



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 9, 2025 – 06:15 PM JST

PDB ID : 8ZN5 / pdb\_00008zn5  
Title : Crystal Structure of Designed Clock Protein KaiC  
Authors : Furuike, Y.; Akiyama, S.  
Deposited on : 2024-05-26  
Resolution : 3.10 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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

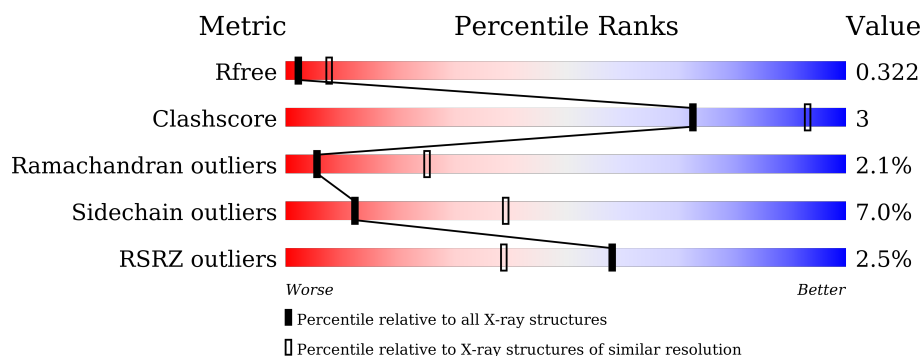
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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))
$R_{free}$	164625	1351 (3.10-3.10)
Clashscore	180529	1454 (3.10-3.10)
Ramachandran outliers	177936	1391 (3.10-3.10)
Sidechain outliers	177891	1391 (3.10-3.10)
RSRZ outliers	164620	1351 (3.10-3.10)

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	518	<div> <div>%</div> <div> <div></div> <div>75%</div> <div>10%</div> <div>•</div> <div>14%</div> </div> </div>
1	B	518	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>9%</div> <div>•</div> <div>12%</div> </div> </div>
1	C	518	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>11%</div> <div>•</div> <div>11%</div> </div> </div>
1	D	518	<div> <div>2%</div> <div> <div></div> <div>74%</div> <div>10%</div> <div>•</div> <div>14%</div> </div> </div>
1	E	518	<div> <div>%</div> <div> <div></div> <div>78%</div> <div>9%</div> <div>•</div> <div>12%</div> </div> </div>
1	F	518	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>8%</div> <div>•</div> <div>14%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	518	 3% 76% 9% • 14%
1	H	518	 6% 77% 6% • 15%
1	I	518	 3% 78% 8% • 14%
1	J	518	 2% 78% 7% • 14%
1	K	518	 2% 77% 7% • 14%
1	L	518	 2% 78% 6% • 15%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 36725 atoms, of which 0 are hydrogens and 0 are deuteriums.

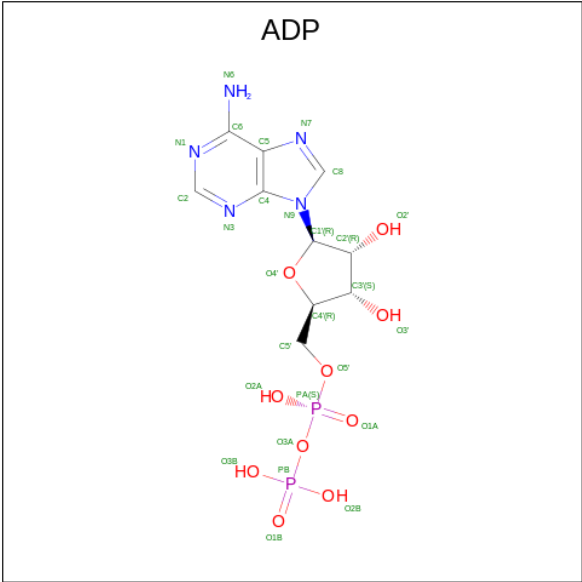
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called KaiC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	454	Total	C	N	O	S	0	0	0
			3201	2036	560	593	12			
1	C	463	Total	C	N	O	S	0	0	0
			3207	2025	572	599	11			
1	F	446	Total	C	N	O	S	0	0	0
			3100	1963	548	577	12			
1	A	446	Total	C	N	O	S	0	0	0
			3151	2002	555	582	12			
1	D	443	Total	C	N	O	S	0	0	0
			3002	1889	533	571	9			
1	E	456	Total	C	N	O	S	0	0	0
			3158	1997	553	596	12			
1	G	447	Total	C	N	O	S	0	0	0
			2853	1785	513	547	8			
1	H	439	Total	C	N	O	S	0	0	0
			2809	1747	513	540	9			
1	K	444	Total	C	N	O	S	0	0	0
			2865	1789	524	546	6			
1	L	439	Total	C	N	O	S	0	0	0
			2784	1738	518	519	9			
1	I	446	Total	C	N	O	S	0	0	0
			2918	1807	527	573	11			
1	J	447	Total	C	N	O	S	0	0	0
			2978	1871	532	568	7			

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	H	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	H	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	K	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	K	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	L	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	L	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	I	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	I	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	J	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	J	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Mg	0	0
			2	2		
3	C	2	Total	Mg	0	0
			2	2		
3	F	2	Total	Mg	0	0
			2	2		
3	A	2	Total	Mg	0	0
			2	2		
3	D	2	Total	Mg	0	0
			2	2		
3	E	2	Total	Mg	0	0
			2	2		
3	G	2	Total	Mg	0	0
			2	2		
3	H	2	Total	Mg	0	0
			2	2		
3	K	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	2	Total 2	Mg 2	0	0
3	I	2	Total 2	Mg 2	0	0
3	J	2	Total 2	Mg 2	0	0

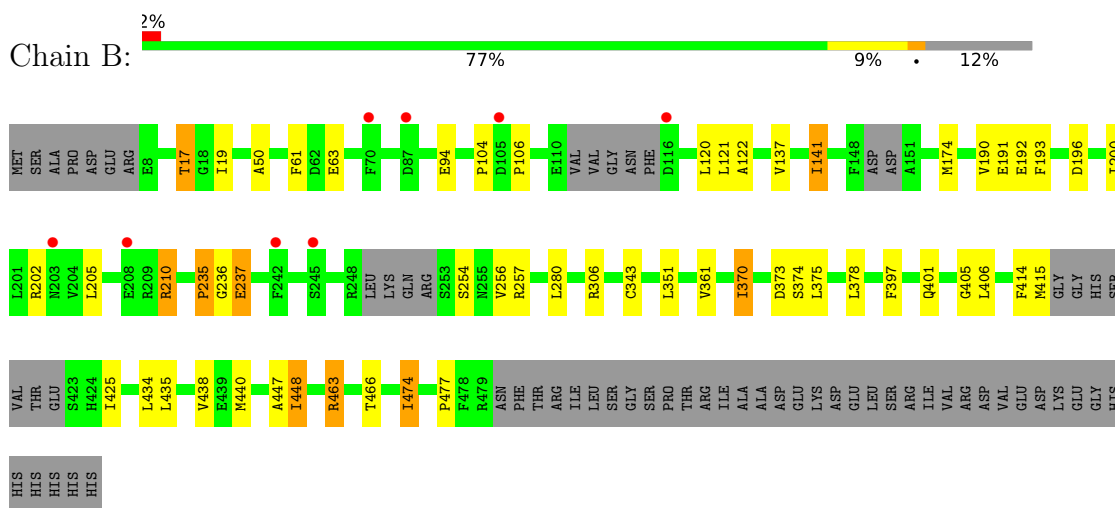
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	O 1	0	0
4	C	4	Total 4	O 4	0	0
4	F	2	Total 2	O 2	0	0
4	A	7	Total 7	O 7	0	0
4	D	2	Total 2	O 2	0	0
4	E	5	Total 5	O 5	0	0
4	K	2	Total 2	O 2	0	0
4	J	4	Total 4	O 4	0	0

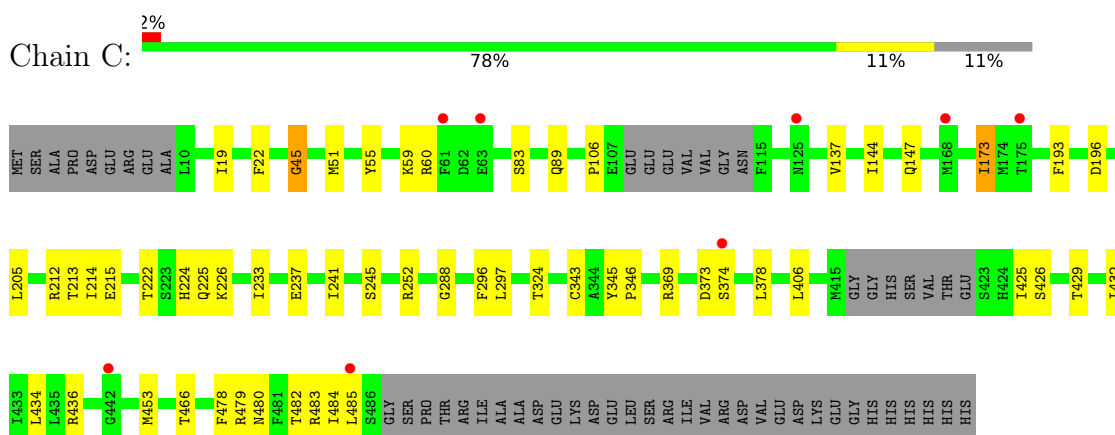
### 3 Residue-property plots [i](#)

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

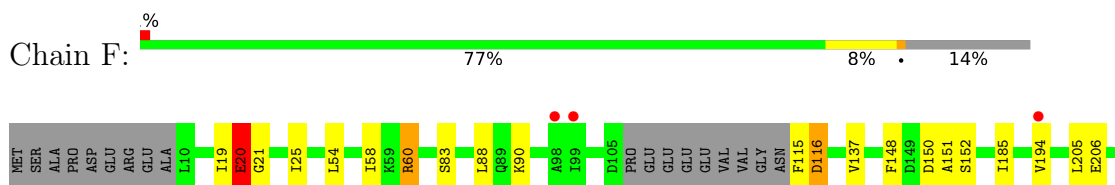
#### • Molecule 1: KaiC

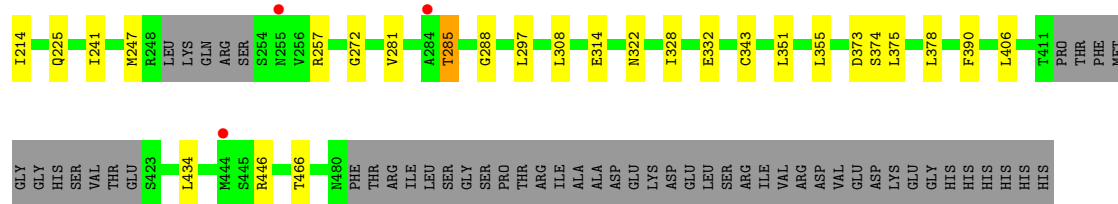


#### • Molecule 1: KaiC

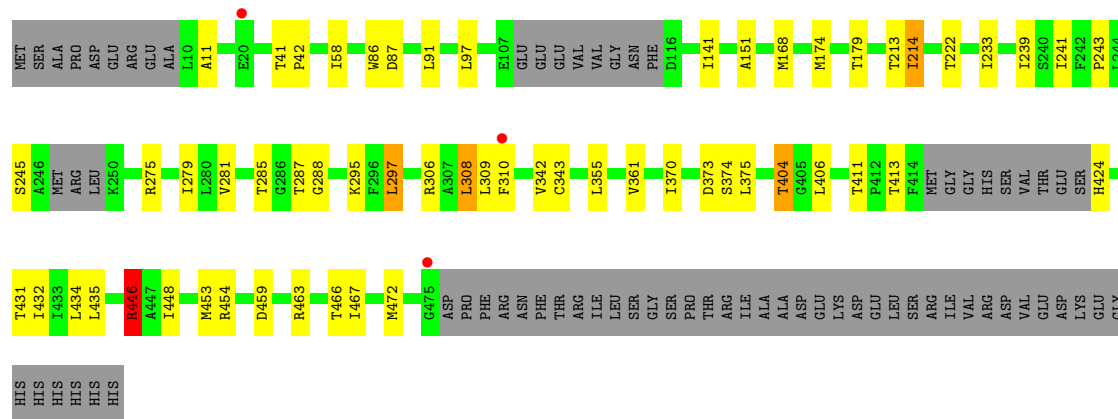
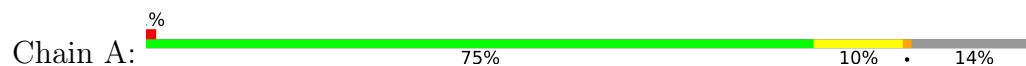


#### • Molecule 1: KaiC

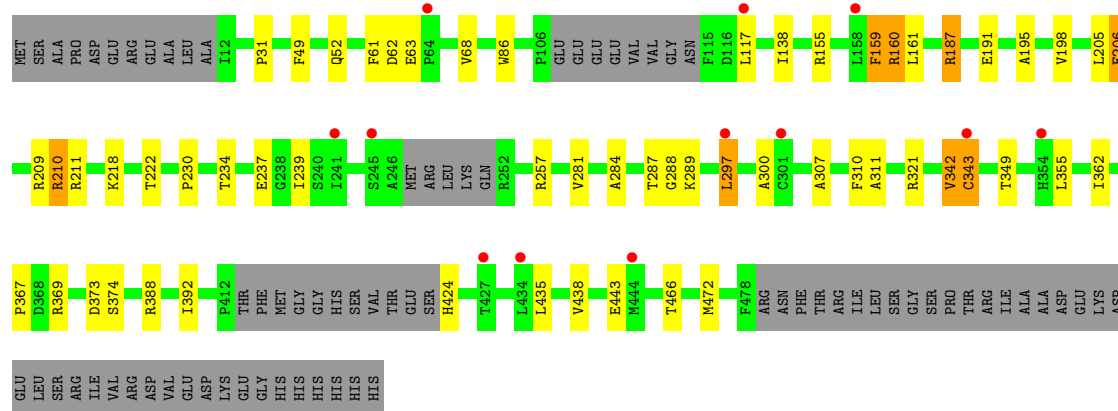
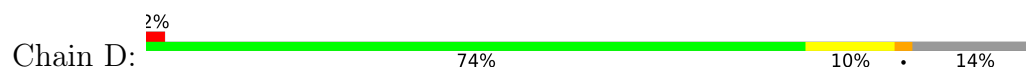




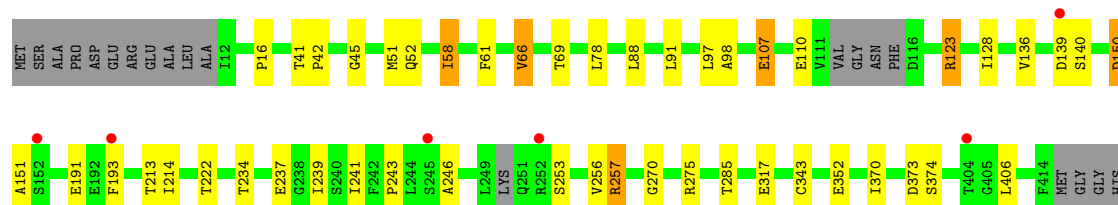
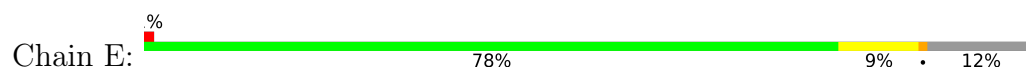
### • Molecule 1: KaiC

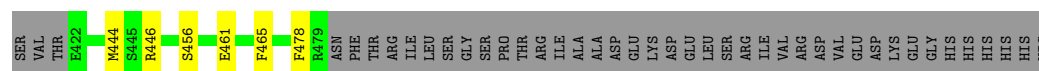


### • Molecule 1: KaiC

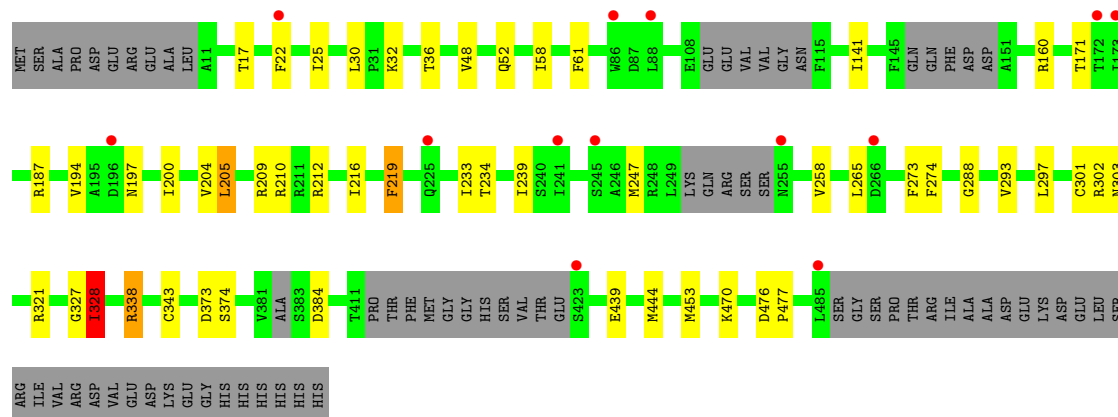
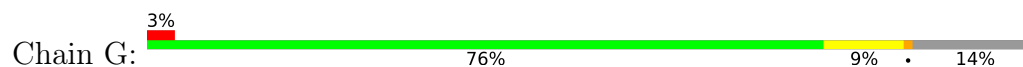


### • Molecule 1: KaiC

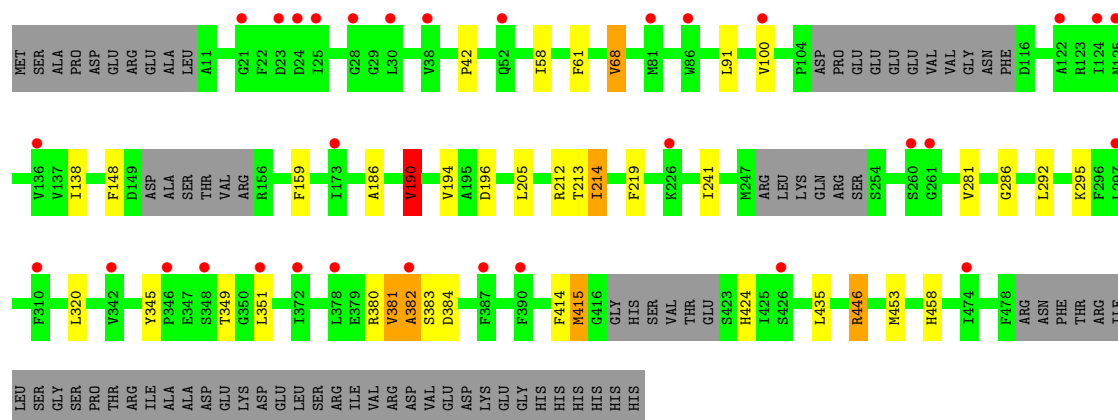
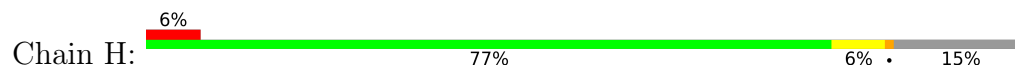




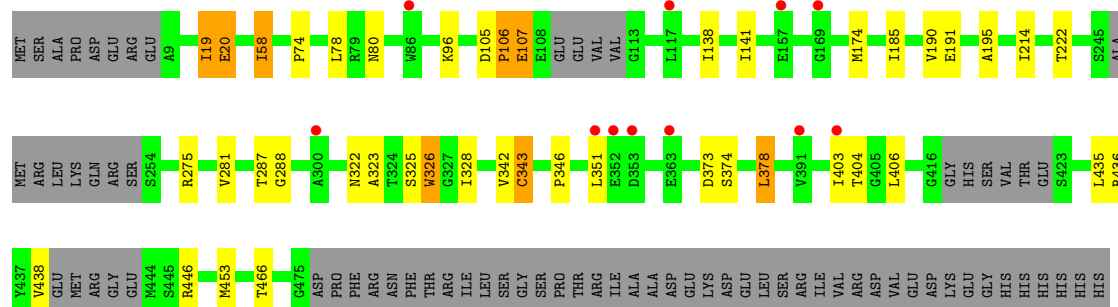
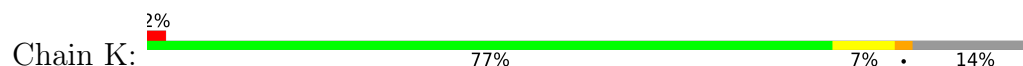
• Molecule 1: KaiC



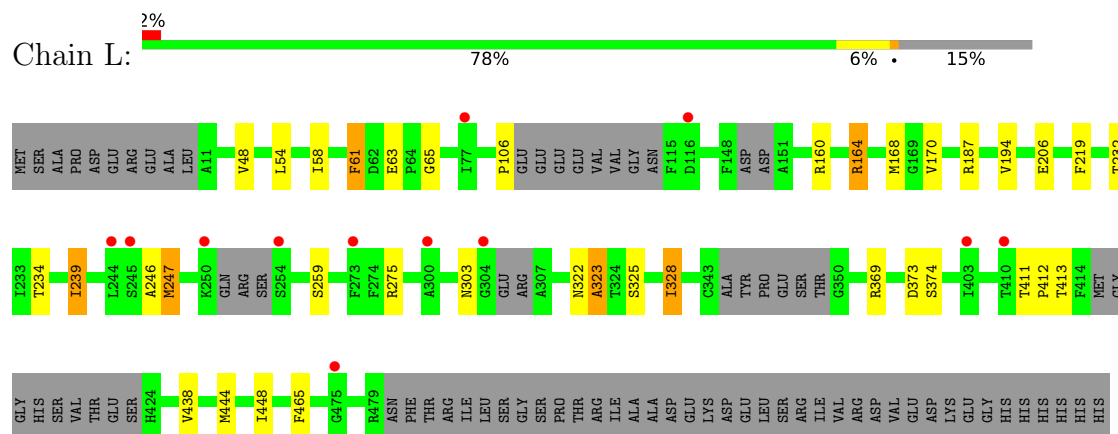
• Molecule 1: KaiC



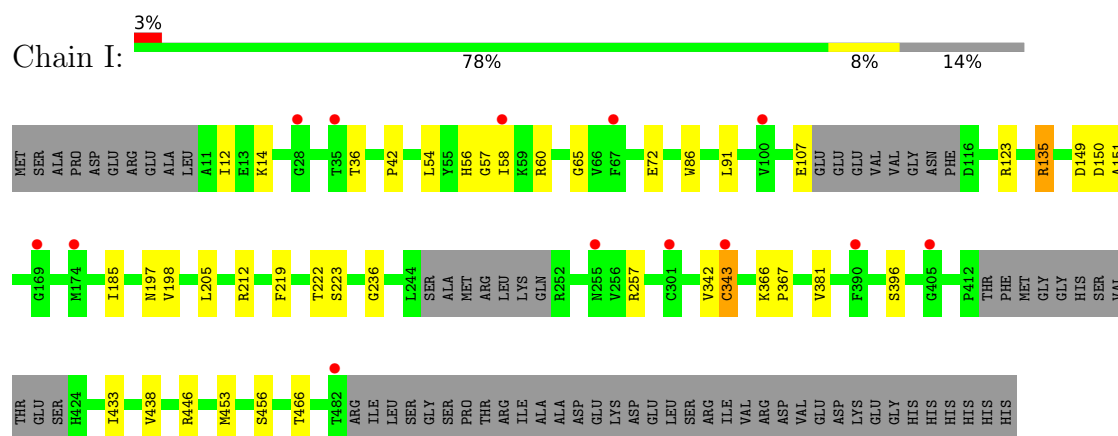
• Molecule 1: KaiC



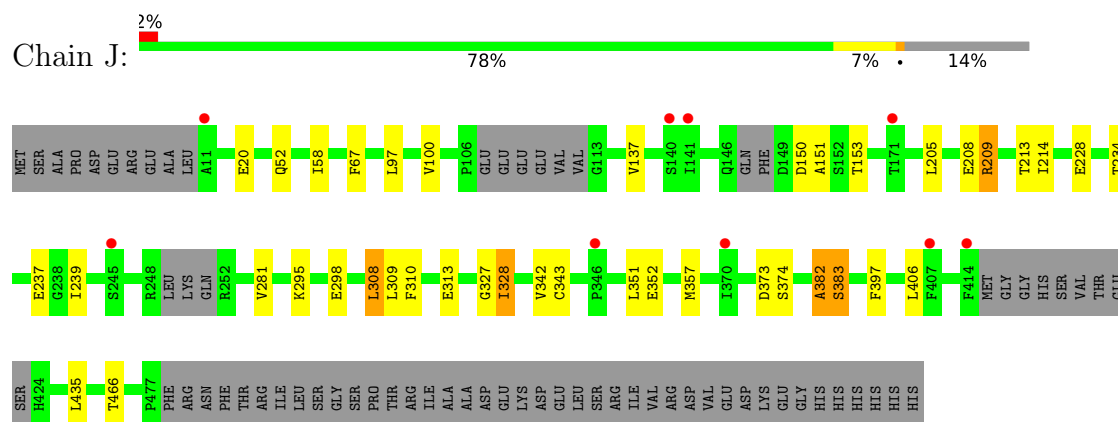
- Molecule 1: KaiC



- Molecule 1: KaiC



- Molecule 1: KaiC



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.13Å 385.57Å 108.11Å 90.00° 113.15° 90.00°	Depositor
Resolution (Å)	49.35 – 3.10 49.35 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.35-3.10) 99.8 (49.35-3.10)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.77 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.8.0415	Depositor
R, $R_{free}$	0.280 , 0.329 0.278 , 0.322	Depositor DCC
$R_{free}$ test set	6299 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	86.9	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 104.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	36725	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% 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: ADP, MG

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	0.26	0/3206	0.44	0/4355
1	B	0.26	0/3259	0.44	0/4432
1	C	0.26	0/3262	0.44	0/4440
1	D	0.27	0/3055	0.45	0/4166
1	E	0.27	0/3214	0.45	0/4375
1	F	0.27	0/3151	0.44	0/4282
1	G	0.27	0/2895	0.45	0/3963
1	H	0.27	0/2854	0.44	0/3902
1	I	0.27	0/2967	0.44	0/4055
1	J	0.27	0/3029	0.44	0/4137
1	K	0.27	0/2909	0.44	0/3982
1	L	0.27	0/2824	0.45	0/3859
All	All	0.27	0/36625	0.44	0/49948

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	J	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	446	ARG	Sidechain
1	J	209	ARG	Sidechain

## 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	3151	0	2880	21	0
1	B	3201	0	2896	23	0
1	C	3207	0	2851	18	0
1	D	3002	0	2586	28	0
1	E	3158	0	2782	22	0
1	F	3100	0	2780	16	0
1	G	2853	0	2281	16	0
1	H	2809	0	2200	9	0
1	I	2918	0	2332	12	0
1	J	2978	0	2502	18	0
1	K	2865	0	2339	20	0
1	L	2784	0	2217	13	0
2	A	54	0	24	0	0
2	B	54	0	24	0	0
2	C	54	0	24	1	0
2	D	54	0	24	0	0
2	E	54	0	24	0	0
2	F	54	0	24	1	0
2	G	54	0	24	0	0
2	H	54	0	24	0	0
2	I	54	0	24	1	0
2	J	54	0	24	0	0
2	K	54	0	24	1	0
2	L	54	0	24	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
3	G	2	0	0	0	0
3	H	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	I	2	0	0	0	0
3	J	2	0	0	0	0
3	K	2	0	0	0	0
3	L	2	0	0	0	0
4	A	7	0	0	0	0
4	B	1	0	0	0	0
4	C	4	0	0	0	0
4	D	2	0	0	0	0
4	E	5	0	0	0	0
4	F	2	0	0	0	0
4	J	4	0	0	0	0
4	K	2	0	0	0	0
All	All	36725	0	30934	207	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 3.

The worst 5 of 207 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:ILE:HD11	1:A:174:MET:HB3	1.48	0.93
1:D:187:ARG:HH11	1:D:187:ARG:HB3	1.50	0.76
1:A:58:ILE:HD11	1:A:91:LEU:HD13	1.67	0.76
1:A:446:ARG:HH11	1:A:467:ILE:HD12	1.55	0.72
1:J:209:ARG:HH21	1:J:209:ARG:HG2	1.55	0.71

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	438/518 (85%)	405 (92%)	27 (6%)	6 (1%)	9	34
1	B	444/518 (86%)	401 (90%)	34 (8%)	9 (2%)	6	26
1	C	457/518 (88%)	412 (90%)	35 (8%)	10 (2%)	5	24
1	D	435/518 (84%)	391 (90%)	37 (8%)	7 (2%)	8	31
1	E	448/518 (86%)	409 (91%)	30 (7%)	9 (2%)	6	26
1	F	438/518 (85%)	398 (91%)	28 (6%)	12 (3%)	4	21
1	G	435/518 (84%)	373 (86%)	54 (12%)	8 (2%)	7	29
1	H	429/518 (83%)	365 (85%)	52 (12%)	12 (3%)	4	20
1	I	438/518 (85%)	393 (90%)	35 (8%)	10 (2%)	5	23
1	J	437/518 (84%)	391 (90%)	38 (9%)	8 (2%)	7	29
1	K	434/518 (84%)	379 (87%)	47 (11%)	8 (2%)	7	29
1	L	425/518 (82%)	373 (88%)	43 (10%)	9 (2%)	5	25
All	All	5258/6216 (85%)	4690 (89%)	460 (9%)	108 (2%)	5	25

5 of 108 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	235	PRO
1	F	20	GLU
1	F	116	ASP
1	F	151	ALA
1	A	413	THR

### 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	282/442 (64%)	260 (92%)	22 (8%)	10	35
1	B	285/442 (64%)	266 (93%)	19 (7%)	13	40
1	C	275/442 (62%)	258 (94%)	17 (6%)	15	43
1	D	248/442 (56%)	234 (94%)	14 (6%)	17	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	272/442 (62%)	253 (93%)	19 (7%)	12	39
1	F	267/442 (60%)	249 (93%)	18 (7%)	13	40
1	G	201/442 (46%)	181 (90%)	20 (10%)	6	24
1	H	193/442 (44%)	173 (90%)	20 (10%)	5	22
1	I	219/442 (50%)	205 (94%)	14 (6%)	14	42
1	J	235/442 (53%)	223 (95%)	12 (5%)	20	49
1	K	208/442 (47%)	196 (94%)	12 (6%)	17	45
1	L	186/442 (42%)	171 (92%)	15 (8%)	9	33
All	All	2871/5304 (54%)	2669 (93%)	202 (7%)	12	39

5 of 202 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	200	ILE
1	H	349	THR
1	J	357	MET
1	G	212	ARG
1	H	68	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	197	ASN
1	L	146	GLN
1	K	322	ASN
1	I	303	ASN
1	A	322	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 48 ligands modelled in this entry, 24 are monoatomic - leaving 24 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	$\# Z  > 2$
2	ADP	C	602	3	24,29,29	0.64	0	29,45,45	0.78	1 (3%)
2	ADP	L	601	3	24,29,29	0.64	0	29,45,45	0.69	1 (3%)
2	ADP	G	601	3	24,29,29	0.65	0	29,45,45	0.70	1 (3%)
2	ADP	G	602	3	24,29,29	0.65	0	29,45,45	0.67	1 (3%)
2	ADP	I	602	3	24,29,29	0.64	0	29,45,45	0.73	1 (3%)
2	ADP	A	602	3	24,29,29	0.64	0	29,45,45	0.73	1 (3%)
2	ADP	C	601	3	24,29,29	0.64	0	29,45,45	0.77	1 (3%)
2	ADP	E	601	3	24,29,29	0.64	0	29,45,45	0.75	1 (3%)
2	ADP	K	602	3	24,29,29	0.64	0	29,45,45	0.72	1 (3%)
2	ADP	D	601	3	24,29,29	0.66	0	29,45,45	0.70	1 (3%)
2	ADP	F	601	3	24,29,29	0.66	0	29,45,45	0.74	1 (3%)
2	ADP	L	602	3	24,29,29	0.65	0	29,45,45	0.69	1 (3%)
2	ADP	B	601	3	24,29,29	0.65	0	29,45,45	0.72	1 (3%)
2	ADP	F	602	3	24,29,29	0.64	0	29,45,45	0.72	1 (3%)
2	ADP	H	602	3	24,29,29	0.64	0	29,45,45	0.74	1 (3%)
2	ADP	J	602	3	24,29,29	0.66	0	29,45,45	0.68	1 (3%)
2	ADP	B	602	3	24,29,29	0.66	0	29,45,45	0.70	1 (3%)
2	ADP	H	601	3	24,29,29	0.64	0	29,45,45	0.70	1 (3%)
2	ADP	J	601	3	24,29,29	0.65	0	29,45,45	0.74	1 (3%)
2	ADP	E	602	-	24,29,29	0.65	0	29,45,45	0.69	1 (3%)
2	ADP	A	601	3	24,29,29	0.65	0	29,45,45	0.71	1 (3%)
2	ADP	I	601	3	24,29,29	0.65	0	29,45,45	0.67	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	ADP	D	602	3	24,29,29	0.66	0	29,45,45	0.75	1 (3%)
2	ADP	K	601	3	24,29,29	0.66	0	29,45,45	0.71	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ADP	C	602	3	-	1/12/32/32	0/3/3/3
2	ADP	L	601	3	-	0/12/32/32	0/3/3/3
2	ADP	G	601	3	-	1/12/32/32	0/3/3/3
2	ADP	G	602	3	-	3/12/32/32	0/3/3/3
2	ADP	I	602	3	-	7/12/32/32	0/3/3/3
2	ADP	A	602	3	-	4/12/32/32	0/3/3/3
2	ADP	C	601	3	-	2/12/32/32	0/3/3/3
2	ADP	E	601	3	-	2/12/32/32	0/3/3/3
2	ADP	K	602	3	-	5/12/32/32	0/3/3/3
2	ADP	D	601	3	-	2/12/32/32	0/3/3/3
2	ADP	F	601	3	-	5/12/32/32	0/3/3/3
2	ADP	L	602	3	-	6/12/32/32	0/3/3/3
2	ADP	B	601	3	-	5/12/32/32	0/3/3/3
2	ADP	F	602	3	-	7/12/32/32	0/3/3/3
2	ADP	H	602	3	-	2/12/32/32	0/3/3/3
2	ADP	J	602	3	-	3/12/32/32	0/3/3/3
2	ADP	B	602	3	-	5/12/32/32	0/3/3/3
2	ADP	H	601	3	-	1/12/32/32	0/3/3/3
2	ADP	J	601	3	-	3/12/32/32	0/3/3/3
2	ADP	E	602	-	-	0/12/32/32	0/3/3/3
2	ADP	A	601	3	-	5/12/32/32	0/3/3/3
2	ADP	I	601	3	-	8/12/32/32	0/3/3/3
2	ADP	D	602	3	-	2/12/32/32	0/3/3/3
2	ADP	K	601	3	-	4/12/32/32	0/3/3/3

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	602	ADP	C5-C6-N6	2.29	123.83	120.35
2	L	601	ADP	C5-C6-N6	2.26	123.78	120.35
2	I	602	ADP	C5-C6-N6	2.25	123.78	120.35
2	C	602	ADP	C5-C6-N6	2.25	123.77	120.35
2	D	602	ADP	C5-C6-N6	2.24	123.76	120.35

There are no chirality outliers.

5 of 83 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	ADP	C5'-O5'-PA-O1A
2	B	601	ADP	C5'-O5'-PA-O2A
2	B	601	ADP	C5'-O5'-PA-O3A
2	B	602	ADP	C5'-O5'-PA-O1A
2	B	602	ADP	O4'-C4'-C5'-O5'

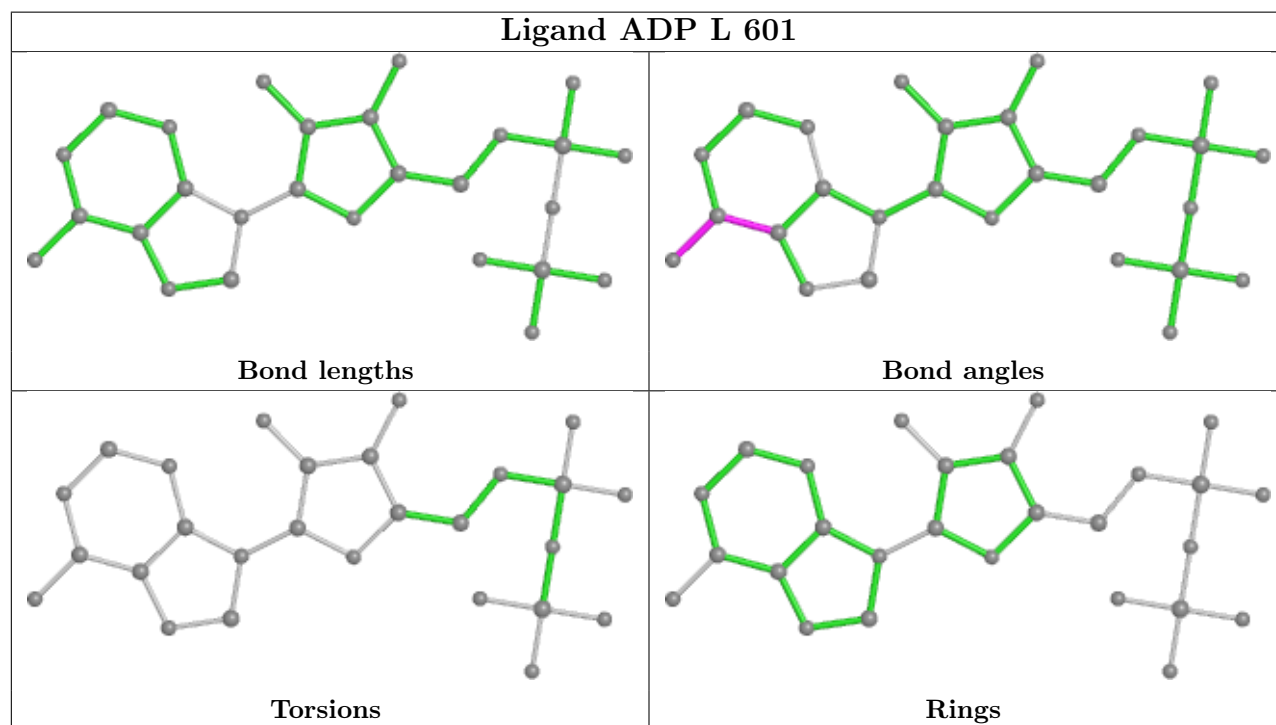
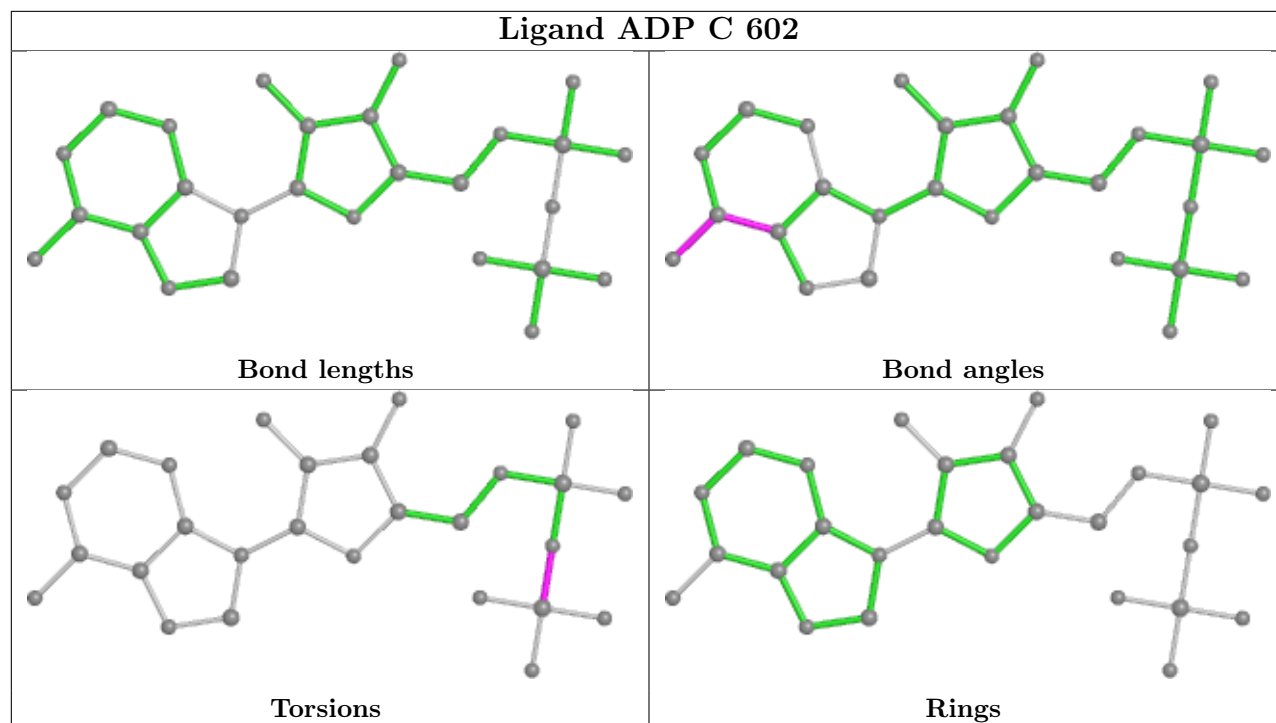
There are no ring outliers.

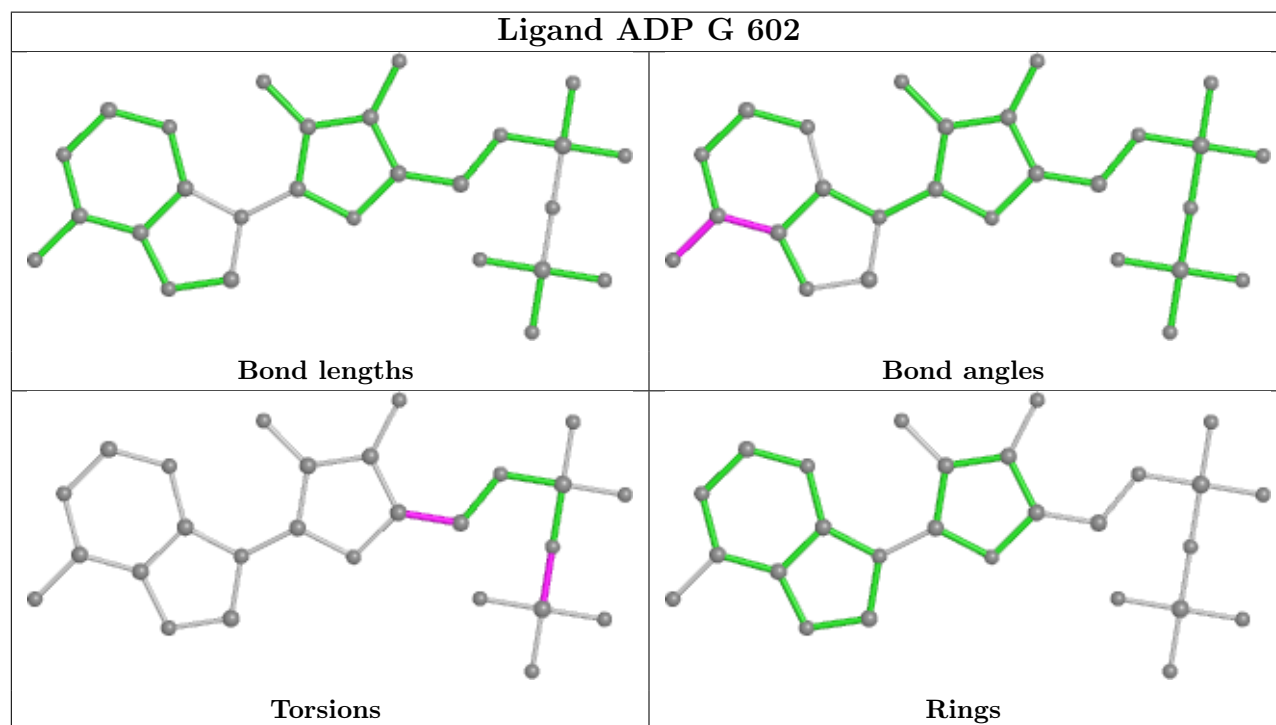
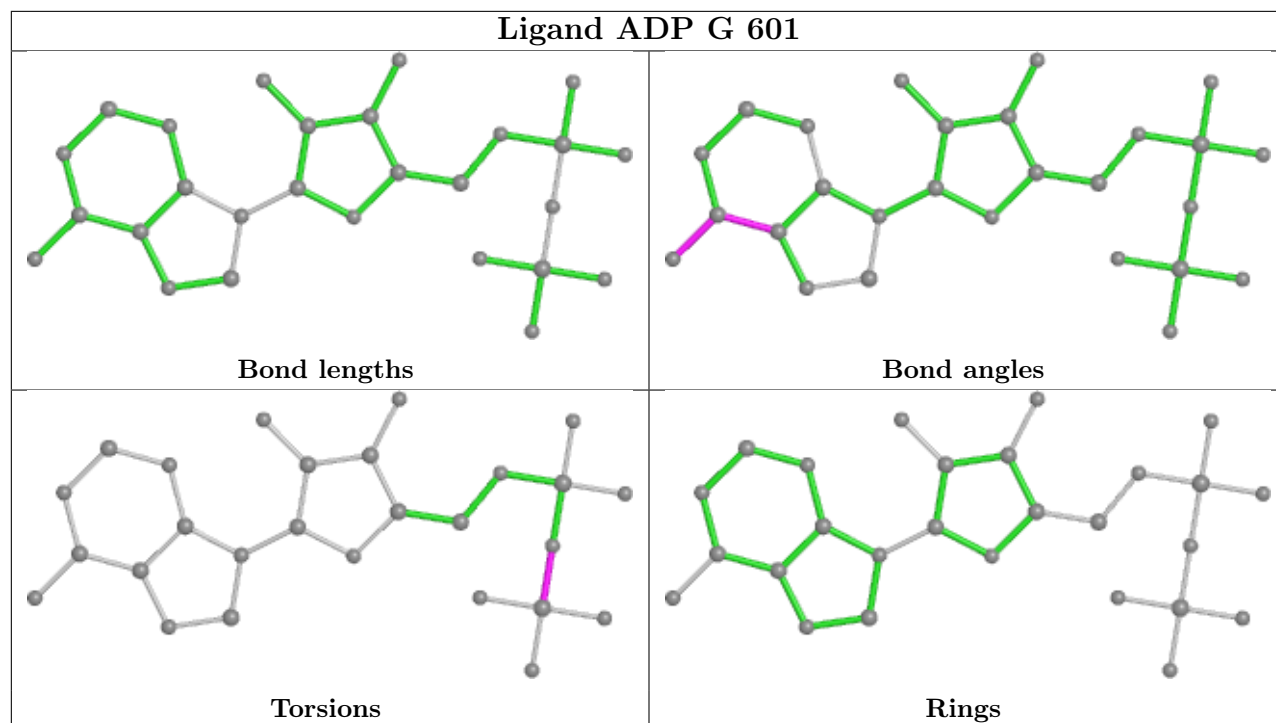
5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	601	ADP	1	0
2	K	602	ADP	1	0
2	F	601	ADP	1	0
2	L	602	ADP	1	0
2	I	601	ADP	1	0

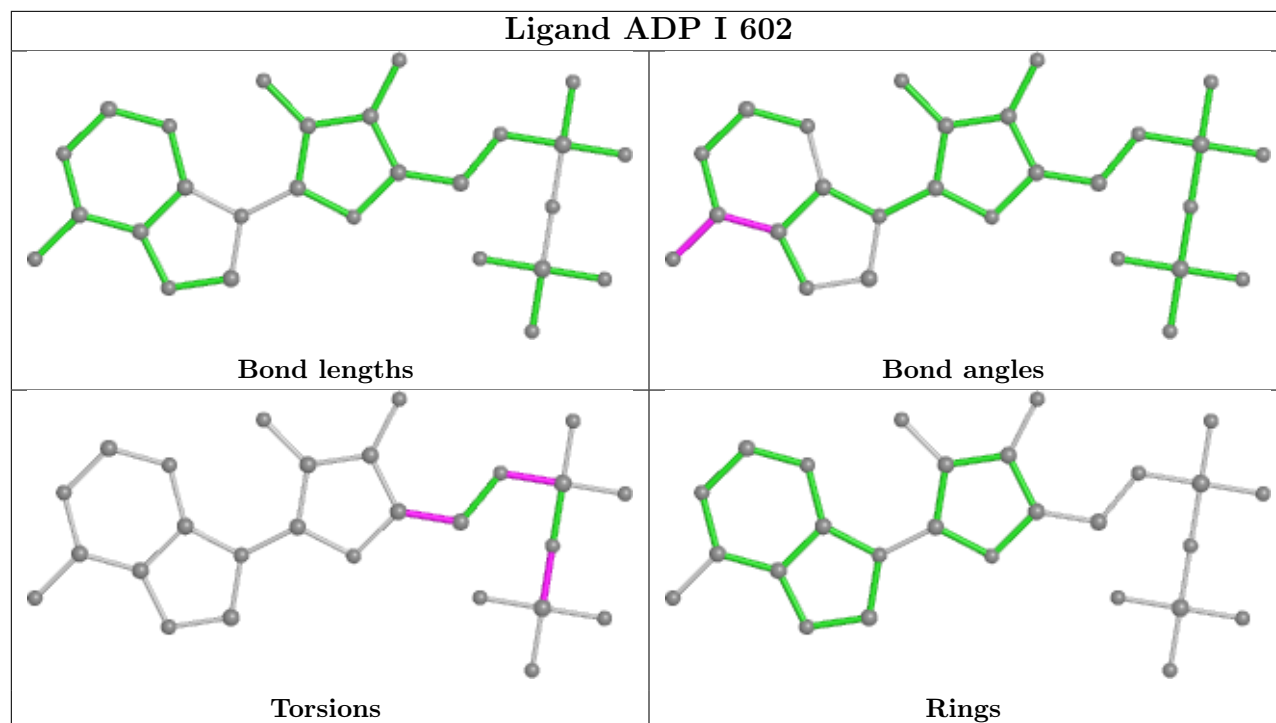
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



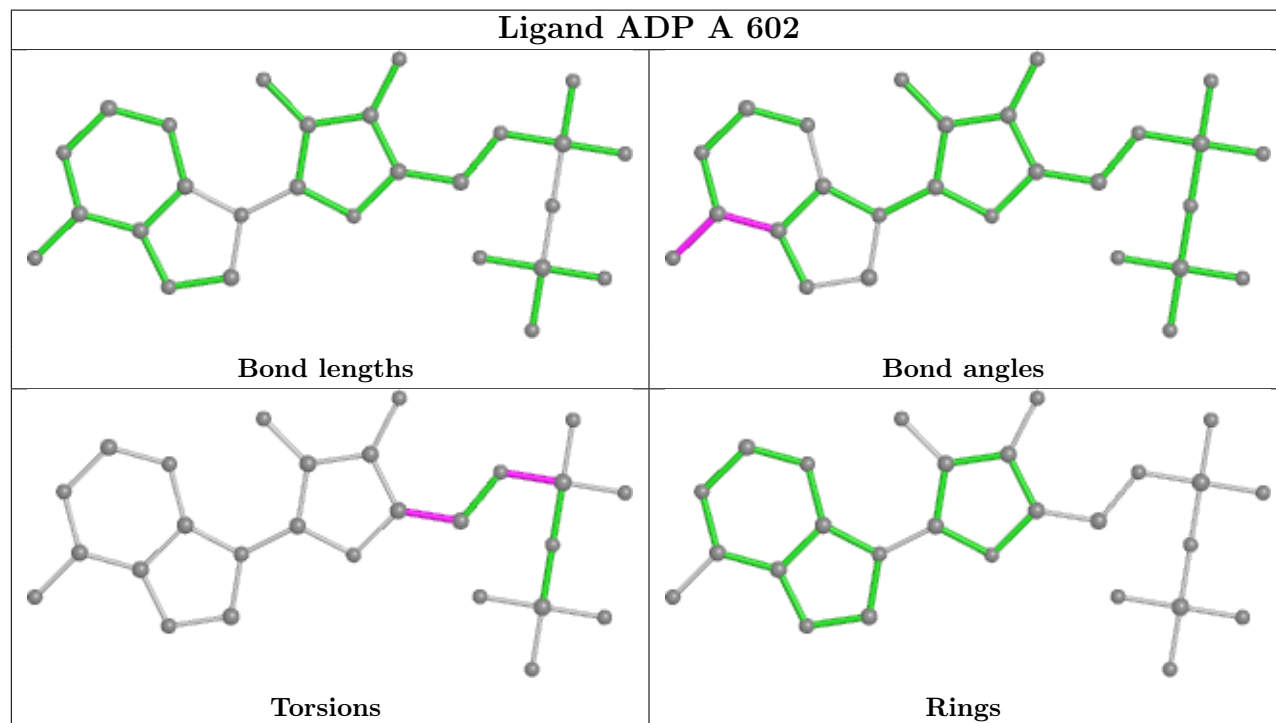




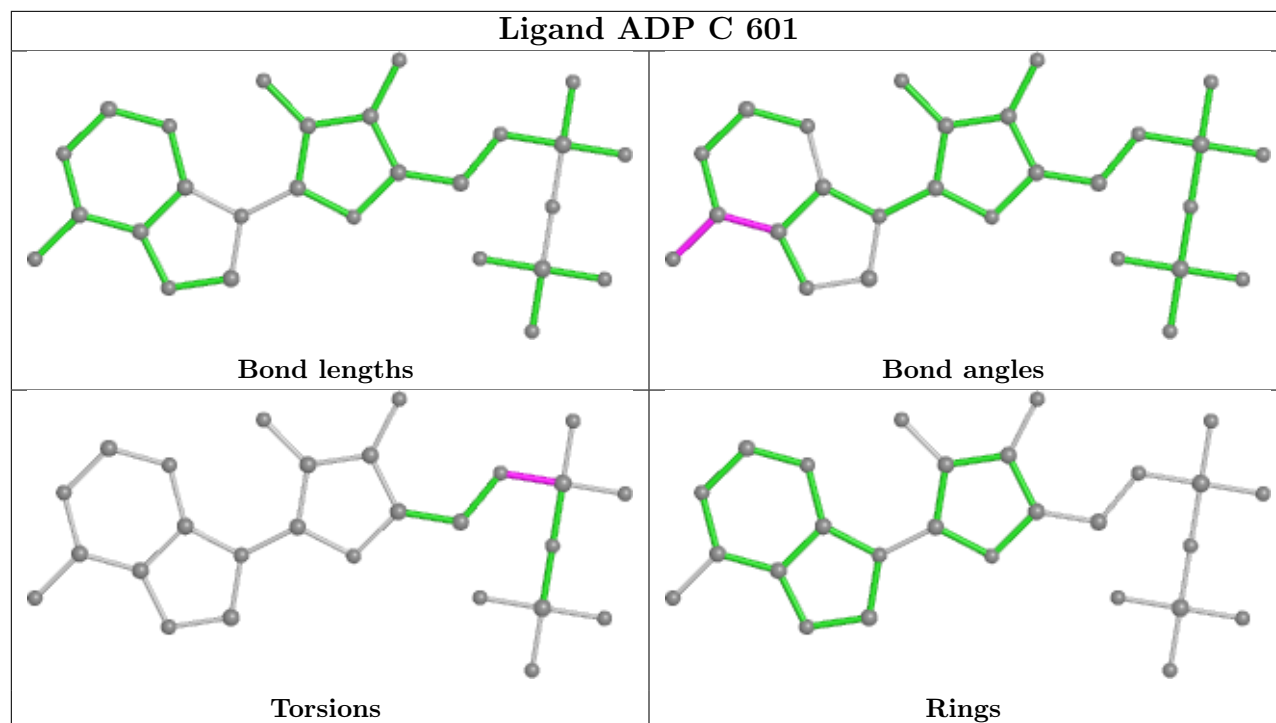
## Ligand ADP I 602



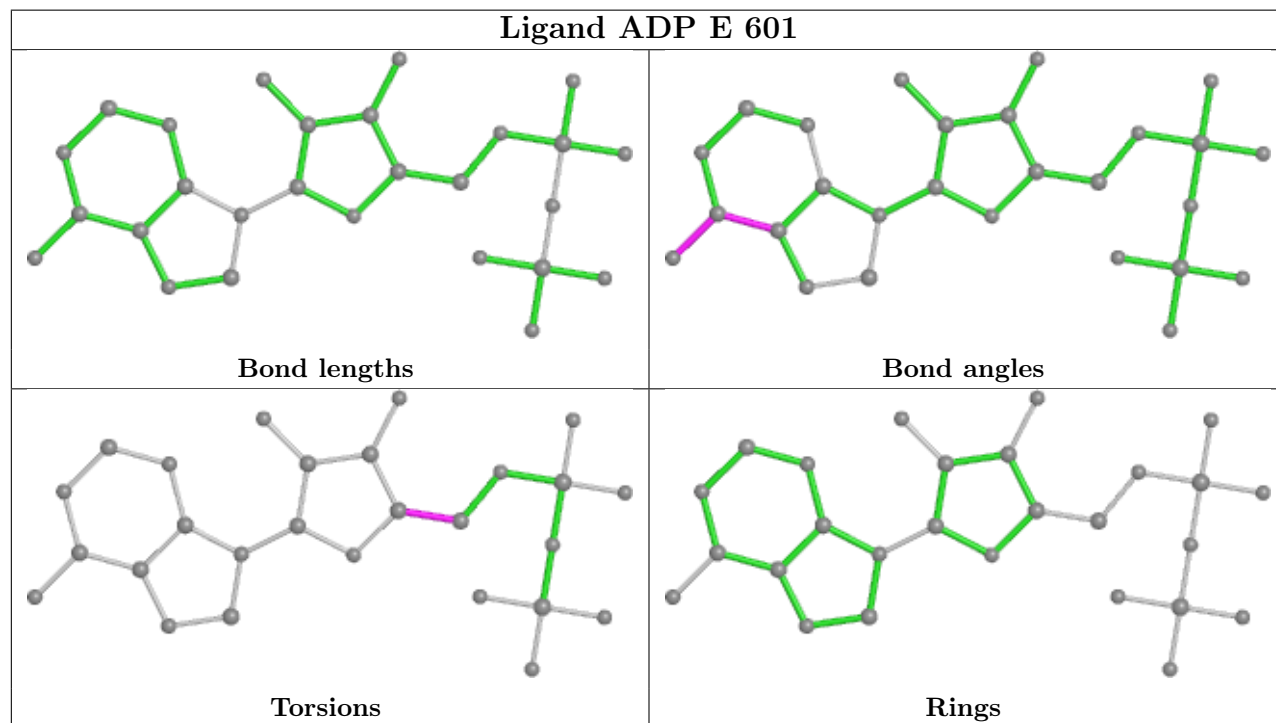
## Ligand ADP A 602

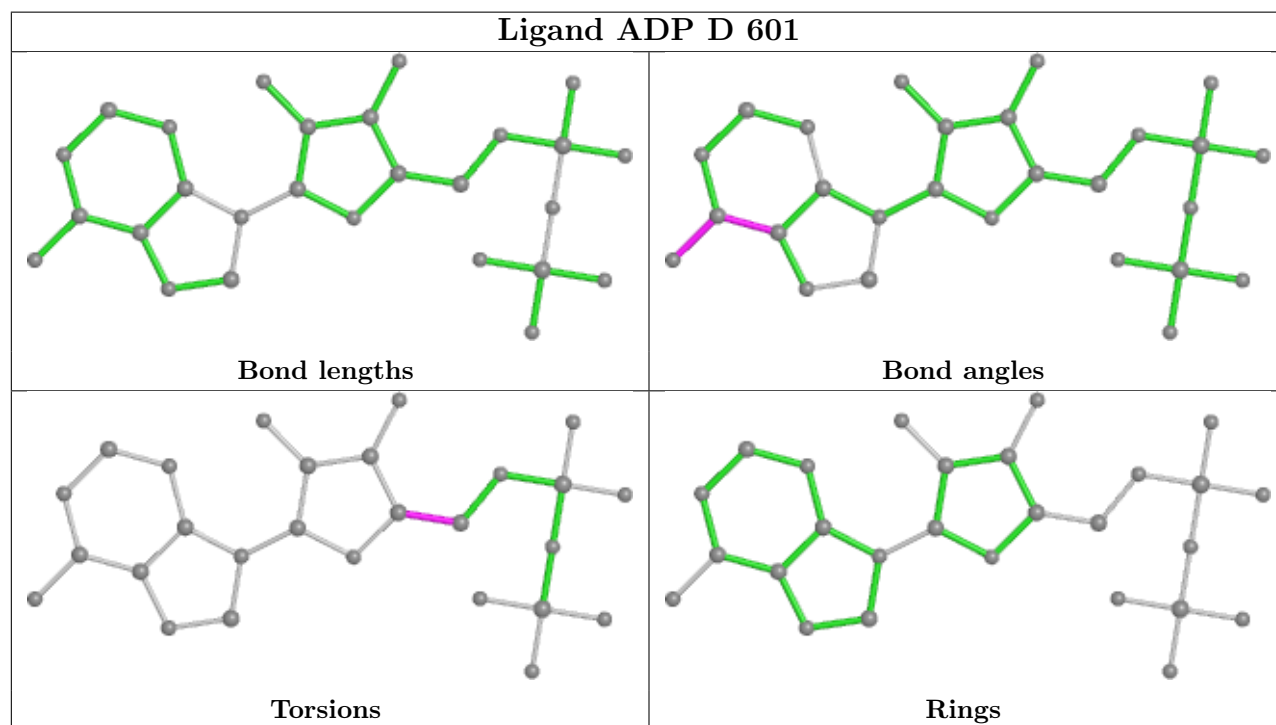
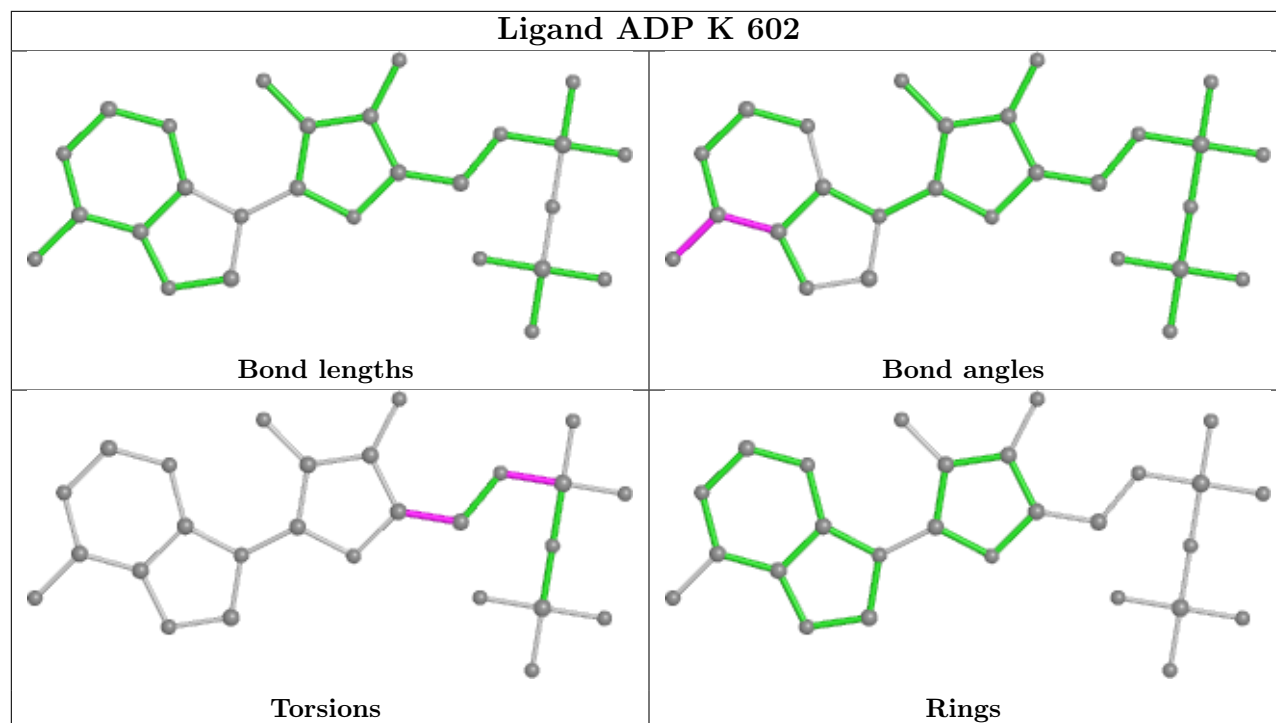


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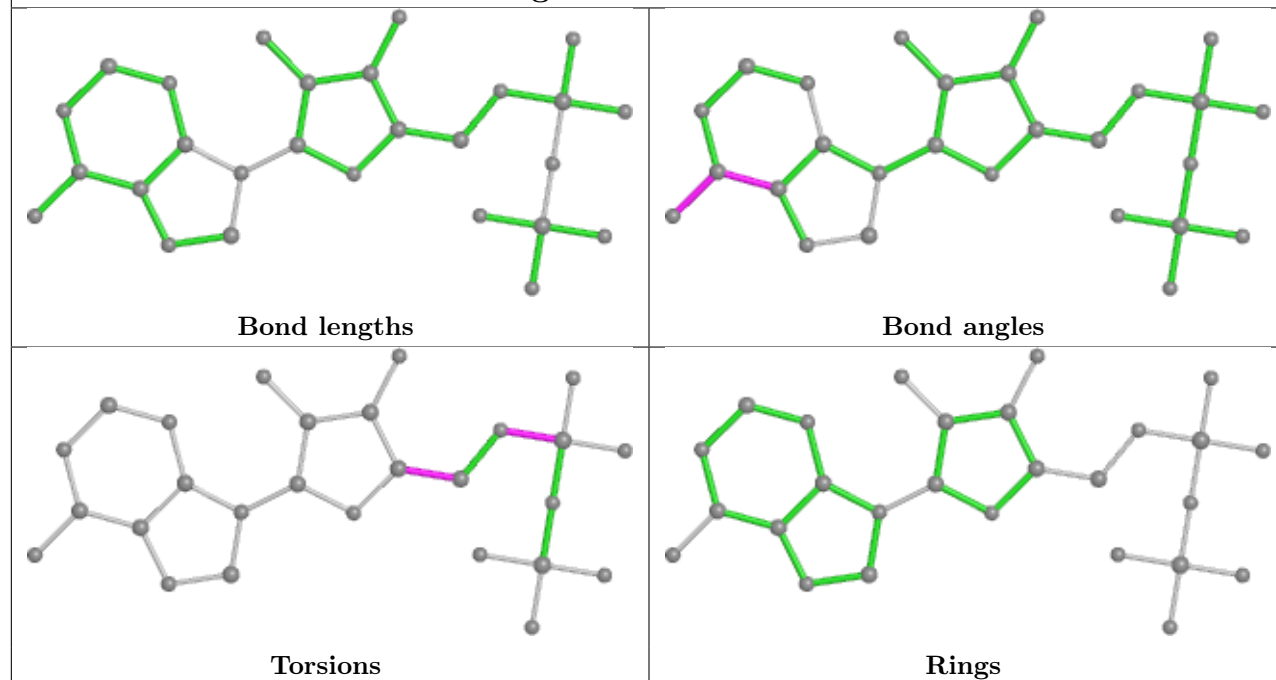


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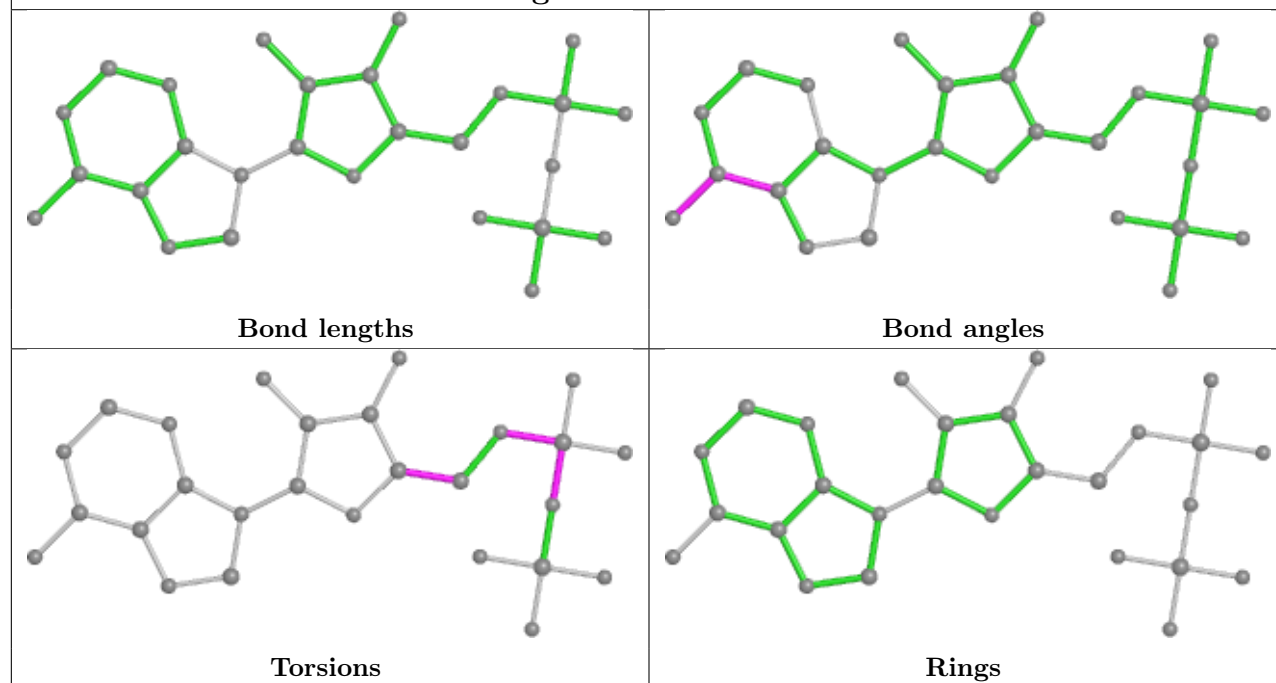


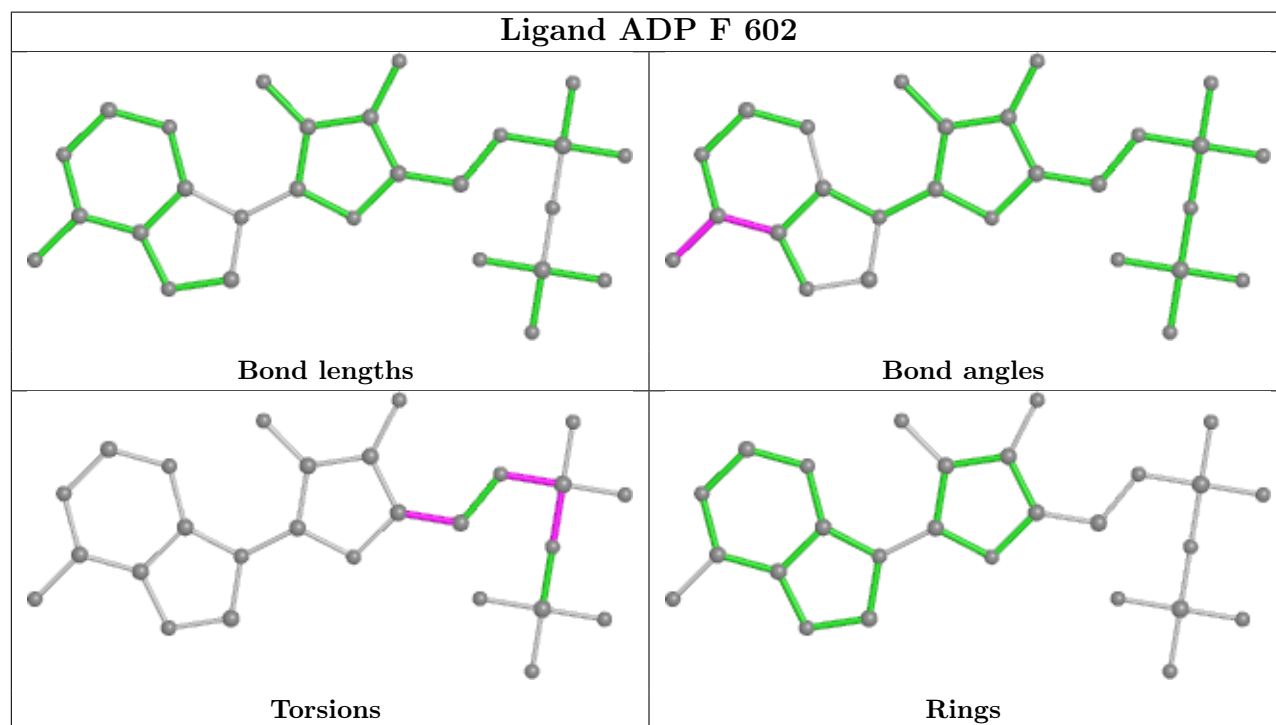
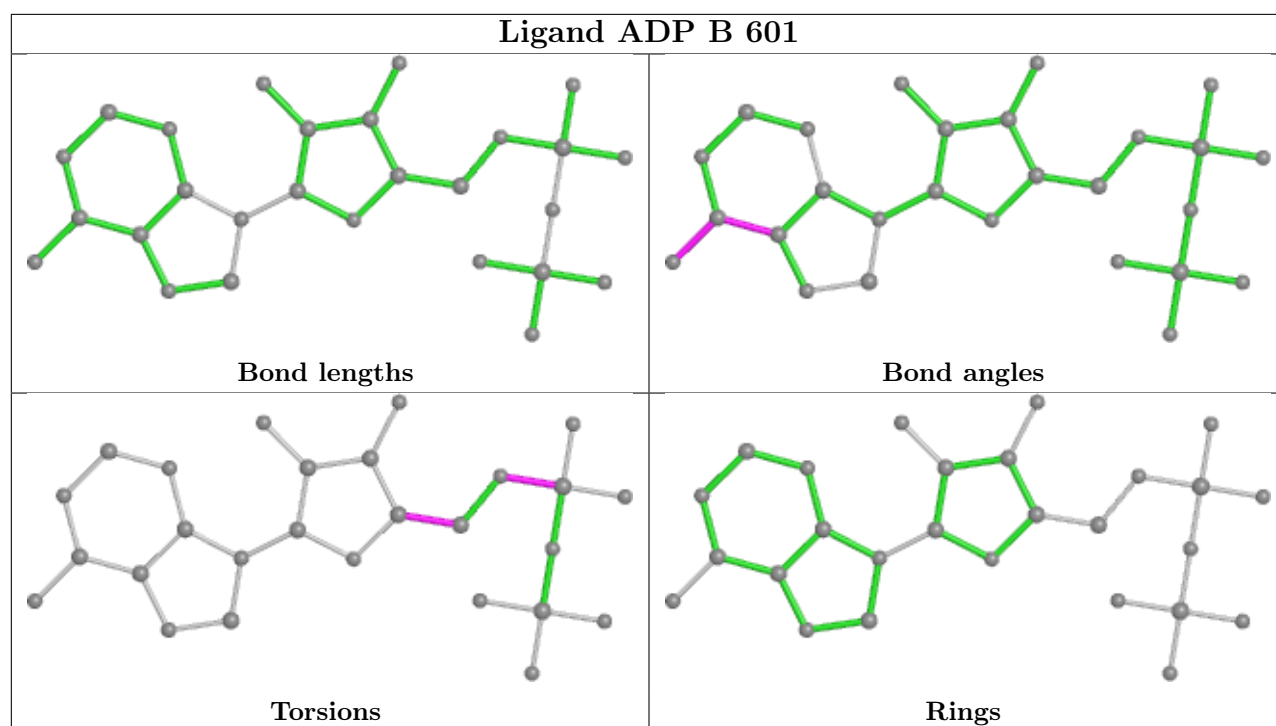


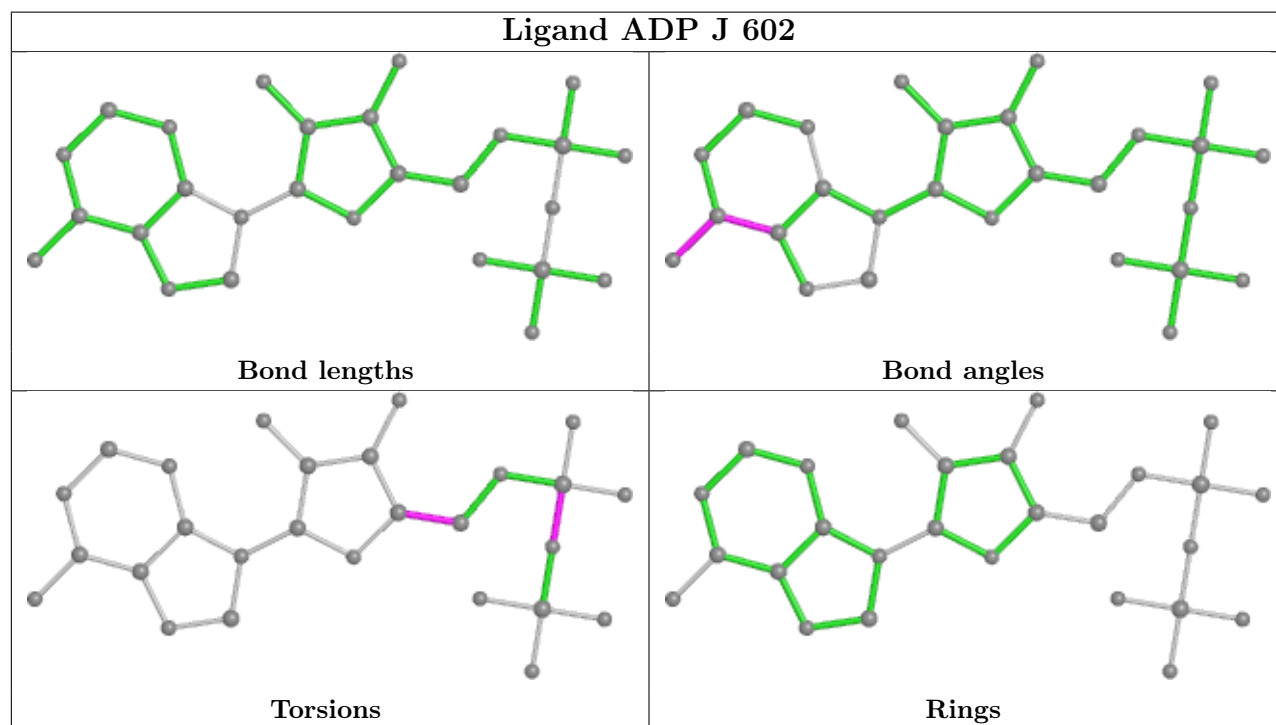
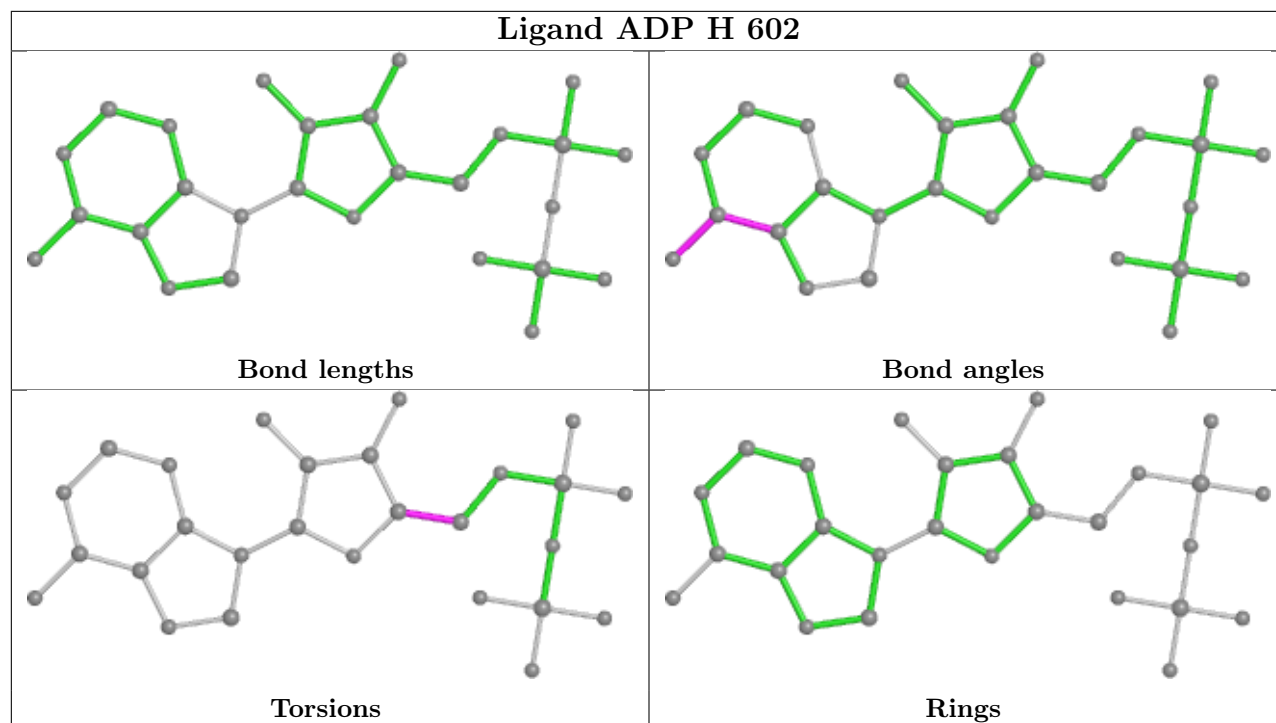
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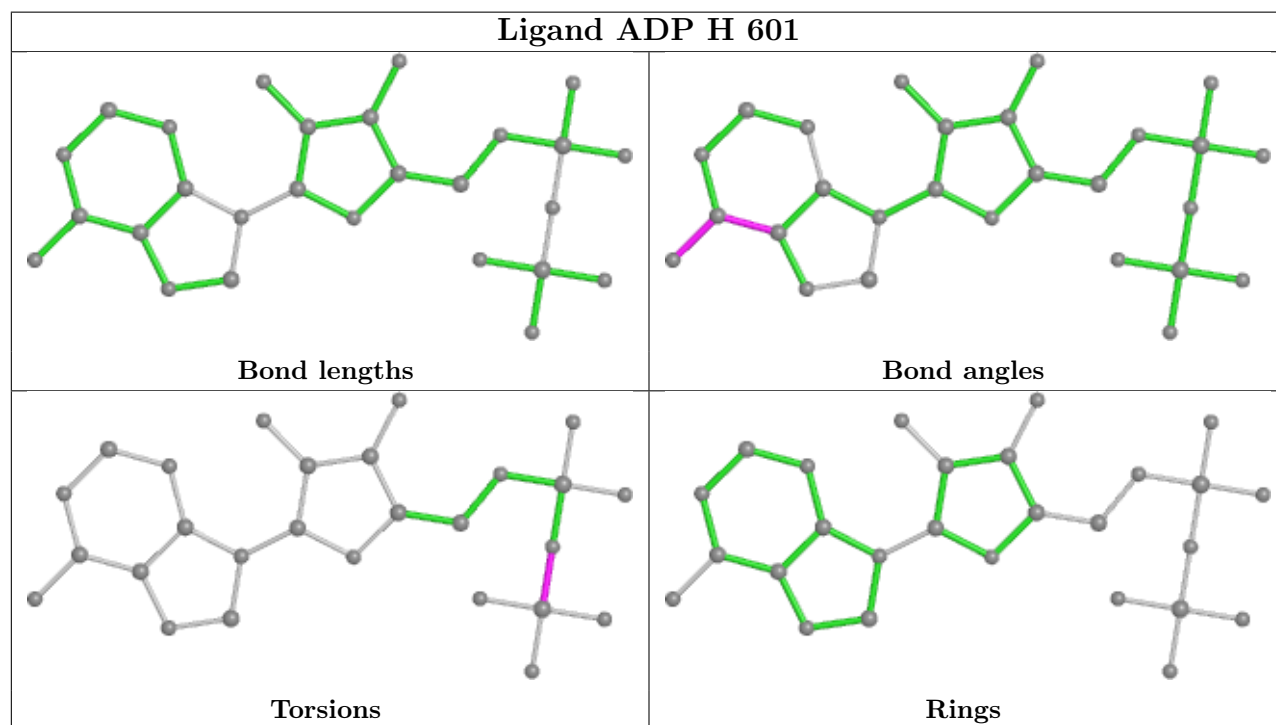
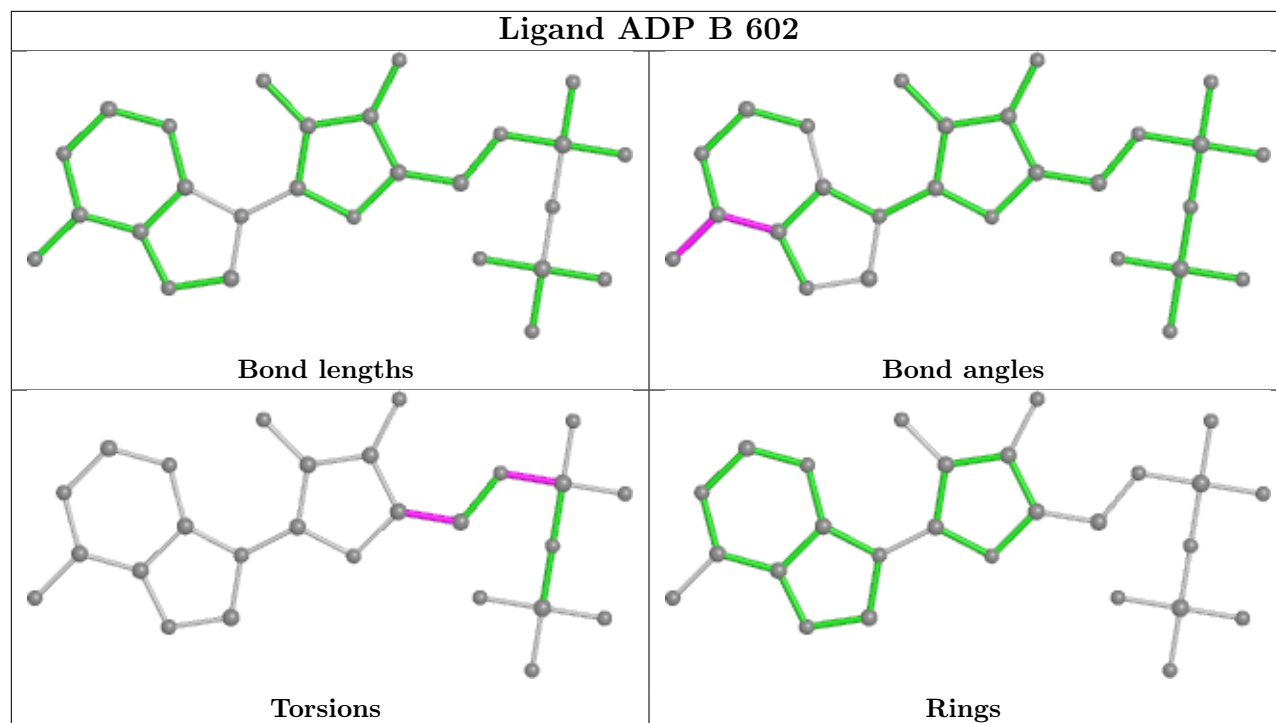
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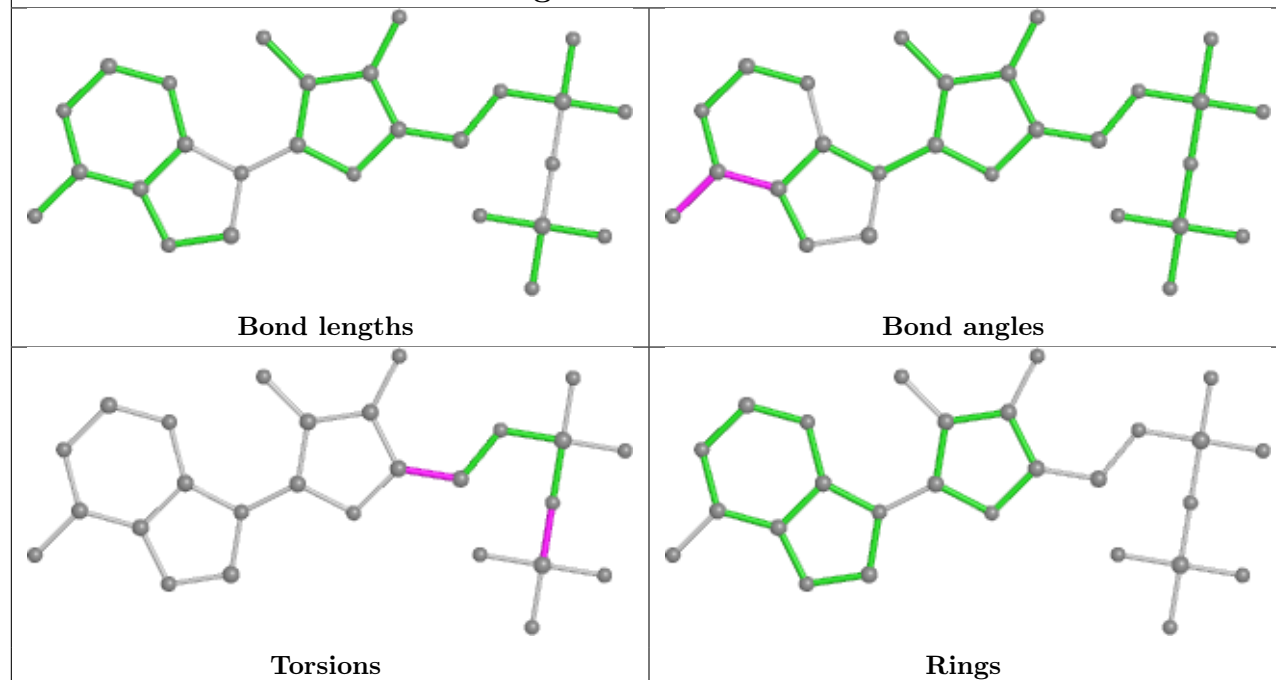




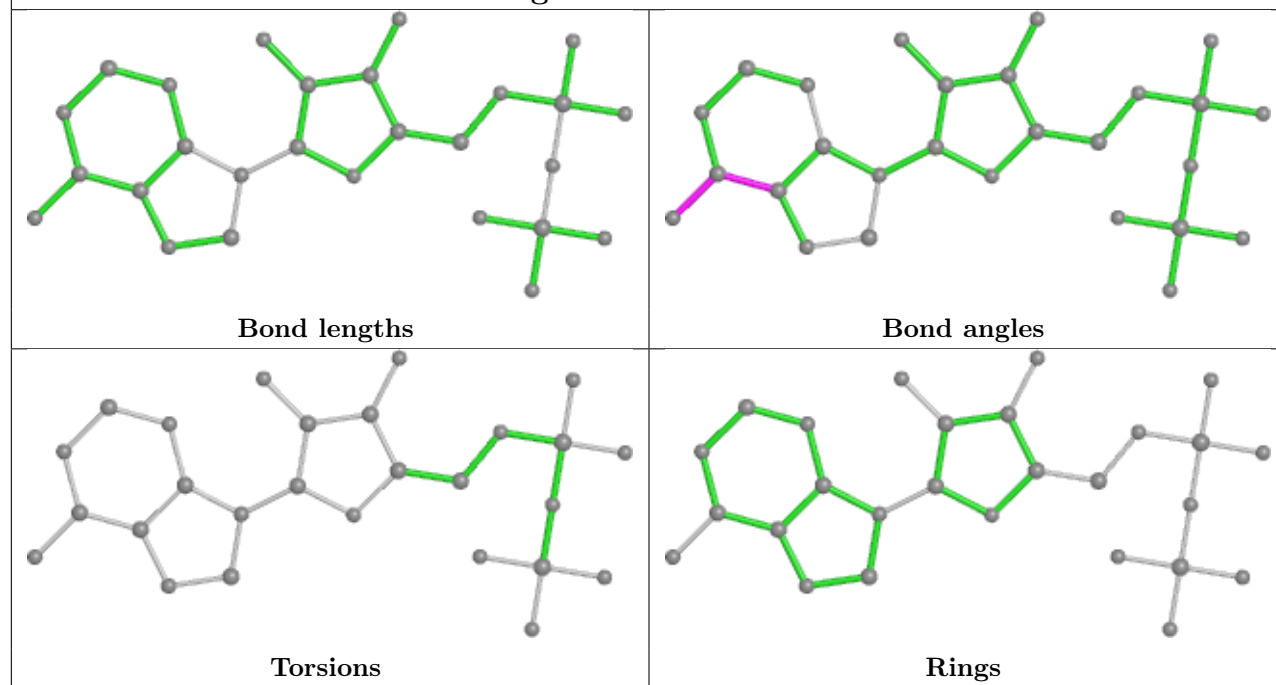


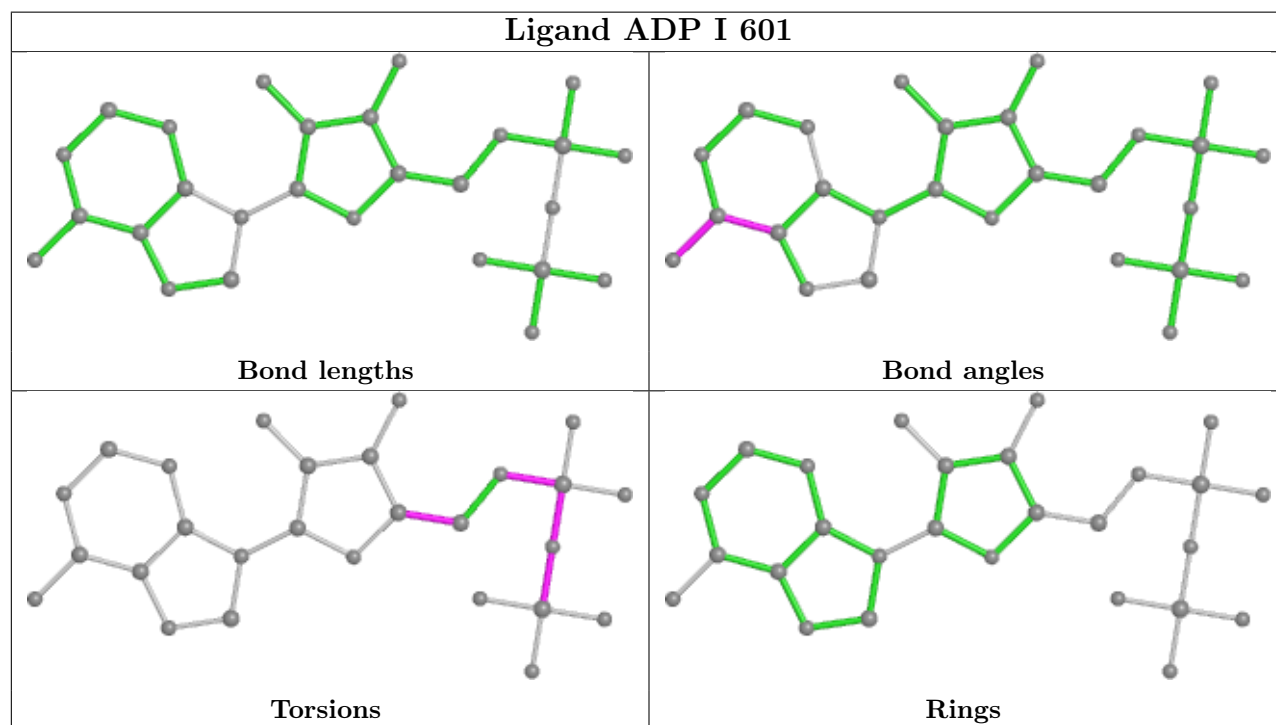
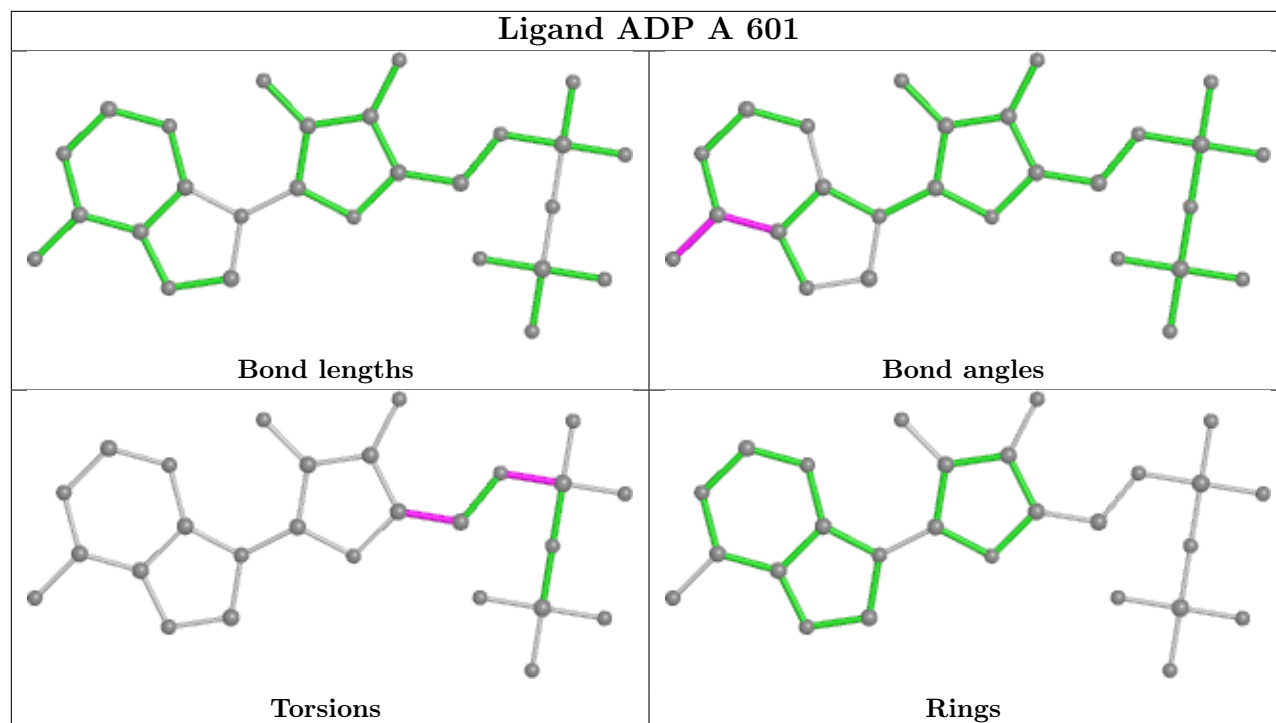


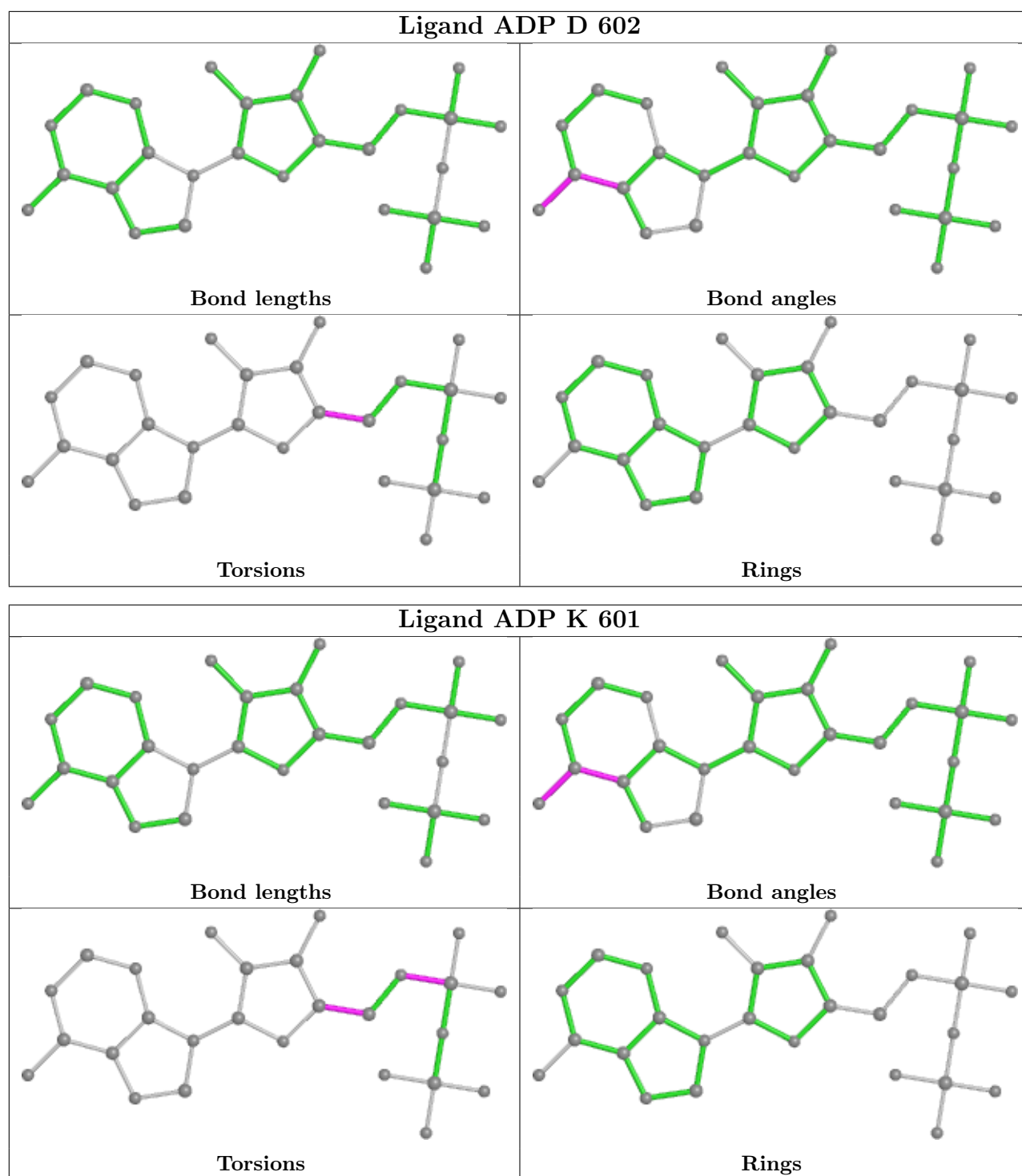
## Ligand ADP J 601



## Ligand ADP E 602







## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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	446/518 (86%)	0.10	3 (0%) 84 70	46, 68, 95, 120	0
1	B	454/518 (87%)	0.20	8 (1%) 67 49	42, 67, 116, 147	0
1	C	463/518 (89%)	0.32	8 (1%) 69 50	49, 80, 108, 130	0
1	D	443/518 (85%)	0.48	12 (2%) 56 36	54, 88, 131, 152	0
1	E	456/518 (88%)	0.18	6 (1%) 74 58	44, 72, 107, 152	0
1	F	446/518 (86%)	0.18	6 (1%) 74 58	45, 74, 100, 119	0
1	G	447/518 (86%)	0.47	13 (2%) 54 34	72, 108, 137, 151	0
1	H	439/518 (84%)	0.63	32 (7%) 22 13	69, 107, 141, 155	0
1	I	446/518 (86%)	0.49	13 (2%) 54 34	63, 97, 125, 138	0
1	J	447/518 (86%)	0.28	9 (2%) 64 45	53, 88, 123, 136	0
1	K	444/518 (85%)	0.39	11 (2%) 58 39	50, 89, 147, 161	0
1	L	439/518 (84%)	0.47	12 (2%) 56 36	61, 96, 141, 176	0
All	All	5370/6216 (86%)	0.35	133 (2%) 58 39	42, 86, 129, 176	0

The worst 5 of 133 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	245	SER	4.5
1	H	173	ILE	4.1
1	D	297	LEU	3.9
1	H	346	PRO	3.8
1	I	67	PHE	3.8

### 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 ⓘ

There are no monosaccharides 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, 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
3	MG	G	604	1/1	0.83	0.18	70,70,70,70	0
3	MG	H	603	1/1	0.85	0.15	97,97,97,97	0
2	ADP	H	602	27/27	0.86	0.13	105,110,115,116	0
3	MG	B	603	1/1	0.86	0.21	61,61,61,61	0
3	MG	L	604	1/1	0.87	0.25	94,94,94,94	0
3	MG	D	604	1/1	0.88	0.17	67,67,67,67	0
2	ADP	G	602	27/27	0.88	0.10	100,103,105,106	0
3	MG	G	603	1/1	0.89	0.16	62,62,62,62	0
2	ADP	K	601	27/27	0.89	0.12	75,100,114,115	0
3	MG	J	604	1/1	0.89	0.15	54,54,54,54	0
2	ADP	L	601	27/27	0.90	0.10	96,99,104,106	0
2	ADP	G	601	27/27	0.90	0.09	72,75,76,77	0
3	MG	F	604	1/1	0.90	0.14	41,41,41,41	0
3	MG	L	603	1/1	0.91	0.25	97,97,97,97	0
2	ADP	L	602	27/27	0.91	0.10	74,79,83,84	0
3	MG	H	604	1/1	0.91	0.08	82,82,82,82	0
3	MG	F	603	1/1	0.92	0.22	69,69,69,69	0
2	ADP	D	602	27/27	0.92	0.09	70,72,73,75	0
2	ADP	I	602	27/27	0.92	0.10	72,79,81,81	0
2	ADP	B	601	27/27	0.92	0.10	62,65,72,73	0
3	MG	B	604	1/1	0.92	0.08	49,49,49,49	0
2	ADP	H	601	27/27	0.93	0.08	76,79,82,83	0
2	ADP	I	601	27/27	0.93	0.09	73,75,76,76	0
2	ADP	C	601	27/27	0.93	0.10	65,69,75,77	0
2	ADP	F	602	27/27	0.93	0.08	57,60,61,63	0
3	MG	I	603	1/1	0.93	0.13	54,54,54,54	0
3	MG	I	604	1/1	0.93	0.07	82,82,82,82	0
2	ADP	A	601	27/27	0.93	0.09	68,70,72,73	0
2	ADP	K	602	27/27	0.94	0.10	60,65,71,71	0
3	MG	C	603	1/1	0.94	0.08	61,61,61,61	0
2	ADP	E	602	27/27	0.94	0.10	64,70,77,78	0
2	ADP	D	601	27/27	0.94	0.09	58,62,64,64	0

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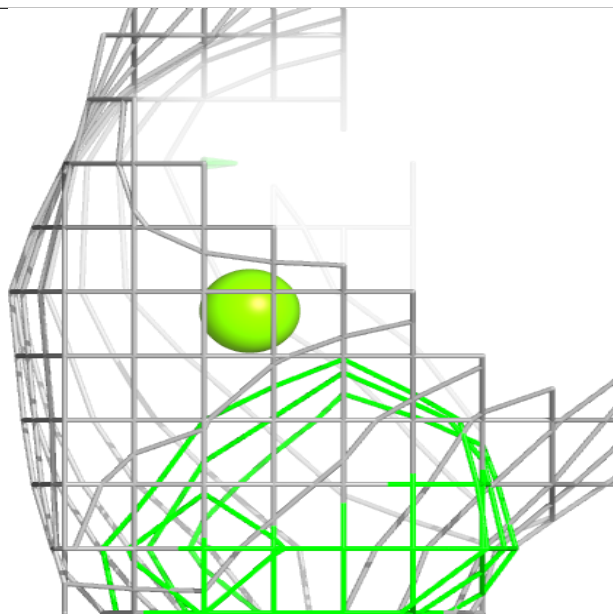
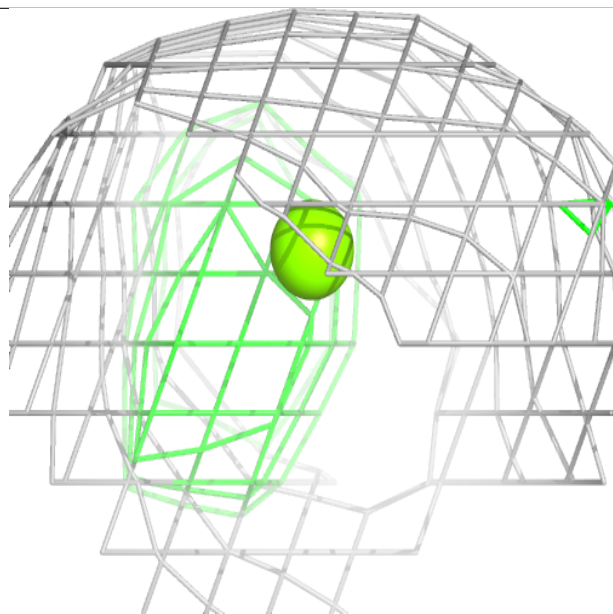
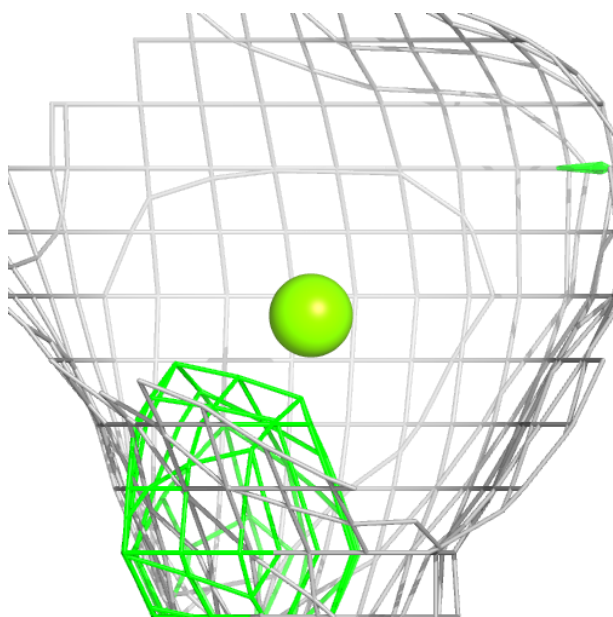
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MG	D	603	1/1	0.94	0.13	53,53,53,53	0
2	ADP	F	601	27/27	0.95	0.09	53,55,58,58	0
2	ADP	J	601	27/27	0.95	0.08	67,80,88,89	0
2	ADP	J	602	27/27	0.95	0.09	55,61,67,69	0
2	ADP	B	602	27/27	0.95	0.08	46,51,54,54	0
3	MG	E	603	1/1	0.95	0.14	61,61,61,61	0
2	ADP	C	602	27/27	0.95	0.08	60,68,72,73	0
2	ADP	A	602	27/27	0.95	0.07	52,54,55,56	0
2	ADP	E	601	27/27	0.96	0.08	46,53,59,60	0
3	MG	E	604	1/1	0.96	0.11	71,71,71,71	0
3	MG	A	603	1/1	0.96	0.05	70,70,70,70	0
3	MG	K	603	1/1	0.96	0.16	38,38,38,38	0
3	MG	K	604	1/1	0.96	0.13	66,66,66,66	0
3	MG	J	603	1/1	0.98	0.10	38,38,38,38	0
3	MG	C	604	1/1	0.98	0.07	71,71,71,71	0
3	MG	A	604	1/1	0.99	0.06	37,37,37,37	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.



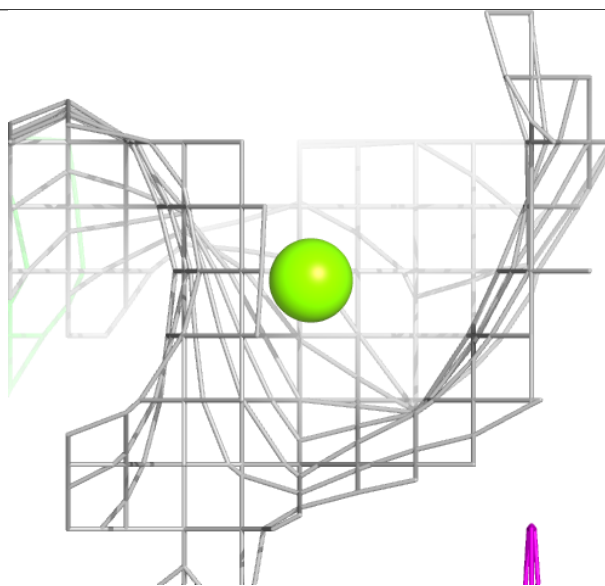
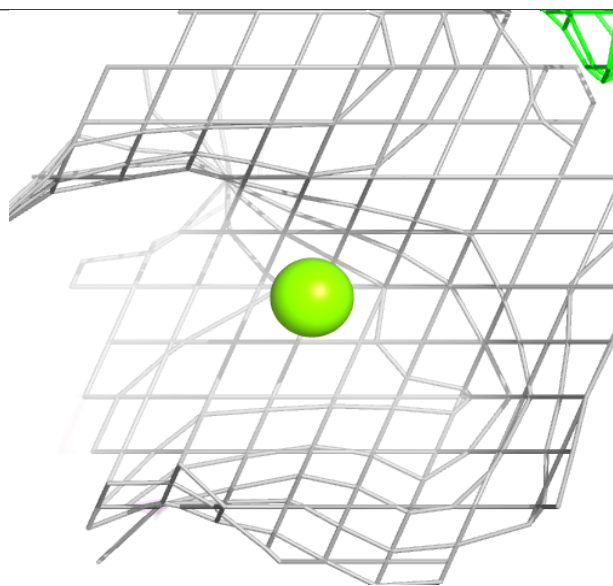
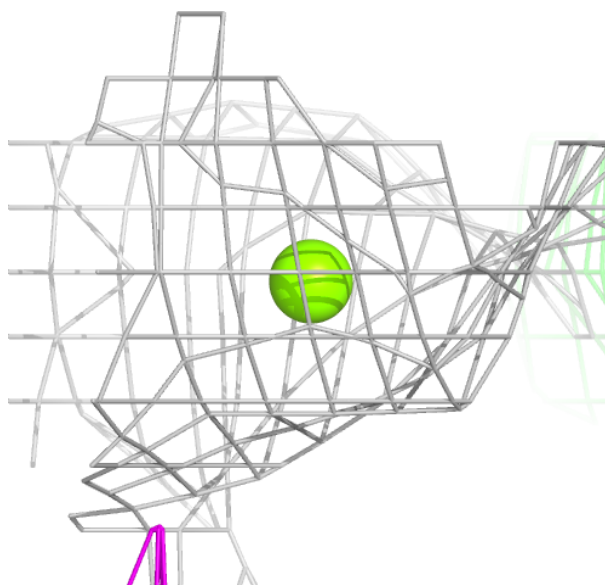
**Electron density around MG G 604:**

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



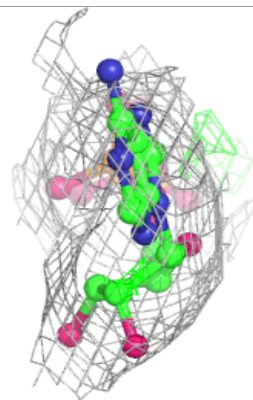
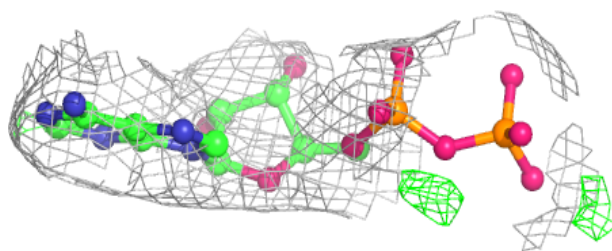
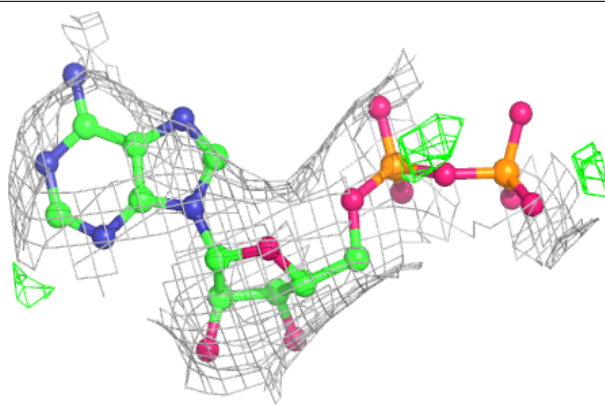
**Electron density around MG H 603:**

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



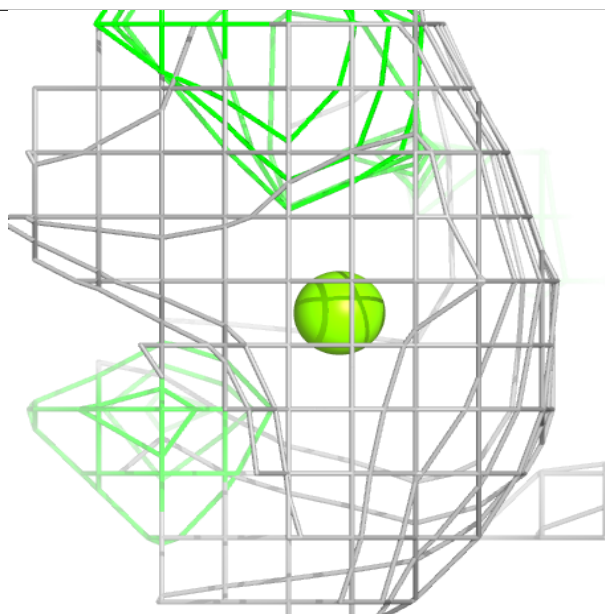
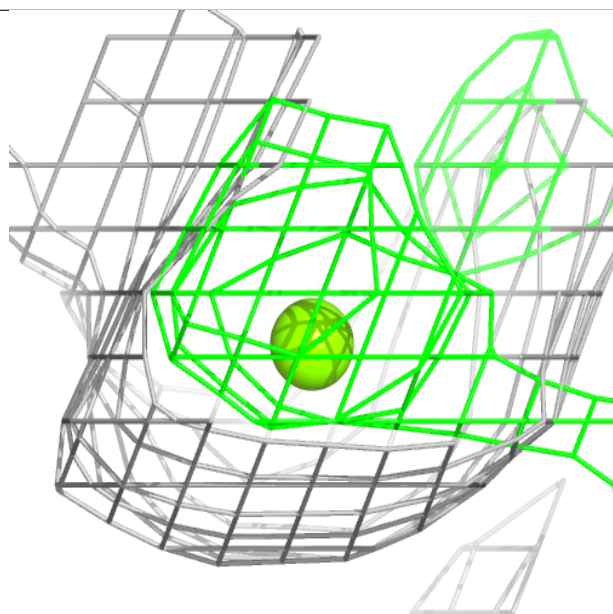
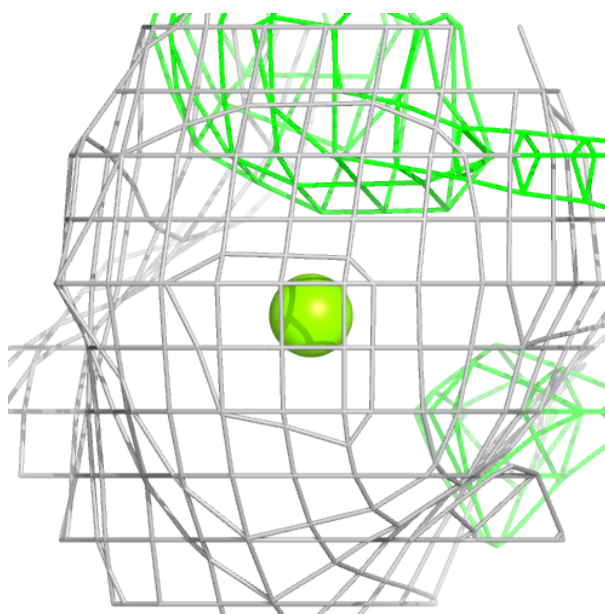
**Electron density around ADP H 602:**

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



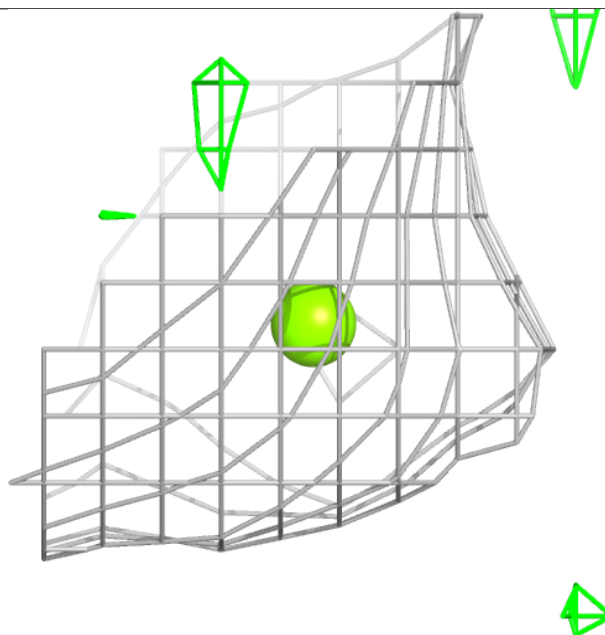
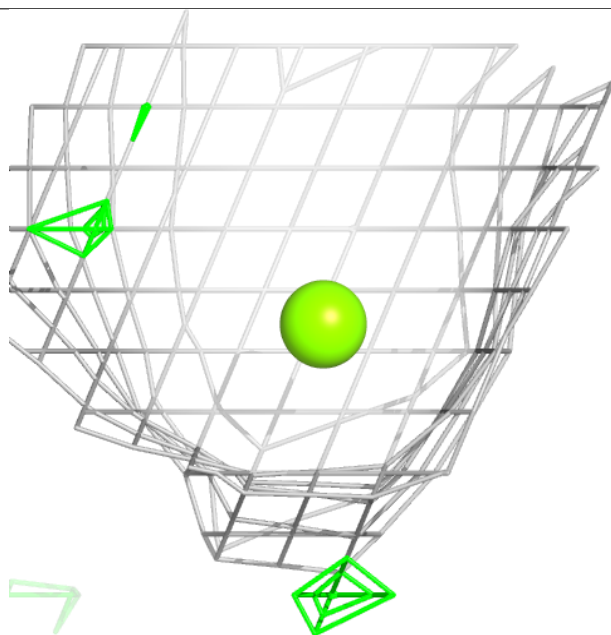
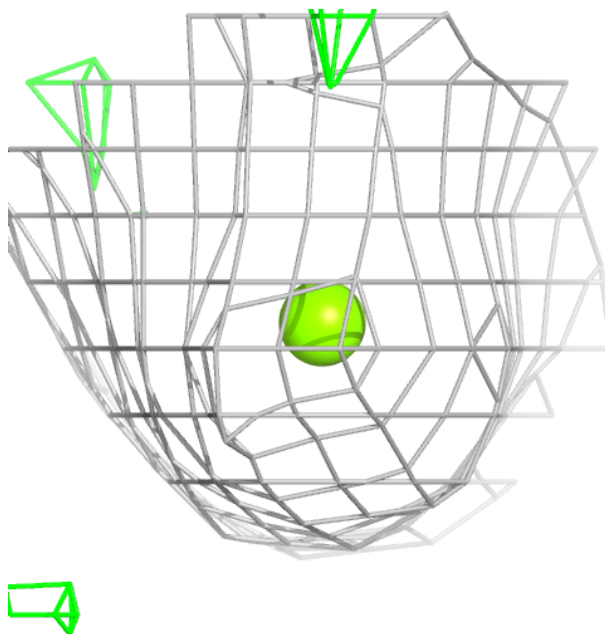
**Electron density around MG B 603:**

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



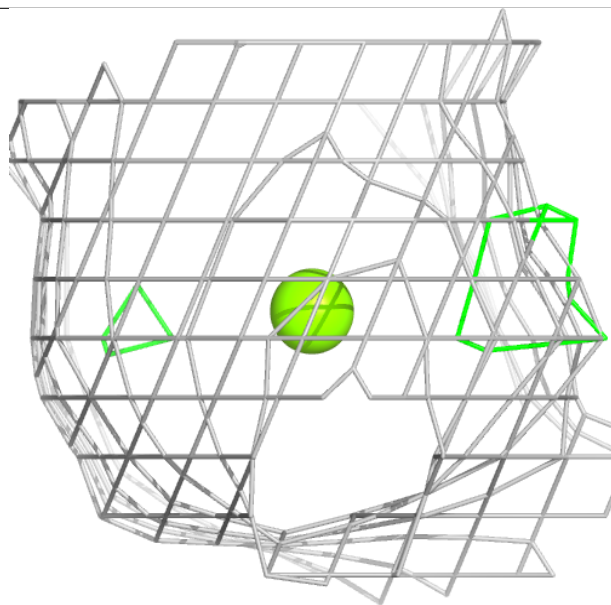
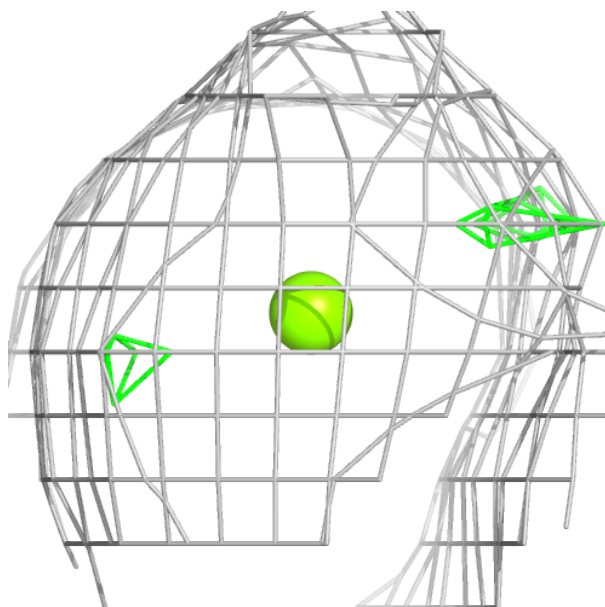
**Electron density around MG L 604:**

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



**Electron density around MG D 604:**

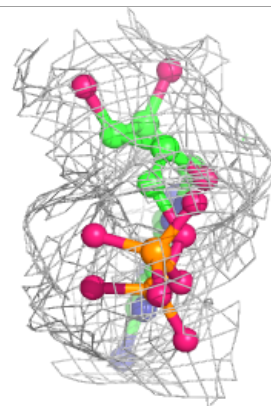
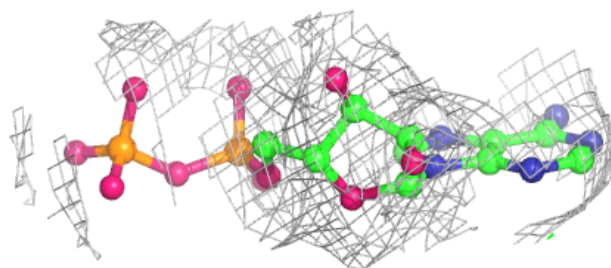
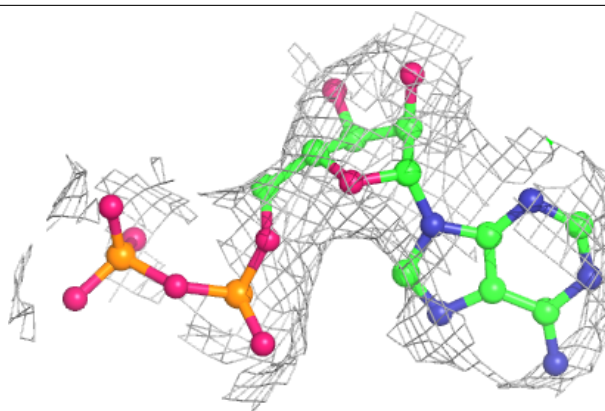
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





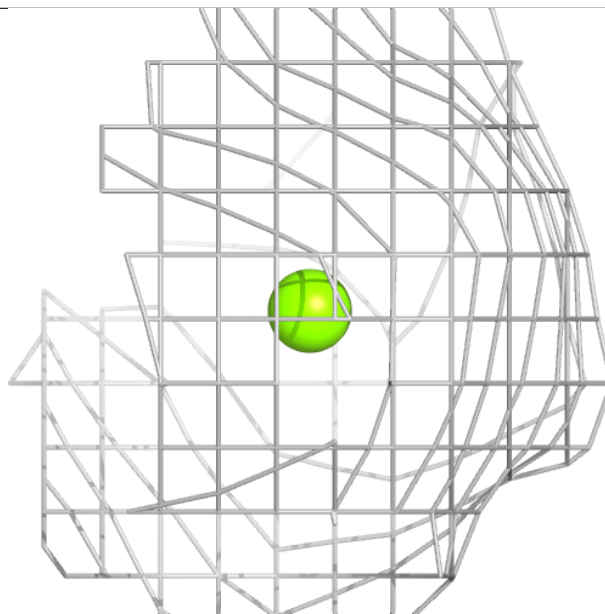
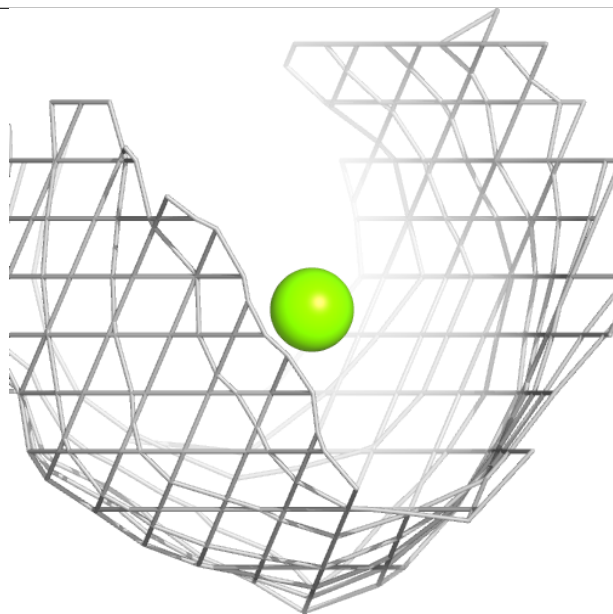
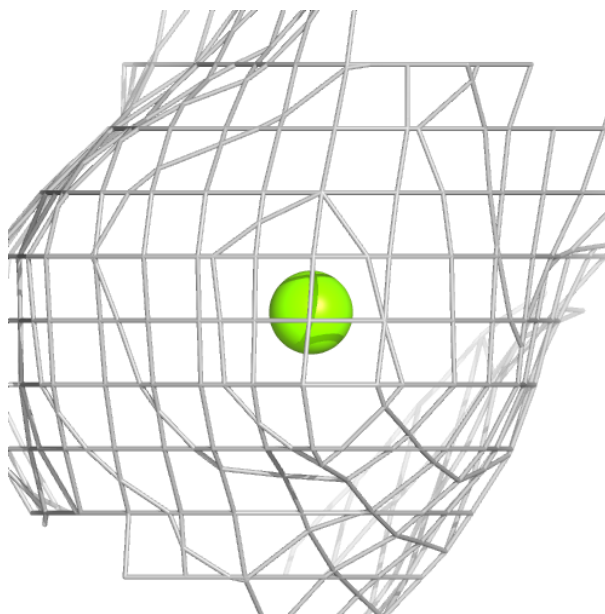
**Electron density around ADP G 602:**

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



**Electron density around MG G 603:**

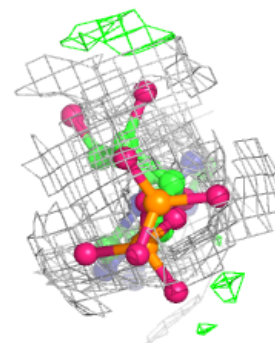
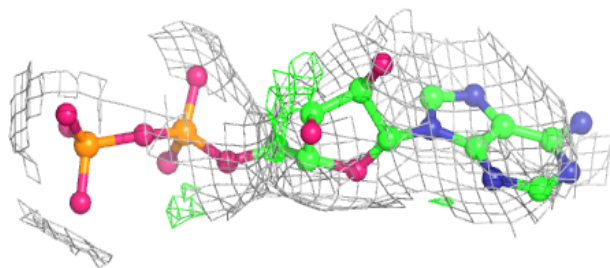
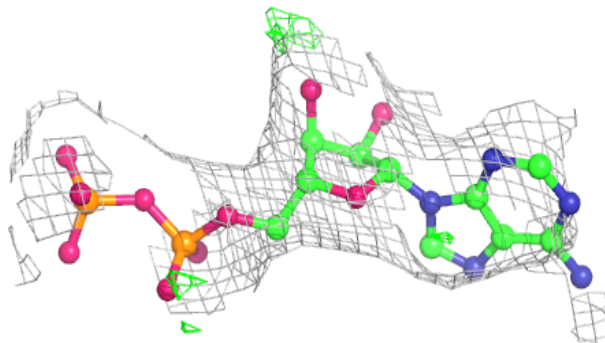
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





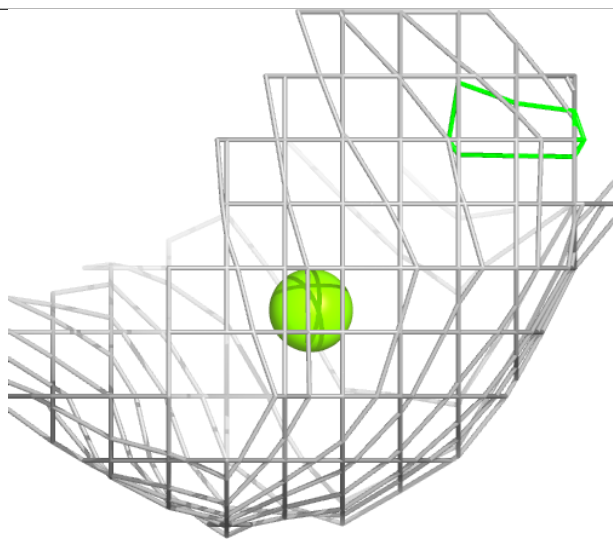
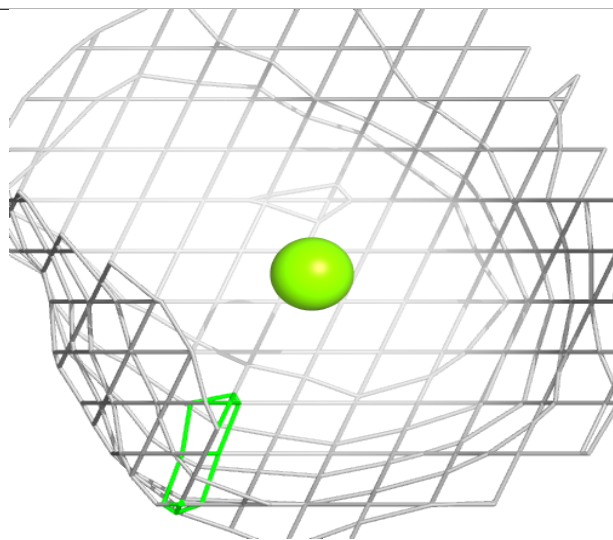
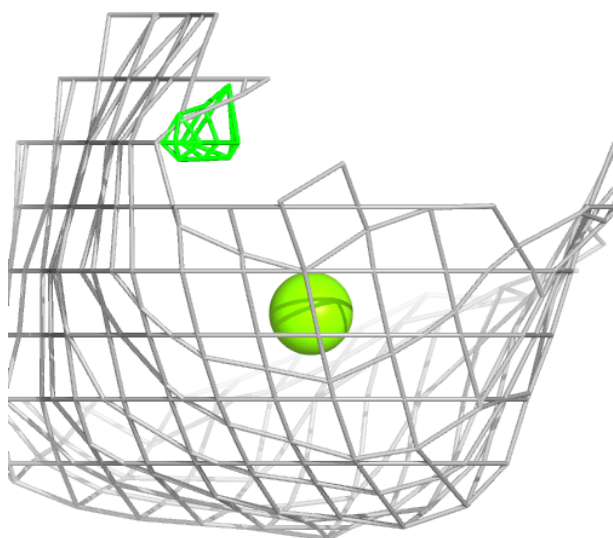
**Electron density around ADP K 601:**

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



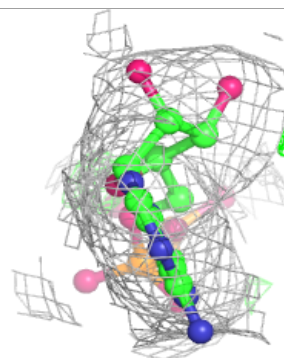
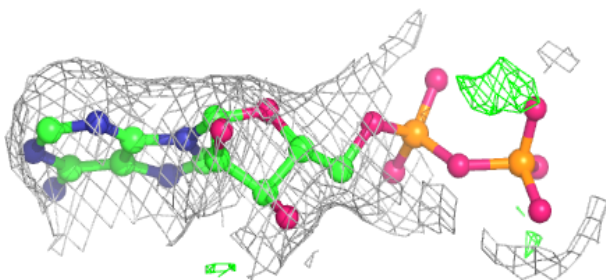
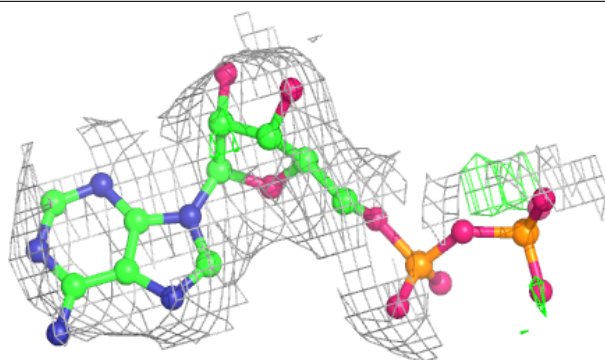
**Electron density around MG J 604:**

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

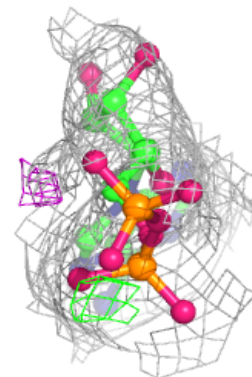
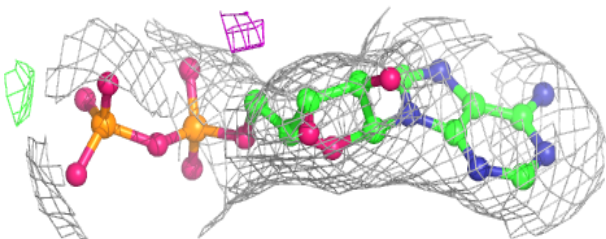
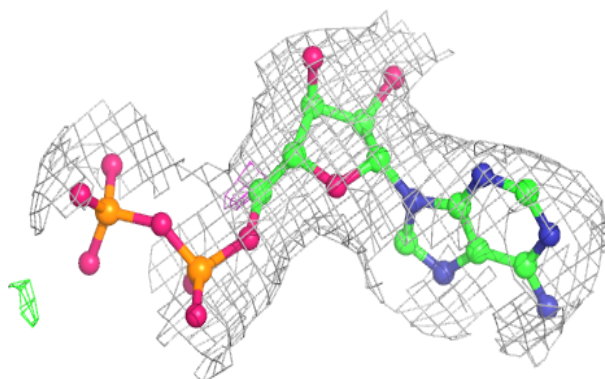


**Electron density around ADP L 601:**

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

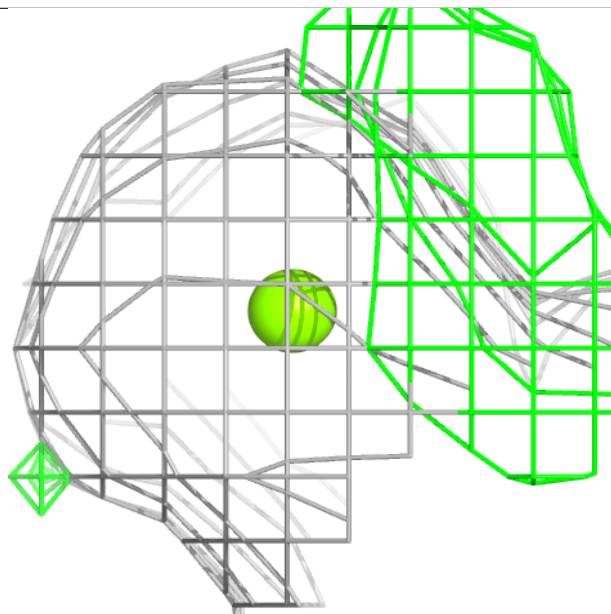
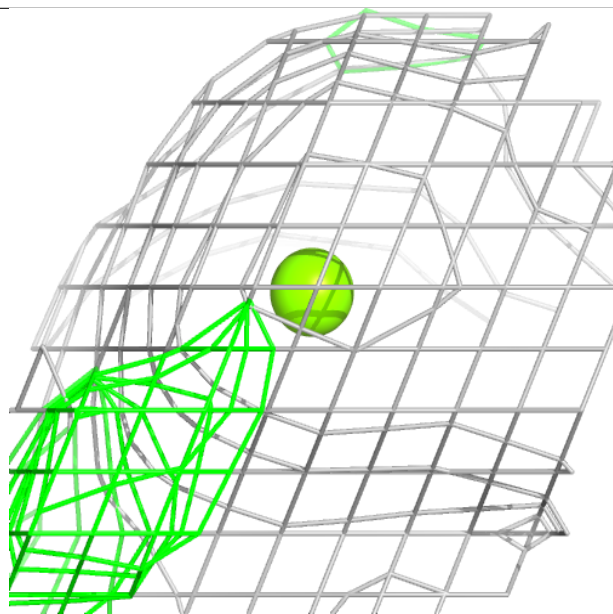
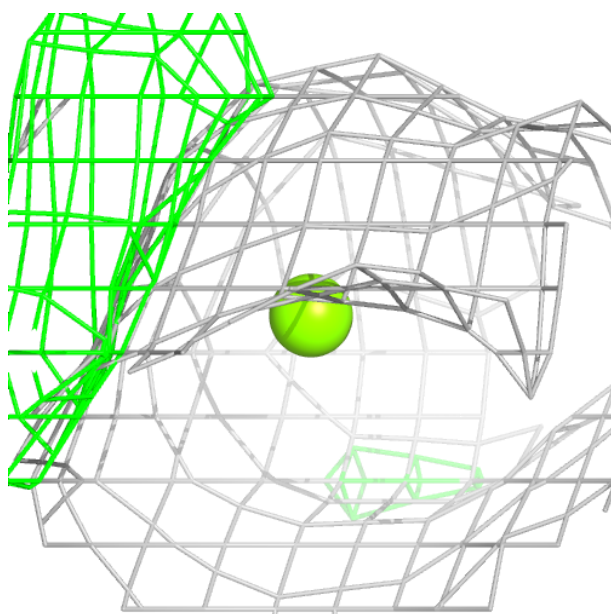
**Electron density around ADP G 601:**

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



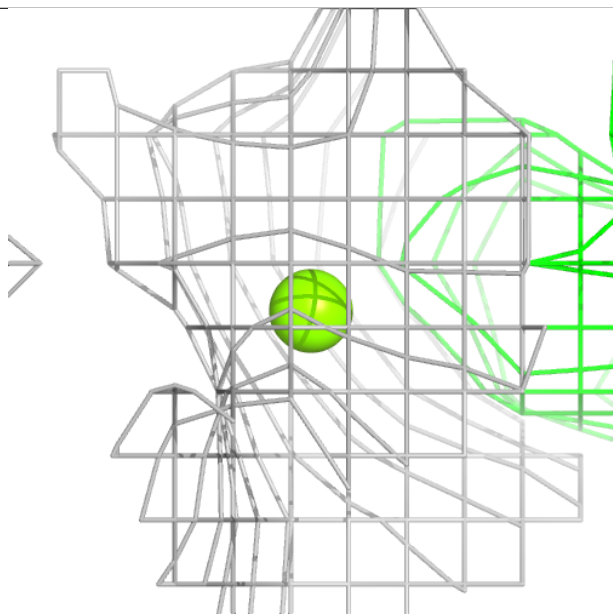
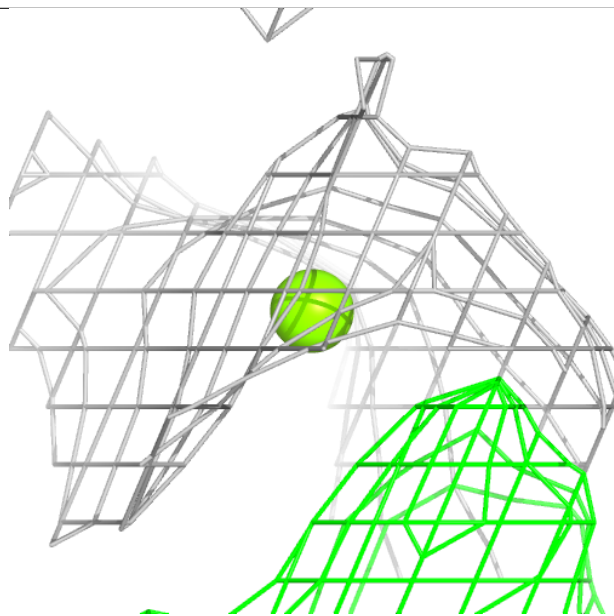
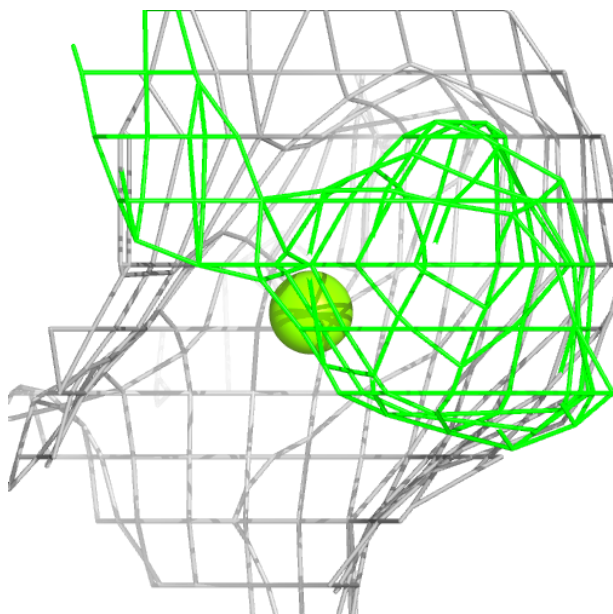
**Electron density around MG F 604:**

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



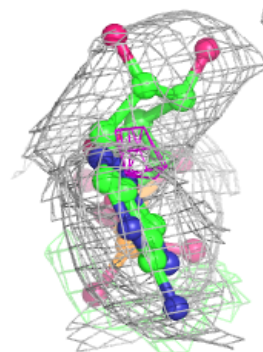
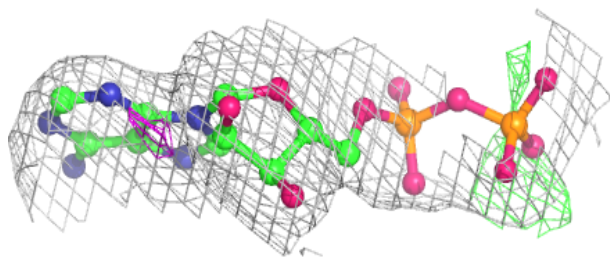
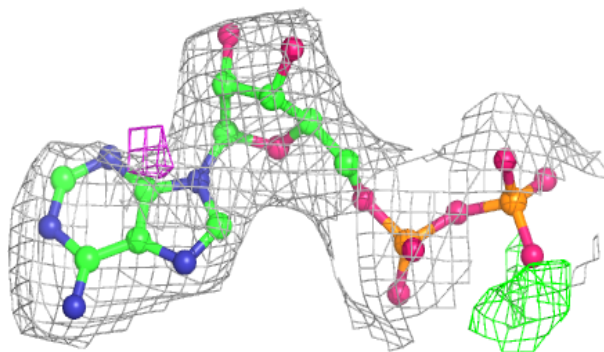
**Electron density around MG L 603:**

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



**Electron density around ADP L 602:**

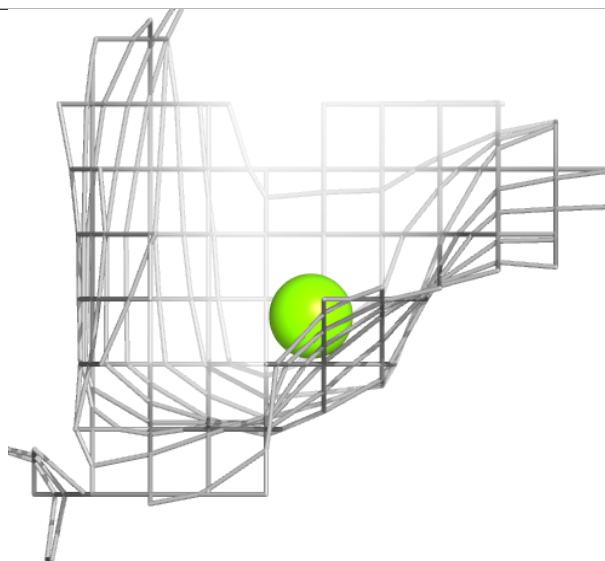
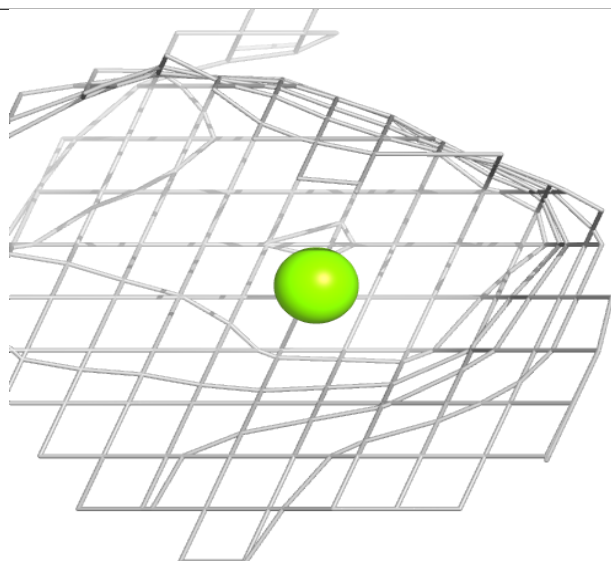
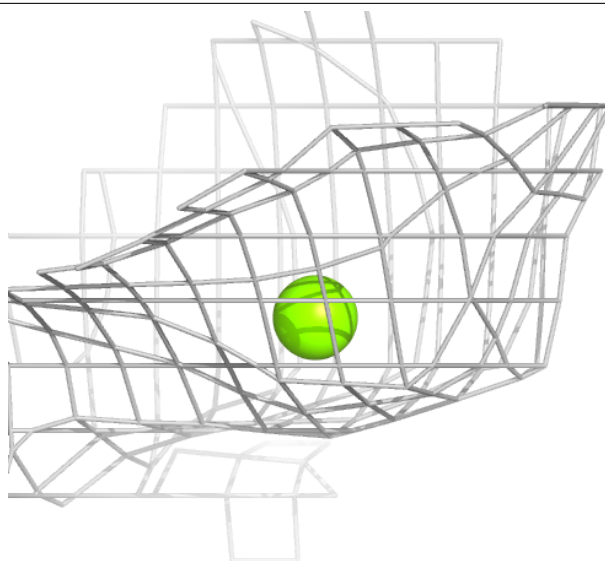
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





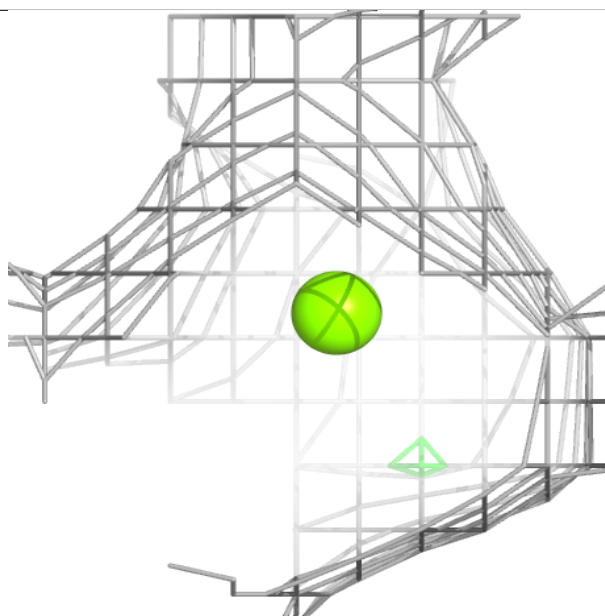
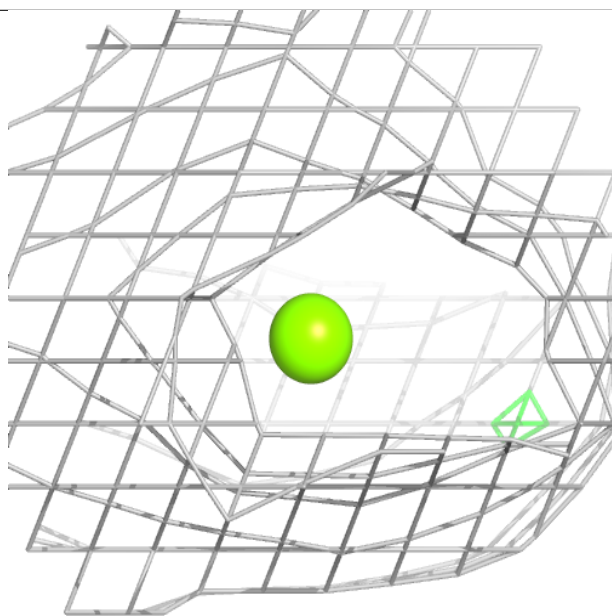
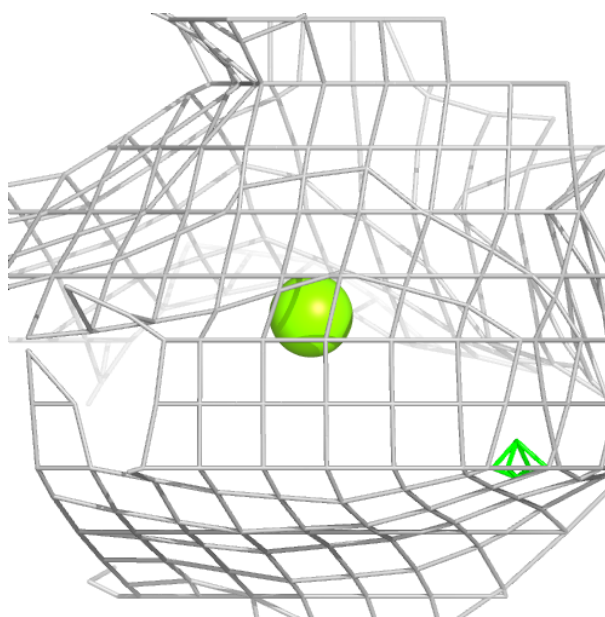
**Electron density around MG H 604:**

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



**Electron density around MG F 603:**

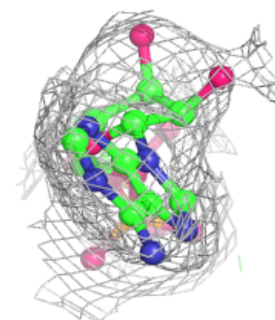
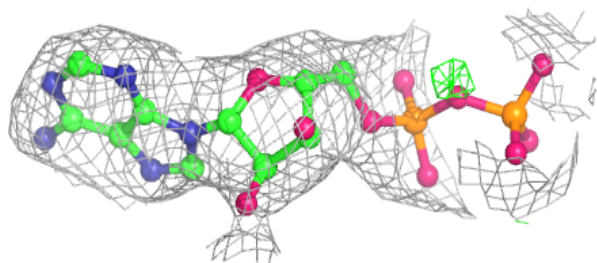
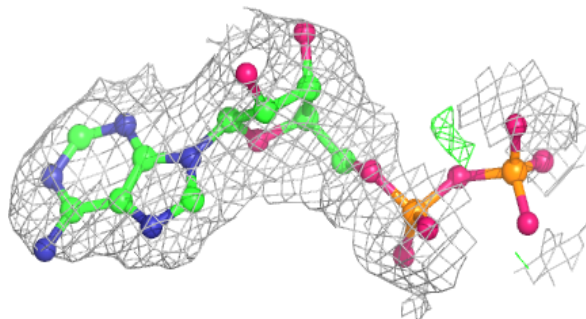
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



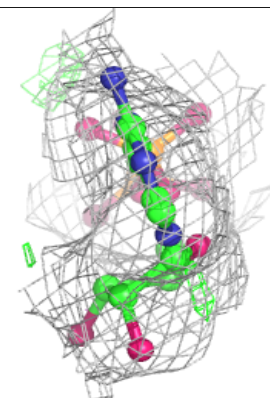
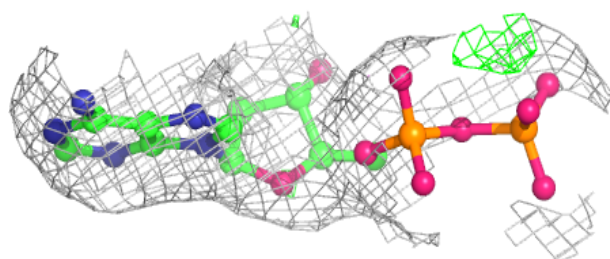
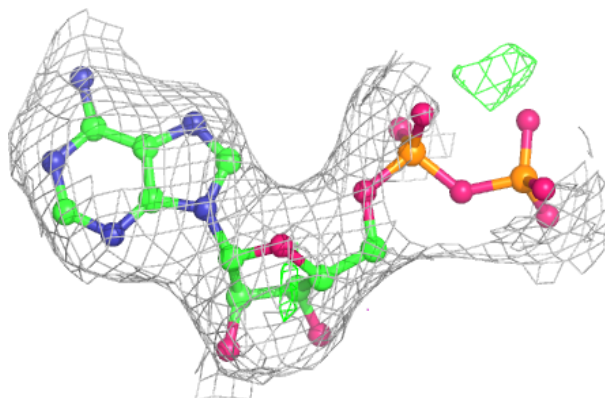


**Electron density around ADP D 602:**

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and green (positive)

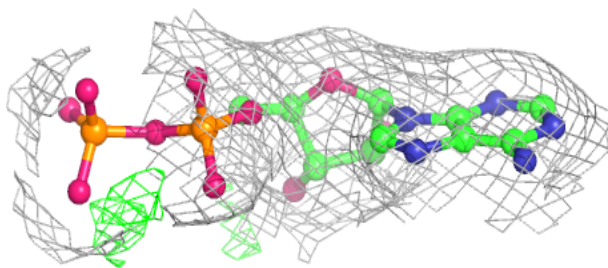
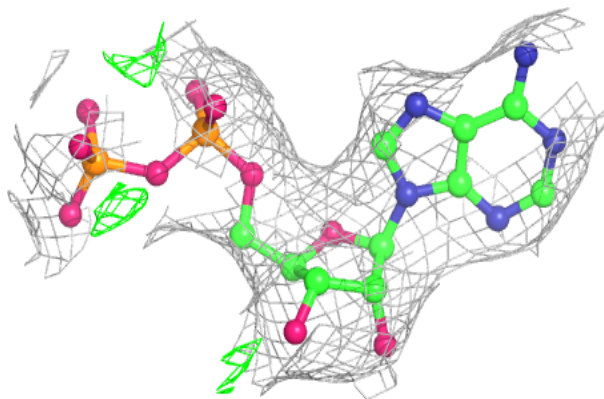
**Electron density around ADP I 602:**

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and green (positive)



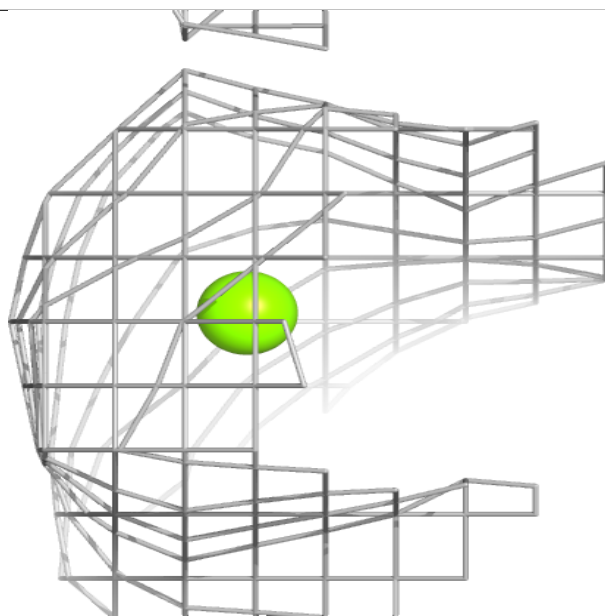
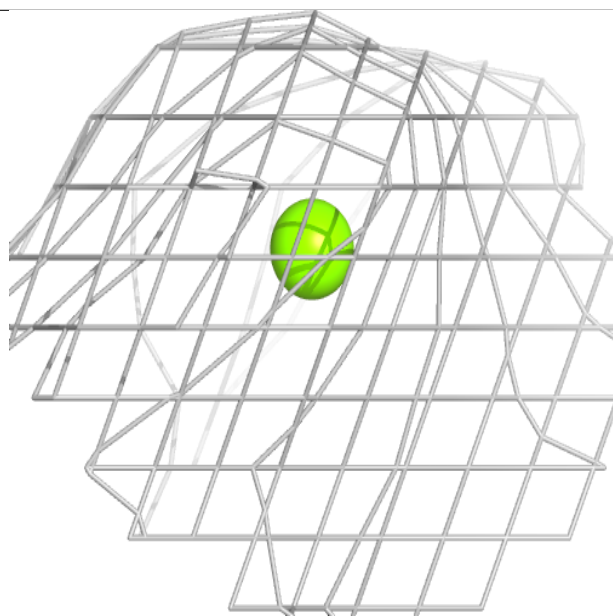
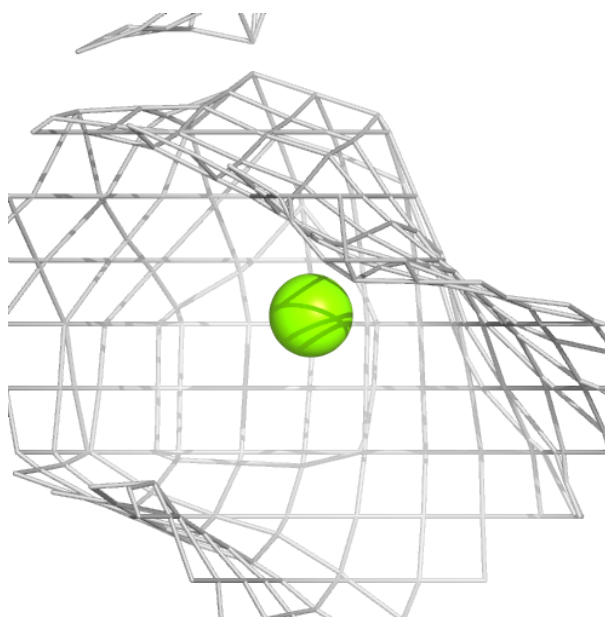
**Electron density around ADP B 601:**

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and green (positive)



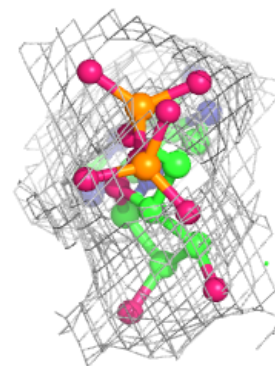
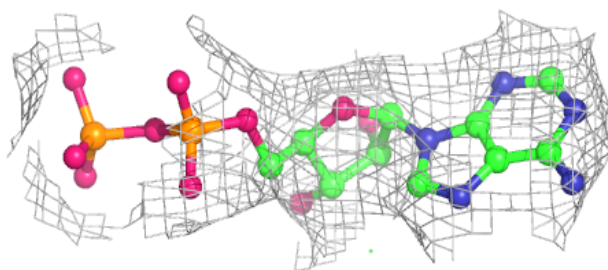
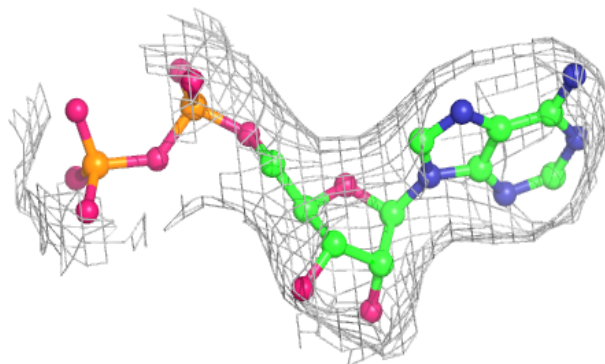
**Electron density around MG B 604:**

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and green (positive)

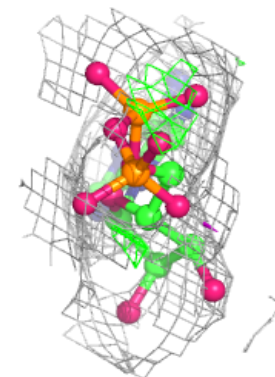
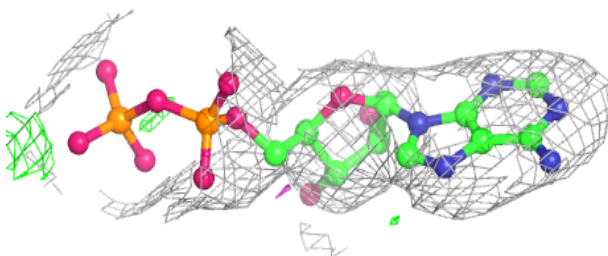
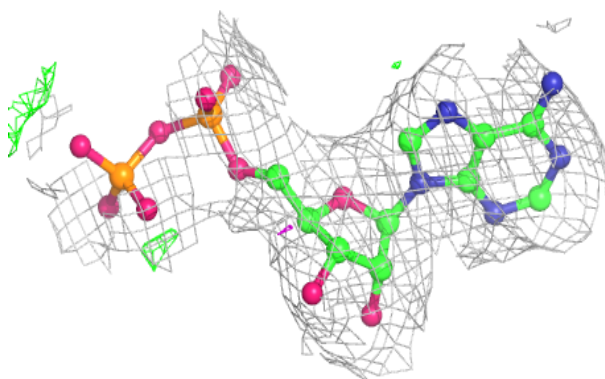


**Electron density around ADP H 601:**

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

**Electron density around ADP I 601:**

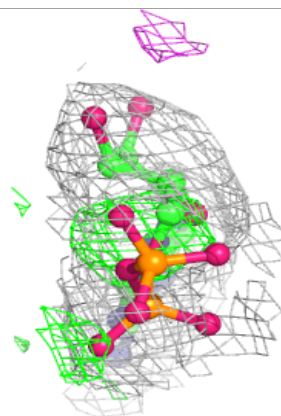
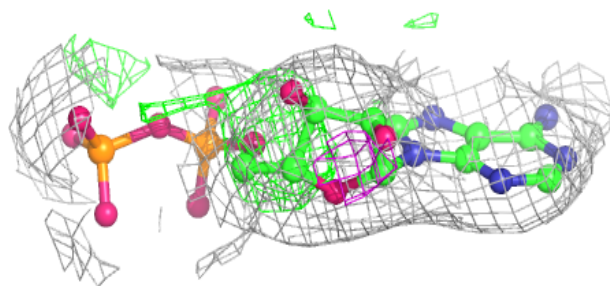
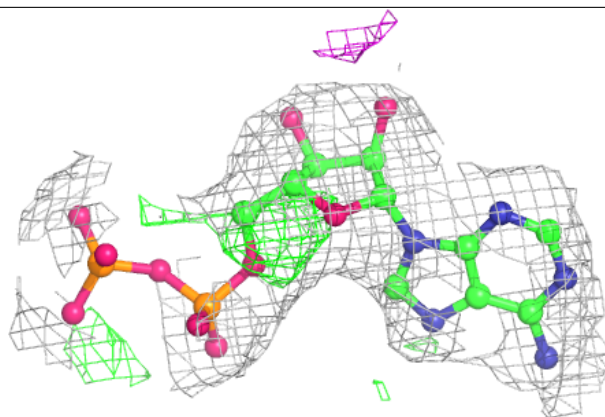
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



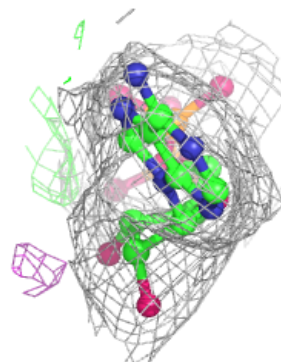
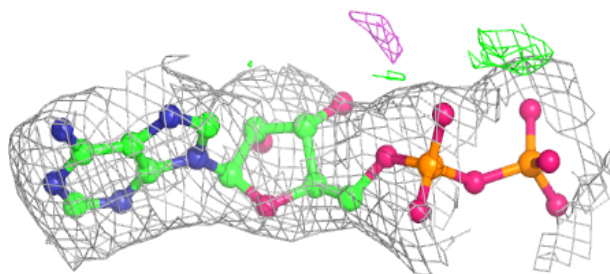
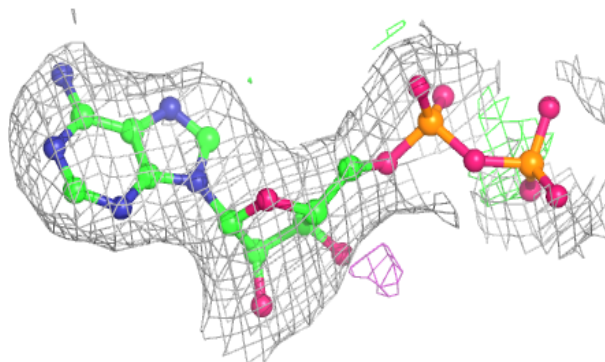


**Electron density around ADP C 601:**

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

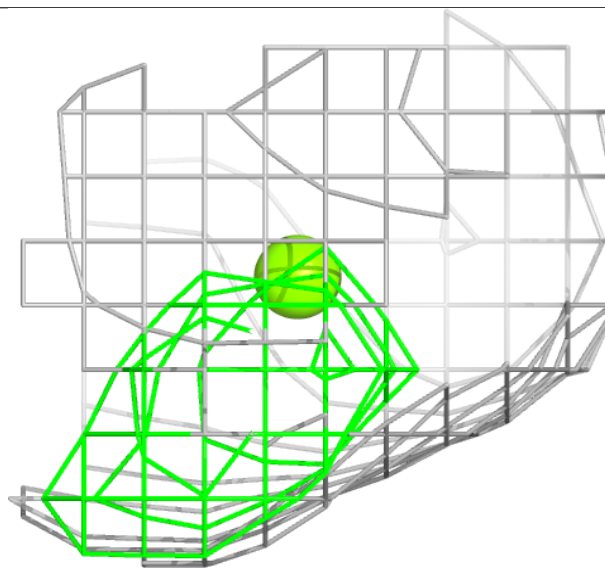
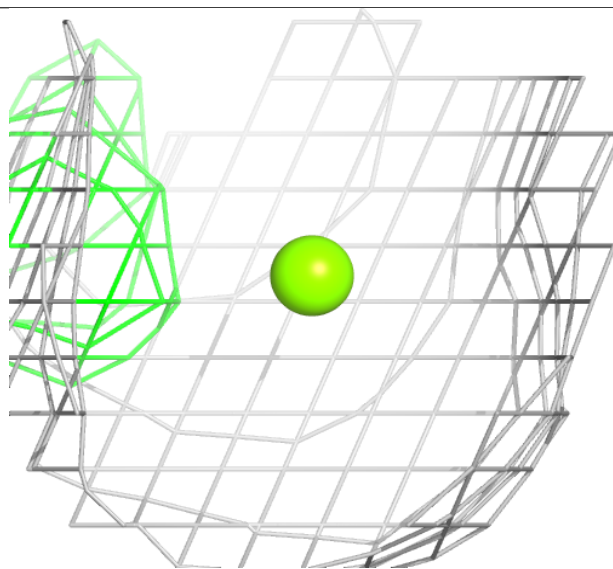
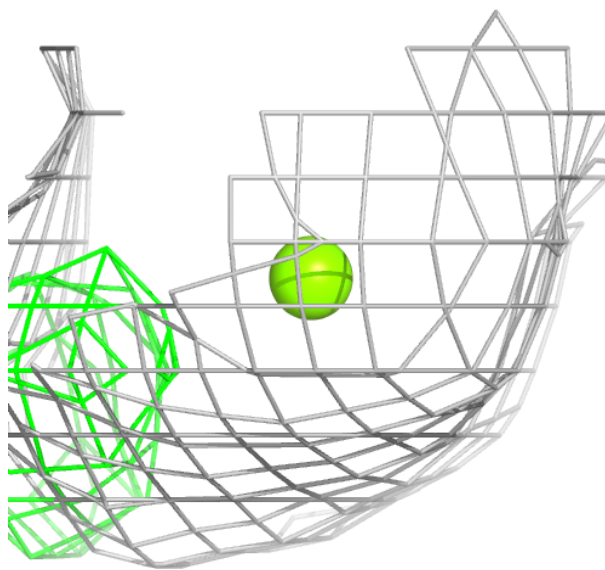
**Electron density around ADP F 602:**

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



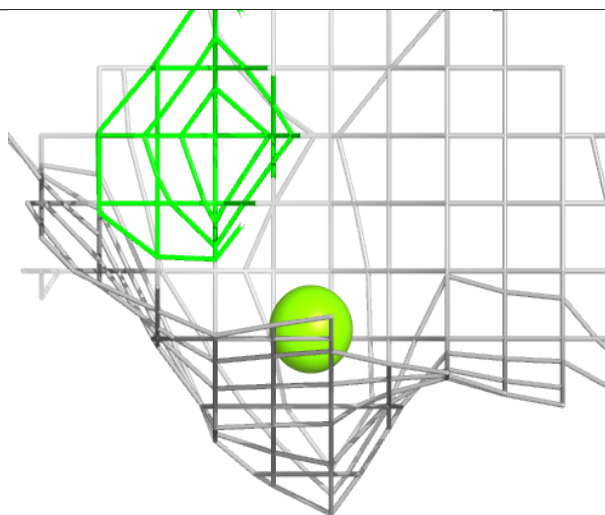
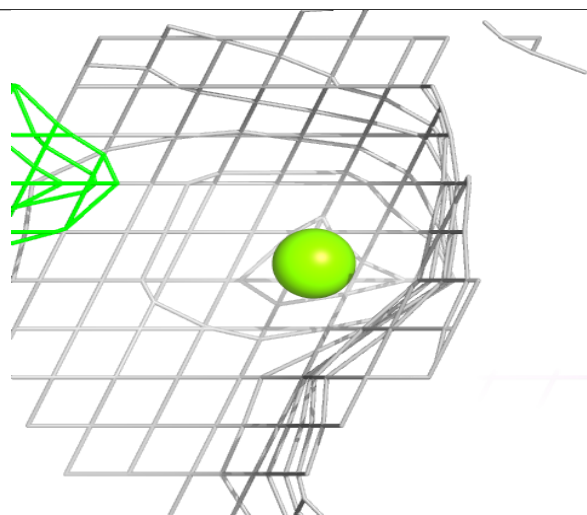
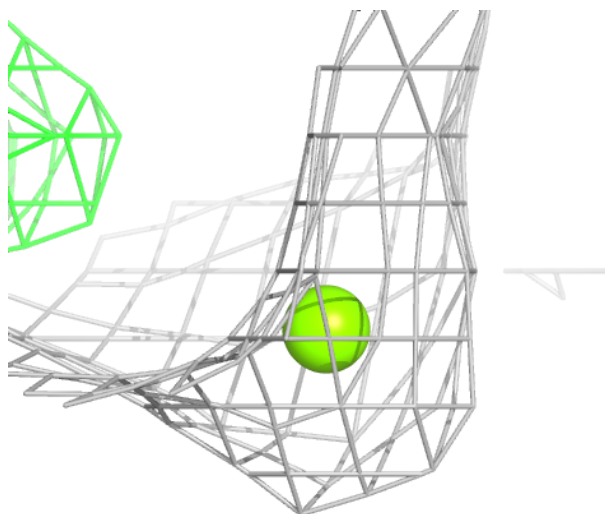
**Electron density around MG I 603:**

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



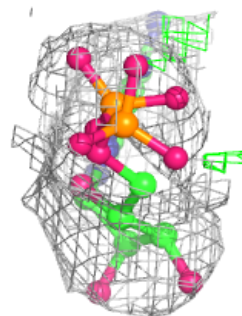
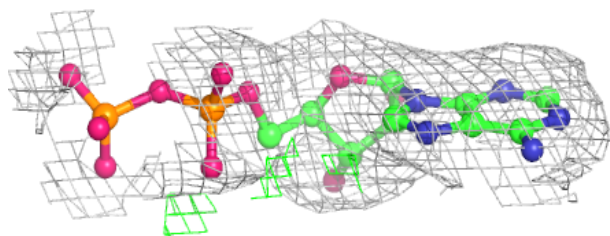
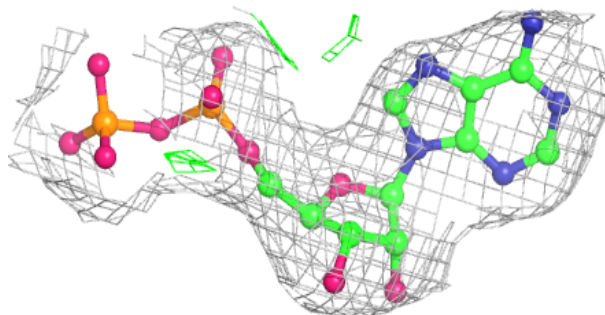
**Electron density around MG I 604:**

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

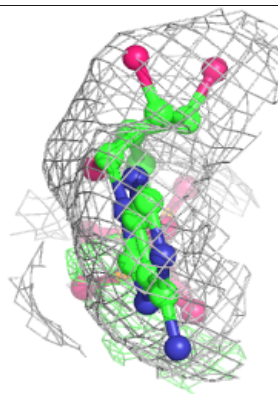
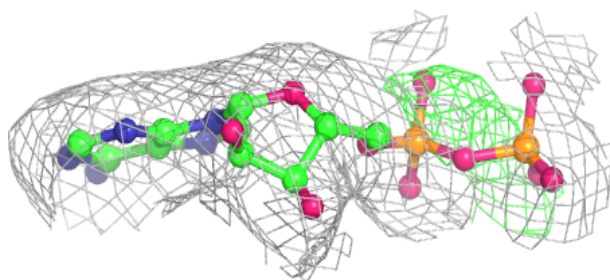
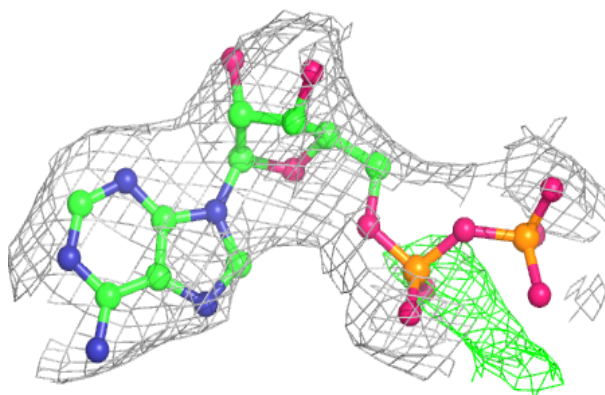


**Electron density around ADP A 601:**

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

**Electron density around ADP K 602:**

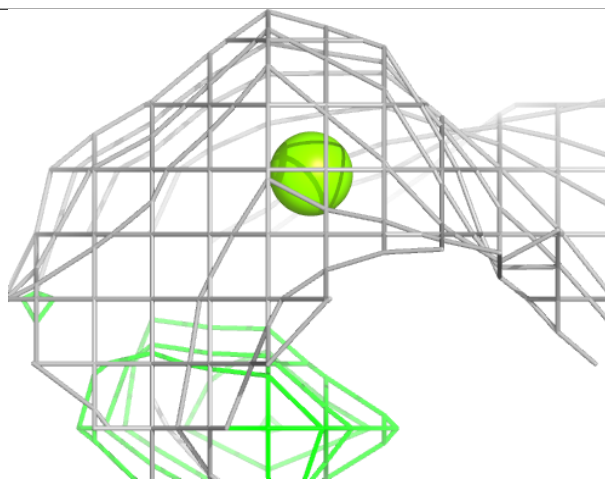
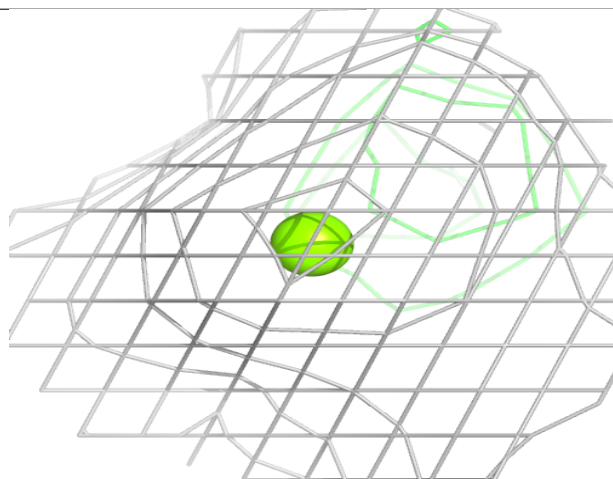
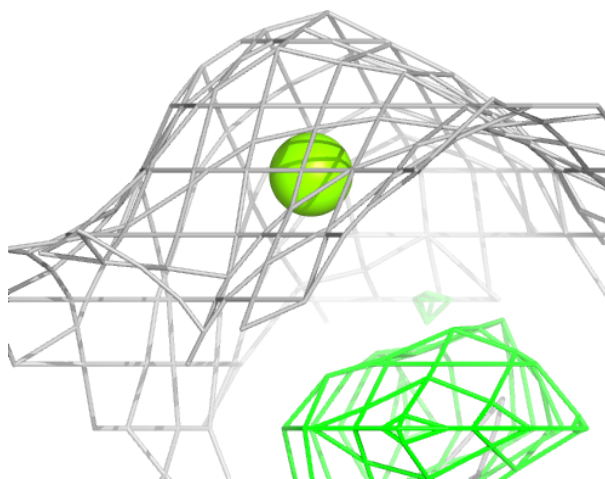
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





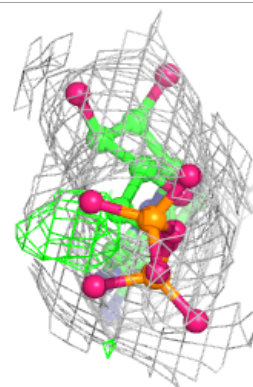
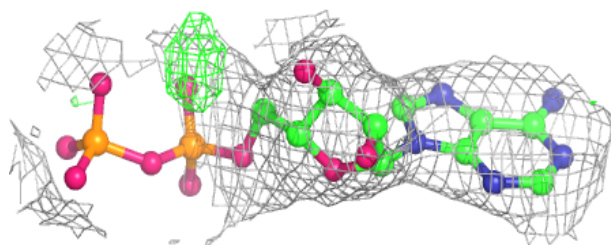
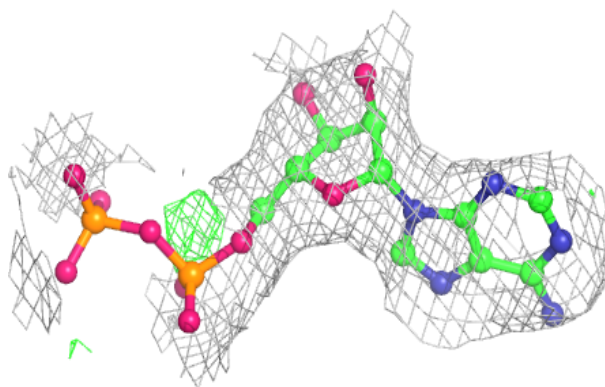
**Electron density around MG C 603:**

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

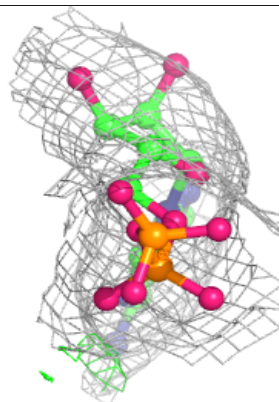
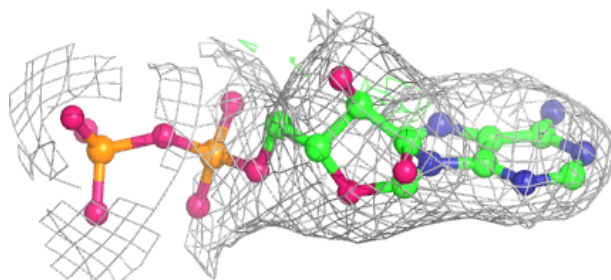
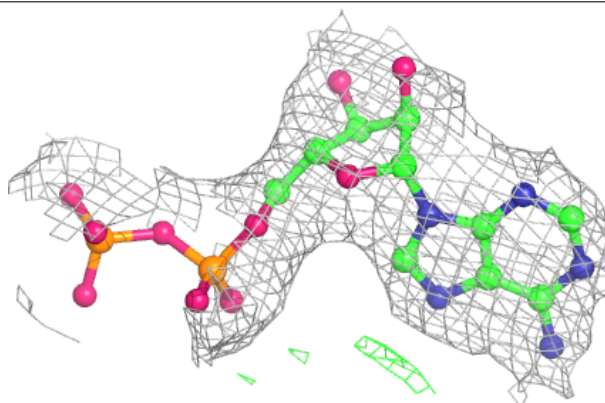


**Electron density around ADP E 602:**

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

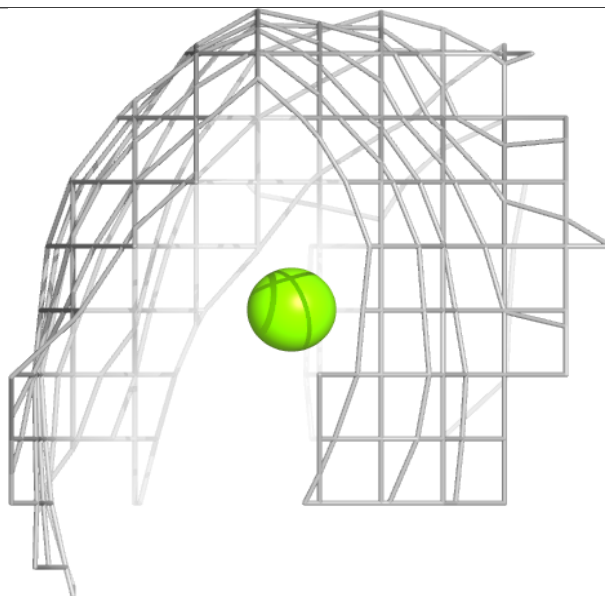
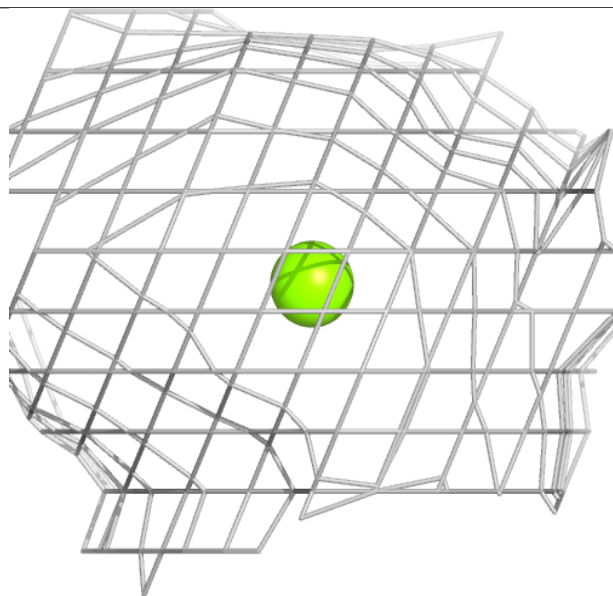
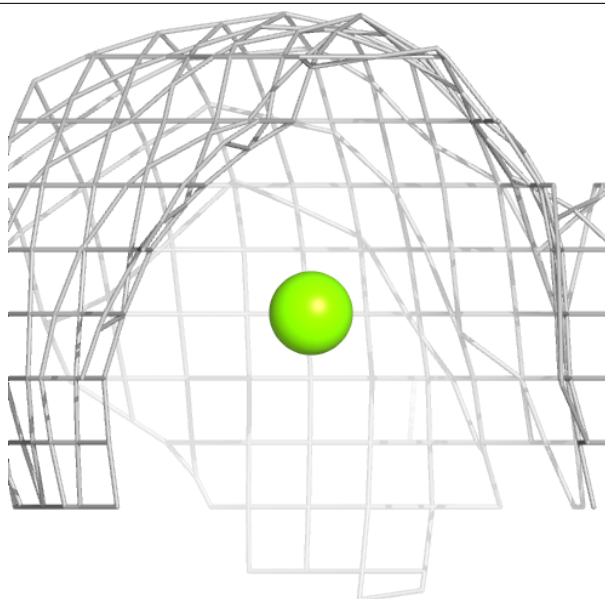
**Electron density around ADP D 601:**

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



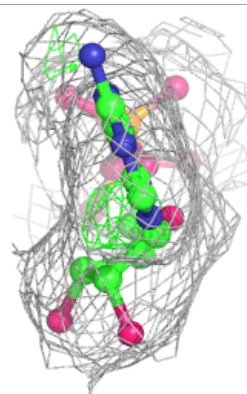
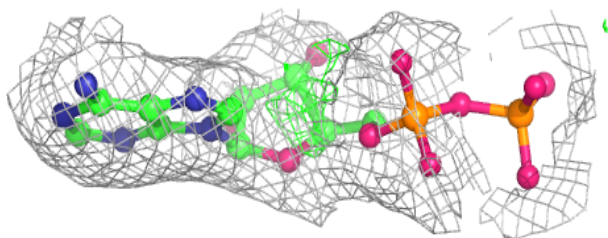
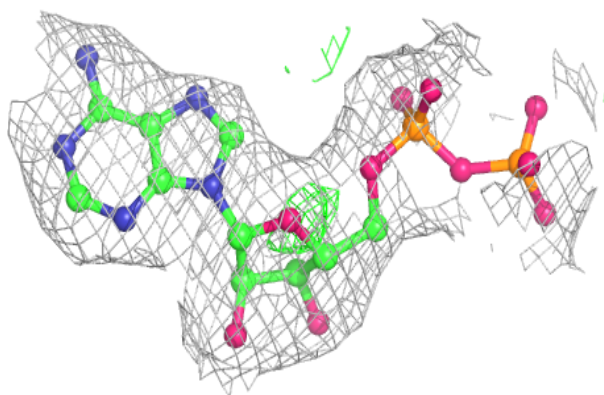
**Electron density around MG D 603:**

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

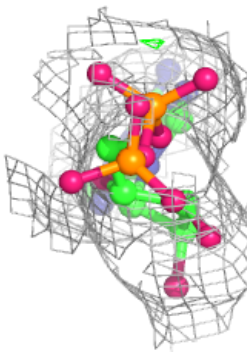
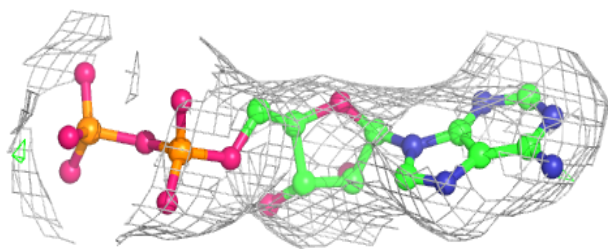
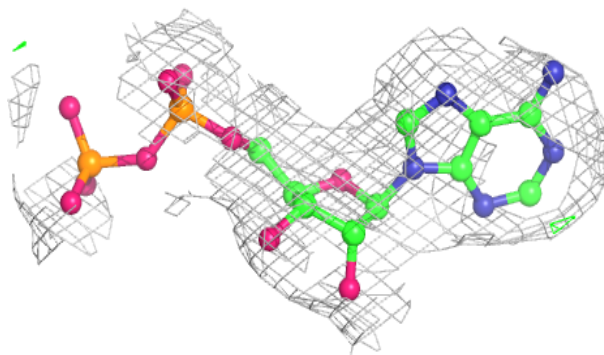


**Electron density around ADP F 601:**

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

**Electron density around ADP J 601:**

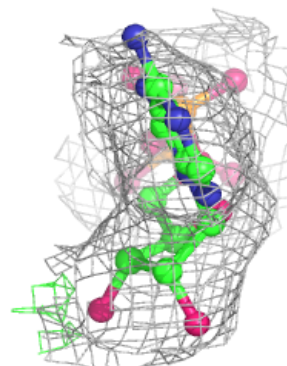
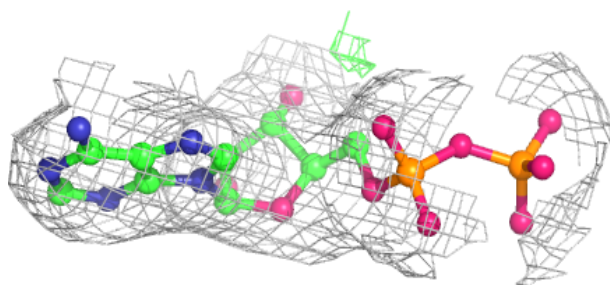
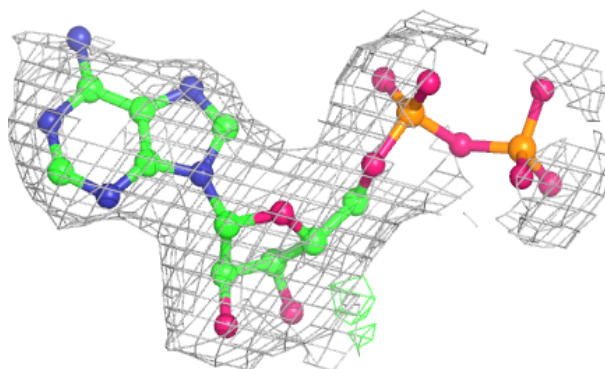
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



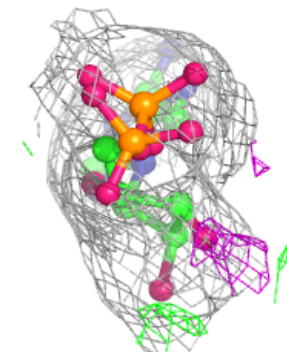
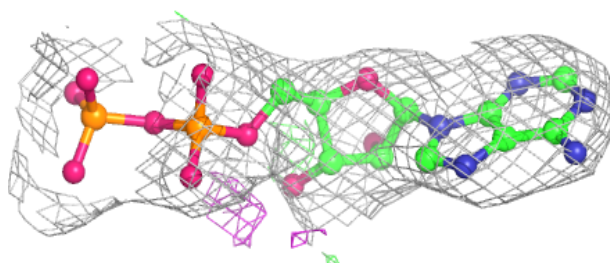


**Electron density around ADP J 602:**

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

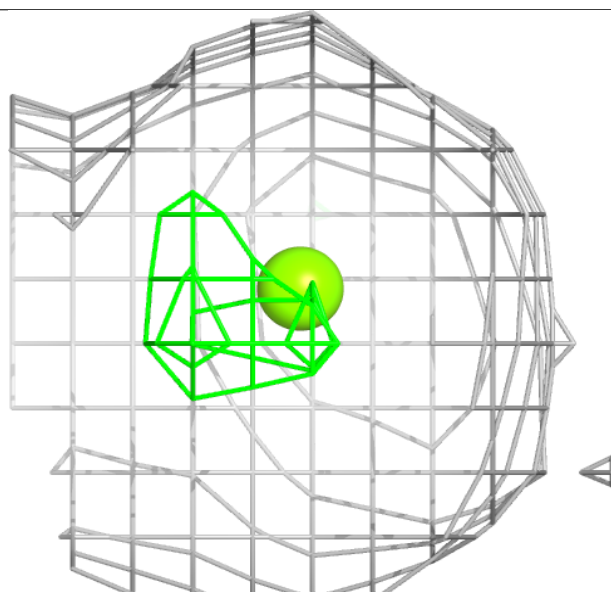
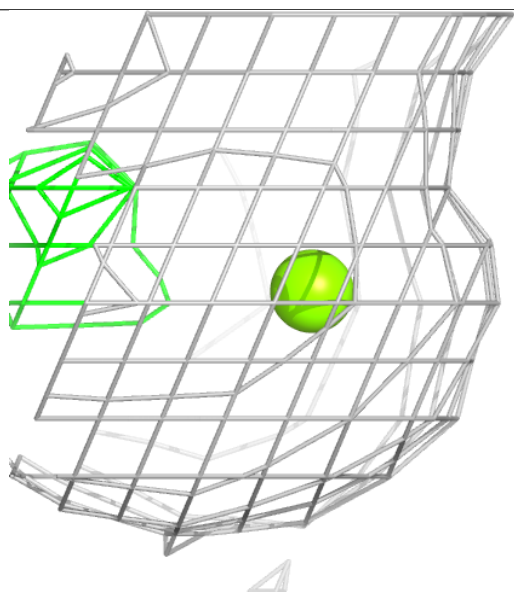
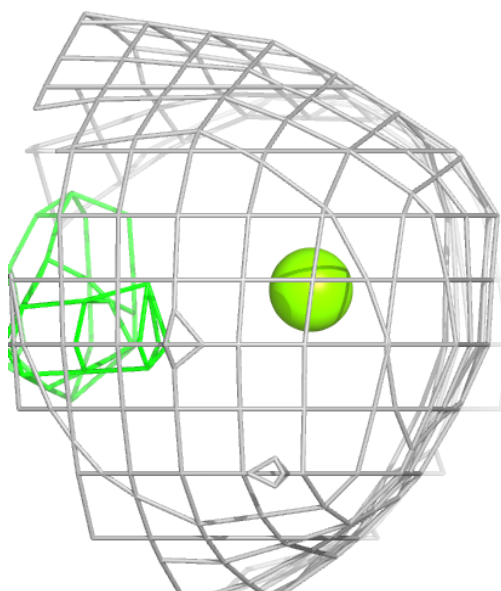
**Electron density around ADP B 602:**

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



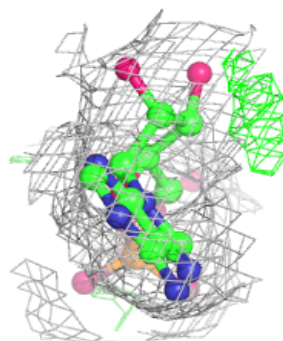
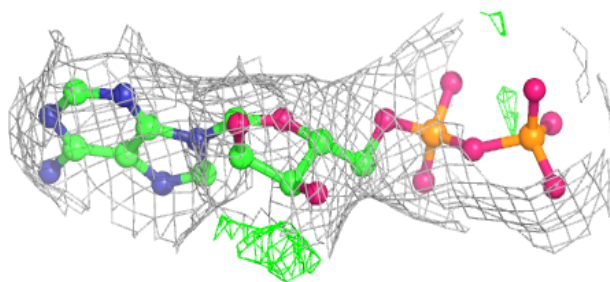
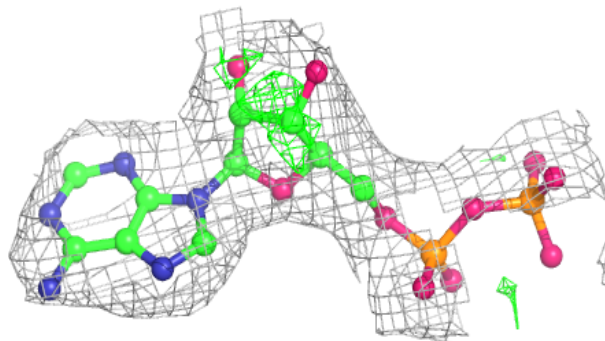
**Electron density around MG E 603:**

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

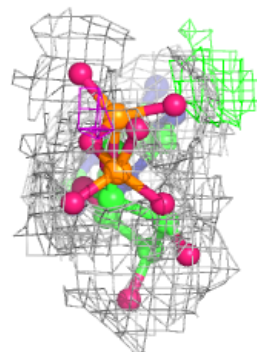
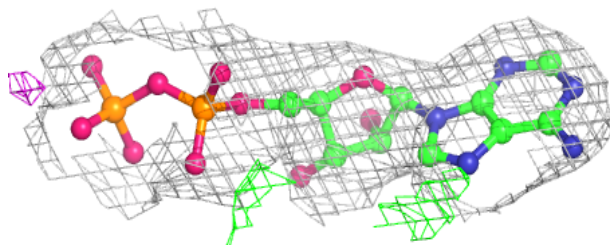
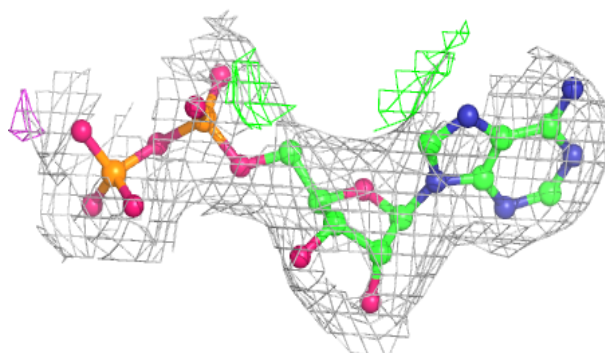


**Electron density around ADP C 602:**

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

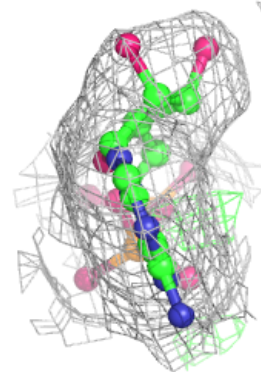
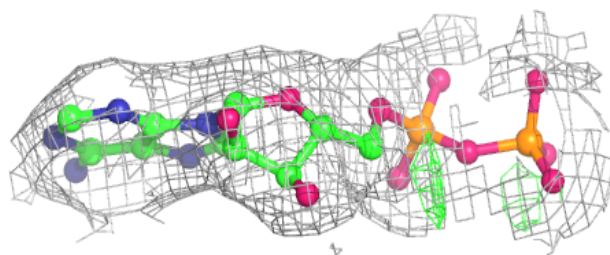
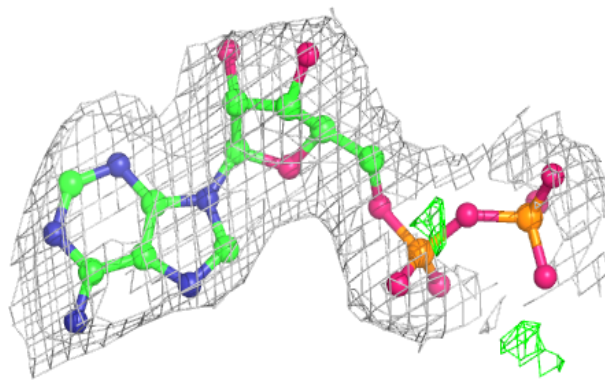
**Electron density around ADP A 602:**

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



**Electron density around ADP E 601:**

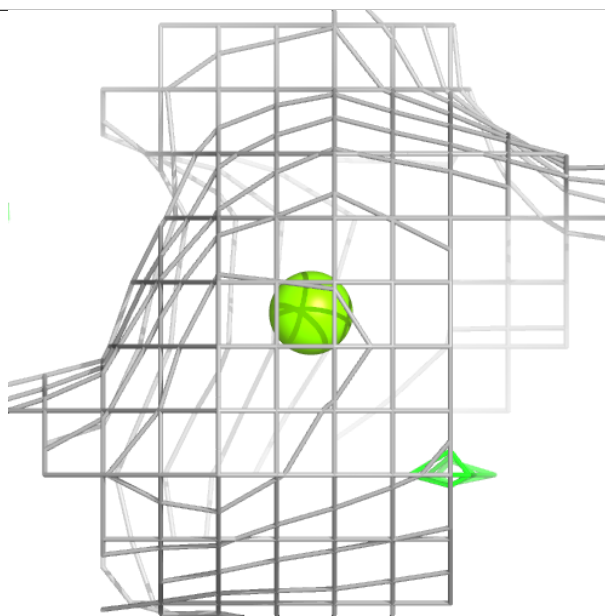
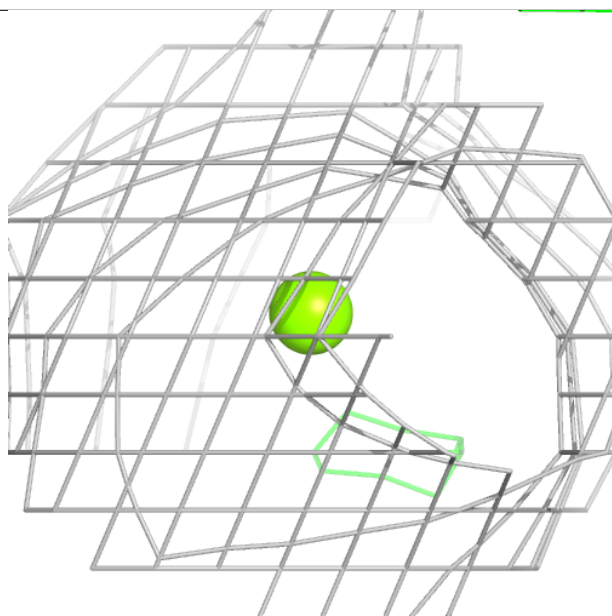
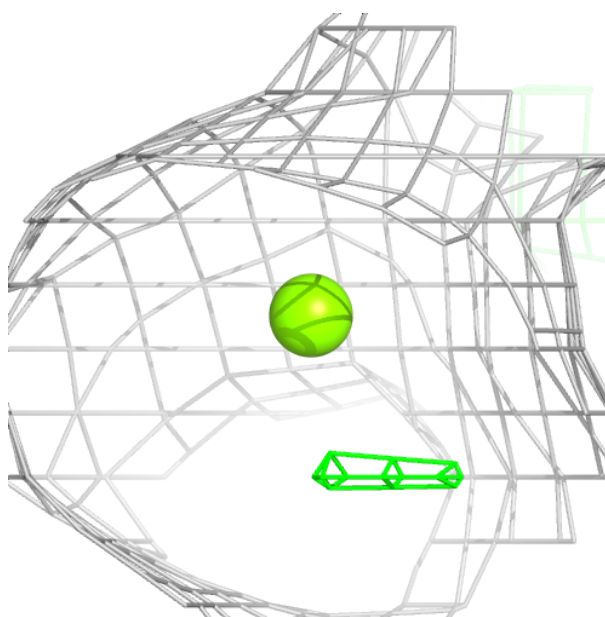
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





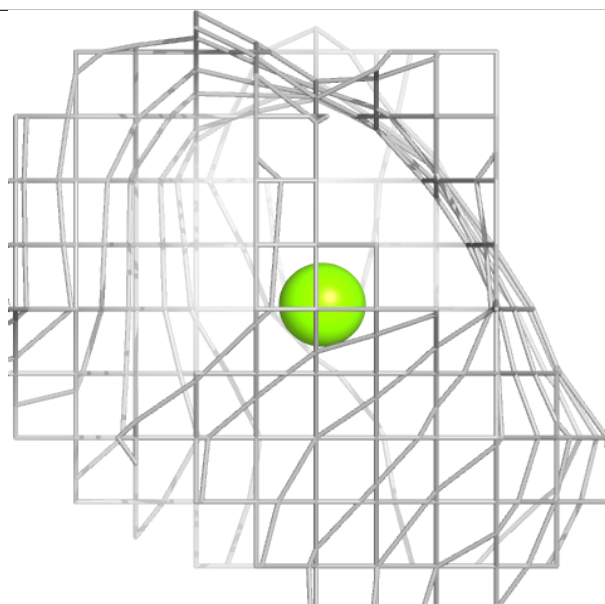
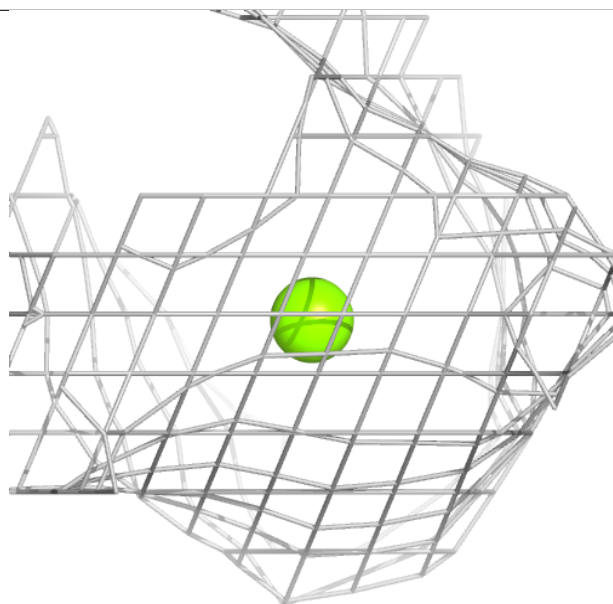
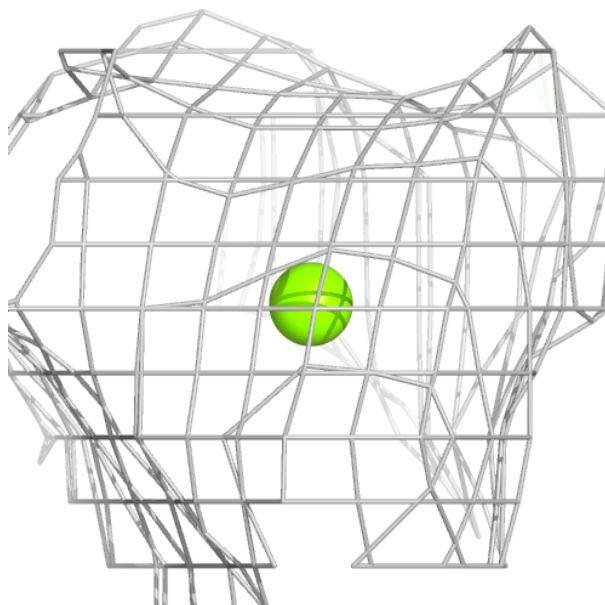
**Electron density around MG E 604:**

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



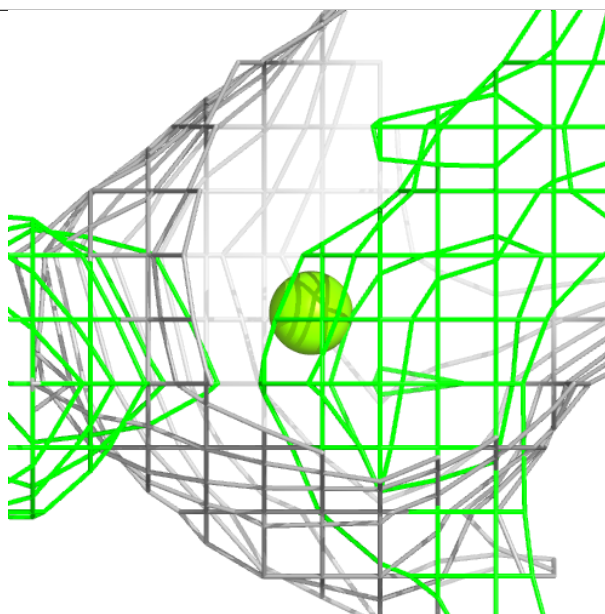
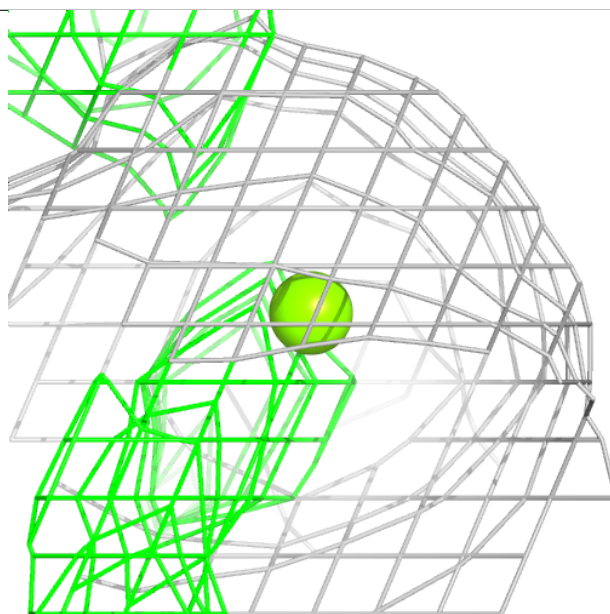
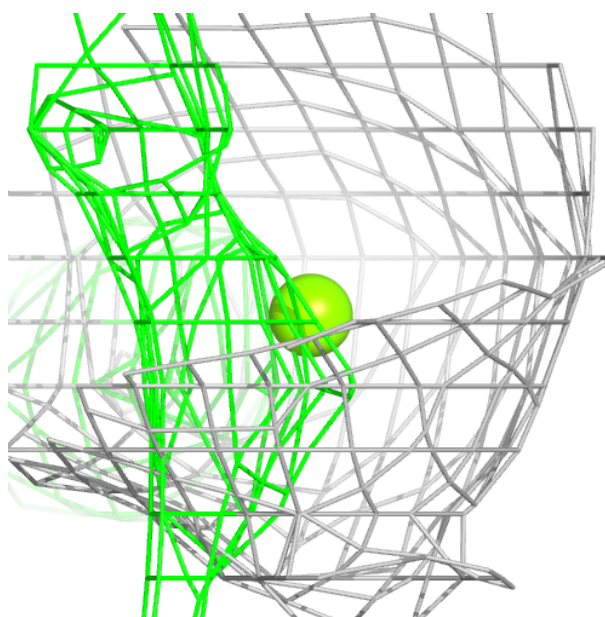
**Electron density around MG A 603:**

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



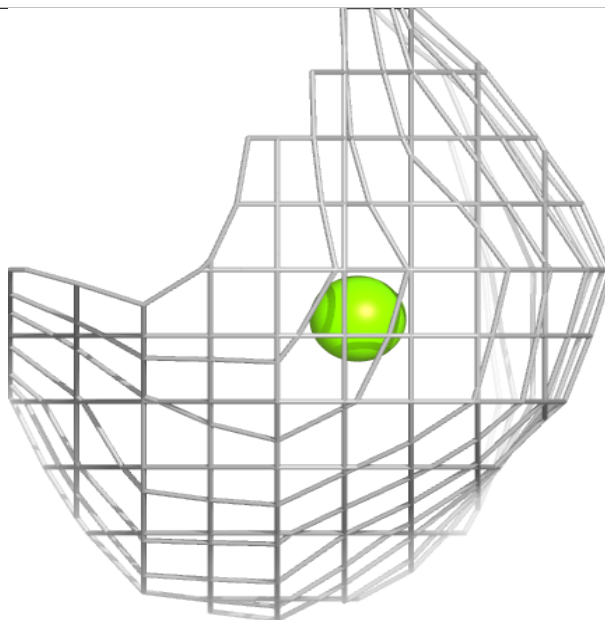
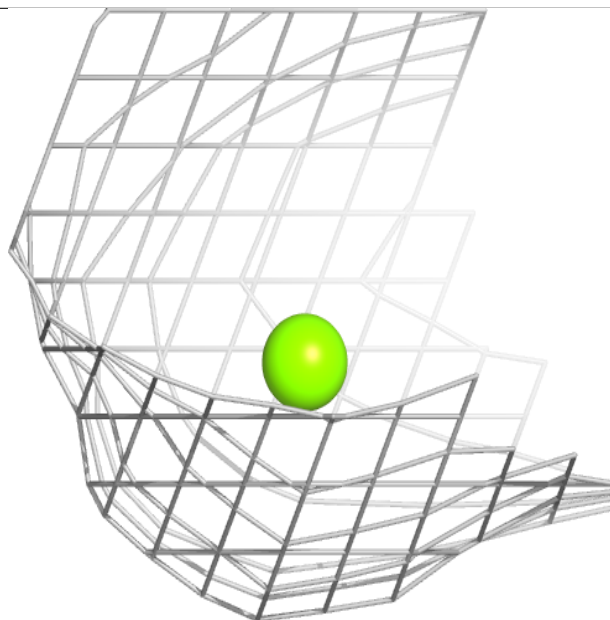
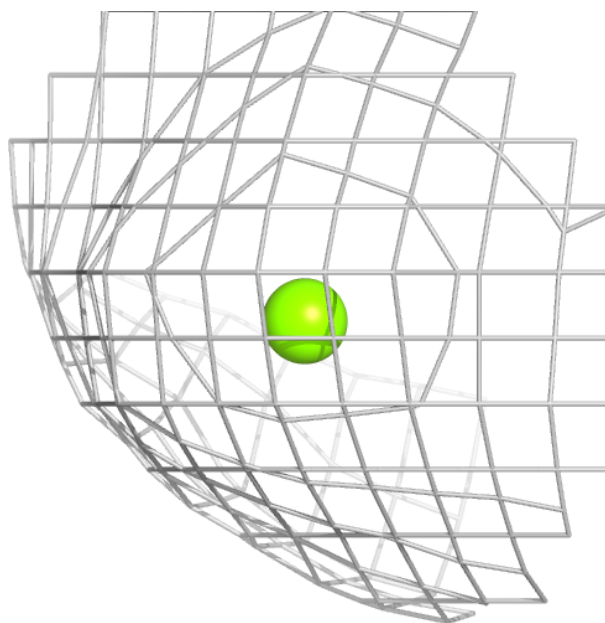
**Electron density around MG K 603:**

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



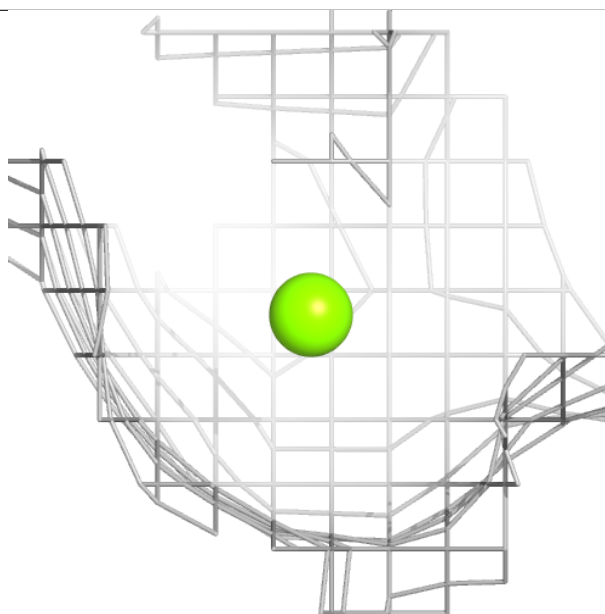
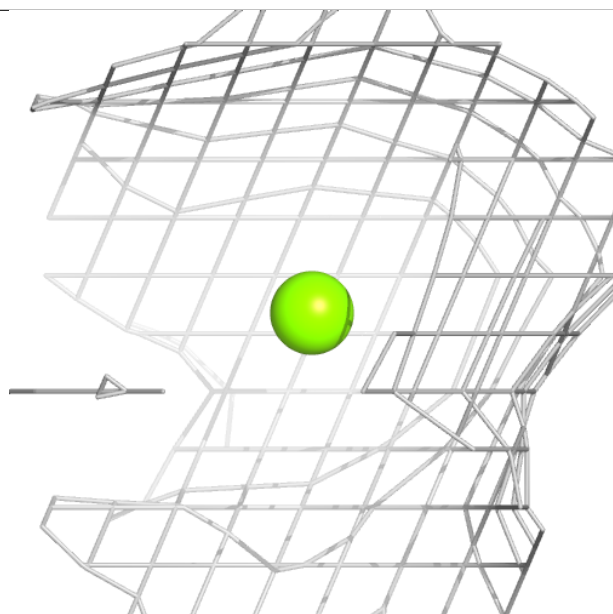
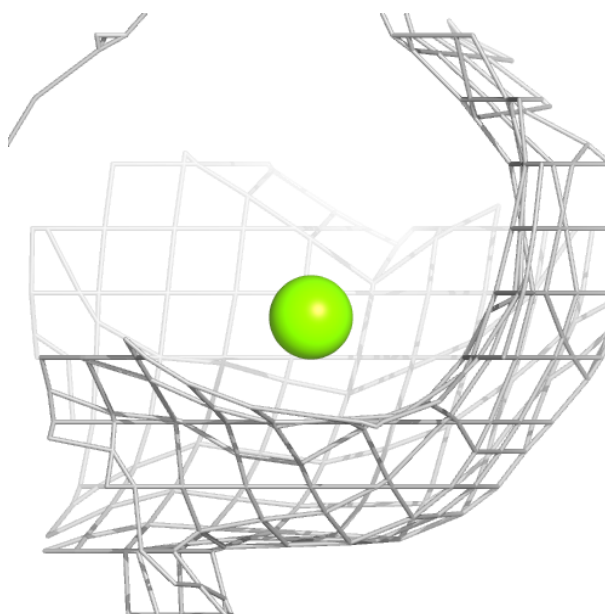
**Electron density around MG K 604:**

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



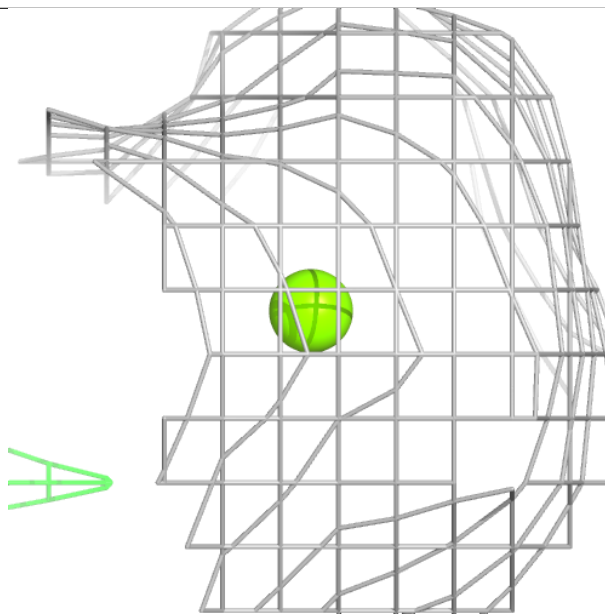
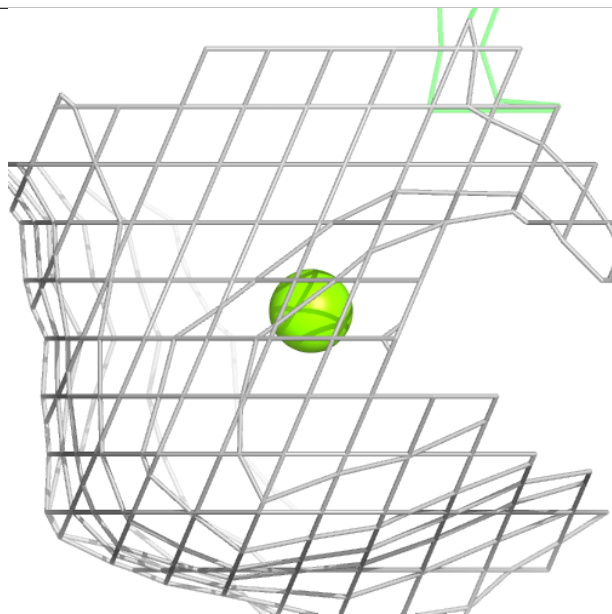
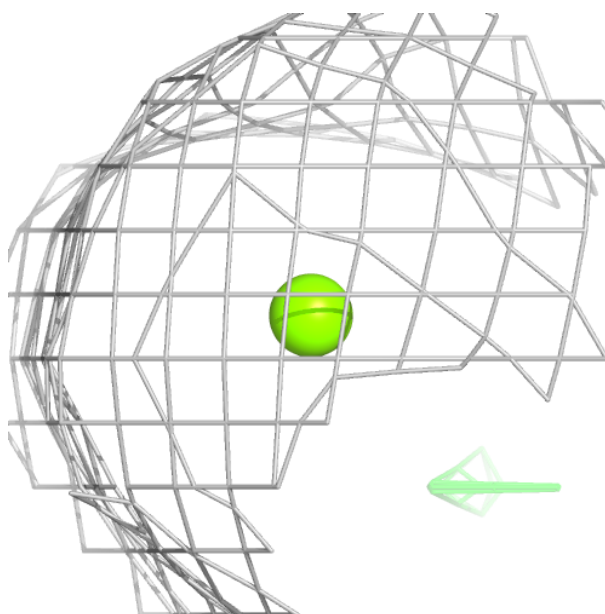
**Electron density around MG J 603:**

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



**Electron density around MG C 604:**

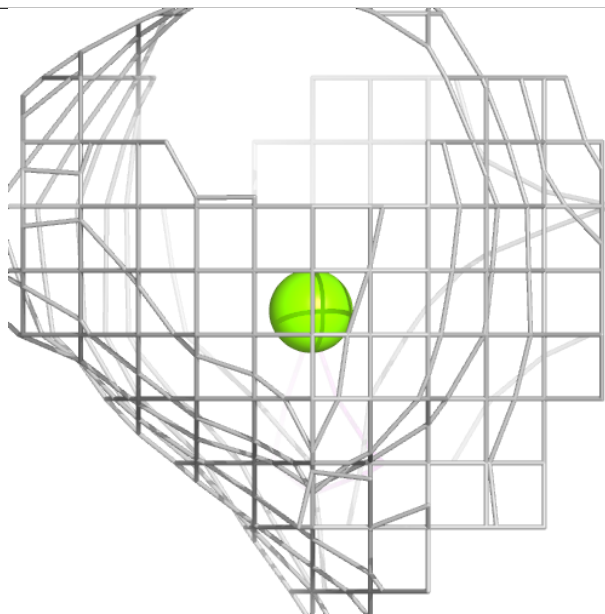
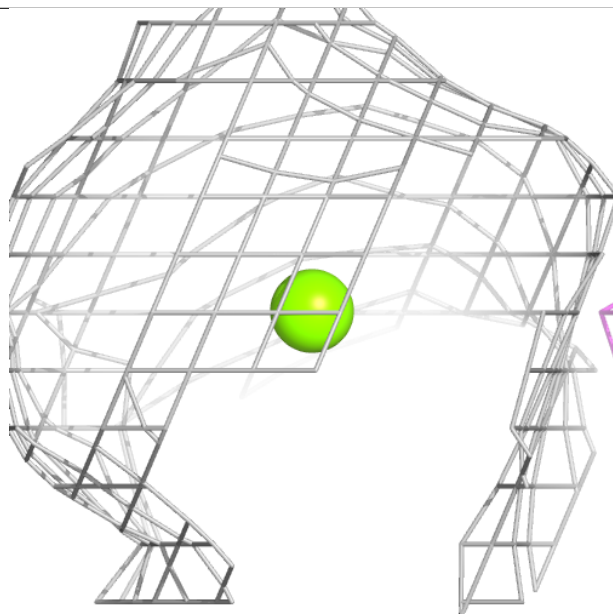
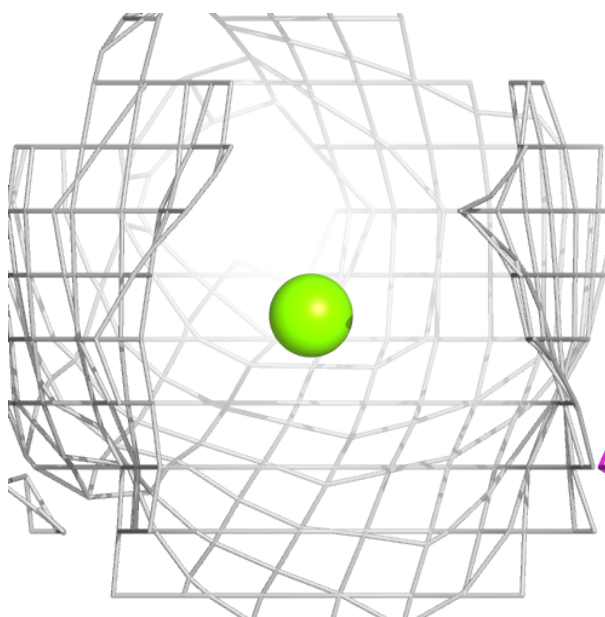
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around MG A 604:**

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



## 6.5 Other polymers ⓘ

There are no such residues in this entry.