N1N-C2N
5	C	704	NDP	C2D-C1D-N1N-C2N
5	D	704	NDP	C2D-C1D-N1N-C2N
5	E	704	NDP	C2D-C1D-N1N-C2N
5	G	704	NDP	C2D-C1D-N1N-C2N
5	A	704	NDP	C3D-C4D-C5D-O5D
3	A	702	CB3	CT-CA-CB-CG
5	C	704	NDP	C3D-C4D-C5D-O5D
5	E	704	NDP	C3D-C4D-C5D-O5D
3	H	702	CB3	CB-CA-CT-O2
5	G	704	NDP	C3D-C4D-C5D-O5D
5	G	704	NDP	O4D-C1D-N1N-C6N
5	D	704	NDP	C3D-C4D-C5D-O5D
5	A	704	NDP	C4D-C5D-O5D-PN
3	E	702	CB3	CT-CA-N-C
2	G	701	UMP	C4'-C5'-O5'-P
5	C	704	NDP	C4D-C5D-O5D-PN
5	D	704	NDP	C4D-C5D-O5D-PN
5	G	704	NDP	C4D-C5D-O5D-PN
5	D	704	NDP	O4D-C1D-N1N-C6N
4	B	703	FOL	N-CA-CT-O1
3	C	702	CB3	CB-CA-N-C
5	A	704	NDP	O4D-C1D-N1N-C6N
5	C	704	NDP	O4D-C1D-N1N-C6N
5	E	704	NDP	O4D-C1D-N1N-C6N
3	H	702	CB3	CB-CA-CT-O1
2	C	701	UMP	C4'-C5'-O5'-P
5	E	704	NDP	C4D-C5D-O5D-PN
4	B	703	FOL	N-CA-CT-O2
4	B	703	FOL	CB-CA-N-C
5	D	704	NDP	C2B-O2B-P2B-O3X
5	H	704	NDP	C2B-O2B-P2B-O3X
2	A	701	UMP	C4'-C5'-O5'-P
5	F	704	NDP	C2D-C1D-N1N-C2N
2	E	701	UMP	C4'-C5'-O5'-P
4	G	703	FOL	OE1-CD-CG-CB

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Mol	Chain	Res	Type	Atoms
3	E	702	CB3	OE1-CD-CG-CB
4	G	703	FOL	OE2-CD-CG-CB
4	F	703	FOL	OE1-CD-CG-CB
4	F	703	FOL	OE2-CD-CG-CB
3	C	702	CB3	OE2-CD-CG-CB
3	C	702	CB3	OE1-CD-CG-CB
3	E	702	CB3	OE2-CD-CG-CB
5	D	704	NDP	C2N-C3N-C7N-N7N
5	E	704	NDP	C2N-C3N-C7N-N7N
4	E	703	FOL	OE1-CD-CG-CB
5	B	704	NDP	C2B-O2B-P2B-O1X
5	E	704	NDP	C2B-O2B-P2B-O1X
5	F	704	NDP	C2B-O2B-P2B-O1X
5	G	704	NDP	C2B-O2B-P2B-O1X
5	B	704	NDP	C2D-C1D-N1N-C2N
5	H	704	NDP	C2D-C1D-N1N-C2N
3	B	702	CB3	CB-CA-CT-O1
3	B	702	CB3	CB-CA-CT-O2
3	B	702	CB3	OE2-CD-CG-CB
3	F	702	CB3	OE2-CD-CG-CB
3	C	702	CB3	CT-CA-CB-CG
3	B	702	CB3	OE1-CD-CG-CB
3	F	702	CB3	OE1-CD-CG-CB
4	E	703	FOL	OE2-CD-CG-CB
2	D	701	UMP	C5'-O5'-P-OP3
2	E	701	UMP	C5'-O5'-P-OP1
3	C	702	CB3	CA-CB-CG-CD
4	B	703	FOL	OE2-CD-CG-CB
5	D	704	NDP	C2D-C1D-N1N-C6N
2	H	701	UMP	C4'-C5'-O5'-P
3	D	702	CB3	OE1-CD-CG-CB
3	D	702	CB3	OE2-CD-CG-CB
5	C	704	NDP	O4D-C1D-N1N-C2N
5	B	704	NDP	PA-O3-PN-O1N
4	D	703	FOL	OE2-CD-CG-CB
4	B	703	FOL	OE1-CD-CG-CB
4	B	703	FOL	CT-CA-N-C
5	G	704	NDP	O4D-C1D-N1N-C2N
3	E	702	CB3	CT-CA-CB-CG
4	H	703	FOL	OE1-CD-CG-CB
3	A	702	CB3	N-CA-CT-O1
4	D	703	FOL	OE1-CD-CG-CB

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Mol	Chain	Res	Type	Atoms
2	D	701	UMP	C4'-C5'-O5'-P
2	F	701	UMP	C4'-C5'-O5'-P
4	C	703	FOL	OE1-CD-CG-CB
5	A	704	NDP	O4D-C1D-N1N-C2N
5	E	704	NDP	O4D-C1D-N1N-C2N
5	A	704	NDP	C2B-O2B-P2B-O1X
5	C	704	NDP	C2B-O2B-P2B-O1X
4	H	703	FOL	OE2-CD-CG-CB
5	A	704	NDP	C2D-C1D-N1N-C6N
5	C	704	NDP	C2D-C1D-N1N-C6N
5	E	704	NDP	C2D-C1D-N1N-C6N
5	D	704	NDP	O4D-C1D-N1N-C2N
3	H	702	CB3	C6-C9-N10-CP1
3	B	702	CB3	CT-CA-CB-CG
5	B	704	NDP	PN-O3-PA-O2A
5	C	704	NDP	PN-O3-PA-O2A
5	F	704	NDP	PN-O3-PA-O2A
5	F	704	NDP	PA-O3-PN-O2N
5	H	704	NDP	PN-O3-PA-O2A
2	A	701	UMP	O4'-C4'-C5'-O5'
2	G	701	UMP	O4'-C4'-C5'-O5'
3	E	702	CB3	C6-C9-N10-CP1

There are no ring outliers.

32 monomers are involved in 104 short contacts:

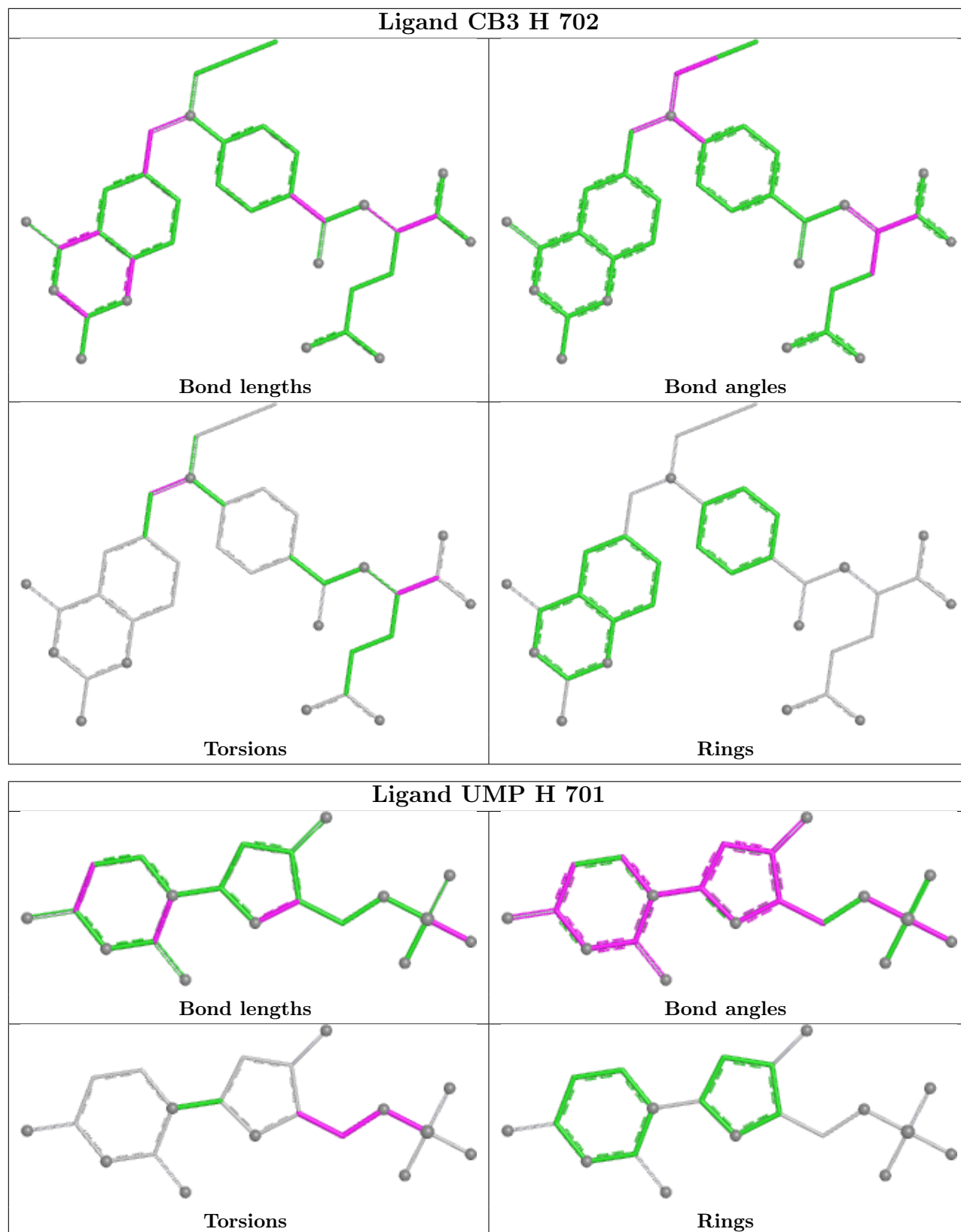
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	702	CB3	4	0
2	H	701	UMP	5	0
3	C	702	CB3	4	0
4	B	703	FOL	2	0
4	E	703	FOL	4	0
2	B	701	UMP	7	0
2	A	701	UMP	3	0
2	E	701	UMP	3	0
5	F	704	NDP	8	0
2	C	701	UMP	4	0
4	F	703	FOL	3	0
5	D	704	NDP	7	0
5	G	704	NDP	3	0
5	E	704	NDP	4	0
4	C	703	FOL	5	0

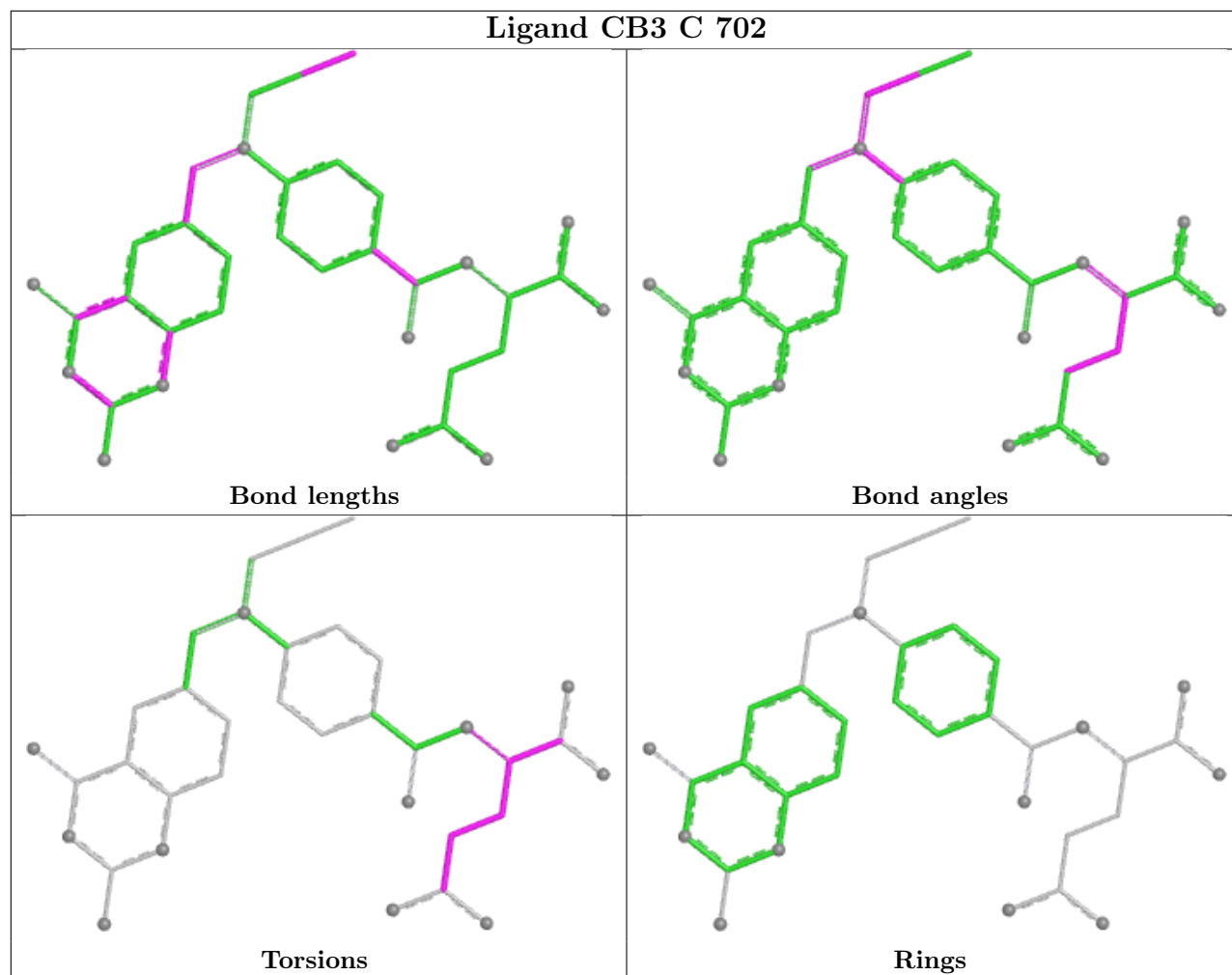
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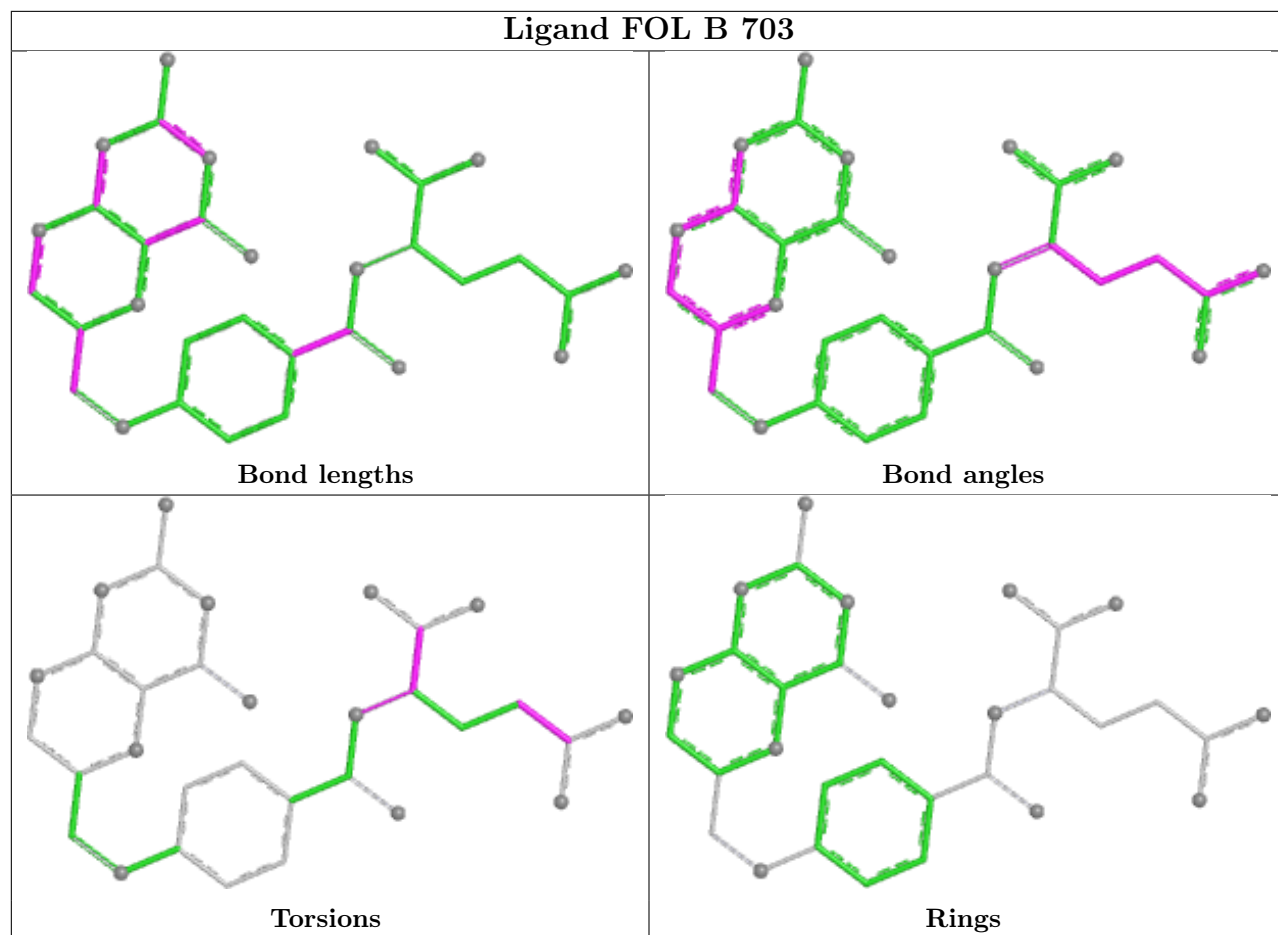
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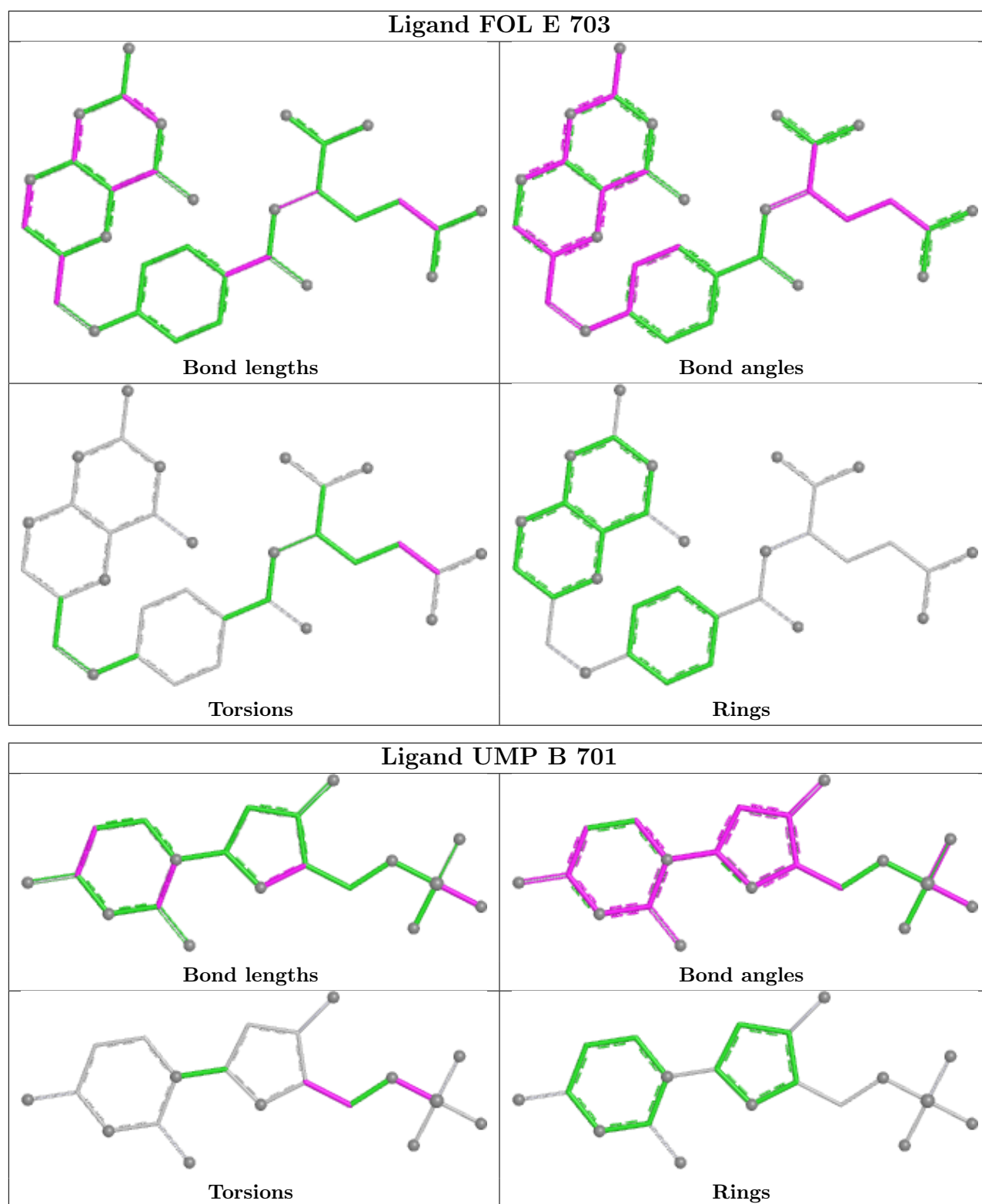
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	704	NDP	3	0
5	C	704	NDP	5	0
3	A	702	CB3	2	0
2	F	701	UMP	4	0
5	H	704	NDP	8	0
5	B	704	NDP	7	0
4	D	703	FOL	2	0
3	B	702	CB3	4	0
3	D	702	CB3	4	0
4	G	703	FOL	4	0
3	F	702	CB3	3	0
2	G	701	UMP	2	0
4	A	703	FOL	4	0
4	H	703	FOL	2	0
3	G	702	CB3	1	0
2	D	701	UMP	4	0
3	E	702	CB3	1	0

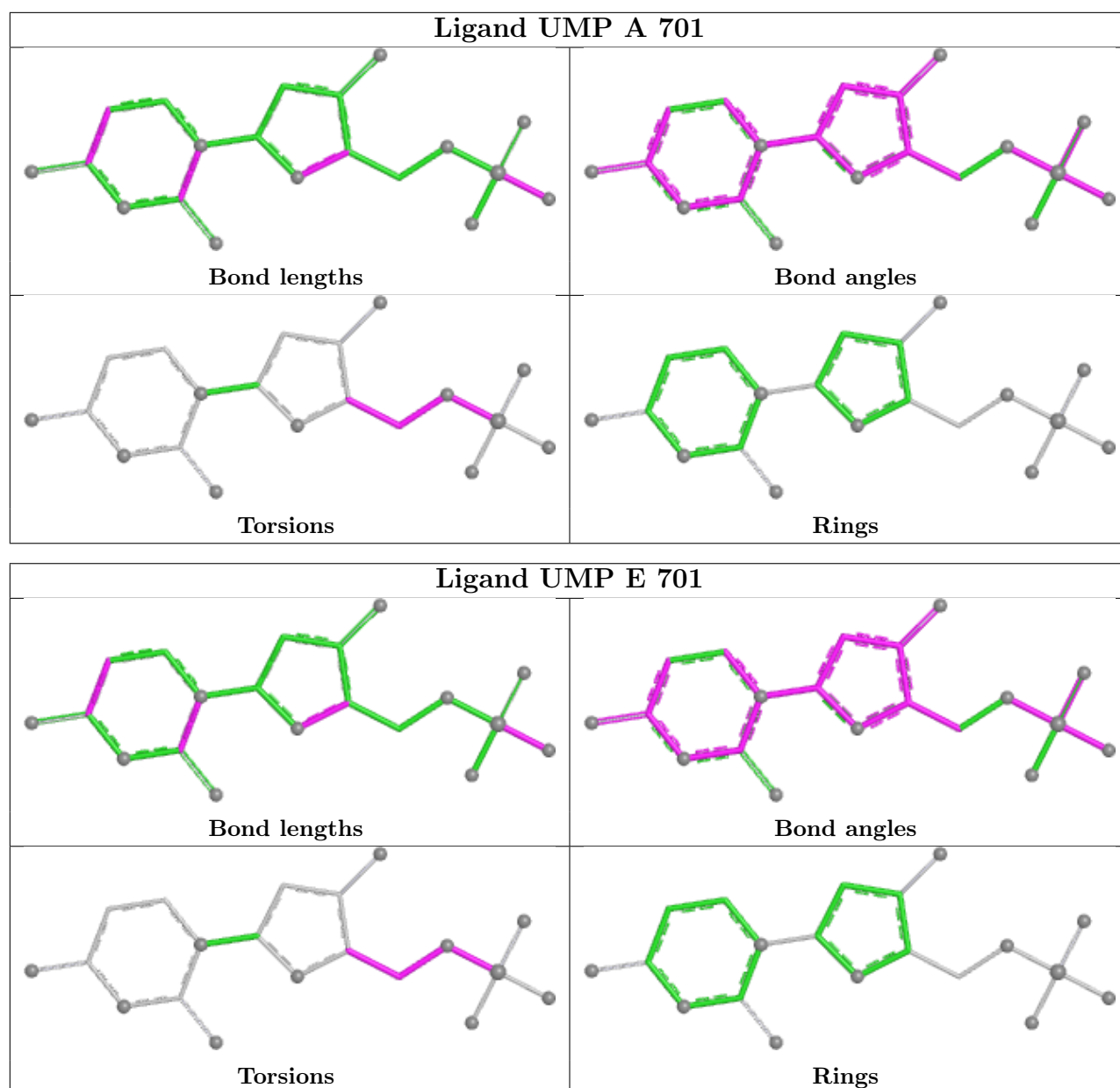
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

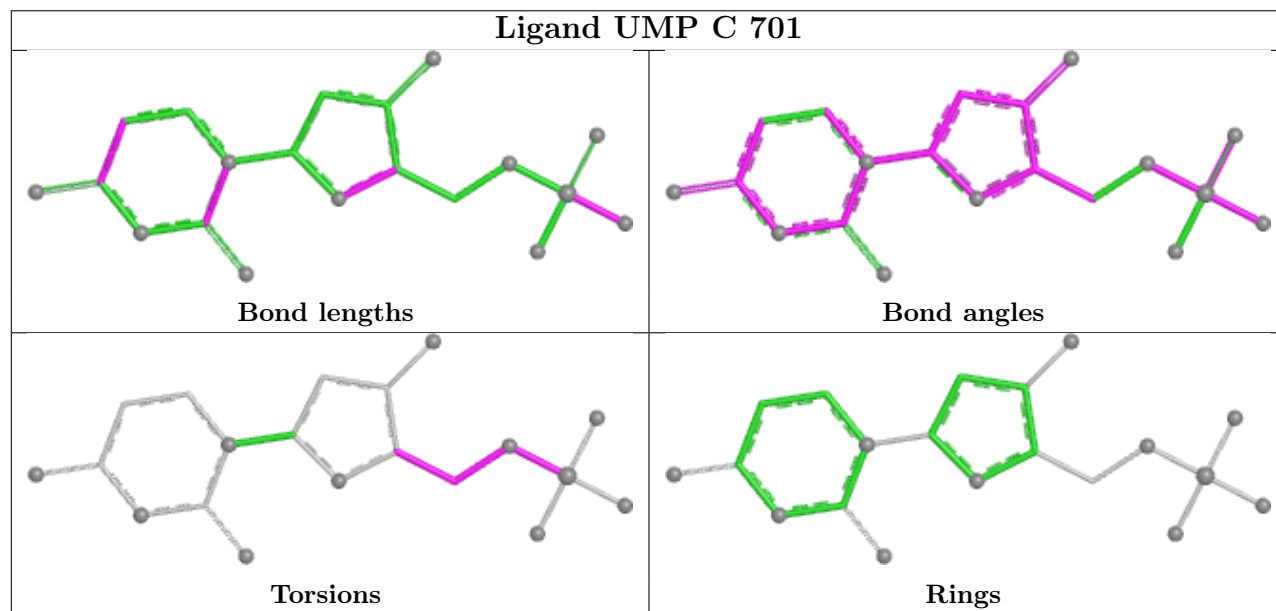
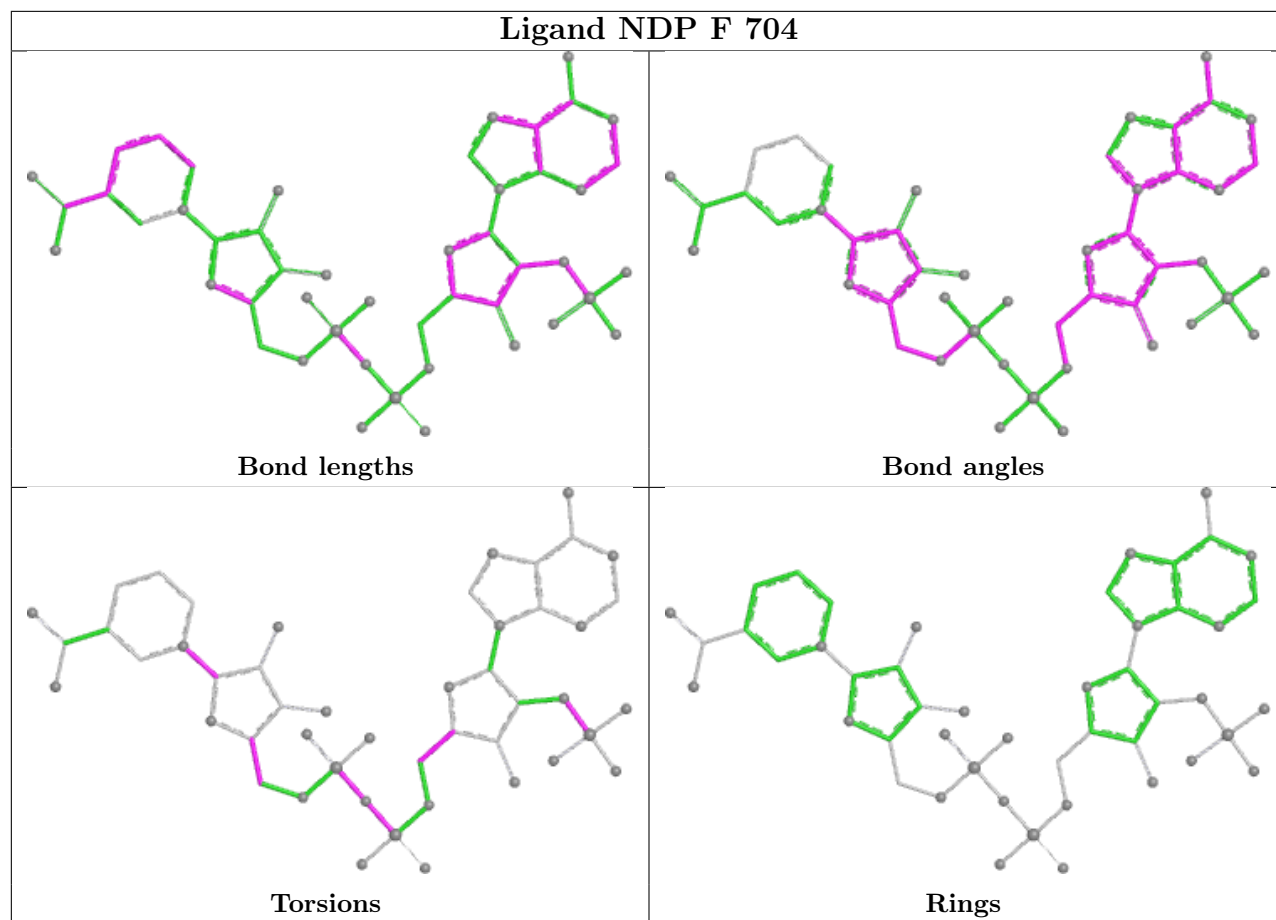


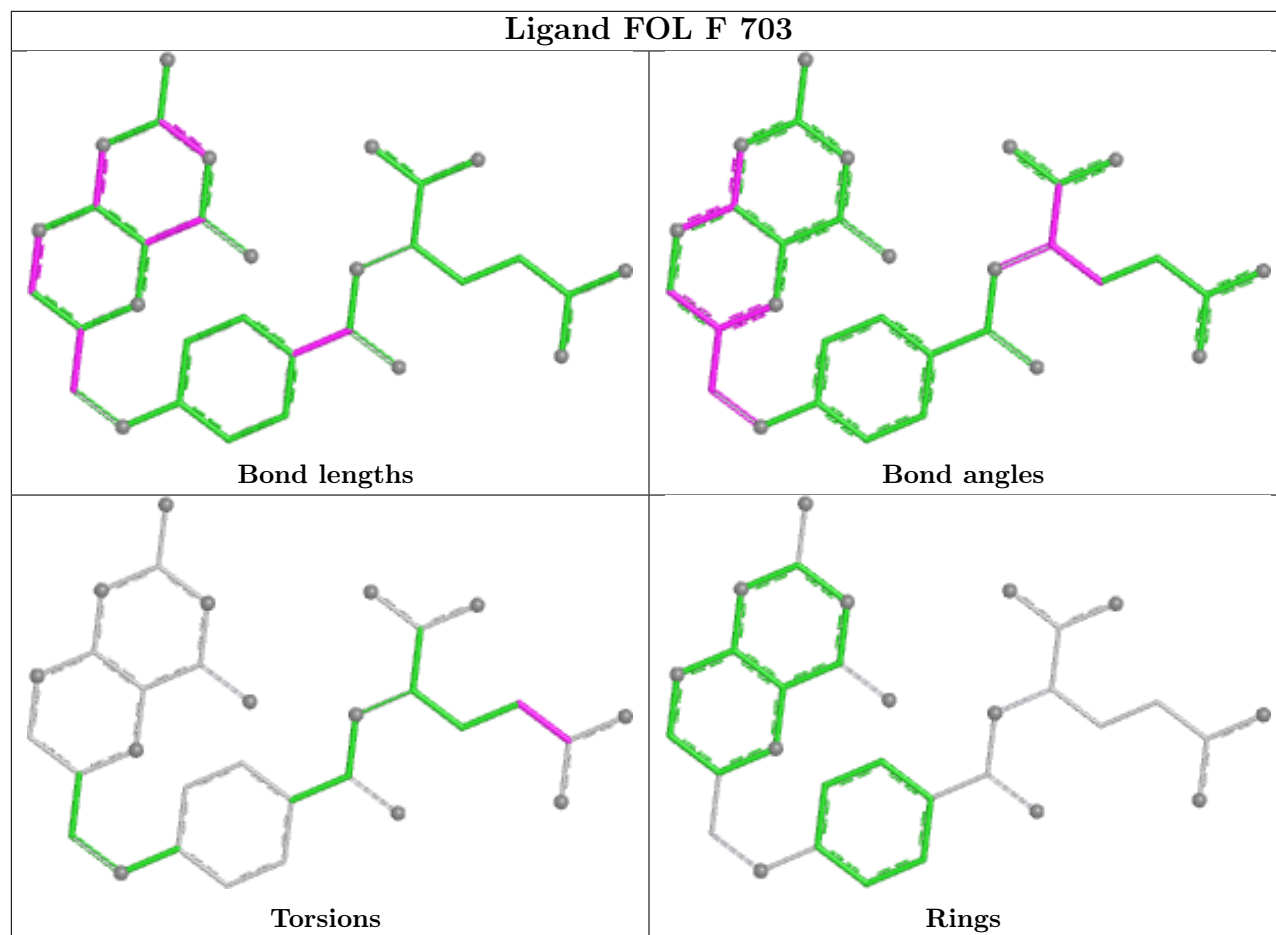


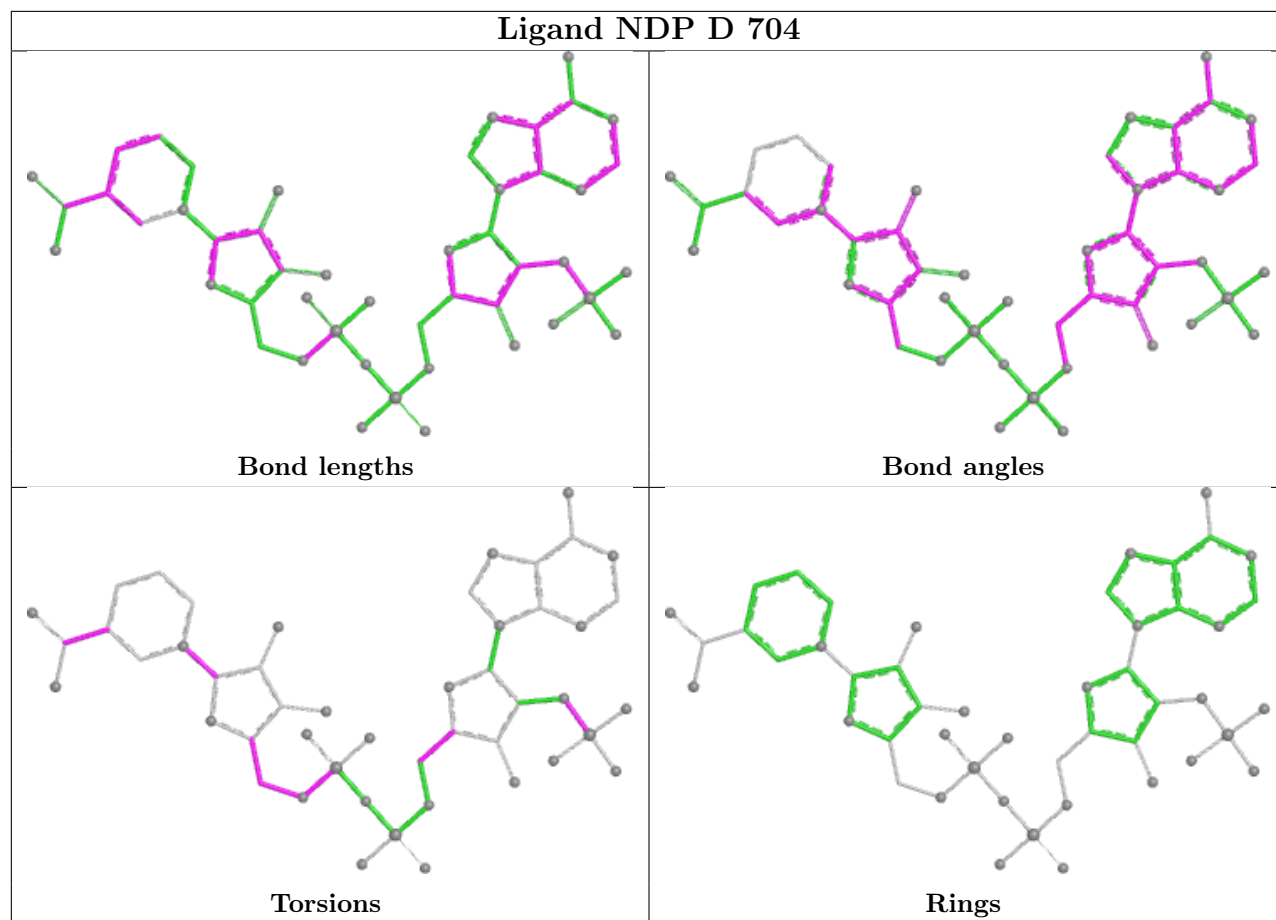


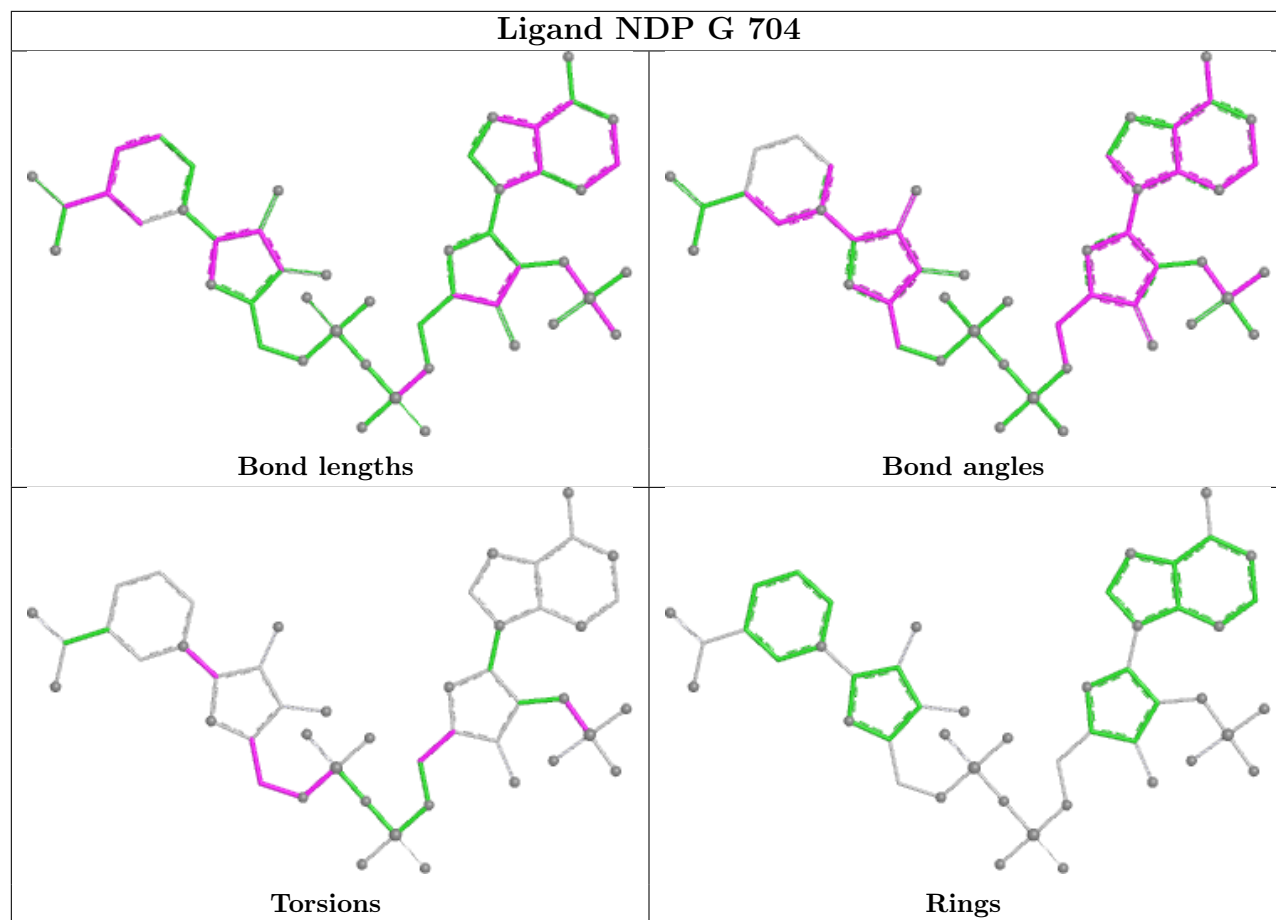


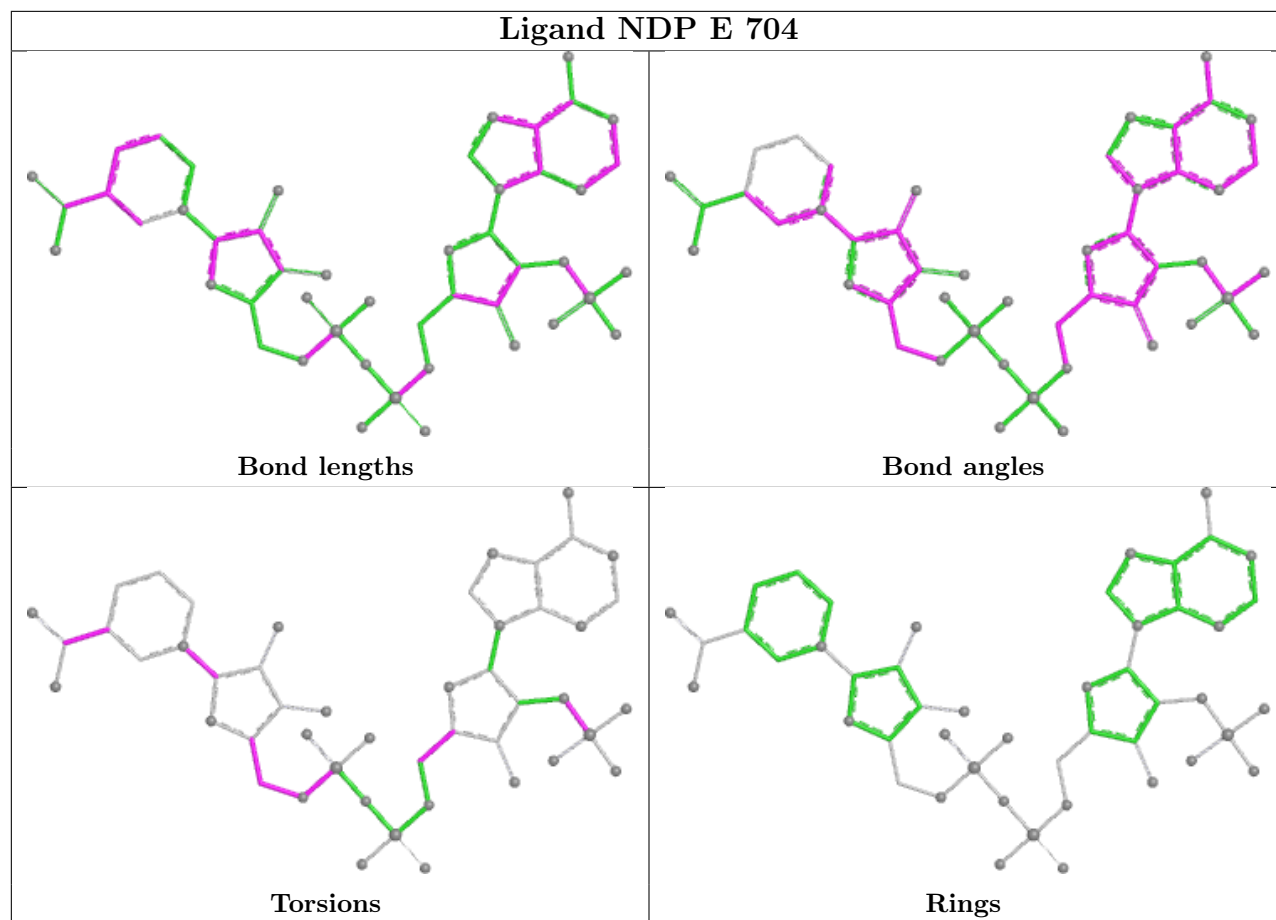


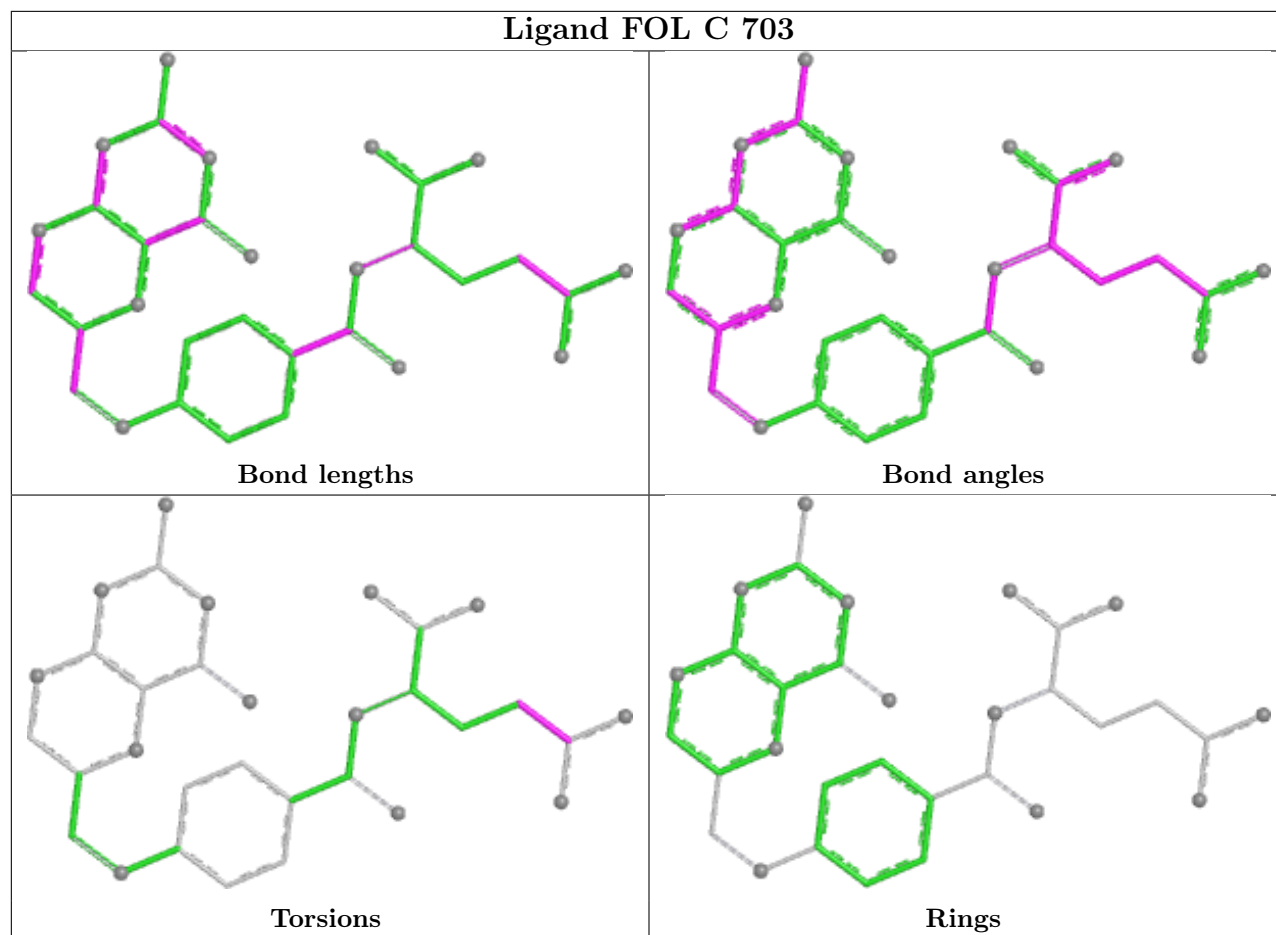


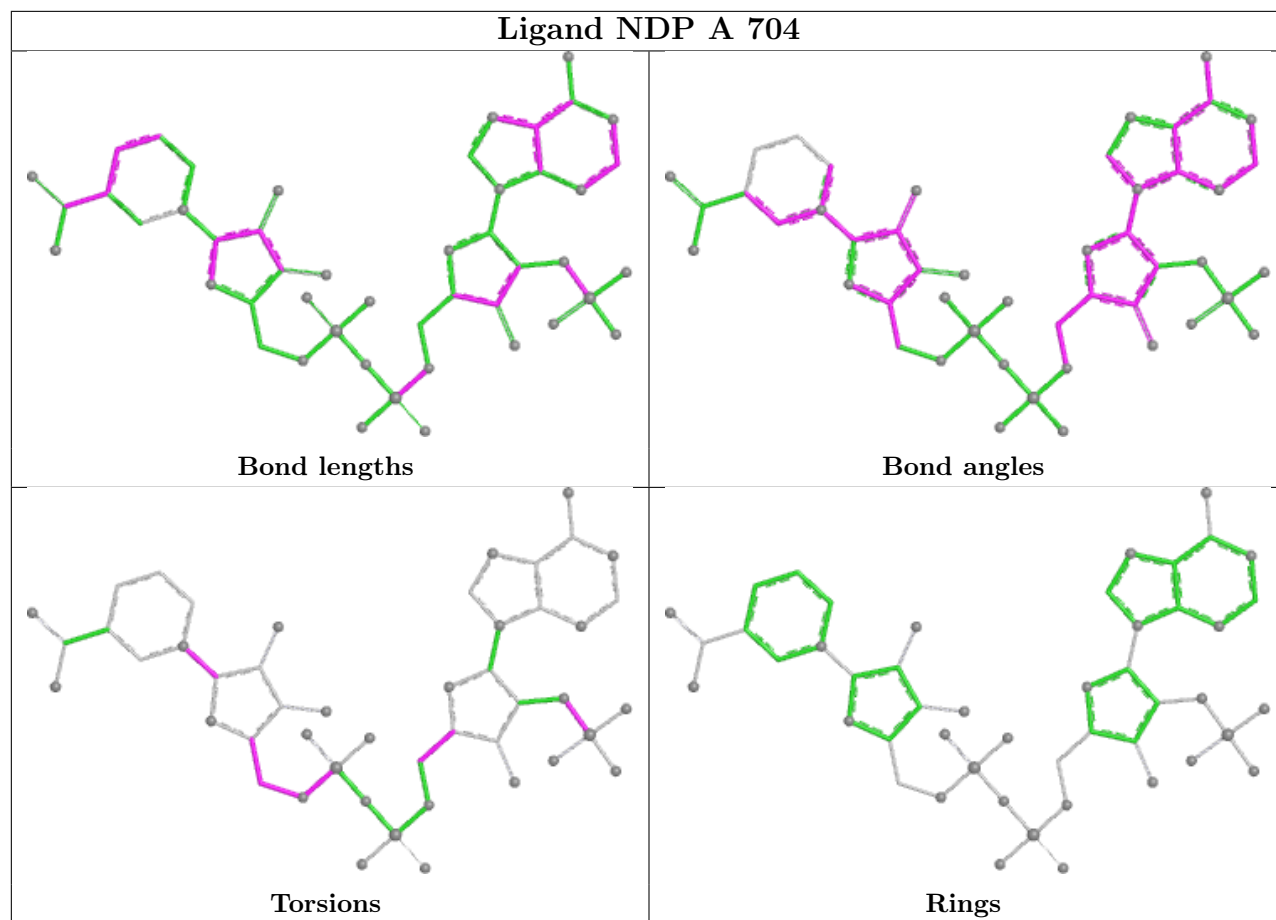


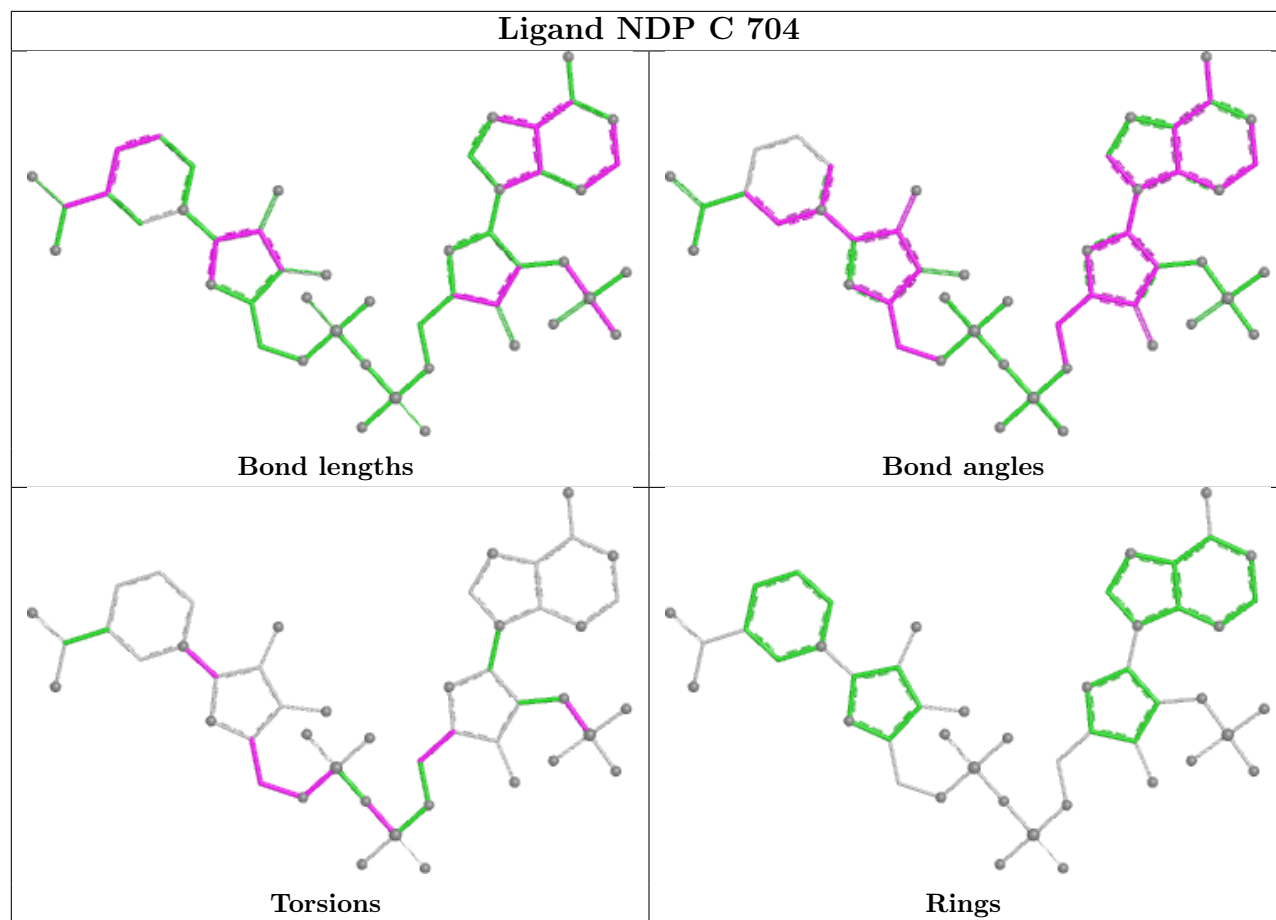


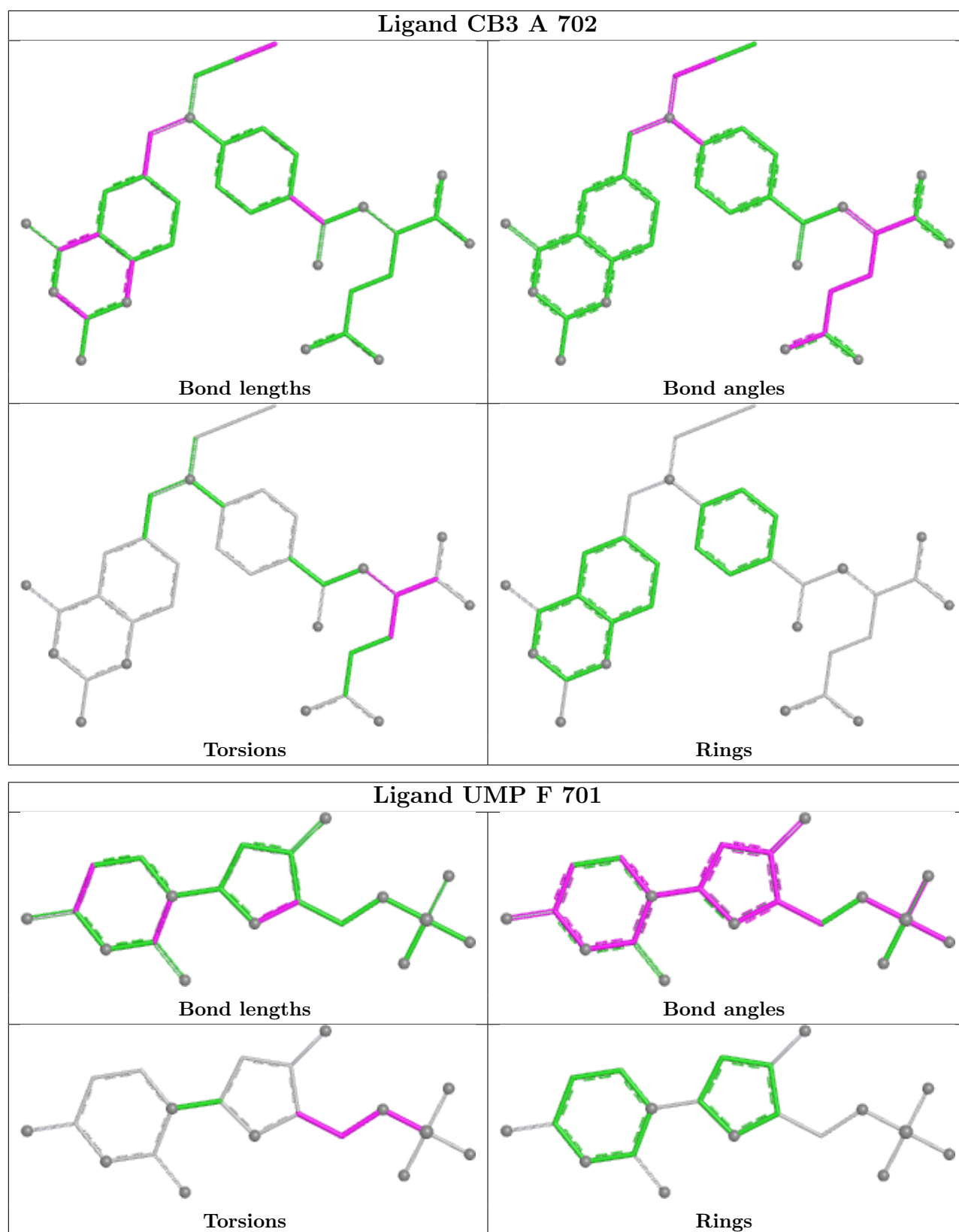


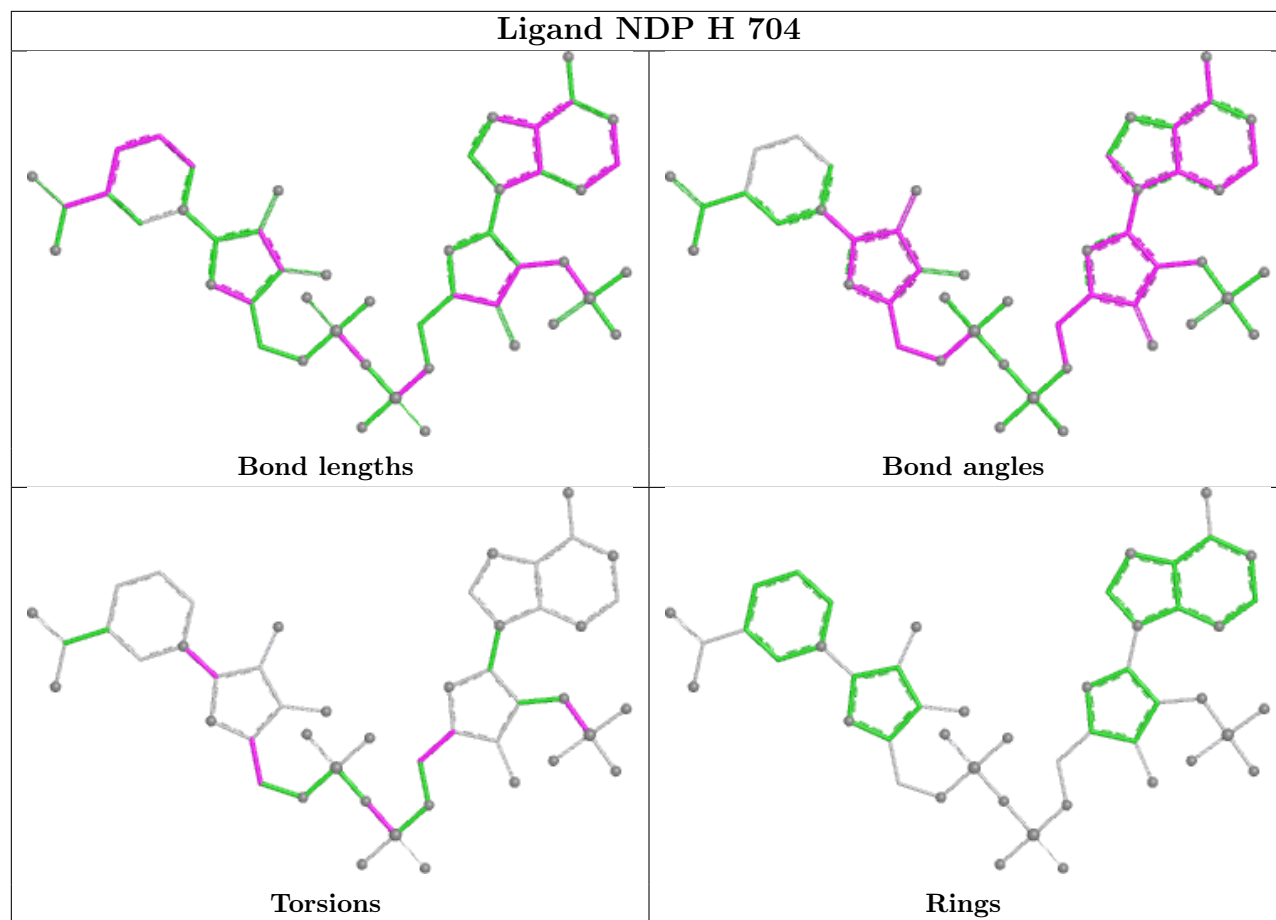


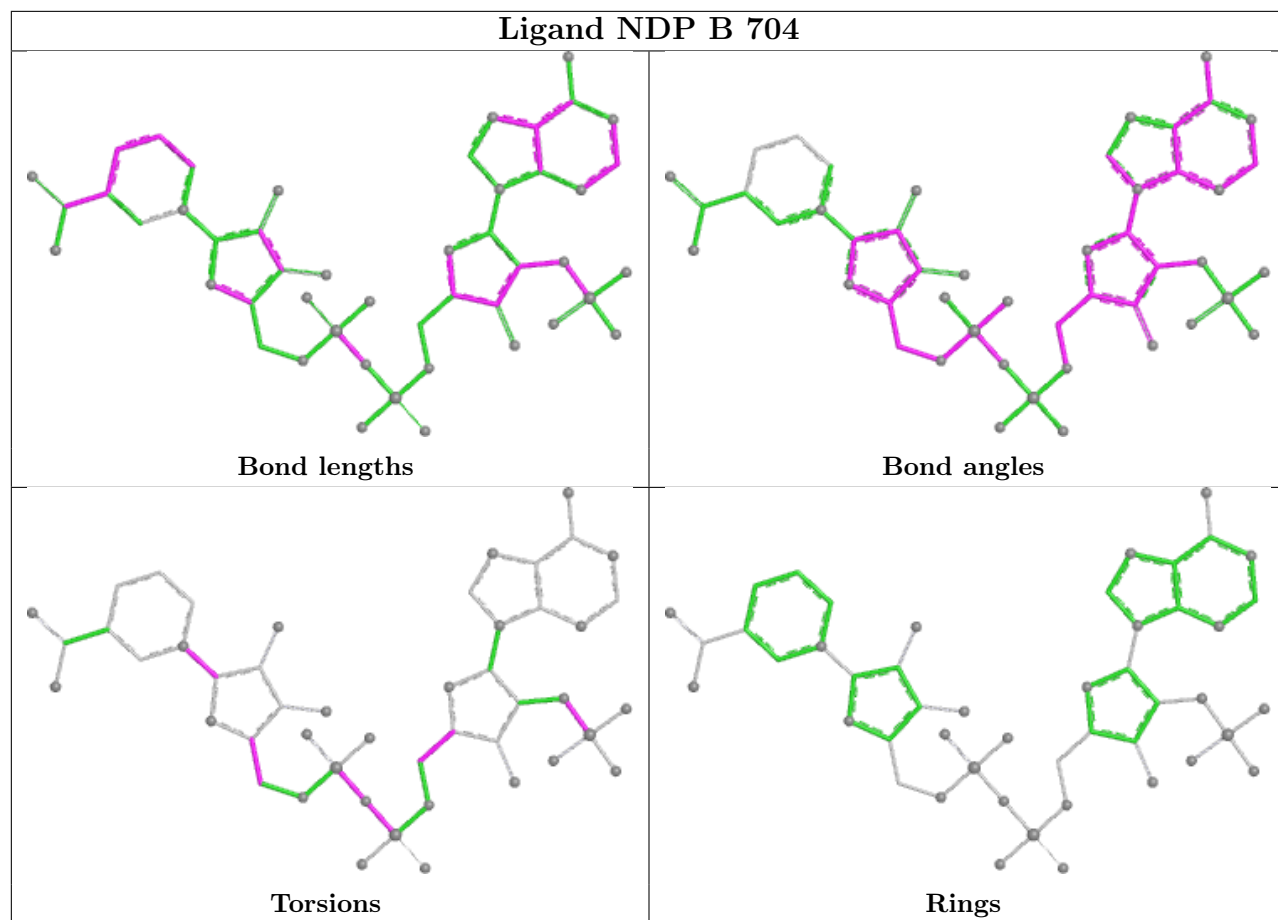


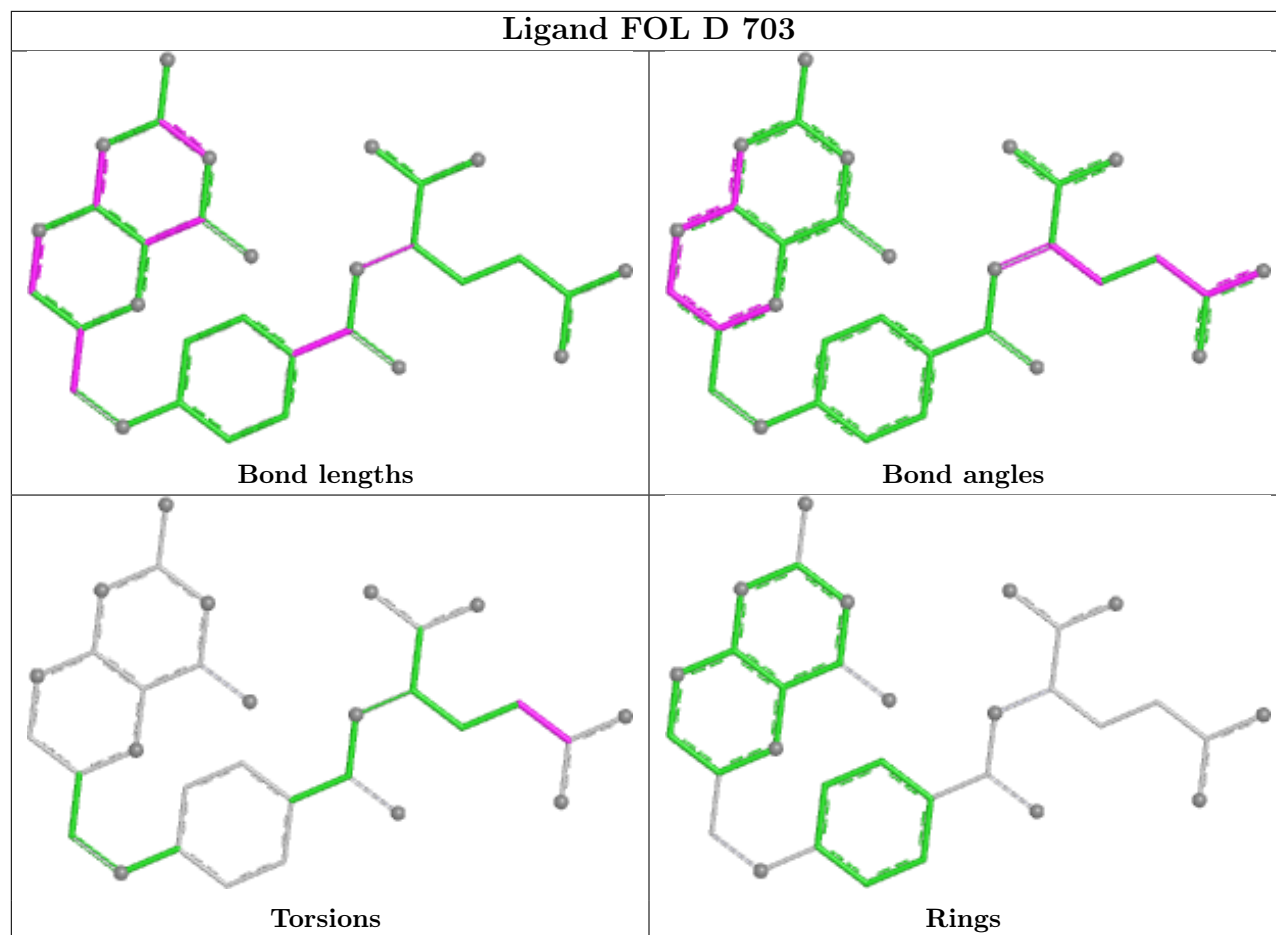


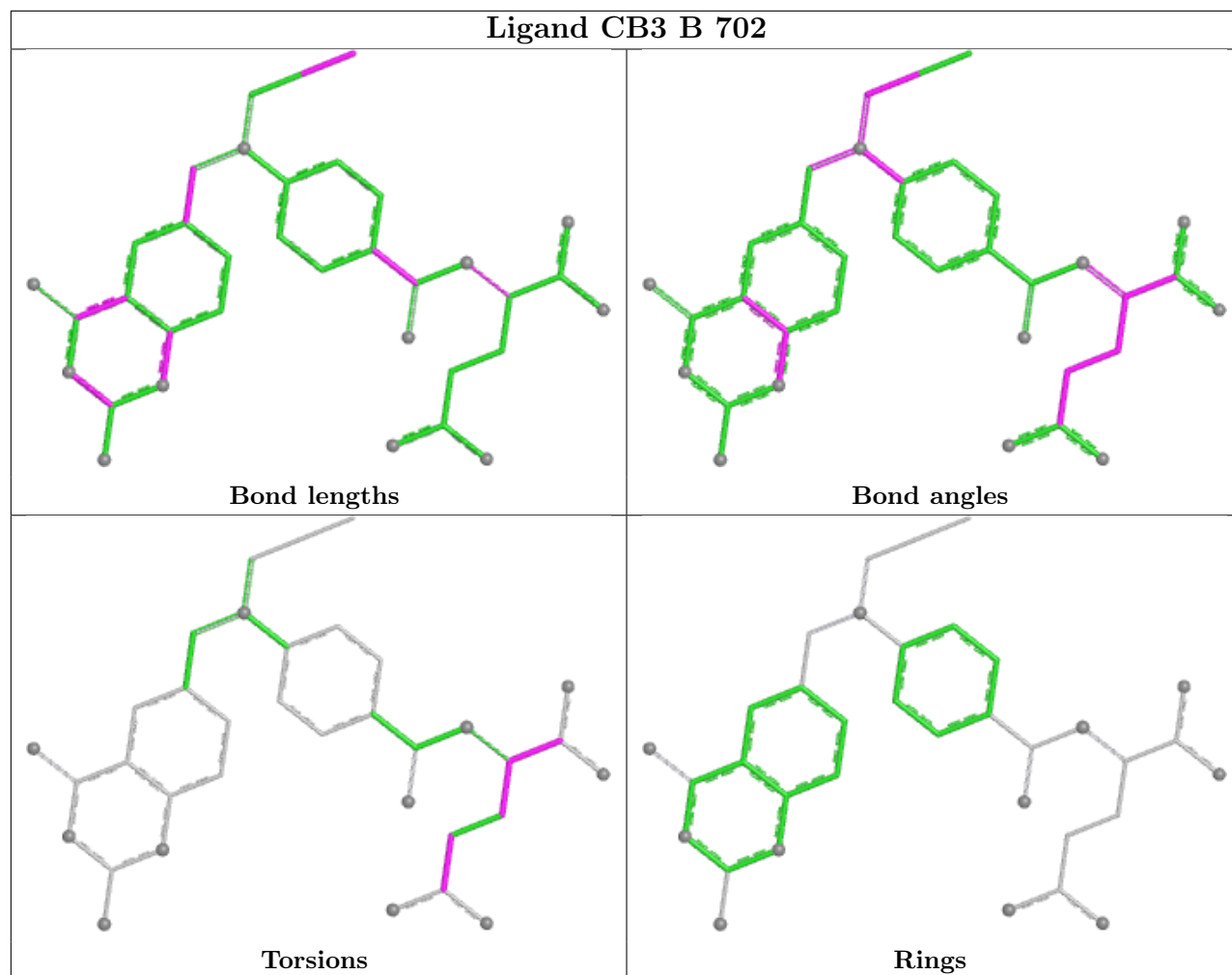


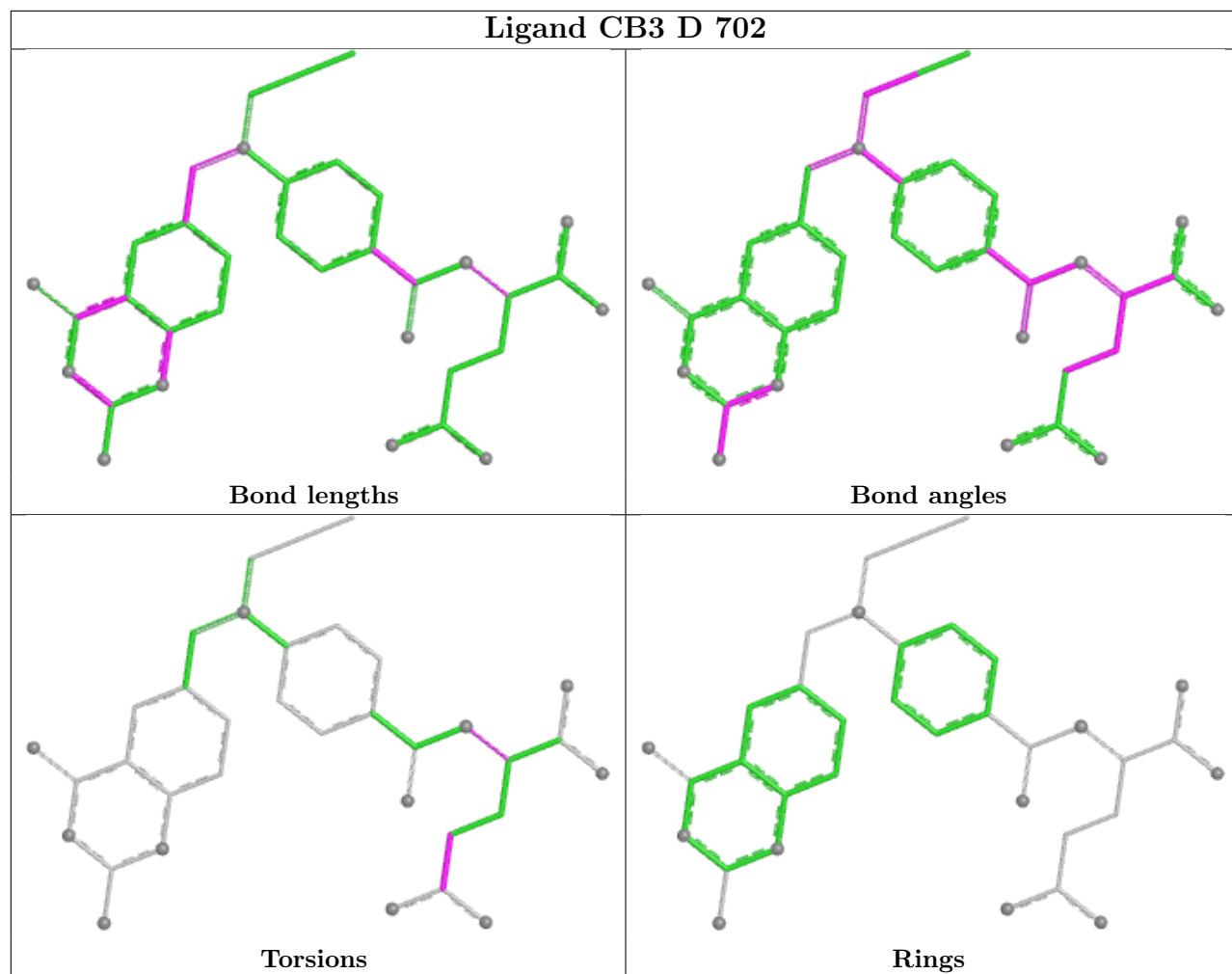


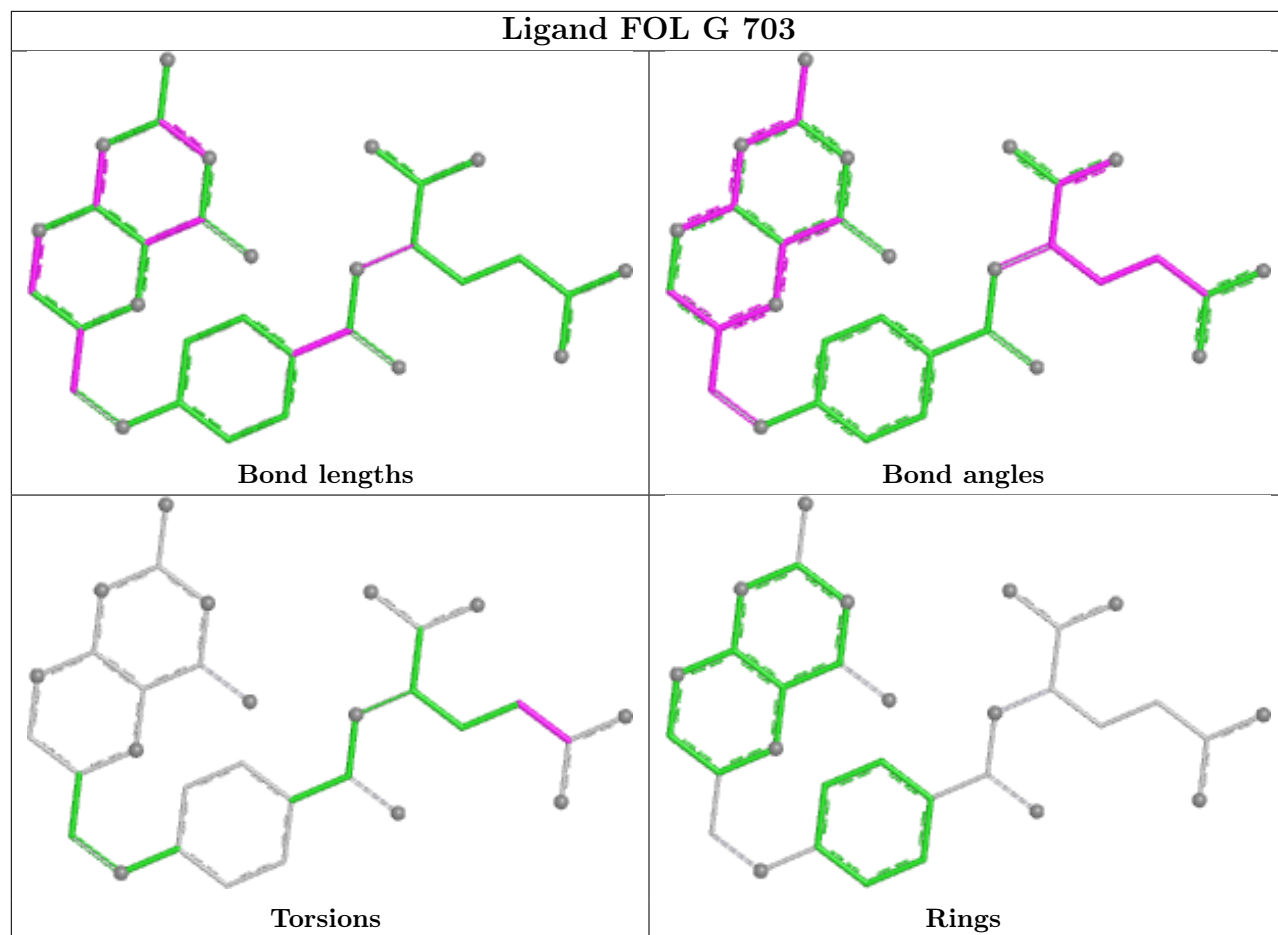


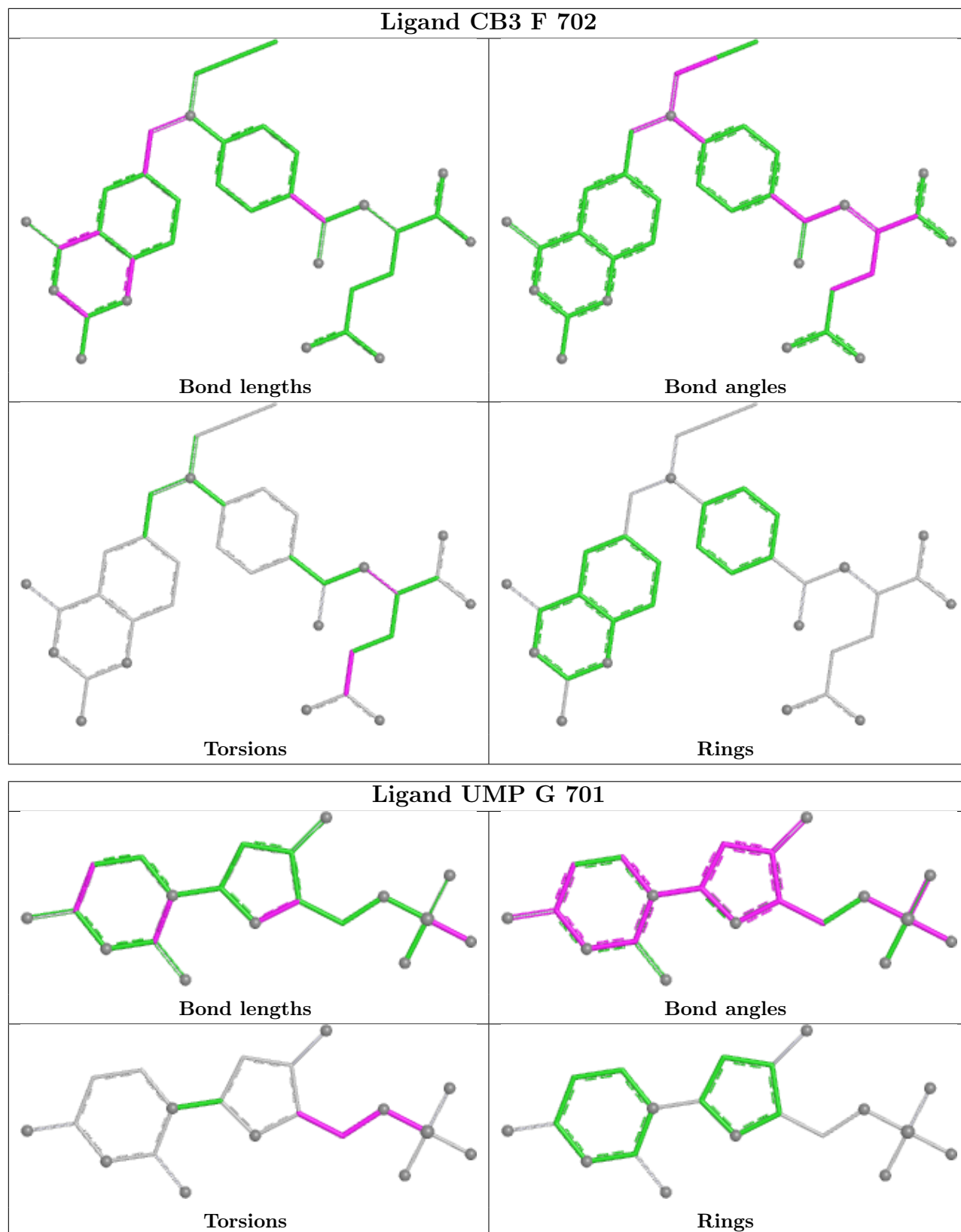


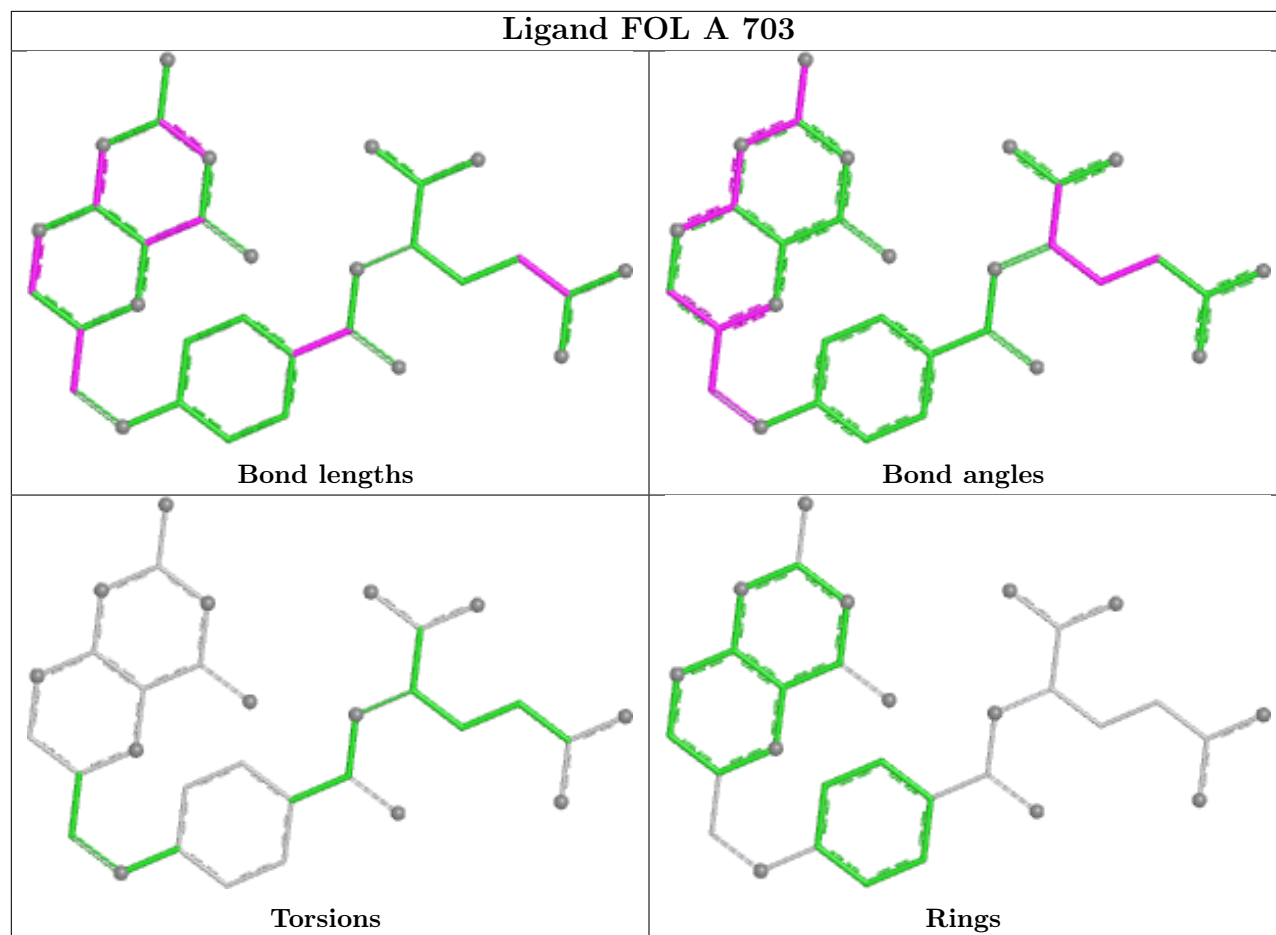


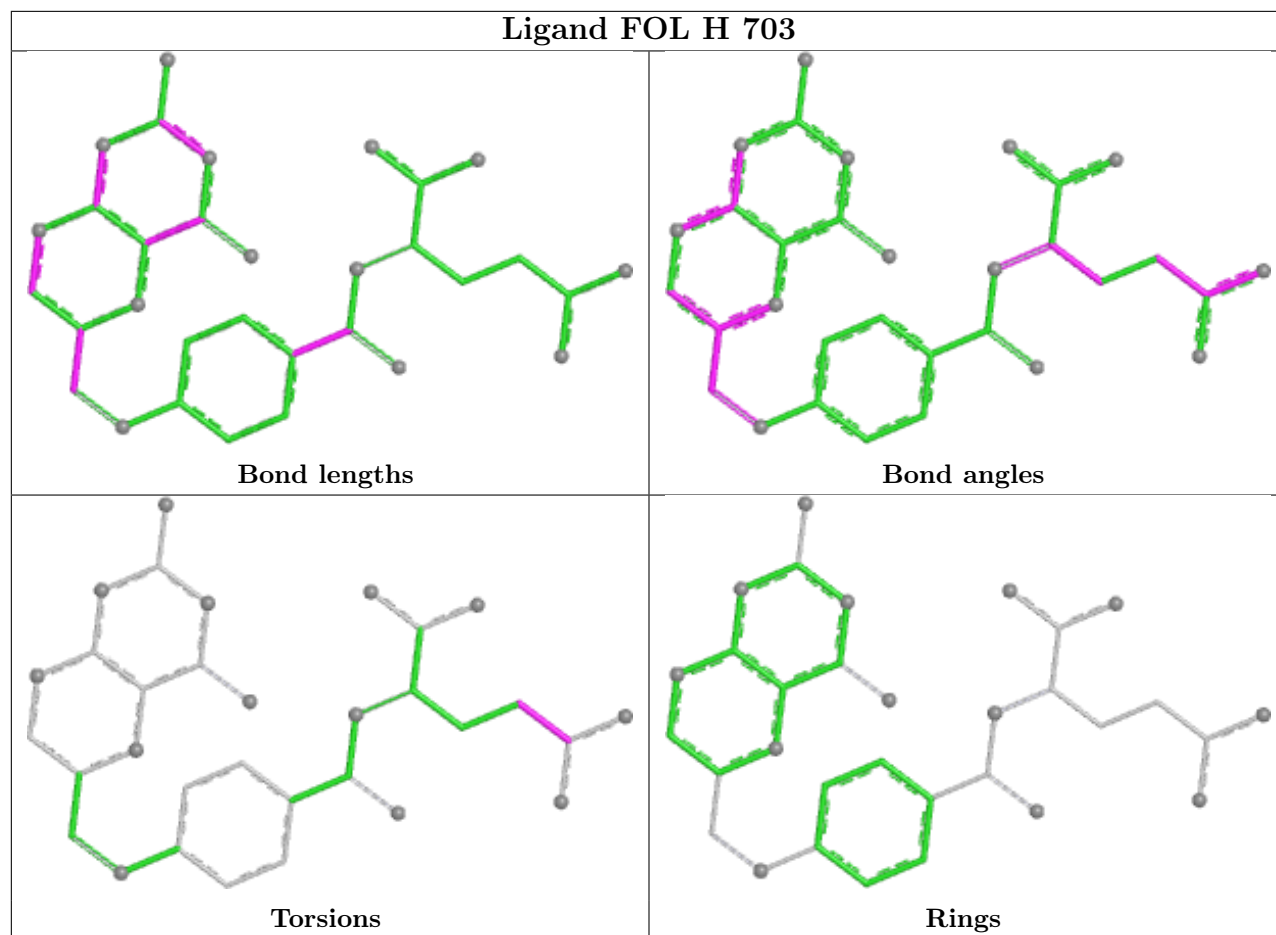


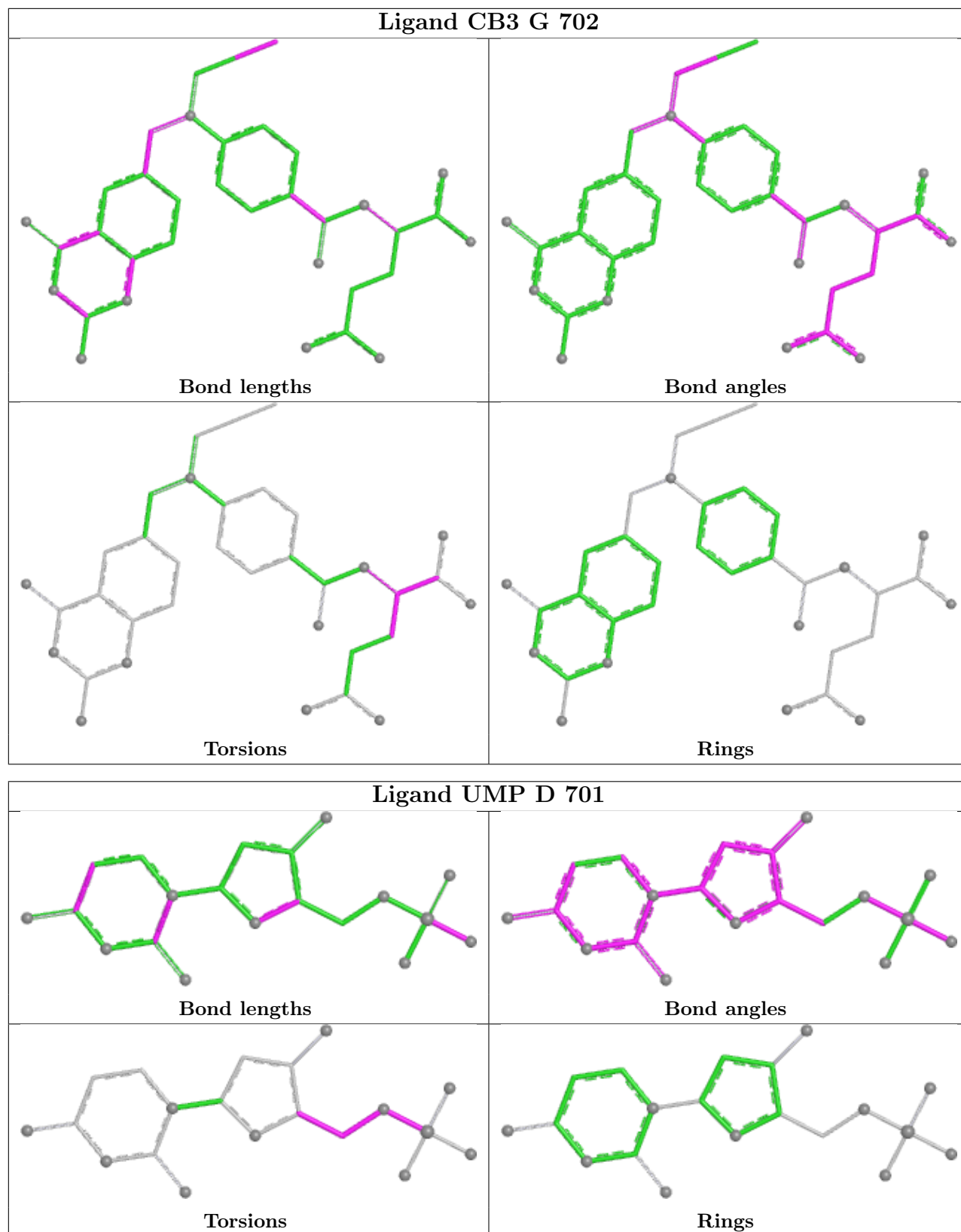


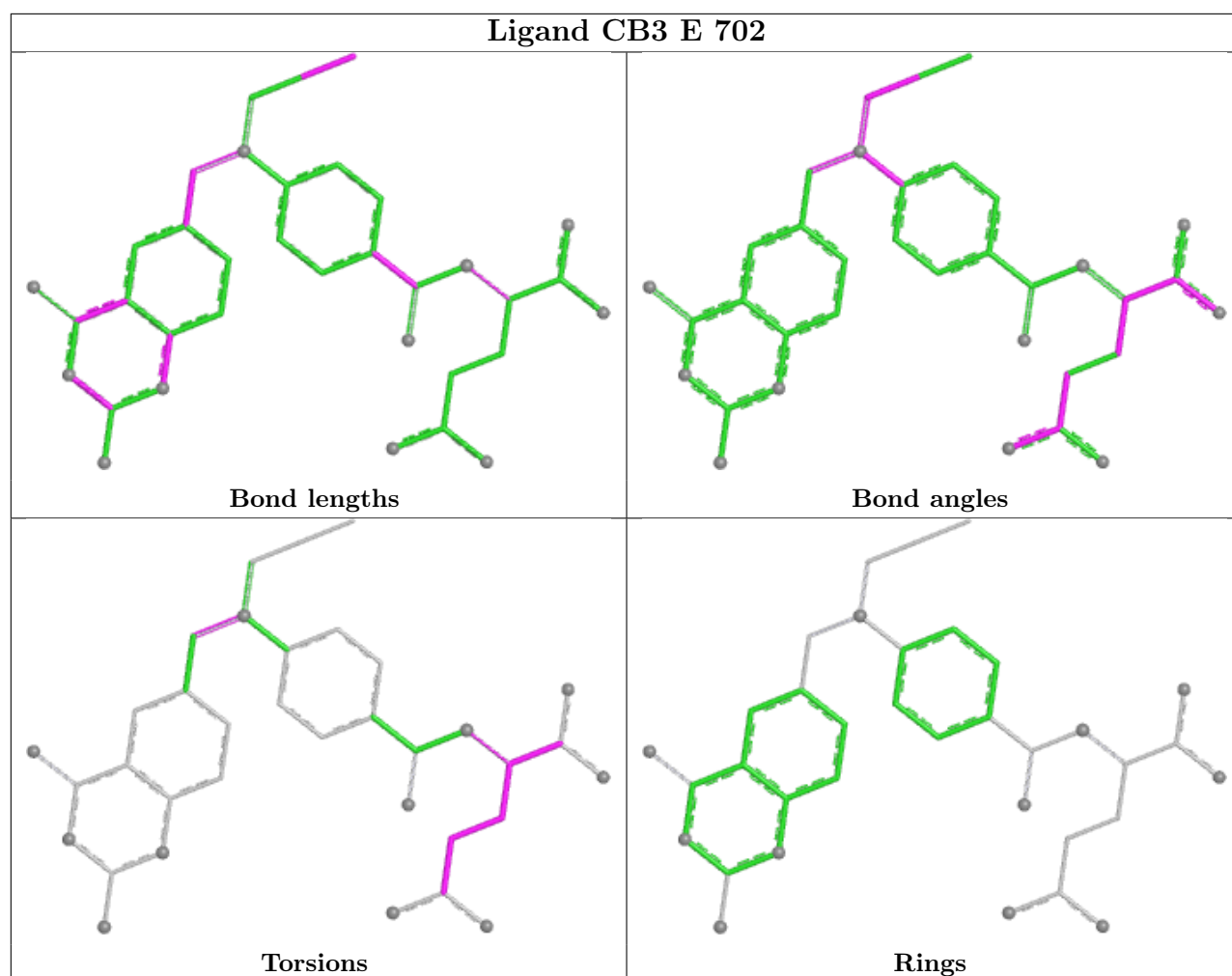












5.7 Other polymers [i](#)

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, 95th 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 ²)	Q<0.9
1	A	510/566 (90%)	-1.09	0 100 100	20, 39, 75, 107	2 (0%)
1	B	491/566 (86%)	-1.03	0 100 100	22, 40, 90, 113	1 (0%)
1	C	510/566 (90%)	-1.08	0 100 100	19, 39, 73, 105	2 (0%)
1	D	491/566 (86%)	-1.03	0 100 100	21, 40, 89, 112	1 (0%)
1	E	510/566 (90%)	-1.10	0 100 100	21, 39, 74, 109	2 (0%)
1	F	491/566 (86%)	-1.03	0 100 100	22, 41, 87, 114	1 (0%)
1	G	510/566 (90%)	-1.09	0 100 100	20, 39, 74, 107	2 (0%)
1	H	491/566 (86%)	-1.03	0 100 100	22, 40, 86, 118	1 (0%)
All	All	4004/4528 (88%)	-1.06	0 100 100	19, 39, 83, 118	12 (0%)

There are no RSRZ outliers to report.

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](#)

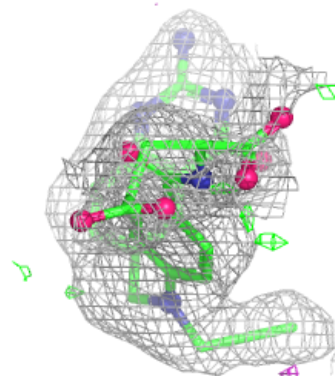
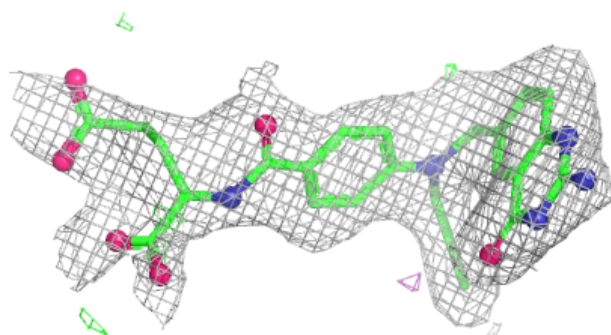
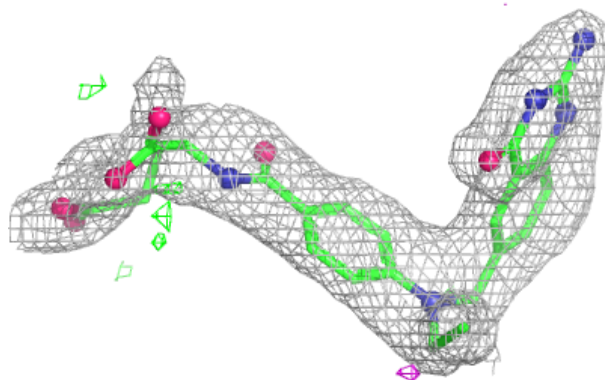
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	CB3	E	702	35/35	0.98	0.06	30,44,86,91	0
4	FOL	B	703	32/32	0.98	0.06	38,71,99,107	0
4	FOL	F	703	32/32	0.98	0.06	33,70,96,101	0
2	UMP	E	701	20/20	0.99	0.03	27,39,50,58	0
2	UMP	F	701	20/20	0.99	0.03	27,35,42,52	0
2	UMP	G	701	20/20	0.99	0.04	29,37,51,65	0
2	UMP	H	701	20/20	0.99	0.03	25,34,44,54	0
3	CB3	A	702	35/35	0.99	0.05	27,41,88,93	0
3	CB3	B	702	35/35	0.99	0.05	26,36,82,106	0
3	CB3	C	702	35/35	0.99	0.04	30,41,86,93	0
3	CB3	D	702	35/35	0.99	0.05	26,35,101,111	0
2	UMP	A	701	20/20	0.99	0.04	28,36,50,57	0
3	CB3	F	702	35/35	0.99	0.05	21,34,103,108	0
3	CB3	G	702	35/35	0.99	0.05	32,40,86,90	0
3	CB3	H	702	35/35	0.99	0.05	22,33,84,109	0
4	FOL	A	703	32/32	0.99	0.04	28,52,83,88	0
2	UMP	C	701	20/20	0.99	0.04	31,38,50,54	0
4	FOL	C	703	32/32	0.99	0.04	33,53,75,84	0
4	FOL	D	703	32/32	0.99	0.05	34,71,93,102	0
4	FOL	E	703	32/32	0.99	0.04	30,57,81,94	0
2	UMP	D	701	20/20	0.99	0.03	27,36,43,52	0
4	FOL	G	703	32/32	0.99	0.05	32,57,85,109	0
4	FOL	H	703	32/32	0.99	0.05	37,71,89,102	0
5	NDP	A	704	48/48	0.99	0.03	25,42,56,64	0
5	NDP	B	704	48/48	0.99	0.04	35,65,114,126	0
5	NDP	C	704	48/48	0.99	0.03	24,41,53,62	0
5	NDP	D	704	48/48	0.99	0.04	38,66,111,114	0
5	NDP	E	704	48/48	0.99	0.03	24,41,58,61	0
5	NDP	F	704	48/48	0.99	0.04	38,61,107,116	0
5	NDP	G	704	48/48	0.99	0.03	23,41,53,67	0
5	NDP	H	704	48/48	0.99	0.04	31,62,108,114	0
2	UMP	B	701	20/20	1.00	0.03	28,33,41,54	0

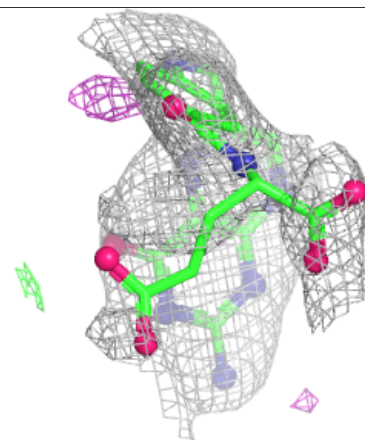
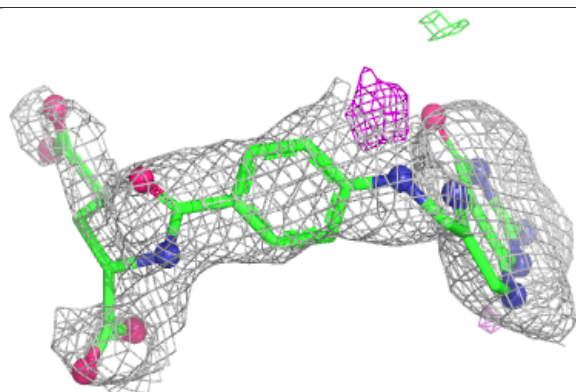
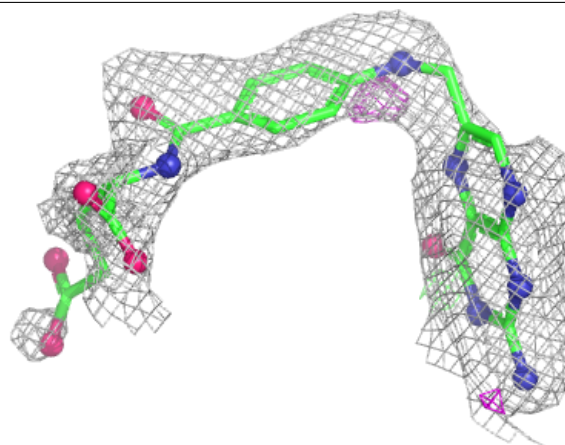
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around CB3 E 702:

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

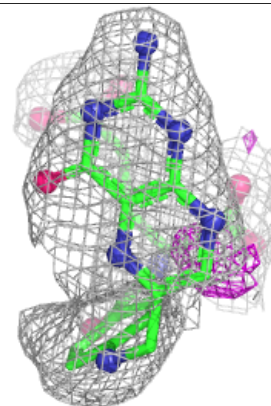
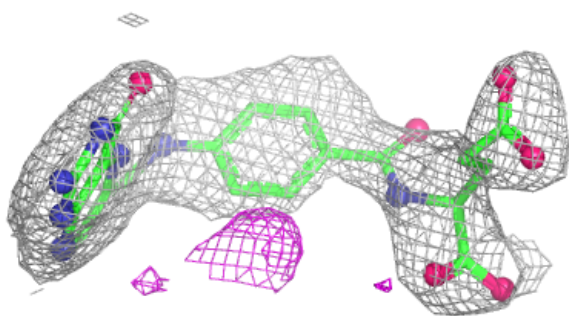
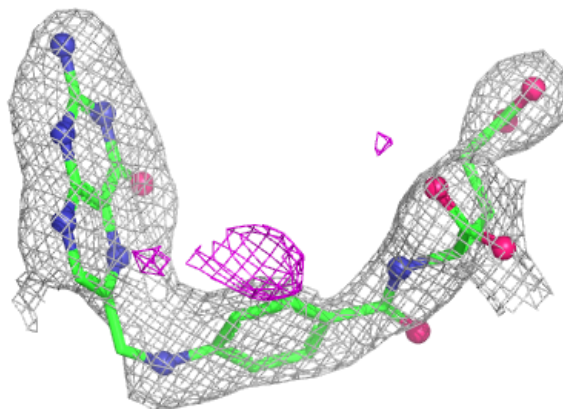
**Electron density around FOL B 703:**

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

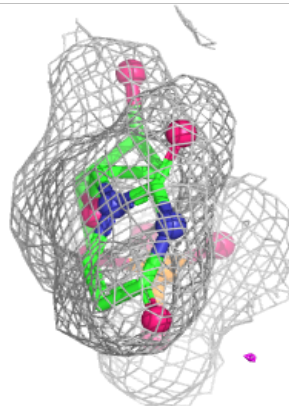
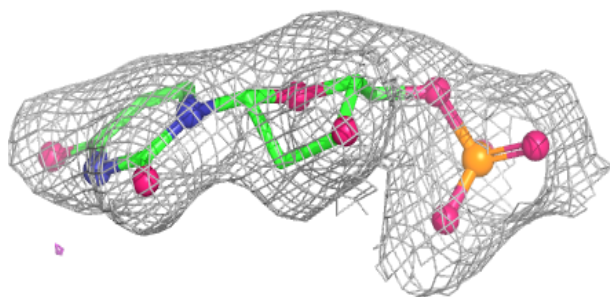
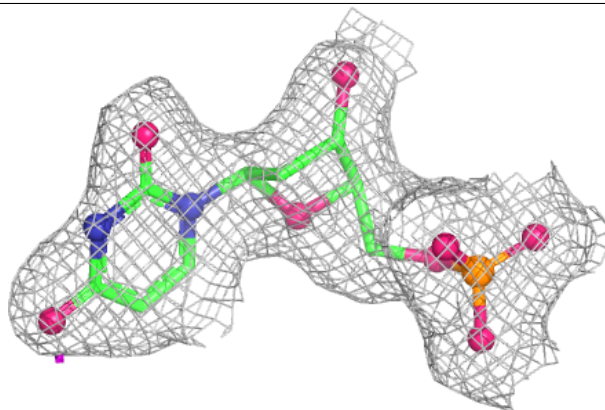


Electron density around FOL F 703:

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

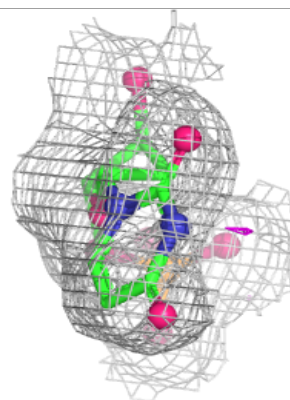
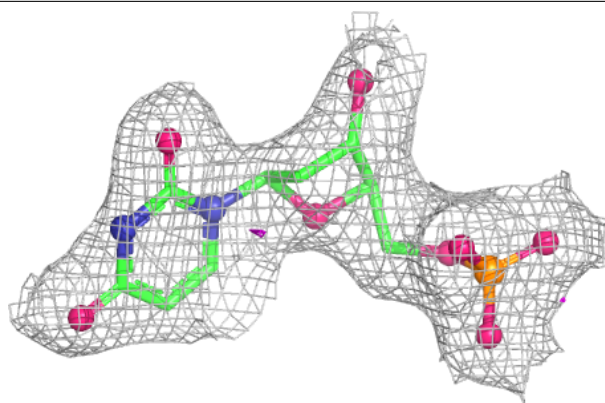
**Electron density around UMP E 701:**

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

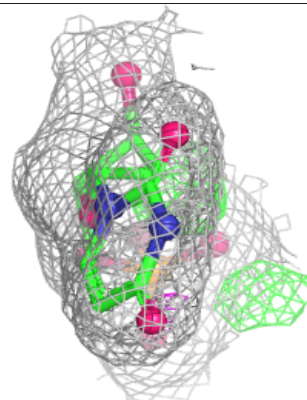
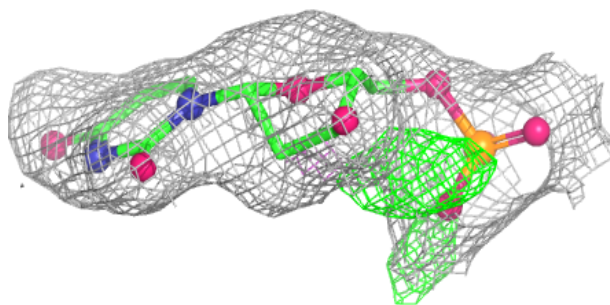
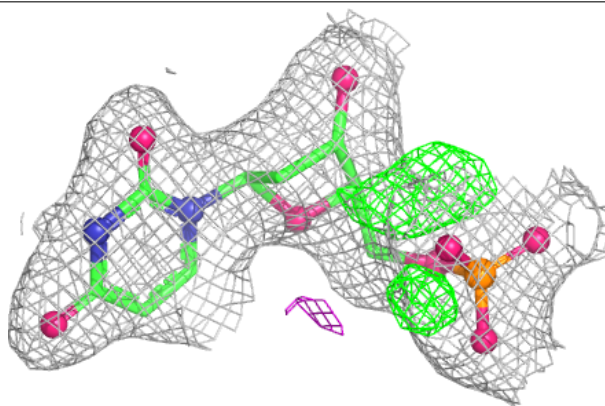


Electron density around UMP F 701:

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and green (positive)

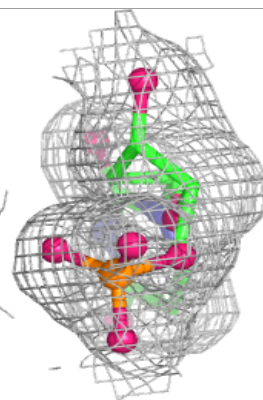
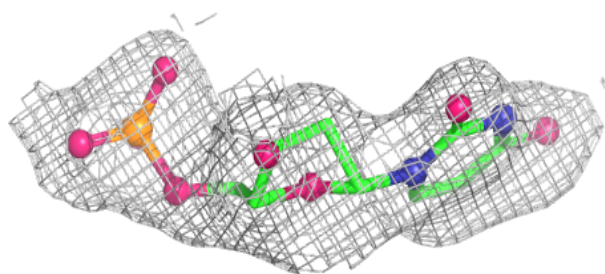
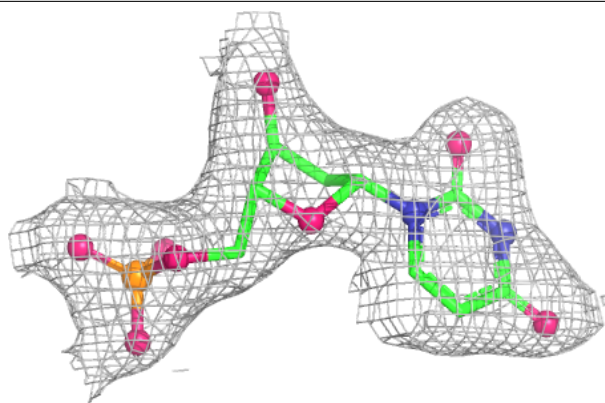
**Electron density around UMP G 701:**

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

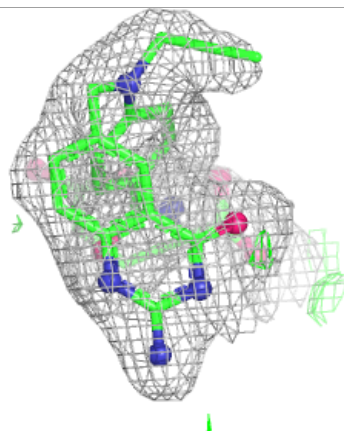
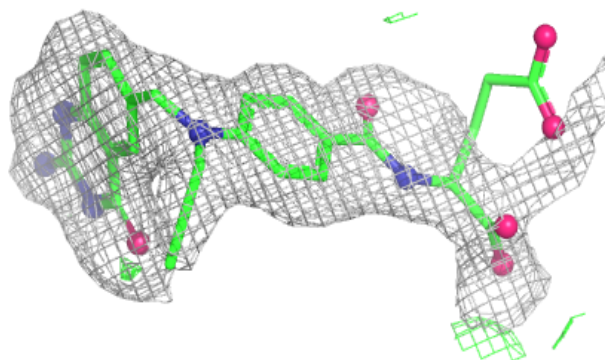
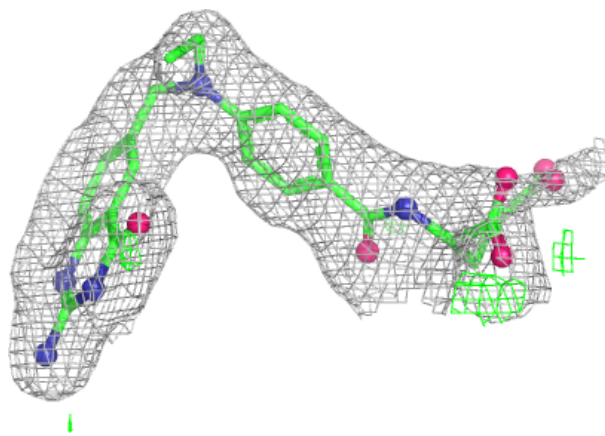


Electron density around UMP H 701:

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and green (positive)

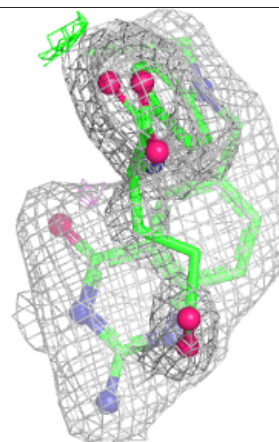
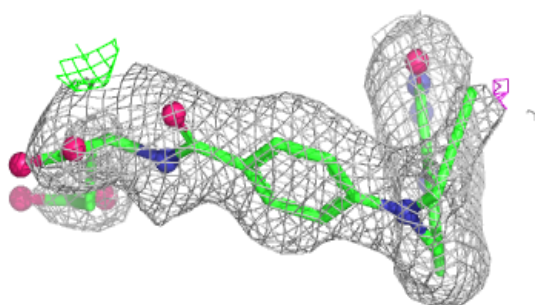
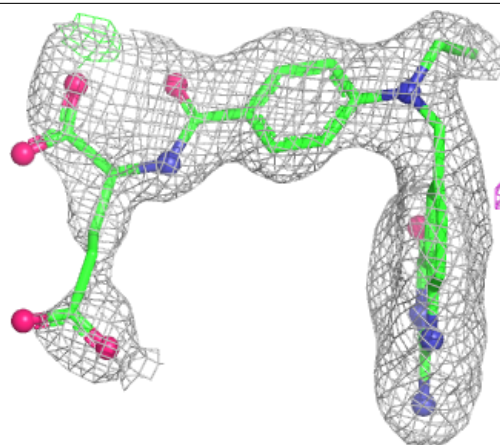
**Electron density around CB3 A 702:**

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

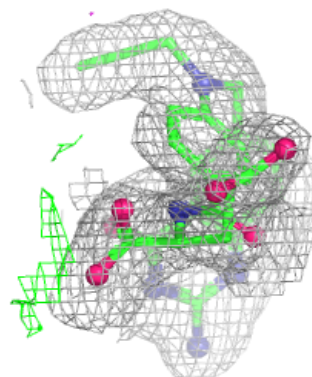
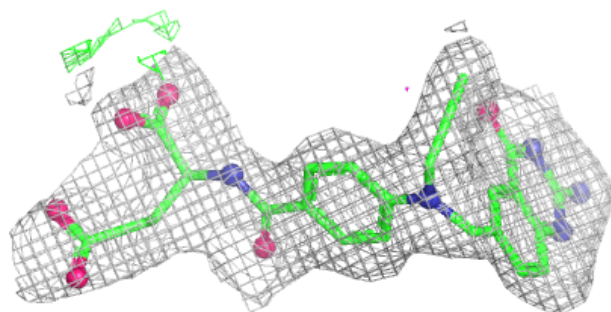
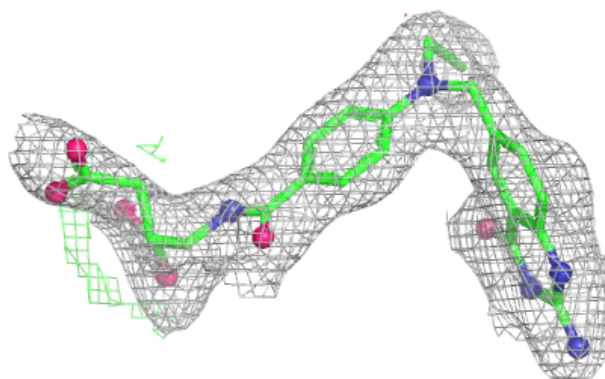


Electron density around CB3 B 702:

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and green (positive)

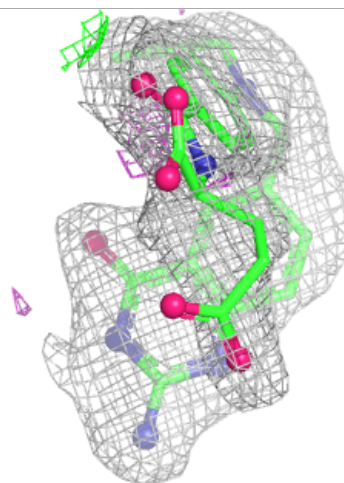
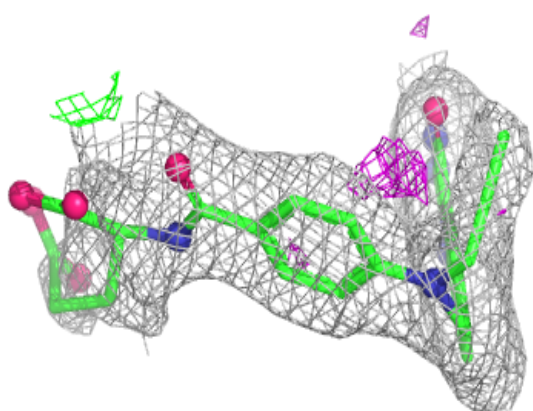
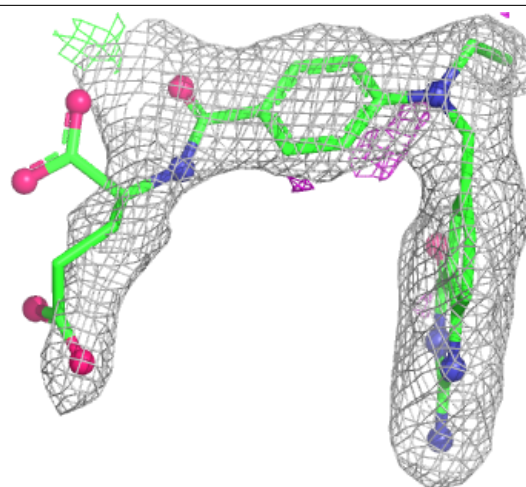
**Electron density around CB3 C 702:**

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



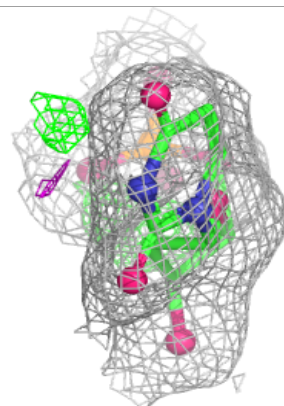
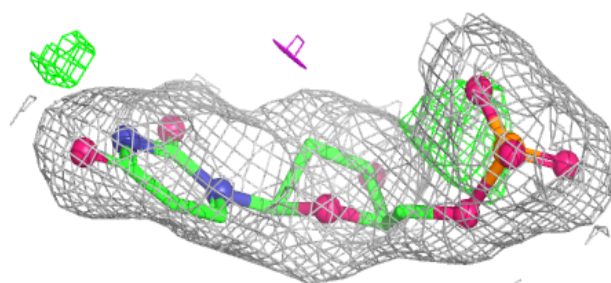
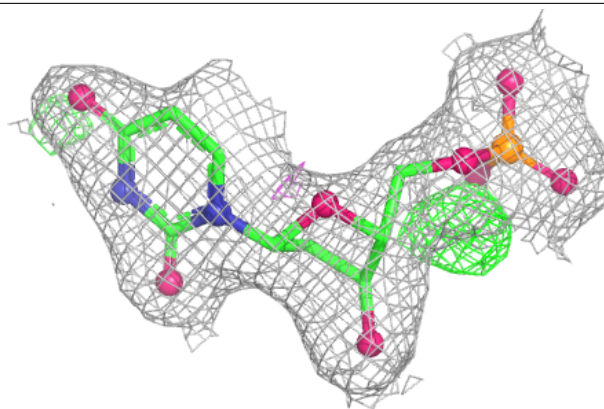
Electron density around CB3 D 702:

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



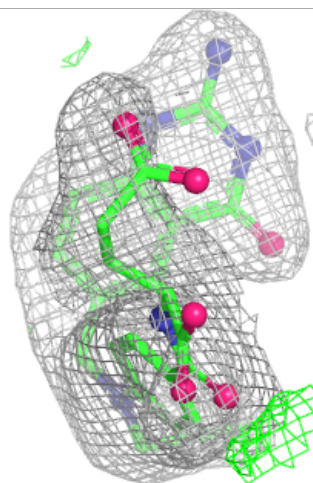
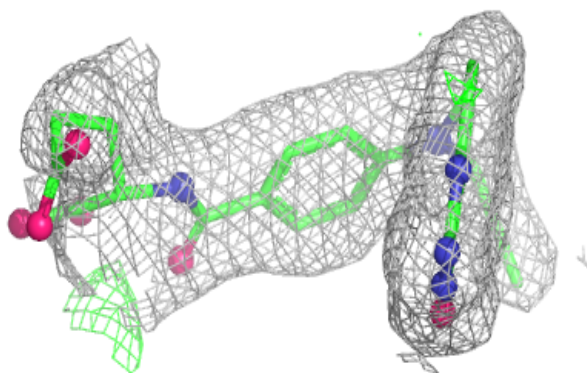
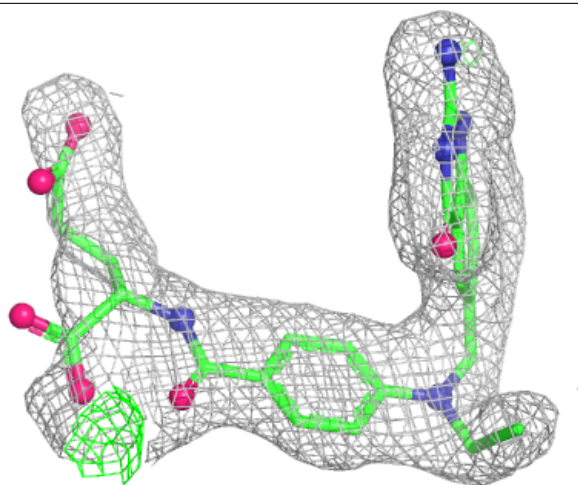
Electron density around UMP A 701:

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



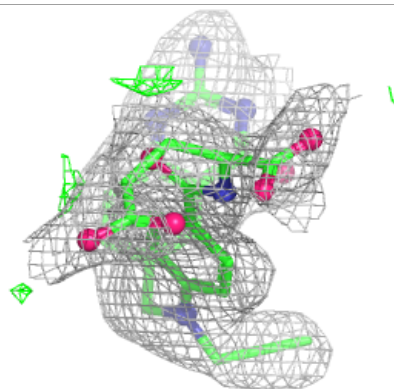
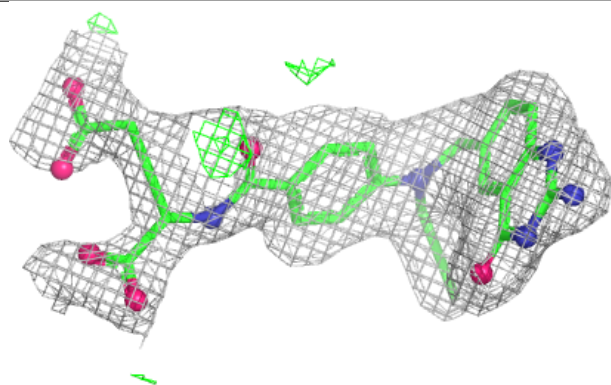
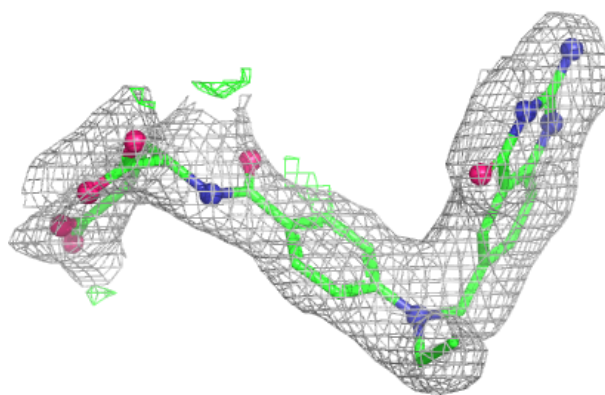
Electron density around CB3 F 702:

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and green (positive)



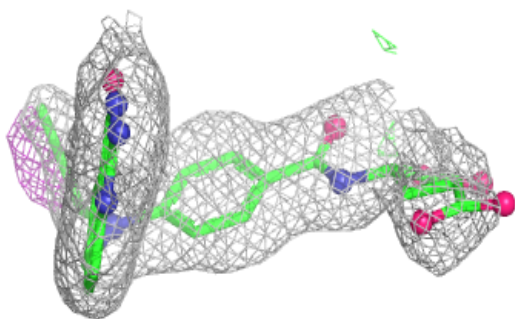
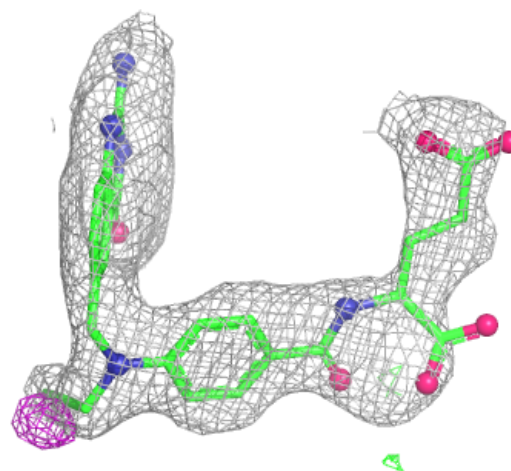
Electron density around CB3 G 702:

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and green (positive)



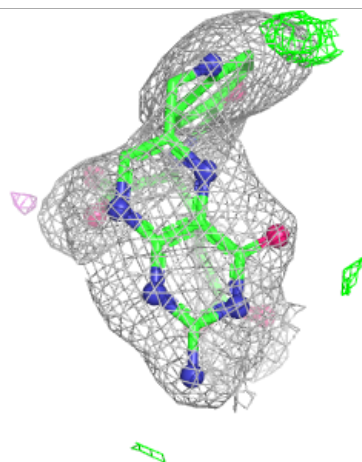
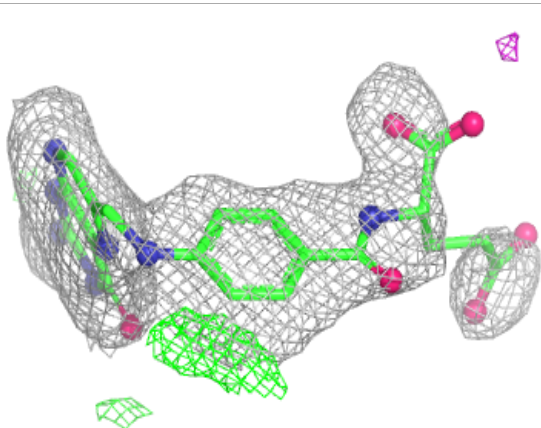
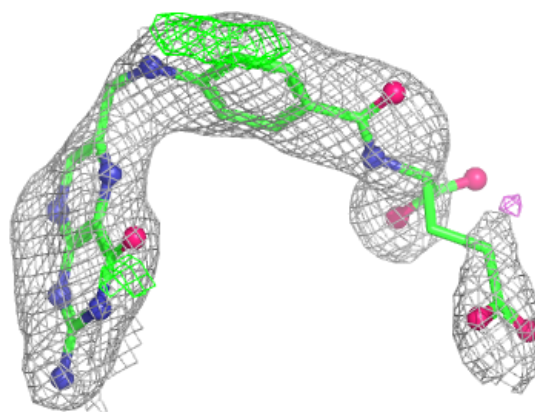
Electron density around CB3 H 702:

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and green (positive)



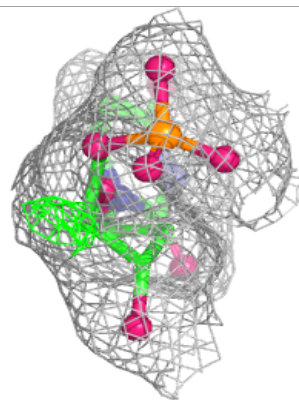
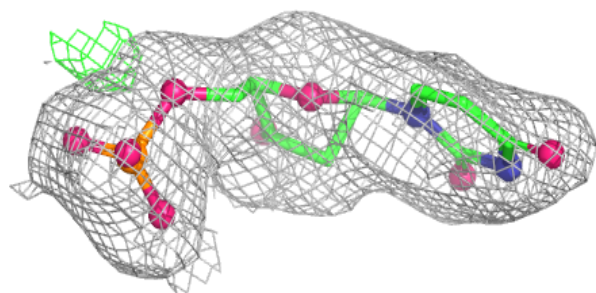
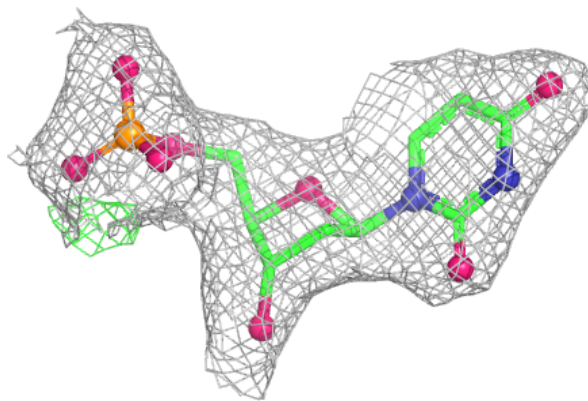
Electron density around FOL A 703:

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



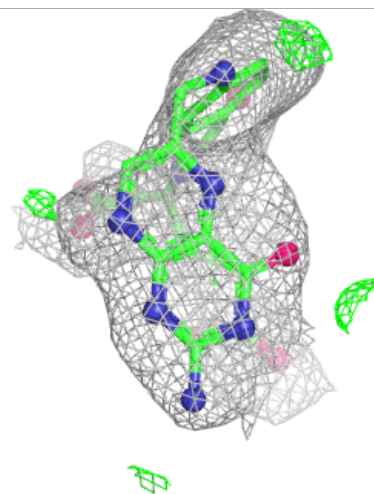
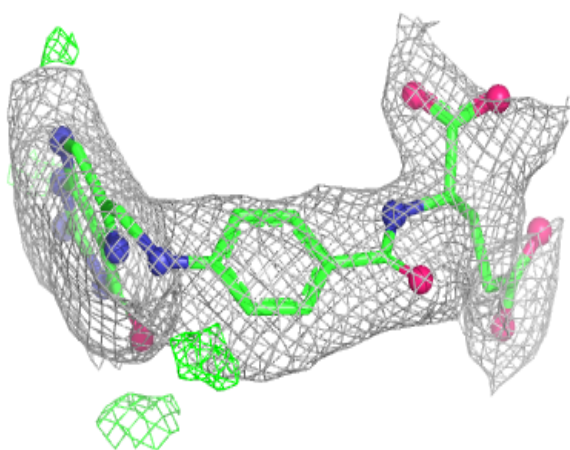
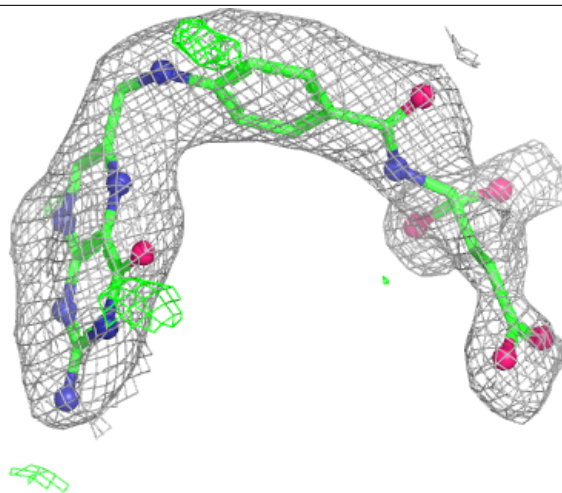
Electron density around UMP C 701:

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



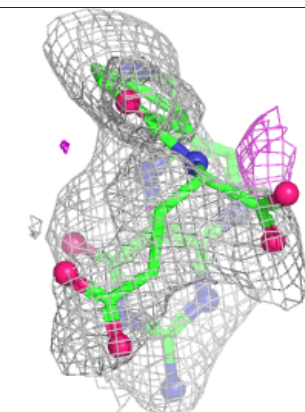
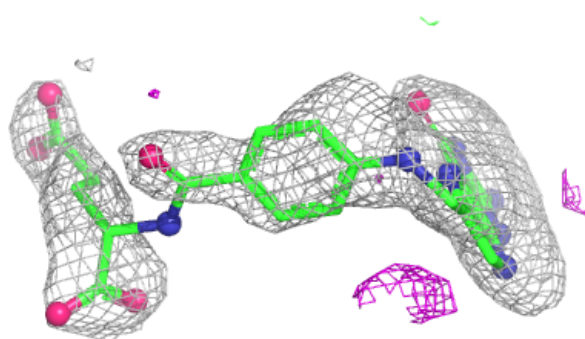
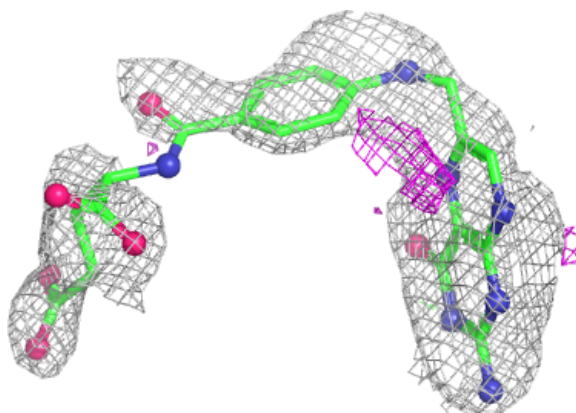
Electron density around FOL C 703:

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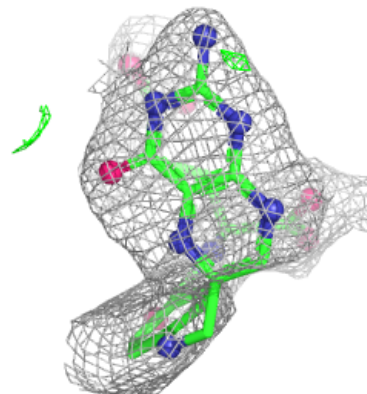
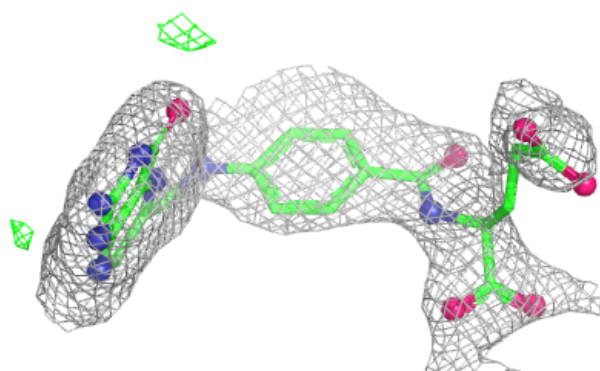
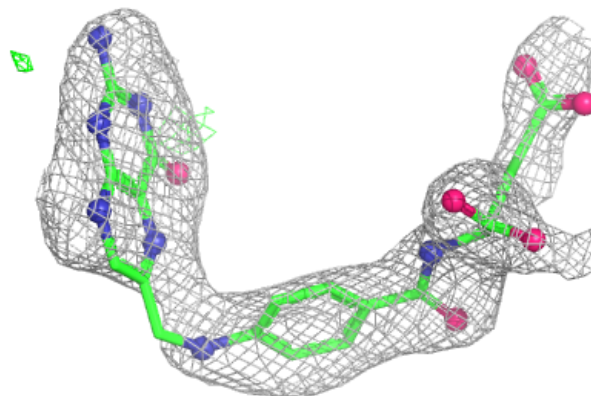


Electron density around FOL D 703:

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and green (positive)

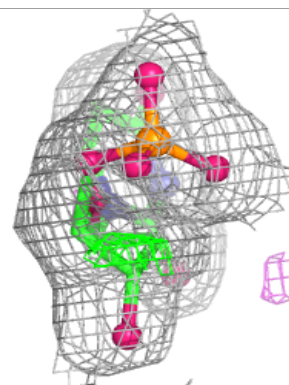
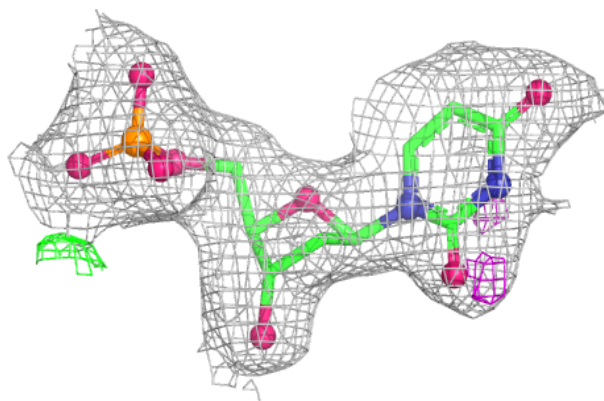
**Electron density around FOL E 703:**

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and green (positive)

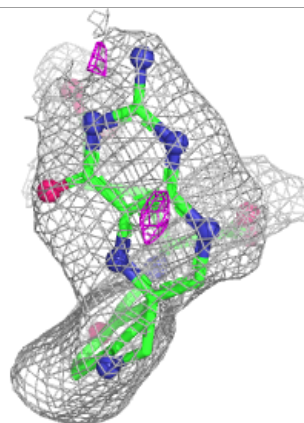
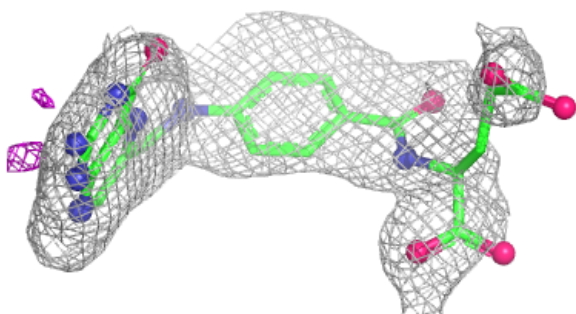
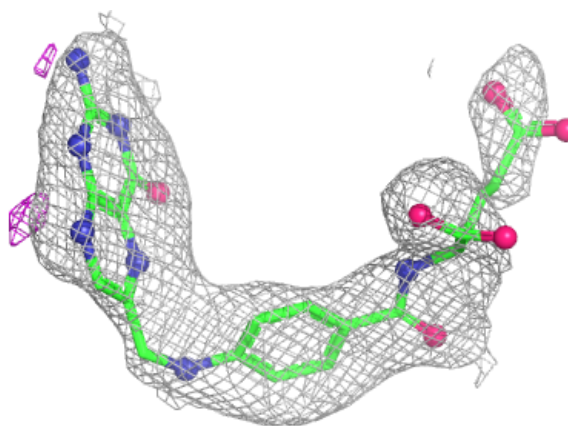


Electron density around UMP D 701:

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and green (positive)

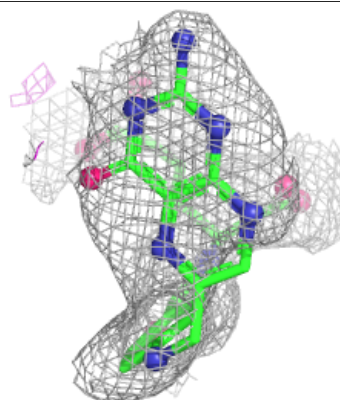
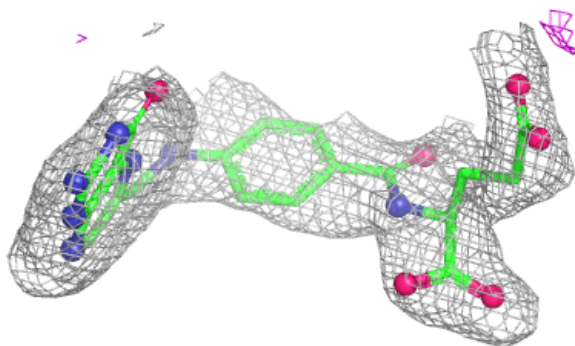
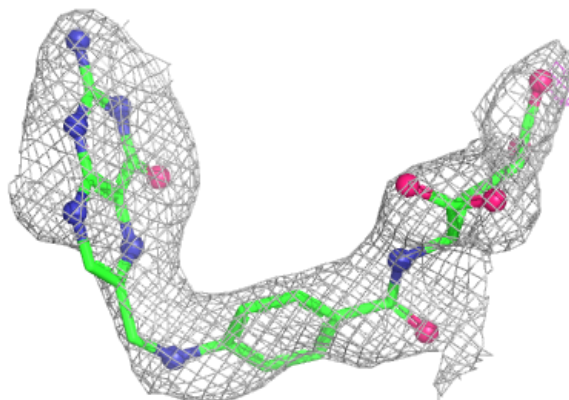
**Electron density around FOL G 703:**

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and green (positive)

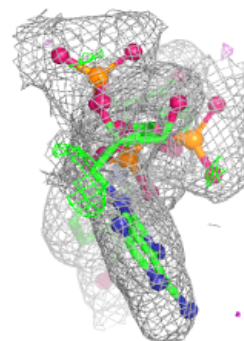
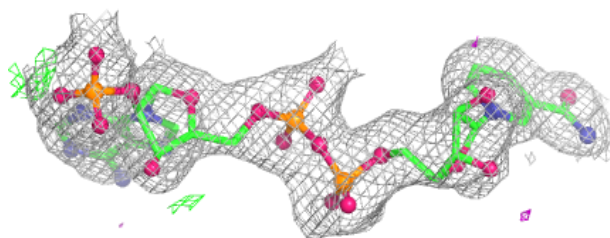
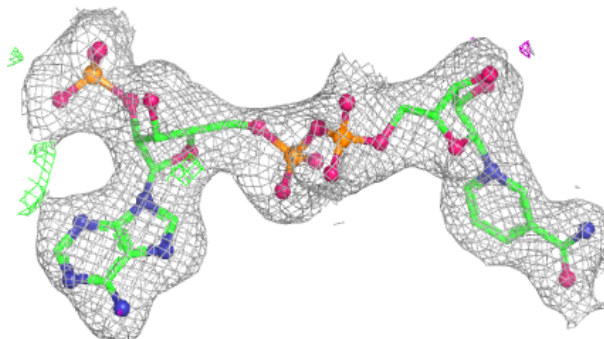


Electron density around FOL H 703:

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

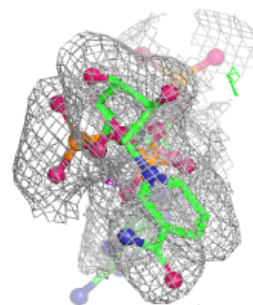
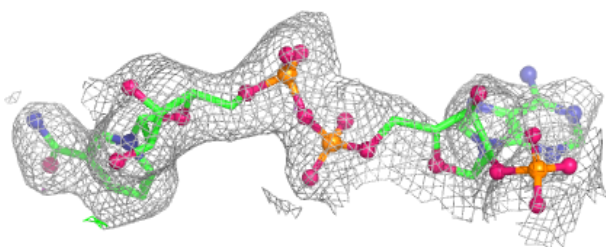
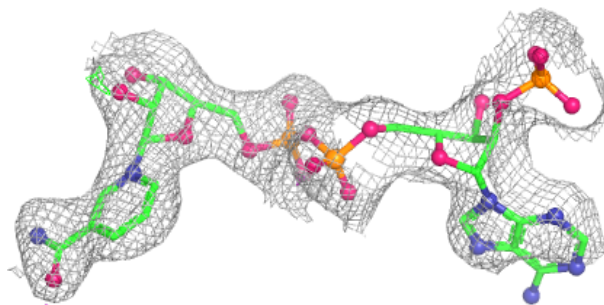
**Electron density around NDP A 704:**

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

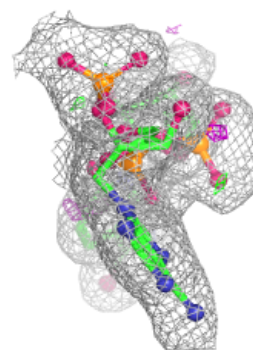
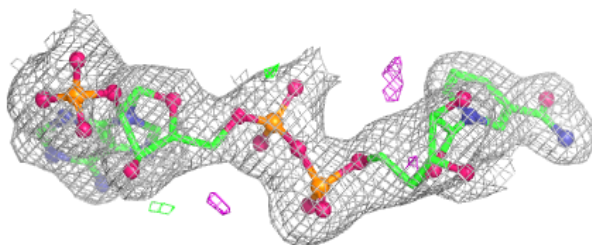
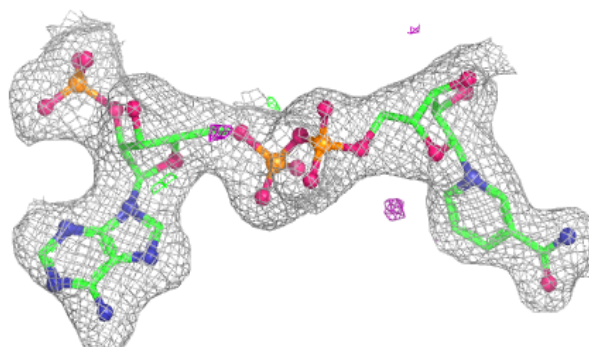


Electron density around NDP B 704:

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

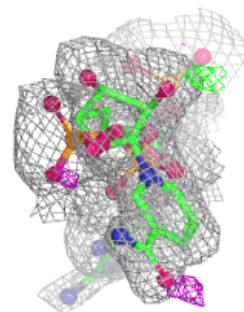
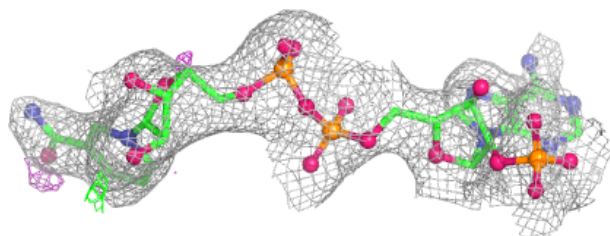
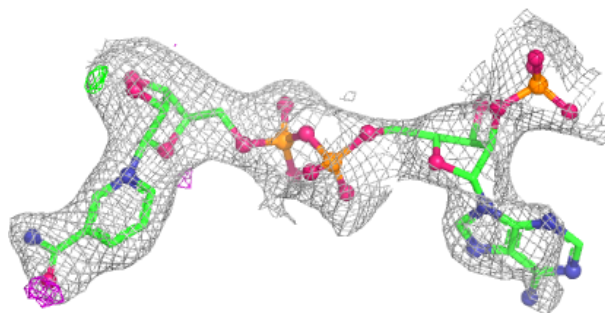
**Electron density around NDP C 704:**

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

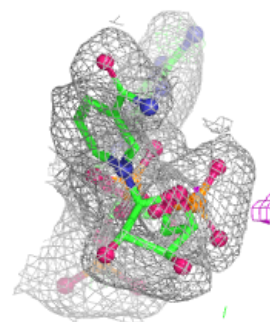
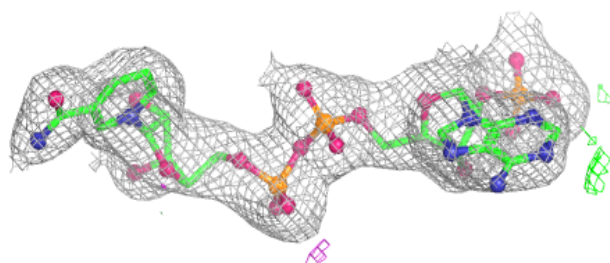
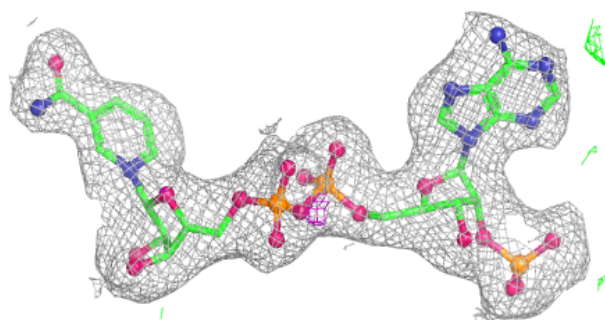


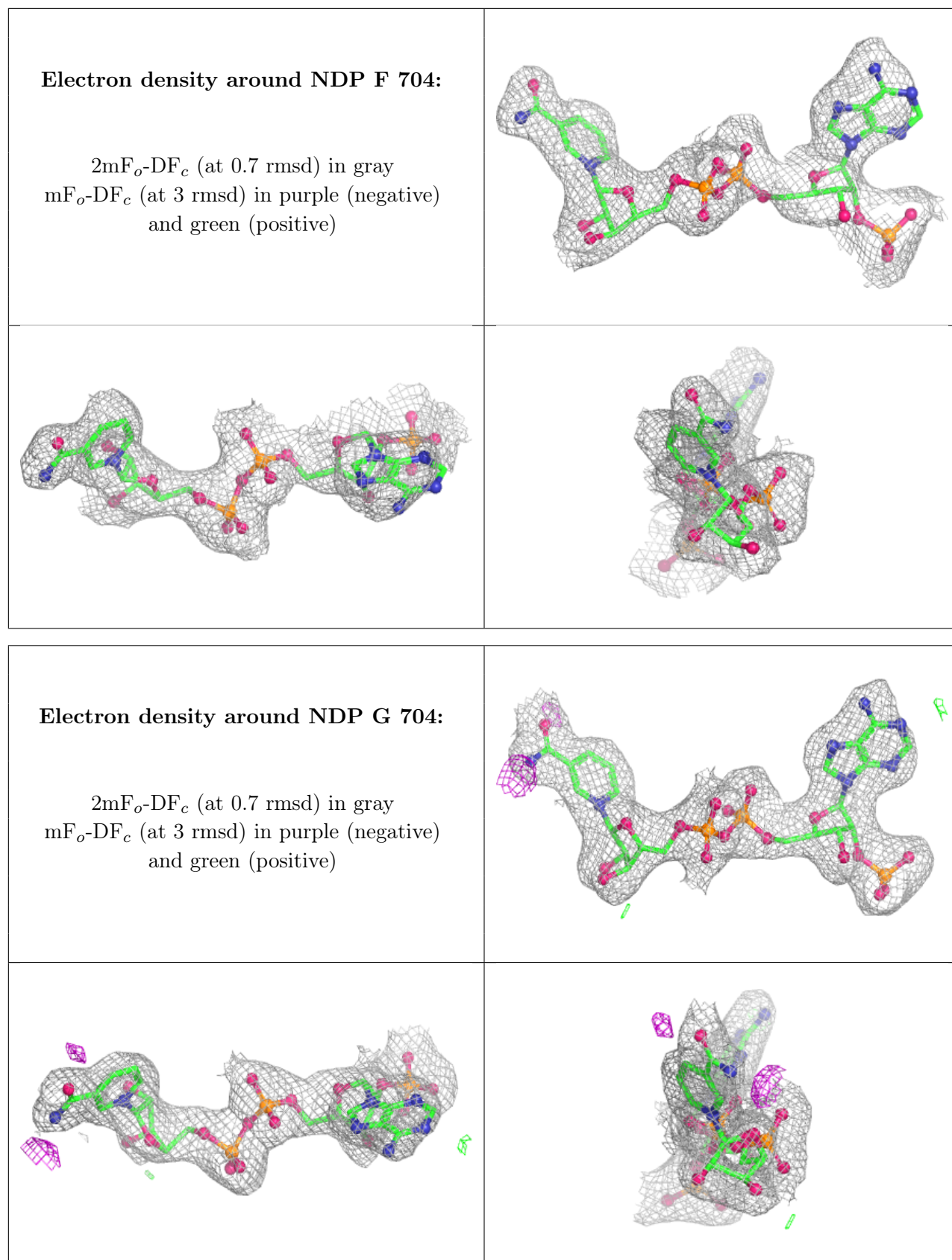
Electron density around NDP D 704:

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

**Electron density around NDP E 704:**

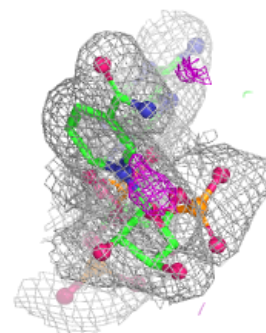
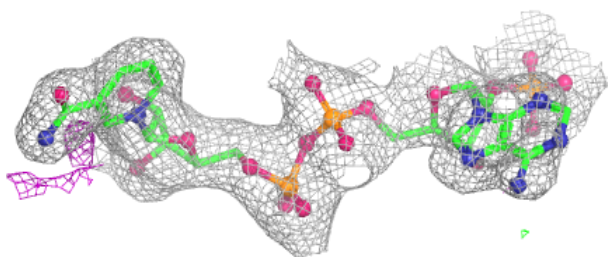
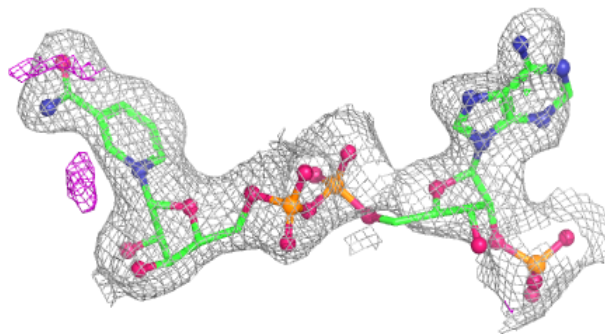
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



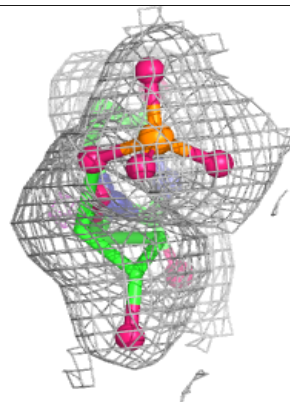
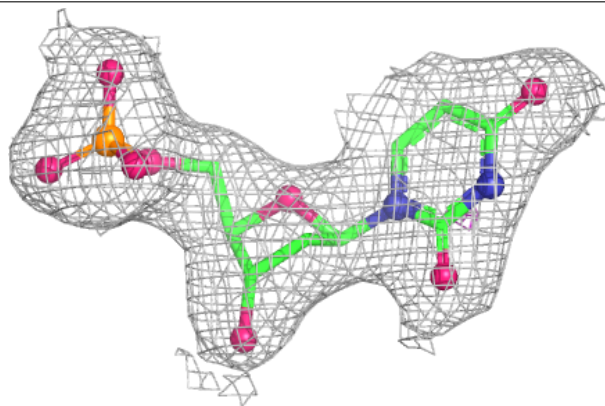


Electron density around NDP H 704:

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

**Electron density around UMP B 701:**

$2mF_o-DF_c$ (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.