



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 03:30 AM UTC

PDB ID : 2C37 / pdb_00002c37
Title : RNASE PH CORE OF THE ARCHAEAL EXOSOME IN COMPLEX WITH
U8 RNA
Authors : Lorentzen, E.; Conti, E.
Deposited on : 2005-10-04
Resolution : 2.80 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

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)
Xtriage (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

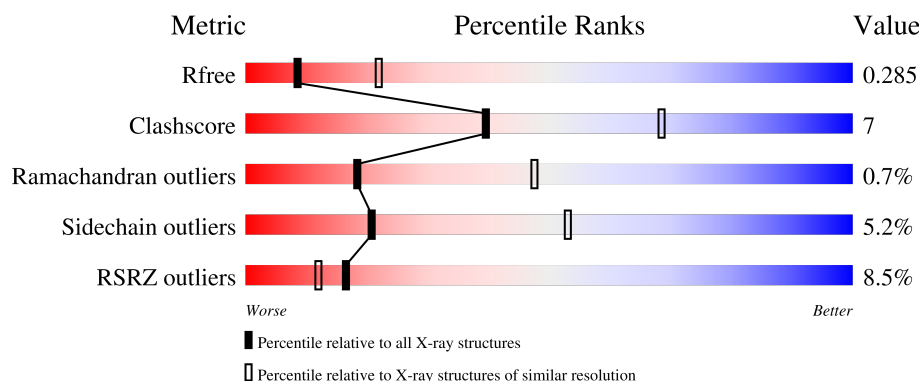
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	275	12% 80% 13% • 5%
1	C	275	8% 81% 12% • 5%
1	E	275	9% 82% 11% • 5%
1	G	275	13% 80% 13% • 5%
1	I	275	9% 81% 13% • 5%

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Mol	Chain	Length	Quality of chain
1	K	275	
1	M	275	
1	O	275	
1	Q	275	
1	S	275	
1	U	275	
1	W	275	
2	B	248	
2	D	248	
2	F	248	
2	H	248	
2	J	248	
2	L	248	
2	N	248	
2	P	248	
2	R	248	
2	T	248	
2	V	248	
2	X	248	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 46570 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 PROBABLE EXOSOME COMPLEX EXONUCLEASE 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	0	0
			1963	1249	323	386	5			
1	C	260	Total	C	N	O	S	0	0	0
			1972	1255	325	387	5			
1	E	260	Total	C	N	O	S	0	0	0
			1968	1253	324	386	5			
1	G	260	Total	C	N	O	S	0	0	0
			1964	1251	324	384	5			
1	I	260	Total	C	N	O	S	0	0	0
			1961	1250	323	383	5			
1	K	260	Total	C	N	O	S	0	0	0
			1964	1251	324	384	5			
1	M	260	Total	C	N	O	S	0	0	0
			1975	1256	325	389	5			
1	O	260	Total	C	N	O	S	0	0	0
			1968	1253	325	385	5			
1	Q	260	Total	C	N	O	S	0	0	0
			1968	1253	325	385	5			
1	S	260	Total	C	N	O	S	0	0	0
			1967	1253	324	385	5			
1	U	260	Total	C	N	O	S	0	0	0
			1968	1253	325	385	5			
1	W	260	Total	C	N	O	S	0	0	0
			1975	1256	324	390	5			

- Molecule 2 is a protein called PROBABLE EXOSOME COMPLEX EXONUCLEASE 1.

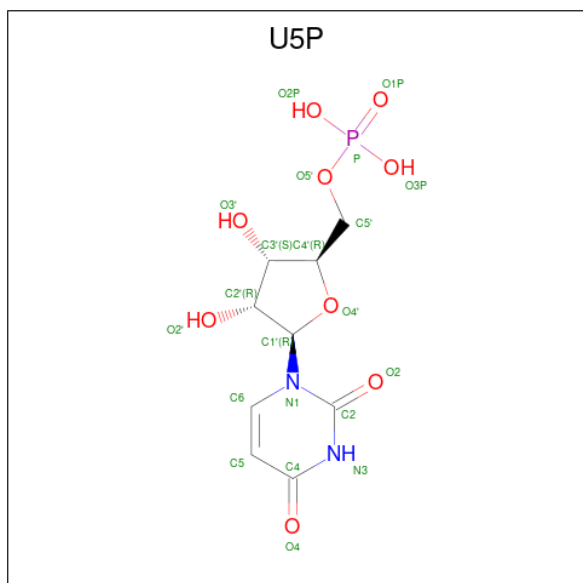
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	241	Total	C	N	O	S	0	0	0
			1859	1172	321	356	10			
2	D	247	Total	C	N	O	S	0	0	0
			1901	1199	328	363	11			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	241	Total	C	N	O	S	0	0	0
			1851	1168	321	352	10			
2	H	241	Total	C	N	O	S	0	0	0
			1859	1172	321	356	10			
2	J	241	Total	C	N	O	S	0	0	0
			1859	1172	321	356	10			
2	L	247	Total	C	N	O	S	0	0	0
			1905	1201	328	365	11			
2	N	241	Total	C	N	O	S	0	0	0
			1859	1172	321	356	10			
2	P	248	Total	C	N	O	S	0	0	0
			1903	1201	326	364	12			
2	R	245	Total	C	N	O	S	0	0	0
			1885	1189	326	359	11			
2	T	247	Total	C	N	O	S	0	0	0
			1901	1199	328	363	11			
2	V	244	Total	C	N	O	S	0	0	0
			1879	1186	324	359	10			
2	X	241	Total	C	N	O	S	0	0	0
			1859	1172	321	356	10			

- Molecule 3 is URIDINE-5'-MONOPHOSPHATE (CCD ID: U5P) (formula: $C_9H_{13}N_2O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			21	9	2	9	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	B	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	B	1	Total	O	P			0	0
			4	3	1				
3	E	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
3	E	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	E	1	Total	C	O	P		0	0
			12	5	6	1			
3	F	1	Total	C	O	P		0	0
			12	5	6	1			
3	G	1	Total	C	O	P		0	0
			13	5	7	1			
3	G	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	H	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	I	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
3	I	1	Total	O	P			0	0
			4	3	1				
3	J	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	M	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
3	M	1	Total	C	O	P		0	0
			12	5	6	1			
3	N	1	Total	C	O	P		0	0
			12	5	6	1			
3	U	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
3	U	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	U	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	V	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	W	1	Total	C	N	O	P	0	0
			21	9	2	9	1		

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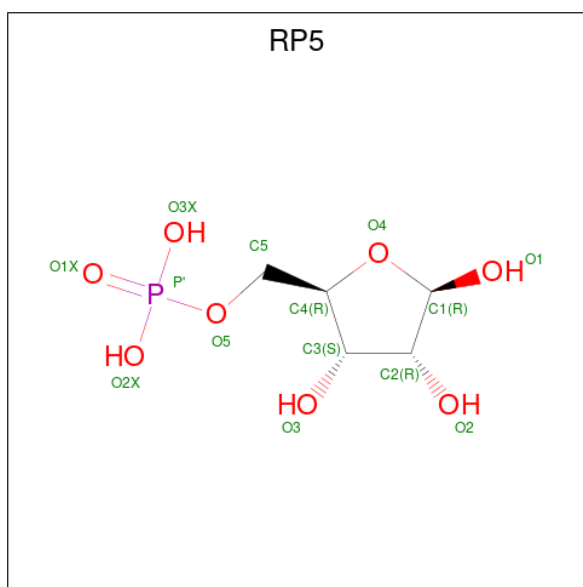
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	W	1	Total	C	N	O	P	0	0
			20	9	2	8	1		
3	W	1	Total	C	O	P		0	0
			12	5	6	1			
3	X	1	Total	O	P			0	0
			4	3	1				

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cl	0	0
			1	1		
4	D	1	Total	Cl	0	0
			1	1		
4	F	1	Total	Cl	0	0
			1	1		
4	H	1	Total	Cl	0	0
			1	1		
4	J	1	Total	Cl	0	0
			1	1		
4	L	1	Total	Cl	0	0
			1	1		
4	N	1	Total	Cl	0	0
			1	1		
4	P	1	Total	Cl	0	0
			1	1		
4	R	1	Total	Cl	0	0
			1	1		
4	T	1	Total	Cl	0	0
			1	1		
4	V	1	Total	Cl	0	0
			1	1		
4	X	1	Total	Cl	0	0
			1	1		

- Molecule 5 is 5-O-phosphono-beta-D-ribofuranose (CCD ID: RP5) (formula: C₅H₁₁O₈P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	N	1	Total	C	O	P	0	0
			13	5	7	1		

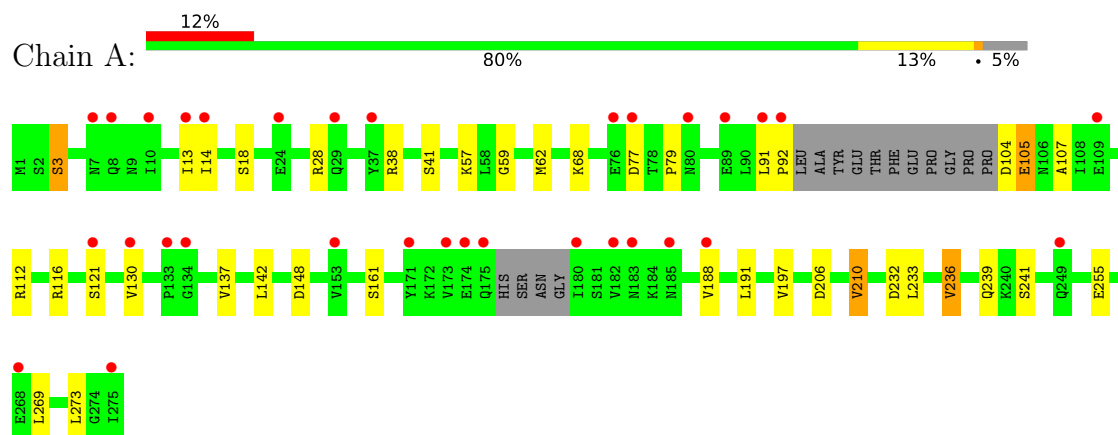
- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	V	1	Total	Na	0	0
			1	1		

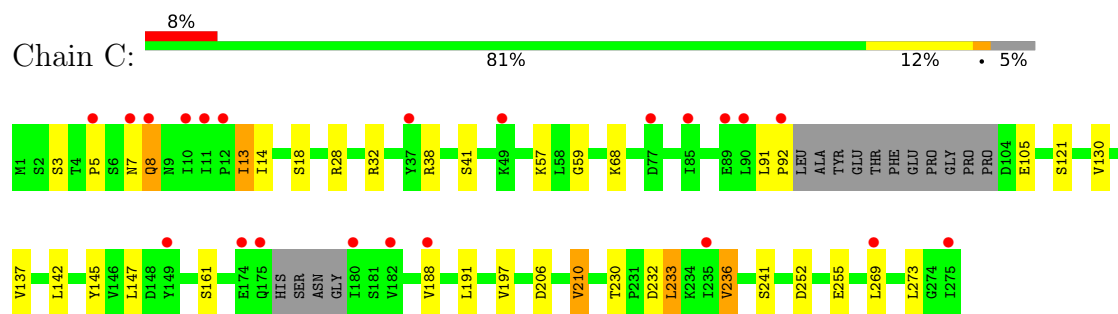
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

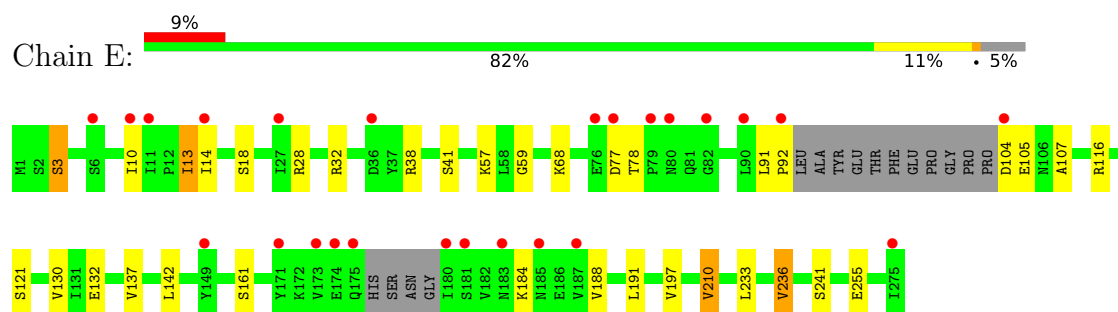
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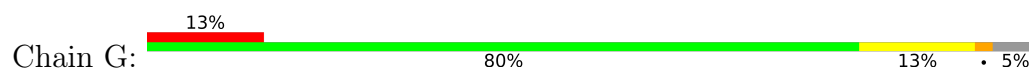
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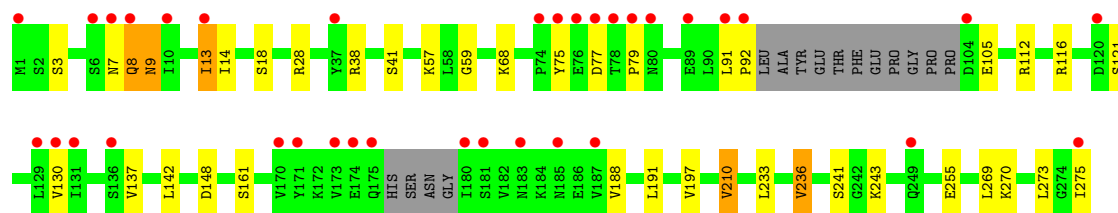


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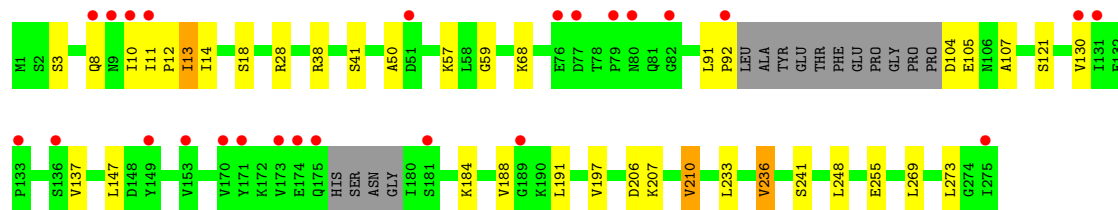
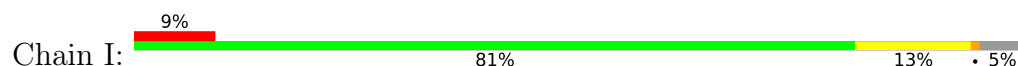


• Molecule 1: PROBABLE EXOSOME COMPLEX EXONUCLEASE 2

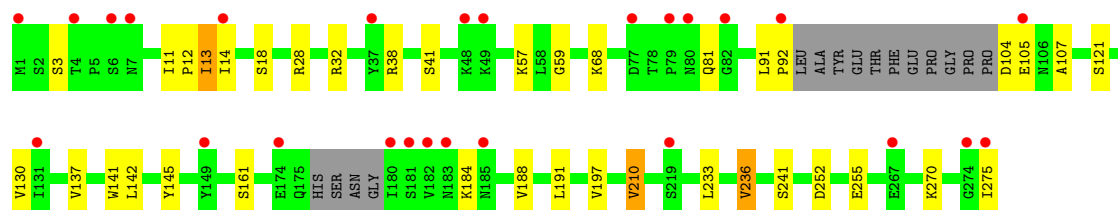
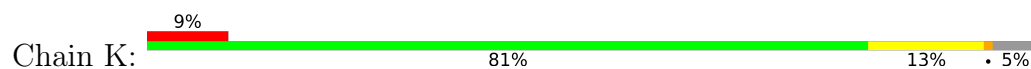




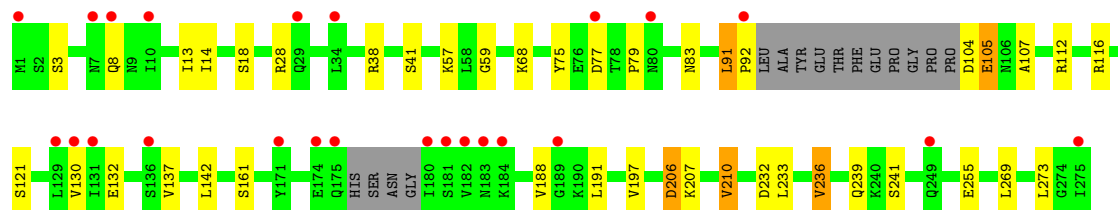
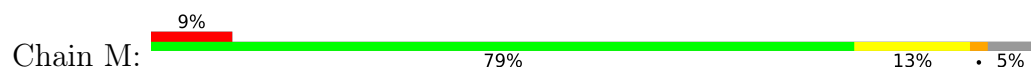
● Molecule 1: PROBABLE EXOSOME COMPLEX EXONUCLEASE 2



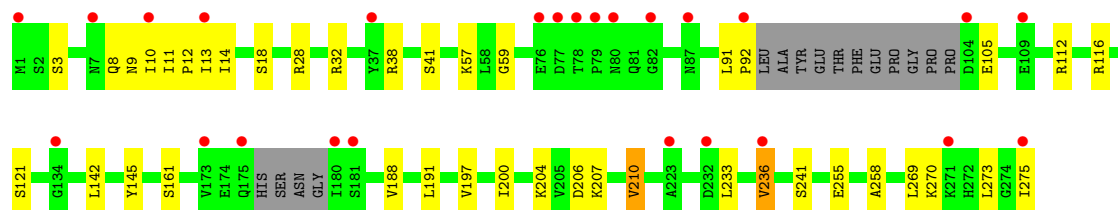
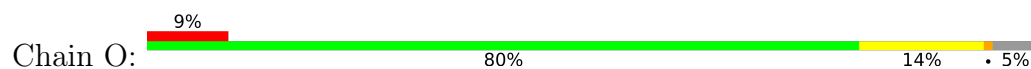
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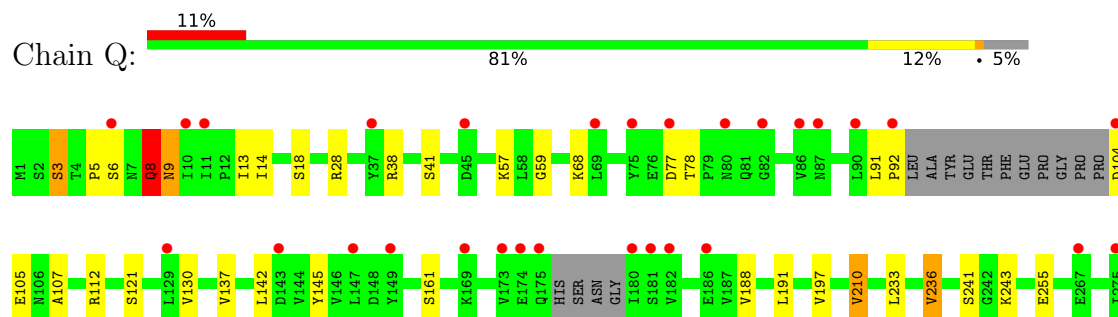
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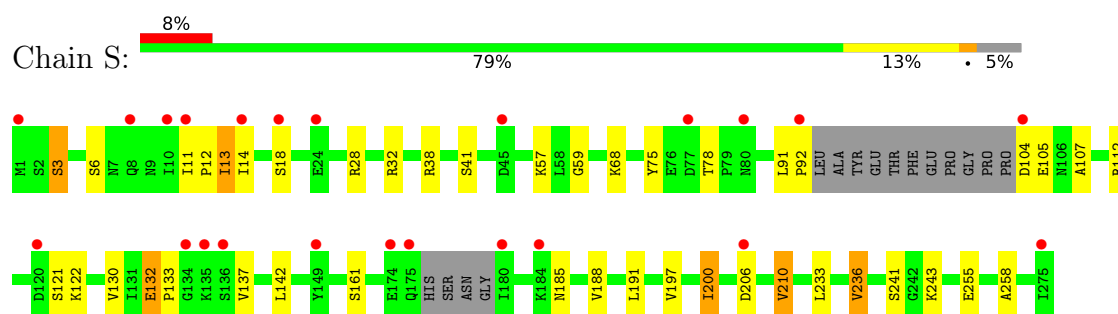
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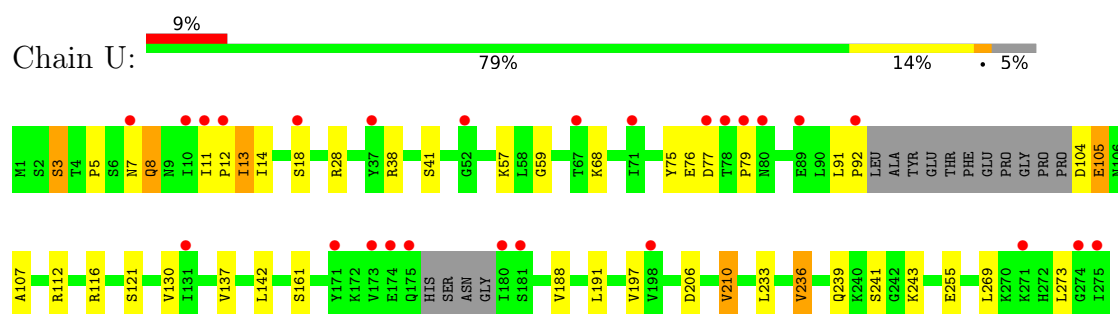
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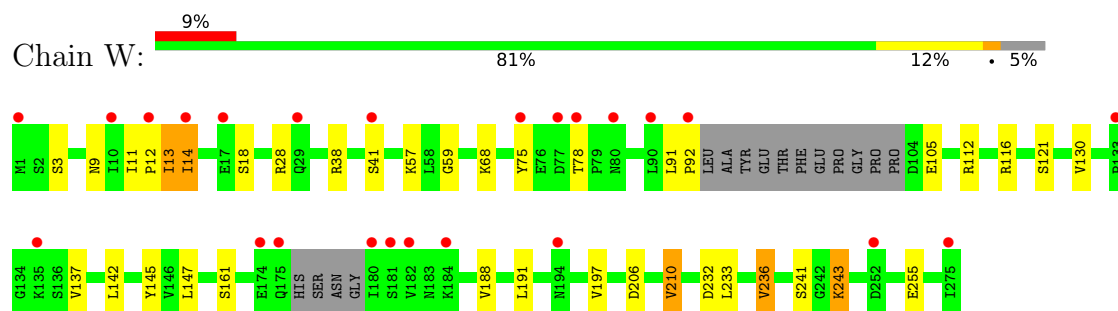
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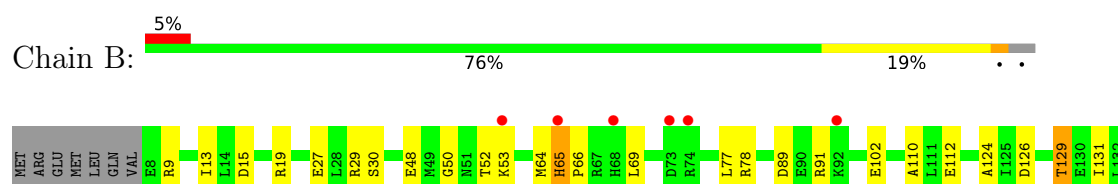
• Molecule 1: PROBABLE EXOSOME COMPLEX EXONUCLEASE 2



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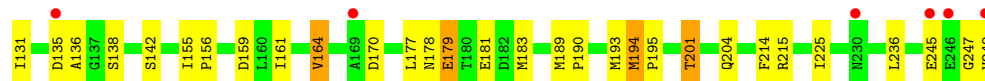
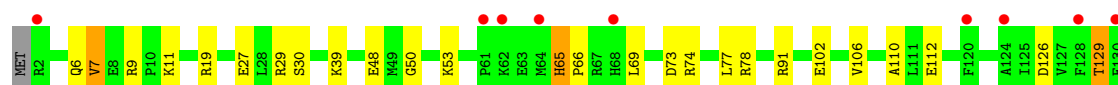
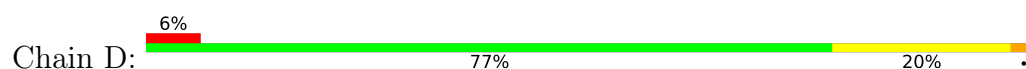


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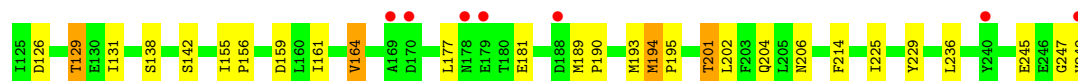
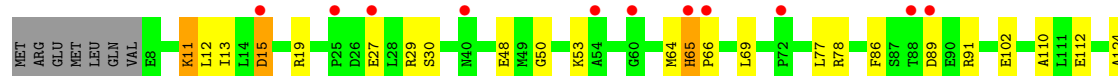
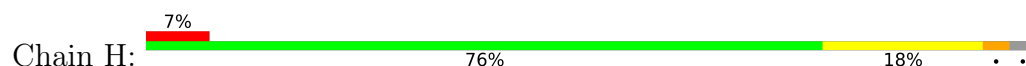
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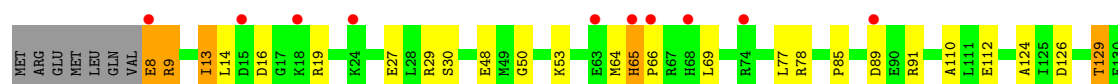
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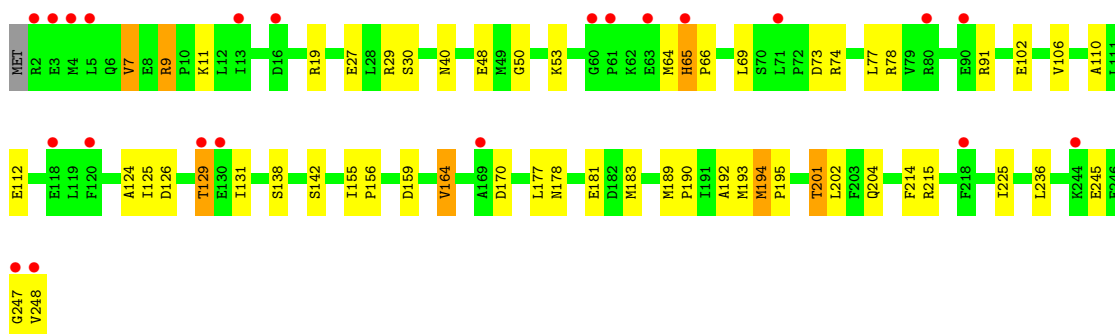


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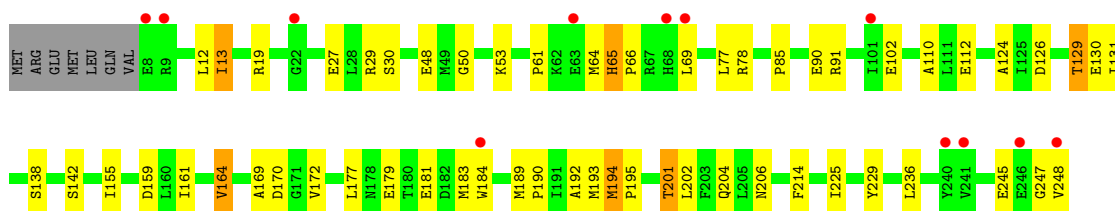
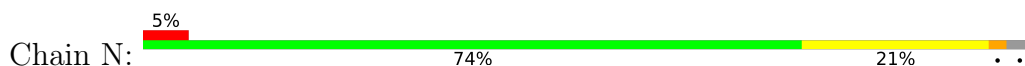


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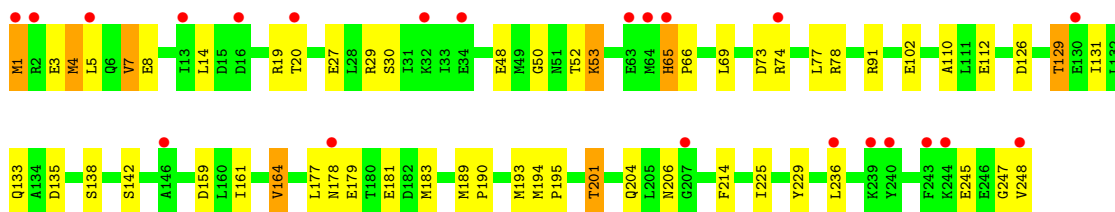
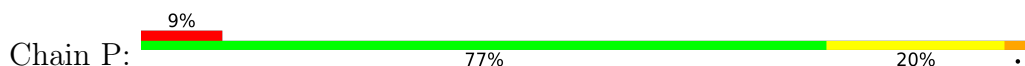




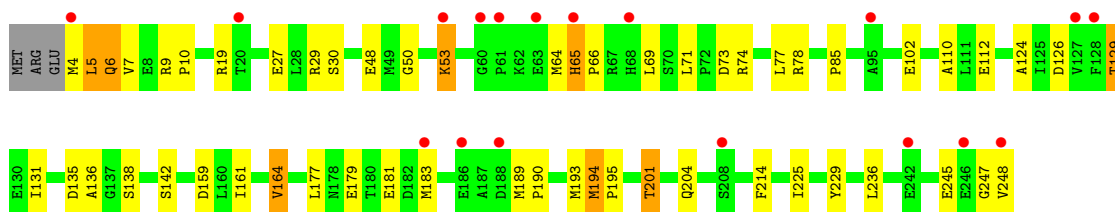
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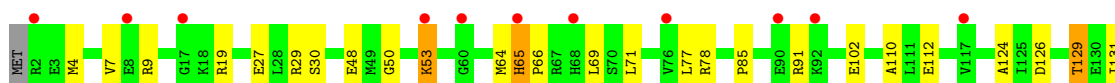
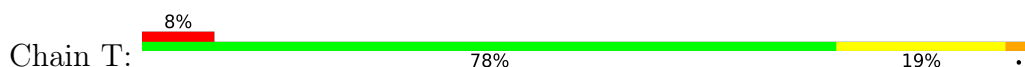
• Molecule 2: PROBABLE EXOSOME COMPLEX EXONUCLEASE 1



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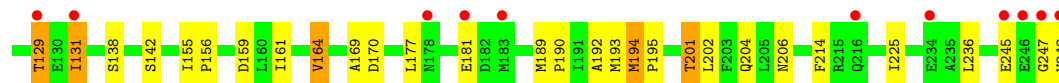
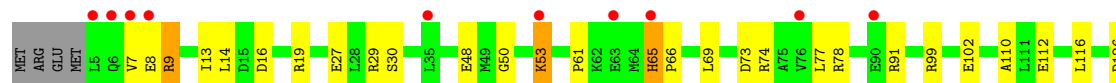
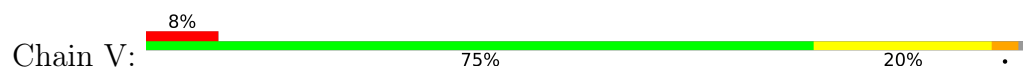


• Molecule 2: PROBABLE EXOSOME COMPLEX EXONUCLEASE 1

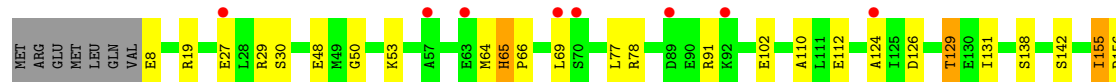
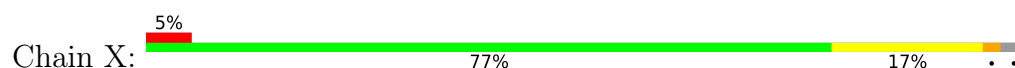




• Molecule 2: PROBABLE EXOSOME COMPLEX EXONUCLEASE 1



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4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	207.02Å 212.94Å 433.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	93.25 – 2.80 93.25 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (93.25-2.80) 93.3 (93.25-2.80)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 2.82Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.266 , 0.282 0.272 , 0.285	Depositor DCC
R_{free} test set	6530 reflections (3.00%)	wwPDB-VP
Wilson B-factor (Å ²)	57.0	Xtriage
Anisotropy	0.195	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 14.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.045 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	46570	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.38% 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: CL, RP5, NA, U5P

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	0.59	0/1988	0.80	0/2701
1	C	0.63	0/1997	0.83	0/2711
1	E	0.59	0/1993	0.80	0/2706
1	G	0.60	0/1989	0.83	1/2701 (0.0%)
1	I	0.59	0/1986	0.82	0/2697
1	K	0.62	0/1989	0.81	0/2701
1	M	0.59	0/2000	0.81	2/2715 (0.1%)
1	O	0.65	0/1993	0.85	0/2706
1	Q	0.62	0/1993	0.83	0/2706
1	S	0.63	0/1992	0.85	2/2706 (0.1%)
1	U	0.60	0/1993	0.83	0/2706
1	W	0.60	0/2000	0.82	0/2715
2	B	0.59	0/1887	0.88	3/2549 (0.1%)
2	D	0.61	0/1929	0.90	3/2606 (0.1%)
2	F	0.60	0/1879	0.88	4/2539 (0.2%)
2	H	0.59	0/1887	0.88	2/2549 (0.1%)
2	J	0.58	0/1887	0.87	2/2549 (0.1%)
2	L	0.64	0/1933	0.88	2/2611 (0.1%)
2	N	0.60	0/1887	0.86	2/2549 (0.1%)
2	P	0.67	0/1931	0.89	0/2609
2	R	0.66	0/1913	0.89	2/2584 (0.1%)
2	T	0.62	0/1929	0.89	2/2606 (0.1%)
2	V	0.60	0/1907	0.86	2/2577 (0.1%)
2	X	0.61	0/1887	0.87	5/2549 (0.2%)
All	All	0.61	0/46769	0.85	34/63348 (0.1%)

There are no bond length outliers.

The worst 5 of 34 bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	194	MET	CA-C-N	6.79	126.59	119.05
2	H	194	MET	C-N-CA	6.79	126.59	119.05
2	J	194	MET	CA-C-N	6.72	126.67	119.28
2	J	194	MET	C-N-CA	6.72	126.67	119.28
1	S	132	GLU	CA-C-N	6.49	126.88	119.93

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	1963	0	1998	24	0
1	C	1972	0	2017	21	0
1	E	1968	0	2011	19	0
1	G	1964	0	2007	20	0
1	I	1961	0	2003	21	0
1	K	1964	0	2007	20	1
1	M	1975	0	2019	23	0
1	O	1968	0	2013	21	0
1	Q	1968	0	2013	22	0
1	S	1967	0	2011	20	1
1	U	1968	0	2013	26	0
1	W	1975	0	2017	20	0
2	B	1859	0	1884	34	0
2	D	1901	0	1925	34	1
2	F	1851	0	1876	33	0
2	H	1859	0	1884	35	0
2	J	1859	0	1884	38	0
2	L	1905	0	1929	32	0
2	N	1859	0	1884	40	0
2	P	1903	0	1926	35	0
2	R	1885	0	1910	38	1
2	T	1901	0	1925	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	V	1879	0	1906	37	0
2	X	1859	0	1884	28	0
3	A	41	0	20	1	0
3	B	24	0	10	0	0
3	E	53	0	26	1	0
3	F	12	0	7	0	0
3	G	33	0	17	1	0
3	H	20	0	10	1	0
3	I	25	0	10	0	0
3	J	20	0	10	0	0
3	M	33	0	17	5	0
3	N	12	0	6	2	0
3	U	61	0	30	1	0
3	V	20	0	11	1	0
3	W	53	0	26	0	0
3	X	4	0	0	0	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
4	F	1	0	0	0	0
4	H	1	0	0	0	0
4	J	1	0	0	0	0
4	L	1	0	0	0	0
4	N	1	0	0	0	0
4	P	1	0	0	0	0
4	R	1	0	0	0	0
4	T	1	0	0	0	0
4	V	1	0	0	0	0
4	X	1	0	0	0	0
5	N	13	0	0	0	0
6	V	1	0	0	0	0
All	All	46570	0	47146	623	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 623 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)
3:M:401:U5P:H5'1	3:M:401:U5P:H6	1.37	1.05
2:X:77:LEU:HD12	2:X:112:GLU:HG3	1.55	0.88
2:N:77:LEU:HD12	2:N:112:GLU:HG3	1.59	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:77:LEU:HD12	2:P:112:GLU:HG3	1.60	0.84
2:H:77:LEU:HD12	2:H:112:GLU:HG3	1.60	0.84

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:6:GLN:O	1:K:81:GLN:NE2[8_545]	2.02	0.18
2:R:9:ARG:O	1:S:122:LYS:NZ[5_455]	2.19	0.01

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	254/275 (92%)	244 (96%)	9 (4%)	1 (0%)	30	60
1	C	254/275 (92%)	244 (96%)	9 (4%)	1 (0%)	30	60
1	E	254/275 (92%)	243 (96%)	9 (4%)	2 (1%)	16	44
1	G	254/275 (92%)	245 (96%)	7 (3%)	2 (1%)	16	44
1	I	254/275 (92%)	244 (96%)	7 (3%)	3 (1%)	10	34
1	K	254/275 (92%)	244 (96%)	9 (4%)	1 (0%)	30	60
1	M	254/275 (92%)	242 (95%)	10 (4%)	2 (1%)	16	44
1	O	254/275 (92%)	244 (96%)	8 (3%)	2 (1%)	16	44
1	Q	254/275 (92%)	245 (96%)	7 (3%)	2 (1%)	16	44
1	S	254/275 (92%)	247 (97%)	6 (2%)	1 (0%)	30	60
1	U	254/275 (92%)	244 (96%)	8 (3%)	2 (1%)	16	44
1	W	254/275 (92%)	245 (96%)	8 (3%)	1 (0%)	30	60
2	B	239/248 (96%)	228 (95%)	10 (4%)	1 (0%)	30	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	245/248 (99%)	231 (94%)	12 (5%)	2 (1%)	16	44
2	F	239/248 (96%)	227 (95%)	10 (4%)	2 (1%)	16	44
2	H	239/248 (96%)	226 (95%)	12 (5%)	1 (0%)	30	60
2	J	239/248 (96%)	227 (95%)	11 (5%)	1 (0%)	30	60
2	L	245/248 (99%)	230 (94%)	13 (5%)	2 (1%)	16	44
2	N	239/248 (96%)	229 (96%)	9 (4%)	1 (0%)	30	60
2	P	246/248 (99%)	232 (94%)	12 (5%)	2 (1%)	16	44
2	R	243/248 (98%)	228 (94%)	11 (4%)	4 (2%)	7	27
2	T	245/248 (99%)	235 (96%)	9 (4%)	1 (0%)	30	60
2	V	242/248 (98%)	228 (94%)	13 (5%)	1 (0%)	30	60
2	X	239/248 (96%)	227 (95%)	11 (5%)	1 (0%)	30	60
All	All	5948/6276 (95%)	5679 (96%)	230 (4%)	39 (1%)	18	47

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	7	VAL
1	O	8	GLN
1	U	76	GLU
1	A	105	GLU
1	C	105	GLU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	217/242 (90%)	204 (94%)	13 (6%)	17	47
1	C	219/242 (90%)	206 (94%)	13 (6%)	18	48
1	E	218/242 (90%)	206 (94%)	12 (6%)	19	51
1	G	217/242 (90%)	205 (94%)	12 (6%)	19	51
1	I	216/242 (89%)	205 (95%)	11 (5%)	21	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	217/242 (90%)	206 (95%)	11 (5%)	21	54
1	M	220/242 (91%)	207 (94%)	13 (6%)	18	48
1	O	218/242 (90%)	207 (95%)	11 (5%)	22	54
1	Q	218/242 (90%)	205 (94%)	13 (6%)	17	47
1	S	218/242 (90%)	203 (93%)	15 (7%)	14	41
1	U	218/242 (90%)	205 (94%)	13 (6%)	17	47
1	W	220/242 (91%)	204 (93%)	16 (7%)	13	38
2	B	198/208 (95%)	190 (96%)	8 (4%)	28	63
2	D	202/208 (97%)	194 (96%)	8 (4%)	28	63
2	F	196/208 (94%)	187 (95%)	9 (5%)	24	58
2	H	198/208 (95%)	189 (96%)	9 (4%)	24	58
2	J	198/208 (95%)	188 (95%)	10 (5%)	21	54
2	L	203/208 (98%)	194 (96%)	9 (4%)	25	59
2	N	198/208 (95%)	190 (96%)	8 (4%)	28	63
2	P	202/208 (97%)	191 (95%)	11 (5%)	20	51
2	R	200/208 (96%)	193 (96%)	7 (4%)	32	67
2	T	202/208 (97%)	191 (95%)	11 (5%)	20	51
2	V	200/208 (96%)	189 (94%)	11 (6%)	19	51
2	X	198/208 (95%)	190 (96%)	8 (4%)	28	63
All	All	5011/5400 (93%)	4749 (95%)	262 (5%)	21	53

5 of 262 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	V	129	THR
1	W	3	SER
2	X	236	LEU
2	J	13	ILE
1	I	255	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
2	P	178	ASN

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Mol	Chain	Res	Type
1	S	83	ASN
1	Q	8	GLN
1	Q	183	ASN
2	T	178	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](#)

Of 39 ligands modelled in this entry, 13 are monoatomic - leaving 26 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	U5P	A	401	3	22,22,22	0.75	0	32,33,33	1.19	4 (12%)
3	U5P	X	302	3	0,3,22	-	-	0,3,33	-	-
3	U5P	E	402	3	18,21,22	0.72	1 (5%)	25,30,33	0.94	0
3	U5P	G	401	3	13,13,22	0.96	0	16,19,33	1.29	2 (12%)
3	U5P	U	402	3	18,21,22	0.79	1 (5%)	25,30,33	1.05	1 (4%)
3	U5P	B	303	3	0,3,22	-	-	0,3,33	-	-
3	U5P	N	302	3	9,12,22	0.39	0	9,16,33	1.52	1 (11%)
3	U5P	U	403	6,3	18,21,22	0.79	1 (5%)	25,30,33	0.84	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	U5P	E	403	3	9,12,22	0.90	0	9,16,33	1.16	1 (11%)
3	U5P	U	401	3	22,22,22	0.68	0	32,33,33	0.87	1 (3%)
3	U5P	H	302	3	18,21,22	0.76	1 (5%)	25,30,33	0.98	0
3	U5P	F	302	3	9,12,22	0.60	0	9,16,33	1.07	1 (11%)
3	U5P	W	403	3	9,12,22	0.89	0	9,16,33	1.20	0
3	U5P	G	402	3	18,21,22	0.73	0	25,30,33	1.04	3 (12%)
3	U5P	I	402	3	0,3,22	-	-	0,3,33	-	-
5	RP5	N	303	-	13,13,14	1.35	1 (7%)	16,19,21	1.18	1 (6%)
3	U5P	M	401	3	22,22,22	0.92	1 (4%)	32,33,33	1.08	1 (3%)
3	U5P	W	402	3	18,21,22	0.59	0	25,30,33	1.25	4 (16%)
3	U5P	E	401	3	22,22,22	0.81	1 (4%)	32,33,33	1.12	3 (9%)
3	U5P	J	302	3	18,21,22	0.78	1 (5%)	25,30,33	0.93	1 (4%)
3	U5P	I	401	3	22,22,22	0.76	0	32,33,33	0.95	1 (3%)
3	U5P	W	401	3	22,22,22	0.89	1 (4%)	32,33,33	1.13	4 (12%)
3	U5P	A	402	3	18,21,22	0.73	1 (5%)	25,30,33	1.50	5 (20%)
3	U5P	M	402	3	9,12,22	0.68	0	9,16,33	0.93	0
3	U5P	B	302	3	18,21,22	0.88	1 (5%)	25,30,33	1.74	6 (24%)
3	U5P	V	302	6,3	18,21,22	0.75	1 (5%)	25,30,33	0.94	2 (8%)

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	U5P	A	401	3	-	4/10/26/26	0/2/2/2
3	U5P	E	402	3	-	1/7/25/26	0/2/2/2
3	U5P	G	401	3	-	3/6/19/26	0/1/1/2
3	U5P	U	402	3	-	0/7/25/26	0/2/2/2
3	U5P	N	302	3	-	0/3/18/26	0/1/1/2
3	U5P	U	403	6,3	-	0/7/25/26	0/2/2/2
3	U5P	E	403	3	-	0/3/18/26	0/1/1/2
3	U5P	U	401	3	-	0/10/26/26	0/2/2/2
3	U5P	H	302	3	-	0/7/25/26	0/2/2/2
3	U5P	F	302	3	-	1/3/18/26	0/1/1/2
3	U5P	W	403	3	-	3/3/18/26	0/1/1/2
3	U5P	G	402	3	-	2/7/25/26	0/2/2/2
5	RP5	N	303	-	-	1/6/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	U5P	M	401	3	-	4/10/26/26	0/2/2/2
3	U5P	W	402	3	-	4/7/25/26	0/2/2/2
3	U5P	E	401	3	-	2/10/26/26	0/2/2/2
3	U5P	J	302	3	-	2/7/25/26	0/2/2/2
3	U5P	I	401	3	-	6/10/26/26	0/2/2/2
3	U5P	W	401	3	-	5/10/26/26	0/2/2/2
3	U5P	A	402	3	-	3/7/25/26	0/2/2/2
3	U5P	M	402	3	-	3/3/18/26	0/1/1/2
3	U5P	B	302	3	-	4/7/25/26	0/2/2/2
3	U5P	V	302	6,3	-	0/7/25/26	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	N	303	RP5	P'-O1X	3.72	1.62	1.50
3	M	401	U5P	C1'-N1	2.62	1.55	1.47
3	W	401	U5P	C1'-N1	2.58	1.54	1.47
3	E	402	U5P	C1'-N1	2.54	1.54	1.47
3	B	302	U5P	C1'-N1	2.53	1.54	1.47

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	302	U5P	C1'-N1-C2	3.76	124.35	117.59
3	B	302	U5P	O4'-C1'-N1	3.70	116.75	108.36
3	A	402	U5P	C1'-N1-C2	3.70	124.23	117.59
3	B	302	U5P	O4'-C4'-C3'	-3.58	98.04	105.15
3	N	302	U5P	O4'-C4'-C3'	-3.41	101.49	104.63

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

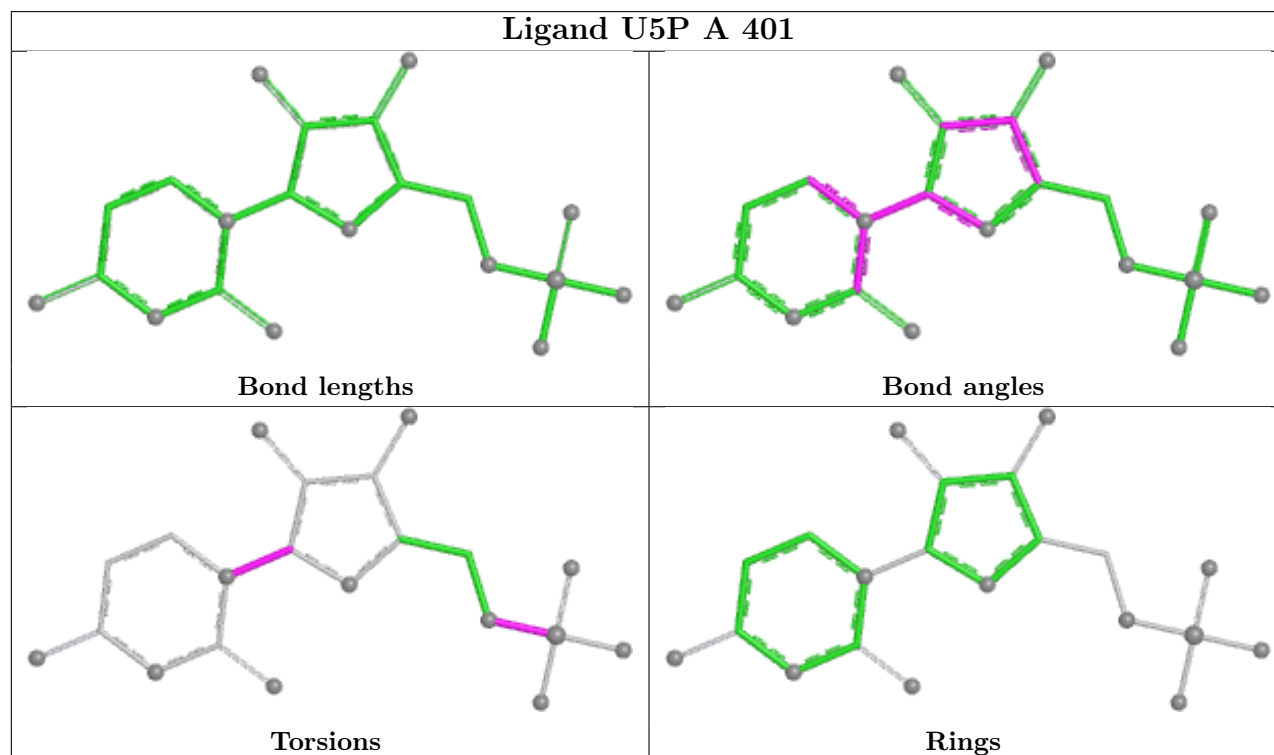
Mol	Chain	Res	Type	Atoms
3	A	401	U5P	O4'-C1'-N1-C2
3	A	401	U5P	O4'-C1'-N1-C6
3	A	401	U5P	C5'-O5'-P-O3P
3	B	302	U5P	O4'-C1'-N1-C2
3	B	302	U5P	O4'-C1'-N1-C6

There are no ring outliers.

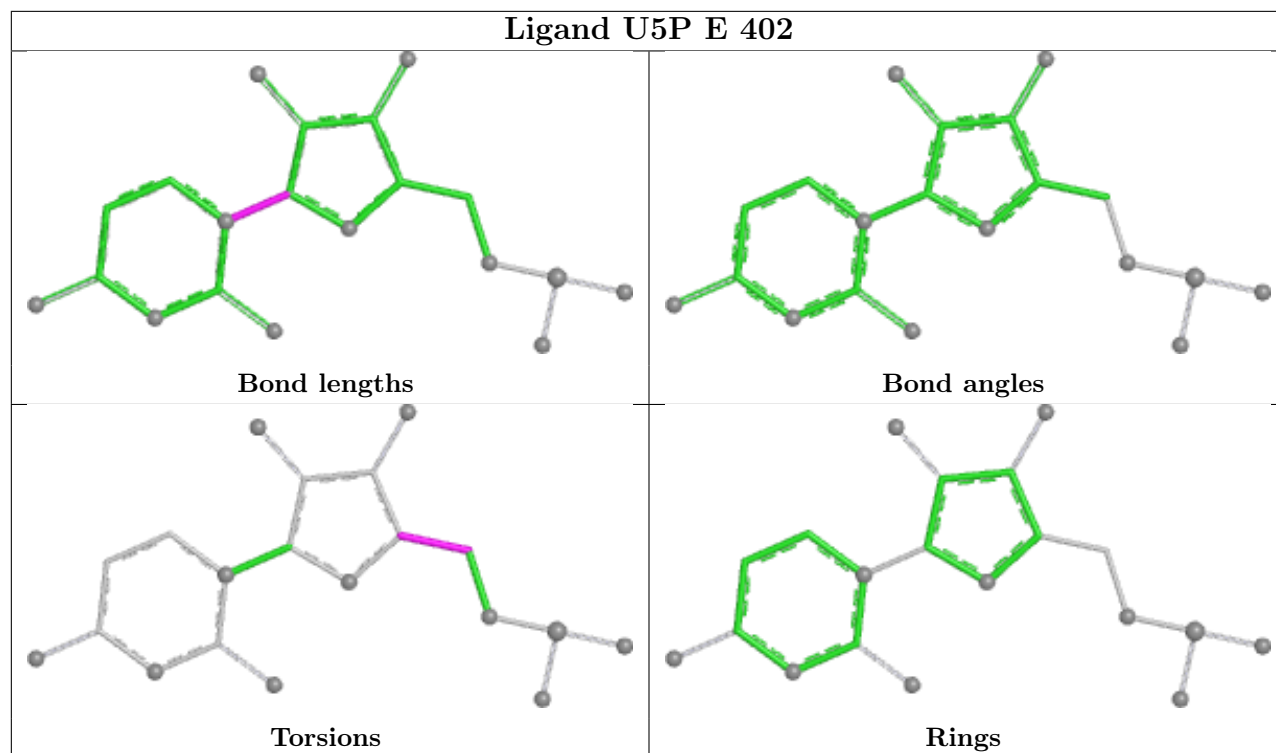
9 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	402	U5P	1	0
3	G	401	U5P	1	0
3	U	402	U5P	1	0
3	N	302	U5P	2	0
3	H	302	U5P	1	0
3	M	401	U5P	2	0
3	A	402	U5P	1	0
3	M	402	U5P	3	0
3	V	302	U5P	1	0

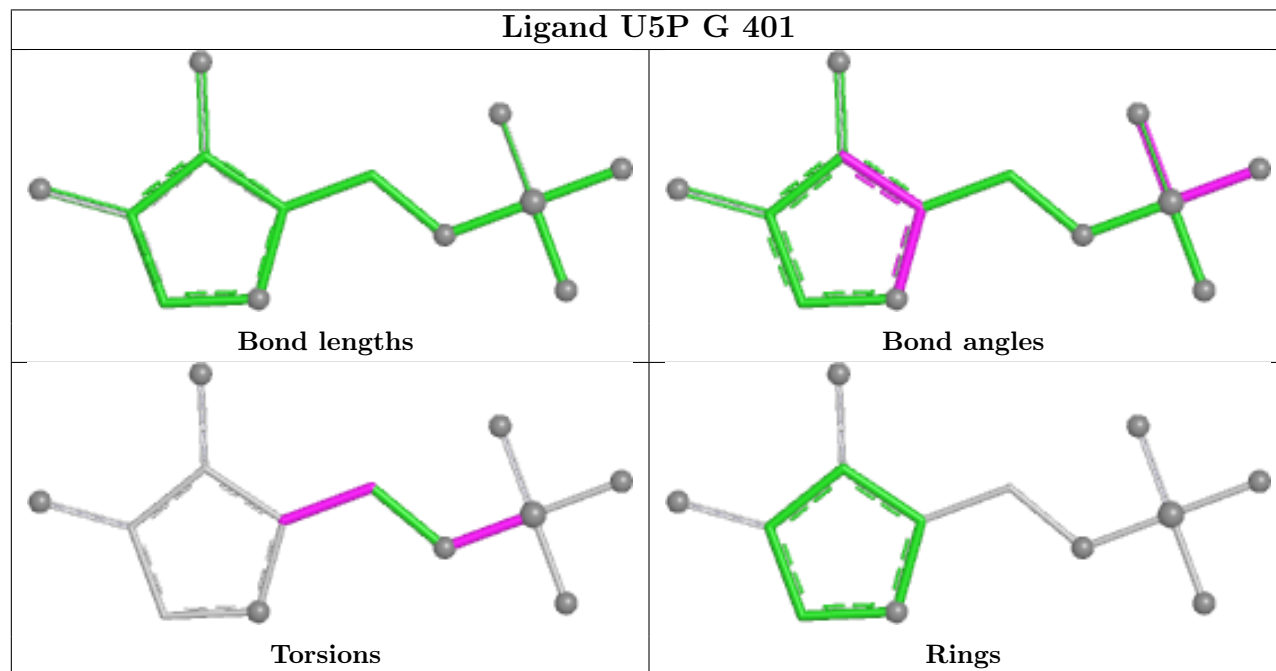
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



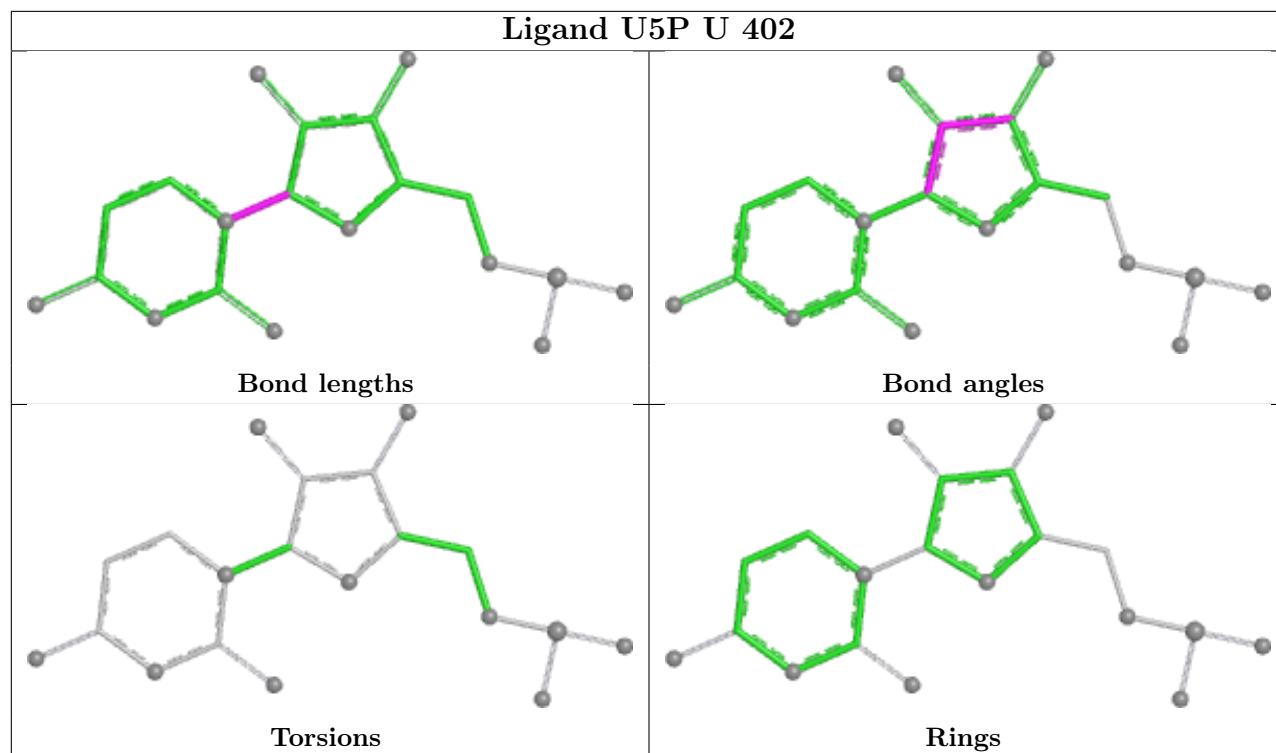
Ligand U5P E 402



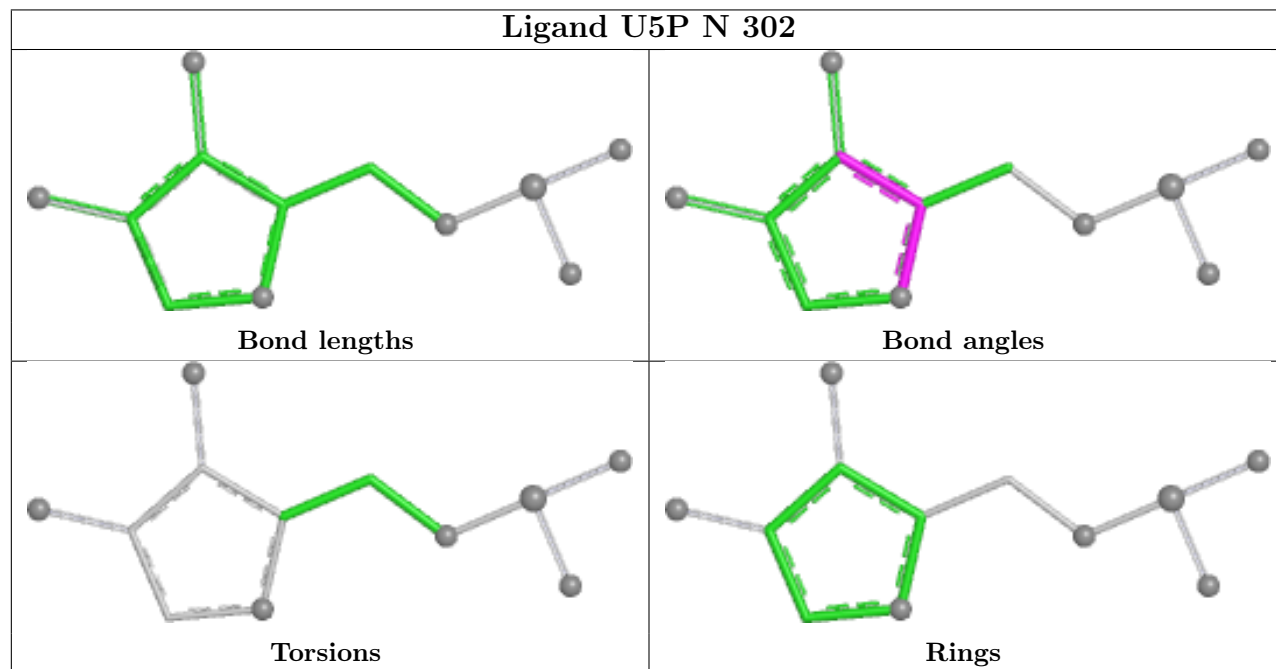
Ligand U5P G 401



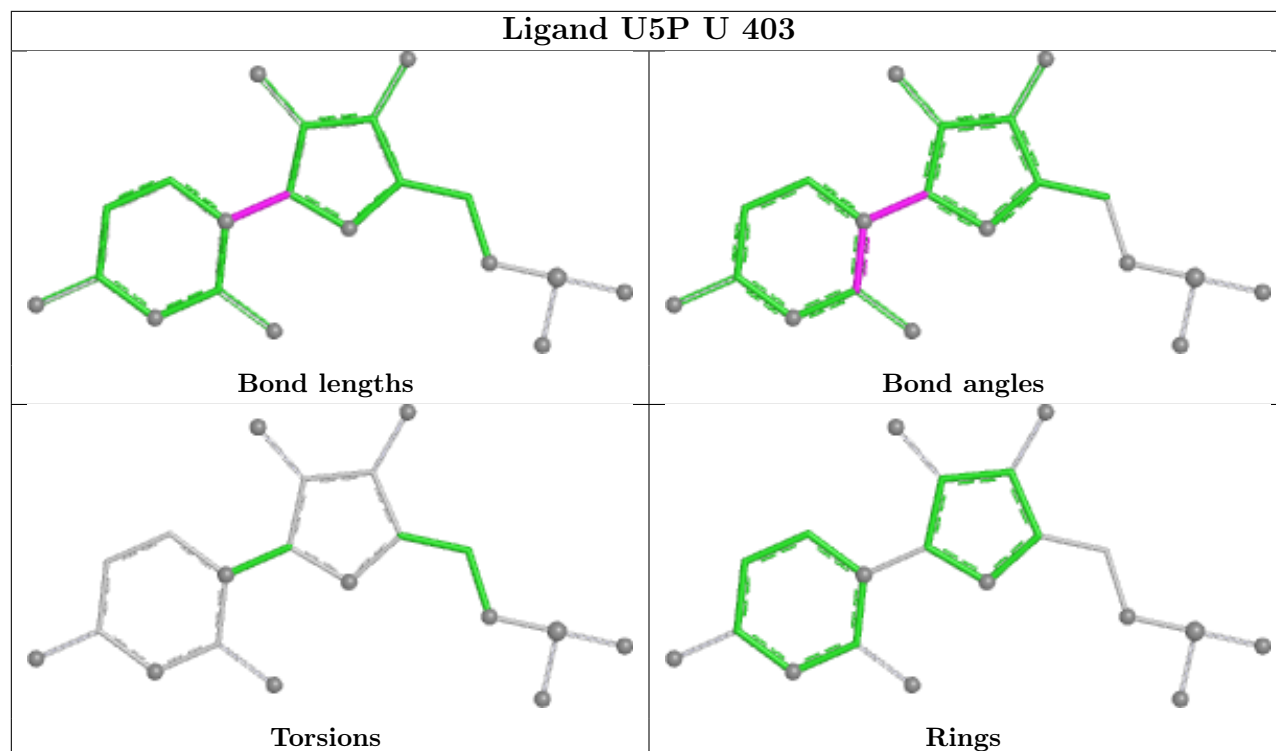
Ligand U5P U 402



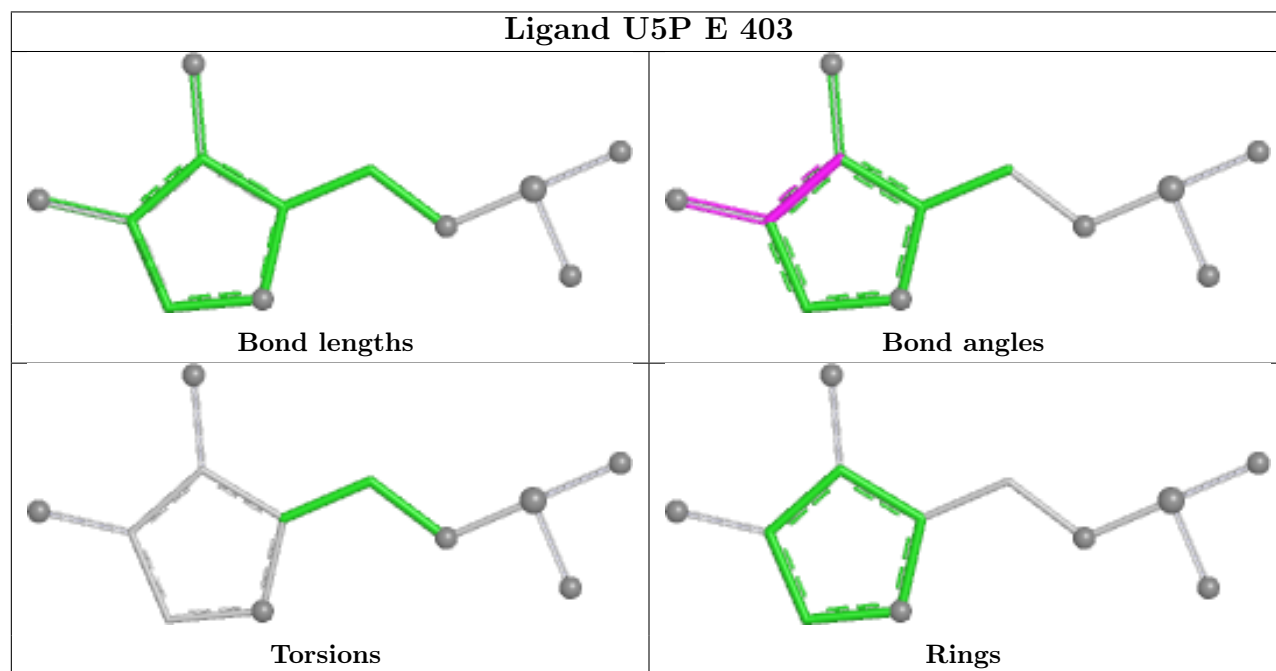
Ligand U5P N 302



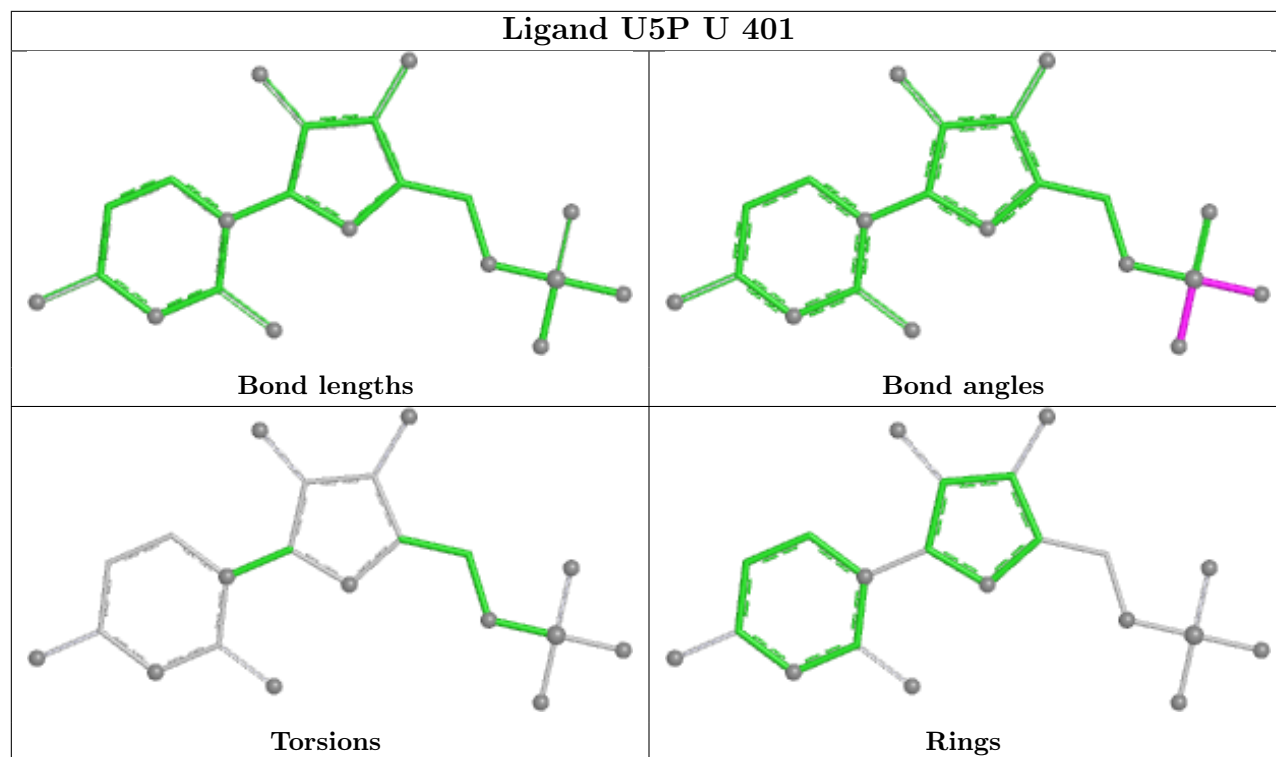
Ligand U5P U 403



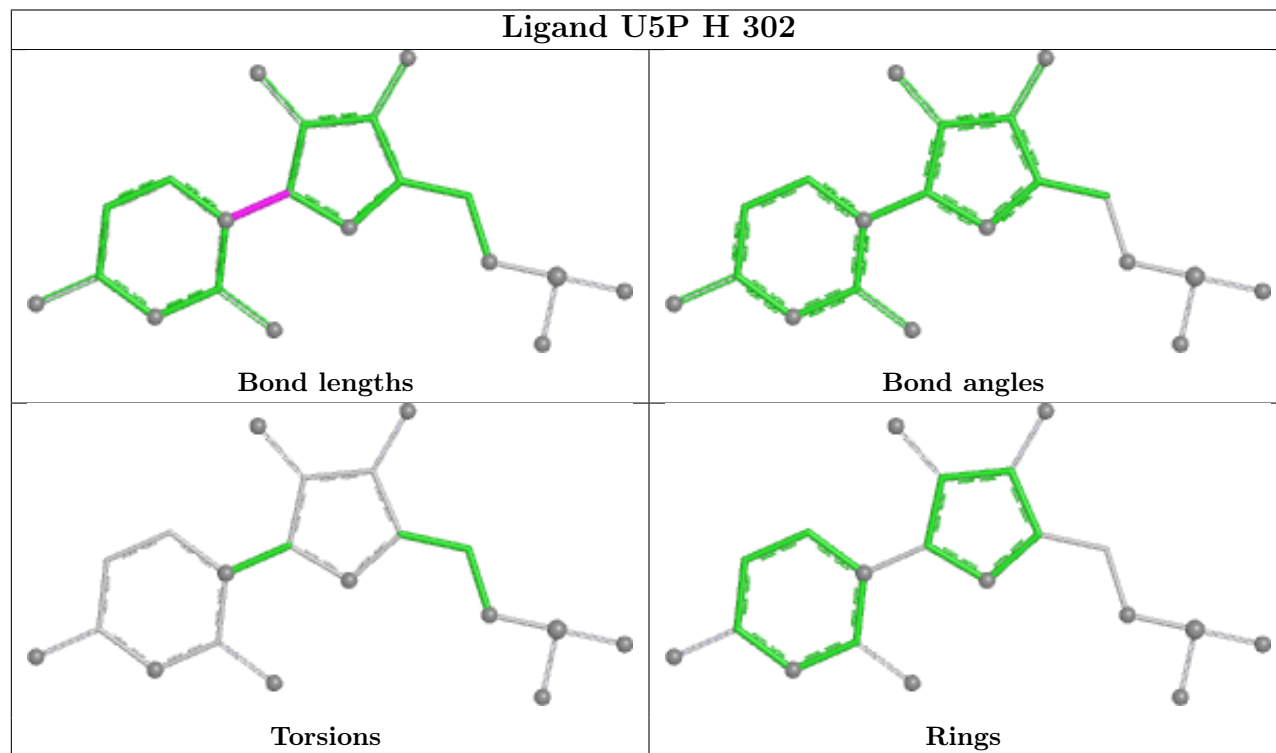
Ligand U5P E 403



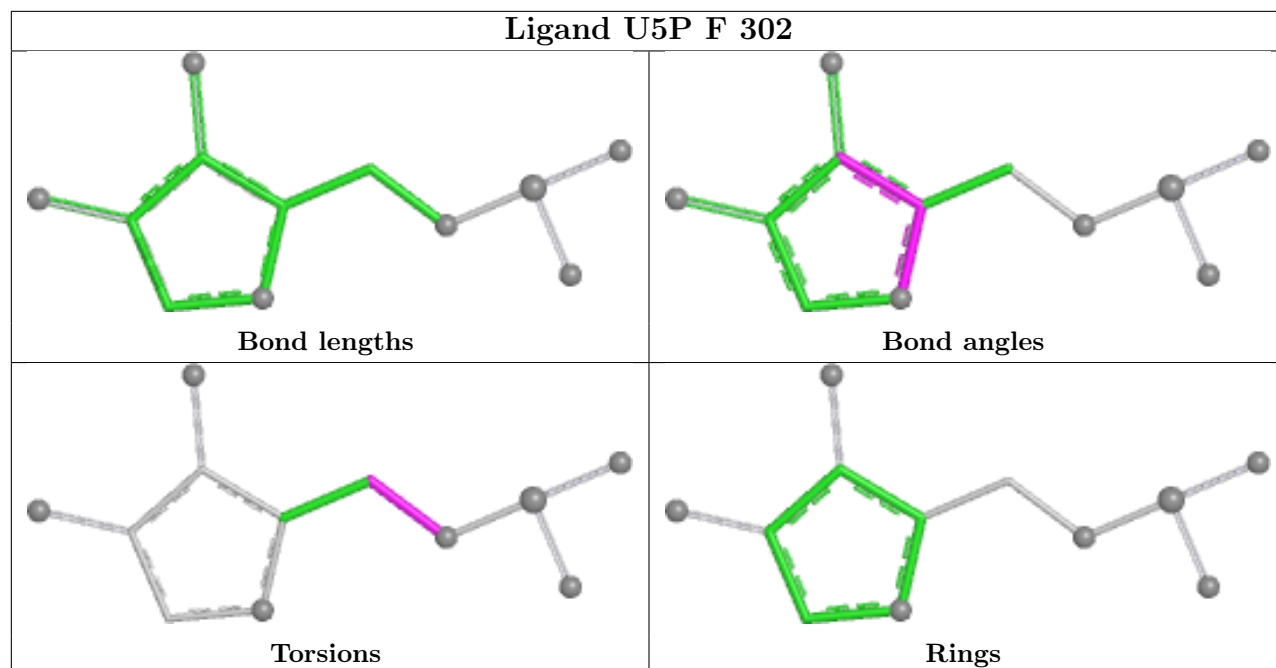
Ligand U5P U 401



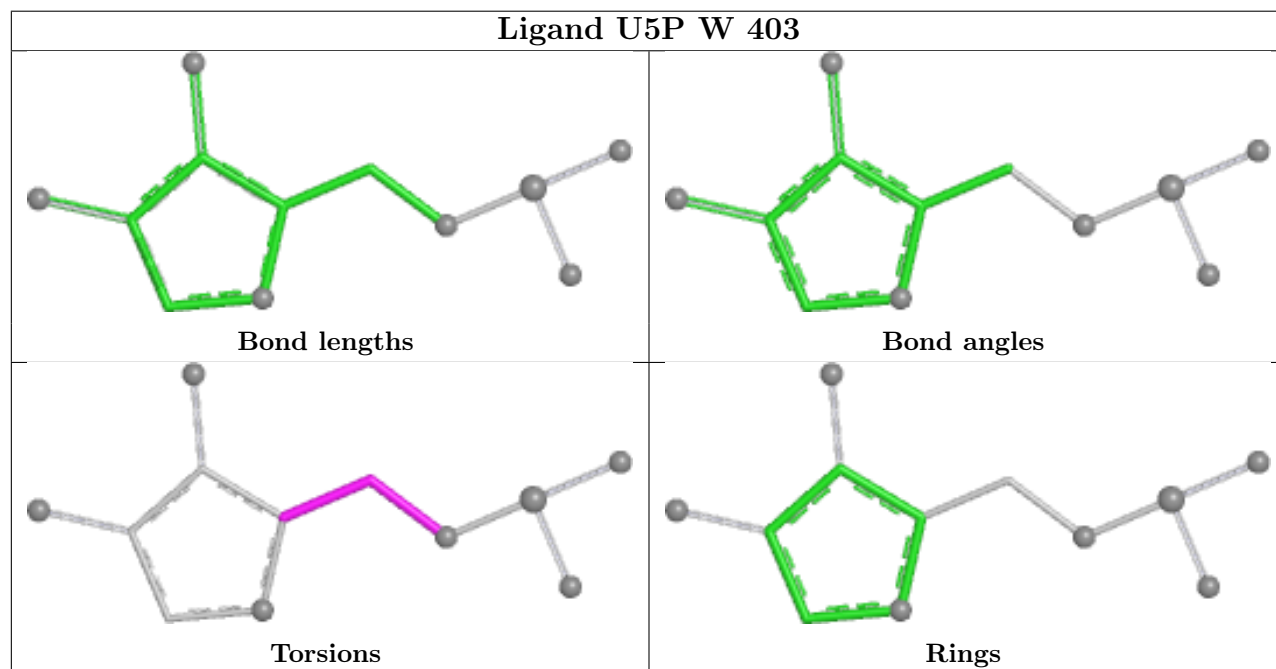
Ligand U5P H 302



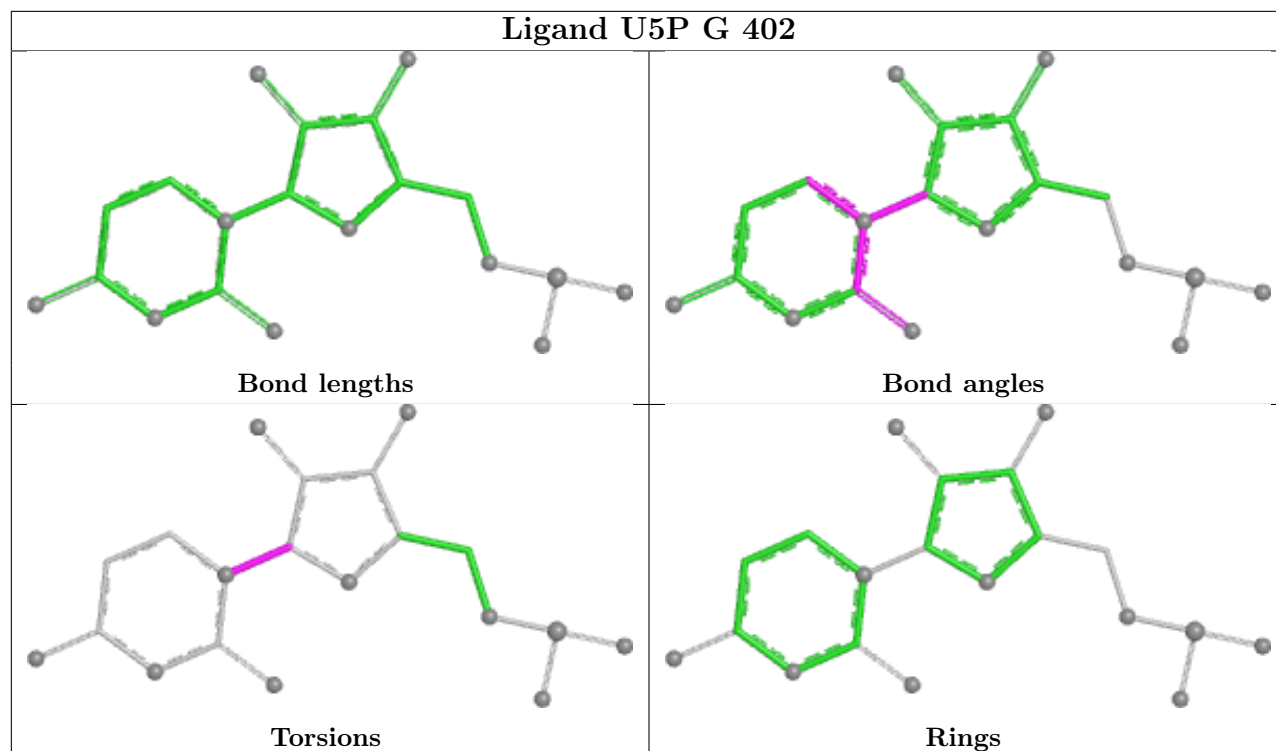
Ligand U5P F 302



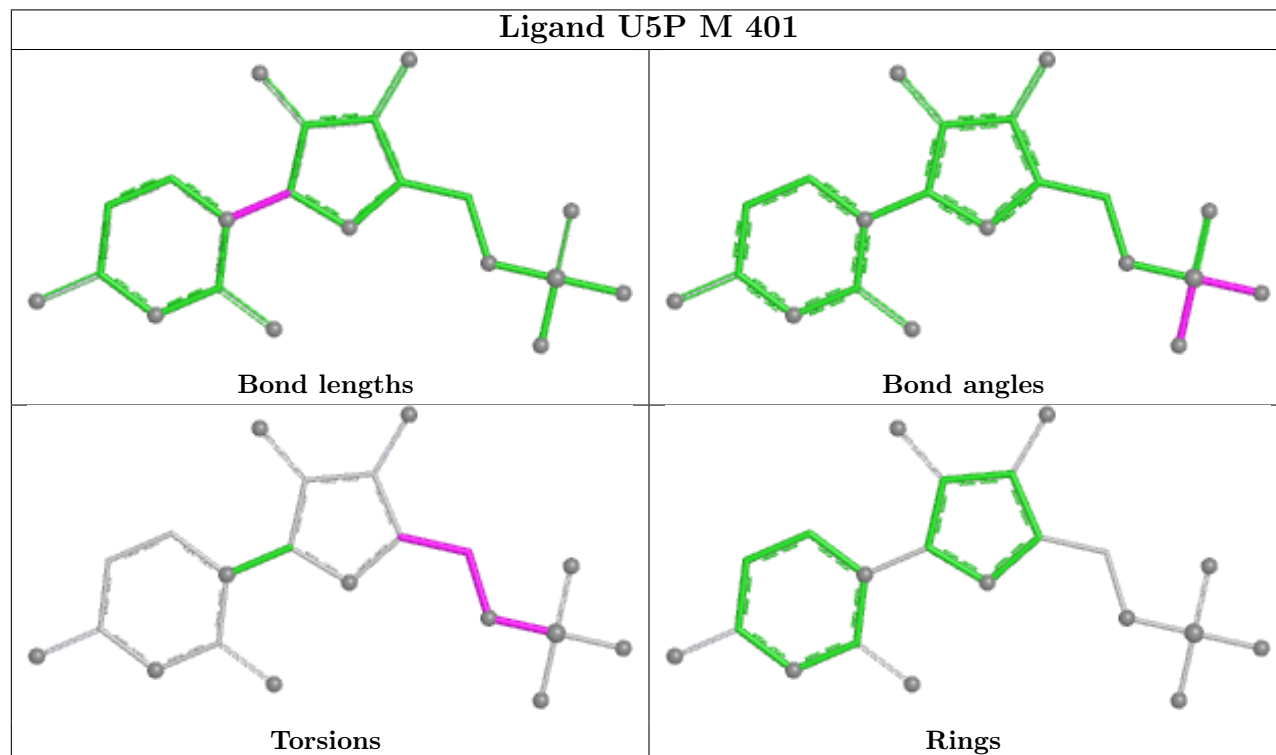
Ligand U5P W 403

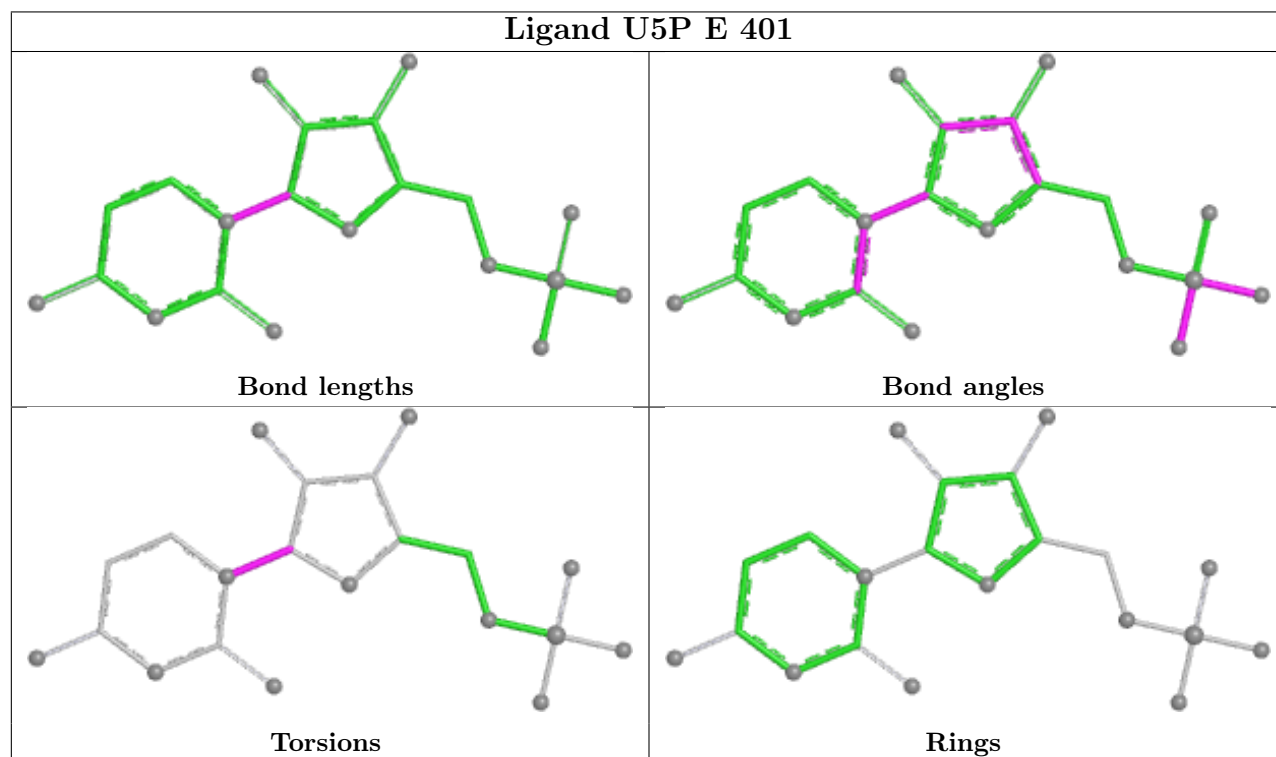
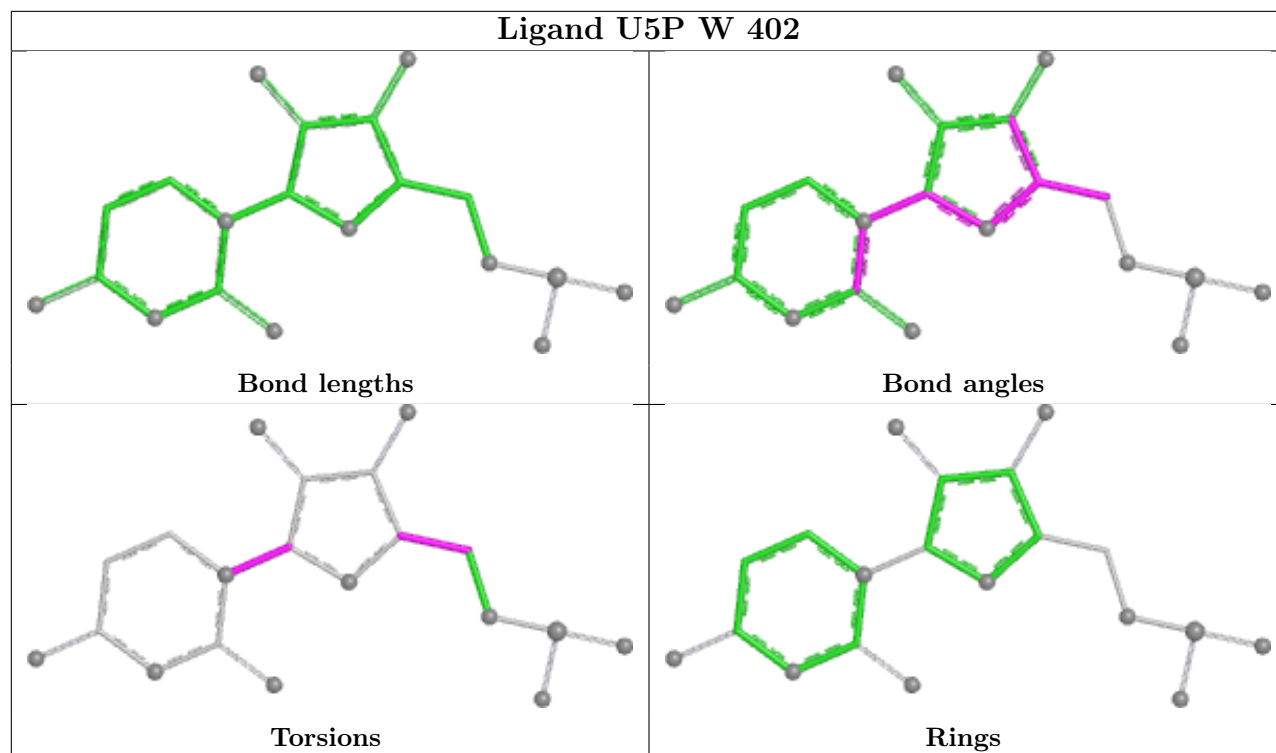


Ligand U5P G 402

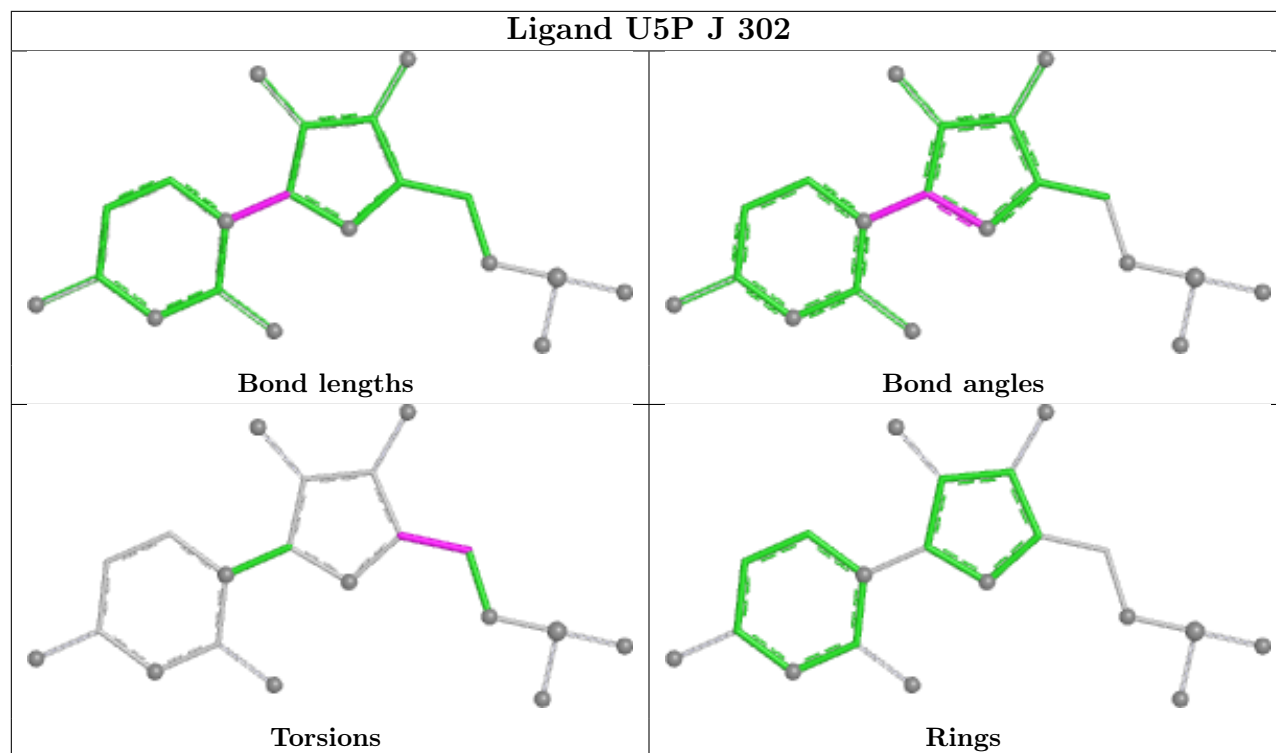


Ligand U5P M 401

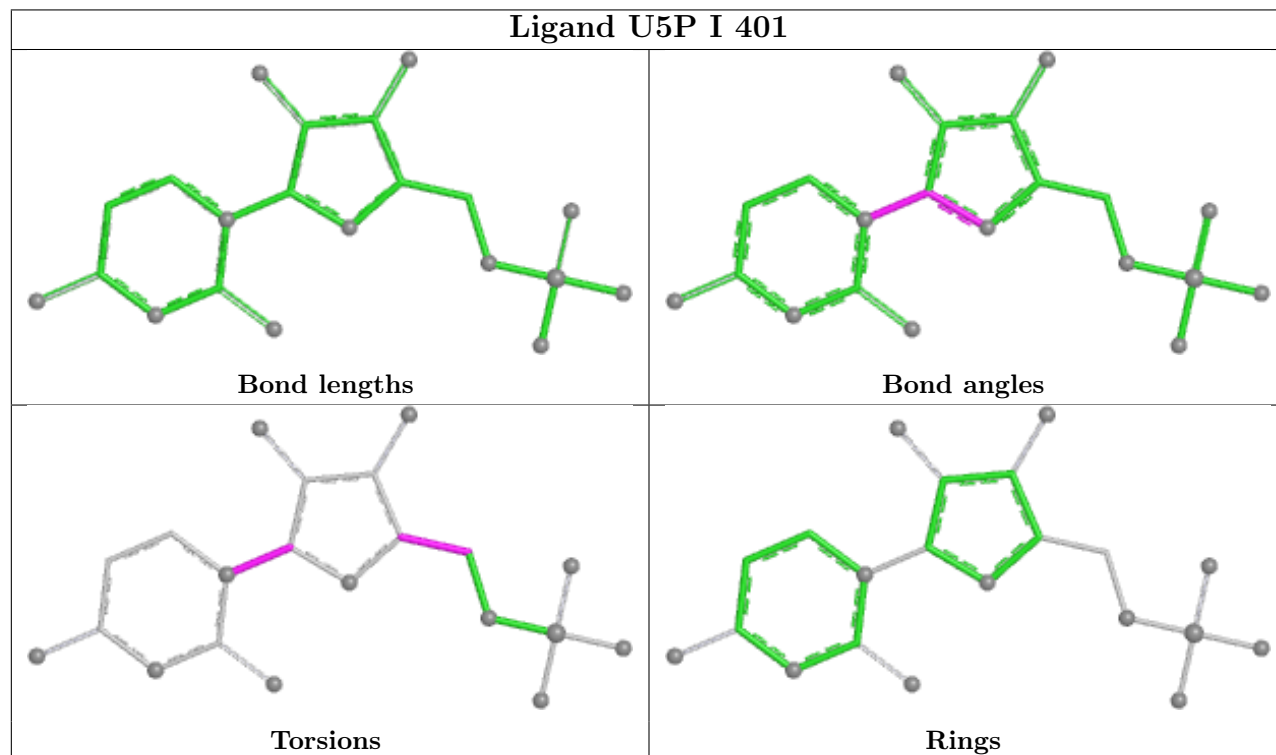


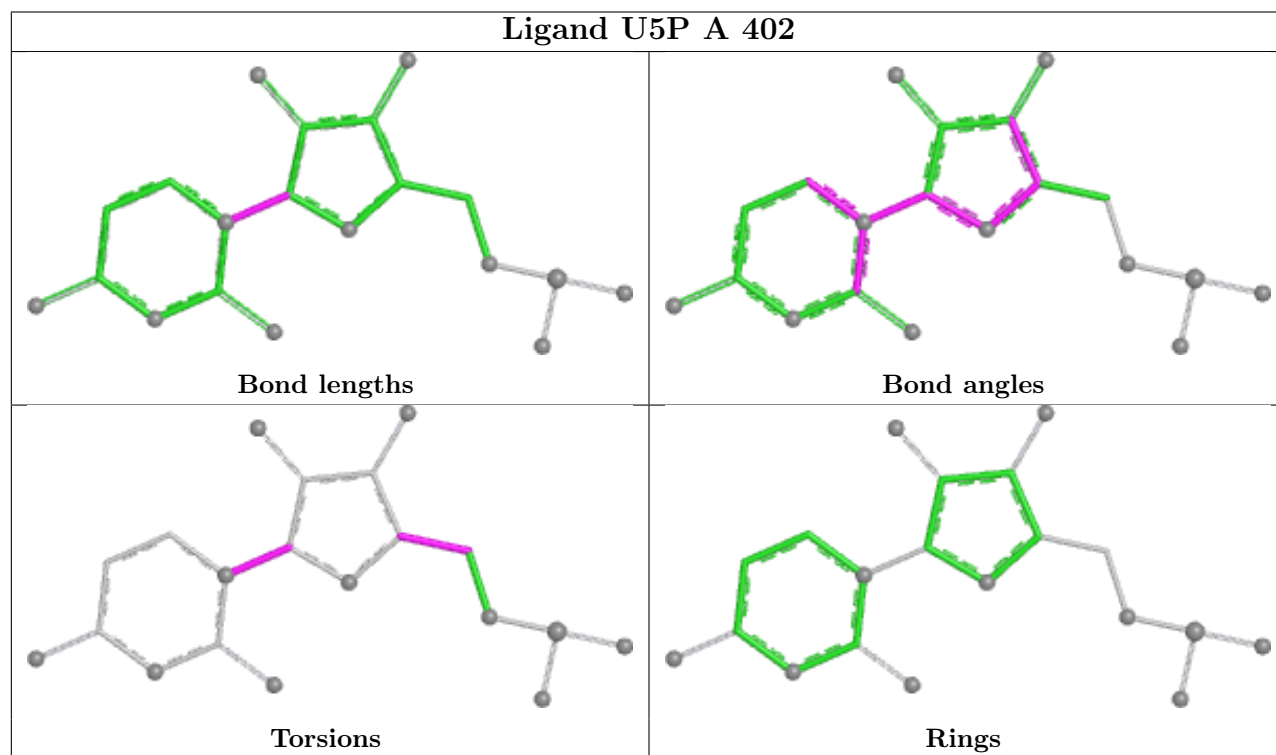
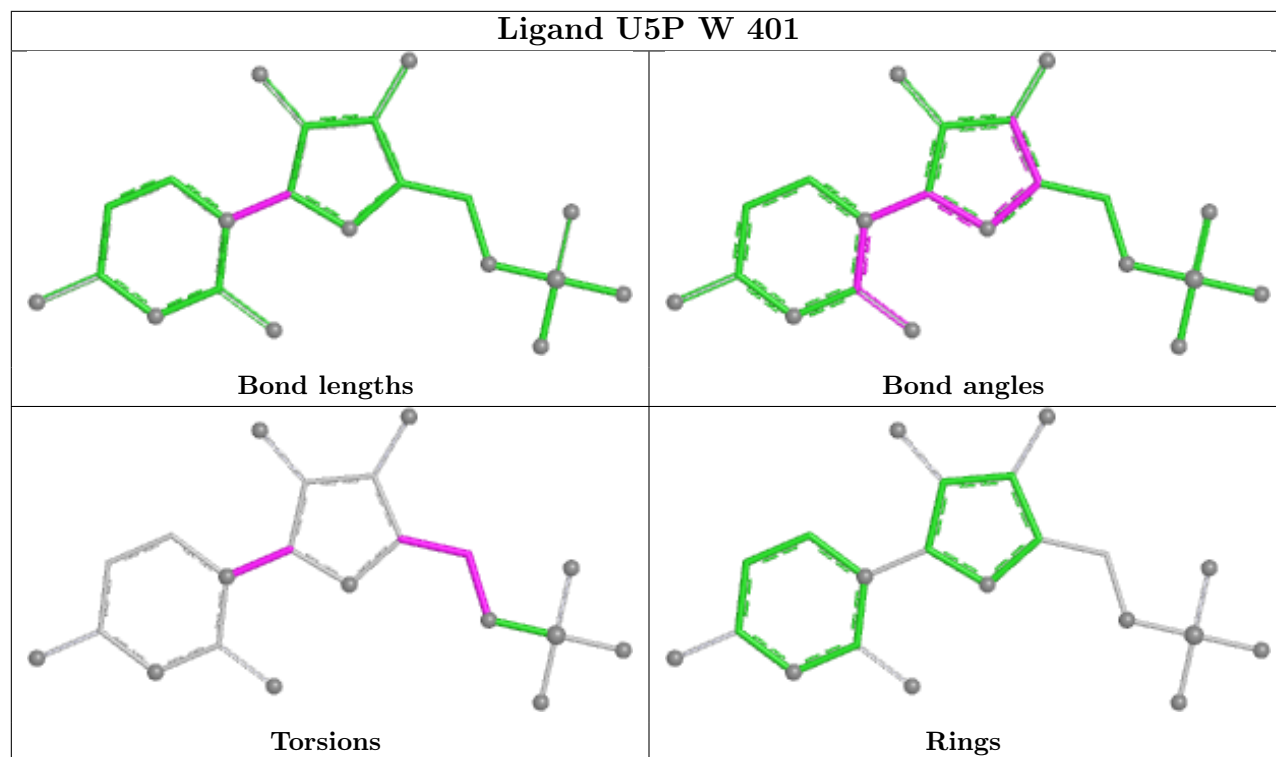


Ligand U5P J 302

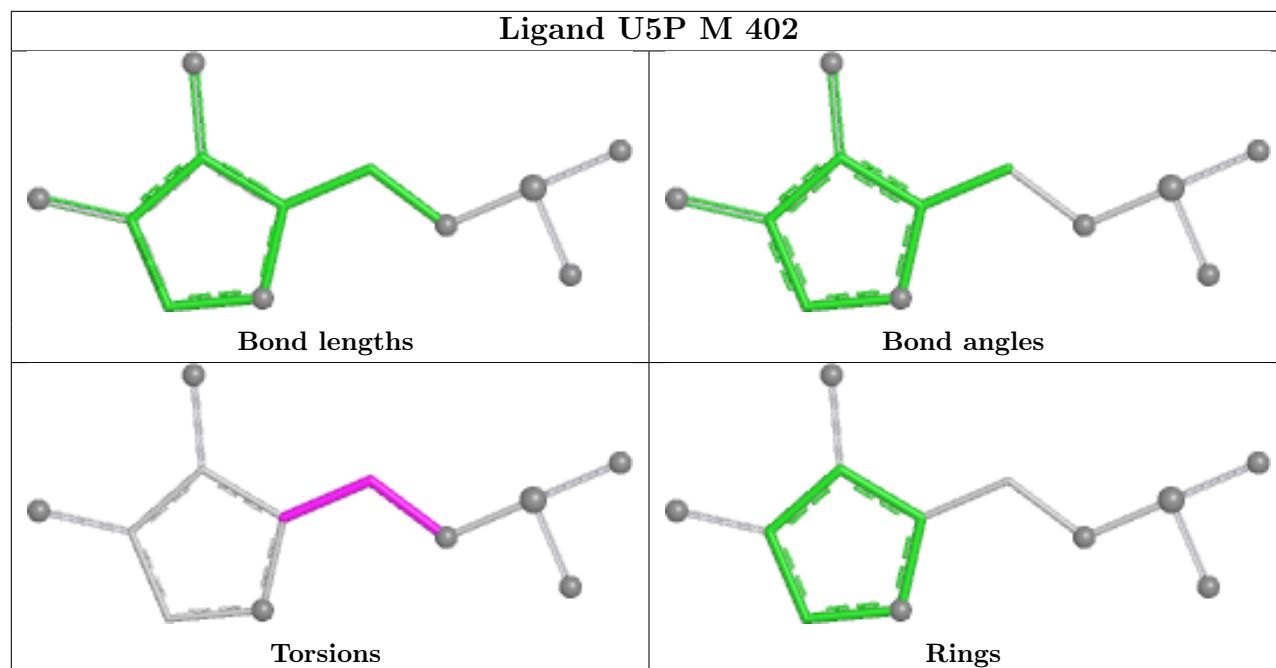


Ligand U5P I 401

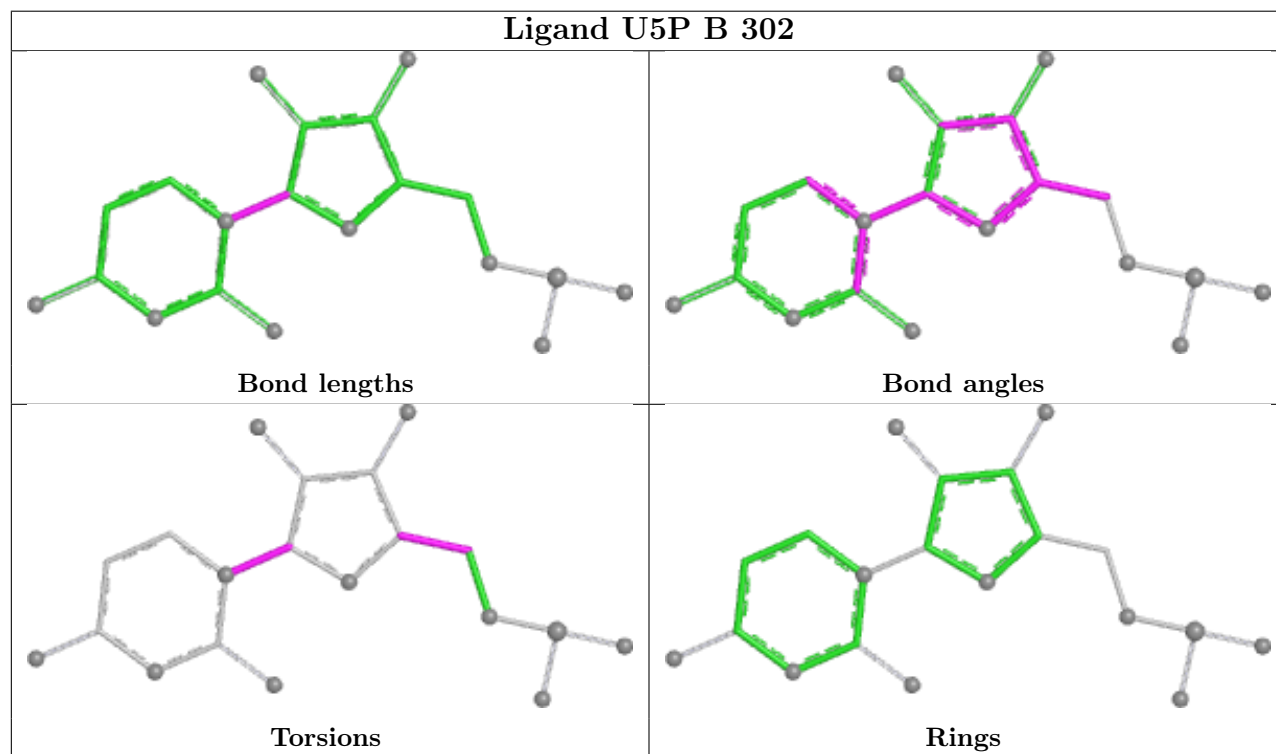


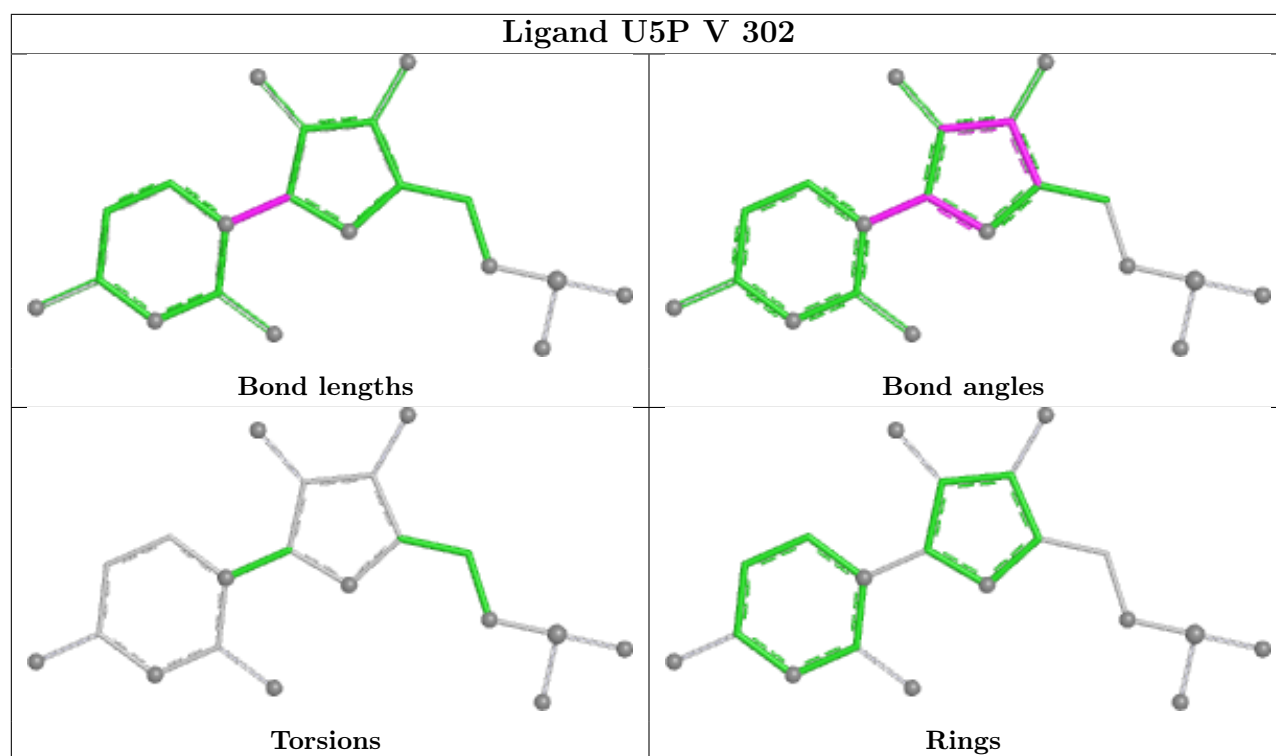


Ligand U5P M 402



Ligand U5P B 302





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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	260/275 (94%)	0.99	32 (12%) 8 6	42, 50, 64, 71	0
1	C	260/275 (94%)	0.90	22 (8%) 16 12	42, 50, 64, 71	0
1	E	260/275 (94%)	0.84	25 (9%) 13 10	42, 50, 64, 71	0
1	G	260/275 (94%)	1.02	35 (13%) 7 5	42, 50, 64, 72	0
1	I	260/275 (94%)	0.91	25 (9%) 13 10	42, 50, 64, 71	0
1	K	260/275 (94%)	0.86	26 (10%) 12 9	42, 50, 64, 71	0
1	M	260/275 (94%)	0.86	24 (9%) 14 10	42, 50, 64, 72	0
1	O	260/275 (94%)	0.89	25 (9%) 13 10	42, 50, 64, 71	0
1	Q	260/275 (94%)	0.96	29 (11%) 10 7	42, 50, 64, 71	0
1	S	260/275 (94%)	0.92	23 (8%) 15 11	42, 50, 64, 71	0
1	U	260/275 (94%)	0.91	26 (10%) 12 9	42, 50, 64, 72	0
1	W	260/275 (94%)	0.85	24 (9%) 14 10	42, 50, 64, 71	0
2	B	241/248 (97%)	0.74	12 (4%) 34 26	42, 49, 65, 78	0
2	D	247/248 (99%)	0.77	15 (6%) 27 20	42, 49, 65, 78	0
2	F	241/248 (97%)	0.79	12 (4%) 34 26	42, 49, 65, 78	0
2	H	241/248 (97%)	0.83	18 (7%) 20 15	42, 49, 65, 78	0
2	J	241/248 (97%)	0.86	15 (6%) 26 20	42, 49, 65, 78	0
2	L	247/248 (99%)	0.84	22 (8%) 15 11	42, 49, 65, 78	0
2	N	241/248 (97%)	0.75	12 (4%) 34 26	42, 49, 65, 78	0
2	P	248/248 (100%)	0.86	22 (8%) 15 11	42, 49, 65, 78	0
2	R	245/248 (98%)	0.94	18 (7%) 21 15	42, 49, 65, 78	0
2	T	247/248 (99%)	0.86	20 (8%) 18 13	42, 49, 65, 78	0
2	V	244/248 (98%)	0.80	21 (8%) 16 12	42, 49, 65, 78	0
2	X	241/248 (97%)	0.77	13 (5%) 31 24	42, 49, 65, 78	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	6044/6276 (96%)	0.86	516 (8%) 16 12	42, 49, 65, 78	0

The worst 5 of 516 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	S	275	ILE	5.8
1	S	175	GLN	5.5
2	R	65	HIS	5.2
1	Q	175	GLN	5.1
1	G	180	ILE	5.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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(Å ²)	Q<0.9
3	U5P	E	403	12/21	0.54	0.20	107,108,109,110	0
3	U5P	X	302	4/21	0.55	0.22	97,97,98,98	0
3	U5P	G	402	20/21	0.59	0.19	101,106,107,107	0
3	U5P	I	401	21/21	0.62	0.16	114,115,117,117	0
3	U5P	W	403	12/21	0.63	0.18	97,97,98,98	0
3	U5P	H	302	20/21	0.65	0.19	98,100,101,101	0
3	U5P	F	302	12/21	0.65	0.24	109,110,111,111	0
3	U5P	B	302	20/21	0.66	0.18	95,98,99,100	0
3	U5P	M	401	21/21	0.68	0.17	90,93,94,95	0
3	U5P	A	402	20/21	0.69	0.17	100,105,107,107	0
3	U5P	G	401	13/21	0.69	0.15	100,102,105,105	0
3	U5P	J	302	20/21	0.70	0.18	107,108,112,113	0
3	U5P	E	401	21/21	0.70	0.15	107,108,110,110	0

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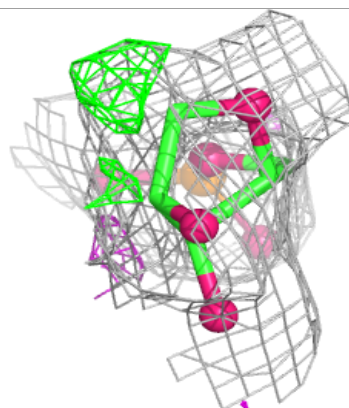
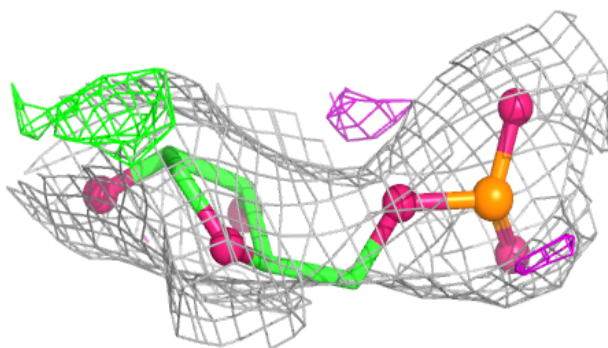
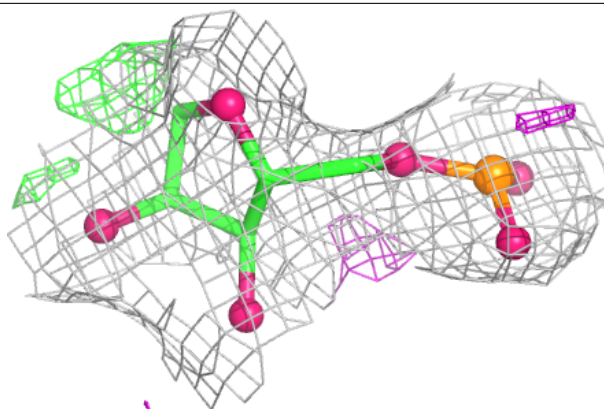
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	U5P	B	303	4/21	0.75	0.16	101,101,102,102	0
3	U5P	M	402	12/21	0.75	0.19	84,85,88,89	0
3	U5P	A	401	21/21	0.76	0.15	94,94,94,96	0
3	U5P	U	403	20/21	0.77	0.15	74,83,84,85	0
3	U5P	W	402	20/21	0.77	0.15	95,98,99,99	0
3	U5P	I	402	4/21	0.80	0.12	106,106,106,107	0
4	CL	R	301	1/1	0.80	0.12	63,63,63,63	0
3	U5P	U	401	21/21	0.81	0.13	78,81,82,83	0
3	U5P	V	302	20/21	0.81	0.17	85,88,89,89	0
3	U5P	W	401	21/21	0.82	0.11	90,92,95,95	0
3	U5P	U	402	20/21	0.83	0.14	73,74,75,76	0
3	U5P	E	402	20/21	0.83	0.15	105,106,107,108	0
4	CL	H	301	1/1	0.84	0.18	66,66,66,66	0
3	U5P	N	302	12/21	0.84	0.13	82,86,89,89	0
4	CL	P	301	1/1	0.85	0.21	80,80,80,80	0
5	RP5	N	303	13/14	0.85	0.14	66,67,69,69	0
4	CL	D	301	1/1	0.90	0.12	76,76,76,76	0
4	CL	T	301	1/1	0.91	0.11	57,57,57,57	0
4	CL	L	301	1/1	0.91	0.20	76,76,76,76	0
6	NA	V	303	1/1	0.91	0.06	40,40,40,40	0
4	CL	N	301	1/1	0.92	0.20	59,59,59,59	0
4	CL	B	301	1/1	0.92	0.11	55,55,55,55	0
4	CL	J	301	1/1	0.93	0.18	50,50,50,50	0
4	CL	X	301	1/1	0.93	0.15	52,52,52,52	0
4	CL	V	301	1/1	0.96	0.15	45,45,45,45	0
4	CL	F	301	1/1	0.97	0.05	36,36,36,36	0

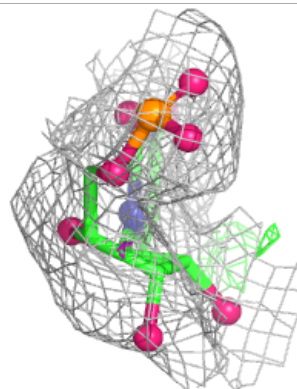
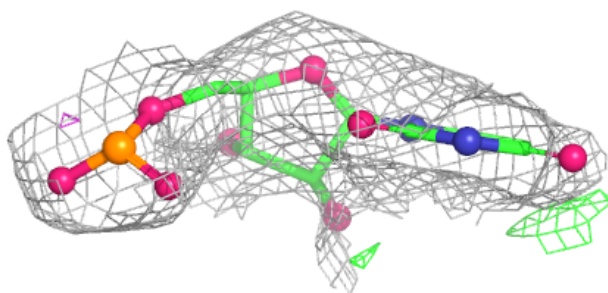
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around U5P E 403:

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

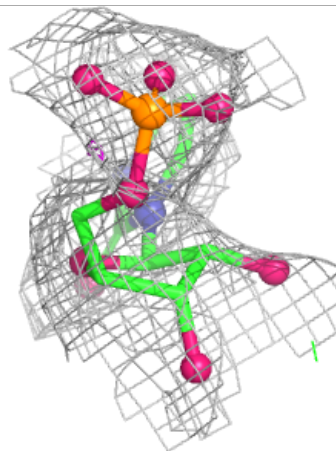
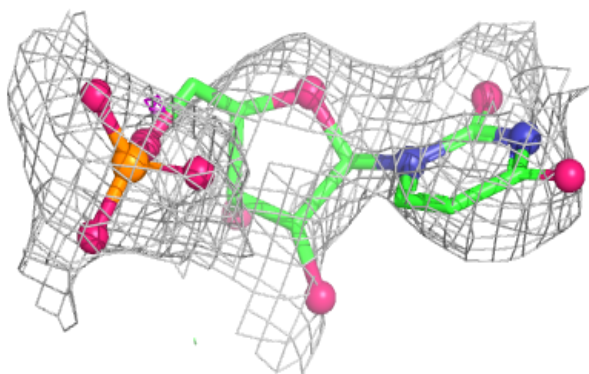
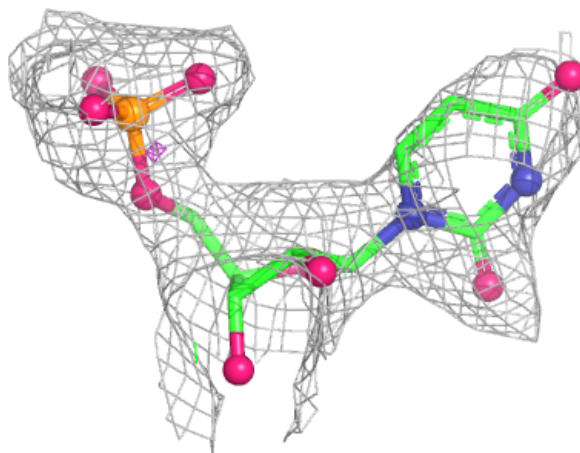
**Electron density around U5P G 402:**

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



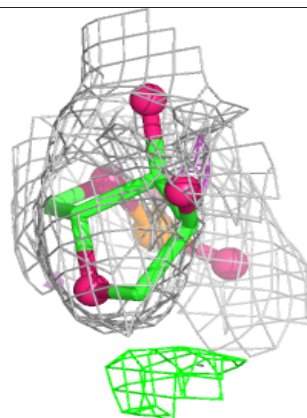
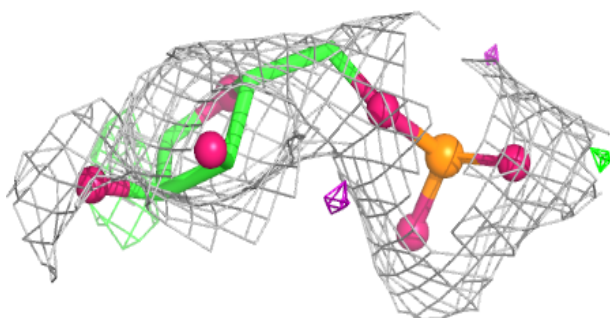
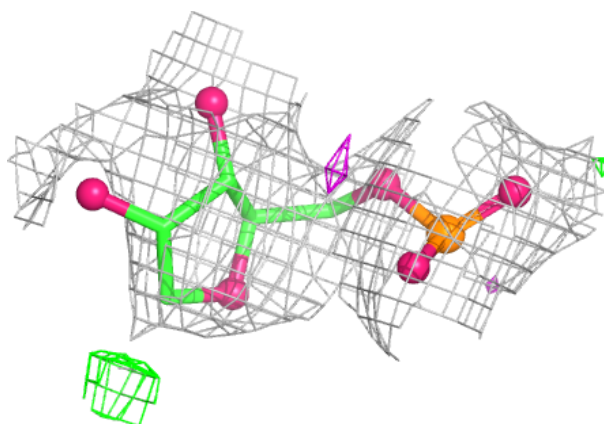
Electron density around U5P I 401:

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



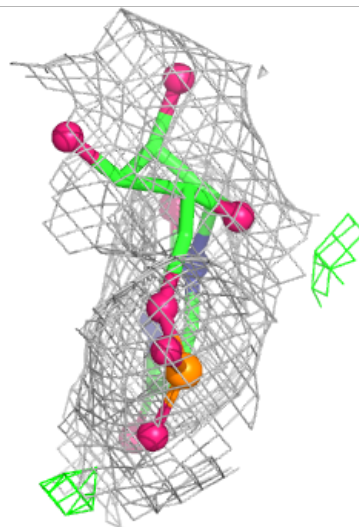
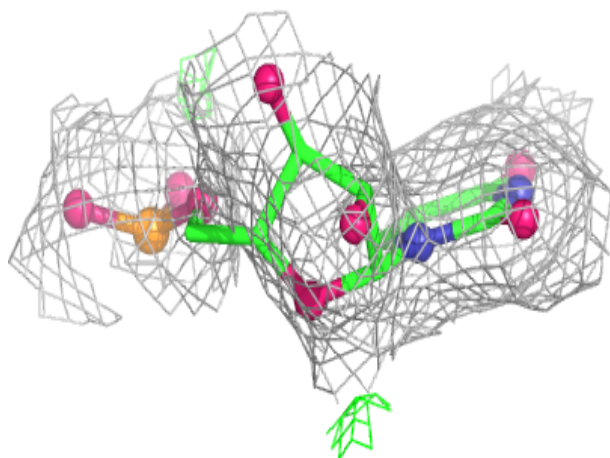
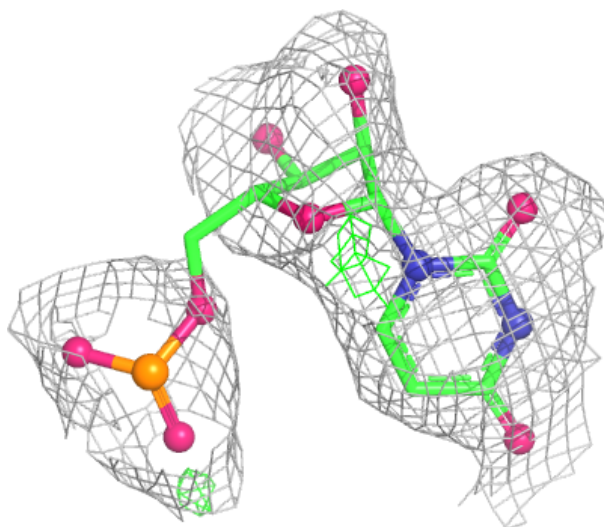
Electron density around U5P W 403:

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



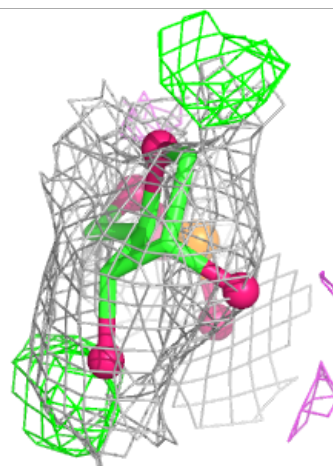
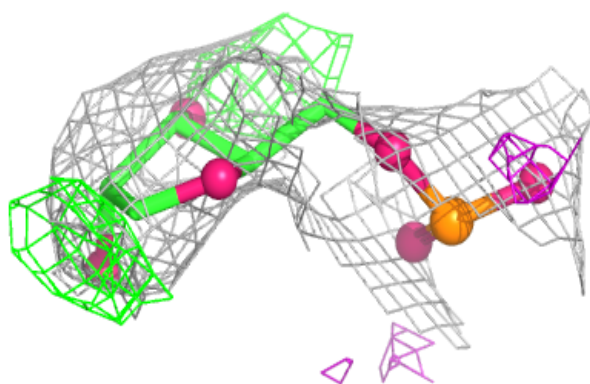
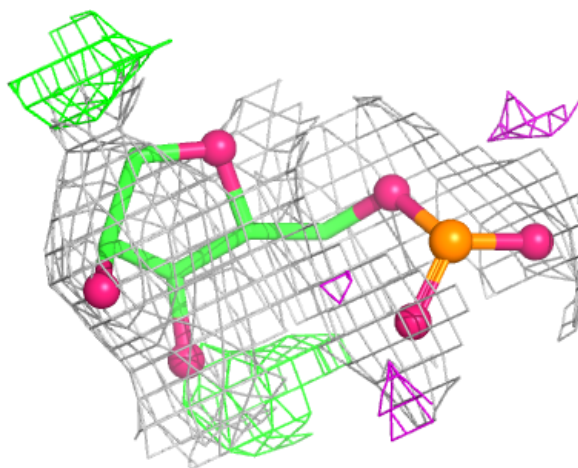
Electron density around U5P H 302:

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



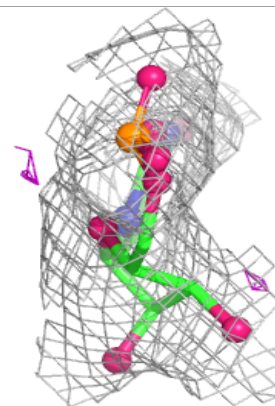
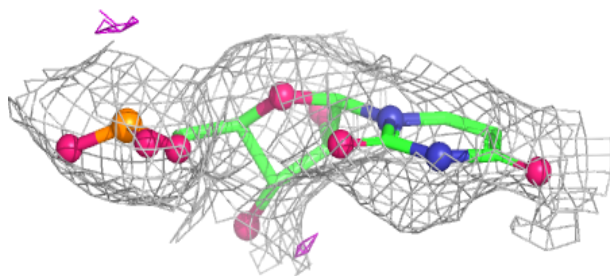
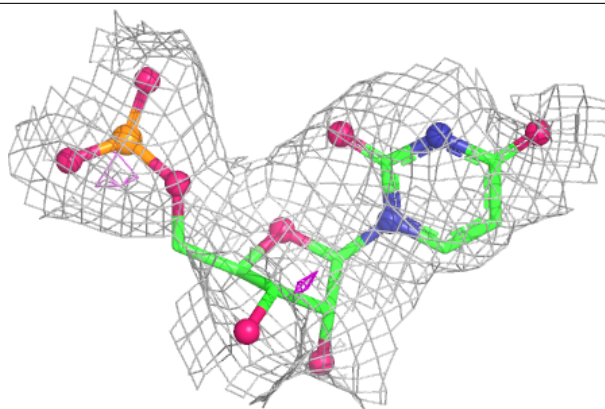
Electron density around U5P F 302:

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

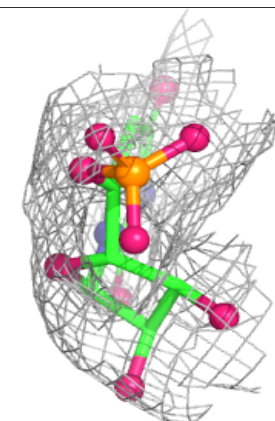
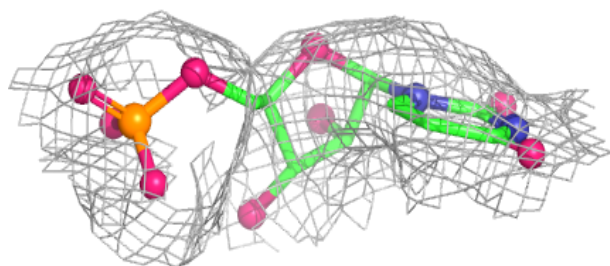
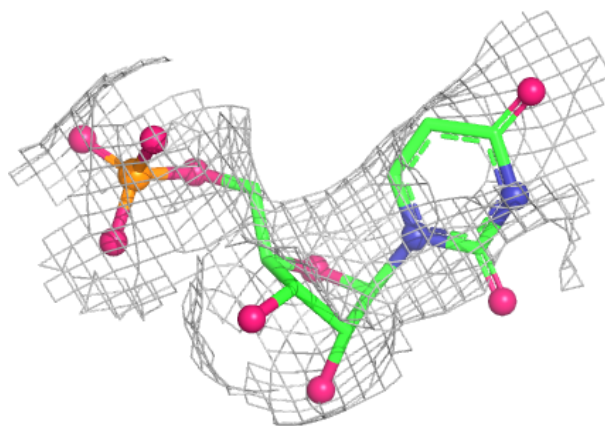


Electron density around U5P B 302:

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

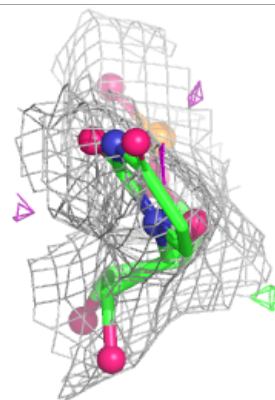
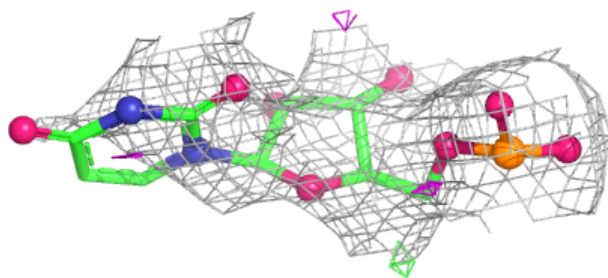
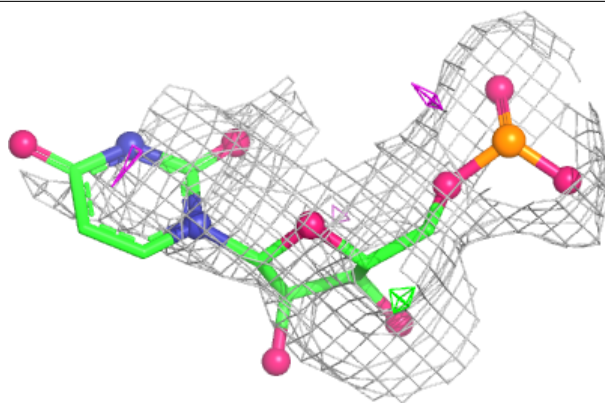
**Electron density around U5P M 401:**

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

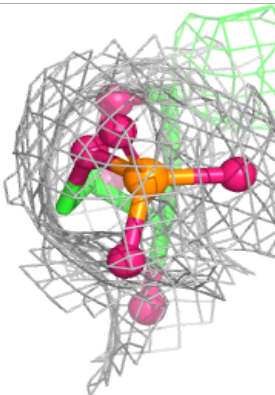
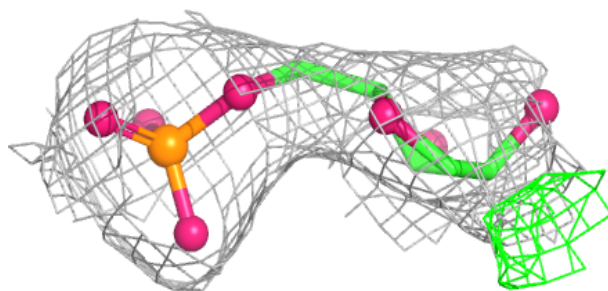
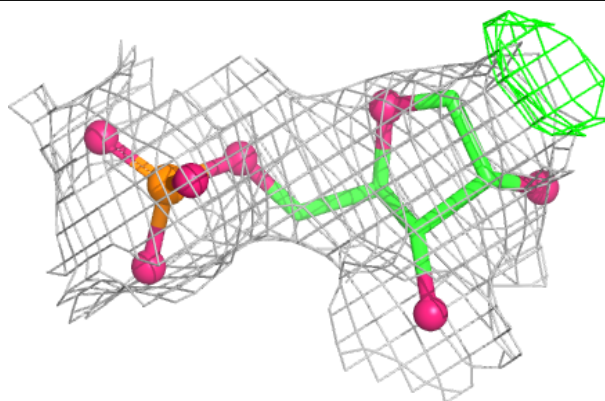


Electron density around U5P A 402:

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

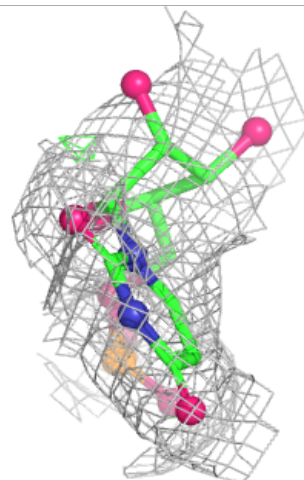
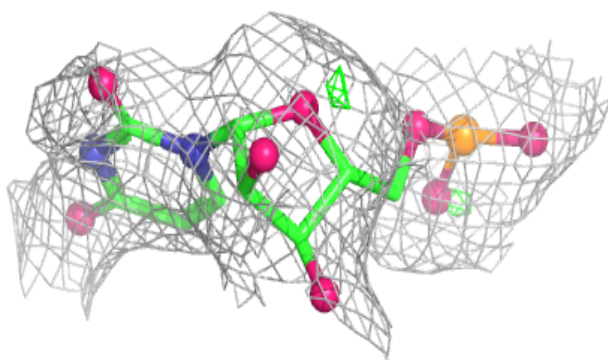
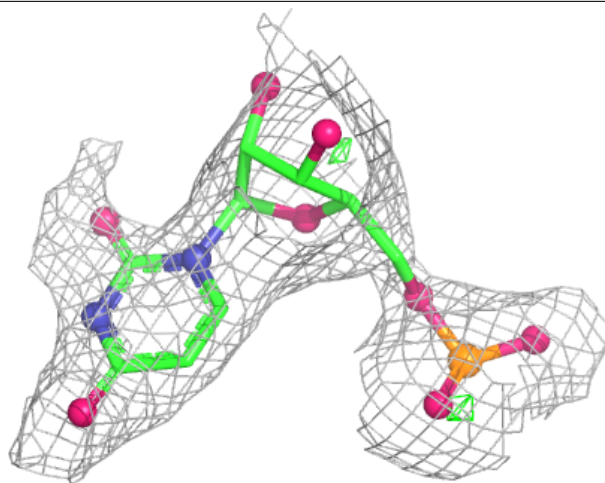
**Electron density around U5P G 401:**

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



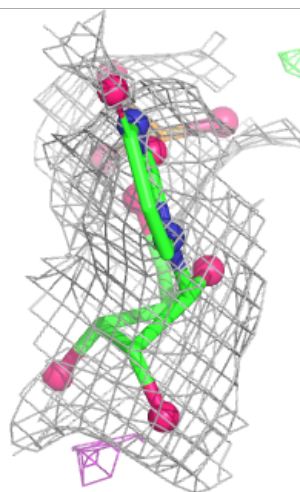
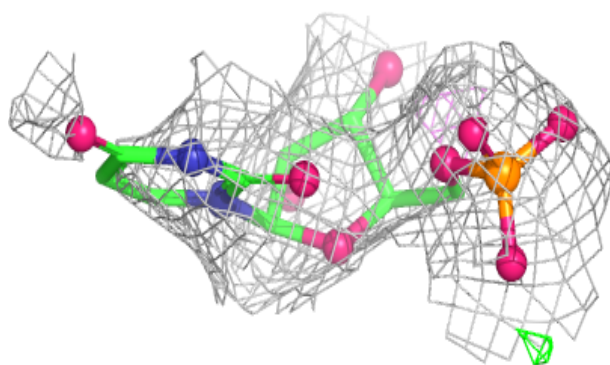
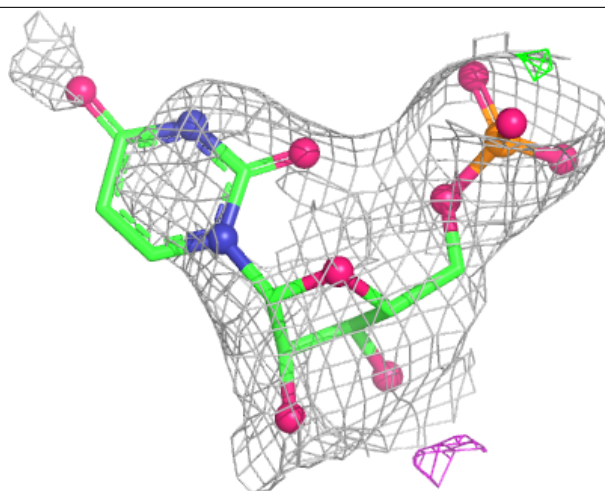
Electron density around U5P J 302:

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



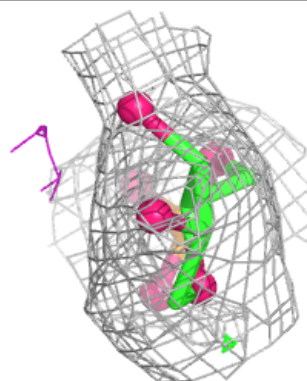
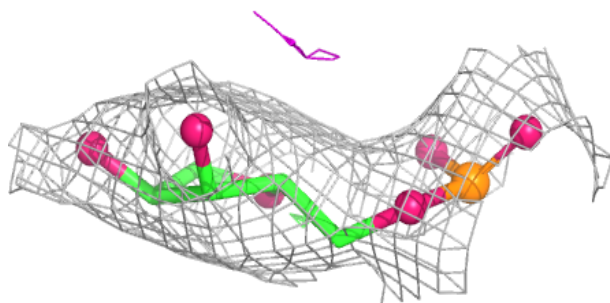
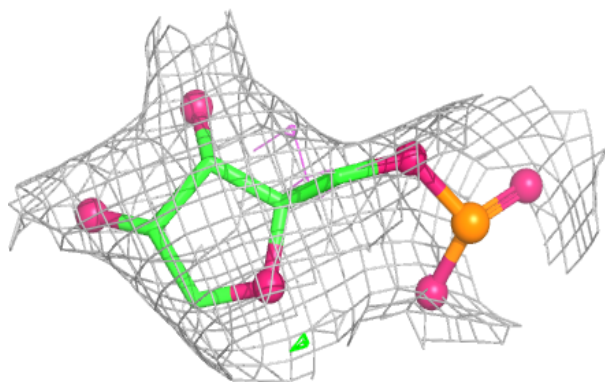
Electron density around U5P E 401:

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

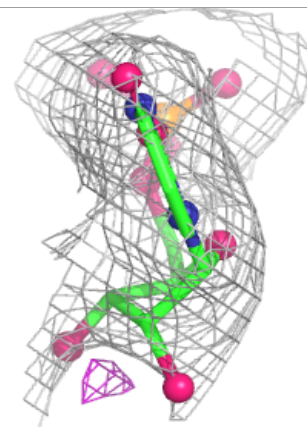
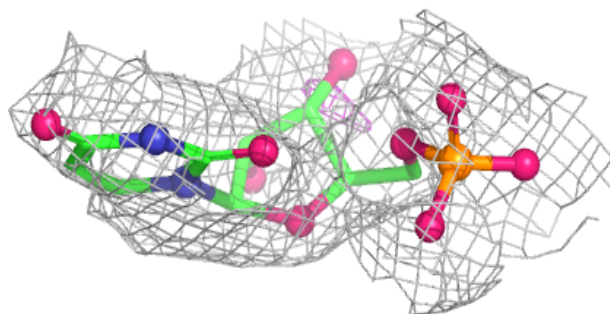
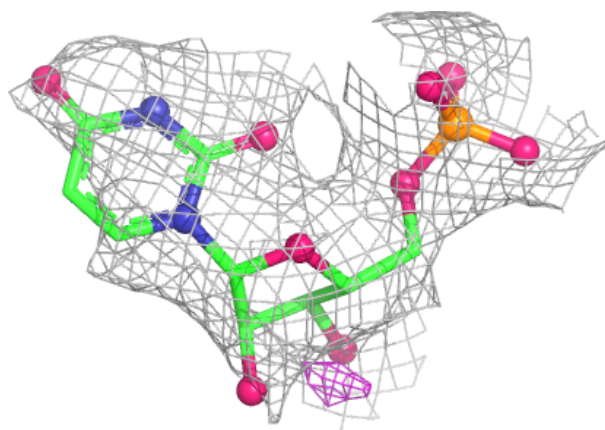


Electron density around U5P M 402:

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

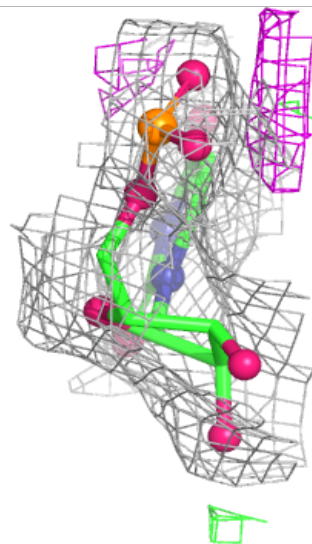
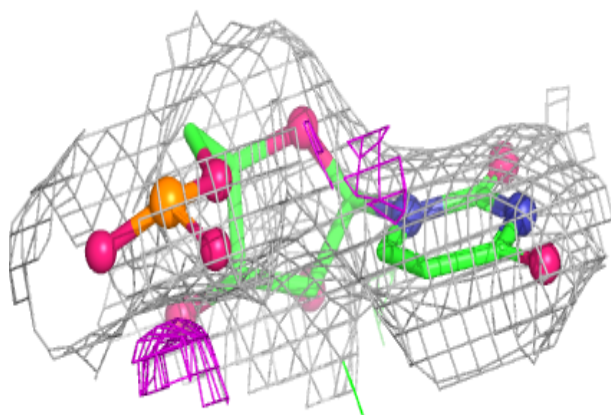
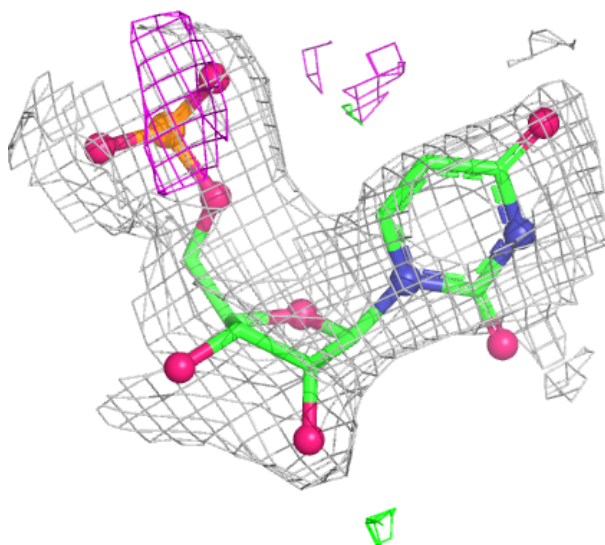
**Electron density around U5P A 401:**

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



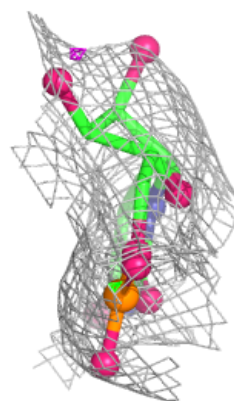
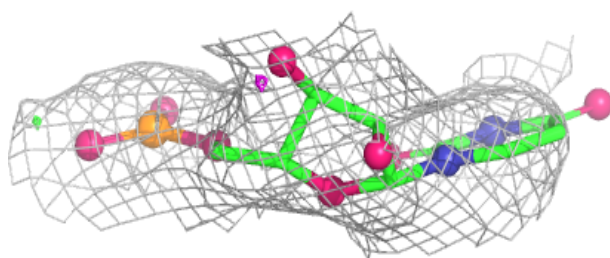
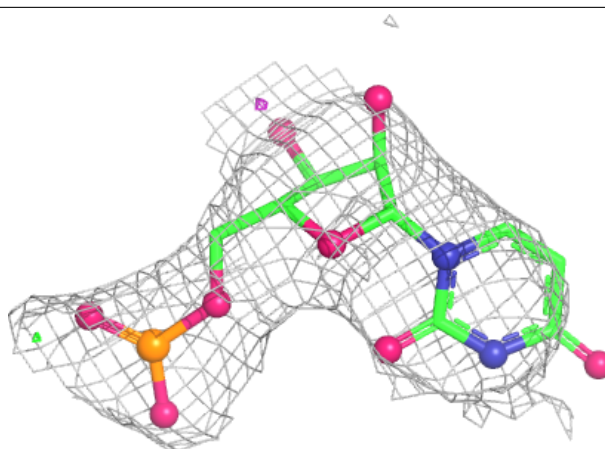
Electron density around U5P U 403:

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



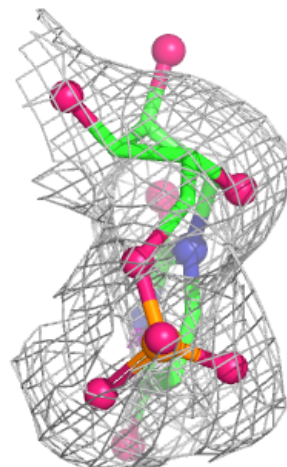
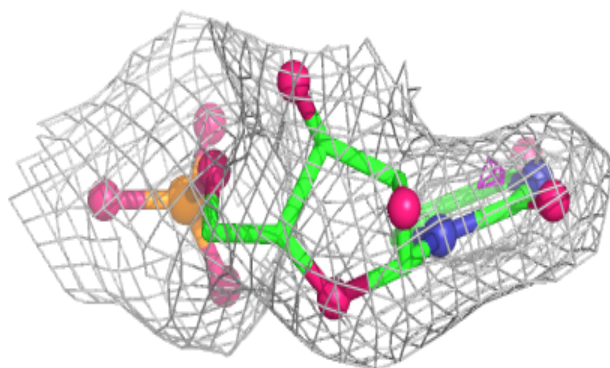
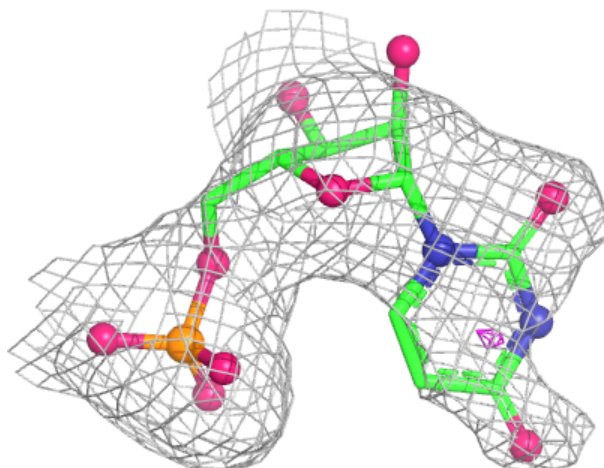
Electron density around U5P W 402:

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



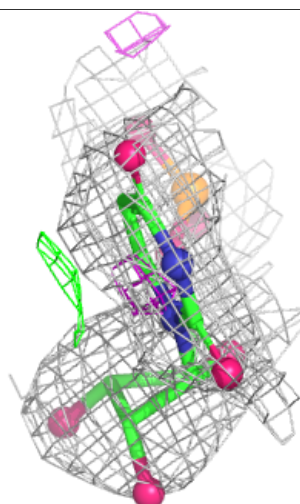
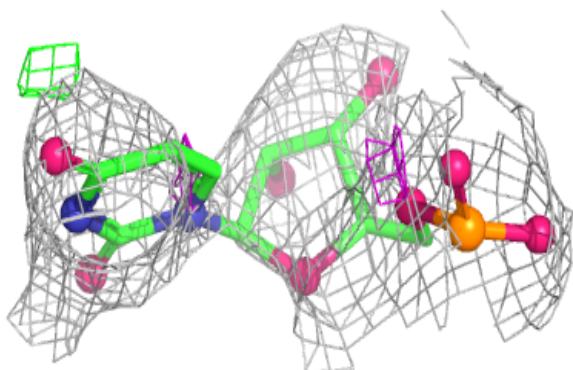
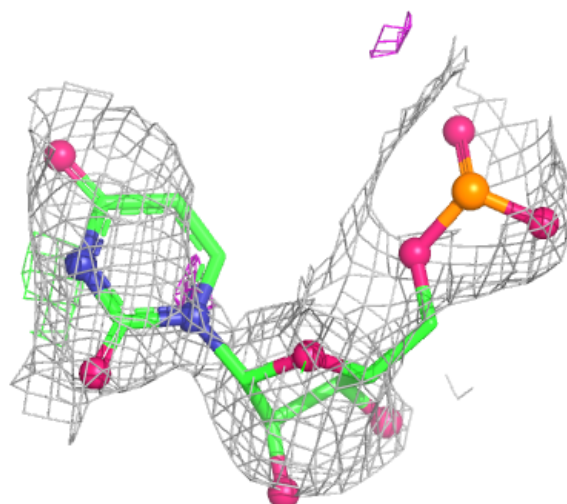
Electron density around U5P U 401:

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



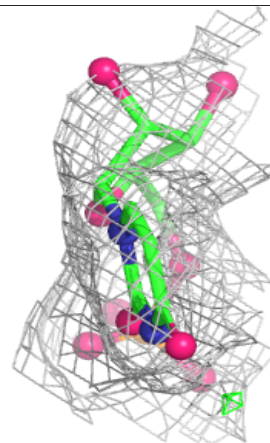
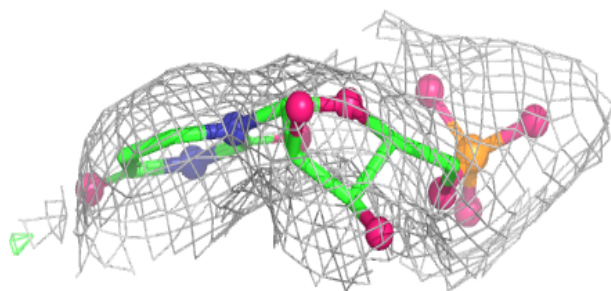
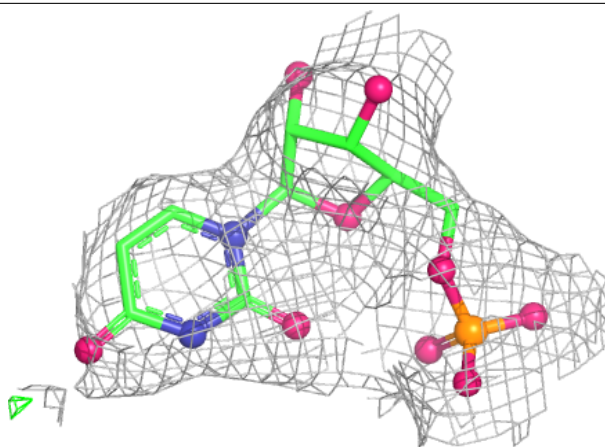
Electron density around U5P V 302:

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



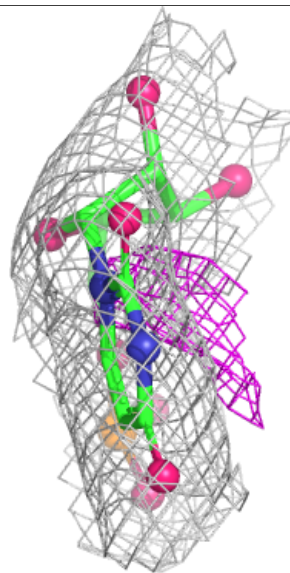
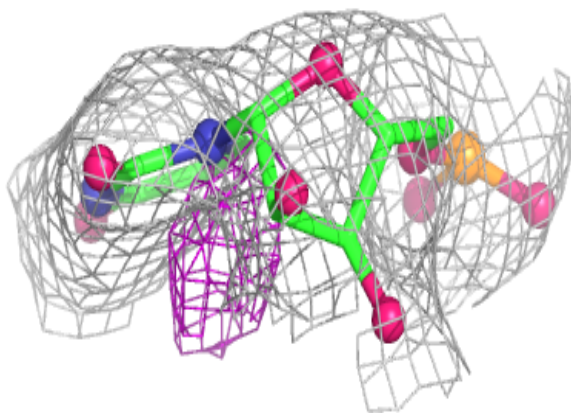
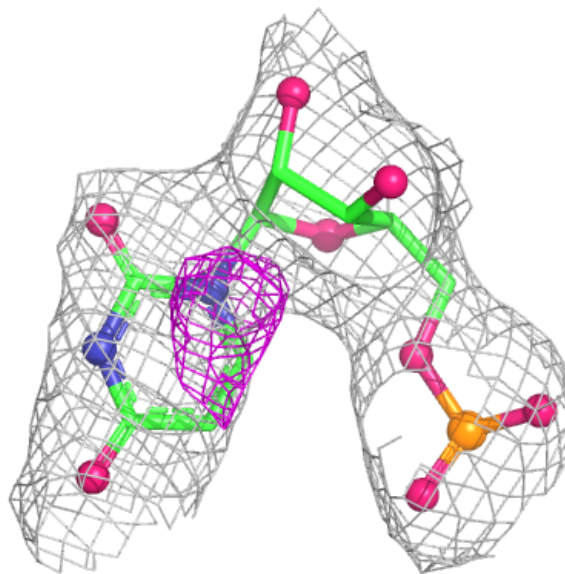
Electron density around U5P W 401:

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



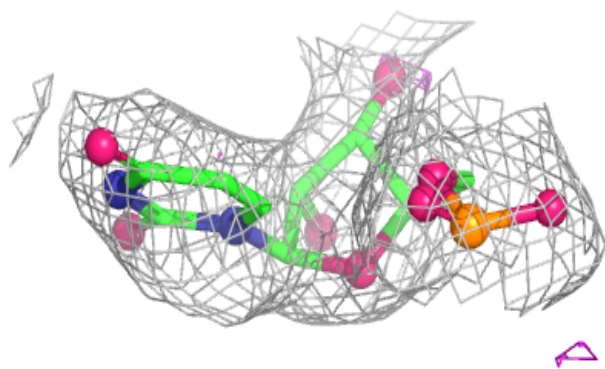
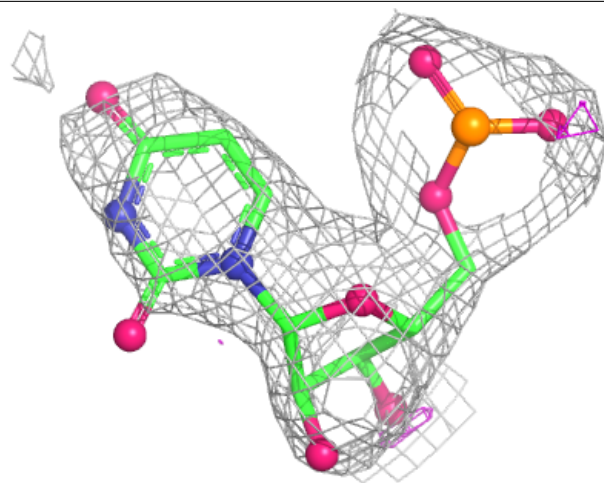
Electron density around U5P U 402:

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



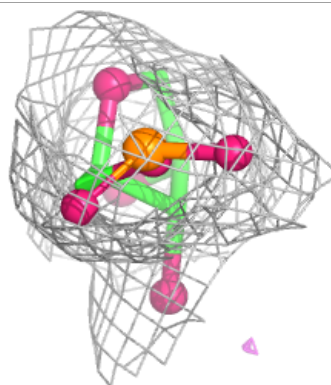
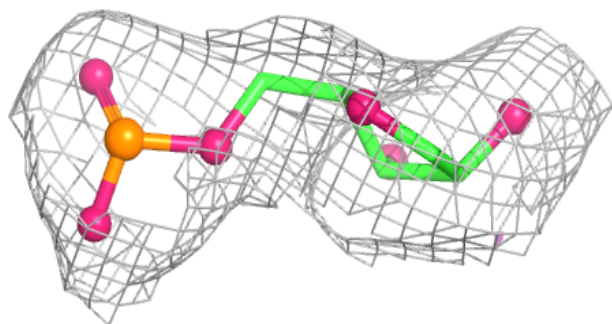
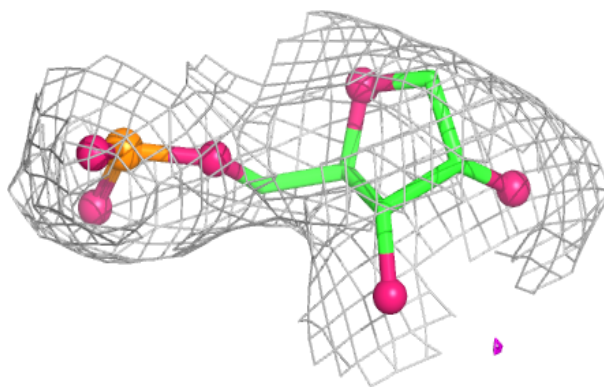
Electron density around U5P E 402:

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



Electron density around U5P N 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.