



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 12:41 PM UTC

PDB ID : 7BIX / pdb\_00007bix  
Title : Crystal structure of UMPK from *M. tuberculosis* in complex with UDP and UTP (C2 form)  
Authors : Labesse, G.; Walter, P.; Haouz, A.; Mechaly, A.E.; Munier-Lehmann, H.  
Deposited on : 2021-01-13  
Resolution : 3.12 Å (reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

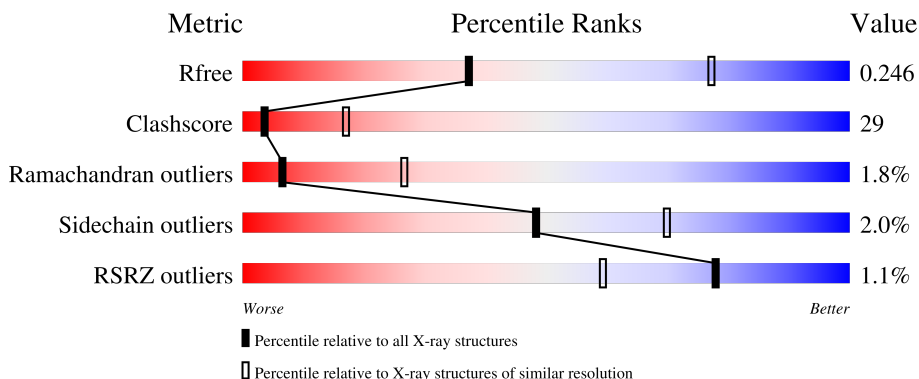
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.12 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	1816 (3.14-3.10)
Clashscore	190562	1906 (3.14-3.10)
Ramachandran outliers	187476	1802 (3.14-3.10)
Sidechain outliers	187428	1802 (3.14-3.10)
RSRZ outliers	180081	1816 (3.14-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	281	
1	B	281	
1	C	281	
1	D	281	
1	E	281	

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Mol	Chain	Length	Quality of chain
1	F	281	<p>2% 36% 38% 22%</p>
1	G	281	<p>46% 31% 22%</p>
1	H	281	<p>46% 34% 20%</p>
1	I	281	<p>46% 33% 20%</p>
1	J	281	<p>44% 36% 19%</p>
1	K	281	<p>47% 33% 19%</p>
1	L	281	<p>43% 36% 19%</p>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 20295 atoms, of which 66 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 Uridylate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	224	Total 1625	C 1023	N 284	O 307	S 11	0	0	0
1	B	226	Total 1655	C 1040	N 291	O 313	S 11	0	0	0
1	C	229	Total 1694	C 1066	N 298	O 319	S 11	0	0	0
1	D	225	Total 1656	C 1042	N 294	O 309	S 11	0	0	0
1	E	224	Total 1652	C 1039	N 293	O 309	S 11	0	0	0
1	F	220	Total 1614	C 1021	N 281	O 301	S 11	0	0	0
1	G	219	Total 1584	C 1000	N 275	O 298	S 11	0	0	0
1	H	225	Total 1662	C 1046	N 294	O 311	S 11	0	0	0
1	I	226	Total 1656	C 1043	N 292	O 310	S 11	0	0	0
1	J	228	Total 1675	C 1056	N 294	O 314	S 11	0	0	0
1	K	228	Total 1673	C 1053	N 296	O 313	S 11	0	0	0
1	L	227	Total 1654	C 1040	N 291	O 313	S 10	0	0	0

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP P9WHK5
A	-18	GLY	-	expression tag	UNP P9WHK5
A	-17	SER	-	expression tag	UNP P9WHK5
A	-16	SER	-	expression tag	UNP P9WHK5
A	-15	HIS	-	expression tag	UNP P9WHK5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	HIS	-	expression tag	UNP P9WHK5
A	-13	HIS	-	expression tag	UNP P9WHK5
A	-12	HIS	-	expression tag	UNP P9WHK5
A	-11	HIS	-	expression tag	UNP P9WHK5
A	-10	HIS	-	expression tag	UNP P9WHK5
A	-9	SER	-	expression tag	UNP P9WHK5
A	-8	SER	-	expression tag	UNP P9WHK5
A	-7	GLY	-	expression tag	UNP P9WHK5
A	-6	LEU	-	expression tag	UNP P9WHK5
A	-5	VAL	-	expression tag	UNP P9WHK5
A	-4	PRO	-	expression tag	UNP P9WHK5
A	-3	ARG	-	expression tag	UNP P9WHK5
A	-2	GLY	-	expression tag	UNP P9WHK5
A	-1	SER	-	expression tag	UNP P9WHK5
A	0	HIS	-	expression tag	UNP P9WHK5
B	-19	MET	-	initiating methionine	UNP P9WHK5
B	-18	GLY	-	expression tag	UNP P9WHK5
B	-17	SER	-	expression tag	UNP P9WHK5
B	-16	SER	-	expression tag	UNP P9WHK5
B	-15	HIS	-	expression tag	UNP P9WHK5
B	-14	HIS	-	expression tag	UNP P9WHK5
B	-13	HIS	-	expression tag	UNP P9WHK5
B	-12	HIS	-	expression tag	UNP P9WHK5
B	-11	HIS	-	expression tag	UNP P9WHK5
B	-10	HIS	-	expression tag	UNP P9WHK5
B	-9	SER	-	expression tag	UNP P9WHK5
B	-8	SER	-	expression tag	UNP P9WHK5
B	-7	GLY	-	expression tag	UNP P9WHK5
B	-6	LEU	-	expression tag	UNP P9WHK5
B	-5	VAL	-	expression tag	UNP P9WHK5
B	-4	PRO	-	expression tag	UNP P9WHK5
B	-3	ARG	-	expression tag	UNP P9WHK5
B	-2	GLY	-	expression tag	UNP P9WHK5
B	-1	SER	-	expression tag	UNP P9WHK5
B	0	HIS	-	expression tag	UNP P9WHK5
C	-19	MET	-	initiating methionine	UNP P9WHK5
C	-18	GLY	-	expression tag	UNP P9WHK5
C	-17	SER	-	expression tag	UNP P9WHK5
C	-16	SER	-	expression tag	UNP P9WHK5
C	-15	HIS	-	expression tag	UNP P9WHK5
C	-14	HIS	-	expression tag	UNP P9WHK5
C	-13	HIS	-	expression tag	UNP P9WHK5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-12	HIS	-	expression tag	UNP P9WHK5
C	-11	HIS	-	expression tag	UNP P9WHK5
C	-10	HIS	-	expression tag	UNP P9WHK5
C	-9	SER	-	expression tag	UNP P9WHK5
C	-8	SER	-	expression tag	UNP P9WHK5
C	-7	GLY	-	expression tag	UNP P9WHK5
C	-6	LEU	-	expression tag	UNP P9WHK5
C	-5	VAL	-	expression tag	UNP P9WHK5
C	-4	PRO	-	expression tag	UNP P9WHK5
C	-3	ARG	-	expression tag	UNP P9WHK5
C	-2	GLY	-	expression tag	UNP P9WHK5
C	-1	SER	-	expression tag	UNP P9WHK5
C	0	HIS	-	expression tag	UNP P9WHK5
D	-19	MET	-	initiating methionine	UNP P9WHK5
D	-18	GLY	-	expression tag	UNP P9WHK5
D	-17	SER	-	expression tag	UNP P9WHK5
D	-16	SER	-	expression tag	UNP P9WHK5
D	-15	HIS	-	expression tag	UNP P9WHK5
D	-14	HIS	-	expression tag	UNP P9WHK5
D	-13	HIS	-	expression tag	UNP P9WHK5
D	-12	HIS	-	expression tag	UNP P9WHK5
D	-11	HIS	-	expression tag	UNP P9WHK5
D	-10	HIS	-	expression tag	UNP P9WHK5
D	-9	SER	-	expression tag	UNP P9WHK5
D	-8	SER	-	expression tag	UNP P9WHK5
D	-7	GLY	-	expression tag	UNP P9WHK5
D	-6	LEU	-	expression tag	UNP P9WHK5
D	-5	VAL	-	expression tag	UNP P9WHK5
D	-4	PRO	-	expression tag	UNP P9WHK5
D	-3	ARG	-	expression tag	UNP P9WHK5
D	-2	GLY	-	expression tag	UNP P9WHK5
D	-1	SER	-	expression tag	UNP P9WHK5
D	0	HIS	-	expression tag	UNP P9WHK5
E	-19	MET	-	initiating methionine	UNP P9WHK5
E	-18	GLY	-	expression tag	UNP P9WHK5
E	-17	SER	-	expression tag	UNP P9WHK5
E	-16	SER	-	expression tag	UNP P9WHK5
E	-15	HIS	-	expression tag	UNP P9WHK5
E	-14	HIS	-	expression tag	UNP P9WHK5
E	-13	HIS	-	expression tag	UNP P9WHK5
E	-12	HIS	-	expression tag	UNP P9WHK5
E	-11	HIS	-	expression tag	UNP P9WHK5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-10	HIS	-	expression tag	UNP P9WHK5
E	-9	SER	-	expression tag	UNP P9WHK5
E	-8	SER	-	expression tag	UNP P9WHK5
E	-7	GLY	-	expression tag	UNP P9WHK5
E	-6	LEU	-	expression tag	UNP P9WHK5
E	-5	VAL	-	expression tag	UNP P9WHK5
E	-4	PRO	-	expression tag	UNP P9WHK5
E	-3	ARG	-	expression tag	UNP P9WHK5
E	-2	GLY	-	expression tag	UNP P9WHK5
E	-1	SER	-	expression tag	UNP P9WHK5
E	0	HIS	-	expression tag	UNP P9WHK5
F	-19	MET	-	initiating methionine	UNP P9WHK5
F	-18	GLY	-	expression tag	UNP P9WHK5
F	-17	SER	-	expression tag	UNP P9WHK5
F	-16	SER	-	expression tag	UNP P9WHK5
F	-15	HIS	-	expression tag	UNP P9WHK5
F	-14	HIS	-	expression tag	UNP P9WHK5
F	-13	HIS	-	expression tag	UNP P9WHK5
F	-12	HIS	-	expression tag	UNP P9WHK5
F	-11	HIS	-	expression tag	UNP P9WHK5
F	-10	HIS	-	expression tag	UNP P9WHK5
F	-9	SER	-	expression tag	UNP P9WHK5
F	-8	SER	-	expression tag	UNP P9WHK5
F	-7	GLY	-	expression tag	UNP P9WHK5
F	-6	LEU	-	expression tag	UNP P9WHK5
F	-5	VAL	-	expression tag	UNP P9WHK5
F	-4	PRO	-	expression tag	UNP P9WHK5
F	-3	ARG	-	expression tag	UNP P9WHK5
F	-2	GLY	-	expression tag	UNP P9WHK5
F	-1	SER	-	expression tag	UNP P9WHK5
F	0	HIS	-	expression tag	UNP P9WHK5
G	-19	MET	-	initiating methionine	UNP P9WHK5
G	-18	GLY	-	expression tag	UNP P9WHK5
G	-17	SER	-	expression tag	UNP P9WHK5
G	-16	SER	-	expression tag	UNP P9WHK5
G	-15	HIS	-	expression tag	UNP P9WHK5
G	-14	HIS	-	expression tag	UNP P9WHK5
G	-13	HIS	-	expression tag	UNP P9WHK5
G	-12	HIS	-	expression tag	UNP P9WHK5
G	-11	HIS	-	expression tag	UNP P9WHK5
G	-10	HIS	-	expression tag	UNP P9WHK5
G	-9	SER	-	expression tag	UNP P9WHK5

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-8	SER	-	expression tag	UNP P9WHK5
G	-7	GLY	-	expression tag	UNP P9WHK5
G	-6	LEU	-	expression tag	UNP P9WHK5
G	-5	VAL	-	expression tag	UNP P9WHK5
G	-4	PRO	-	expression tag	UNP P9WHK5
G	-3	ARG	-	expression tag	UNP P9WHK5
G	-2	GLY	-	expression tag	UNP P9WHK5
G	-1	SER	-	expression tag	UNP P9WHK5
G	0	HIS	-	expression tag	UNP P9WHK5
H	-19	MET	-	initiating methionine	UNP P9WHK5
H	-18	GLY	-	expression tag	UNP P9WHK5
H	-17	SER	-	expression tag	UNP P9WHK5
H	-16	SER	-	expression tag	UNP P9WHK5
H	-15	HIS	-	expression tag	UNP P9WHK5
H	-14	HIS	-	expression tag	UNP P9WHK5
H	-13	HIS	-	expression tag	UNP P9WHK5
H	-12	HIS	-	expression tag	UNP P9WHK5
H	-11	HIS	-	expression tag	UNP P9WHK5
H	-10	HIS	-	expression tag	UNP P9WHK5
H	-9	SER	-	expression tag	UNP P9WHK5
H	-8	SER	-	expression tag	UNP P9WHK5
H	-7	GLY	-	expression tag	UNP P9WHK5
H	-6	LEU	-	expression tag	UNP P9WHK5
H	-5	VAL	-	expression tag	UNP P9WHK5
H	-4	PRO	-	expression tag	UNP P9WHK5
H	-3	ARG	-	expression tag	UNP P9WHK5
H	-2	GLY	-	expression tag	UNP P9WHK5
H	-1	SER	-	expression tag	UNP P9WHK5
H	0	HIS	-	expression tag	UNP P9WHK5
I	-19	MET	-	initiating methionine	UNP P9WHK5
I	-18	GLY	-	expression tag	UNP P9WHK5
I	-17	SER	-	expression tag	UNP P9WHK5
I	-16	SER	-	expression tag	UNP P9WHK5
I	-15	HIS	-	expression tag	UNP P9WHK5
I	-14	HIS	-	expression tag	UNP P9WHK5
I	-13	HIS	-	expression tag	UNP P9WHK5
I	-12	HIS	-	expression tag	UNP P9WHK5
I	-11	HIS	-	expression tag	UNP P9WHK5
I	-10	HIS	-	expression tag	UNP P9WHK5
I	-9	SER	-	expression tag	UNP P9WHK5
I	-8	SER	-	expression tag	UNP P9WHK5
I	-7	GLY	-	expression tag	UNP P9WHK5

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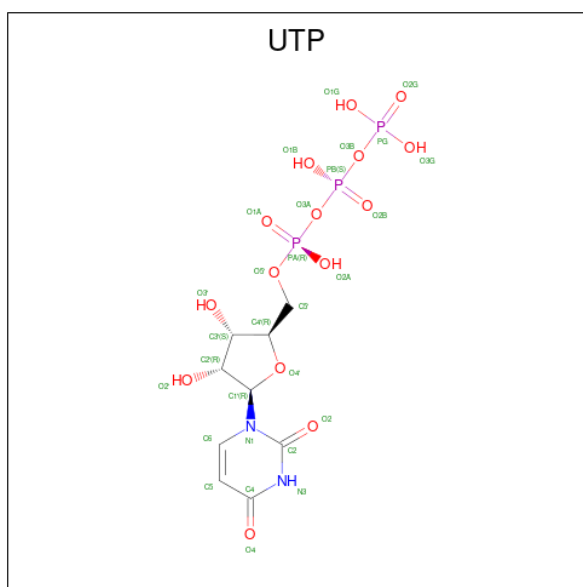
Chain	Residue	Modelled	Actual	Comment	Reference
I	-6	LEU	-	expression tag	UNP P9WHK5
I	-5	VAL	-	expression tag	UNP P9WHK5
I	-4	PRO	-	expression tag	UNP P9WHK5
I	-3	ARG	-	expression tag	UNP P9WHK5
I	-2	GLY	-	expression tag	UNP P9WHK5
I	-1	SER	-	expression tag	UNP P9WHK5
I	0	HIS	-	expression tag	UNP P9WHK5
J	-19	MET	-	initiating methionine	UNP P9WHK5
J	-18	GLY	-	expression tag	UNP P9WHK5
J	-17	SER	-	expression tag	UNP P9WHK5
J	-16	SER	-	expression tag	UNP P9WHK5
J	-15	HIS	-	expression tag	UNP P9WHK5
J	-14	HIS	-	expression tag	UNP P9WHK5
J	-13	HIS	-	expression tag	UNP P9WHK5
J	-12	HIS	-	expression tag	UNP P9WHK5
J	-11	HIS	-	expression tag	UNP P9WHK5
J	-10	HIS	-	expression tag	UNP P9WHK5
J	-9	SER	-	expression tag	UNP P9WHK5
J	-8	SER	-	expression tag	UNP P9WHK5
J	-7	GLY	-	expression tag	UNP P9WHK5
J	-6	LEU	-	expression tag	UNP P9WHK5
J	-5	VAL	-	expression tag	UNP P9WHK5
J	-4	PRO	-	expression tag	UNP P9WHK5
J	-3	ARG	-	expression tag	UNP P9WHK5
J	-2	GLY	-	expression tag	UNP P9WHK5
J	-1	SER	-	expression tag	UNP P9WHK5
J	0	HIS	-	expression tag	UNP P9WHK5
K	-19	MET	-	initiating methionine	UNP P9WHK5
K	-18	GLY	-	expression tag	UNP P9WHK5
K	-17	SER	-	expression tag	UNP P9WHK5
K	-16	SER	-	expression tag	UNP P9WHK5
K	-15	HIS	-	expression tag	UNP P9WHK5
K	-14	HIS	-	expression tag	UNP P9WHK5
K	-13	HIS	-	expression tag	UNP P9WHK5
K	-12	HIS	-	expression tag	UNP P9WHK5
K	-11	HIS	-	expression tag	UNP P9WHK5
K	-10	HIS	-	expression tag	UNP P9WHK5
K	-9	SER	-	expression tag	UNP P9WHK5
K	-8	SER	-	expression tag	UNP P9WHK5
K	-7	GLY	-	expression tag	UNP P9WHK5
K	-6	LEU	-	expression tag	UNP P9WHK5
K	-5	VAL	-	expression tag	UNP P9WHK5

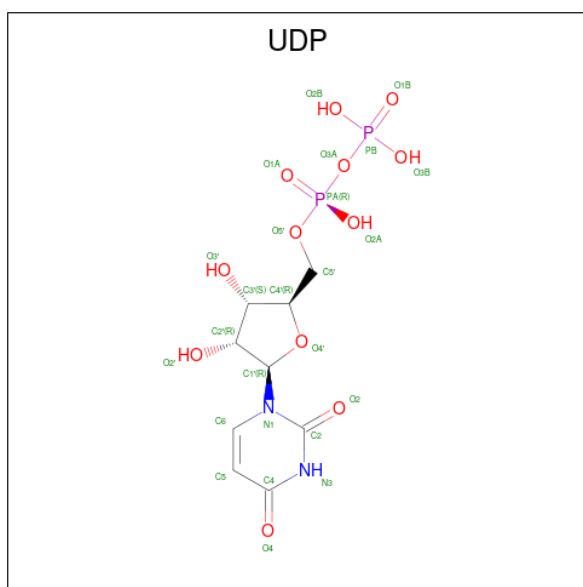
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Chain	Residue	Modelled	Actual	Comment	Reference
K	-4	PRO	-	expression tag	UNP P9WHK5
K	-3	ARG	-	expression tag	UNP P9WHK5
K	-2	GLY	-	expression tag	UNP P9WHK5
K	-1	SER	-	expression tag	UNP P9WHK5
K	0	HIS	-	expression tag	UNP P9WHK5
L	-19	MET	-	initiating methionine	UNP P9WHK5
L	-18	GLY	-	expression tag	UNP P9WHK5
L	-17	SER	-	expression tag	UNP P9WHK5
L	-16	SER	-	expression tag	UNP P9WHK5
L	-15	HIS	-	expression tag	UNP P9WHK5
L	-14	HIS	-	expression tag	UNP P9WHK5
L	-13	HIS	-	expression tag	UNP P9WHK5
L	-12	HIS	-	expression tag	UNP P9WHK5
L	-11	HIS	-	expression tag	UNP P9WHK5
L	-10	HIS	-	expression tag	UNP P9WHK5
L	-9	SER	-	expression tag	UNP P9WHK5
L	-8	SER	-	expression tag	UNP P9WHK5
L	-7	GLY	-	expression tag	UNP P9WHK5
L	-6	LEU	-	expression tag	UNP P9WHK5
L	-5	VAL	-	expression tag	UNP P9WHK5
L	-4	PRO	-	expression tag	UNP P9WHK5
L	-3	ARG	-	expression tag	UNP P9WHK5
L	-2	GLY	-	expression tag	UNP P9WHK5
L	-1	SER	-	expression tag	UNP P9WHK5
L	0	HIS	-	expression tag	UNP P9WHK5

- Molecule 2 is URIDINE 5'-TRIPHOSPHATE (CCD ID: UTP) (formula: C<sub>9</sub>H<sub>15</sub>N<sub>2</sub>O<sub>15</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	B	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	C	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	D	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	E	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	H	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	I	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	J	1	Total 25	C 9	N 2	O 12	P 2	0	0
3	K	1	Total 25	C 9	N 2	O 12	P 2	0	0

- Molecule 4 is water.

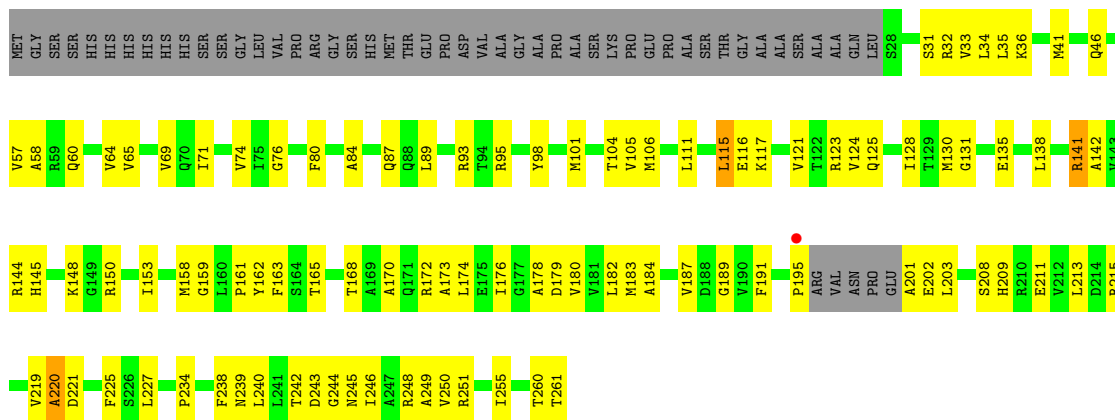
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	3	Total 3 O 3	0	0
4	B	2	Total 2 O 2	0	0
4	C	4	Total 4 O 4	0	0
4	D	5	Total 5 O 5	0	0

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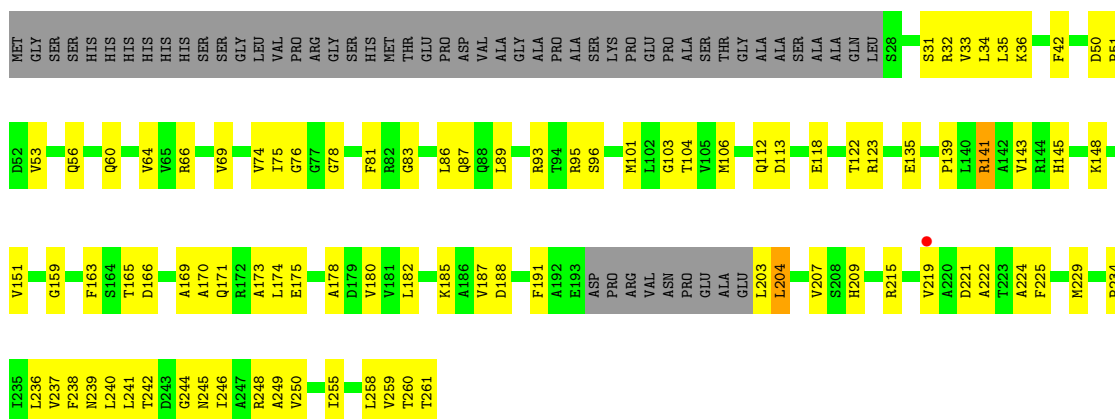
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
4	E	5	Total O 5 5	0	0
4	F	6	Total O 6 6	0	0
4	G	6	Total O 6 6	0	0
4	H	1	Total O 1 1	0	0
4	I	5	Total O 5 5	0	0
4	J	8	Total O 8 8	0	0
4	K	4	Total O 4 4	0	0
4	L	6	Total O 6 6	0	0

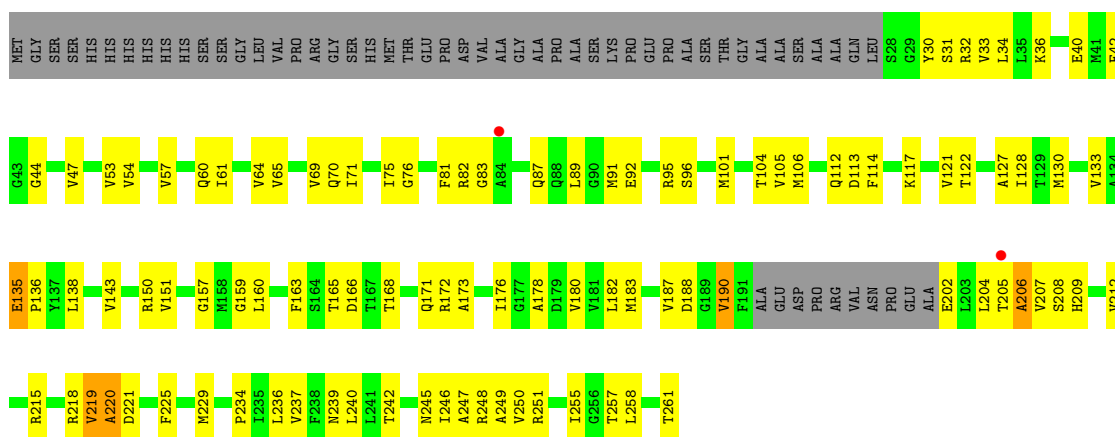




• Molecule 1: Uridylate kinase

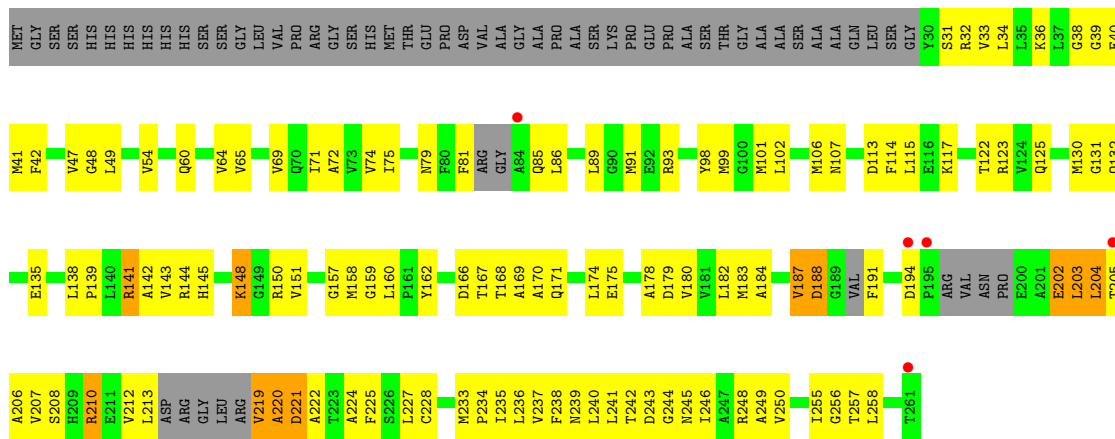


• Molecule 1: Uridylate kinase

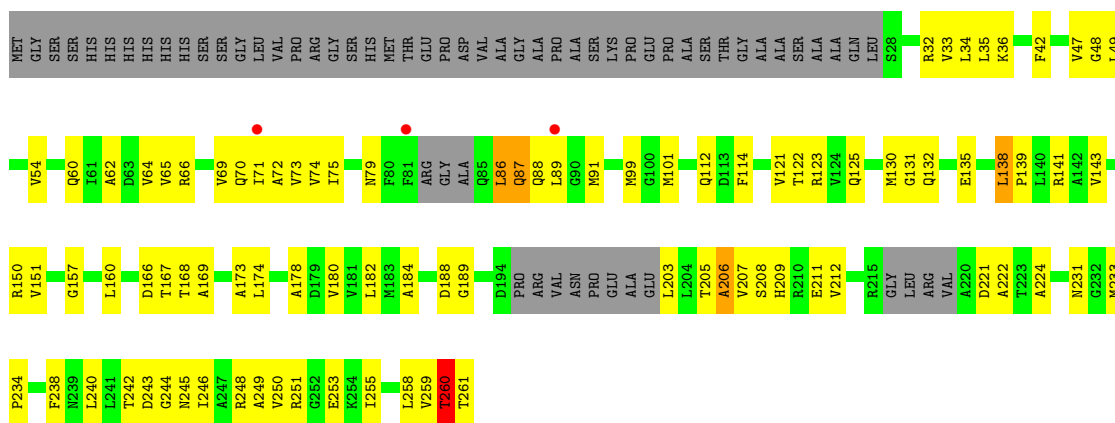


• Molecule 1: Uridylate kinase

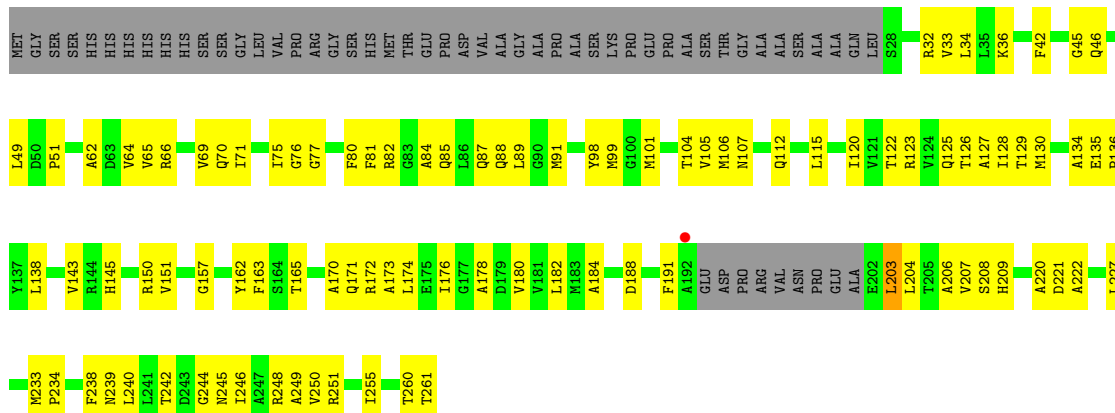




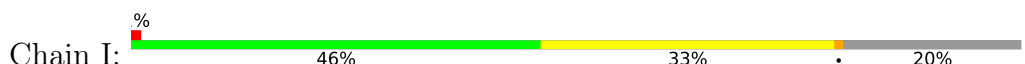
• Molecule 1: Uridylate kinase

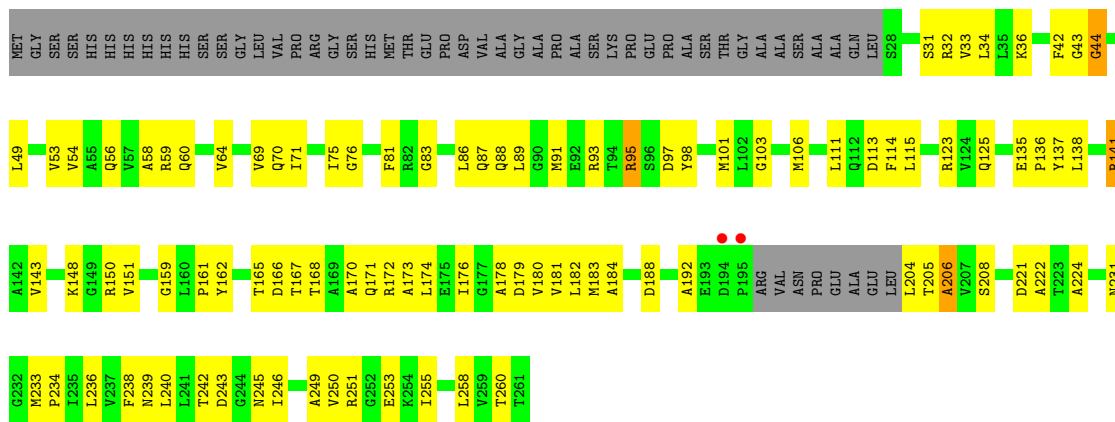


• Molecule 1: Uridylate kinase

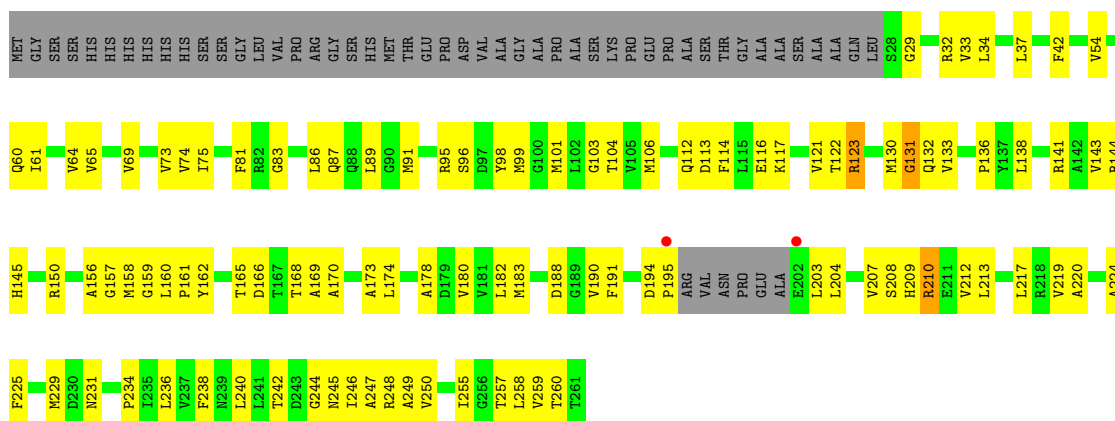
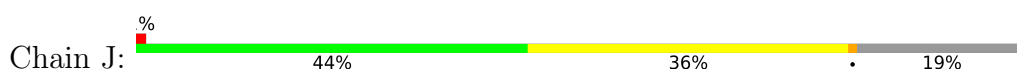


• Molecule 1: Uridylate kinase

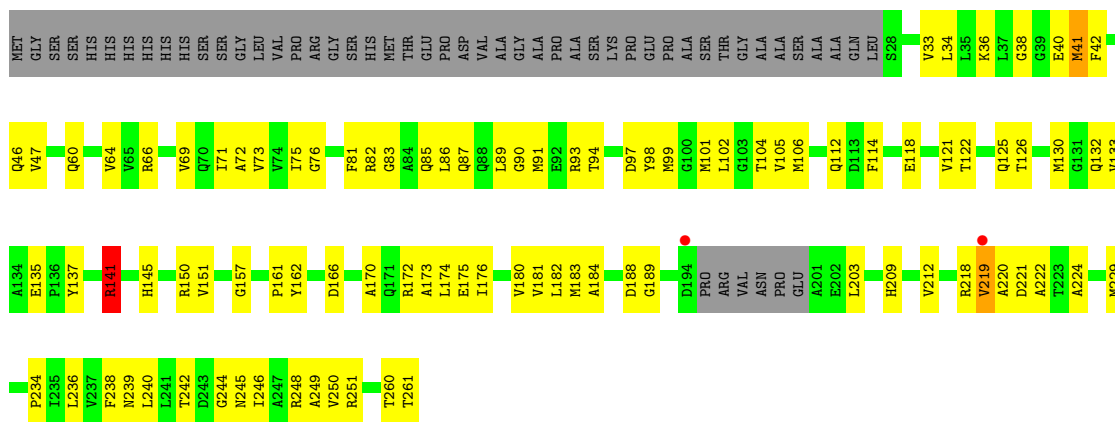




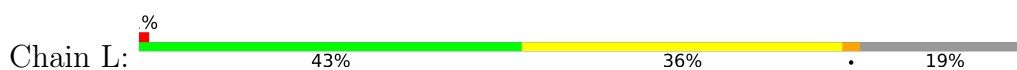
• Molecule 1: Uridylate kinase



• Molecule 1: Uridylate kinase



• Molecule 1: Uridylate kinase





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	197.47Å 152.82Å 125.11Å 90.00° 121.39° 90.00°	Depositor
Resolution (Å)	27.98 – 3.12 27.98 – 3.12	Depositor EDS
% Data completeness (in resolution range)	93.9 (27.98-3.12) 94.0 (27.98-3.12)	Depositor EDS
$R_{merge}$	0.21	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.65 (at 2.82Å)	Xtrriage
Refinement program	PHENIX 1.18	Depositor
R, $R_{free}$	0.191 , (Not available) 0.190 , 0.246	Depositor DCC
$R_{free}$ test set	2651 reflections (4.27%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.9	Xtrriage
Anisotropy	0.013	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 61.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	20295	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.88% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: UTP, UDP

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	0.31	0/1642	0.42	1/2220 (0.0%)
1	B	0.37	1/1672 (0.1%)	0.59	5/2259 (0.2%)
1	C	0.50	3/1713 (0.2%)	0.48	2/2314 (0.1%)
1	D	0.42	0/1674	0.44	0/2260
1	E	0.53	0/1670	0.51	1/2253 (0.0%)
1	F	0.28	0/1629	0.46	1/2198 (0.0%)
1	G	0.35	0/1599	0.43	1/2160 (0.0%)
1	H	0.13	0/1680	0.32	0/2268
1	I	0.28	0/1675	0.37	0/2264
1	J	0.42	1/1694 (0.1%)	0.41	0/2290
1	K	0.37	1/1691 (0.1%)	0.39	0/2284
1	L	0.43	0/1671	0.54	1/2260 (0.0%)
All	All	0.38	6/20010 (0.0%)	0.45	12/27030 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	138	LEU	C-O	-7.65	1.17	1.24
1	B	138	LEU	C-O	-6.65	1.19	1.25
1	C	138	LEU	CA-C	-6.52	1.45	1.52
1	K	141	ARG	C-O	-5.83	1.17	1.24
1	J	123	ARG	C-O	-5.73	1.17	1.23

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	217	LEU	N-CA-C	9.60	123.25	109.71
1	B	219	VAL	N-CA-C	8.12	119.54	108.17
1	B	218	ARG	N-CA-C	6.87	125.43	110.80
1	L	196	ARG	N-CA-C	-6.81	103.79	111.14
1	G	260	THR	N-CA-C	6.54	124.73	110.80

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1625	0	1634	107	0
1	B	1655	0	1672	101	0
1	C	1694	0	1721	86	0
1	D	1656	0	1679	88	0
1	E	1652	0	1674	107	0
1	F	1614	0	1630	130	0
1	G	1584	0	1585	96	0
1	H	1662	0	1690	98	0
1	I	1656	0	1673	104	0
1	J	1675	0	1697	102	0
1	K	1673	0	1693	104	0
1	L	1654	0	1654	124	0
2	A	29	11	11	5	0
2	C	29	11	11	4	0
2	D	29	11	11	3	0
2	G	29	11	11	1	0
2	I	29	11	11	6	0
2	J	29	11	11	1	0
3	B	25	0	11	3	0
3	C	25	0	11	0	0
3	D	25	0	11	2	0
3	E	25	0	11	3	0
3	H	25	0	11	0	0
3	I	25	0	11	2	0
3	J	25	0	11	3	0
3	K	25	0	11	5	0
4	A	3	0	0	0	0
4	B	2	0	0	0	0
4	C	4	0	0	0	0
4	D	5	0	0	0	0
4	E	5	0	0	1	0
4	F	6	0	0	0	0
4	G	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	1	0	0	0	0
4	I	5	0	0	0	0
4	J	8	0	0	1	0
4	K	4	0	0	0	0
4	L	6	0	0	0	0
All	All	20229	66	20156	1181	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 29.

The worst 5 of 1181 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:I:184:ALA:HB1	1:I:240:LEU:HD22	1.28	1.16
1:L:122:THR:HG22	1:L:151:VAL:HB	1.27	1.12
1:L:191:PHE:CE1	1:L:203:LEU:HD13	1.84	1.12
1:E:190:VAL:HG23	1:E:257:THR:CB	1.83	1.09
1:H:69:VAL:HG21	1:H:250:VAL:HG11	1.35	1.09

There are no symmetry-related clashes.

## 5.3 Torsion angles [\(i\)](#)

### 5.3.1 Protein backbone [\(i\)](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	218/281 (78%)	205 (94%)	12 (6%)	1 (0%)	24 55
1	B	222/281 (79%)	199 (90%)	16 (7%)	7 (3%)	3 16
1	C	225/281 (80%)	212 (94%)	11 (5%)	2 (1%)	14 42
1	D	221/281 (79%)	211 (96%)	9 (4%)	1 (0%)	24 55
1	E	220/281 (78%)	203 (92%)	14 (6%)	3 (1%)	9 31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	210/281 (75%)	186 (89%)	15 (7%)	9 (4%)	2	11
1	G	211/281 (75%)	196 (93%)	9 (4%)	6 (3%)	4	19
1	H	221/281 (79%)	211 (96%)	6 (3%)	4 (2%)	6	26
1	I	222/281 (79%)	203 (91%)	17 (8%)	2 (1%)	14	42
1	J	224/281 (80%)	211 (94%)	12 (5%)	1 (0%)	30	60
1	K	224/281 (80%)	202 (90%)	18 (8%)	4 (2%)	6	26
1	L	221/281 (79%)	204 (92%)	10 (4%)	7 (3%)	3	16
All	All	2639/3372 (78%)	2443 (93%)	149 (6%)	47 (2%)	6	26

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	131	GLY
1	B	220	ALA
1	B	243	ASP
1	E	219	VAL
1	F	188	ASP

### 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	164/215 (76%)	160 (98%)	4 (2%)	43	67
1	B	168/215 (78%)	164 (98%)	4 (2%)	43	67
1	C	174/215 (81%)	171 (98%)	3 (2%)	53	72
1	D	168/215 (78%)	165 (98%)	3 (2%)	51	71
1	E	168/215 (78%)	162 (96%)	6 (4%)	31	59
1	F	163/215 (76%)	155 (95%)	8 (5%)	22	51
1	G	158/215 (74%)	156 (99%)	2 (1%)	61	75
1	H	170/215 (79%)	170 (100%)	0	100	100
1	I	168/215 (78%)	166 (99%)	2 (1%)	63	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	171/215 (80%)	168 (98%)	3 (2%)	51	71
1	K	169/215 (79%)	167 (99%)	2 (1%)	63	76
1	L	166/215 (77%)	163 (98%)	3 (2%)	51	71
All	All	2007/2580 (78%)	1967 (98%)	40 (2%)	48	70

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	138	LEU
1	K	85	GLN
1	G	211	GLU
1	J	141	ARG
1	L	93	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	46	GLN
1	I	245	ASN
1	L	60	GLN
1	J	245	ASN
1	K	245	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](#)

14 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	UDP	J	302	-	25,26,26	0.46	0	38,40,40	0.60	1 (2%)
3	UDP	I	302	-	25,26,26	0.46	0	38,40,40	0.68	1 (2%)
3	UDP	D	302	-	25,26,26	0.25	0	38,40,40	0.37	0
2	UTP	G	301	-	29,30,30	2.72	13 (44%)	43,47,47	1.81	10 (23%)
3	UDP	B	300	-	25,26,26	0.43	0	38,40,40	0.61	1 (2%)
2	UTP	J	301	-	29,30,30	2.25	17 (58%)	43,47,47	2.04	16 (37%)
3	UDP	E	301	-	25,26,26	0.50	0	38,40,40	0.69	1 (2%)
2	UTP	D	301	-	29,30,30	2.69	12 (41%)	43,47,47	1.72	8 (18%)
2	UTP	A	301	-	29,30,30	2.80	12 (41%)	43,47,47	1.88	12 (27%)
3	UDP	K	301	-	25,26,26	0.52	0	38,40,40	0.68	1 (2%)
2	UTP	C	301	-	29,30,30	2.58	11 (37%)	43,47,47	1.82	12 (27%)
2	UTP	I	301	-	29,30,30	2.23	15 (51%)	43,47,47	2.00	13 (30%)
3	UDP	C	302	-	25,26,26	0.47	0	38,40,40	0.67	1 (2%)
3	UDP	H	301	-	25,26,26	0.23	0	38,40,40	0.38	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	UDP	J	302	-	-	4/16/32/32	0/2/2/2
3	UDP	I	302	-	-	1/16/32/32	0/2/2/2
3	UDP	D	302	-	-	4/16/32/32	0/2/2/2
2	UTP	G	301	-	-	8/22/38/38	0/2/2/2
3	UDP	B	300	-	-	3/16/32/32	0/2/2/2
2	UTP	J	301	-	-	1/22/38/38	0/2/2/2
3	UDP	E	301	-	-	1/16/32/32	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UTP	D	301	-	-	2/22/38/38	0/2/2/2
2	UTP	A	301	-	-	5/22/38/38	0/2/2/2
3	UDP	K	301	-	-	2/16/32/32	0/2/2/2
2	UTP	C	301	-	-	9/22/38/38	0/2/2/2
2	UTP	I	301	-	-	8/22/38/38	0/2/2/2
3	UDP	C	302	-	-	1/16/32/32	0/2/2/2
3	UDP	H	301	-	-	3/16/32/32	0/2/2/2

The worst 5 of 80 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	UTP	PA-O3A	6.15	1.66	1.59
2	A	301	UTP	PB-O3A	6.06	1.66	1.59
2	G	301	UTP	PA-O3A	5.78	1.65	1.59
2	D	301	UTP	PA-O3A	5.69	1.65	1.59
2	G	301	UTP	PB-O3A	5.62	1.65	1.59

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	301	UTP	C4-N3-C2	-5.57	119.70	126.61
2	D	301	UTP	C4-N3-C2	-5.57	119.70	126.61
2	I	301	UTP	C4-N3-C2	-5.47	119.82	126.61
2	A	301	UTP	C4-N3-C2	-5.44	119.86	126.61
2	J	301	UTP	C4-N3-C2	-5.38	119.94	126.61

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

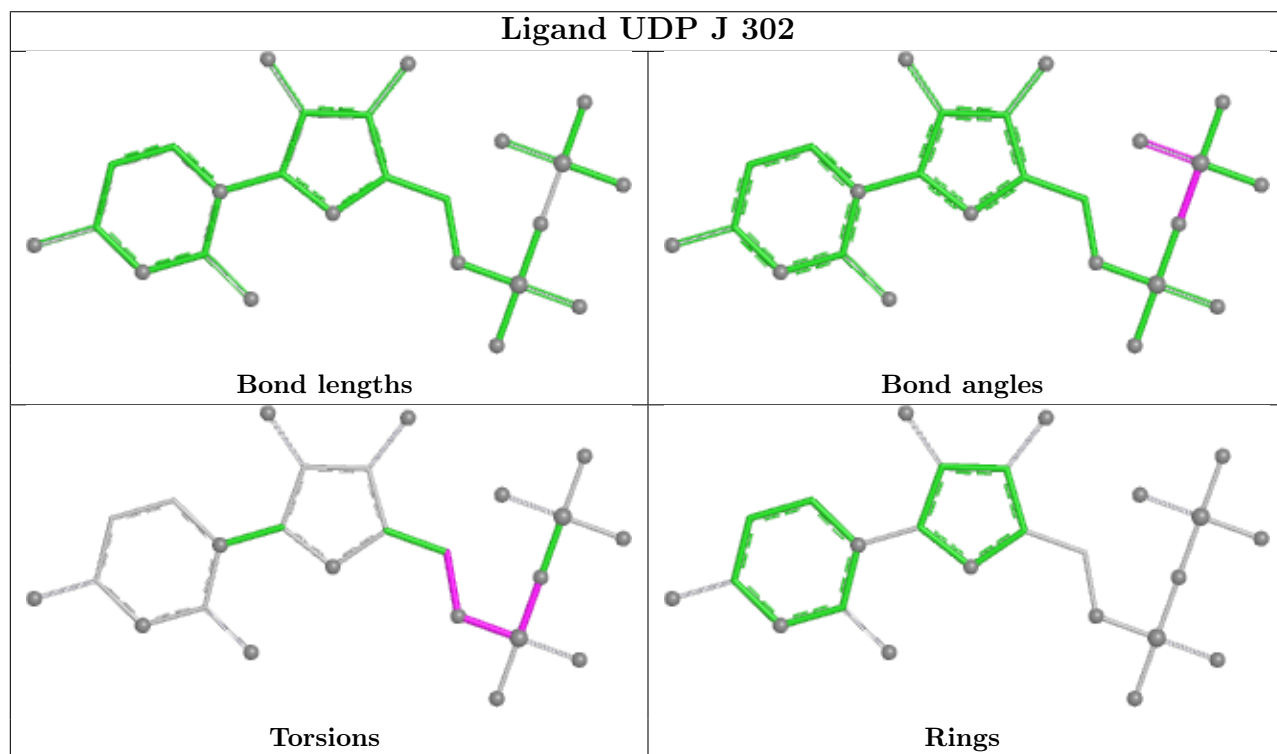
Mol	Chain	Res	Type	Atoms
2	A	301	UTP	C5'-O5'-PA-O2A
2	A	301	UTP	C5'-O5'-PA-O3A
2	A	301	UTP	O4'-C4'-C5'-O5'
2	D	301	UTP	PB-O3B-PG-O1G
2	G	301	UTP	PB-O3B-PG-O1G

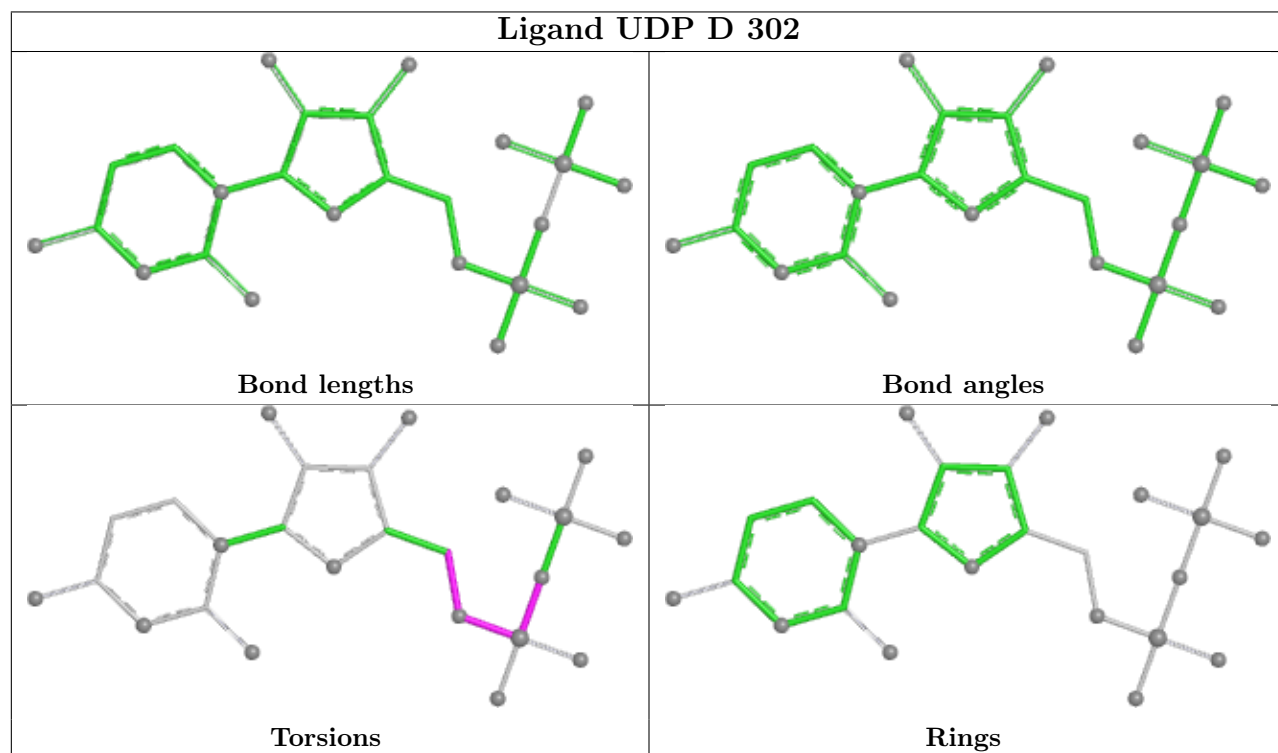
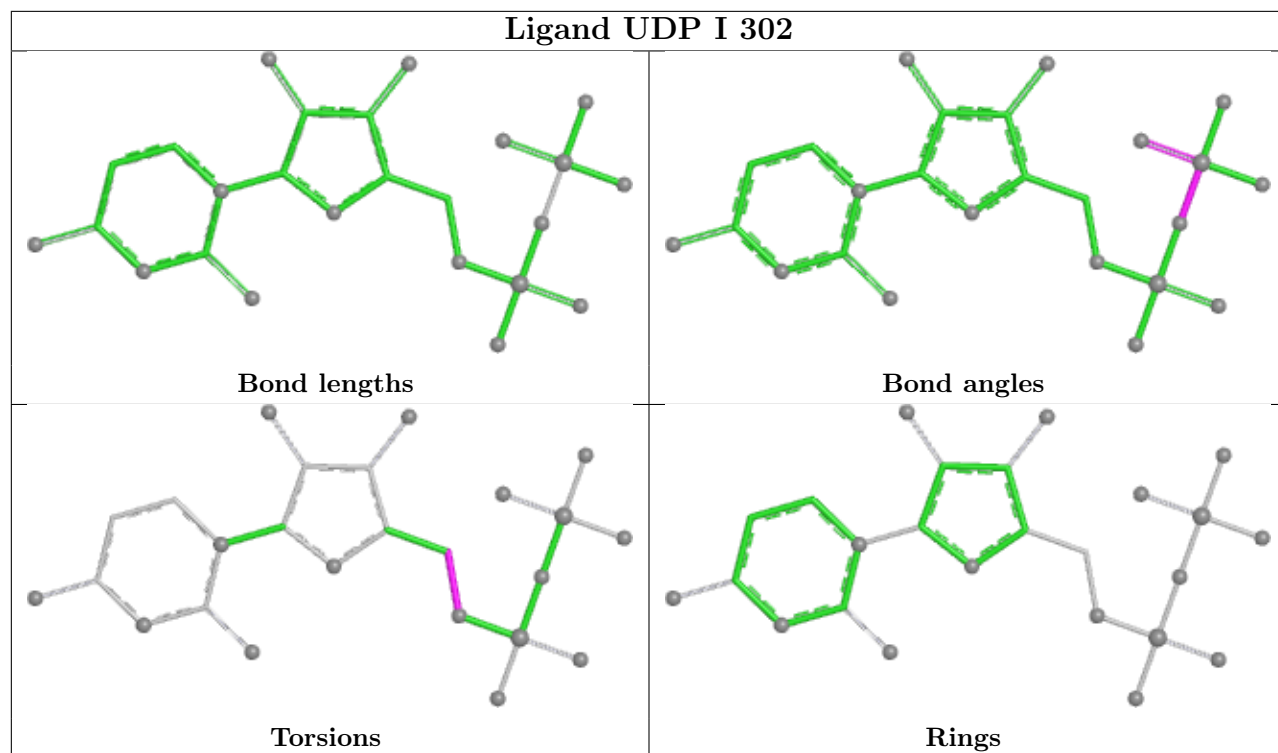
There are no ring outliers.

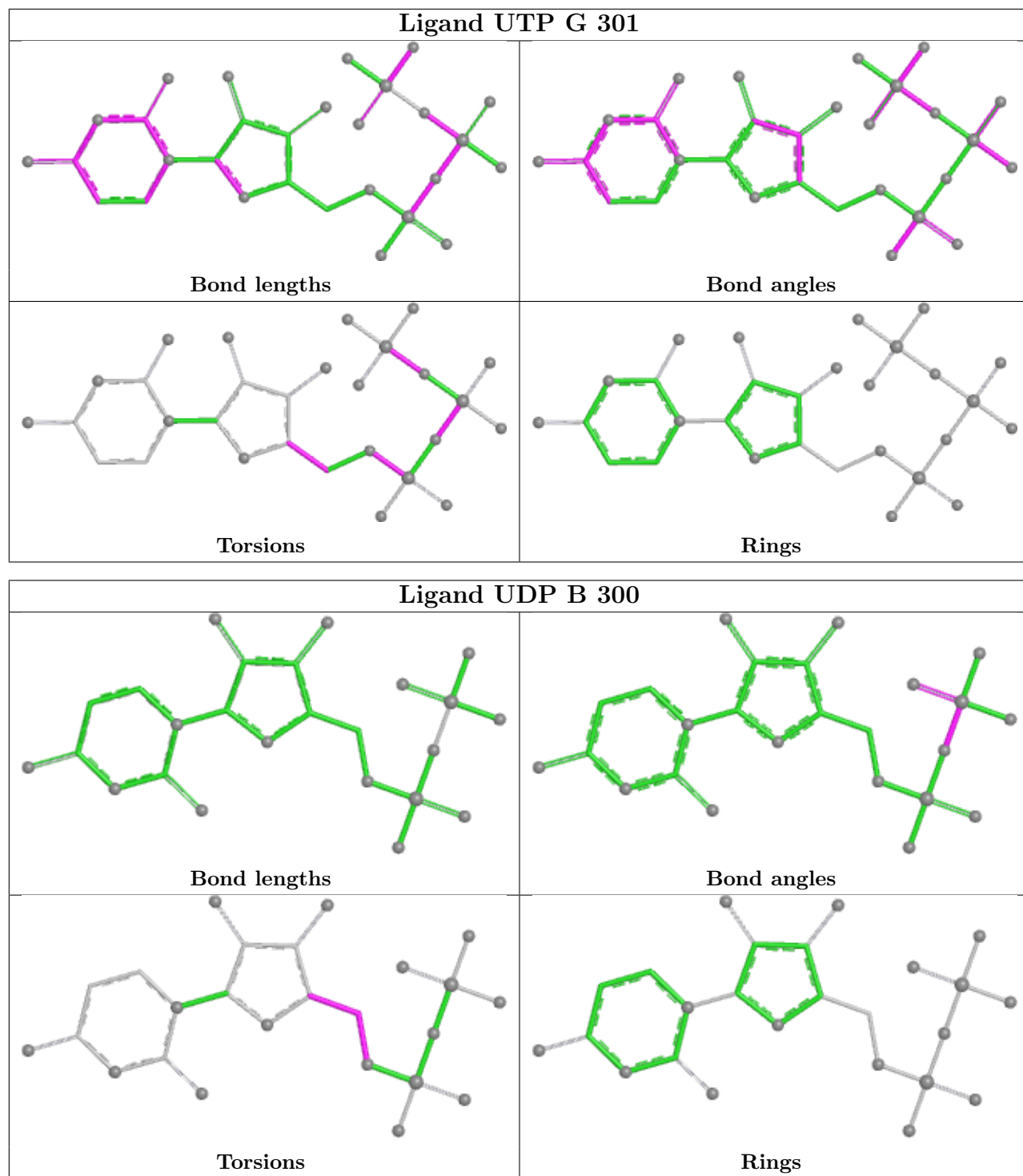
12 monomers are involved in 38 short contacts:

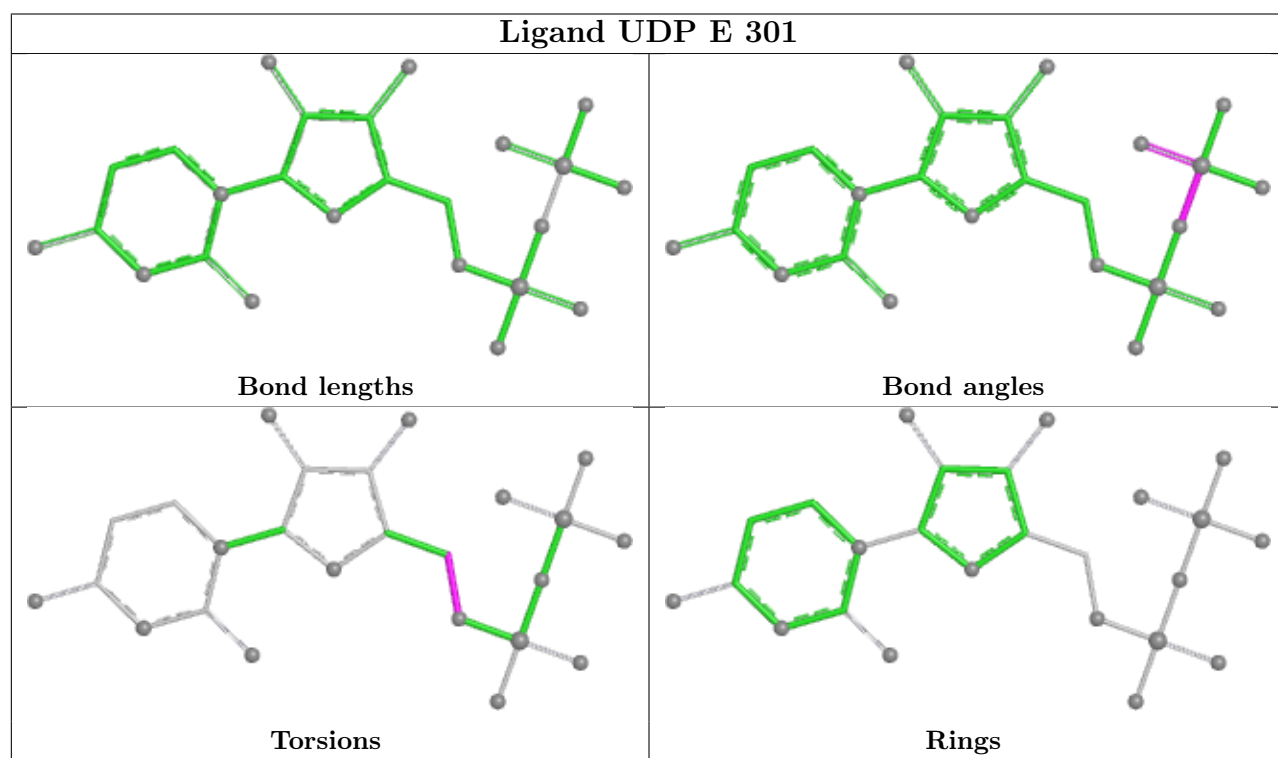
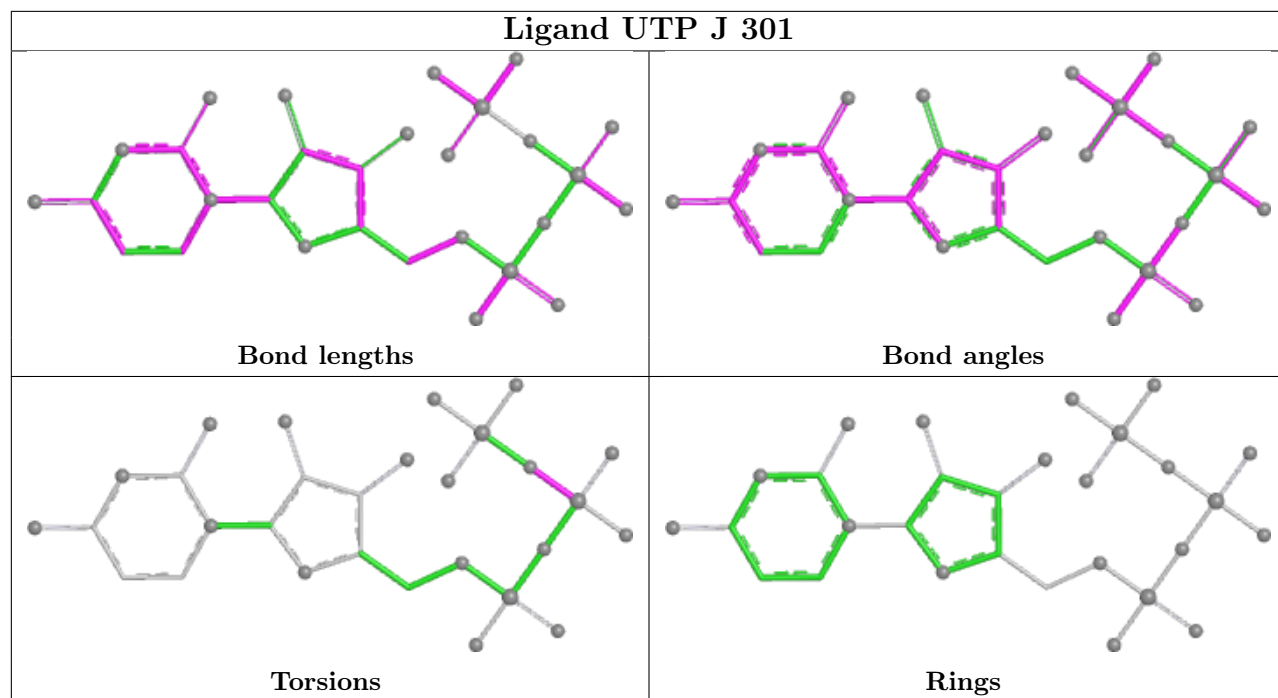
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	J	302	UDP	3	0
3	I	302	UDP	2	0
3	D	302	UDP	2	0
2	G	301	UTP	1	0
3	B	300	UDP	3	0
2	J	301	UTP	1	0
3	E	301	UDP	3	0
2	D	301	UTP	3	0
2	A	301	UTP	5	0
3	K	301	UDP	5	0
2	C	301	UTP	4	0
2	I	301	UTP	6	0

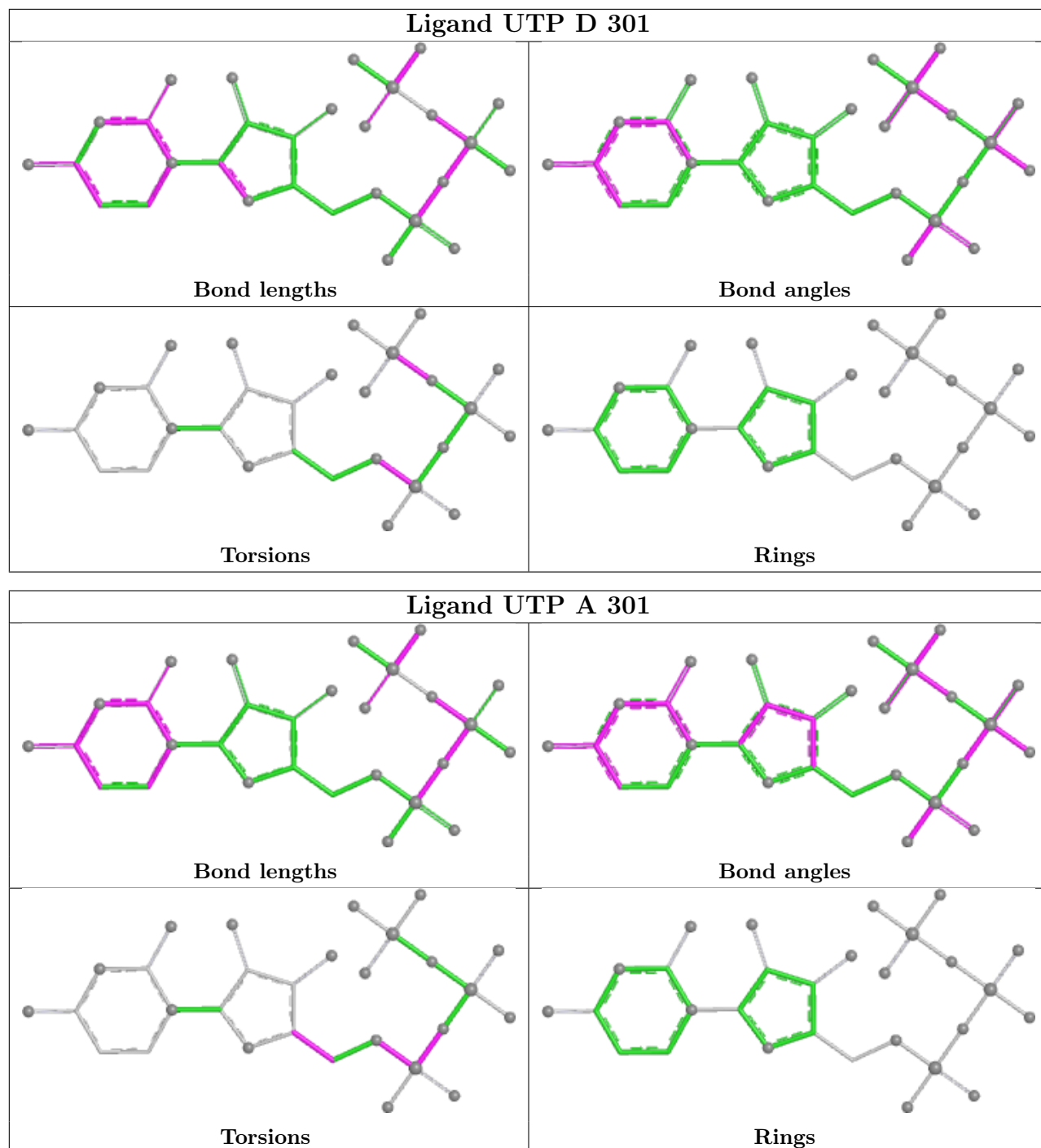
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

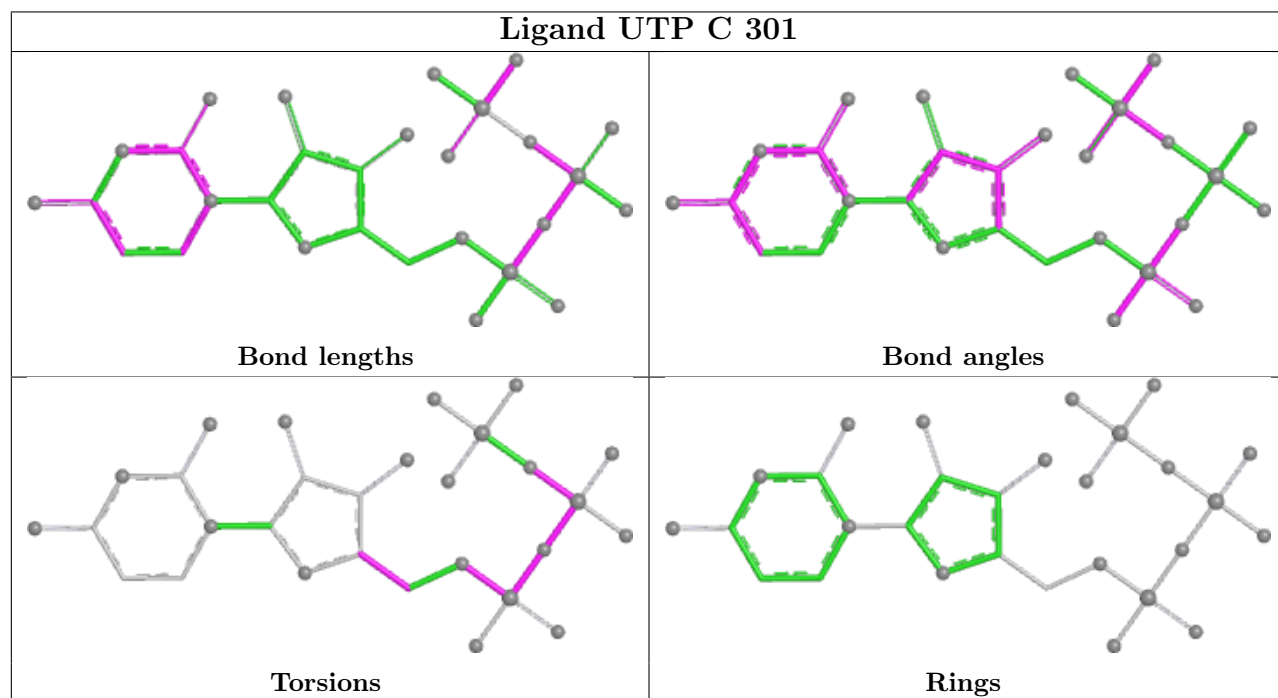
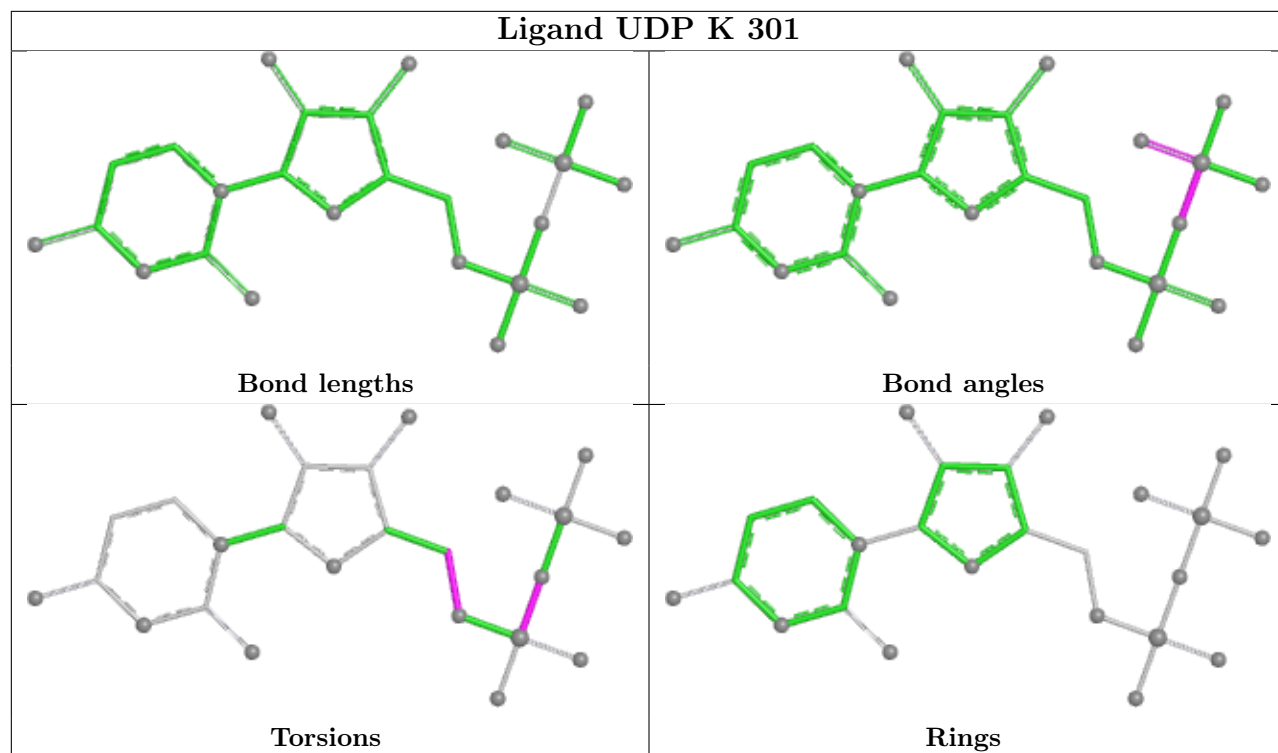


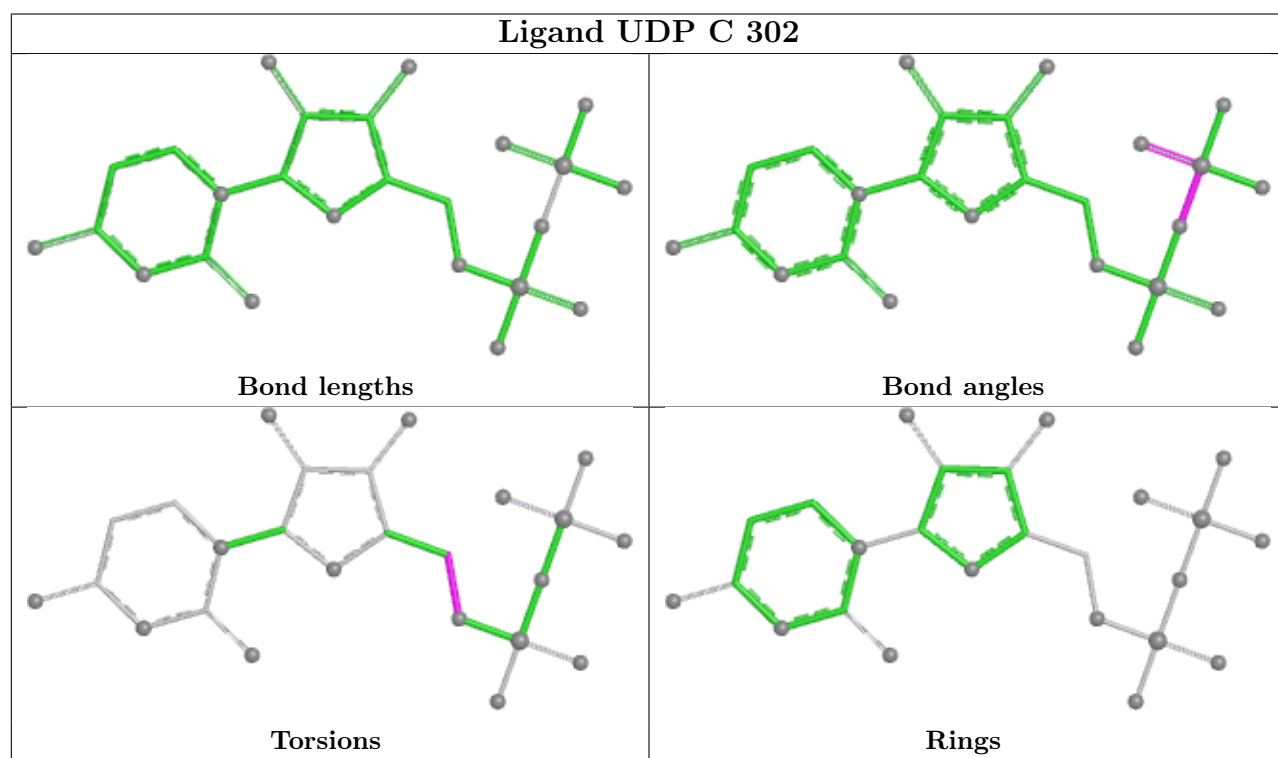
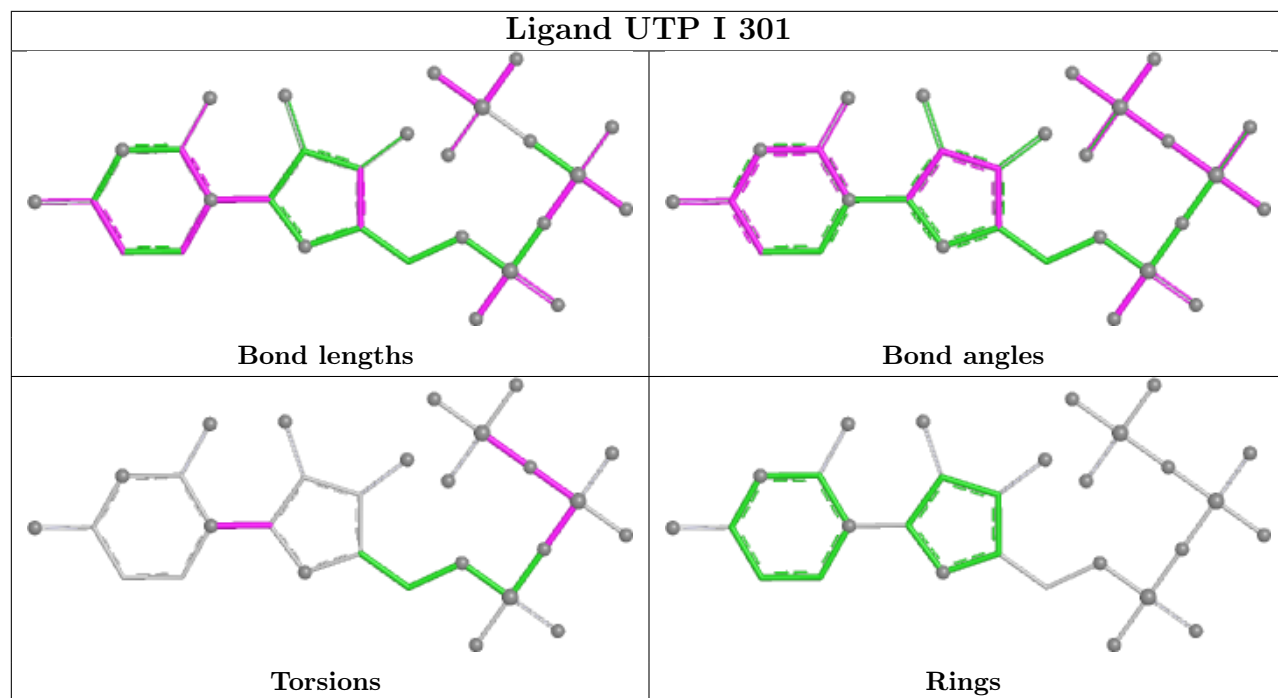


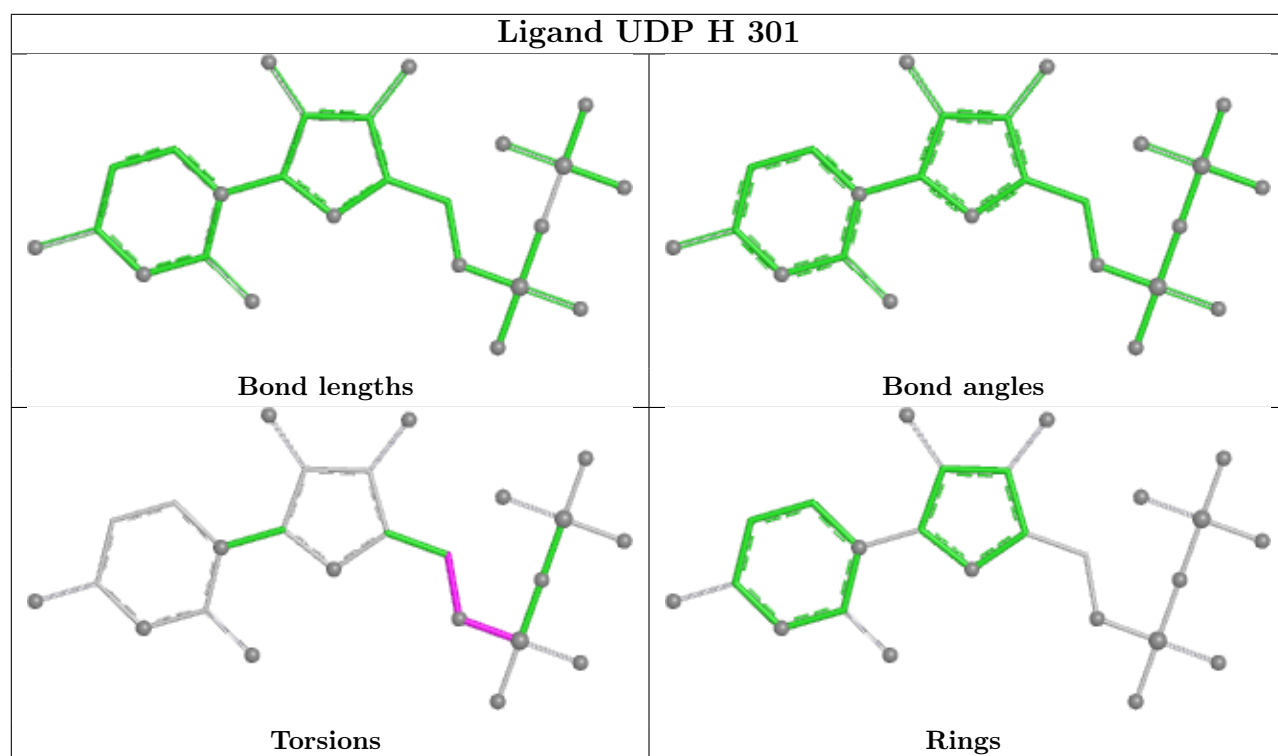












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	224/281 (79%)	-0.06	6 (2%) 56 35	30, 63, 105, 134	13 (5%)
1	B	226/281 (80%)	-0.23	1 (0%) 88 76	29, 62, 114, 135	9 (3%)
1	C	229/281 (81%)	-0.46	1 (0%) 88 76	22, 40, 95, 144	6 (2%)
1	D	225/281 (80%)	-0.33	1 (0%) 88 76	21, 50, 98, 131	4 (1%)
1	E	224/281 (79%)	-0.18	2 (0%) 81 63	20, 51, 102, 133	5 (2%)
1	F	220/281 (78%)	0.18	5 (2%) 61 39	40, 95, 138, 157	8 (3%)
1	G	219/281 (77%)	-0.01	3 (1%) 73 53	34, 75, 119, 145	10 (4%)
1	H	225/281 (80%)	-0.26	1 (0%) 88 76	33, 60, 105, 130	5 (2%)
1	I	226/281 (80%)	-0.27	2 (0%) 81 63	26, 54, 118, 143	7 (3%)
1	J	228/281 (81%)	-0.23	2 (0%) 81 63	23, 48, 103, 135	13 (5%)
1	K	228/281 (81%)	-0.21	2 (0%) 81 63	22, 48, 97, 124	8 (3%)
1	L	227/281 (80%)	-0.03	3 (1%) 75 56	22, 68, 108, 141	8 (3%)
All	All	2701/3372 (80%)	-0.18	29 (1%) 78 59	20, 59, 115, 157	96 (3%)

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	85	GLN	7.0
1	K	194	ASP	5.6
1	A	86	LEU	5.5
1	F	194	ASP	5.3
1	I	195	PRO	4.8

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

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

### 6.3 Carbohydrates [i](#)

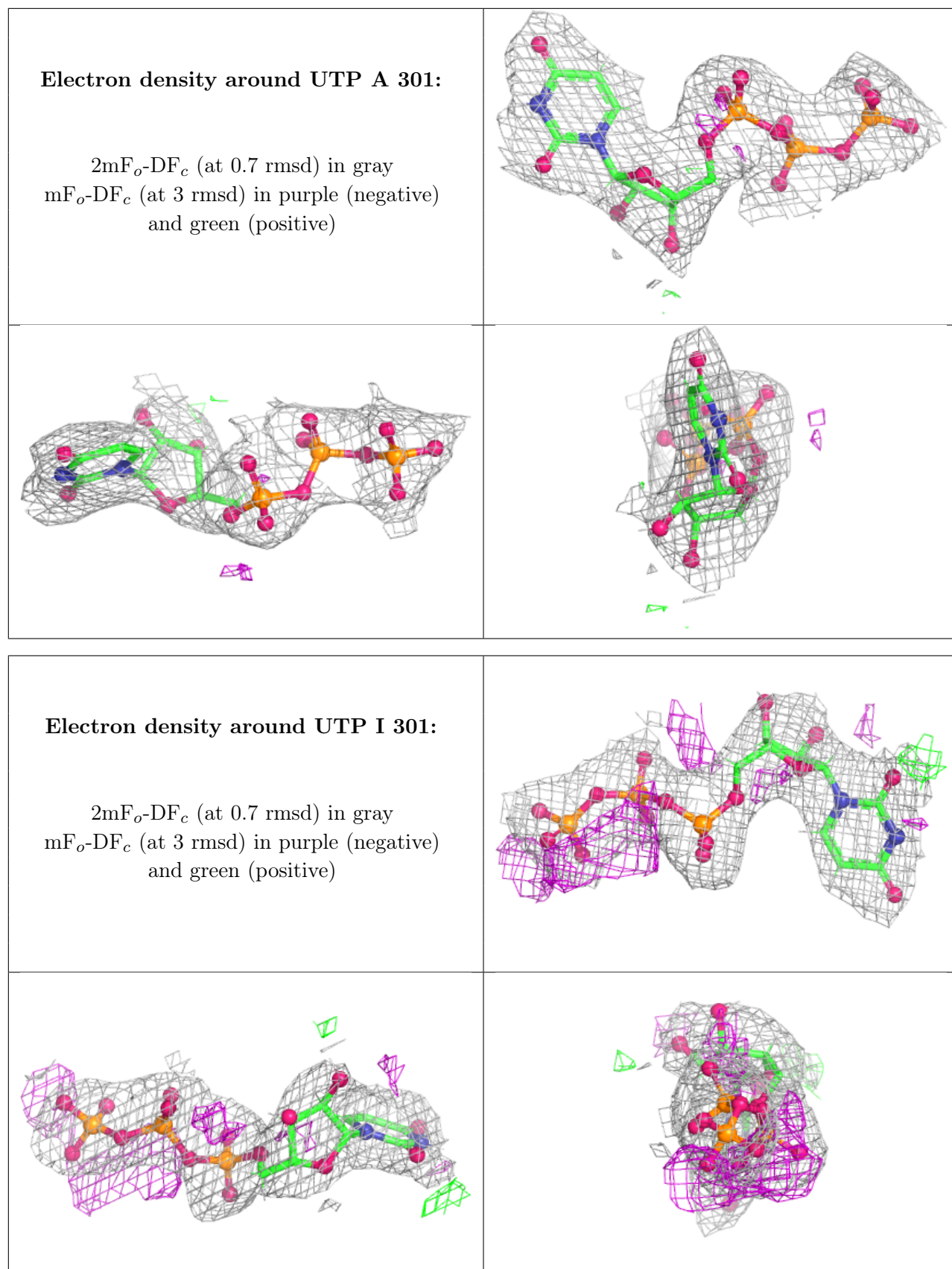
There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

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

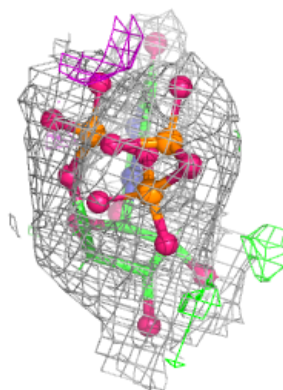
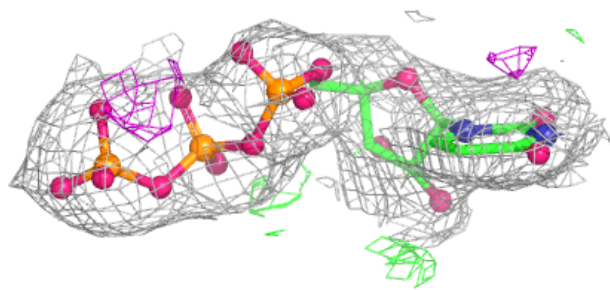
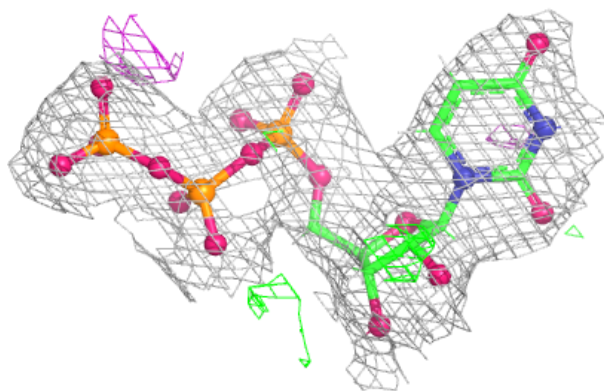
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	UTP	A	301	29/29	0.90	0.09	38,73,97,101	0
2	UTP	I	301	29/29	0.91	0.08	43,68,82,82	0
2	UTP	G	301	29/29	0.92	0.09	53,69,79,84	0
3	UDP	K	301	25/25	0.92	0.11	55,81,90,93	0
3	UDP	H	301	25/25	0.93	0.09	50,66,78,83	0
2	UTP	J	301	29/29	0.93	0.08	44,55,78,79	0
3	UDP	B	300	25/25	0.94	0.08	39,52,61,62	0
3	UDP	E	301	25/25	0.94	0.09	57,64,79,80	0
2	UTP	D	301	29/29	0.95	0.08	2,13,31,38	40
3	UDP	J	302	25/25	0.95	0.07	38,56,66,72	0
2	UTP	C	301	29/29	0.95	0.07	27,43,69,73	0
3	UDP	D	302	25/25	0.96	0.07	36,48,58,62	0
3	UDP	I	302	25/25	0.96	0.07	28,38,54,61	0
3	UDP	C	302	25/25	0.97	0.07	24,32,47,57	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.

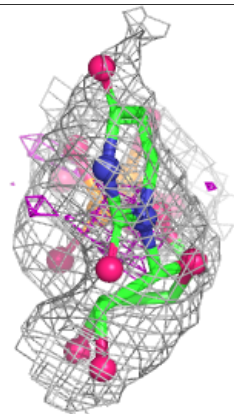
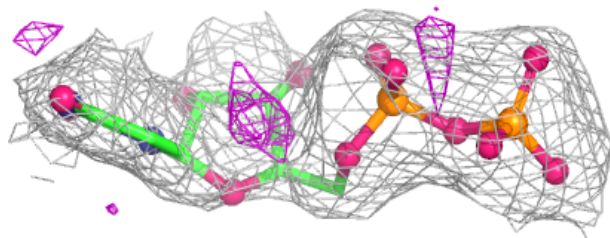
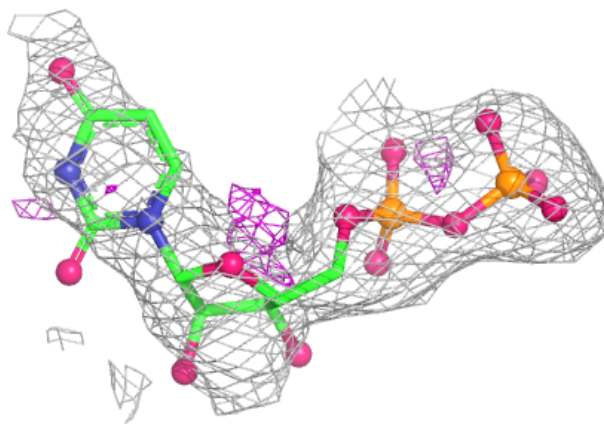


**Electron density around UTP G 301:**

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

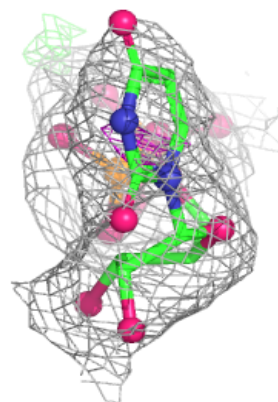
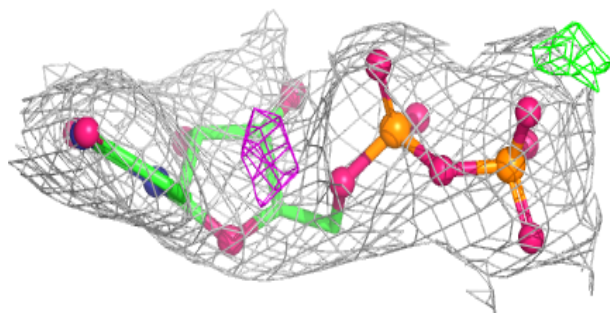
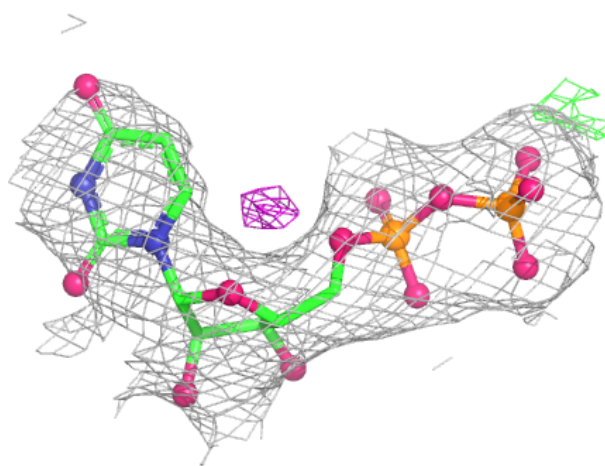
**Electron density around UDP K 301:**

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



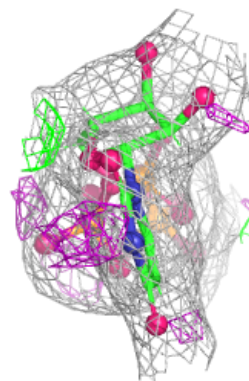
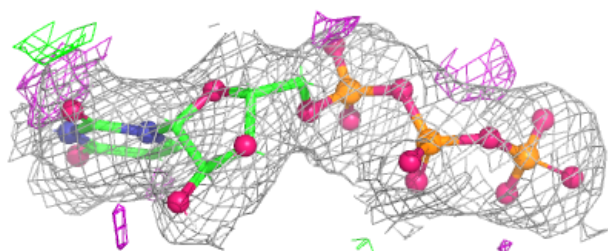
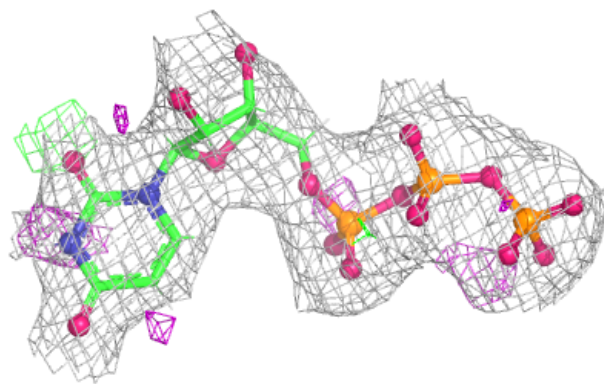
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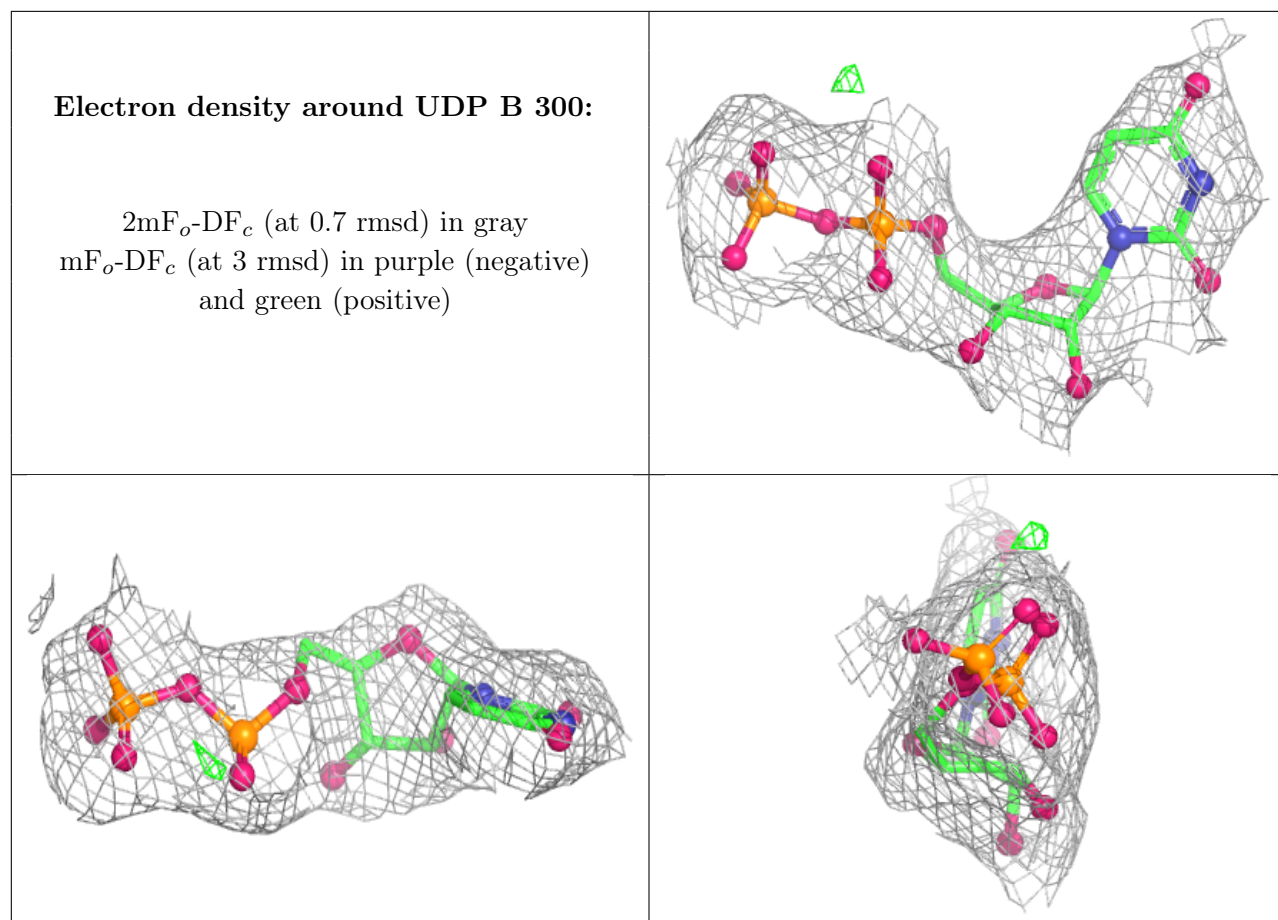
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around UTP J 301:**

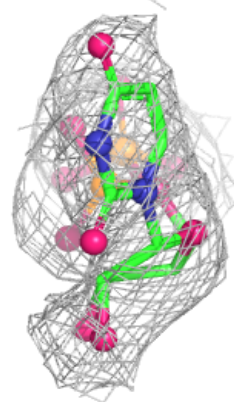
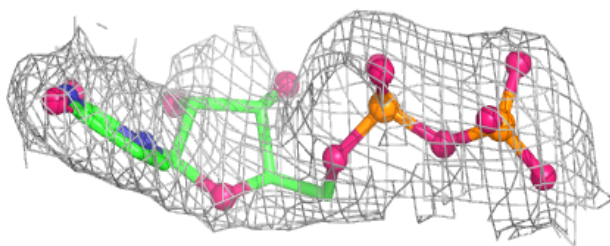
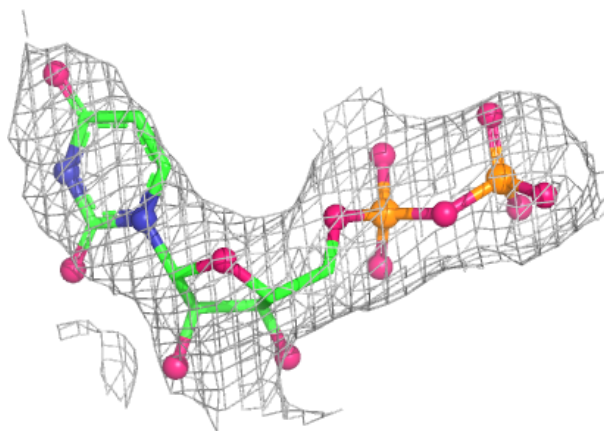
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



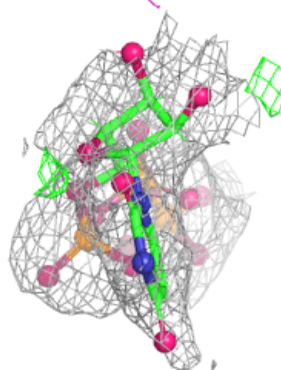
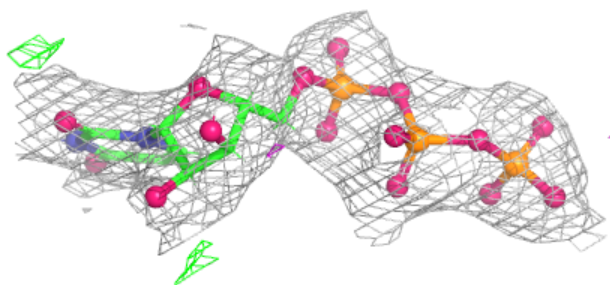
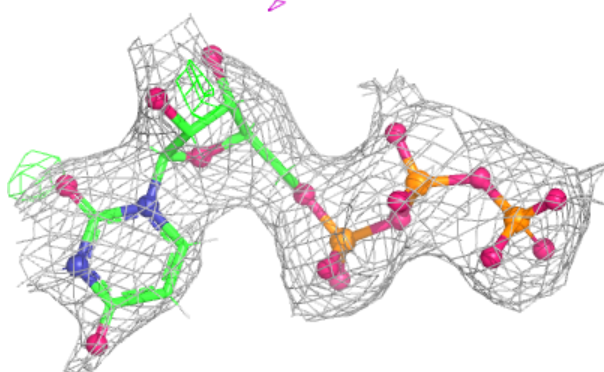


**Electron density around UDP E 301:**

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and green (positive)

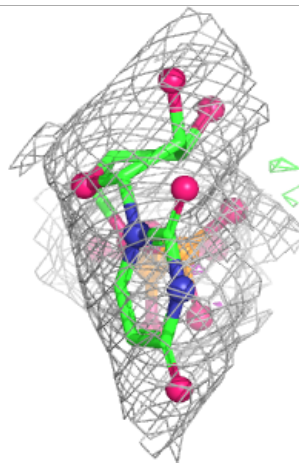
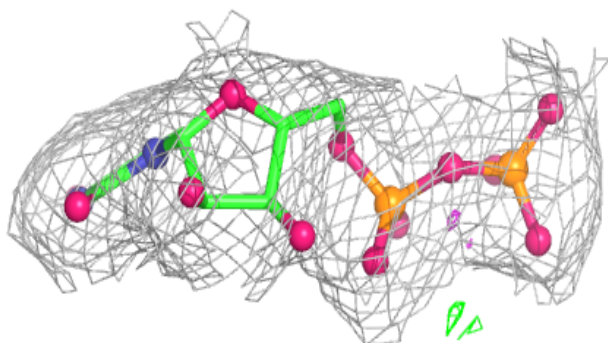
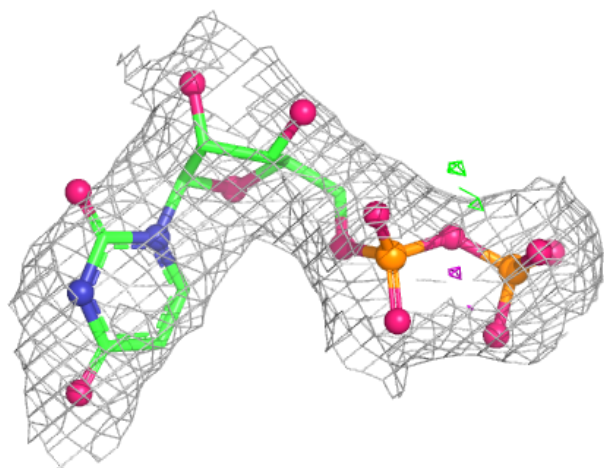
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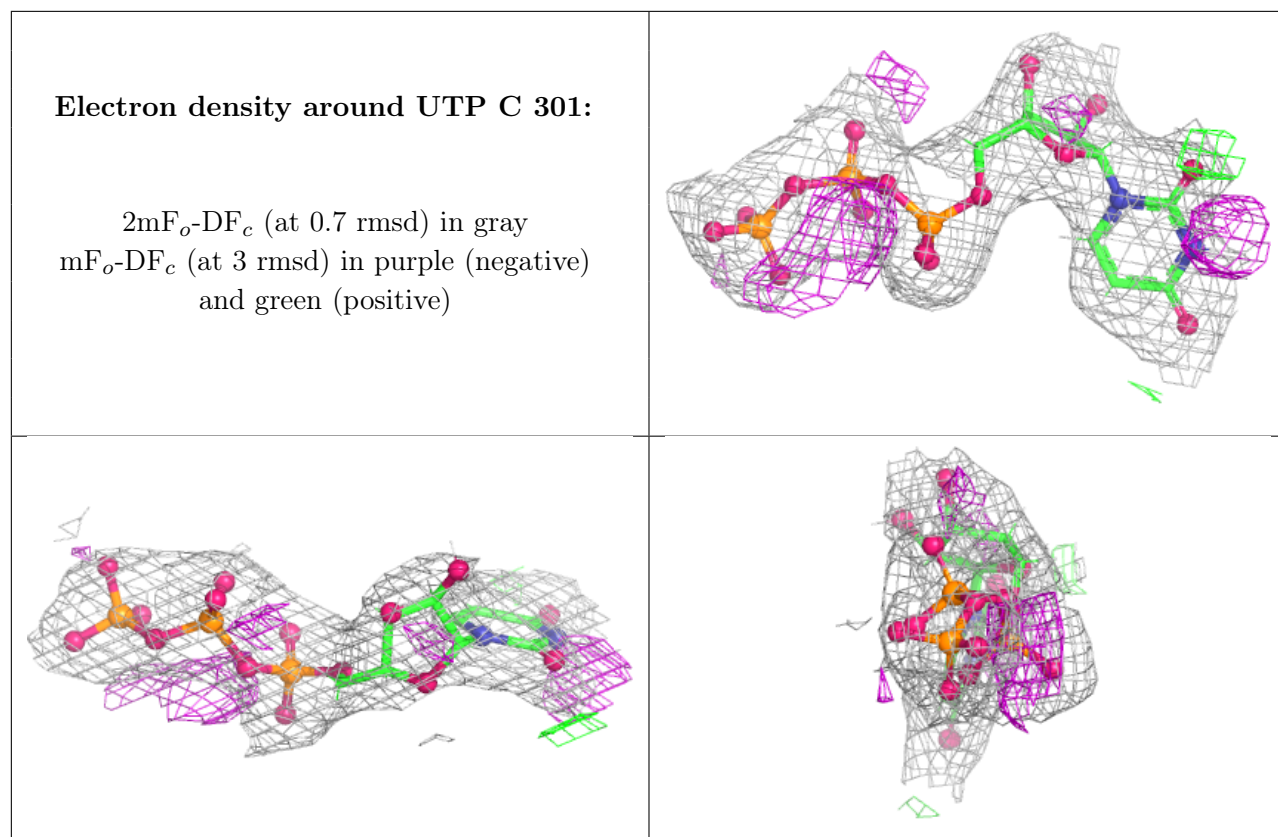
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around UDP J 302:**

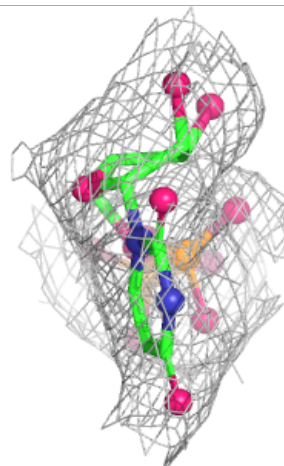
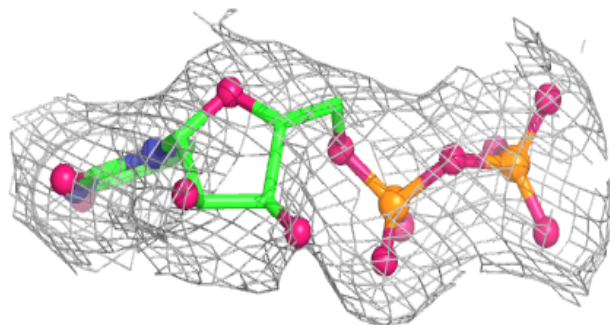
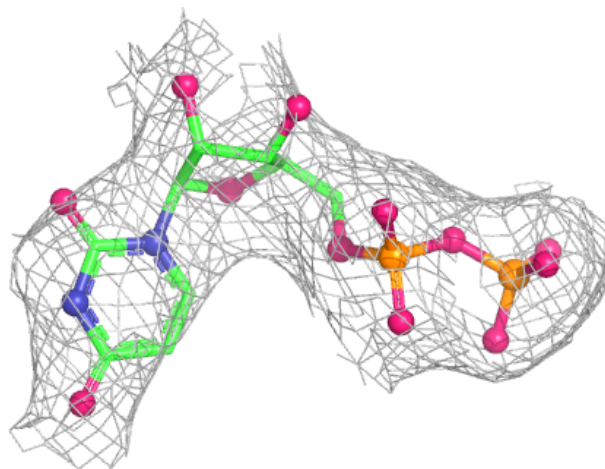
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





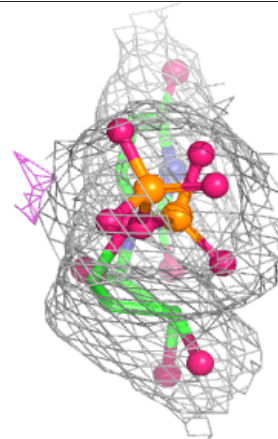
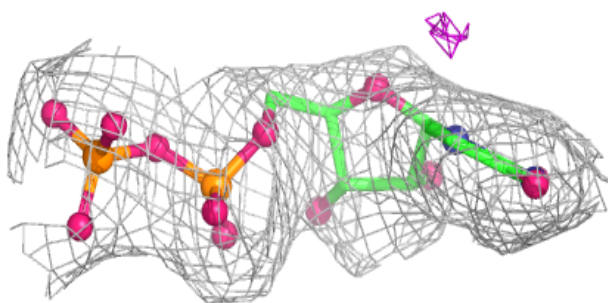
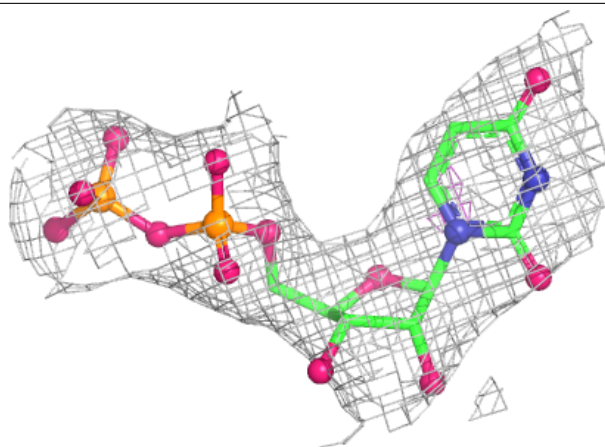
**Electron density around UDP D 302:**

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

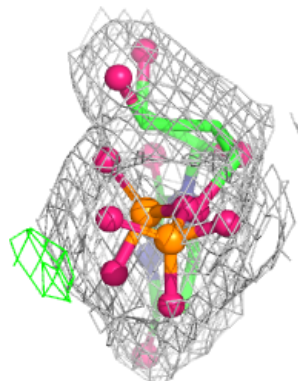
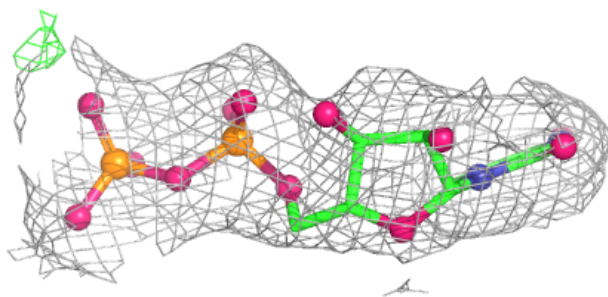
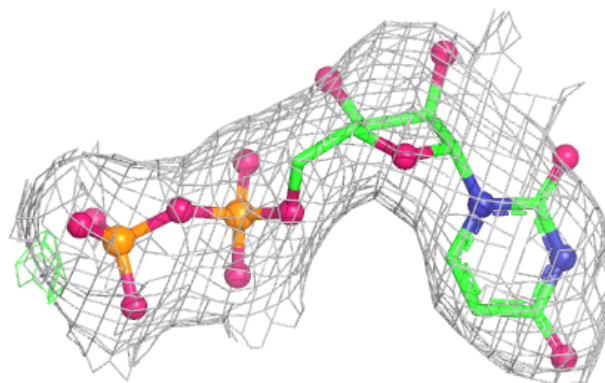


**Electron density around UDP I 302:**

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

**Electron density around UDP C 302:**

$2mF_o-DF_c$  (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.