



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:09 PM UTC

PDB ID : 3WVL / pdb_00003wvl
Title : Crystal structure of the football-shaped GroEL-GroES complex (GroEL: GroES2:ATP14) from Escherichia coli
Authors : Koike-Takeshita, A.; Arakawa, T.; Taguchi, H.; Shimamura, T.
Deposited on : 2014-05-23
Resolution : 3.79 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

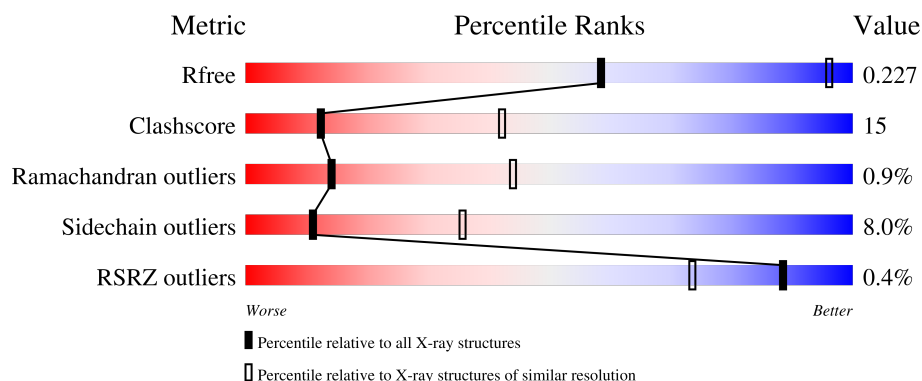
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.79 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.



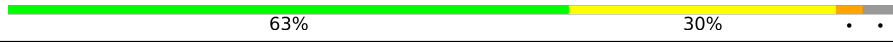
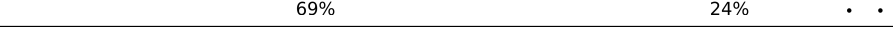
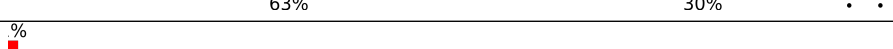
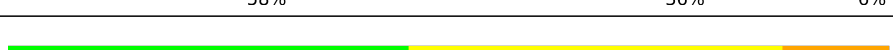
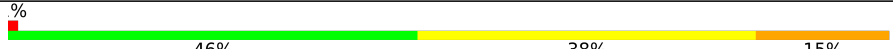
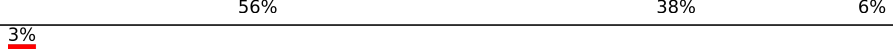
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1085 (3.94-3.62)
Clashscore	190562	1029 (3.92-3.64)
Ramachandran outliers	187476	1064 (3.94-3.62)
Sidechain outliers	187428	1059 (3.94-3.62)
RSRZ outliers	180081	1084 (3.94-3.62)

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	548	 67% 27% . .
1	B	548	 66% 28% . .
1	C	548	 66% 25% . .
1	D	548	 2% 61% 31% . .
1	E	548	 64% 28% . .

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Mol	Chain	Length	Quality of chain
1	F	548	% 
1	G	548	
1	H	548	
1	I	548	
1	J	548	
1	K	548	
1	L	548	% 
1	M	548	
1	N	548	
2	O	97	% 
2	P	97	% 
2	Q	97	
2	R	97	% 
2	S	97	
2	T	97	
2	U	97	
2	V	97	% 
2	W	97	% 
2	X	97	
2	Y	97	
2	Z	97	3% 
2	a	97	
2	b	97	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 64540 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 60 kDa chaperonin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	B	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	C	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	D	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	E	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	F	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	G	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	H	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	I	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	J	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	K	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	L	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	M	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			
1	N	524	Total	C	N	O	S	0	0	0
			3849	2395	665	769	20			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	52	ALA	ASP	engineered mutation	UNP P0A6F5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	398	ALA	ASP	engineered mutation	UNP P0A6F5
B	52	ALA	ASP	engineered mutation	UNP P0A6F5
B	398	ALA	ASP	engineered mutation	UNP P0A6F5
C	52	ALA	ASP	engineered mutation	UNP P0A6F5
C	398	ALA	ASP	engineered mutation	UNP P0A6F5
D	52	ALA	ASP	engineered mutation	UNP P0A6F5
D	398	ALA	ASP	engineered mutation	UNP P0A6F5
E	52	ALA	ASP	engineered mutation	UNP P0A6F5
E	398	ALA	ASP	engineered mutation	UNP P0A6F5
F	52	ALA	ASP	engineered mutation	UNP P0A6F5
F	398	ALA	ASP	engineered mutation	UNP P0A6F5
G	52	ALA	ASP	engineered mutation	UNP P0A6F5
G	398	ALA	ASP	engineered mutation	UNP P0A6F5
H	52	ALA	ASP	engineered mutation	UNP P0A6F5
H	398	ALA	ASP	engineered mutation	UNP P0A6F5
I	52	ALA	ASP	engineered mutation	UNP P0A6F5
I	398	ALA	ASP	engineered mutation	UNP P0A6F5
J	52	ALA	ASP	engineered mutation	UNP P0A6F5
J	398	ALA	ASP	engineered mutation	UNP P0A6F5
K	52	ALA	ASP	engineered mutation	UNP P0A6F5
K	398	ALA	ASP	engineered mutation	UNP P0A6F5
L	52	ALA	ASP	engineered mutation	UNP P0A6F5
L	398	ALA	ASP	engineered mutation	UNP P0A6F5
M	52	ALA	ASP	engineered mutation	UNP P0A6F5
M	398	ALA	ASP	engineered mutation	UNP P0A6F5
N	52	ALA	ASP	engineered mutation	UNP P0A6F5
N	398	ALA	ASP	engineered mutation	UNP P0A6F5

- Molecule 2 is a protein called 10 kDa chaperonin.

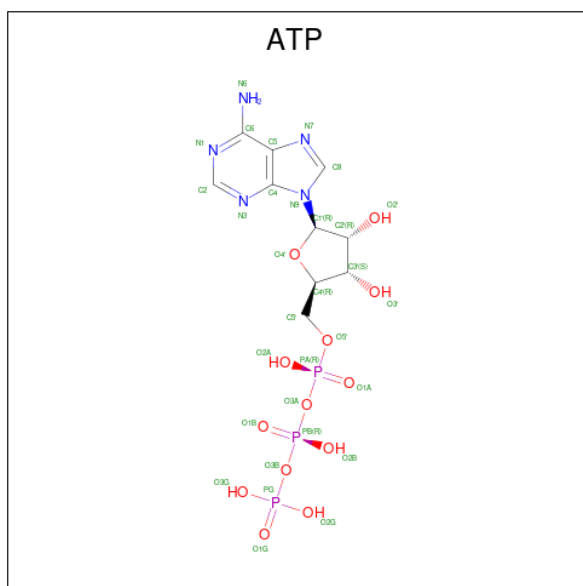
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	O	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	P	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	Q	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	R	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	S	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	T	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	U	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	V	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	W	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	X	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	Y	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	Z	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	a	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			
2	b	97	Total	C	N	O	S	0	0	0
			728	454	127	145	2			

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	D	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	G	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	H	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	I	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	J	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	K	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	L	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	M	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	N	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		
4	B	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		
4	D	1	Total	Mg	0	0
			1	1		
4	E	1	Total	Mg	0	0
			1	1		
4	F	1	Total	Mg	0	0
			1	1		
4	G	1	Total	Mg	0	0
			1	1		
4	H	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	1	Total 1	Mg 1	0	0
4	J	1	Total 1	Mg 1	0	0
4	K	1	Total 1	Mg 1	0	0
4	L	1	Total 1	Mg 1	0	0
4	M	1	Total 1	Mg 1	0	0
4	N	1	Total 1	Mg 1	0	0

- Molecule 5 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total 1	K 1	0	0
5	B	1	Total 1	K 1	0	0
5	C	1	Total 1	K 1	0	0
5	D	1	Total 1	K 1	0	0
5	E	1	Total 1	K 1	0	0
5	F	1	Total 1	K 1	0	0
5	G	1	Total 1	K 1	0	0
5	H	1	Total 1	K 1	0	0
5	I	1	Total 1	K 1	0	0
5	J	1	Total 1	K 1	0	0
5	K	1	Total 1	K 1	0	0
5	L	1	Total 1	K 1	0	0
5	M	1	Total 1	K 1	0	0

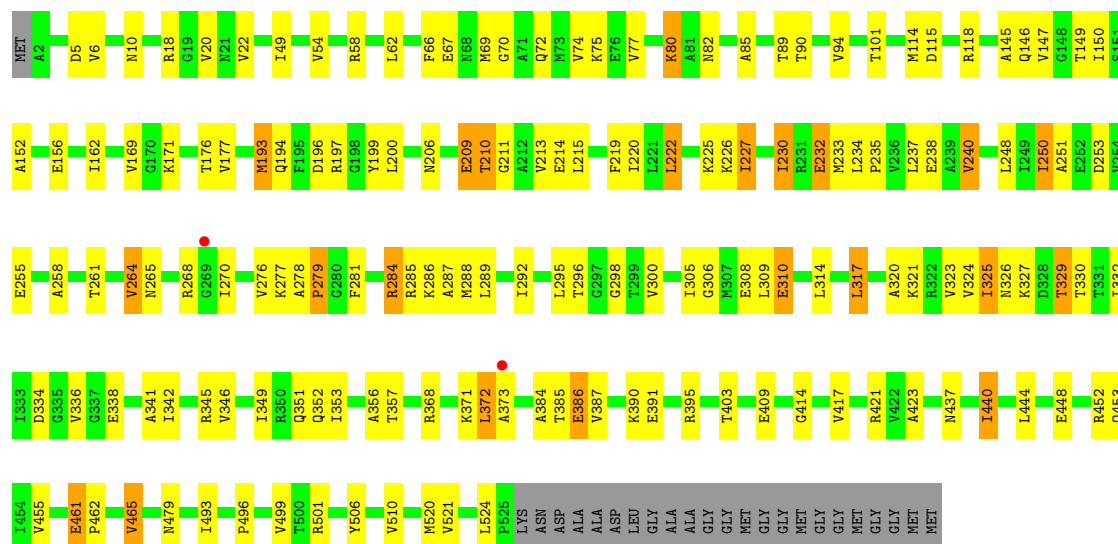
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	N	1	Total	K	0	0
			1	1		

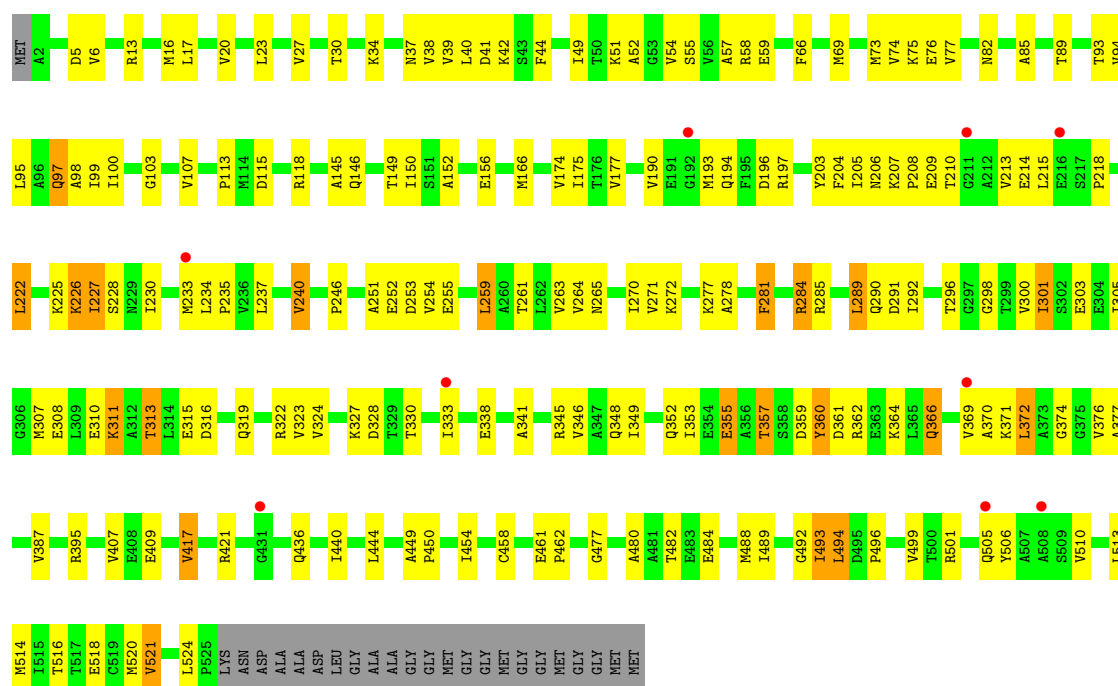
- Molecule 1: 60 kDa chaperonin

Chain C:



- Molecule 1: 60 kDa chaperonin

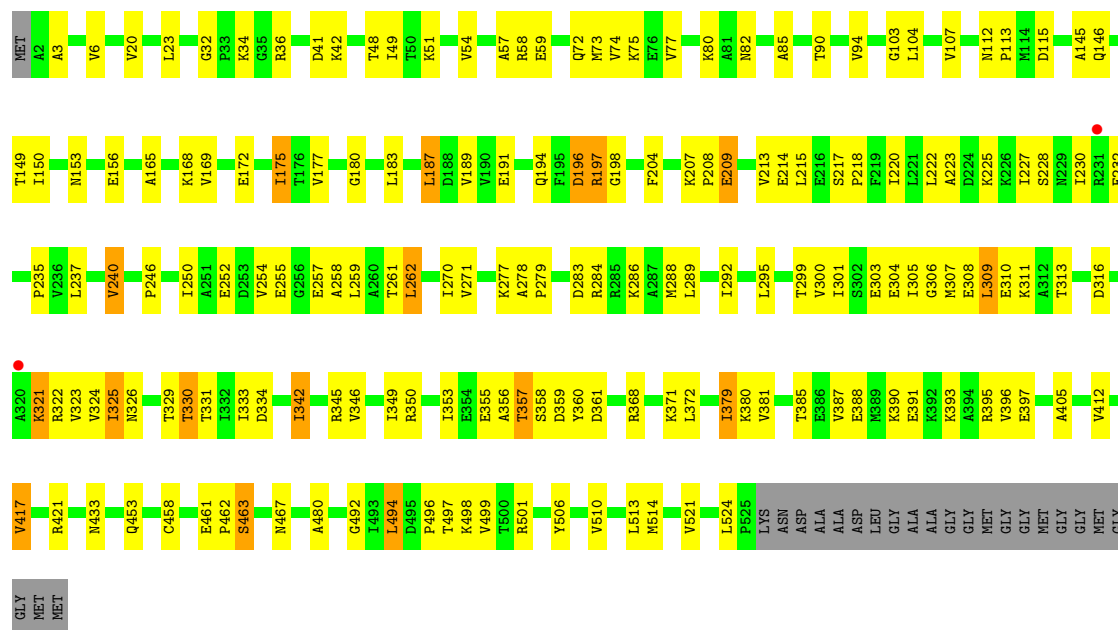
Chain D:



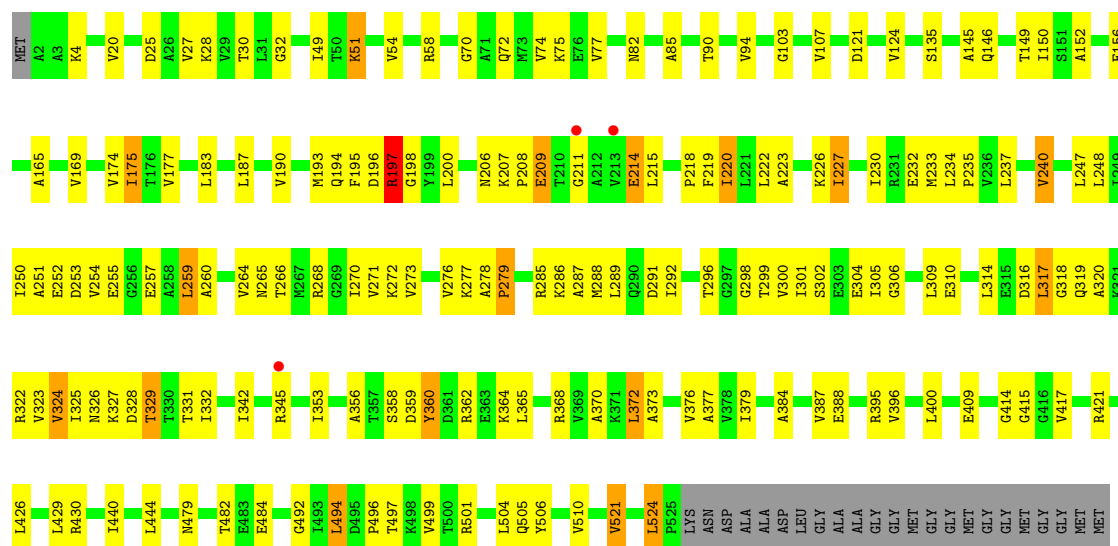
- Molecule 1: 60 kDa chaperonin

Chain E:

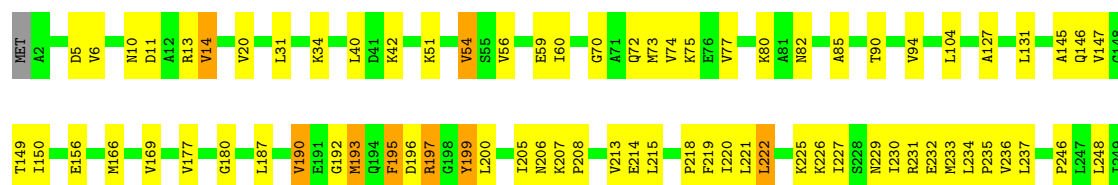




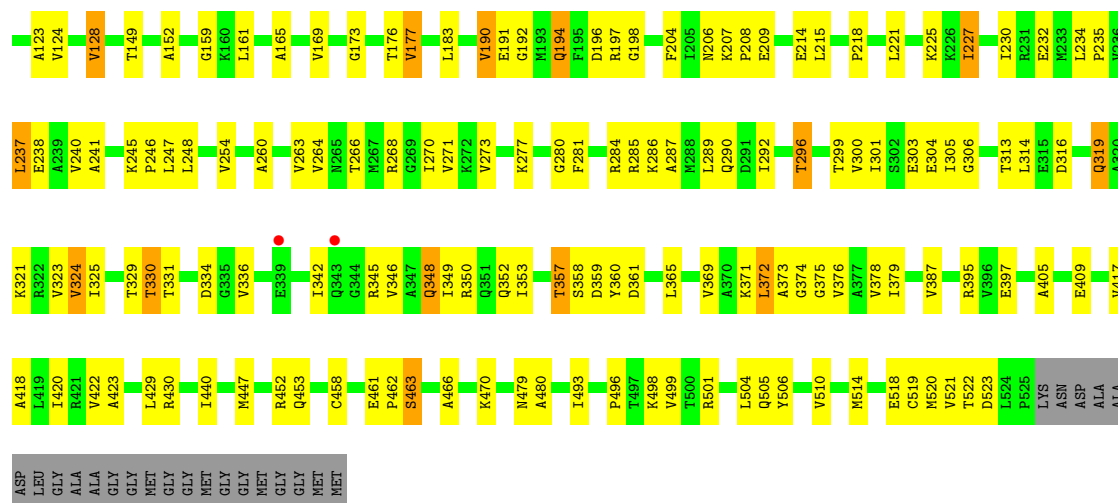
• Molecule 1: 60 kDa chaperonin



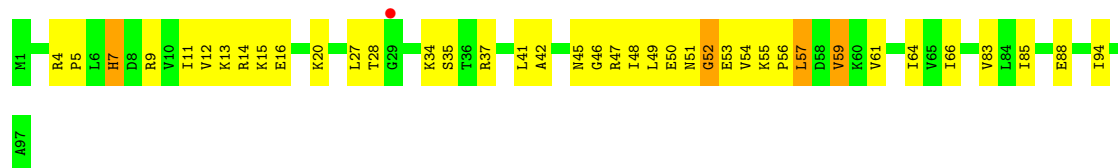
• Molecule 1: 60 kDa chaperonin



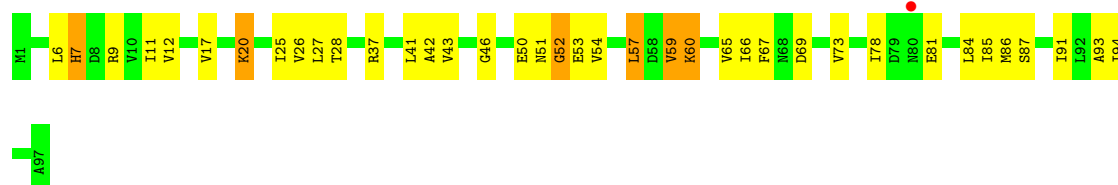




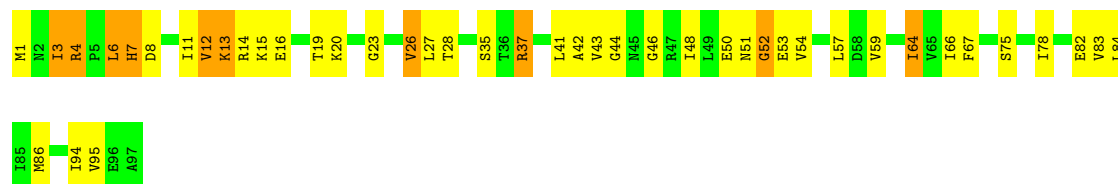
• Molecule 2: 10 kDa chaperonin



• Molecule 2: 10 kDa chaperonin

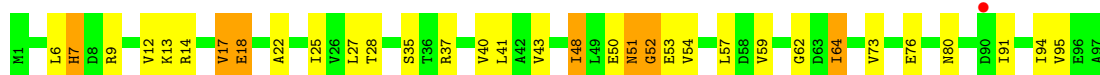


• Molecule 2: 10 kDa chaperonin



• Molecule 2: 10 kDa chaperonin

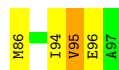




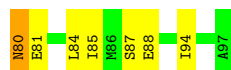
- Molecule 2: 10 kDa chaperonin



- Molecule 2: 10 kDa chaperonin



- Molecule 2: 10 kDa chaperonin

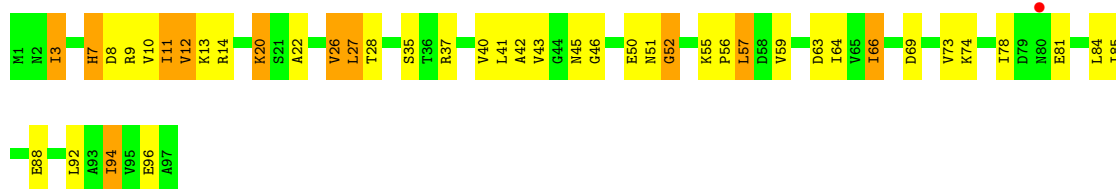


- Molecule 2: 10 kDa chaperonin



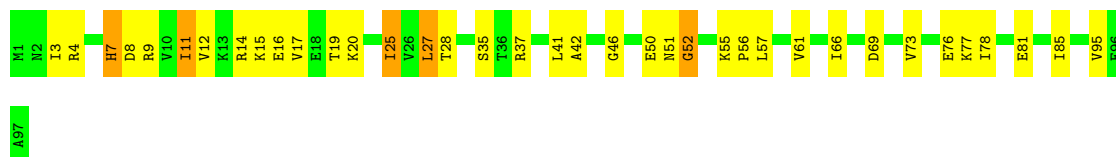
- Molecule 2: 10 kDa chaperonin





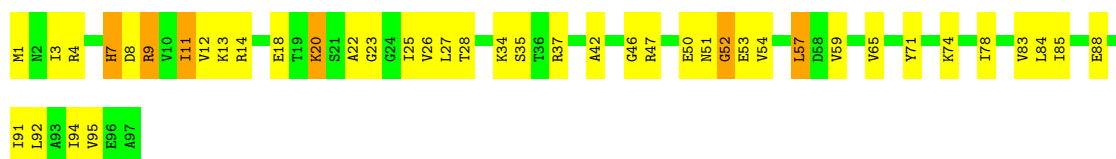
- Molecule 2: 10 kDa chaperonin

Chain X: 62% 33% 5%



- Molecule 2: 10 kDa chaperonin

Chain Y: 56% 38% 6%



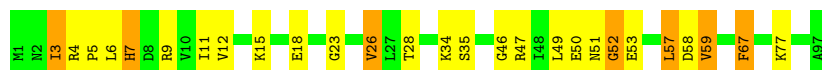
- Molecule 2: 10 kDa chaperonin

Chain Z: 3% 58% 36% 6%



- Molecule 2: 10 kDa chaperonin

Chain a: 72% 21% 7%



- Molecule 2: 10 kDa chaperonin

Chain b: 52% 39% 9%



S87	E88	I91	I94	V95	E96	A97
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	160.28Å 217.12Å 198.48Å 90.00° 98.02° 90.00°	Depositor
Resolution (Å)	49.56 – 3.79 49.56 – 3.79	Depositor EDS
% Data completeness (in resolution range)	91.0 (49.56-3.79) 83.3 (49.56-3.79)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.05 (at 3.77Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1589)	Depositor
R, R_{free}	0.211 , 0.250 0.219 , 0.227	Depositor DCC
R_{free} test set	6142 reflections (4.55%)	wwPDB-VP
Wilson B-factor (Å ²)	111.8	Xtriage
Anisotropy	0.297	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 187.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	64540	wwPDB-VP
Average B, all atoms (Å ²)	175.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 65.58 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.9238e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ATP, K, 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	0.32	0/3877	0.76	0/5235
1	B	0.33	0/3877	0.78	0/5235
1	C	0.34	0/3877	0.78	2/5235 (0.0%)
1	D	0.34	0/3877	0.78	0/5235
1	E	0.34	0/3877	0.76	2/5235 (0.0%)
1	F	0.34	0/3877	0.77	1/5235 (0.0%)
1	G	0.34	0/3877	0.77	2/5235 (0.0%)
1	H	0.33	0/3877	0.77	2/5235 (0.0%)
1	I	0.33	0/3877	0.78	0/5235
1	J	0.33	0/3877	0.77	2/5235 (0.0%)
1	K	0.34	0/3877	0.75	1/5235 (0.0%)
1	L	0.34	0/3877	0.77	0/5235
1	M	0.34	0/3877	0.77	1/5235 (0.0%)
1	N	0.33	0/3877	0.77	1/5235 (0.0%)
2	O	0.24	0/732	0.69	0/983
2	P	0.25	0/732	0.73	0/983
2	Q	0.25	0/732	0.71	0/983
2	R	0.25	0/732	0.70	0/983
2	S	0.24	0/732	0.74	2/983 (0.2%)
2	T	0.24	0/732	0.69	0/983
2	U	0.25	0/732	0.69	1/983 (0.1%)
2	V	0.25	0/732	0.75	3/983 (0.3%)
2	W	0.24	0/732	0.71	0/983
2	X	0.26	0/732	0.73	0/983
2	Y	0.26	0/732	0.68	0/983
2	Z	0.25	0/732	0.66	0/983
2	a	0.24	0/732	0.70	0/983
2	b	0.25	0/732	0.69	0/983
All	All	0.32	0/64526	0.76	20/87052 (0.0%)

There are no bond length outliers.

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	51	LYS	N-CA-C	-5.72	106.28	113.72
2	S	55	LYS	CA-C-N	5.60	125.92	119.92
2	S	55	LYS	C-N-CA	5.60	125.92	119.92
1	C	461	GLU	CA-C-N	5.45	124.80	118.85
1	C	461	GLU	C-N-CA	5.45	124.80	118.85

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3849	0	3978	112	0
1	B	3849	0	3978	112	0
1	C	3849	0	3978	110	0
1	D	3849	0	3977	142	0
1	E	3849	0	3978	115	0
1	F	3849	0	3978	131	0
1	G	3849	0	3978	123	0
1	H	3849	0	3978	109	0
1	I	3849	0	3978	152	0
1	J	3849	0	3978	116	0
1	K	3849	0	3978	132	0
1	L	3849	0	3978	122	0
1	M	3849	0	3978	128	0
1	N	3849	0	3978	127	0
2	O	728	0	762	27	0
2	P	728	0	762	36	0
2	Q	728	0	762	35	0
2	R	728	0	762	25	0
2	S	728	0	762	40	0
2	T	728	0	762	26	0
2	U	728	0	762	45	0
2	V	728	0	762	46	0
2	W	728	0	762	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	X	728	0	762	24	0
2	Y	728	0	762	27	0
2	Z	728	0	762	24	0
2	a	728	0	762	18	0
2	b	728	0	762	36	0
3	A	31	0	12	1	0
3	B	31	0	12	3	0
3	C	31	0	12	0	0
3	D	31	0	12	0	0
3	E	31	0	12	0	0
3	F	31	0	12	1	0
3	G	31	0	12	1	0
3	H	31	0	12	1	0
3	I	31	0	12	4	0
3	J	31	0	12	1	0
3	K	31	0	12	1	0
3	L	31	0	12	2	0
3	M	31	0	12	0	0
3	N	31	0	12	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
4	K	1	0	0	0	0
4	L	1	0	0	0	0
4	M	1	0	0	0	0
4	N	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
5	I	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	J	1	0	0	0	0
5	K	1	0	0	0	0
5	L	1	0	0	0	0
5	M	1	0	0	0	0
5	N	1	0	0	0	0
All	All	64540	0	66527	2021	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 15.

The worst 5 of 2021 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:C:10:ASN:HD21	1:H:10:ASN:HD21	1.11	0.98
1:B:10:ASN:HD21	1:I:10:ASN:HD21	1.11	0.97
1:D:226:LYS:HZ3	1:D:252:GLU:H	1.15	0.90
1:G:10:ASN:HD21	1:K:10:ASN:HD21	1.19	0.90
1:G:77:VAL:HG22	1:G:510:VAL:HG21	1.54	0.90

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	522/548 (95%)	503 (96%)	17 (3%)	2 (0%)	30	61
1	B	522/548 (95%)	504 (97%)	16 (3%)	2 (0%)	30	61
1	C	522/548 (95%)	503 (96%)	15 (3%)	4 (1%)	16	47
1	D	522/548 (95%)	500 (96%)	18 (3%)	4 (1%)	16	47
1	E	522/548 (95%)	500 (96%)	19 (4%)	3 (1%)	21	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	522/548 (95%)	498 (95%)	19 (4%)	5 (1%)	12	42
1	G	522/548 (95%)	500 (96%)	18 (3%)	4 (1%)	16	47
1	H	522/548 (95%)	502 (96%)	17 (3%)	3 (1%)	21	53
1	I	522/548 (95%)	502 (96%)	17 (3%)	3 (1%)	21	53
1	J	522/548 (95%)	497 (95%)	20 (4%)	5 (1%)	12	42
1	K	522/548 (95%)	503 (96%)	16 (3%)	3 (1%)	21	53
1	L	522/548 (95%)	501 (96%)	18 (3%)	3 (1%)	21	53
1	M	522/548 (95%)	501 (96%)	19 (4%)	2 (0%)	30	61
1	N	522/548 (95%)	500 (96%)	18 (3%)	4 (1%)	16	47
2	O	95/97 (98%)	83 (87%)	10 (10%)	2 (2%)	5	30
2	P	95/97 (98%)	84 (88%)	9 (10%)	2 (2%)	5	30
2	Q	95/97 (98%)	83 (87%)	10 (10%)	2 (2%)	5	30
2	R	95/97 (98%)	82 (86%)	10 (10%)	3 (3%)	3	24
2	S	95/97 (98%)	83 (87%)	10 (10%)	2 (2%)	5	30
2	T	95/97 (98%)	81 (85%)	12 (13%)	2 (2%)	5	30
2	U	95/97 (98%)	83 (87%)	9 (10%)	3 (3%)	3	24
2	V	95/97 (98%)	82 (86%)	11 (12%)	2 (2%)	5	30
2	W	95/97 (98%)	83 (87%)	10 (10%)	2 (2%)	5	30
2	X	95/97 (98%)	83 (87%)	10 (10%)	2 (2%)	5	30
2	Y	95/97 (98%)	83 (87%)	10 (10%)	2 (2%)	5	30
2	Z	95/97 (98%)	82 (86%)	10 (10%)	3 (3%)	3	24
2	a	95/97 (98%)	83 (87%)	9 (10%)	3 (3%)	3	24
2	b	95/97 (98%)	83 (87%)	10 (10%)	2 (2%)	5	30
All	All	8638/9030 (96%)	8172 (95%)	387 (4%)	79 (1%)	14	44

5 of 79 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	358	SER
1	C	193	MET
1	C	356	ALA
1	D	360	TYR
1	G	193	MET

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	402/413 (97%)	387 (96%)	15 (4%)	30	53
1	B	402/413 (97%)	377 (94%)	25 (6%)	16	42
1	C	402/413 (97%)	373 (93%)	29 (7%)	13	39
1	D	402/413 (97%)	369 (92%)	33 (8%)	10	34
1	E	402/413 (97%)	368 (92%)	34 (8%)	10	33
1	F	402/413 (97%)	380 (94%)	22 (6%)	19	45
1	G	402/413 (97%)	383 (95%)	19 (5%)	23	47
1	H	402/413 (97%)	381 (95%)	21 (5%)	21	45
1	I	402/413 (97%)	372 (92%)	30 (8%)	12	38
1	J	402/413 (97%)	372 (92%)	30 (8%)	12	38
1	K	402/413 (97%)	367 (91%)	35 (9%)	9	33
1	L	402/413 (97%)	366 (91%)	36 (9%)	9	32
1	M	402/413 (97%)	376 (94%)	26 (6%)	15	41
1	N	402/413 (97%)	374 (93%)	28 (7%)	14	39
2	O	80/80 (100%)	73 (91%)	7 (9%)	9	33
2	P	80/80 (100%)	72 (90%)	8 (10%)	7	28
2	Q	80/80 (100%)	68 (85%)	12 (15%)	3	16
2	R	80/80 (100%)	71 (89%)	9 (11%)	5	23
2	S	80/80 (100%)	70 (88%)	10 (12%)	4	20
2	T	80/80 (100%)	65 (81%)	15 (19%)	1	10
2	U	80/80 (100%)	66 (82%)	14 (18%)	2	12
2	V	80/80 (100%)	65 (81%)	15 (19%)	1	10
2	W	80/80 (100%)	67 (84%)	13 (16%)	2	14
2	X	80/80 (100%)	68 (85%)	12 (15%)	3	16
2	Y	80/80 (100%)	66 (82%)	14 (18%)	2	12
2	Z	80/80 (100%)	69 (86%)	11 (14%)	3	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	a	80/80 (100%)	73 (91%)	7 (9%)	9	33
2	b	80/80 (100%)	68 (85%)	12 (15%)	3	16
All	All	6748/6902 (98%)	6206 (92%)	542 (8%)	11	36

5 of 542 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	V	25	ILE
2	W	12	VAL
2	V	16	GLU
2	Z	61	VAL
1	H	387	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	10	ASN
1	N	319	GLN
1	L	194	GLN
1	L	505	GLN
2	Q	80	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 42 ligands modelled in this entry, 28 are monoatomic - leaving 14 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	ATP	I	601	5,4	32,33,33	1.38	4 (12%)	48,52,52	1.76	9 (18%)
3	ATP	J	601	5,4	32,33,33	1.41	4 (12%)	48,52,52	1.76	9 (18%)
3	ATP	L	601	5,4	32,33,33	1.36	4 (12%)	48,52,52	1.78	10 (20%)
3	ATP	C	601	5,4	32,33,33	1.42	4 (12%)	48,52,52	1.72	9 (18%)
3	ATP	M	601	5,4	32,33,33	1.40	4 (12%)	48,52,52	1.76	10 (20%)
3	ATP	F	601	5,4	32,33,33	1.40	5 (15%)	48,52,52	1.72	9 (18%)
3	ATP	N	601	5,4	32,33,33	1.41	4 (12%)	48,52,52	1.72	9 (18%)
3	ATP	G	601	5,4	32,33,33	1.39	5 (15%)	48,52,52	1.75	10 (20%)
3	ATP	A	601	5,4	32,33,33	1.41	5 (15%)	48,52,52	1.73	9 (18%)
3	ATP	B	601	5,4	32,33,33	1.44	6 (18%)	48,52,52	1.75	8 (16%)
3	ATP	H	601	5,4	32,33,33	1.45	6 (18%)	48,52,52	1.71	7 (14%)
3	ATP	K	601	5,4	32,33,33	1.37	4 (12%)	48,52,52	1.76	10 (20%)
3	ATP	E	601	5,4	32,33,33	1.38	4 (12%)	48,52,52	1.77	9 (18%)
3	ATP	D	601	5,4	32,33,33	1.38	4 (12%)	48,52,52	1.78	9 (18%)

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	ATP	I	601	5,4	-	2/22/38/38	0/3/3/3
3	ATP	J	601	5,4	-	3/22/38/38	0/3/3/3
3	ATP	L	601	5,4	-	4/22/38/38	0/3/3/3
3	ATP	C	601	5,4	-	3/22/38/38	0/3/3/3
3	ATP	M	601	5,4	-	3/22/38/38	0/3/3/3
3	ATP	F	601	5,4	-	2/22/38/38	0/3/3/3
3	ATP	N	601	5,4	-	0/22/38/38	0/3/3/3
3	ATP	G	601	5,4	-	4/22/38/38	0/3/3/3
3	ATP	A	601	5,4	-	3/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ATP	B	601	5,4	-	2/22/38/38	0/3/3/3
3	ATP	H	601	5,4	-	2/22/38/38	0/3/3/3
3	ATP	K	601	5,4	-	4/22/38/38	0/3/3/3
3	ATP	E	601	5,4	-	4/22/38/38	0/3/3/3
3	ATP	D	601	5,4	-	3/22/38/38	0/3/3/3

The worst 5 of 63 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	601	ATP	C5-C4	4.85	1.47	1.39
3	I	601	ATP	C5-C4	4.76	1.47	1.39
3	B	601	ATP	C5-C4	4.74	1.47	1.39
3	C	601	ATP	C5-C4	4.74	1.47	1.39
3	A	601	ATP	C5-C4	4.71	1.47	1.39

The worst 5 of 127 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	601	ATP	C5-C4-N3	-5.88	118.62	126.72
3	H	601	ATP	C5-C4-N3	-5.81	118.71	126.72
3	K	601	ATP	C5-C4-N3	-5.81	118.71	126.72
3	E	601	ATP	C5-C4-N3	-5.76	118.78	126.72
3	I	601	ATP	C5-C4-N3	-5.76	118.79	126.72

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	ATP	PB-O3B-PG-O3G
3	B	601	ATP	PB-O3B-PG-O3G
3	C	601	ATP	PB-O3B-PG-O2G
3	C	601	ATP	PB-O3B-PG-O3G
3	D	601	ATP	C5'-O5'-PA-O2A

There are no ring outliers.

9 monomers are involved in 15 short contacts:

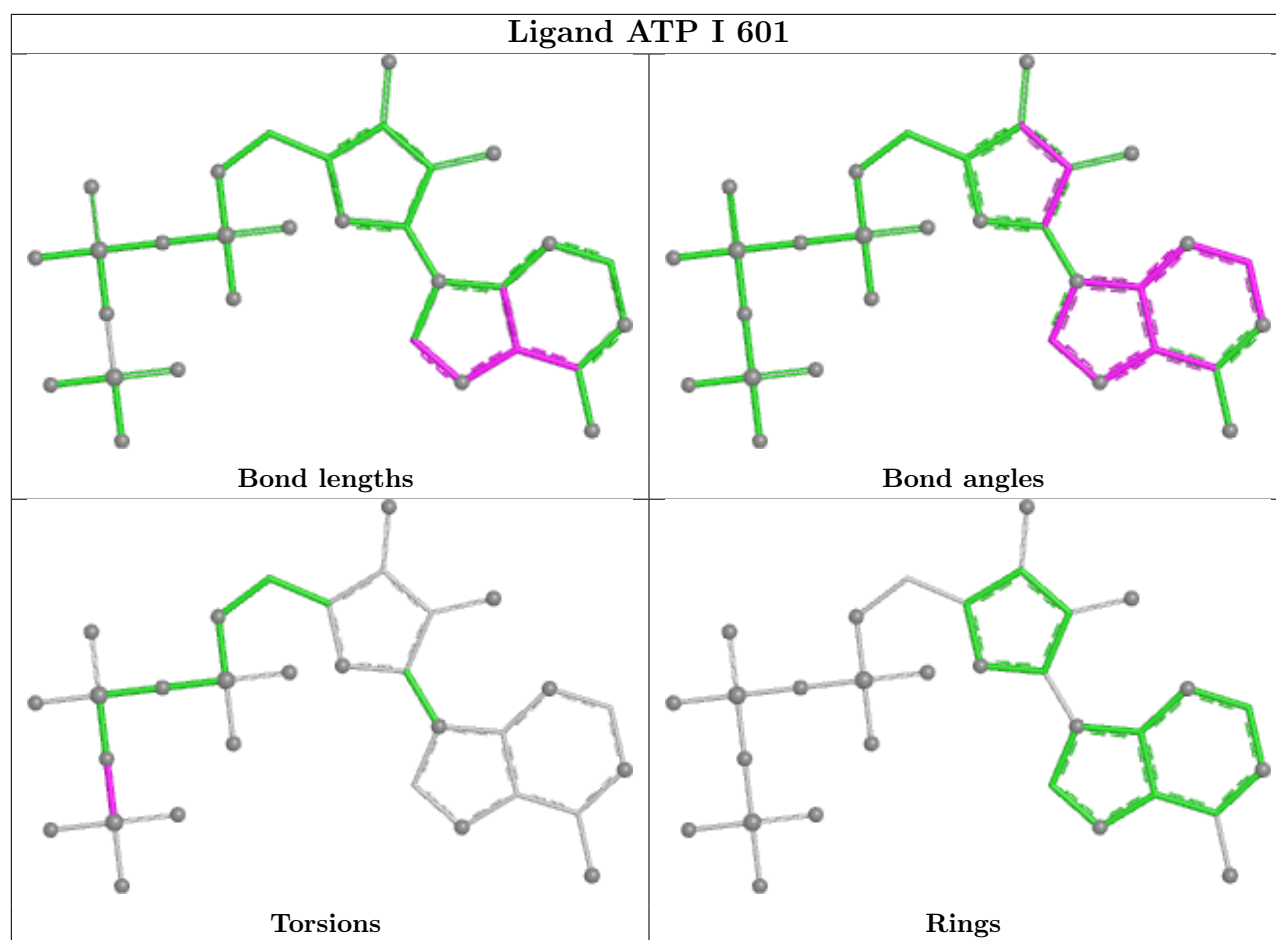
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	601	ATP	4	0
3	J	601	ATP	1	0

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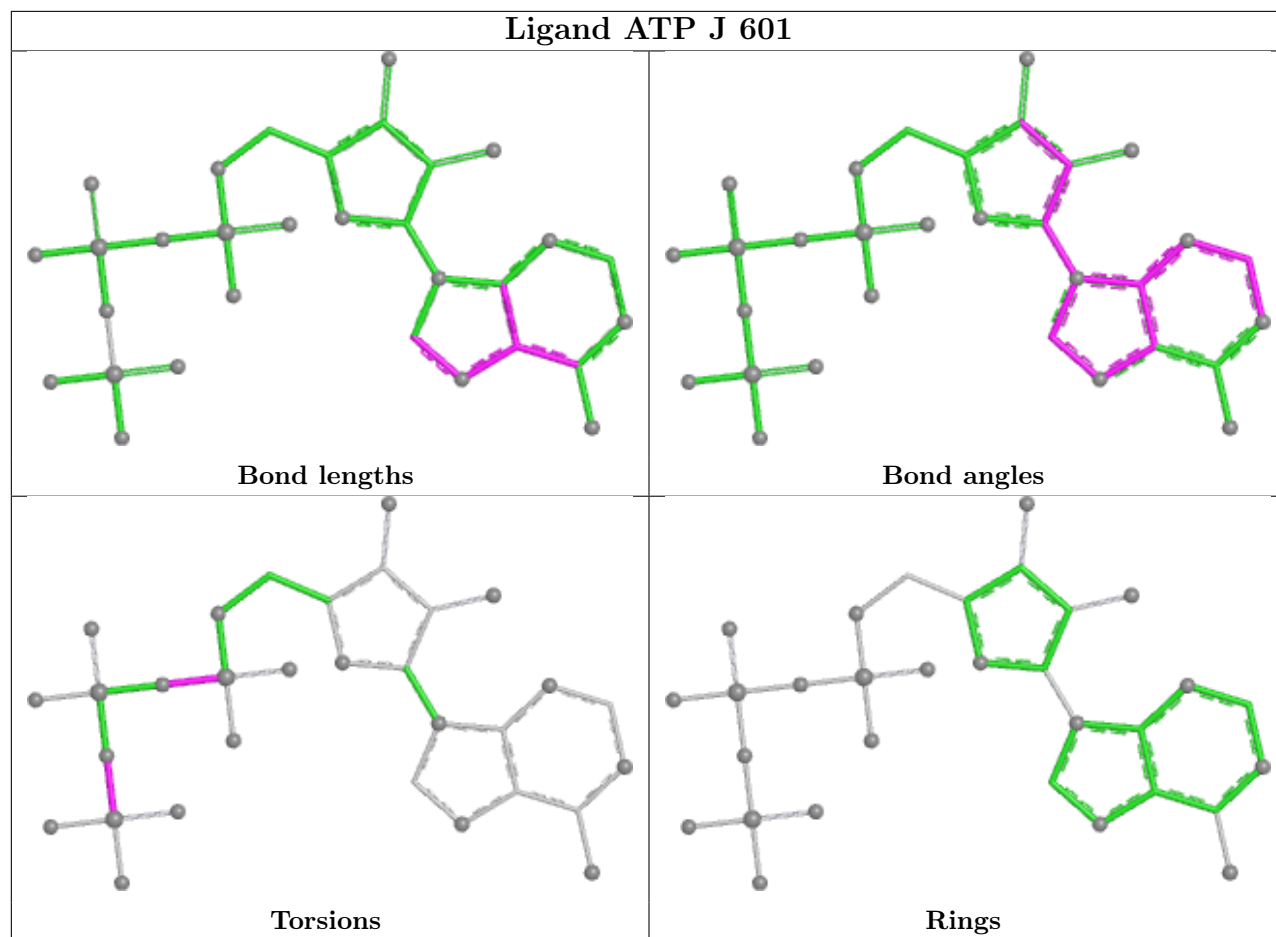
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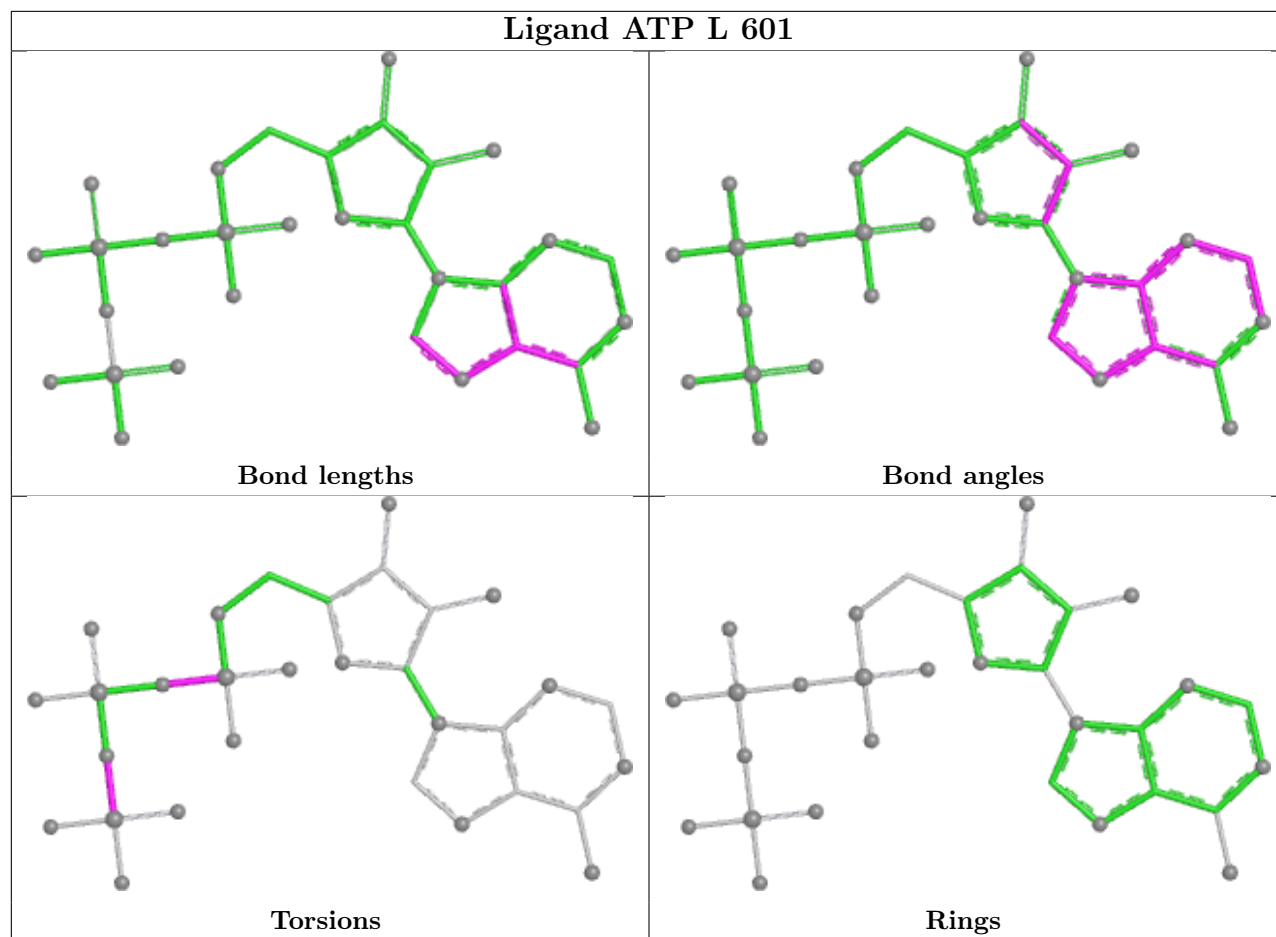
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	601	ATP	2	0
3	F	601	ATP	1	0
3	G	601	ATP	1	0
3	A	601	ATP	1	0
3	B	601	ATP	3	0
3	H	601	ATP	1	0
3	K	601	ATP	1	0

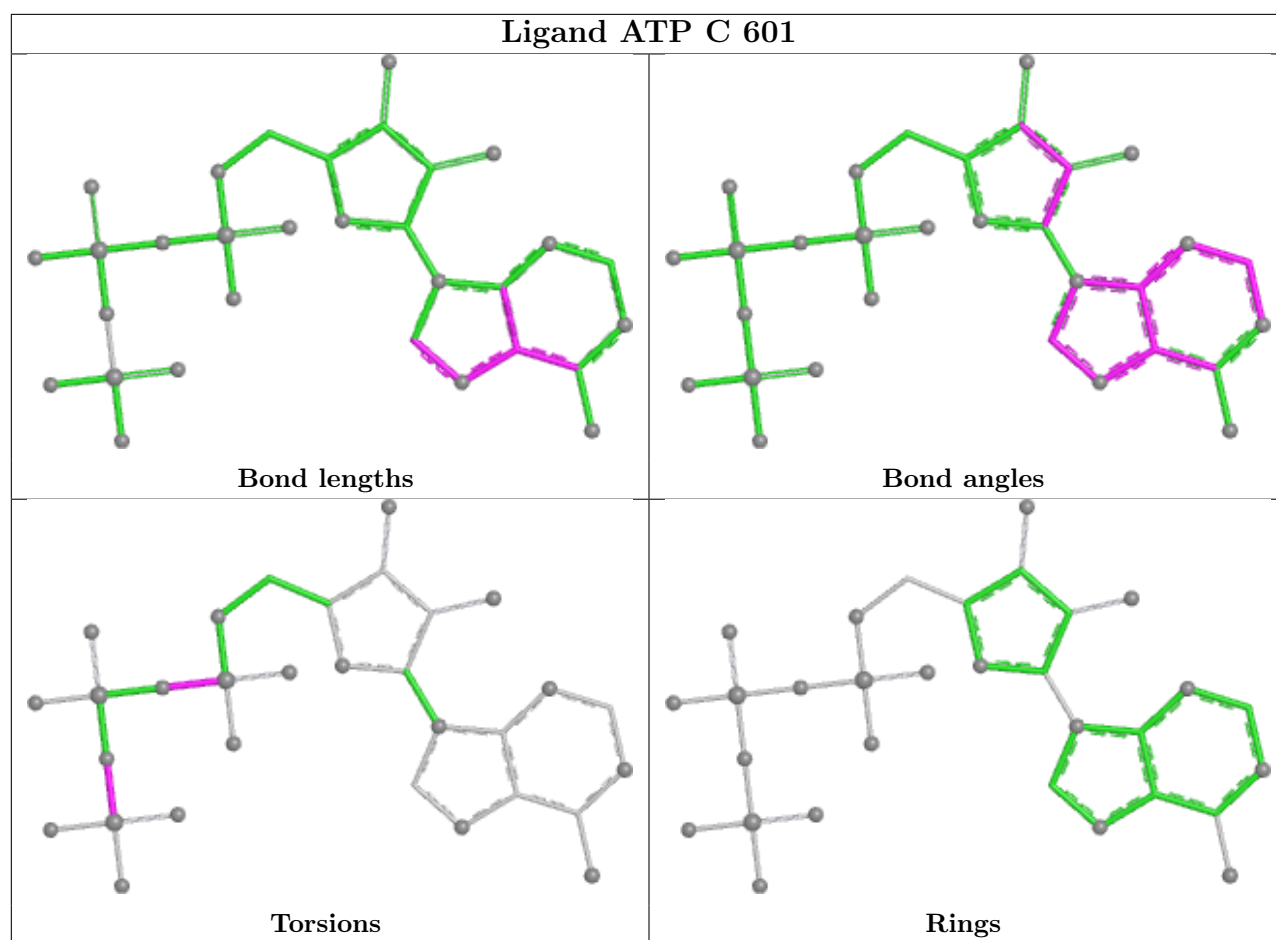
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

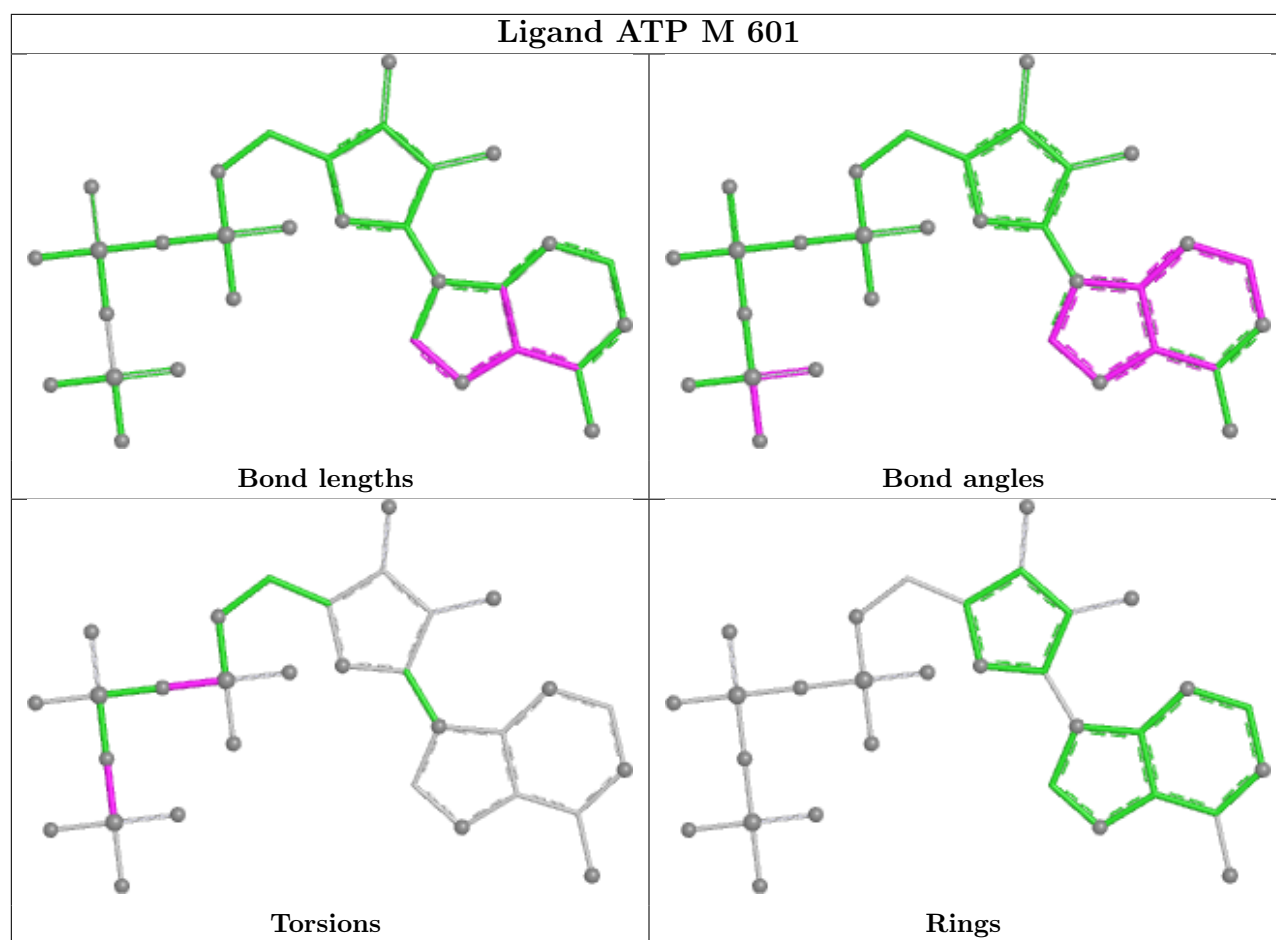


Ligand ATP J 601

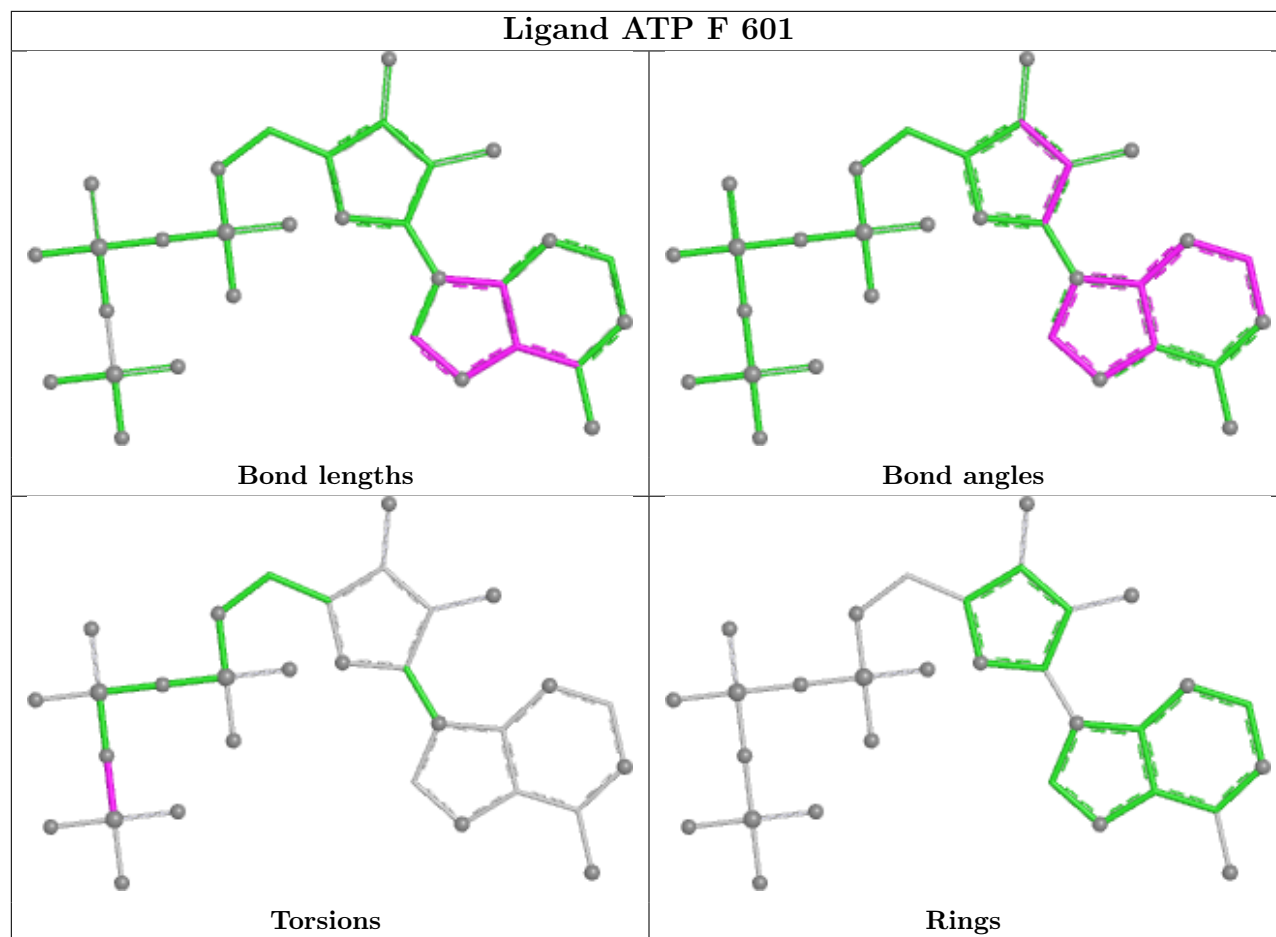


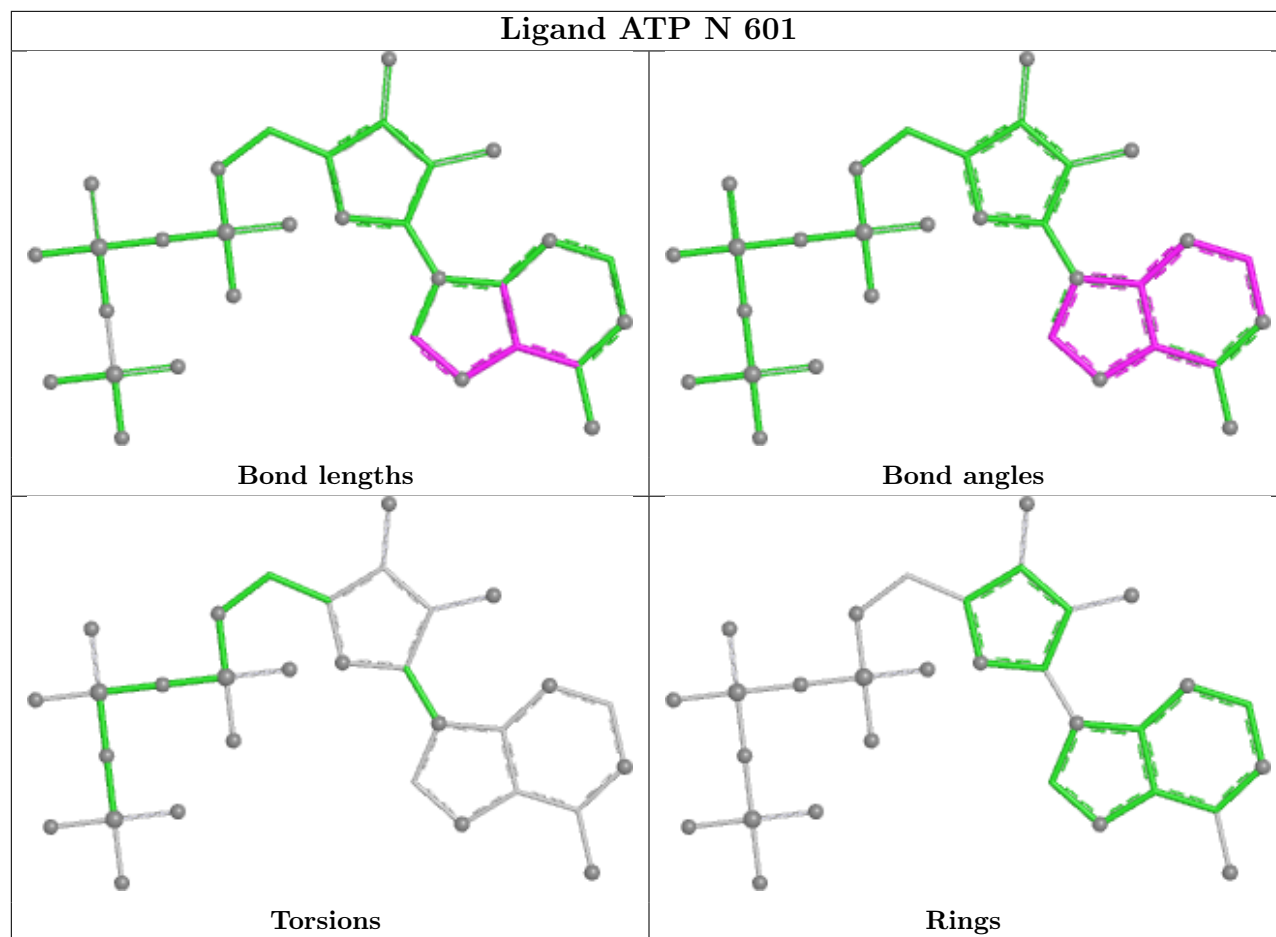


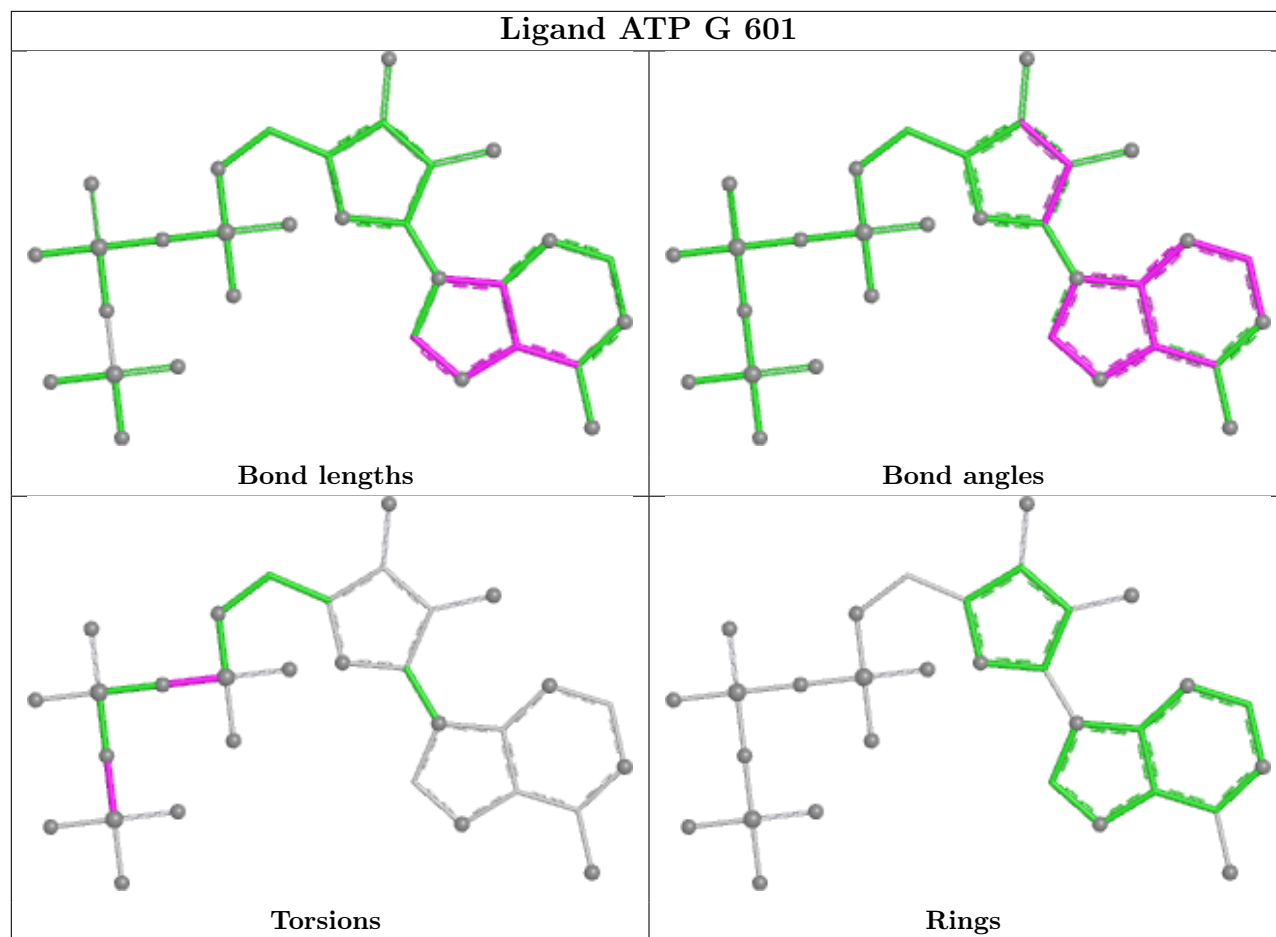


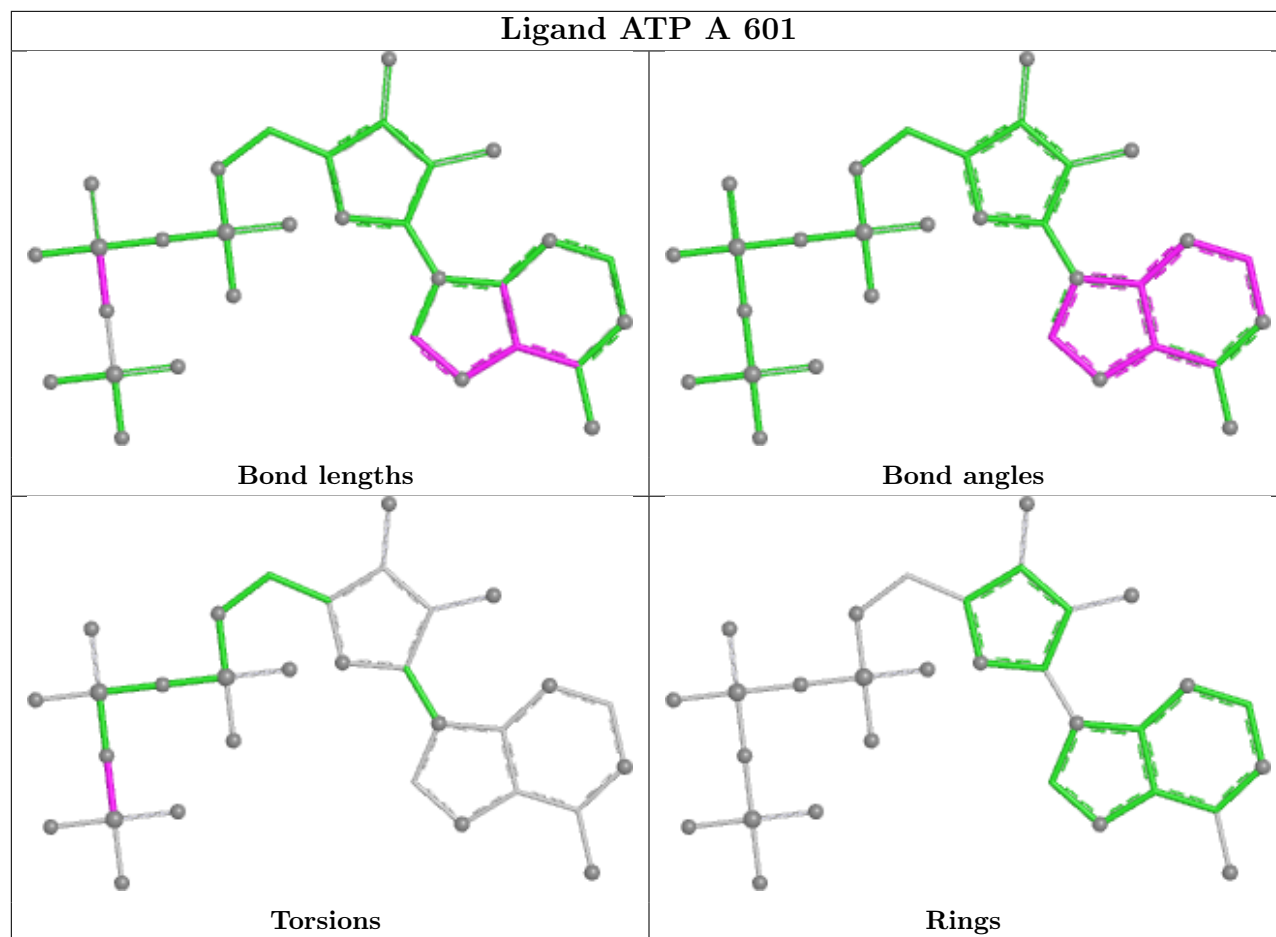


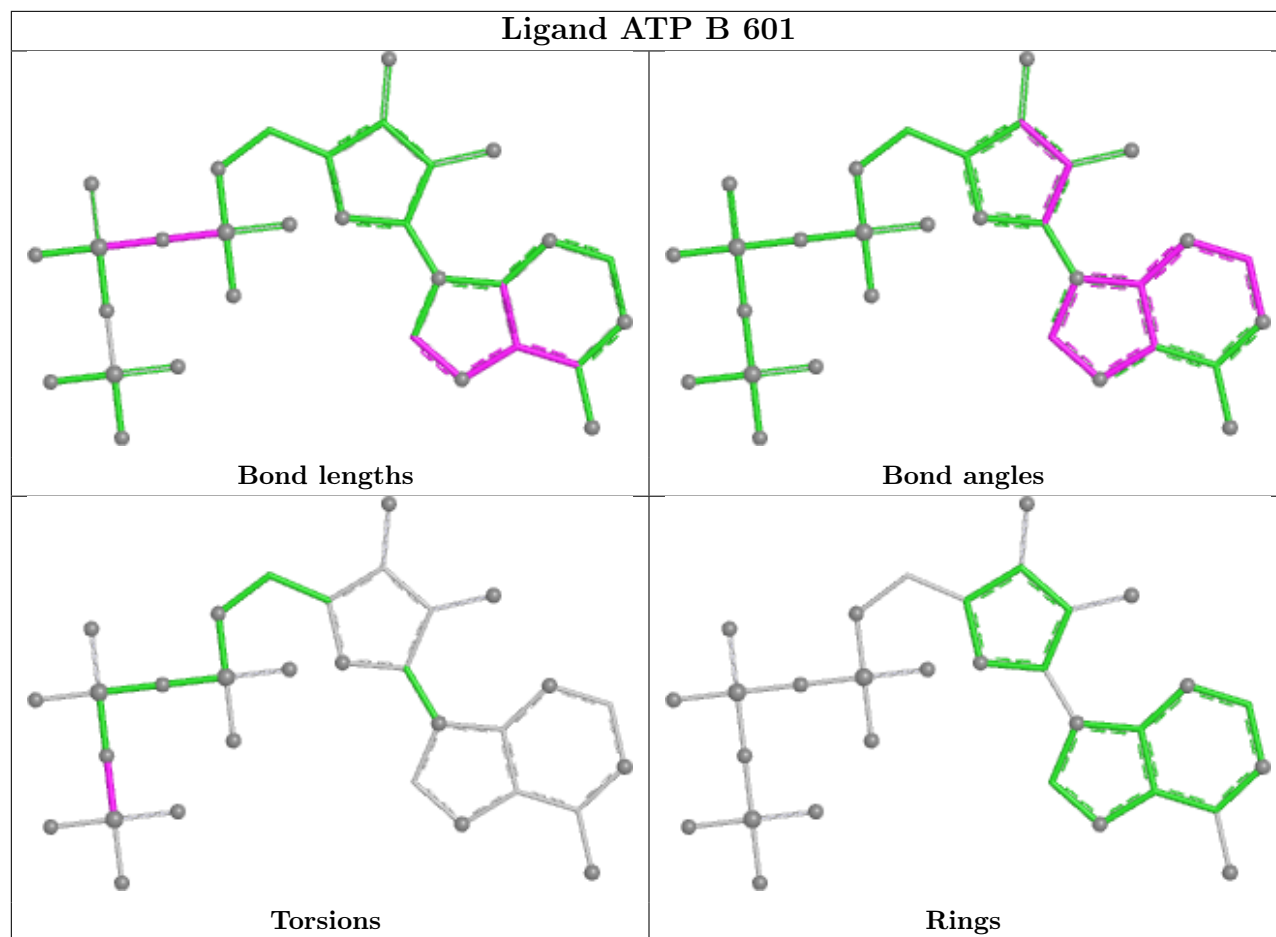
Ligand ATP F 601

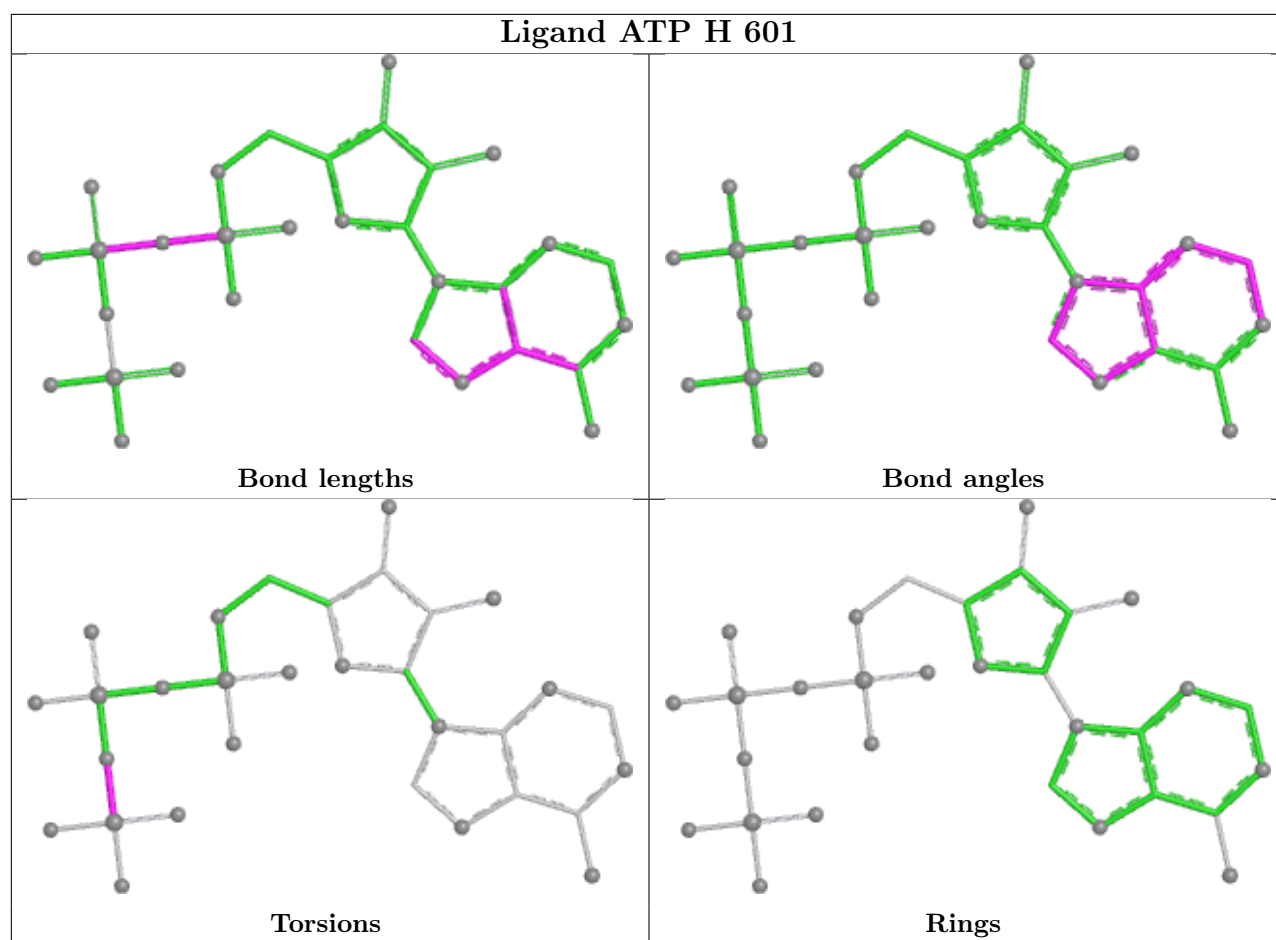


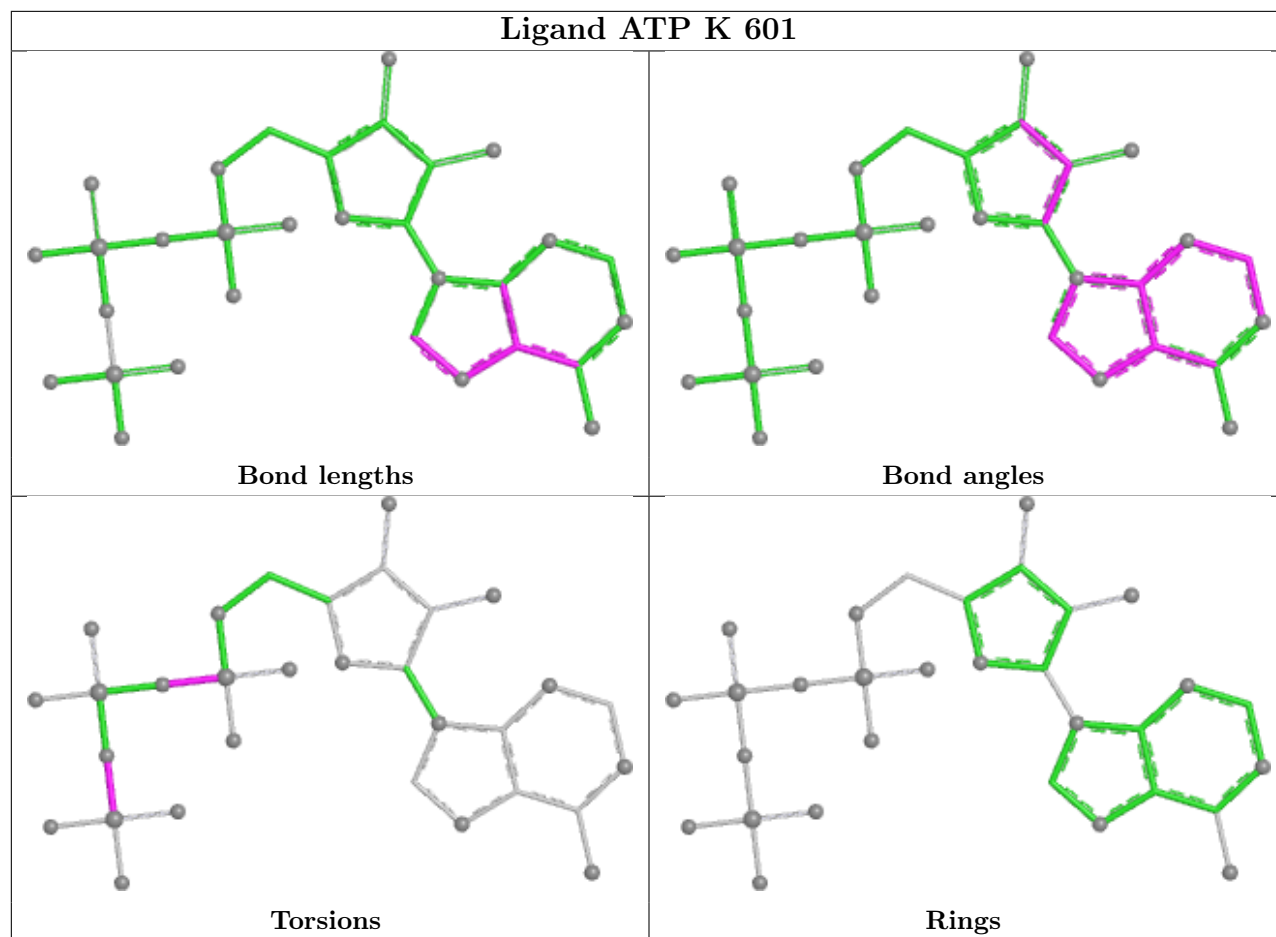


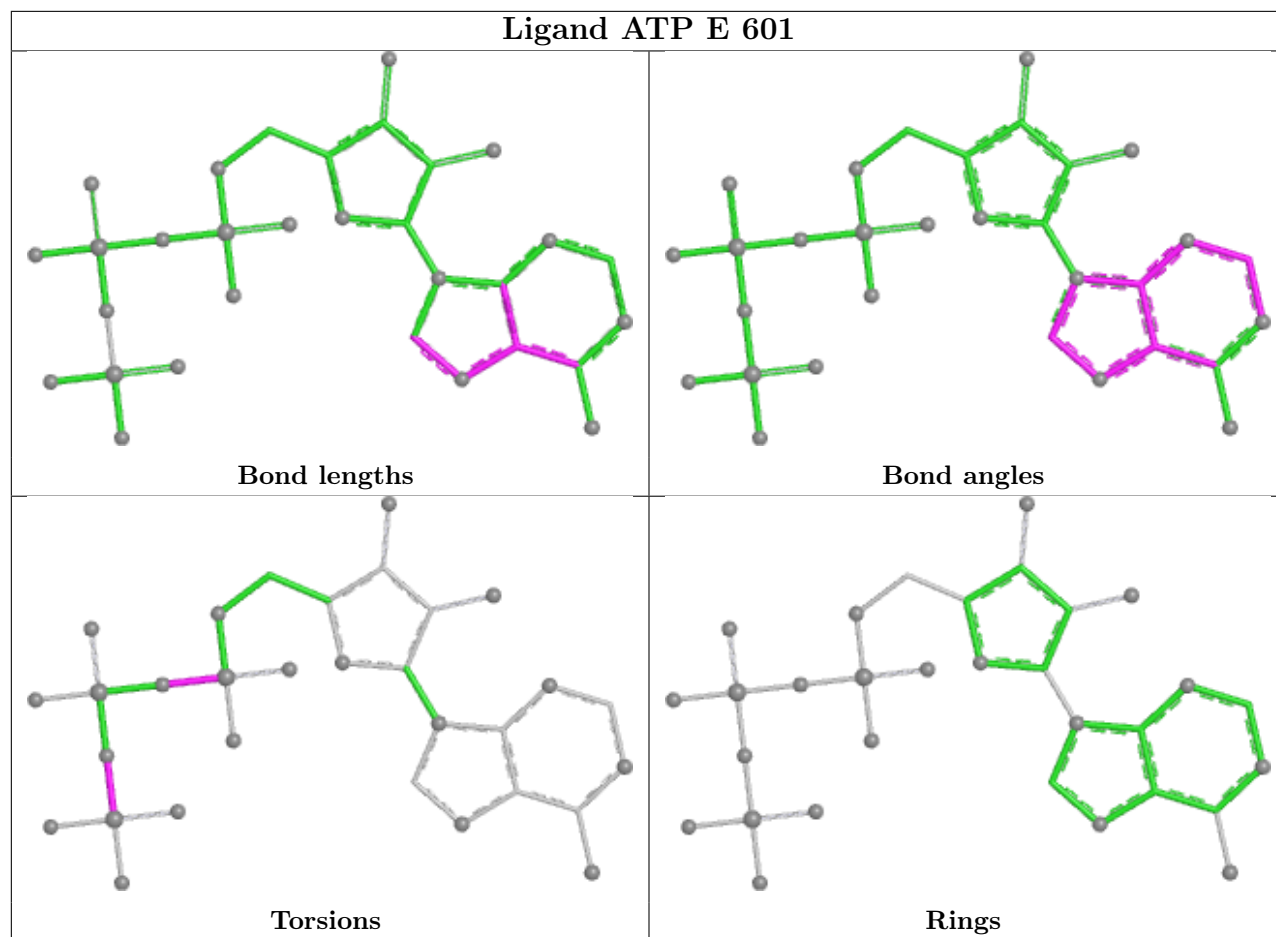


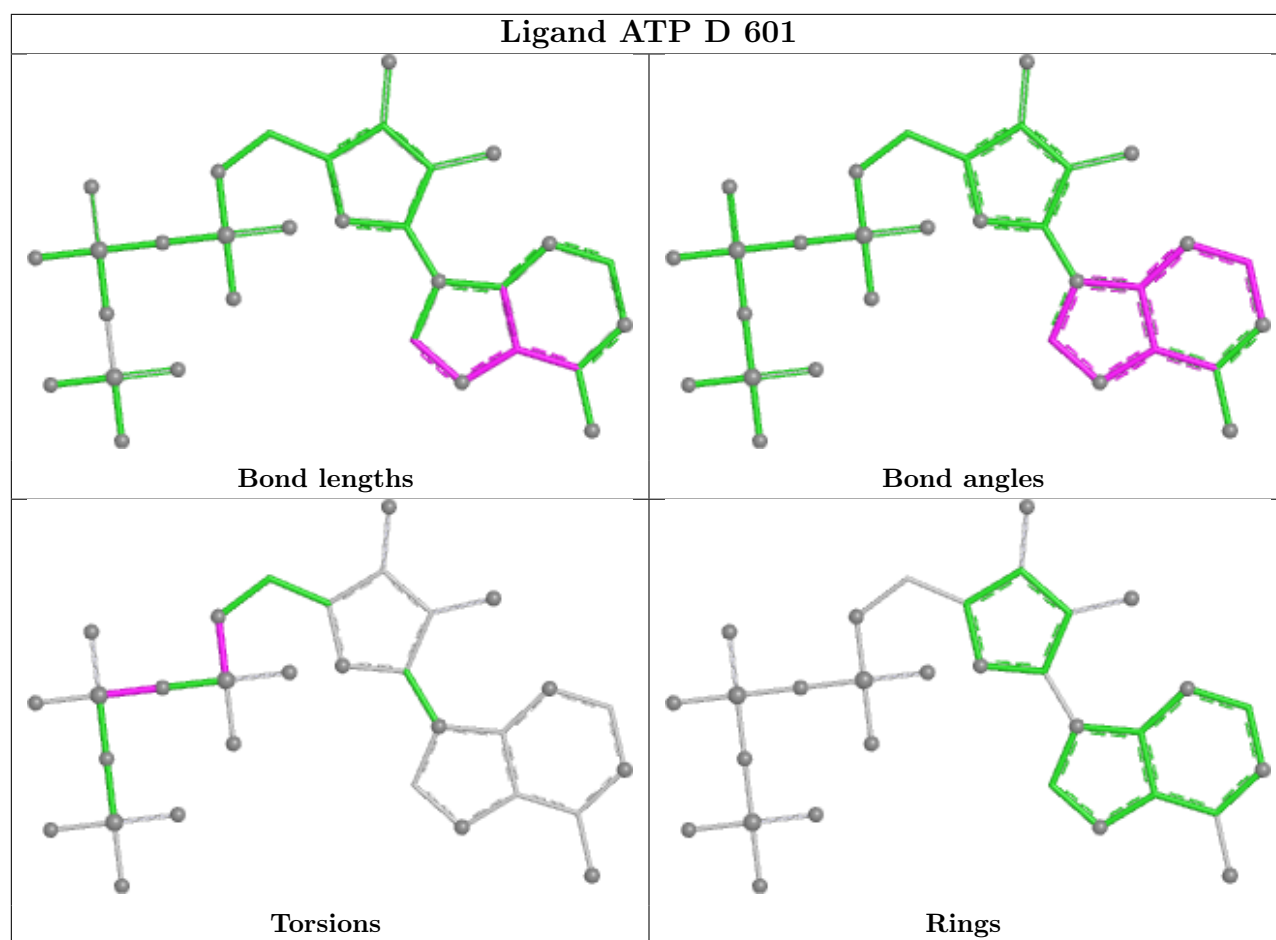












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 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	524/548 (95%)	-0.31	0 100 100	68, 134, 281, 335	0
1	B	524/548 (95%)	-0.26	1 (0%) 91 81	71, 134, 286, 336	0
1	C	524/548 (95%)	-0.22	2 (0%) 88 73	65, 132, 275, 331	0
1	D	524/548 (95%)	-0.13	9 (1%) 69 46	68, 130, 277, 327	0
1	E	524/548 (95%)	-0.17	2 (0%) 88 73	65, 133, 275, 330	0
1	F	524/548 (95%)	-0.24	3 (0%) 85 67	67, 133, 274, 324	0
1	G	524/548 (95%)	-0.26	2 (0%) 88 73	68, 135, 282, 344	0
1	H	524/548 (95%)	-0.32	2 (0%) 88 73	64, 134, 288, 342	0
1	I	524/548 (95%)	-0.26	1 (0%) 91 81	66, 135, 292, 349	0
1	J	524/548 (95%)	-0.28	0 100 100	66, 132, 274, 332	0
1	K	524/548 (95%)	-0.18	1 (0%) 91 81	64, 130, 275, 326	0
1	L	524/548 (95%)	-0.13	5 (0%) 79 57	69, 132, 276, 328	0
1	M	524/548 (95%)	-0.24	1 (0%) 91 81	63, 134, 276, 334	0
1	N	524/548 (95%)	-0.24	2 (0%) 88 73	73, 132, 297, 355	0
2	O	97/97 (100%)	-0.09	1 (1%) 79 57	183, 233, 312, 338	0
2	P	97/97 (100%)	-0.14	1 (1%) 79 57	189, 233, 313, 346	0
2	Q	97/97 (100%)	-0.12	0 100 100	194, 240, 324, 352	0
2	R	97/97 (100%)	-0.06	1 (1%) 79 57	205, 243, 313, 341	0
2	S	97/97 (100%)	0.15	0 100 100	207, 246, 314, 354	0
2	T	97/97 (100%)	0.03	0 100 100	205, 244, 315, 346	0
2	U	97/97 (100%)	-0.13	0 100 100	188, 234, 314, 348	0
2	V	97/97 (100%)	-0.12	1 (1%) 79 57	190, 236, 312, 348	0
2	W	97/97 (100%)	-0.07	1 (1%) 79 57	195, 237, 315, 347	0
2	X	97/97 (100%)	-0.10	0 100 100	186, 232, 316, 346	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
2	Y	97/97 (100%)	-0.03	0 100 100	191, 232, 313, 344	0
2	Z	97/97 (100%)	0.18	3 (3%) 51 34	197, 236, 316, 354	0
2	a	97/97 (100%)	-0.09	0 100 100	189, 233, 316, 342	0
2	b	97/97 (100%)	-0.13	0 100 100	193, 237, 315, 344	0
All	All	8694/9030 (96%)	-0.20	39 (0%) 88 73	63, 157, 291, 355	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	W	80	ASN	3.3
1	D	505	GLN	3.3
1	D	508	ALA	3.2
2	P	80	ASN	3.2
1	L	124	VAL	3.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	K	L	603	1/1	0.71	0.15	185,185,185,185	0
5	K	J	603	1/1	0.80	0.14	251,251,251,251	0
5	K	A	603	1/1	0.82	0.13	200,200,200,200	0
5	K	E	603	1/1	0.83	0.13	140,140,140,140	0
5	K	C	603	1/1	0.86	0.22	291,291,291,291	0
5	K	M	603	1/1	0.86	0.13	192,192,192,192	0
4	MG	A	602	1/1	0.87	0.14	76,76,76,76	0

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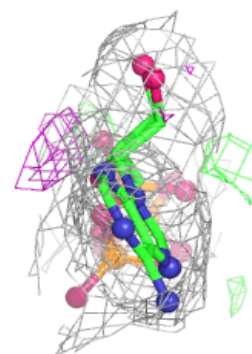
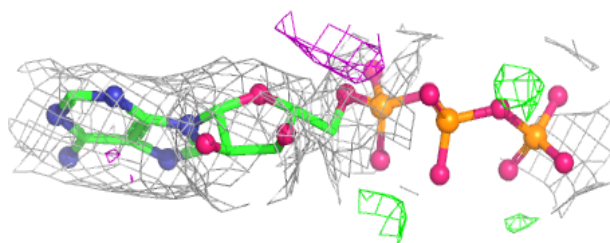
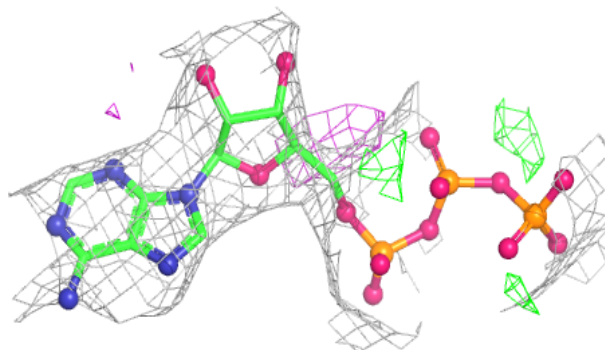
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	K	I	603	1/1	0.88	0.12	138,138,138,138	0
5	K	G	603	1/1	0.88	0.10	197,197,197,197	0
5	K	D	603	1/1	0.89	0.13	139,139,139,139	0
5	K	B	603	1/1	0.90	0.10	200,200,200,200	0
5	K	K	603	1/1	0.90	0.09	149,149,149,149	0
5	K	F	603	1/1	0.91	0.10	132,132,132,132	0
4	MG	J	602	1/1	0.92	0.08	112,112,112,112	0
5	K	N	603	1/1	0.92	0.14	165,165,165,165	0
4	MG	I	602	1/1	0.94	0.06	106,106,106,106	0
4	MG	G	602	1/1	0.95	0.09	88,88,88,88	0
4	MG	N	602	1/1	0.95	0.11	103,103,103,103	0
3	ATP	B	601	31/31	0.95	0.08	70,113,189,206	0
3	ATP	N	601	31/31	0.96	0.08	75,110,162,207	0
4	MG	K	602	1/1	0.96	0.08	71,71,71,71	0
4	MG	H	602	1/1	0.96	0.08	74,74,74,74	0
3	ATP	K	601	31/31	0.96	0.07	55,109,148,207	0
4	MG	E	602	1/1	0.97	0.11	94,94,94,94	0
3	ATP	E	601	31/31	0.97	0.08	61,95,148,174	0
3	ATP	G	601	31/31	0.97	0.07	68,99,162,188	0
3	ATP	H	601	31/31	0.97	0.07	67,95,170,203	0
3	ATP	I	601	31/31	0.97	0.07	58,120,159,197	0
3	ATP	J	601	31/31	0.97	0.07	76,112,176,190	0
3	ATP	A	601	31/31	0.97	0.07	74,112,169,195	0
3	ATP	L	601	31/31	0.97	0.06	66,97,157,198	0
3	ATP	C	601	31/31	0.97	0.08	65,116,176,192	0
3	ATP	D	601	31/31	0.97	0.07	67,95,205,263	0
4	MG	C	602	1/1	0.98	0.09	71,71,71,71	0
3	ATP	F	601	31/31	0.98	0.06	76,101,160,203	0
4	MG	M	602	1/1	0.98	0.04	81,81,81,81	0
5	K	H	603	1/1	0.98	0.04	168,168,168,168	0
4	MG	F	602	1/1	0.98	0.07	77,77,77,77	0
3	ATP	M	601	31/31	0.99	0.05	71,98,158,206	0
4	MG	D	602	1/1	0.99	0.03	87,87,87,87	0
4	MG	B	602	1/1	0.99	0.08	68,68,68,68	0
4	MG	L	602	1/1	0.99	0.04	87,87,87,87	0

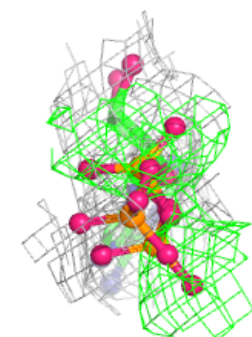
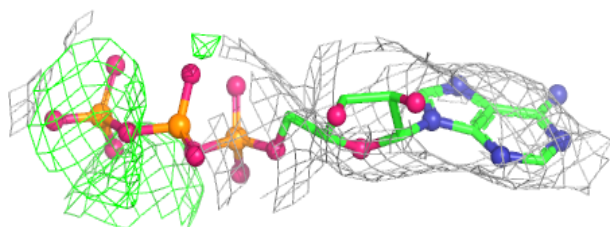
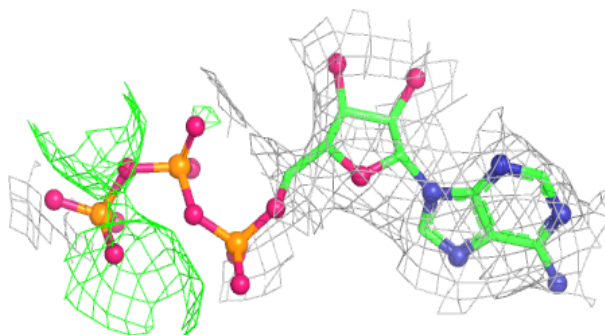
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ATP B 601:

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

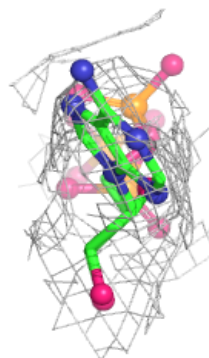
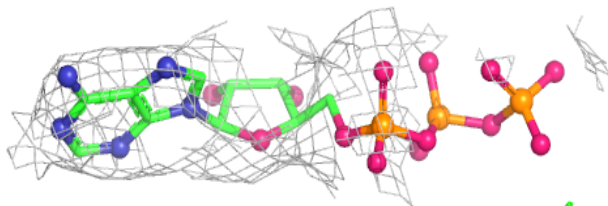
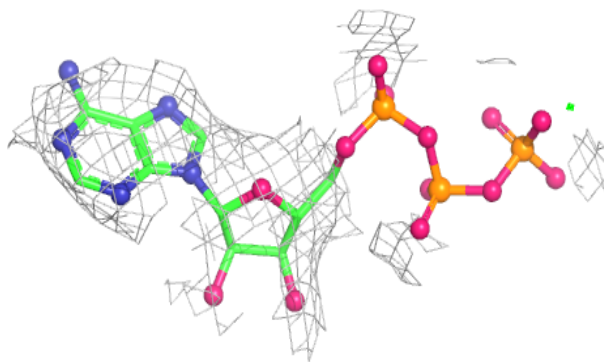
**Electron density around ATP N 601:**

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

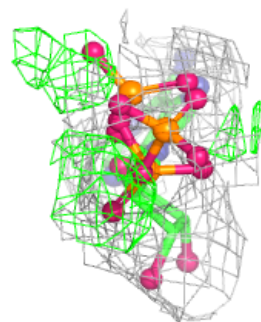
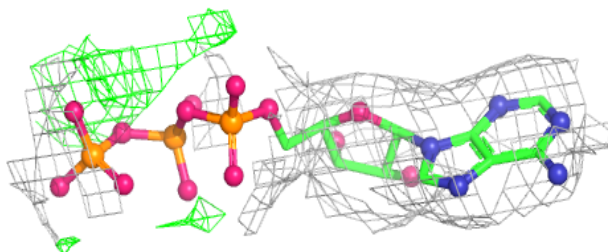
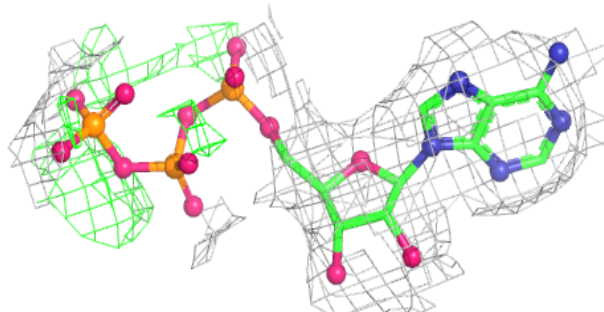


Electron density around ATP K 601:

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

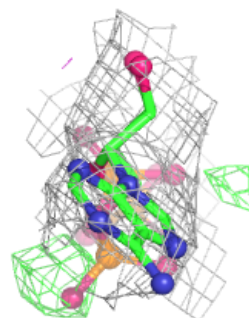
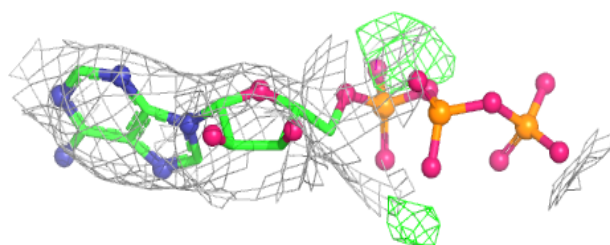
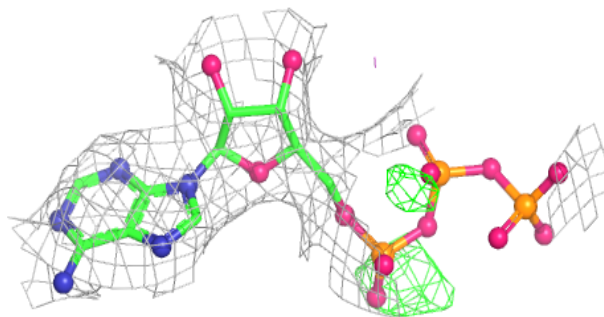
**Electron density around ATP E 601:**

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and green (positive)

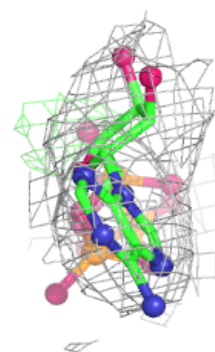
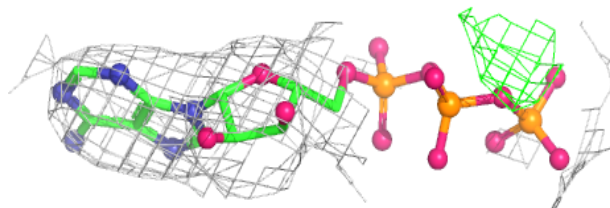
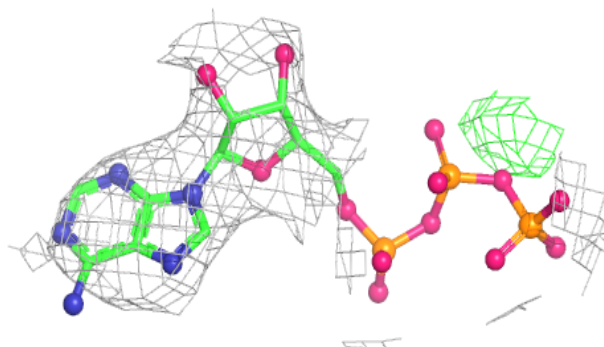


Electron density around ATP G 601:

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

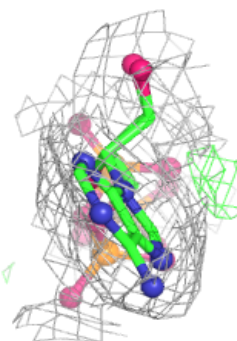
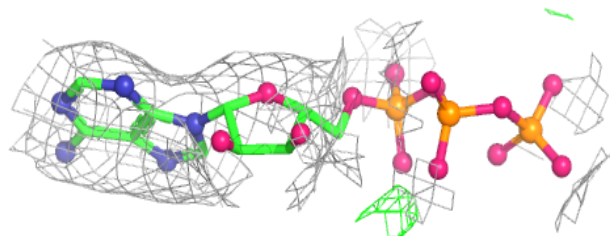
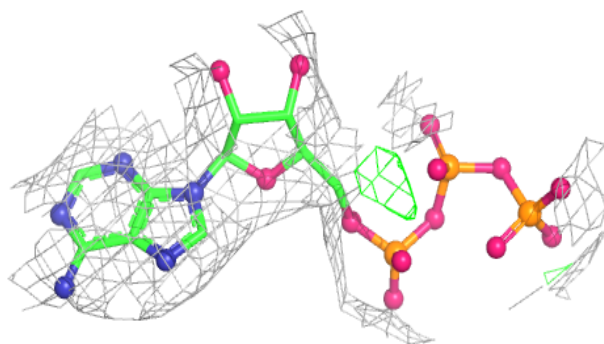
**Electron density around ATP H 601:**

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and green (positive)

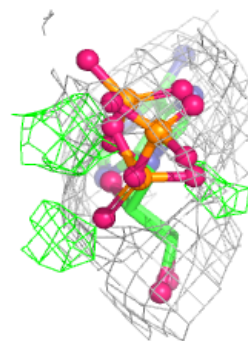
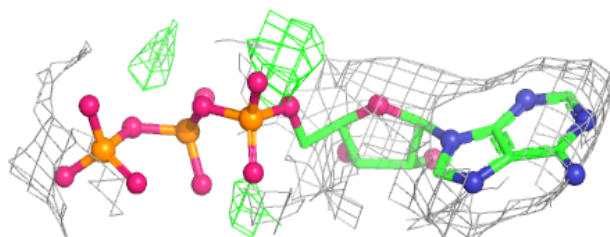
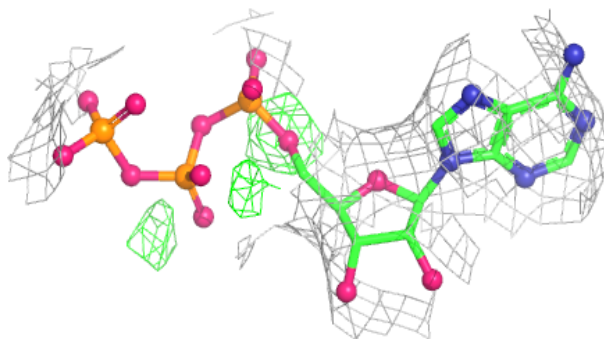


Electron density around ATP I 601:

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

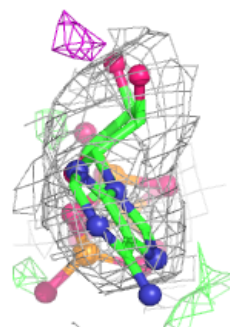
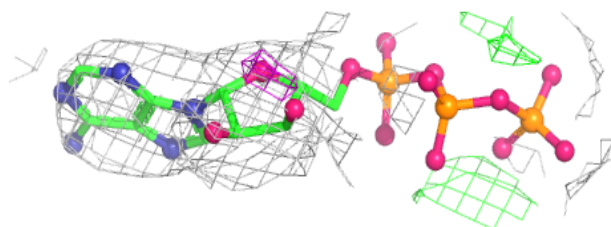
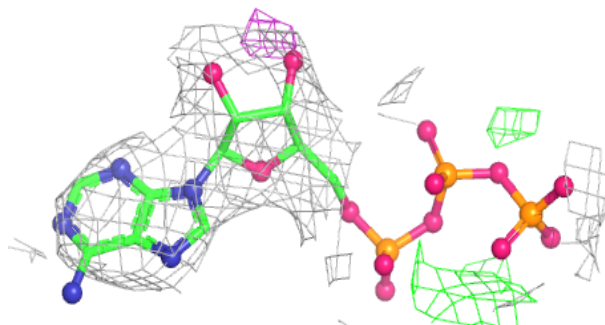
**Electron density around ATP J 601:**

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and green (positive)

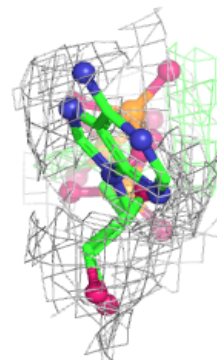
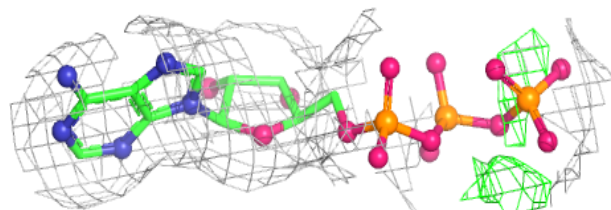
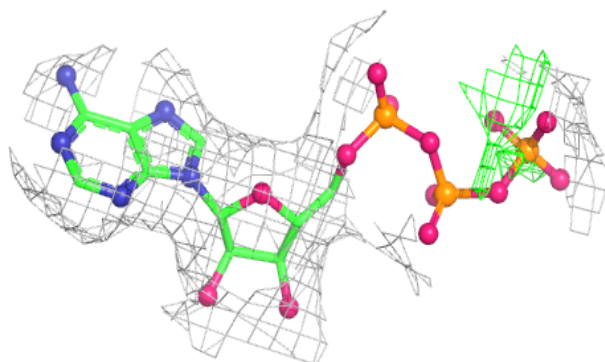


Electron density around ATP A 601:

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

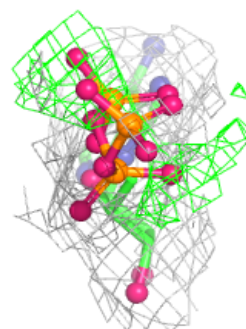
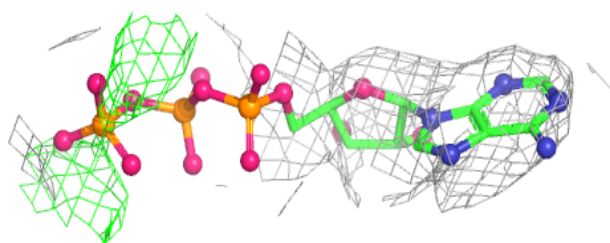
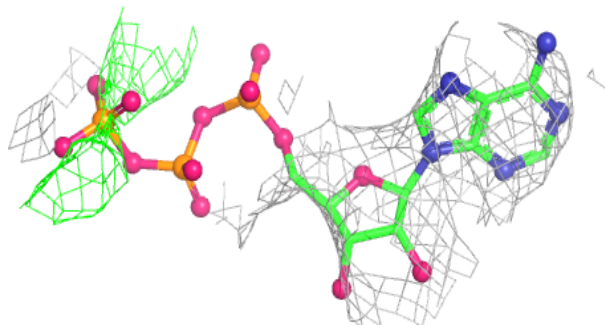
**Electron density around ATP L 601:**

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and green (positive)

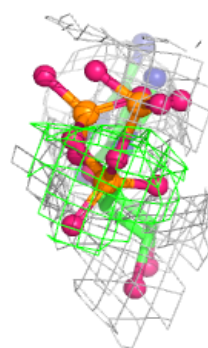
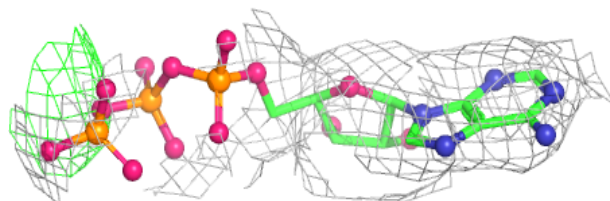
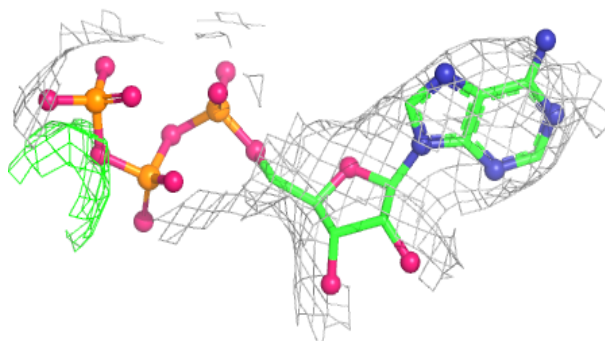


Electron density around ATP C 601:

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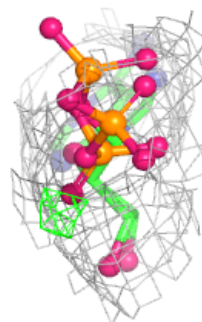
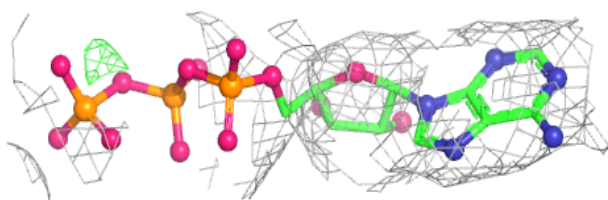
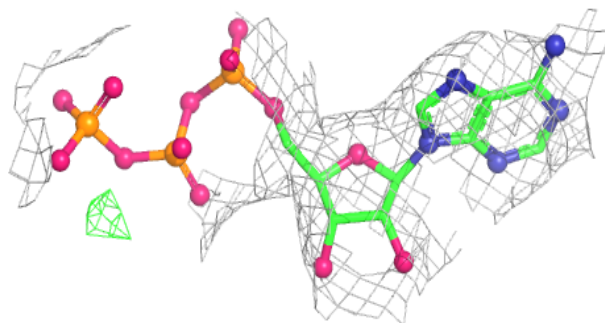
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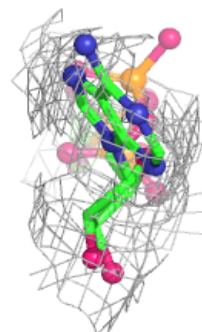
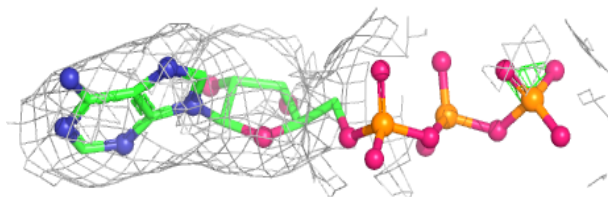
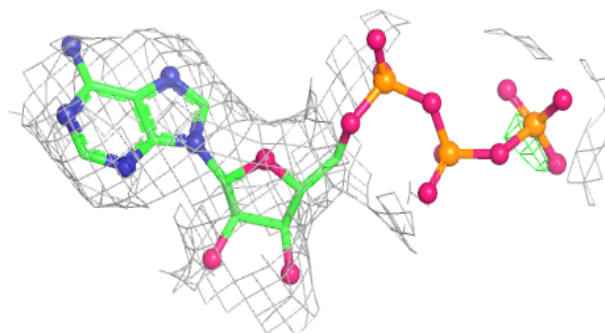


Electron density around ATP F 601:

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

**Electron density around ATP M 601:**

$2mF_o-DF_c$ (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.