



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:25 AM UTC

PDB ID : 3ZKB / pdb_00003zkb
Title : CRYSTAL STRUCTURE OF THE ATPASE REGION OF Mycobacterium tuberculosis GyrB WITH AMPPNP
Authors : Agrawal, A.; Roue, M.; Spitzfaden, C.; Petrella, S.; Aubry, A.; Volker, C.; Mossakowska, D.; Hann, M.; Bax, B.; Mayer, C.
Deposited on : 2013-01-22
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

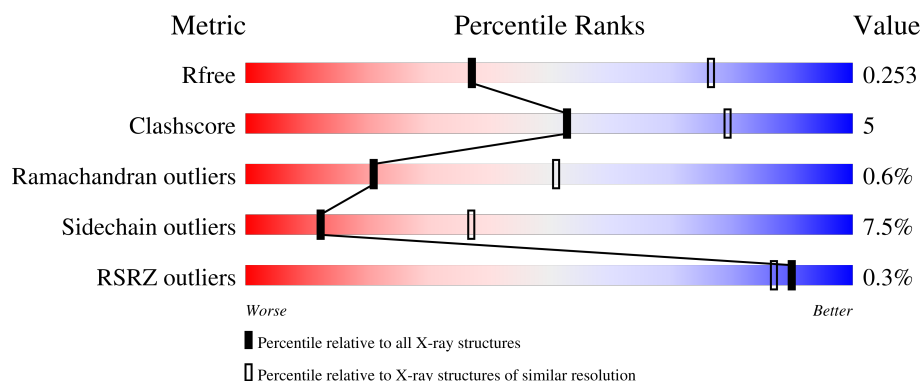
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	432	
1	B	432	
1	C	432	
1	D	432	

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Mol	Chain	Length	Quality of chain
1	E	432	 70%17% • 11%
1	F	432	 75%12% • 11%
1	G	432	 73%14% • 12%
1	H	432	 68%18% • 12%
1	I	432	 72%12% • 13%
1	J	432	 72%17%11%
1	K	432	 70%16% • 13%
1	L	432	 %74%14%12%
1	M	432	 71%17% • 11%
1	N	432	 %76%9% • 14%
1	O	432	 71%16% • 12%
1	P	432	 67%18% • 13%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 46952 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 DNA GYRASE SUBUNIT B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	380	Total	C	N	O	S	0	0	0
			2887	1809	509	563	6			
1	B	382	Total	C	N	O	S	0	0	0
			2874	1798	505	565	6			
1	C	387	Total	C	N	O	S	0	0	0
			2938	1842	516	574	6			
1	D	392	Total	C	N	O	S	0	0	0
			2954	1844	518	586	6			
1	E	386	Total	C	N	O	S	0	0	0
			2912	1821	511	574	6			
1	F	383	Total	C	N	O	S	0	0	0
			2888	1807	505	570	6			
1	G	381	Total	C	N	O	S	0	0	0
			2864	1796	502	560	6			
1	H	379	Total	C	N	O	S	0	0	0
			2866	1794	502	564	6			
1	I	375	Total	C	N	O	S	0	0	0
			2827	1768	494	559	6			
1	J	384	Total	C	N	O	S	0	0	0
			2884	1806	506	566	6			
1	K	376	Total	C	N	O	S	0	0	0
			2838	1778	497	557	6			
1	L	382	Total	C	N	O	S	0	0	0
			2862	1791	501	564	6			
1	M	383	Total	C	N	O	S	0	0	0
			2888	1808	509	565	6			
1	N	373	Total	C	N	O	S	0	0	0
			2816	1763	495	552	6			
1	O	379	Total	C	N	O	S	0	0	0
			2877	1803	506	562	6			
1	P	376	Total	C	N	O	S	0	0	0
			2822	1768	489	559	6			

There are 80 discrepancies between the modelled and reference sequences:

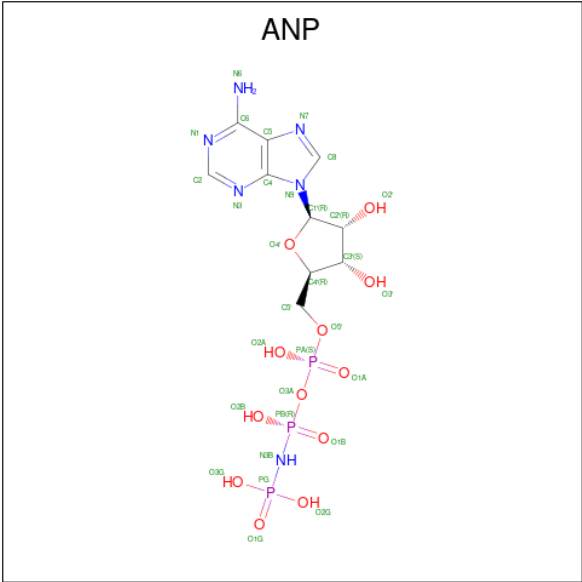
Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP I6WX66
A	-3	PRO	-	expression tag	UNP I6WX66
A	-2	LEU	-	expression tag	UNP I6WX66
A	-1	GLY	-	expression tag	UNP I6WX66
A	0	SER	-	expression tag	UNP I6WX66
B	-4	GLY	-	expression tag	UNP I6WX66
B	-3	PRO	-	expression tag	UNP I6WX66
B	-2	LEU	-	expression tag	UNP I6WX66
B	-1	GLY	-	expression tag	UNP I6WX66
B	0	SER	-	expression tag	UNP I6WX66
C	-4	GLY	-	expression tag	UNP I6WX66
C	-3	PRO	-	expression tag	UNP I6WX66
C	-2	LEU	-	expression tag	UNP I6WX66
C	-1	GLY	-	expression tag	UNP I6WX66
C	0	SER	-	expression tag	UNP I6WX66
D	-4	GLY	-	expression tag	UNP I6WX66
D	-3	PRO	-	expression tag	UNP I6WX66
D	-2	LEU	-	expression tag	UNP I6WX66
D	-1	GLY	-	expression tag	UNP I6WX66
D	0	SER	-	expression tag	UNP I6WX66
E	-4	GLY	-	expression tag	UNP I6WX66
E	-3	PRO	-	expression tag	UNP I6WX66
E	-2	LEU	-	expression tag	UNP I6WX66
E	-1	GLY	-	expression tag	UNP I6WX66
E	0	SER	-	expression tag	UNP I6WX66
F	-4	GLY	-	expression tag	UNP I6WX66
F	-3	PRO	-	expression tag	UNP I6WX66
F	-2	LEU	-	expression tag	UNP I6WX66
F	-1	GLY	-	expression tag	UNP I6WX66
F	0	SER	-	expression tag	UNP I6WX66
G	-4	GLY	-	expression tag	UNP I6WX66
G	-3	PRO	-	expression tag	UNP I6WX66
G	-2	LEU	-	expression tag	UNP I6WX66
G	-1	GLY	-	expression tag	UNP I6WX66
G	0	SER	-	expression tag	UNP I6WX66
H	-4	GLY	-	expression tag	UNP I6WX66
H	-3	PRO	-	expression tag	UNP I6WX66
H	-2	LEU	-	expression tag	UNP I6WX66
H	-1	GLY	-	expression tag	UNP I6WX66
H	0	SER	-	expression tag	UNP I6WX66
I	-4	GLY	-	expression tag	UNP I6WX66
I	-3	PRO	-	expression tag	UNP I6WX66

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-2	LEU	-	expression tag	UNP I6WX66
I	-1	GLY	-	expression tag	UNP I6WX66
I	0	SER	-	expression tag	UNP I6WX66
J	-4	GLY	-	expression tag	UNP I6WX66
J	-3	PRO	-	expression tag	UNP I6WX66
J	-2	LEU	-	expression tag	UNP I6WX66
J	-1	GLY	-	expression tag	UNP I6WX66
J	0	SER	-	expression tag	UNP I6WX66
K	-4	GLY	-	expression tag	UNP I6WX66
K	-3	PRO	-	expression tag	UNP I6WX66
K	-2	LEU	-	expression tag	UNP I6WX66
K	-1	GLY	-	expression tag	UNP I6WX66
K	0	SER	-	expression tag	UNP I6WX66
L	-4	GLY	-	expression tag	UNP I6WX66
L	-3	PRO	-	expression tag	UNP I6WX66
L	-2	LEU	-	expression tag	UNP I6WX66
L	-1	GLY	-	expression tag	UNP I6WX66
L	0	SER	-	expression tag	UNP I6WX66
M	-4	GLY	-	expression tag	UNP I6WX66
M	-3	PRO	-	expression tag	UNP I6WX66
M	-2	LEU	-	expression tag	UNP I6WX66
M	-1	GLY	-	expression tag	UNP I6WX66
M	0	SER	-	expression tag	UNP I6WX66
N	-4	GLY	-	expression tag	UNP I6WX66
N	-3	PRO	-	expression tag	UNP I6WX66
N	-2	LEU	-	expression tag	UNP I6WX66
N	-1	GLY	-	expression tag	UNP I6WX66
N	0	SER	-	expression tag	UNP I6WX66
O	-4	GLY	-	expression tag	UNP I6WX66
O	-3	PRO	-	expression tag	UNP I6WX66
O	-2	LEU	-	expression tag	UNP I6WX66
O	-1	GLY	-	expression tag	UNP I6WX66
O	0	SER	-	expression tag	UNP I6WX66
P	-4	GLY	-	expression tag	UNP I6WX66
P	-3	PRO	-	expression tag	UNP I6WX66
P	-2	LEU	-	expression tag	UNP I6WX66
P	-1	GLY	-	expression tag	UNP I6WX66
P	0	SER	-	expression tag	UNP I6WX66

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	D	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	E	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	F	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	G	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	H	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	I	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	J	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	K	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	L	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	M	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	N	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

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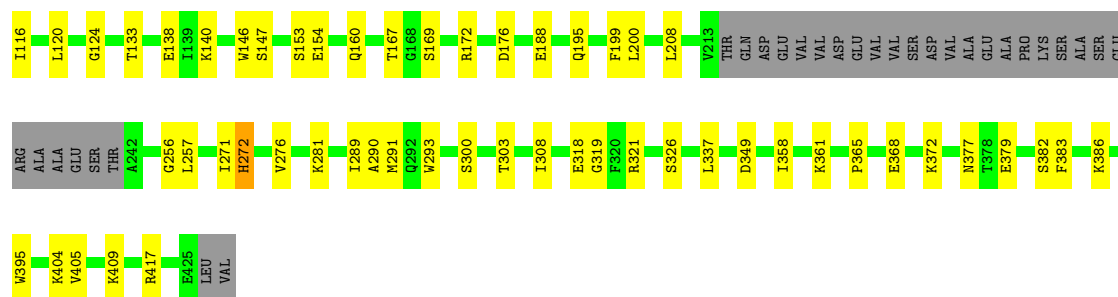
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	O	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	P	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	2	Total	Mg	0	0
			2	2		
3	C	2	Total	Mg	0	0
			2	2		
3	D	2	Total	Mg	0	0
			2	2		
3	E	1	Total	Mg	0	0
			1	1		
3	F	1	Total	Mg	0	0
			1	1		
3	G	2	Total	Mg	0	0
			2	2		
3	H	1	Total	Mg	0	0
			1	1		
3	I	1	Total	Mg	0	0
			1	1		
3	J	1	Total	Mg	0	0
			1	1		
3	K	1	Total	Mg	0	0
			1	1		
3	L	1	Total	Mg	0	0
			1	1		
3	M	1	Total	Mg	0	0
			1	1		
3	N	1	Total	Mg	0	0
			1	1		
3	O	1	Total	Mg	0	0
			1	1		
3	P	1	Total	Mg	0	0
			1	1		

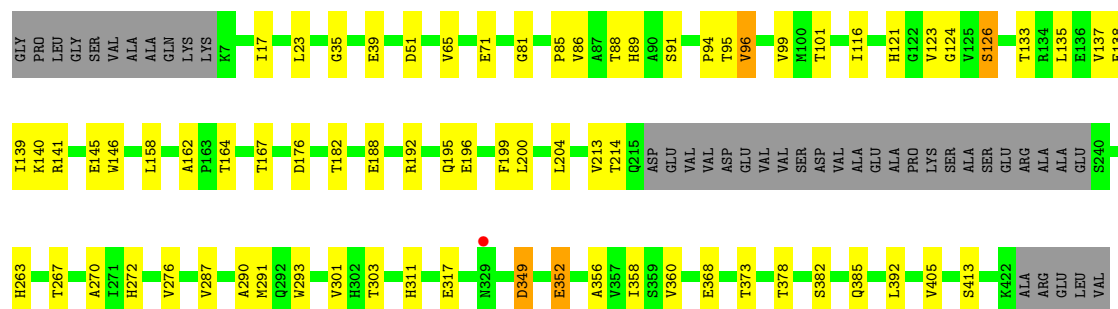
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	44	Total 44	O 44	0	0
4	B	31	Total 31	O 31	0	0
4	C	62	Total 62	O 62	0	0
4	D	40	Total 40	O 40	0	0
4	E	45	Total 45	O 45	0	0
4	F	26	Total 26	O 26	0	0
4	G	25	Total 25	O 25	0	0
4	H	29	Total 29	O 29	0	0
4	I	24	Total 24	O 24	0	0
4	J	33	Total 33	O 33	0	0
4	K	11	Total 11	O 11	0	0
4	L	13	Total 13	O 13	0	0
4	M	16	Total 16	O 16	0	0
4	N	14	Total 14	O 14	0	0
4	O	12	Total 12	O 12	0	0
4	P	14	Total 14	O 14	0	0



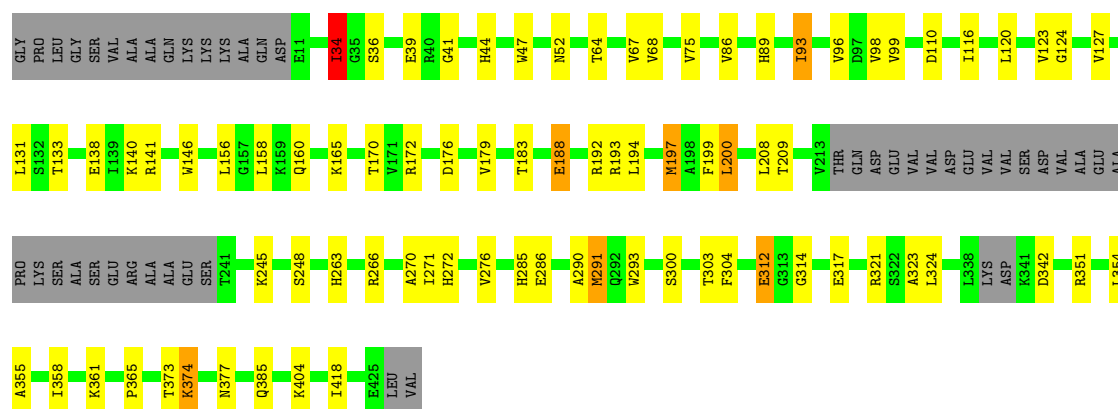
• Molecule 1: DNA GYRASE SUBUNIT B

Chain D: 74% 16% 9%



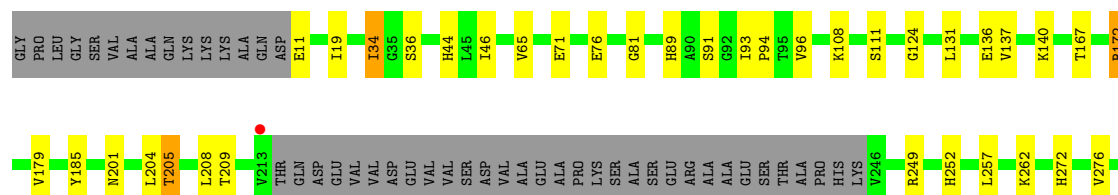
• Molecule 1: DNA GYRASE SUBUNIT B

Chain E: 70% 17% 11%



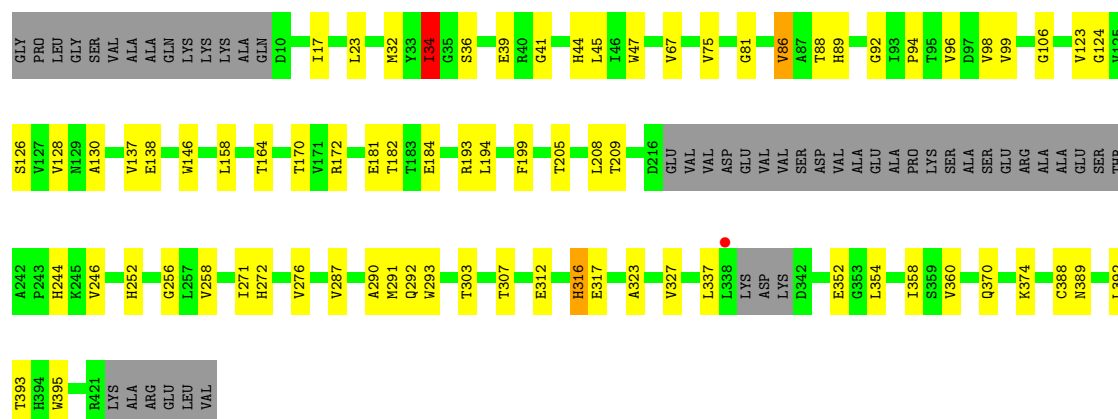
• Molecule 1: DNA GYRASE SUBUNIT B

Chain F: 75% 12% 11%



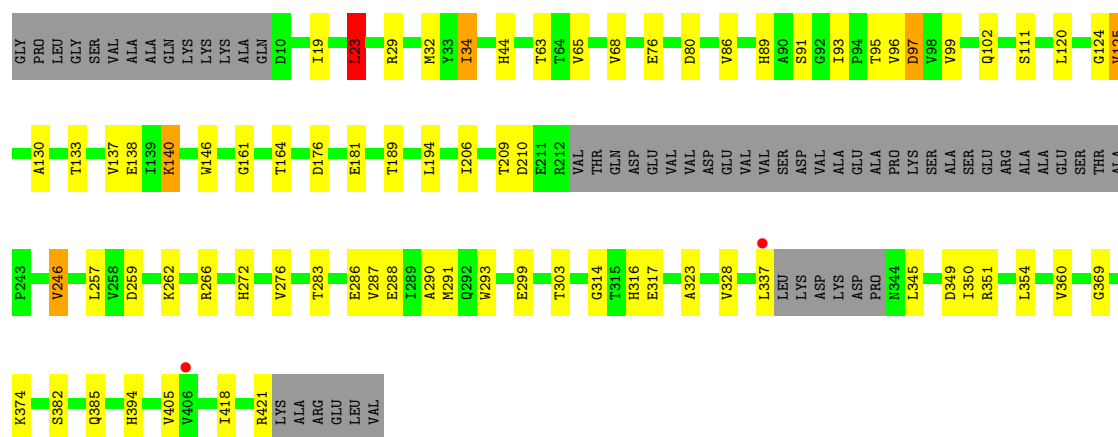


Chain J:  72% 17% 11%



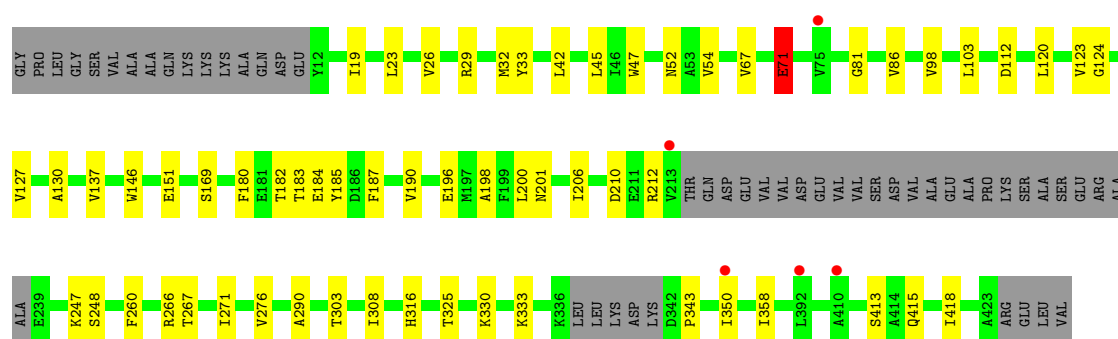
• Molecule 1: DNA GYRASE SUBUNIT B

Chain K:  70% 16% 13%



• Molecule 1: DNA GYRASE SUBUNIT B

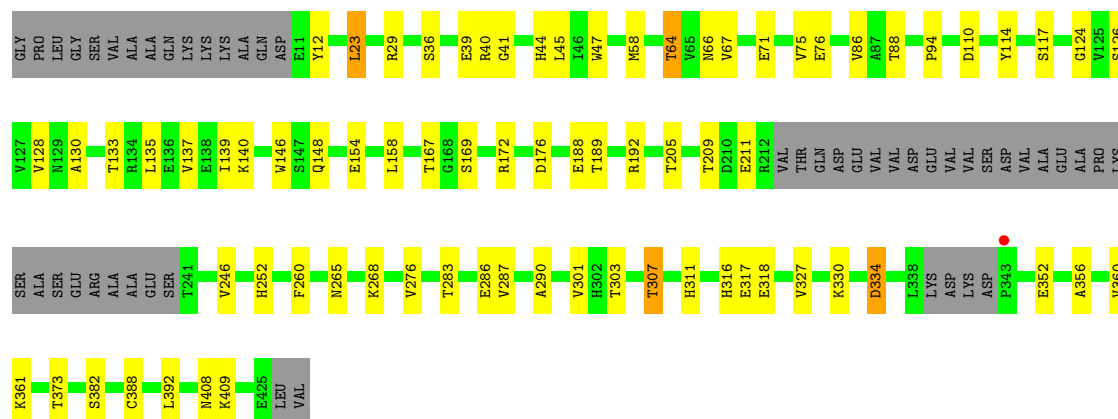
Chain L:  74% 14% 12%



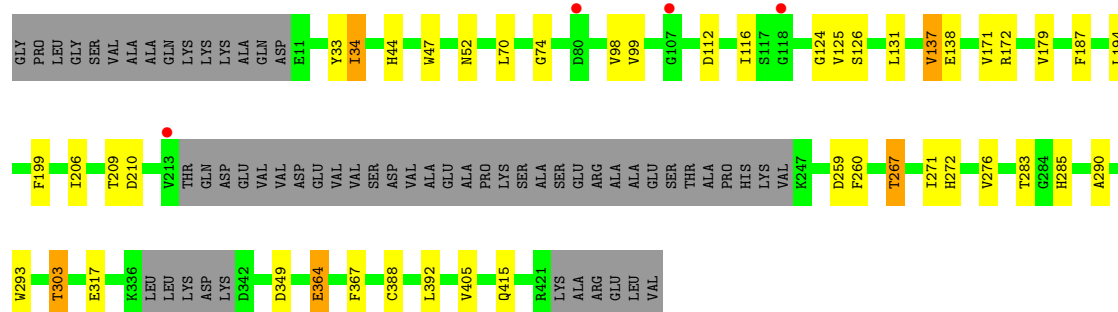
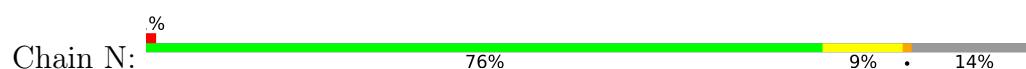
• Molecule 1: DNA GYRASE SUBUNIT B

Chain M:  71% 17% 11%

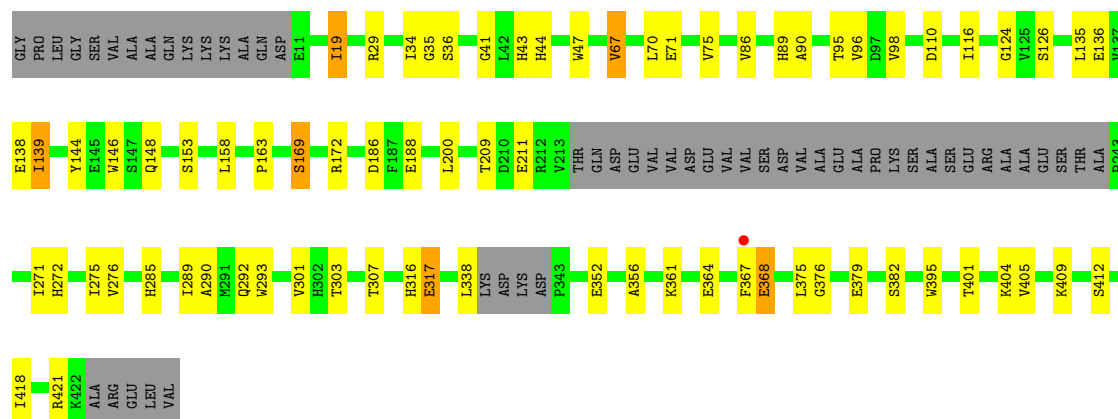




• Molecule 1: DNA GYRASE SUBUNIT B

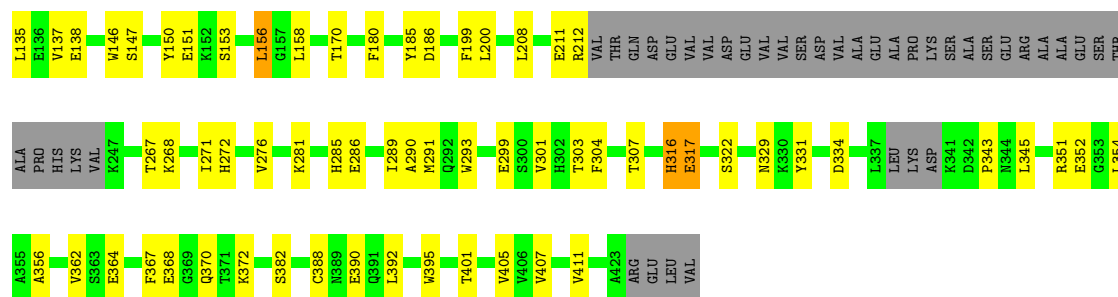


• Molecule 1: DNA GYRASE SUBUNIT B



- Molecule 1: DNA GYRASE SUBUNIT B





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	101.36Å 138.20Å 147.69Å 105.28° 92.31° 107.23°	Depositor
Resolution (Å)	24.94 – 2.90 24.94 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.2 (24.94-2.90) 98.0 (24.94-2.90)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 2.89Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.182 , 0.240 0.195 , 0.253	Depositor DCC
R_{free} test set	7966 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	66.0	Xtriage
Anisotropy	0.668	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 58.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	46952	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ANP, 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	0.80	0/2942	1.40	26/3991 (0.7%)
1	B	0.79	0/2928	1.38	14/3978 (0.4%)
1	C	0.81	0/2994	1.40	26/4062 (0.6%)
1	D	0.79	0/3010	1.40	12/4091 (0.3%)
1	E	0.81	1/2967 (0.0%)	1.39	9/4030 (0.2%)
1	F	0.78	0/2942	1.36	4/3997 (0.1%)
1	G	0.77	0/2919	1.37	12/3967 (0.3%)
1	H	0.78	0/2920	1.40	13/3966 (0.3%)
1	I	0.76	0/2881	1.37	8/3913 (0.2%)
1	J	0.79	0/2938	1.39	7/3993 (0.2%)
1	K	0.80	0/2892	1.35	8/3927 (0.2%)
1	L	0.85	0/2916	1.41	9/3963 (0.2%)
1	M	0.79	0/2943	1.38	6/3995 (0.2%)
1	N	0.78	0/2869	1.38	10/3896 (0.3%)
1	O	0.77	0/2931	1.36	7/3975 (0.2%)
1	P	0.78	1/2875 (0.0%)	1.37	5/3907 (0.1%)
All	All	0.79	2/46867 (0.0%)	1.38	176/63651 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	197	MET	SD-CE	-6.23	1.64	1.79
1	P	364	GLU	CA-C	5.55	1.58	1.52

The worst 5 of 176 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	93	ILE	N-CA-CB	-9.66	105.16	111.83
1	N	34	ILE	N-CA-CB	-8.33	102.42	112.33
1	E	93	ILE	N-CA-CB	-8.24	104.67	111.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	34	ILE	N-CA-CB	-6.94	104.57	112.21
1	N	260	PHE	CA-CB-CG	6.87	120.67	113.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2887	0	2803	35	0
1	B	2874	0	2760	27	0
1	C	2938	0	2857	33	0
1	D	2954	0	2823	30	0
1	E	2912	0	2795	40	0
1	F	2888	0	2772	21	0
1	G	2864	0	2755	30	0
1	H	2866	0	2764	34	0
1	I	2827	0	2701	27	0
1	J	2884	0	2769	34	0
1	K	2838	0	2730	34	0
1	L	2862	0	2749	21	0
1	M	2888	0	2784	30	0
1	N	2816	0	2714	15	0
1	O	2877	0	2791	32	0
1	P	2822	0	2700	39	0
2	A	31	0	13	1	0
2	B	31	0	13	0	0
2	C	31	0	13	0	0
2	D	31	0	13	0	0
2	E	31	0	13	1	0
2	F	31	0	13	1	0
2	G	31	0	13	1	0
2	H	31	0	13	0	0
2	I	31	0	13	2	0
2	J	31	0	13	1	0
2	K	31	0	13	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	31	0	13	1	0
2	M	31	0	13	0	0
2	N	31	0	13	0	0
2	O	31	0	13	2	0
2	P	31	0	13	0	0
3	A	1	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	1	0	0	0	0
3	F	1	0	0	0	0
3	G	2	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	K	1	0	0	0	0
3	L	1	0	0	0	0
3	M	1	0	0	0	0
3	N	1	0	0	0	0
3	O	1	0	0	0	0
3	P	1	0	0	0	0
4	A	44	0	0	0	0
4	B	31	0	0	0	0
4	C	62	0	0	0	0
4	D	40	0	0	1	0
4	E	45	0	0	0	0
4	F	26	0	0	0	0
4	G	25	0	0	1	0
4	H	29	0	0	0	0
4	I	24	0	0	0	0
4	J	33	0	0	0	0
4	K	11	0	0	0	0
4	L	13	0	0	0	0
4	M	16	0	0	0	0
4	N	14	0	0	0	0
4	O	12	0	0	1	0
4	P	14	0	0	0	0
All	All	46952	0	44475	458	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 5.

The worst 5 of 458 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)
2:O:601:ANP:H8	2:O:601:ANP:H5'2	1.55	0.87
1:P:272:HIS:HE1	1:P:293:TRP:H	1.22	0.85
1:A:287:VAL:HG23	1:A:360:VAL:HG12	1.61	0.82
1:C:89:HIS:HD2	1:C:91:SER:HB2	1.44	0.81
1:H:272:HIS:HE1	1:H:293:TRP:H	1.28	0.80

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	374/432 (87%)	354 (95%)	17 (4%)	3 (1%)	16	44
1	B	378/432 (88%)	362 (96%)	13 (3%)	3 (1%)	16	44
1	C	383/432 (89%)	368 (96%)	13 (3%)	2 (0%)	24	54
1	D	388/432 (90%)	375 (97%)	11 (3%)	2 (0%)	24	54
1	E	380/432 (88%)	365 (96%)	14 (4%)	1 (0%)	36	65
1	F	379/432 (88%)	366 (97%)	11 (3%)	2 (0%)	24	54
1	G	375/432 (87%)	361 (96%)	13 (4%)	1 (0%)	36	65
1	H	375/432 (87%)	360 (96%)	13 (4%)	2 (0%)	24	54
1	I	369/432 (85%)	355 (96%)	12 (3%)	2 (0%)	24	54
1	J	378/432 (88%)	360 (95%)	13 (3%)	5 (1%)	9	32
1	K	370/432 (86%)	351 (95%)	17 (5%)	2 (0%)	24	54
1	L	376/432 (87%)	356 (95%)	17 (4%)	3 (1%)	16	44
1	M	377/432 (87%)	358 (95%)	18 (5%)	1 (0%)	36	65
1	N	367/432 (85%)	350 (95%)	16 (4%)	1 (0%)	36	65
1	O	373/432 (86%)	358 (96%)	14 (4%)	1 (0%)	36	65
1	P	370/432 (86%)	353 (95%)	14 (4%)	3 (1%)	16	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	6012/6912 (87%)	5752 (96%)	226 (4%)	34 (1%)	21 51

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	344	ASN
1	L	343	PRO
1	B	124	GLY
1	D	124	GLY
1	E	124	GLY

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	302/350 (86%)	279 (92%)	23 (8%)	12 36
1	B	297/350 (85%)	281 (95%)	16 (5%)	20 51
1	C	307/350 (88%)	282 (92%)	25 (8%)	11 33
1	D	306/350 (87%)	283 (92%)	23 (8%)	12 37
1	E	302/350 (86%)	280 (93%)	22 (7%)	13 38
1	F	299/350 (85%)	278 (93%)	21 (7%)	14 40
1	G	296/350 (85%)	275 (93%)	21 (7%)	13 40
1	H	299/350 (85%)	271 (91%)	28 (9%)	8 26
1	I	293/350 (84%)	270 (92%)	23 (8%)	11 35
1	J	298/350 (85%)	275 (92%)	23 (8%)	12 35
1	K	295/350 (84%)	275 (93%)	20 (7%)	14 42
1	L	297/350 (85%)	276 (93%)	21 (7%)	13 40
1	M	299/350 (85%)	277 (93%)	22 (7%)	13 38
1	N	293/350 (84%)	276 (94%)	17 (6%)	18 49
1	O	301/350 (86%)	277 (92%)	24 (8%)	11 34
1	P	292/350 (83%)	265 (91%)	27 (9%)	8 27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	4776/5600 (85%)	4420 (92%)	356 (8%)	12	37

5 of 356 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	125	VAL
1	M	408	ASN
1	K	286	GLU
1	L	248	SER
1	N	303	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 120 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	316	HIS
1	O	316	HIS
1	J	399	ASN
1	O	311	HIS
1	P	389	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 36 ligands modelled in this entry, 20 are monoatomic - leaving 16 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	ANP	E	601	3	33,33,33	3.54	15 (45%)	45,52,52	2.08	10 (22%)
2	ANP	N	601	3	33,33,33	3.56	14 (42%)	45,52,52	2.02	9 (20%)
2	ANP	D	601	3	33,33,33	3.40	14 (42%)	45,52,52	2.00	9 (20%)
2	ANP	A	601	3	33,33,33	3.51	15 (45%)	45,52,52	1.95	9 (20%)
2	ANP	C	601	3	33,33,33	3.51	14 (42%)	45,52,52	1.94	10 (22%)
2	ANP	H	601	3	33,33,33	3.57	13 (39%)	45,52,52	2.00	10 (22%)
2	ANP	B	601	3	33,33,33	3.63	15 (45%)	45,52,52	2.04	12 (26%)
2	ANP	K	601	3	33,33,33	3.52	14 (42%)	45,52,52	1.99	11 (24%)
2	ANP	O	601	3	33,33,33	3.53	15 (45%)	45,52,52	2.02	11 (24%)
2	ANP	I	601	3	33,33,33	3.54	15 (45%)	45,52,52	2.12	11 (24%)
2	ANP	P	601	3	33,33,33	3.56	14 (42%)	45,52,52	2.10	11 (24%)
2	ANP	L	601	3	33,33,33	3.48	13 (39%)	45,52,52	2.02	11 (24%)
2	ANP	F	601	3	33,33,33	3.54	14 (42%)	45,52,52	1.93	10 (22%)
2	ANP	M	601	3	33,33,33	3.57	15 (45%)	45,52,52	2.03	11 (24%)
2	ANP	J	601	3	33,33,33	3.51	13 (39%)	45,52,52	1.90	9 (20%)
2	ANP	G	601	3	33,33,33	3.55	14 (42%)	45,52,52	2.01	11 (24%)

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	ANP	E	601	3	-	2/18/38/38	0/3/3/3
2	ANP	N	601	3	-	3/18/38/38	0/3/3/3
2	ANP	D	601	3	-	4/18/38/38	0/3/3/3
2	ANP	A	601	3	-	5/18/38/38	0/3/3/3
2	ANP	C	601	3	-	4/18/38/38	0/3/3/3
2	ANP	H	601	3	-	4/18/38/38	0/3/3/3
2	ANP	B	601	3	-	3/18/38/38	0/3/3/3
2	ANP	K	601	3	-	1/18/38/38	0/3/3/3
2	ANP	O	601	3	-	4/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ANP	I	601	3	-	3/18/38/38	0/3/3/3
2	ANP	P	601	3	-	3/18/38/38	0/3/3/3
2	ANP	L	601	3	-	3/18/38/38	0/3/3/3
2	ANP	F	601	3	-	2/18/38/38	0/3/3/3
2	ANP	M	601	3	-	2/18/38/38	0/3/3/3
2	ANP	J	601	3	-	5/18/38/38	0/3/3/3
2	ANP	G	601	3	-	3/18/38/38	0/3/3/3

The worst 5 of 227 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	ANP	PB-O1B	11.32	1.63	1.46
2	C	601	ANP	PB-O1B	11.31	1.63	1.46
2	M	601	ANP	PB-O1B	11.24	1.63	1.46
2	P	601	ANP	PB-O1B	11.22	1.63	1.46
2	H	601	ANP	PB-O1B	11.19	1.63	1.46

The worst 5 of 165 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	601	ANP	C5-C4-N3	-6.51	117.75	126.72
2	B	601	ANP	N3-C2-N1	-6.42	118.86	128.58
2	I	601	ANP	C5-C4-N3	-6.40	117.91	126.72
2	L	601	ANP	C5-C4-N3	-6.38	117.93	126.72
2	H	601	ANP	C5-C4-N3	-6.32	118.01	126.72

There are no chirality outliers.

5 of 51 torsion outliers are listed below:

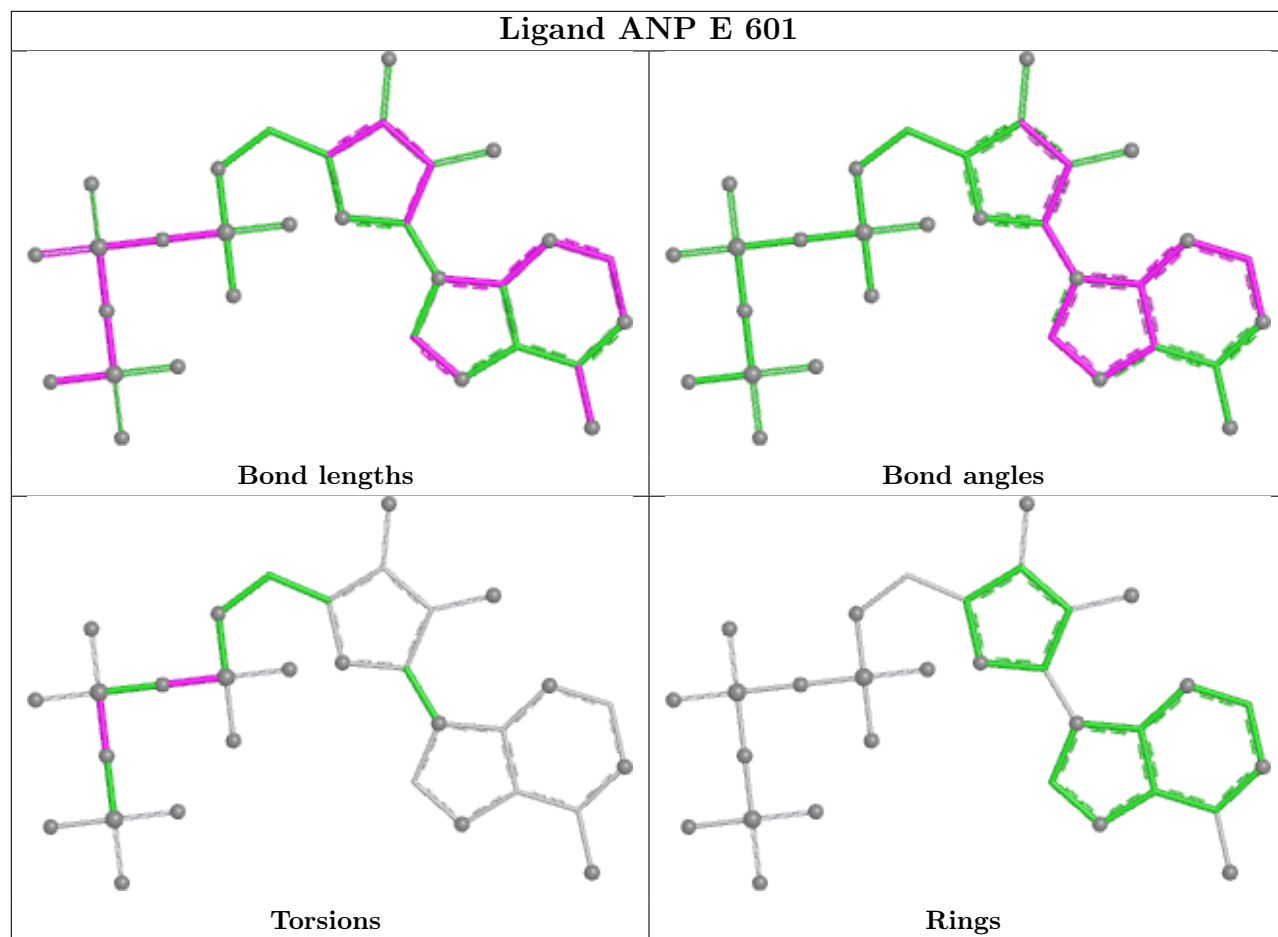
Mol	Chain	Res	Type	Atoms
2	A	601	ANP	PB-N3B-PG-O1G
2	A	601	ANP	PG-N3B-PB-O1B
2	A	601	ANP	PA-O3A-PB-O2B
2	B	601	ANP	PG-N3B-PB-O1B
2	B	601	ANP	PA-O3A-PB-O1B

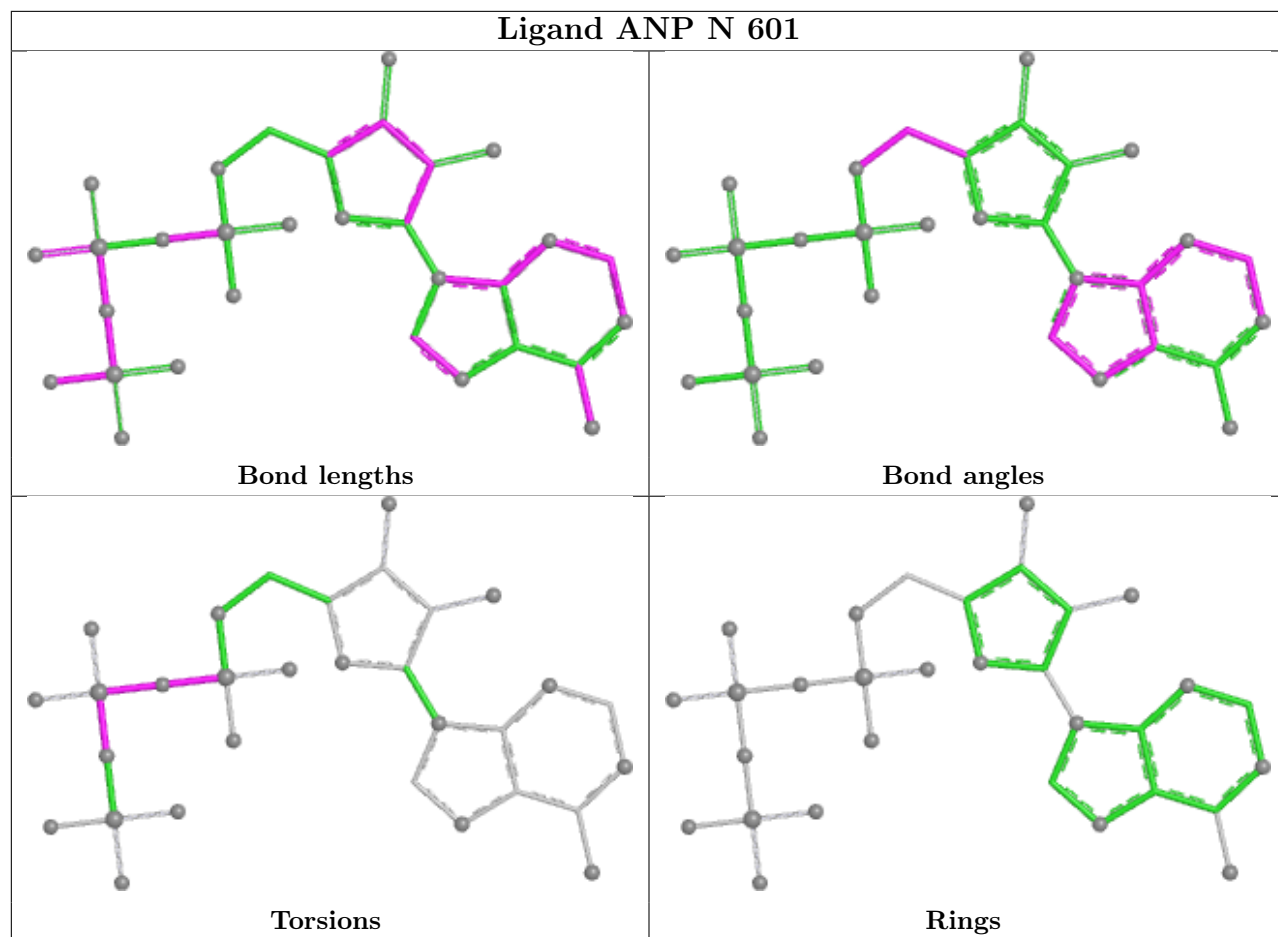
There are no ring outliers.

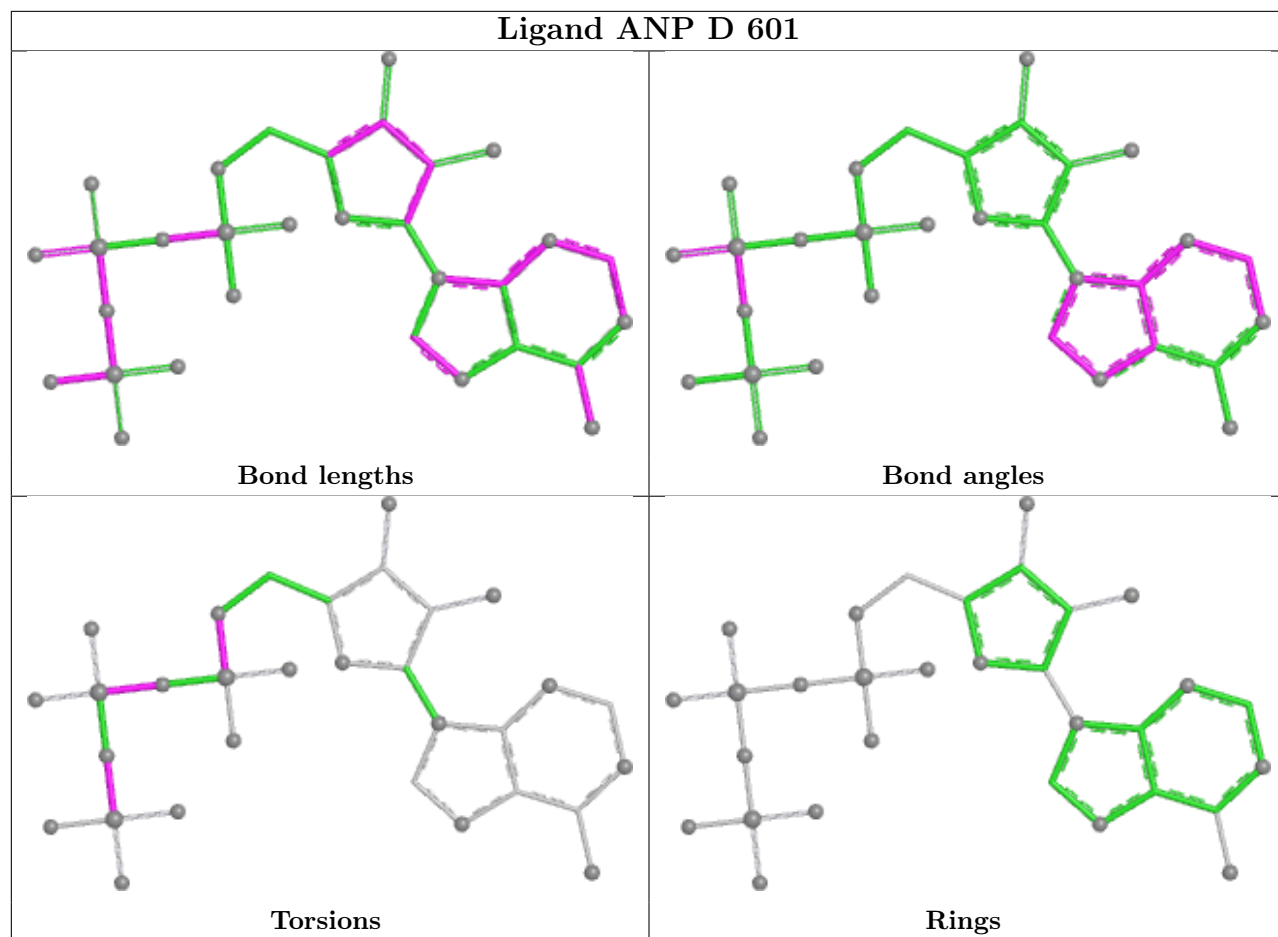
9 monomers are involved in 11 short contacts:

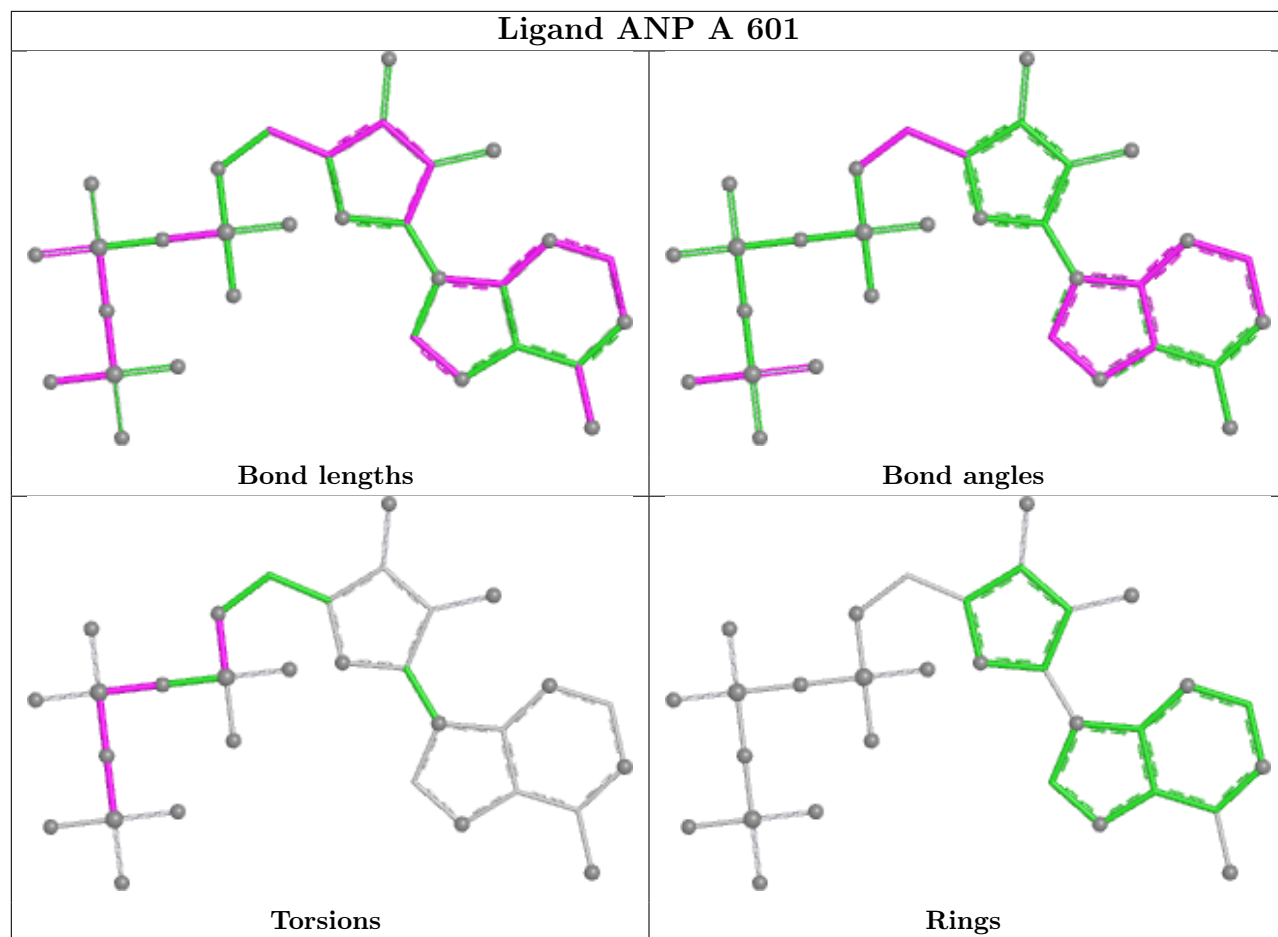
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	601	ANP	1	0
2	A	601	ANP	1	0
2	K	601	ANP	1	0
2	O	601	ANP	2	0
2	I	601	ANP	2	0
2	L	601	ANP	1	0
2	F	601	ANP	1	0
2	J	601	ANP	1	0
2	G	601	ANP	1	0

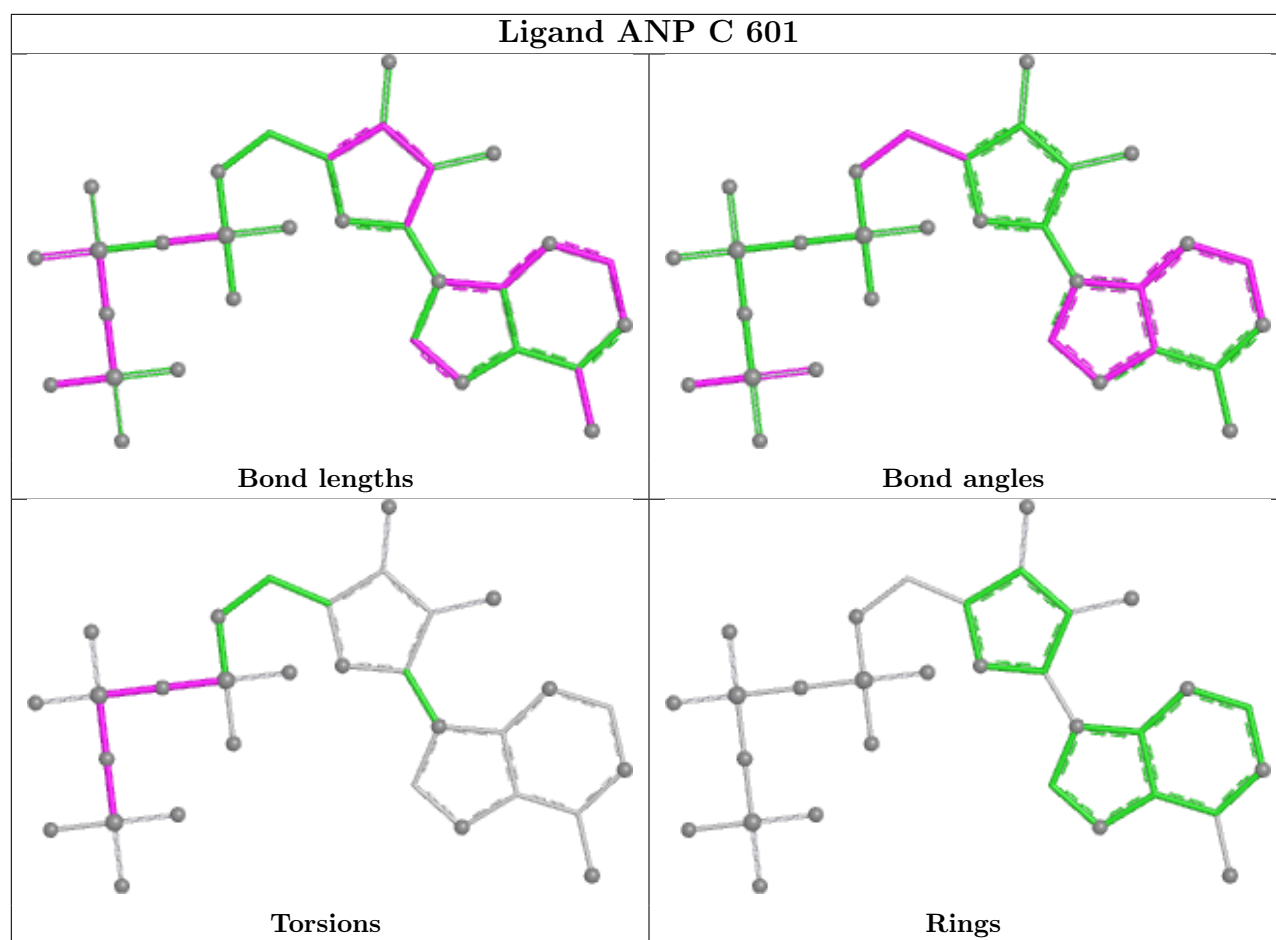
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

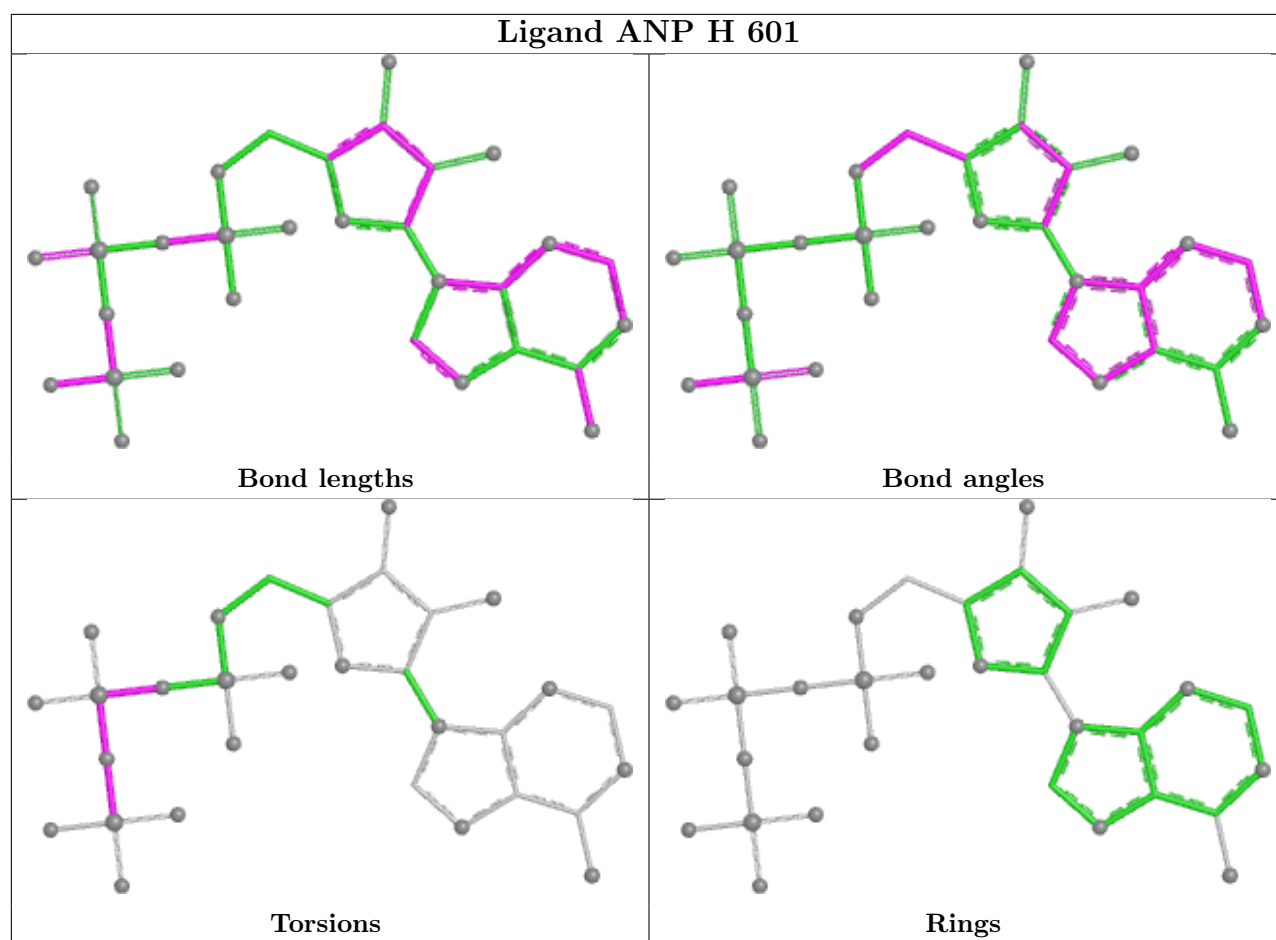


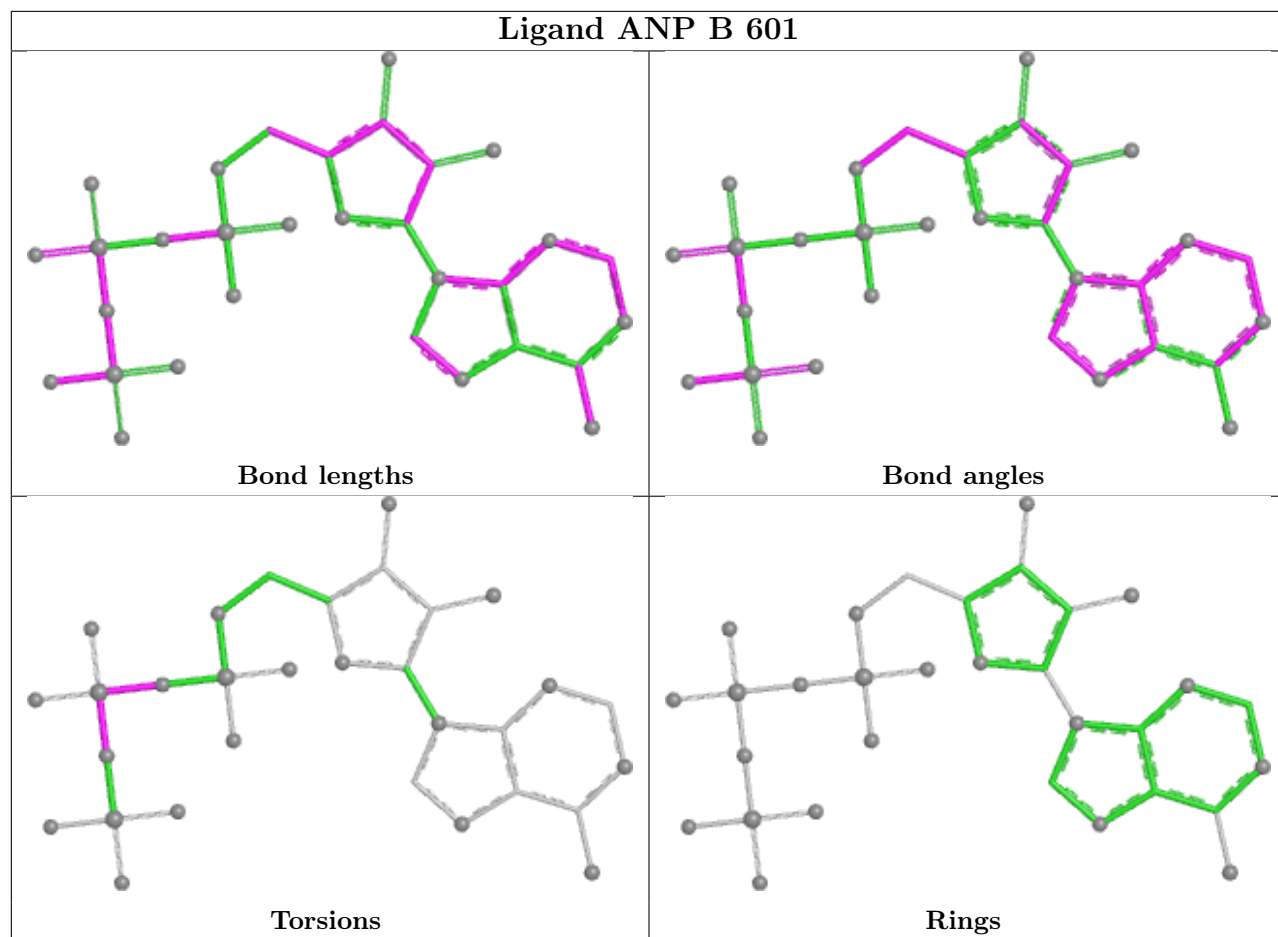


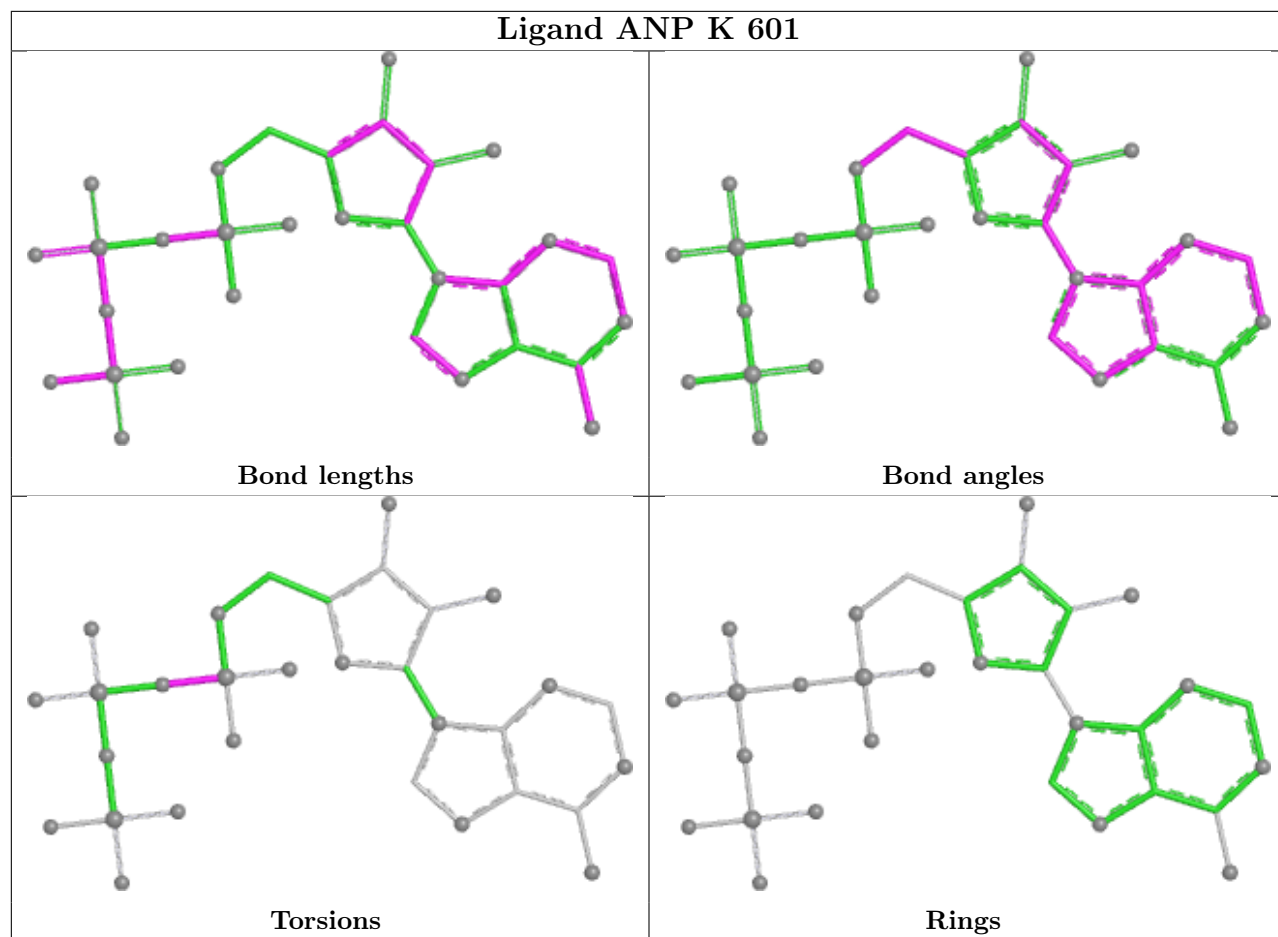


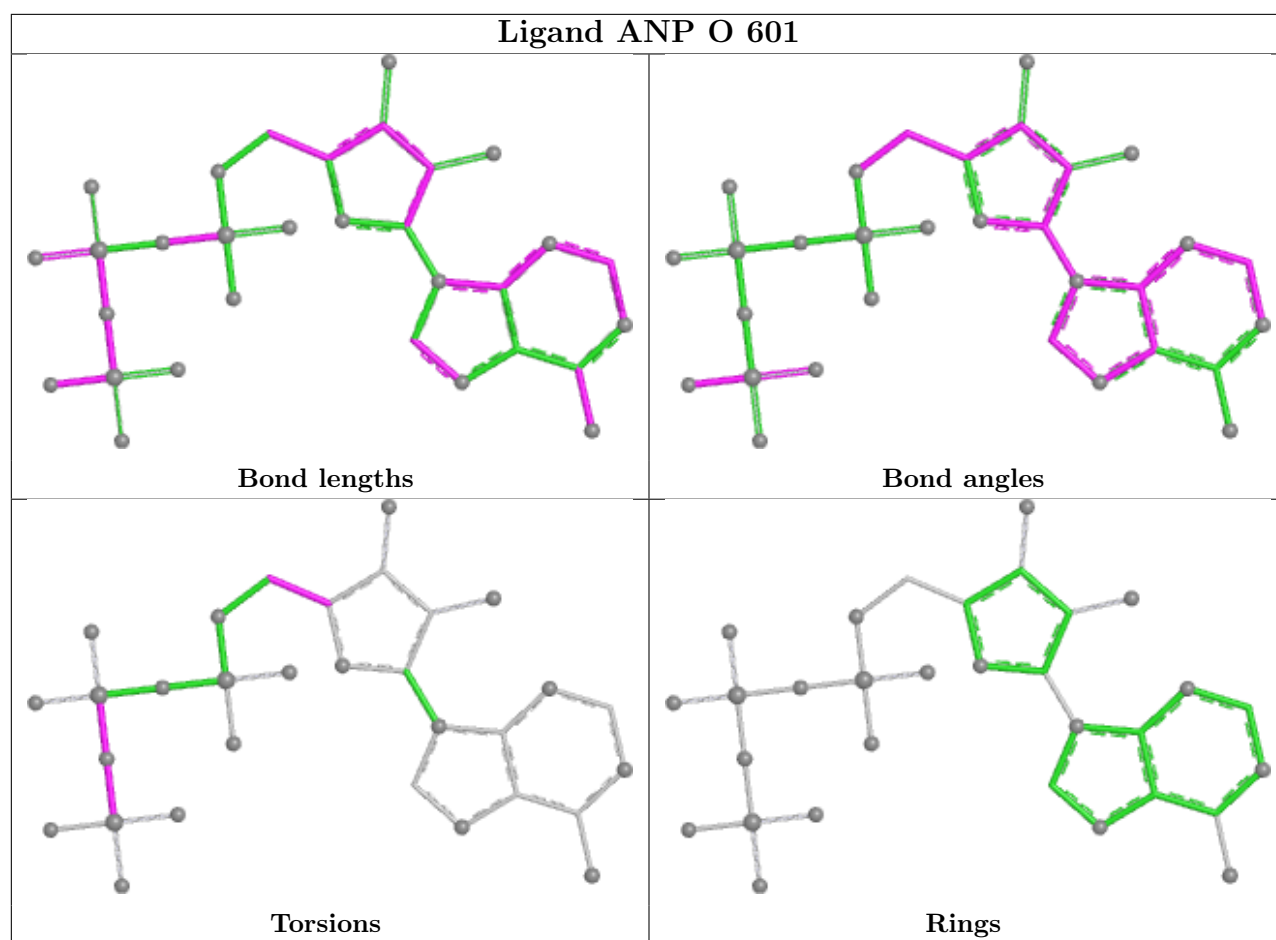




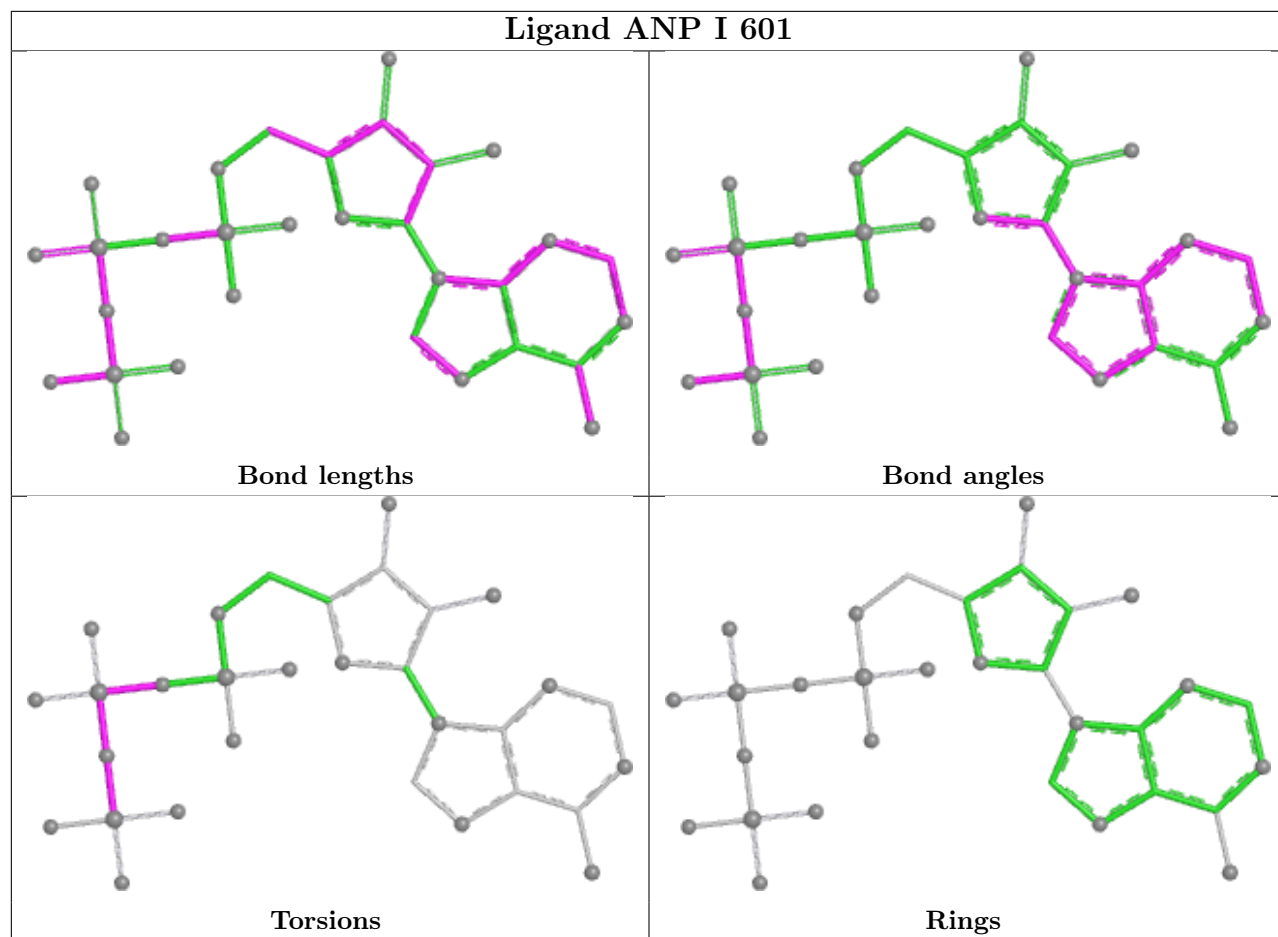


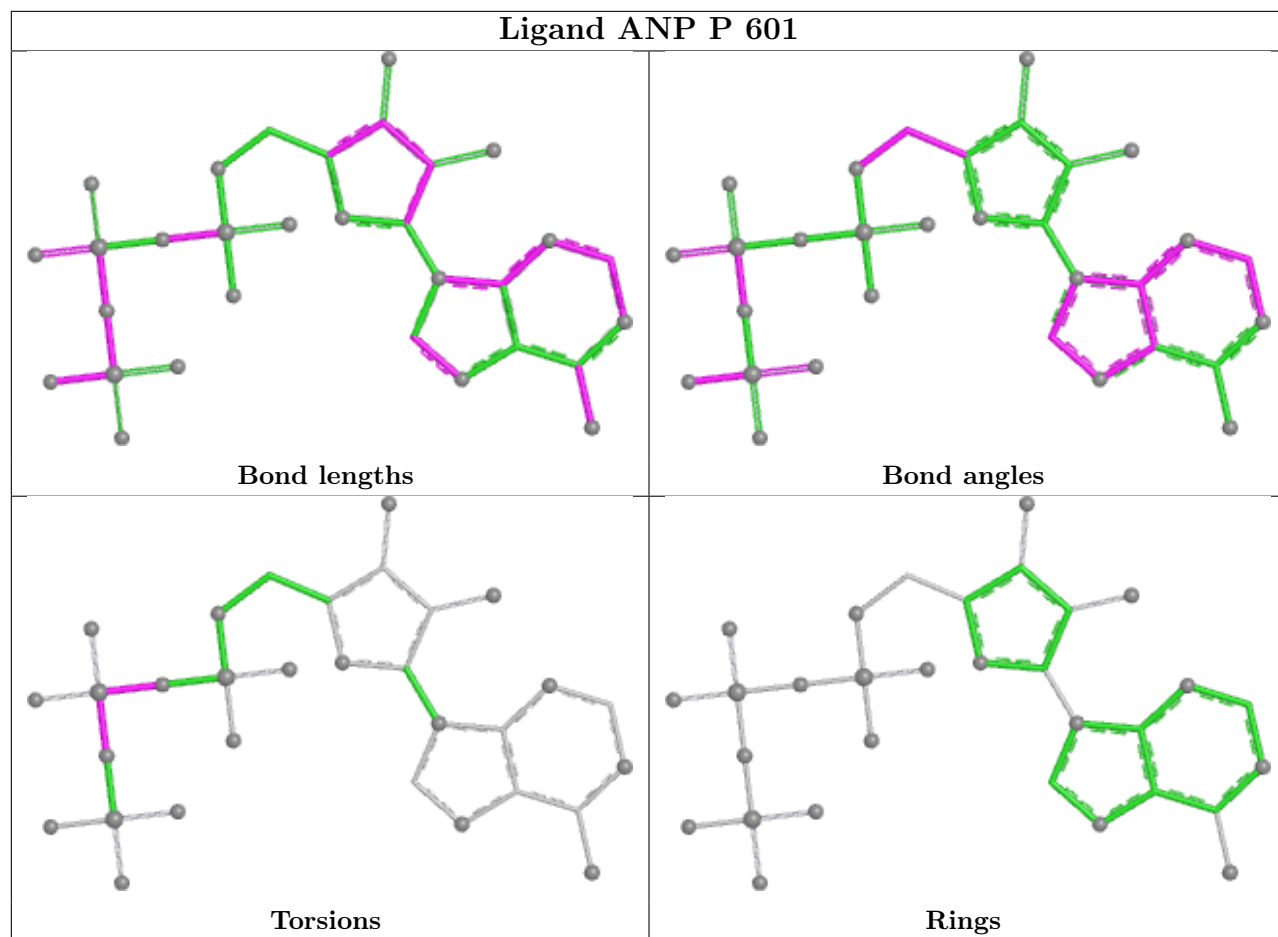


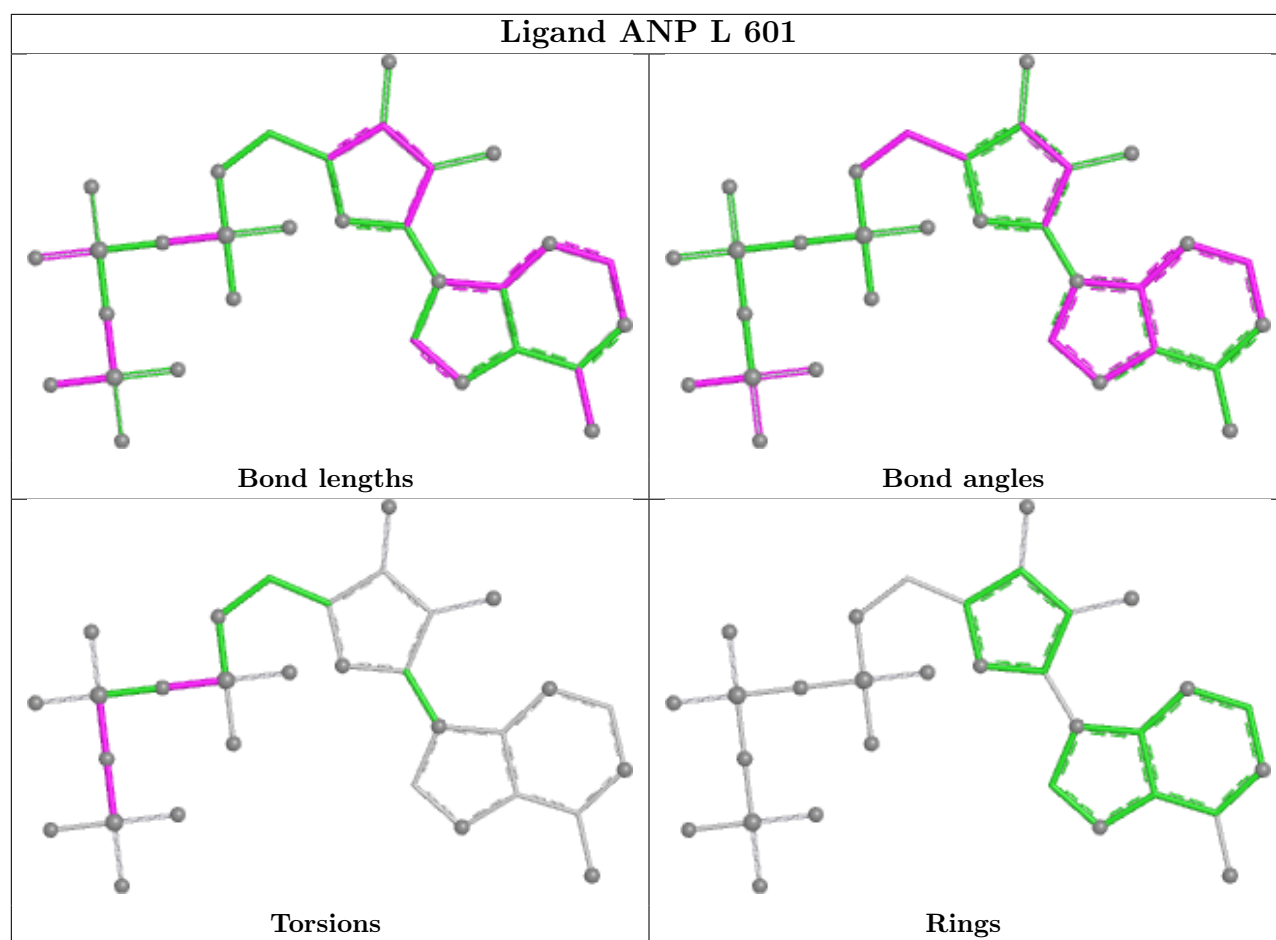


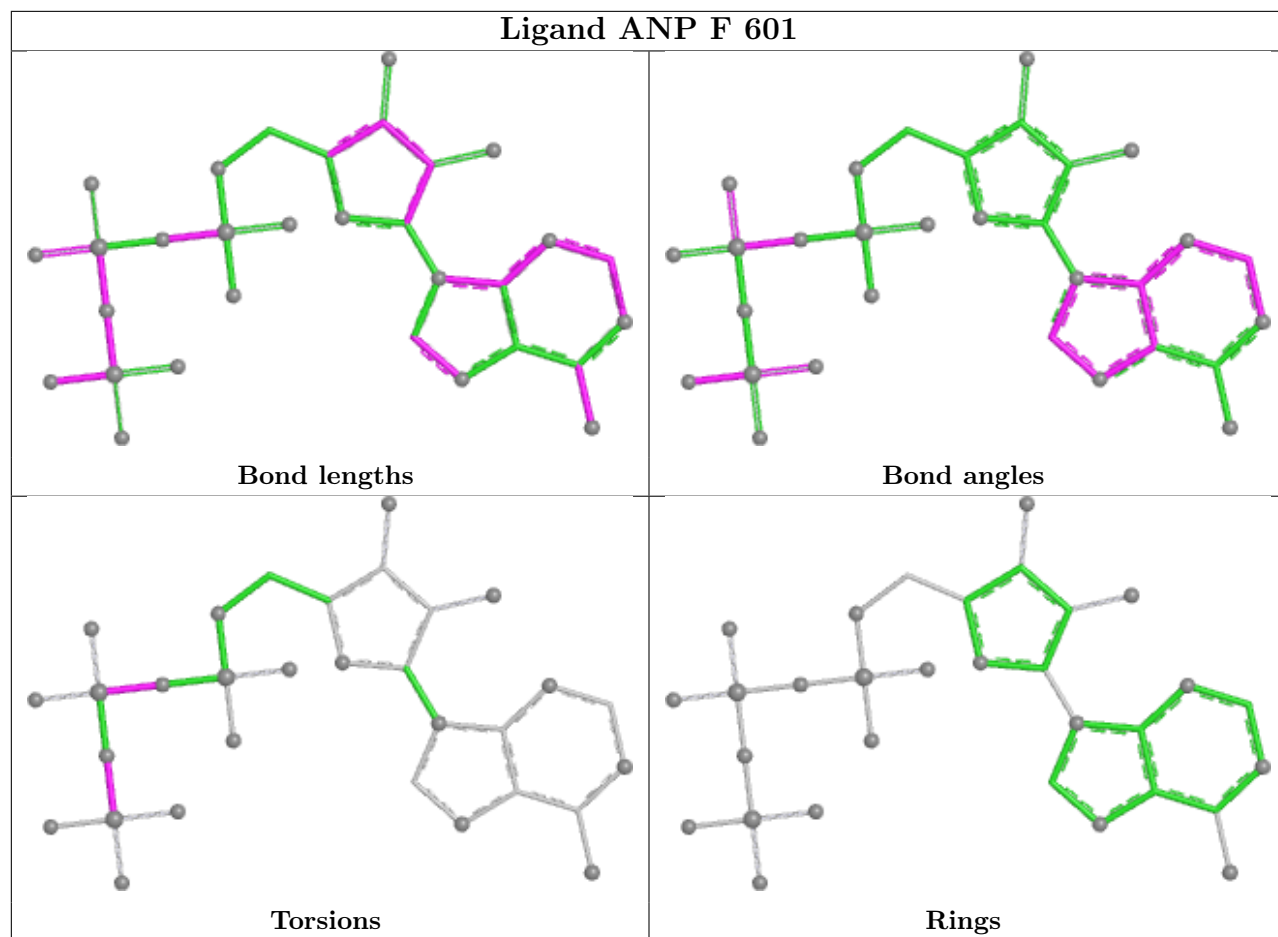


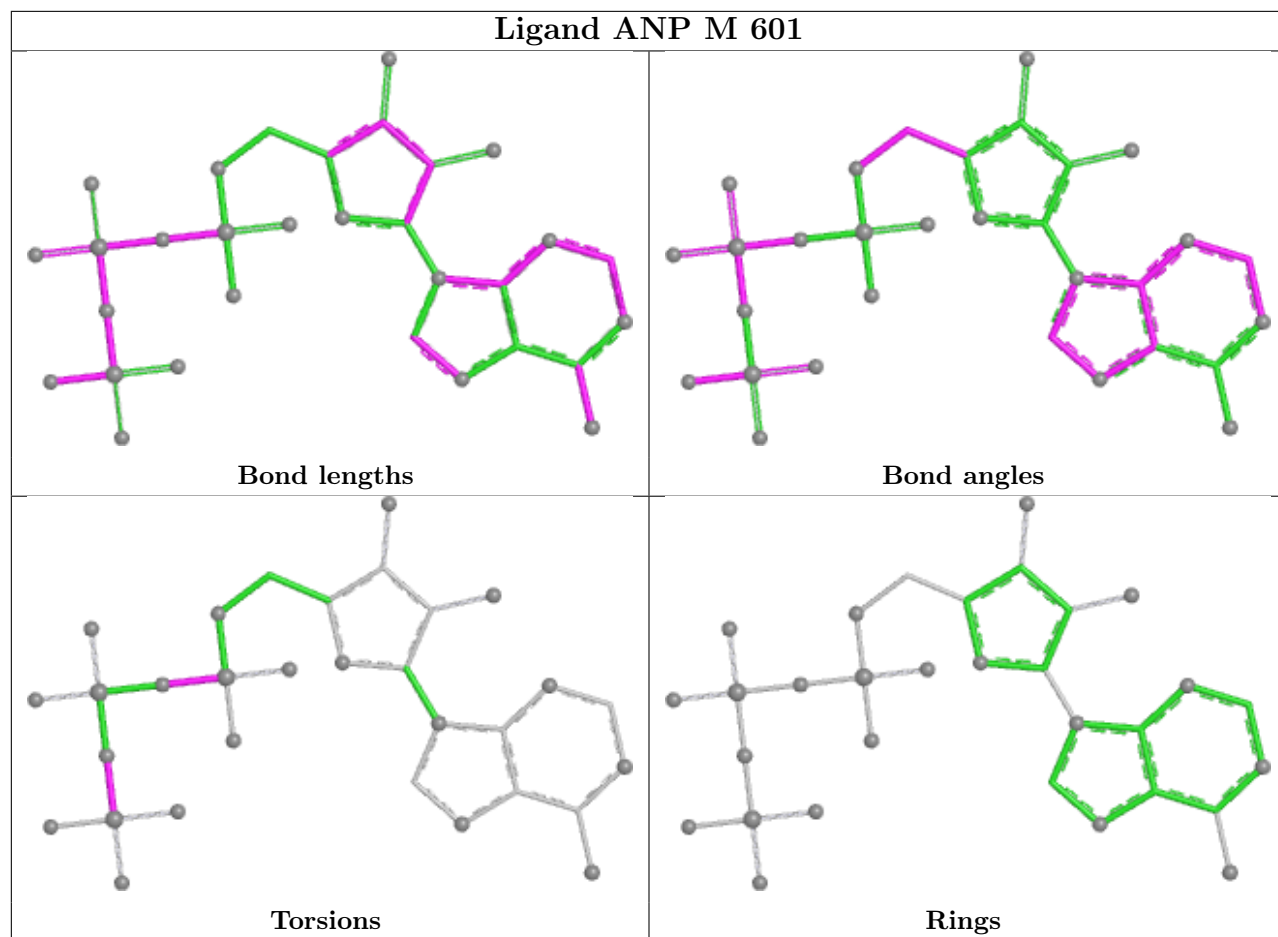
Ligand ANP I 601



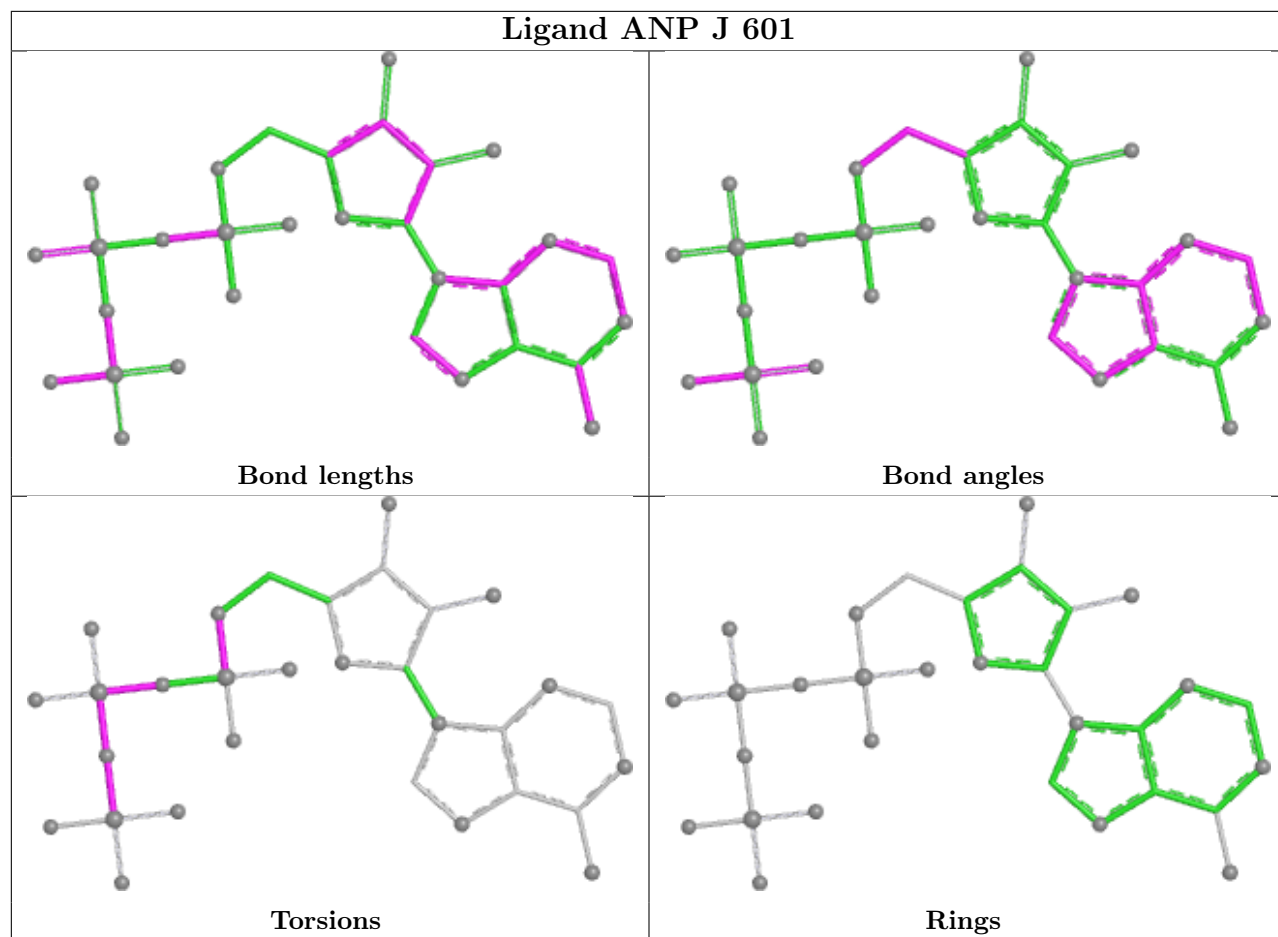


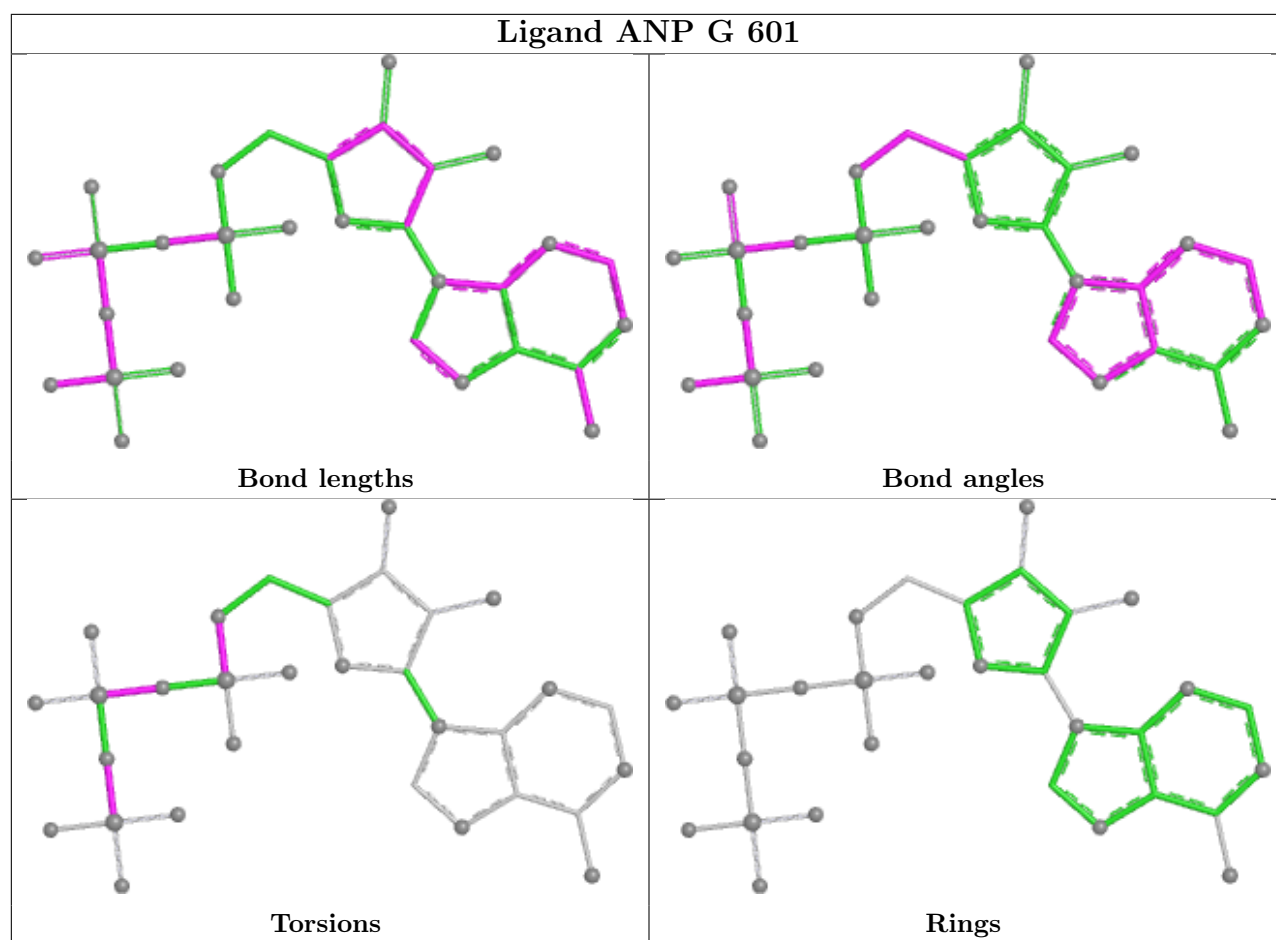






Ligand ANP J 601





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	380/432 (87%)	-0.46	2 (0%) 87 83	53, 85, 146, 167	0
1	B	382/432 (88%)	-0.46	0 100 100	49, 93, 147, 176	0
1	C	387/432 (89%)	-0.61	0 100 100	50, 72, 122, 151	0
1	D	392/432 (90%)	-0.53	1 (0%) 90 87	51, 79, 132, 170	0
1	E	386/432 (89%)	-0.58	0 100 100	50, 78, 132, 161	0
1	F	383/432 (88%)	-0.46	1 (0%) 90 87	65, 96, 138, 156	0
1	G	381/432 (88%)	-0.48	0 100 100	67, 93, 122, 156	0
1	H	379/432 (87%)	-0.43	0 100 100	64, 91, 122, 137	0
1	I	375/432 (86%)	-0.39	1 (0%) 90 87	66, 101, 176, 192	0
1	J	384/432 (88%)	-0.50	1 (0%) 90 87	56, 83, 144, 172	0
1	K	376/432 (87%)	-0.29	2 (0%) 87 83	71, 104, 176, 190	0
1	L	382/432 (88%)	-0.11	5 (1%) 75 67	74, 112, 180, 195	0
1	M	383/432 (88%)	-0.35	1 (0%) 90 87	78, 108, 145, 166	0
1	N	373/432 (86%)	-0.27	4 (1%) 78 71	74, 109, 152, 173	0
1	O	379/432 (87%)	-0.38	1 (0%) 90 87	78, 100, 131, 161	0
1	P	376/432 (87%)	-0.30	2 (0%) 87 83	76, 108, 139, 151	0
All	All	6098/6912 (88%)	-0.41	21 (0%) 90 87	49, 96, 149, 195	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	75	VAL	3.6
1	K	406	VAL	3.0
1	N	107	GLY	3.0
1	F	213	VAL	2.9
1	A	342	ASP	2.7

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.

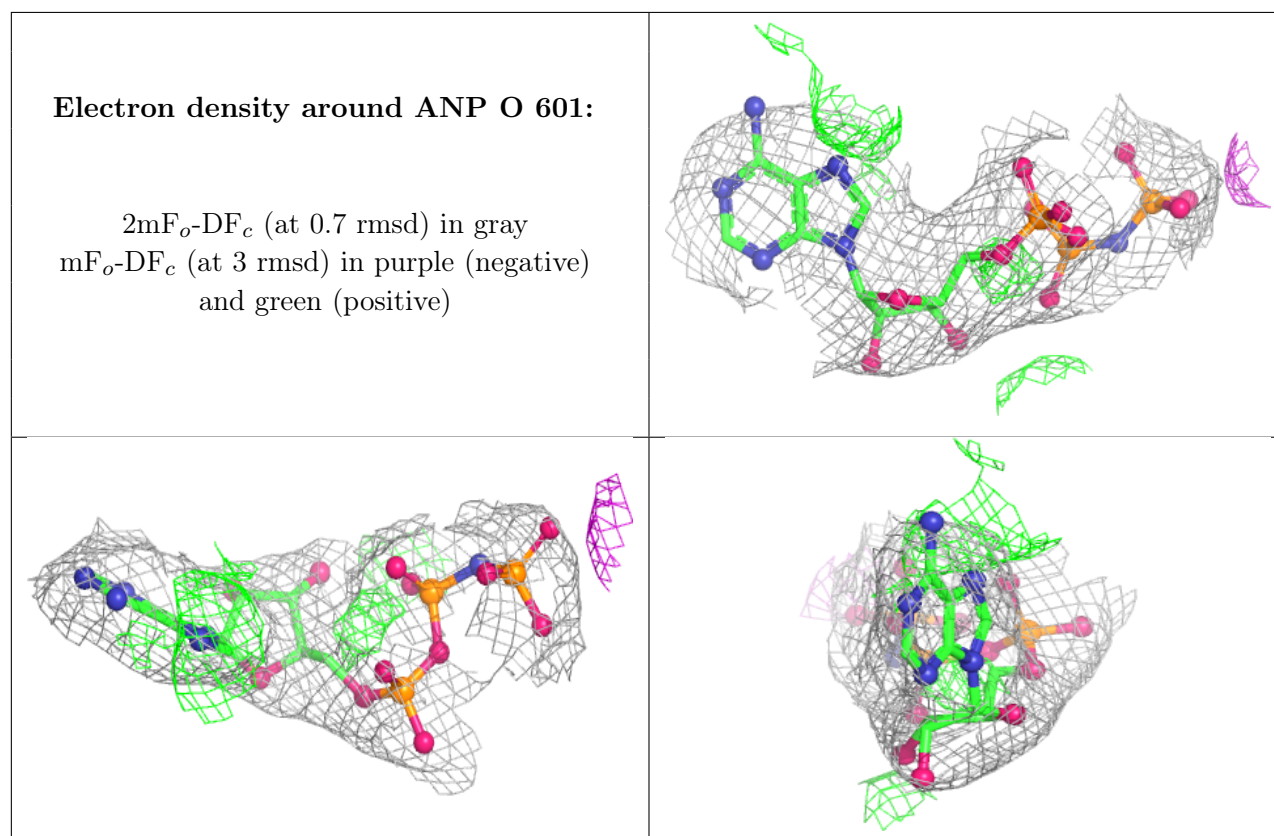
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	C	1001	1/1	0.81	0.23	85,85,85,85	0
3	MG	B	1001	1/1	0.83	0.06	83,83,83,83	0
3	MG	G	1001	1/1	0.92	0.04	76,76,76,76	0
3	MG	B	602	1/1	0.93	0.06	57,57,57,57	0
2	ANP	O	601	31/31	0.93	0.08	98,102,105,106	0
3	MG	D	1001	1/1	0.95	0.06	78,78,78,78	0
2	ANP	K	601	31/31	0.95	0.07	90,96,104,106	0
3	MG	I	602	1/1	0.95	0.18	82,82,82,82	0
3	MG	J	602	1/1	0.95	0.12	60,60,60,60	0
3	MG	O	602	1/1	0.95	0.09	76,76,76,76	0
2	ANP	P	601	31/31	0.96	0.07	94,98,108,111	0
2	ANP	F	601	31/31	0.96	0.07	72,90,100,102	0
3	MG	L	602	1/1	0.96	0.05	74,74,74,74	0
2	ANP	H	601	31/31	0.96	0.06	69,77,80,83	0
2	ANP	D	601	31/31	0.97	0.06	58,64,68,74	0
2	ANP	I	601	31/31	0.97	0.07	70,75,80,83	0
2	ANP	J	601	31/31	0.97	0.06	49,63,68,69	0
2	ANP	E	601	31/31	0.97	0.06	62,69,73,76	0
2	ANP	L	601	31/31	0.97	0.06	74,92,98,99	0
2	ANP	M	601	31/31	0.97	0.05	76,87,92,93	0
2	ANP	N	601	31/31	0.97	0.06	81,89,95,97	0
2	ANP	B	601	31/31	0.97	0.06	56,81,90,93	0
2	ANP	G	601	31/31	0.97	0.05	63,78,82,83	0
3	MG	P	602	1/1	0.97	0.05	97,97,97,97	0
2	ANP	C	601	31/31	0.98	0.05	43,56,63,65	0
3	MG	K	602	1/1	0.98	0.04	54,54,54,54	0
2	ANP	A	601	31/31	0.98	0.06	56,65,76,81	0

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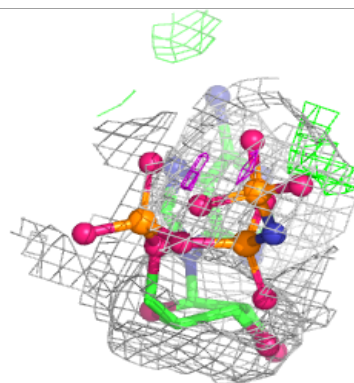
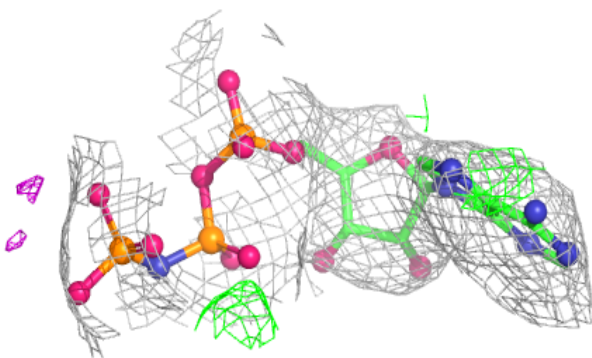
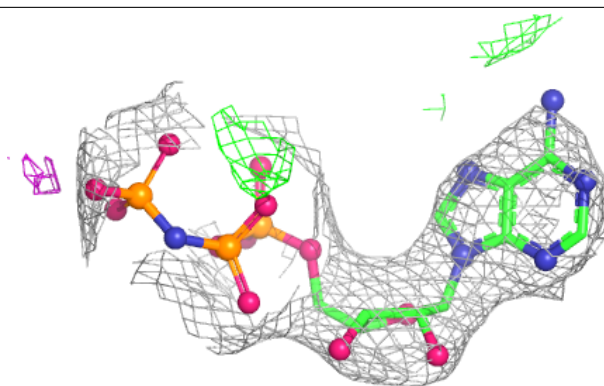
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	H	602	1/1	0.98	0.09	58,58,58,58	0
3	MG	A	602	1/1	0.98	0.09	50,50,50,50	0
3	MG	F	602	1/1	0.99	0.07	53,53,53,53	0
3	MG	G	602	1/1	0.99	0.04	63,63,63,63	0
3	MG	D	602	1/1	0.99	0.04	58,58,58,58	0
3	MG	N	602	1/1	0.99	0.05	75,75,75,75	0
3	MG	C	602	1/1	0.99	0.07	51,51,51,51	0
3	MG	E	602	1/1	0.99	0.03	56,56,56,56	0
3	MG	M	602	1/1	1.00	0.04	51,51,51,51	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.

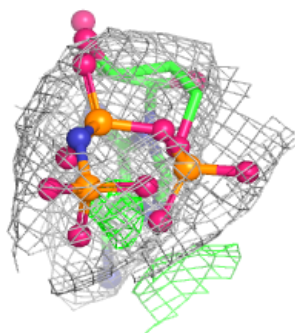
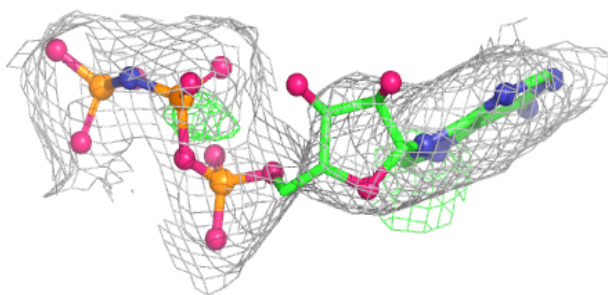
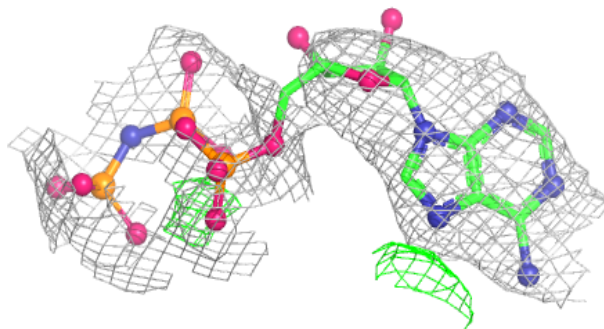


Electron density around ANP K 601:

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

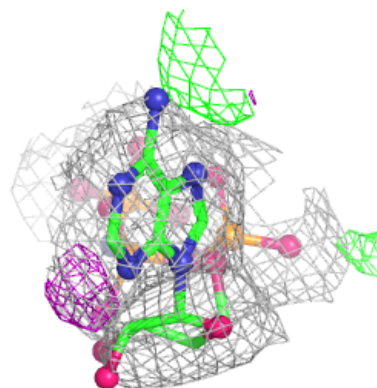
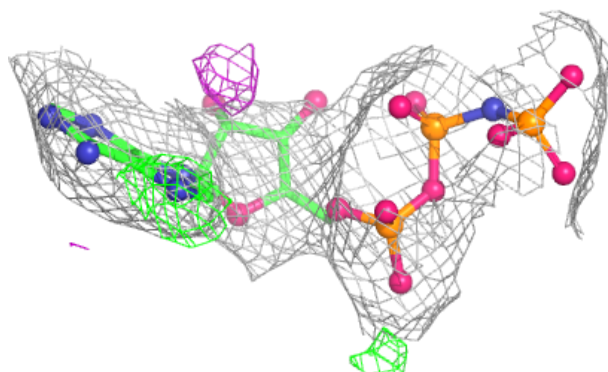
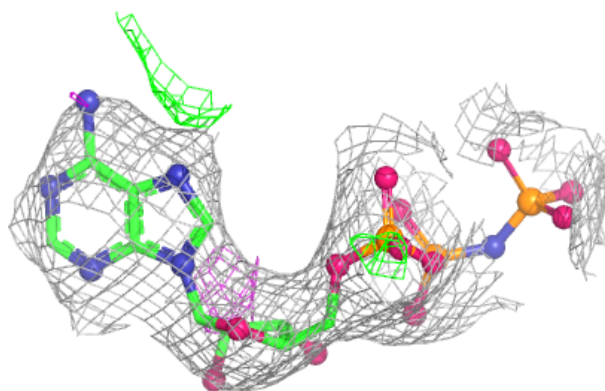
**Electron density around ANP P 601:**

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

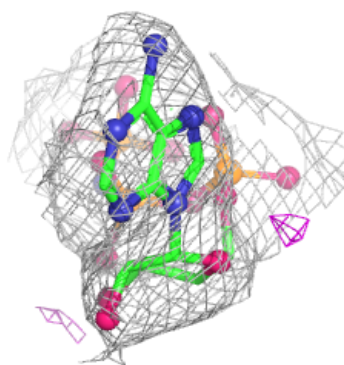
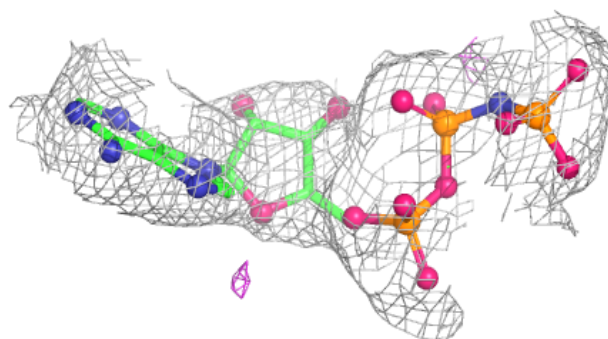
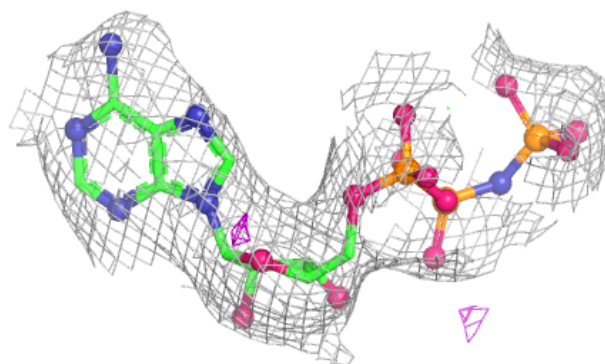


Electron density around ANP F 601:

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

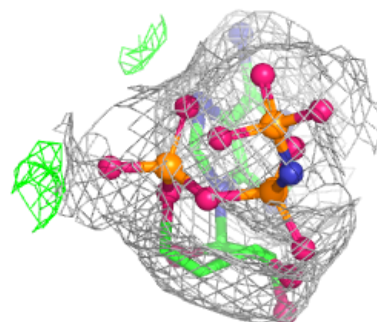
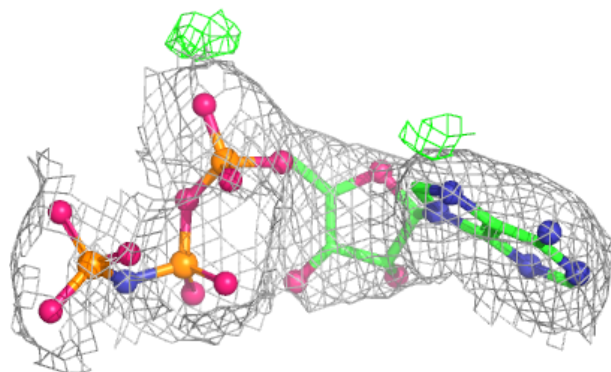
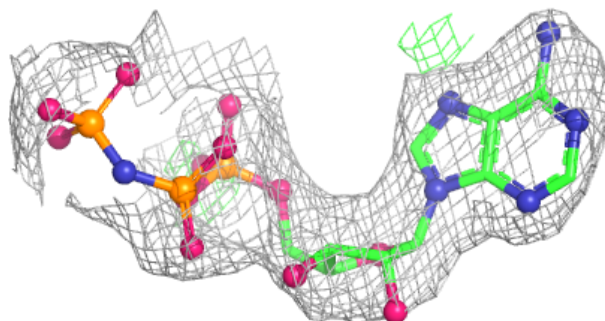
**Electron density around ANP H 601:**

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and green (positive)

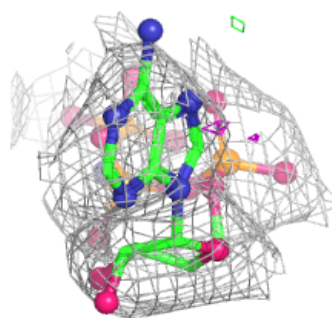
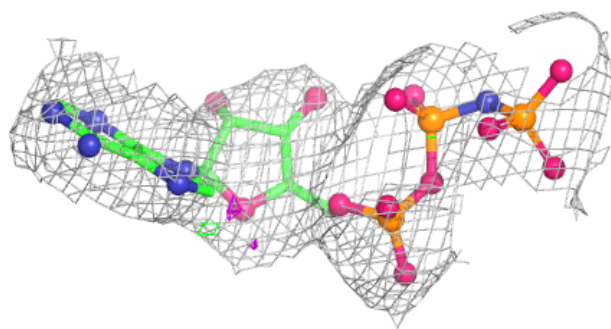
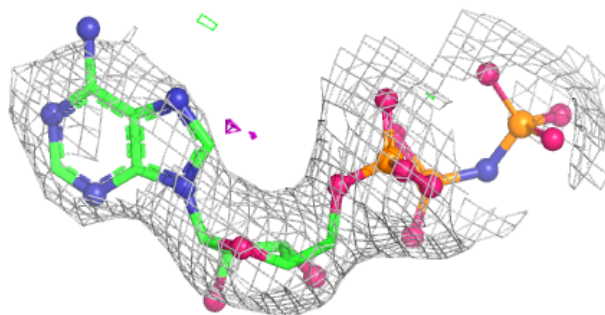


Electron density around ANP D 601:

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

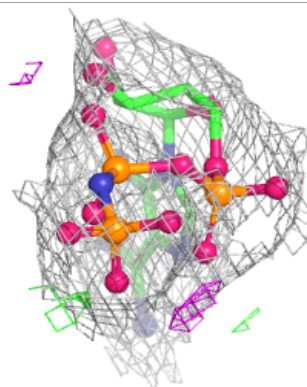
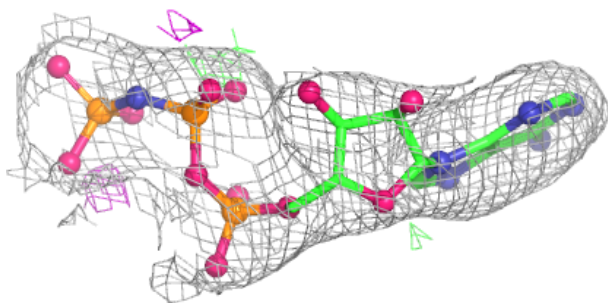
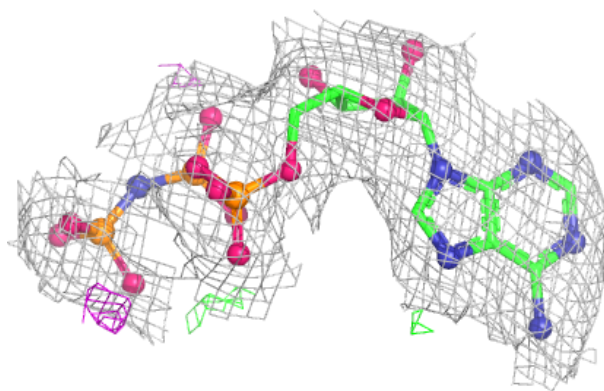
**Electron density around ANP I 601:**

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

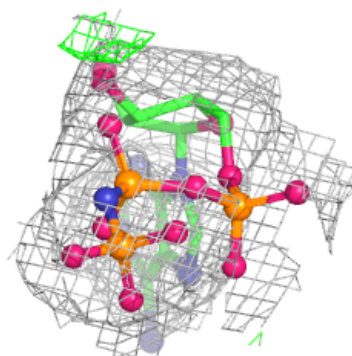
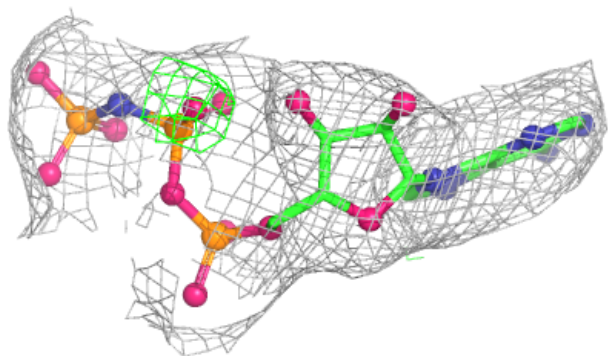
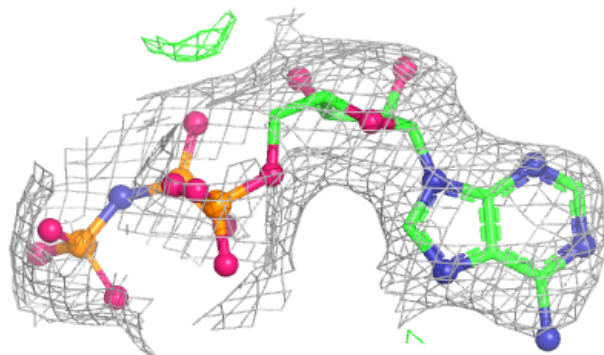


Electron density around ANP J 601:

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

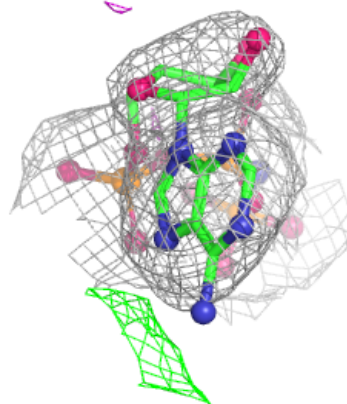
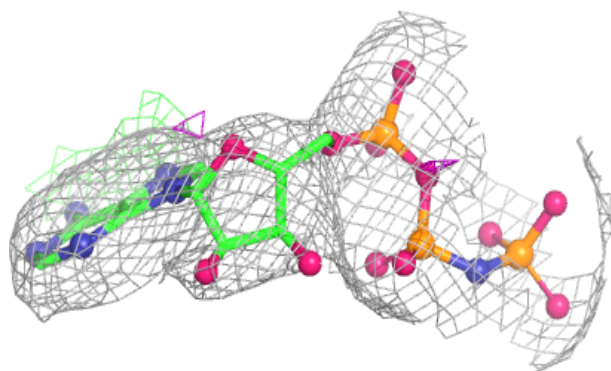
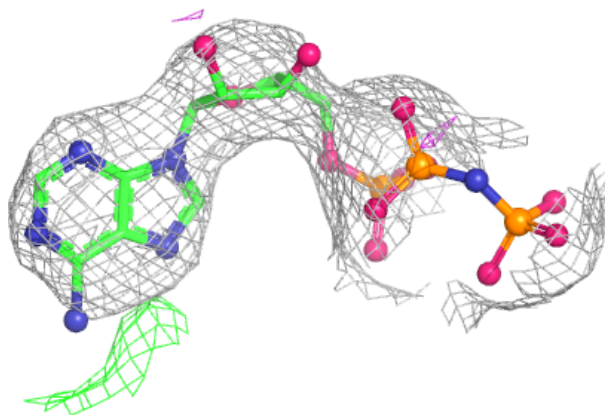
**Electron density around ANP E 601:**

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and green (positive)

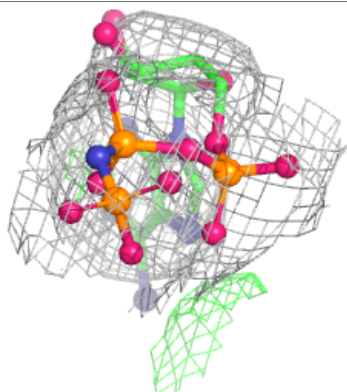
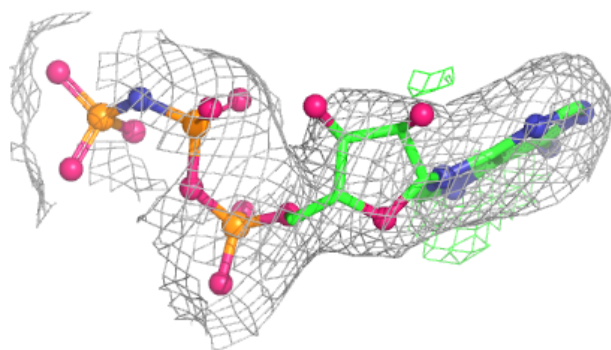
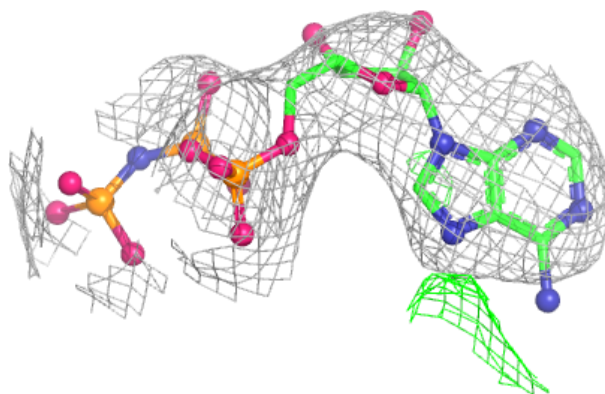


Electron density around ANP L 601:

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

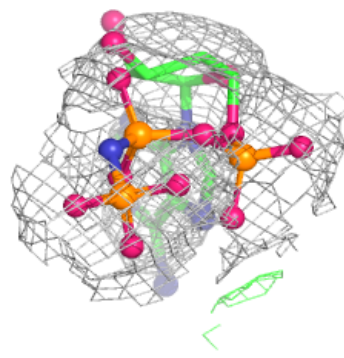
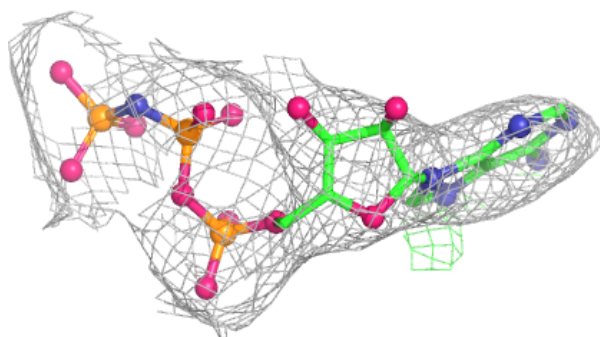
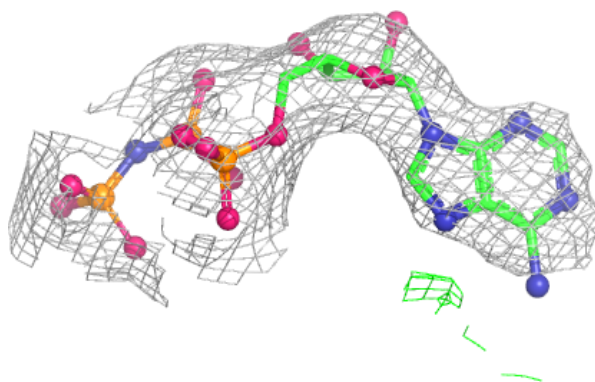
**Electron density around ANP M 601:**

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

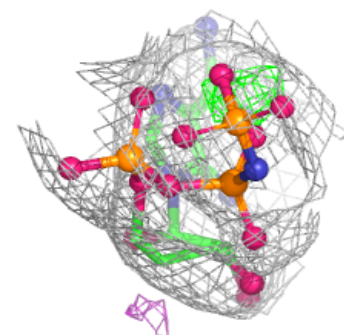
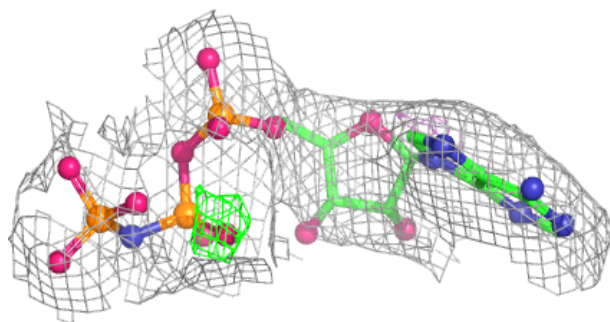
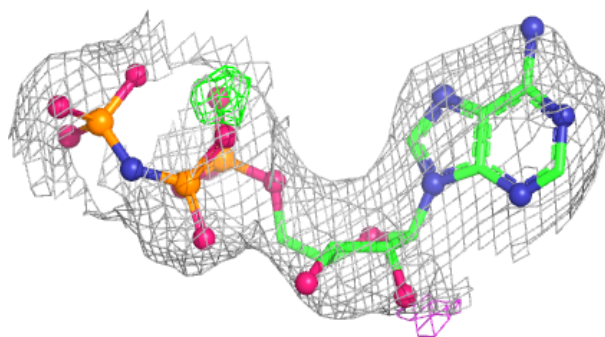


Electron density around ANP N 601:

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

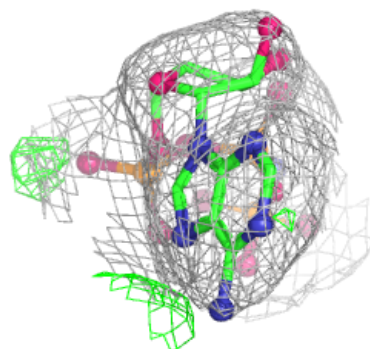
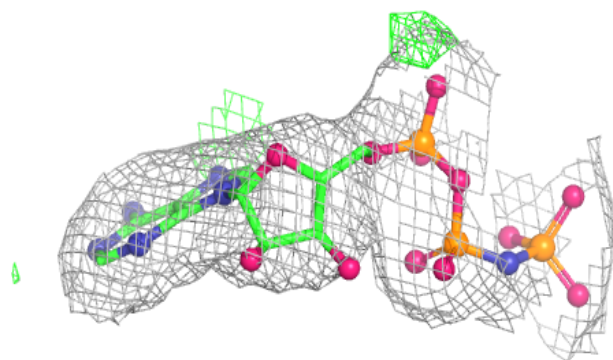
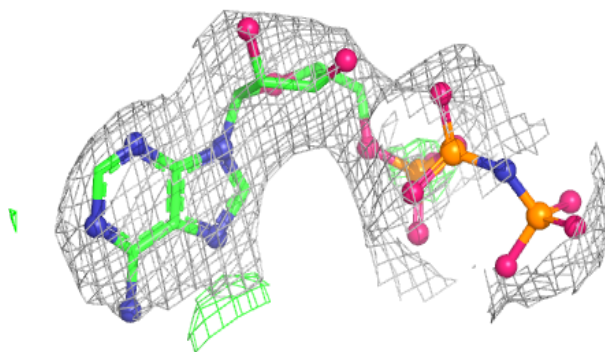
**Electron density around ANP B 601:**

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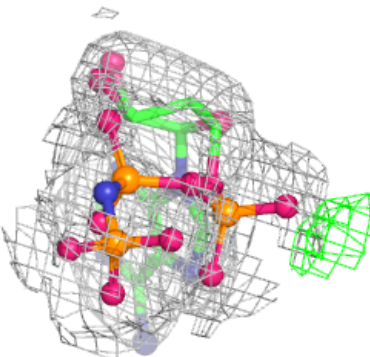
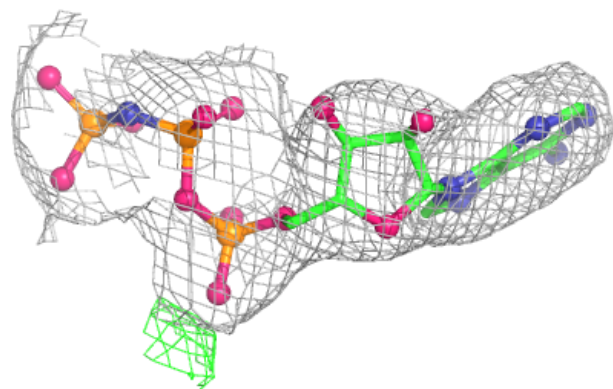
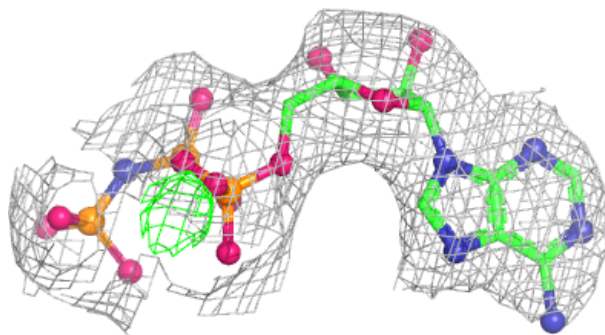


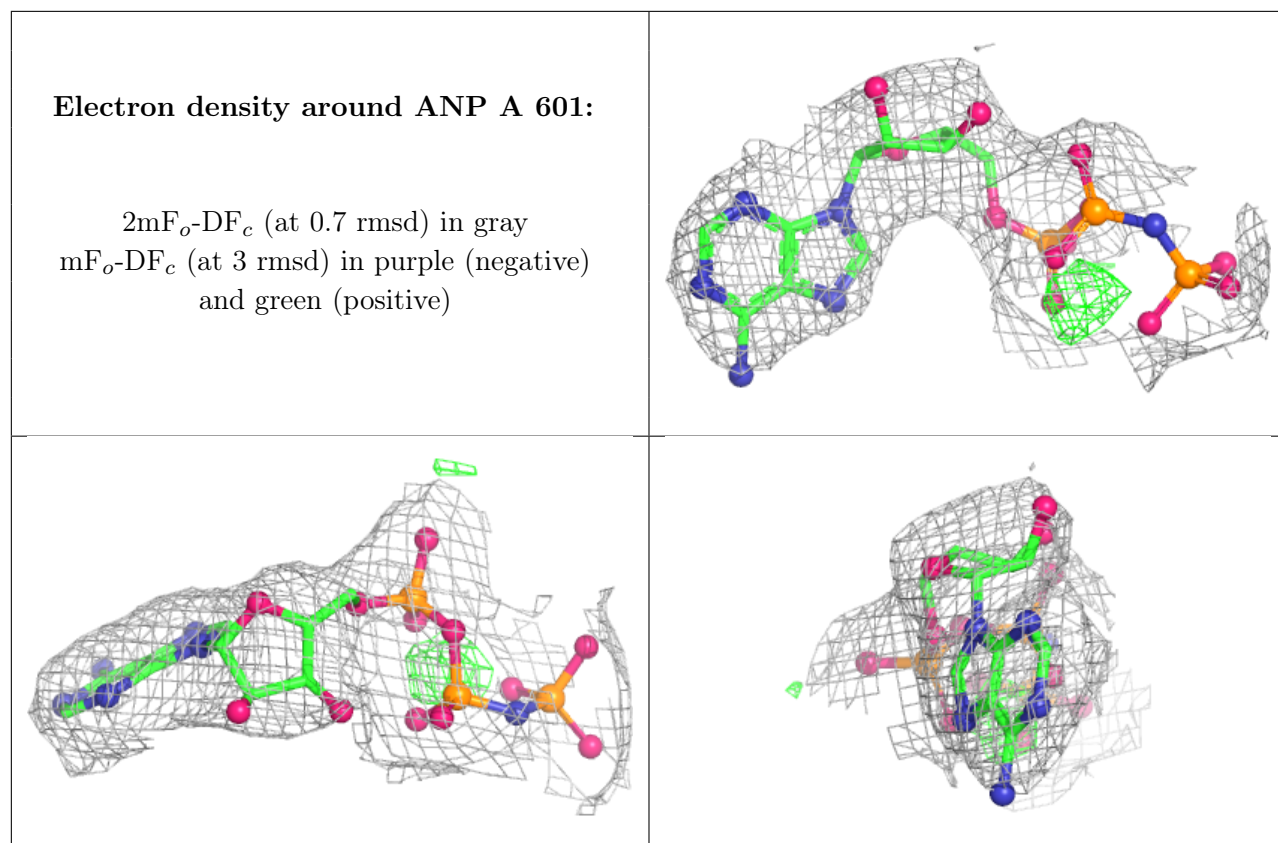
Electron density around ANP G 601:

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

**Electron density around ANP 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.