



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2024 – 12:33 PM JST

PDB ID : 5ZLP
Title : Crystal structure of glutamine synthetase from helicobacter pylori
Authors : Joo, H.K.; Lee, J.Y.
Deposited on : 2018-03-29
Resolution : 2.93 Å(reported)

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

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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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

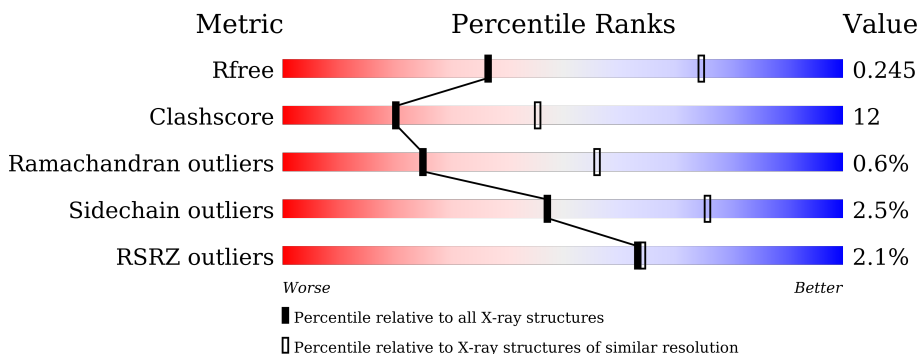
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.93 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}	130704	2969 (2.98-2.90)
Clashscore	141614	3218 (2.98-2.90)
Ramachandran outliers	138981	3122 (2.98-2.90)
Sidechain outliers	138945	3124 (2.98-2.90)
RSRZ outliers	127900	2902 (2.98-2.90)

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	481	
1	B	481	
1	C	481	
1	D	481	
1	E	481	
1	F	481	

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Mol	Chain	Length	Quality of chain	
1	G	481	%	
1	H	481	2%	
1	I	481	2%	
1	J	481	2%	
1	K	481	%	
1	L	481		

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	PPQ	I	502	-	X	-	-
5	MG	J	503	-	-	-	X

2 Entry composition [i](#)

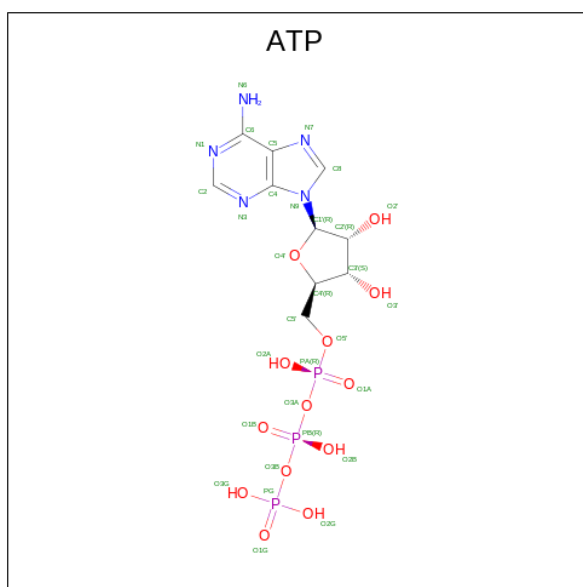
There are 7 unique types of molecules in this entry. The entry contains 46003 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glutamine synthetase.

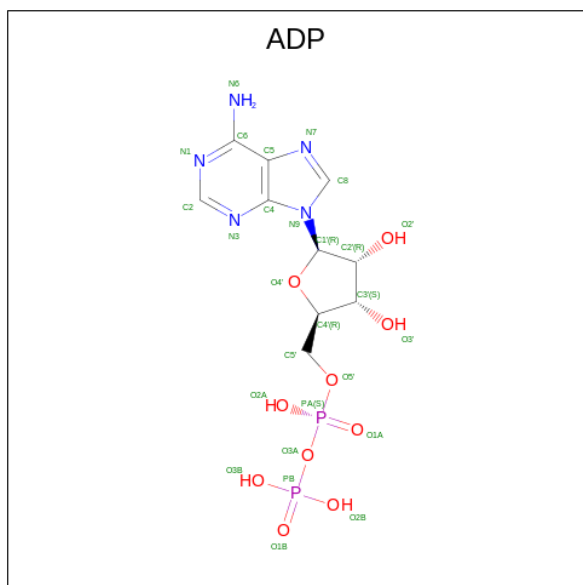
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	476	3782	2422	629	713	18	0	0	0
1	B	475	3769	2414	627	710	18	0	0	0
1	C	474	3768	2414	626	710	18	0	0	0
1	D	476	3782	2422	630	712	18	0	0	0
1	E	473	3753	2407	625	703	18	0	0	0
1	F	475	3763	2411	627	707	18	0	0	0
1	H	475	3763	2411	627	707	18	0	0	0
1	J	478	3789	2424	634	713	18	0	0	0
1	K	475	3769	2415	628	708	18	0	0	0
1	L	476	3774	2417	629	710	18	0	0	0
1	G	476	3777	2418	630	711	18	0	0	0
1	I	475	3766	2412	627	709	18	0	0	0

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



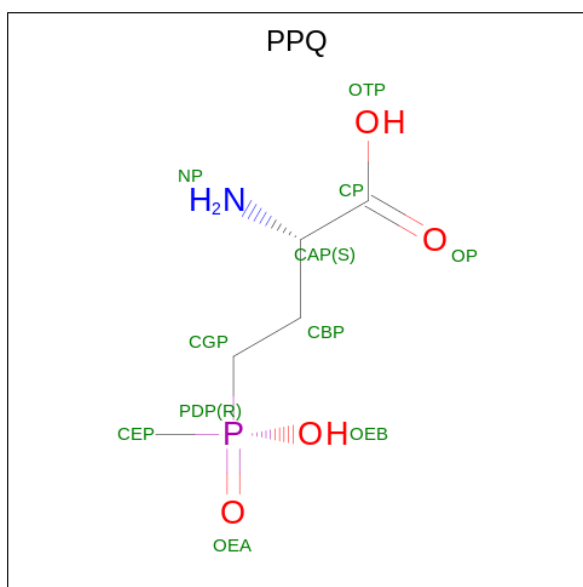
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total 31	C 10	N 5	O 13	P 3	0	0
2	B	1	Total 31	C 10	N 5	O 13	P 3	0	0
2	C	1	Total 31	C 10	N 5	O 13	P 3	0	0
2	F	1	Total 31	C 10	N 5	O 13	P 3	0	0
2	K	1	Total 31	C 10	N 5	O 13	P 3	0	0
2	G	1	Total 31	C 10	N 5	O 13	P 3	0	0

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



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

- Molecule 4 is PHOSPHINOTHRICIN (three-letter code: PPQ) (formula: C₅H₁₂NO₄P).

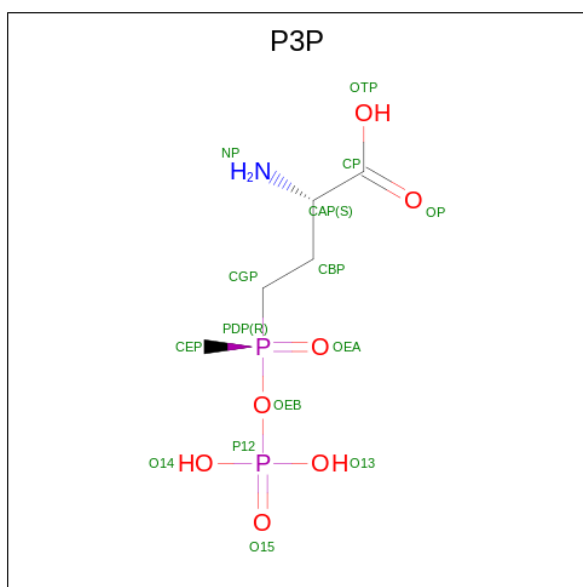


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	J	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
4	K	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
4	I	1	Total	C	N	O	P	0	0
			11	5	1	4	1		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	J	1	Total	Mg	0	0
			1	1		
5	L	2	Total	Mg	0	0
			2	2		
5	I	1	Total	Mg	0	0
			1	1		

- Molecule 6 is (2S)-2-AMINO-4-[METHYL(PHOSPHONOOXY)PHOSPHORYL]BUTANOIC ACID (three-letter code: P3P) (formula: C₅H₁₃NO₇P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
6	L	1	15	5	1	7	2	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	25	Total	O	0	0
			25	25		
7	B	20	Total	O	0	0
			20	20		
7	C	17	Total	O	0	0
			17	17		
7	D	26	Total	O	0	0
			26	26		
7	E	26	Total	O	0	0
			26	26		
7	F	19	Total	O	0	0
			19	19		
7	H	27	Total	O	0	0
			27	27		
7	J	40	Total	O	0	0
			40	40		
7	K	36	Total	O	0	0
			36	36		
7	L	42	Total	O	0	0
			42	42		
7	G	42	Total	O	0	0
			42	42		

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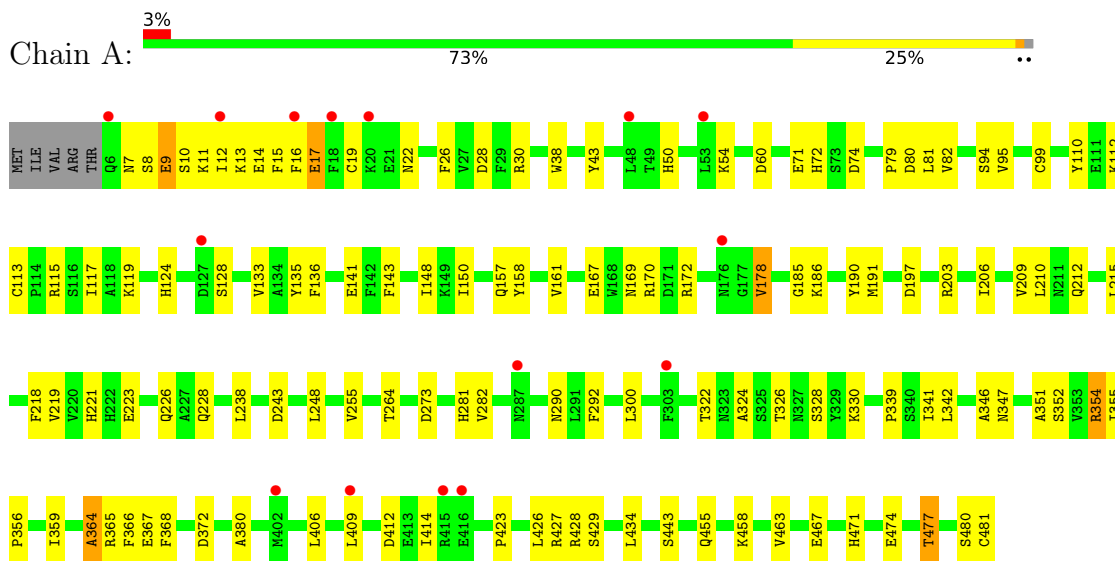
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	I	28	Total	O	0	0
			28	28		

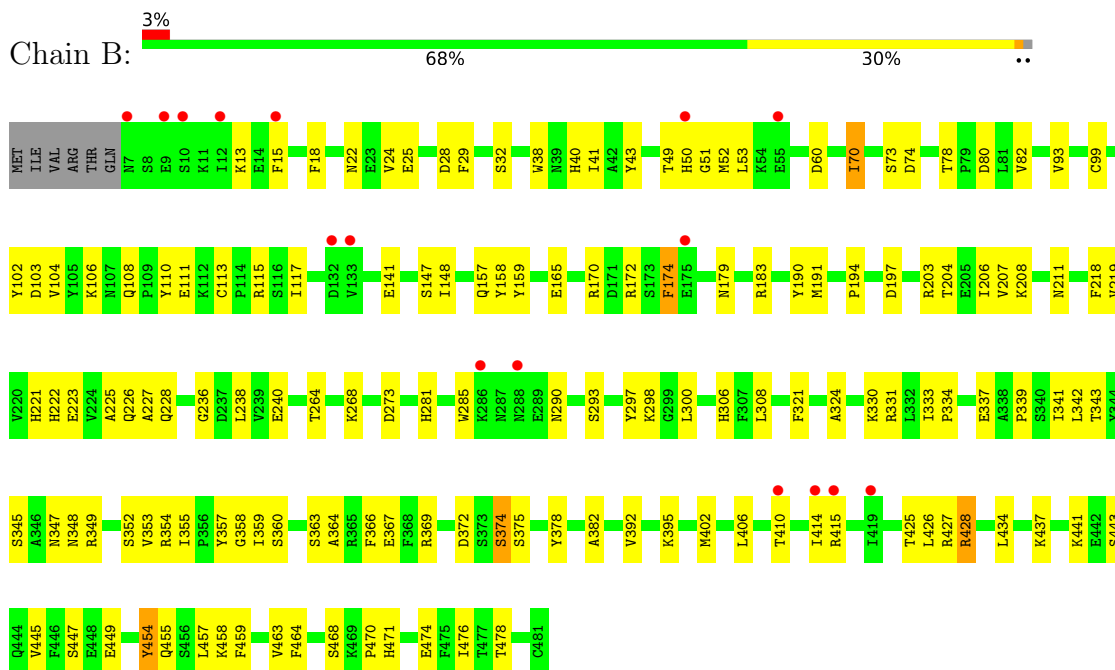
3 Residue-property plots [i](#)

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.

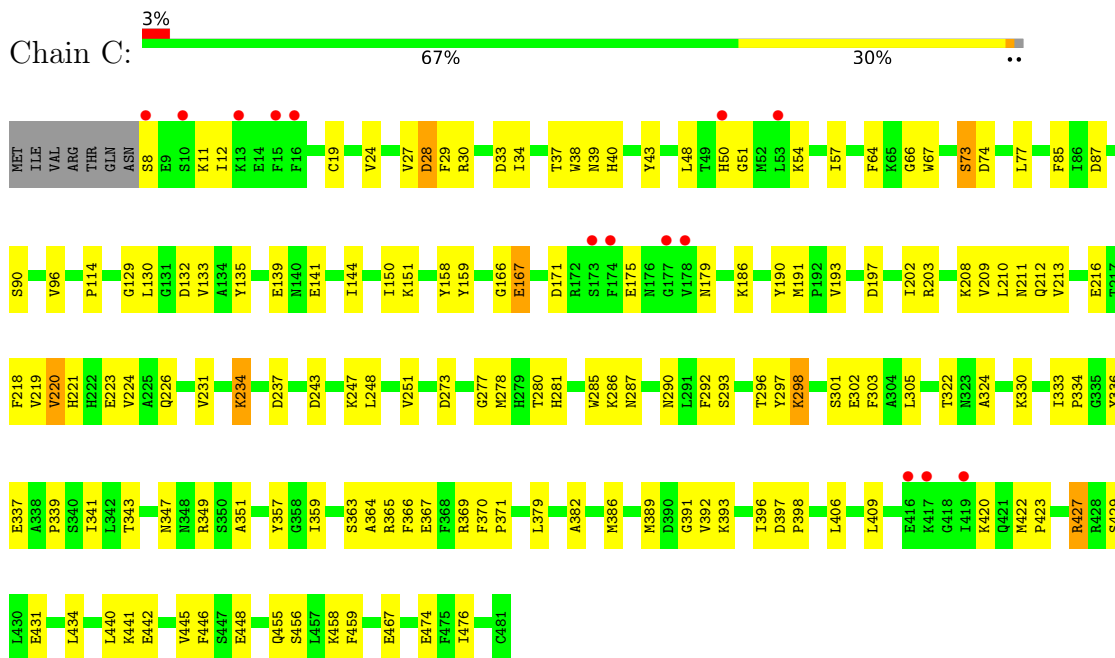
- Molecule 1: Glutamine synthetase



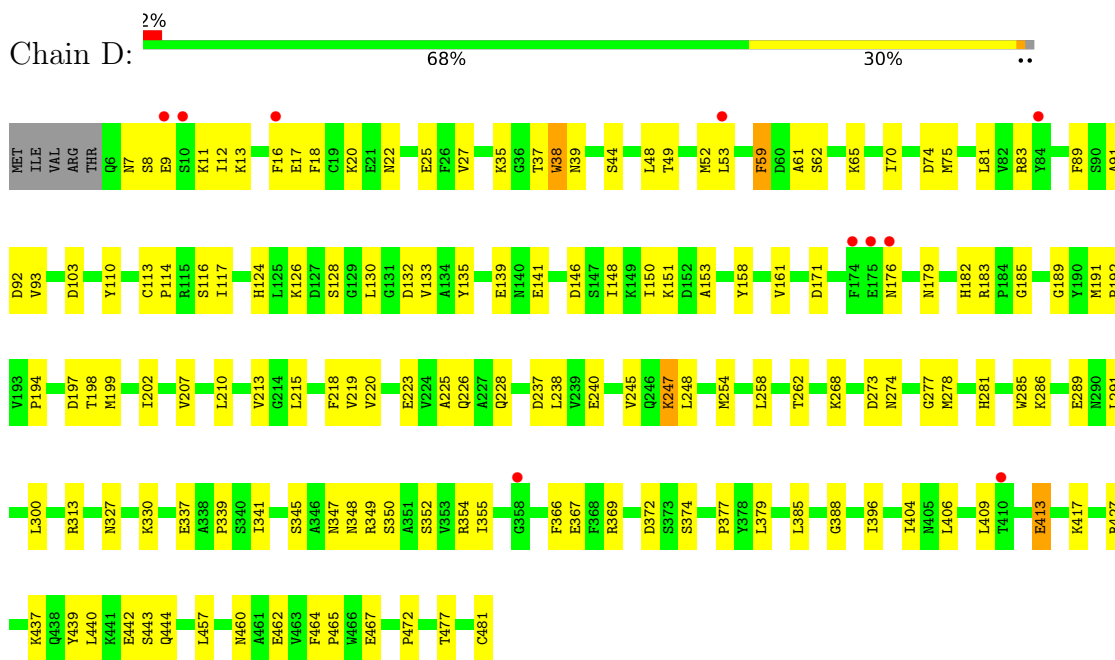
- Molecule 1: Glutamine synthetase



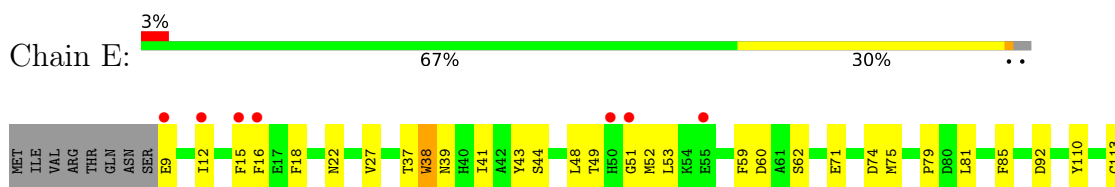
- Molecule 1: Glutamine synthetase

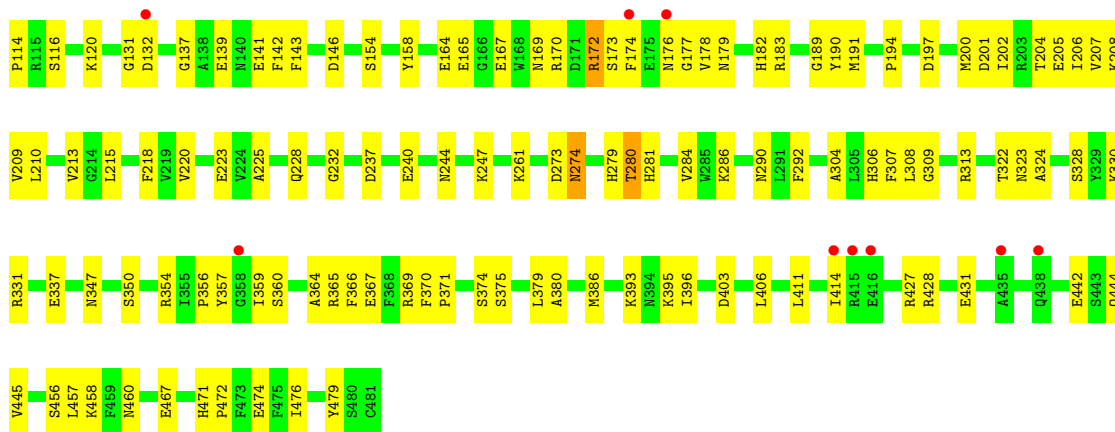


- Molecule 1: Glutamine synthetase

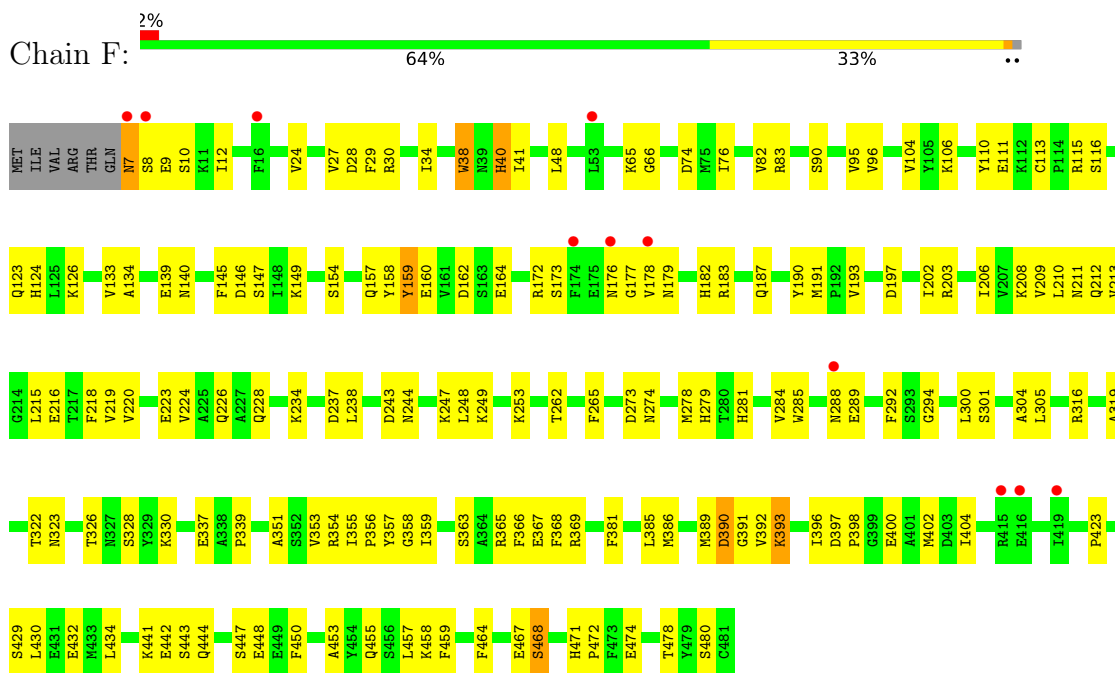


- Molecule 1: Glutamine synthetase

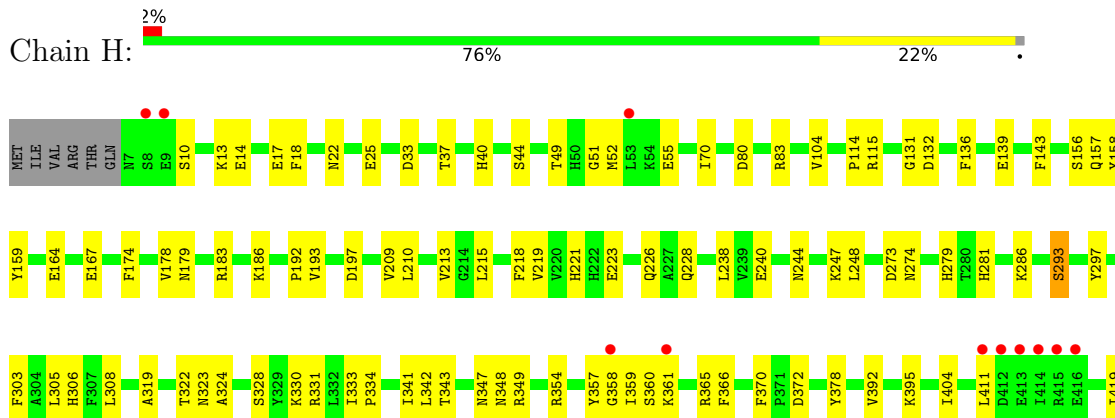




● Molecule 1: Glutamine synthetase

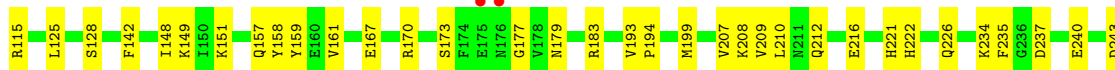


● Molecule 1: Glutamine synthetase

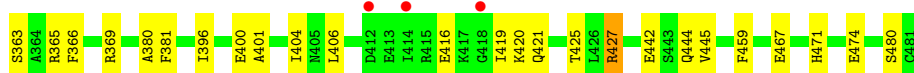
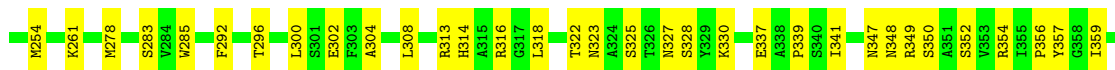
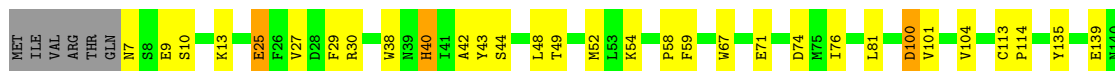




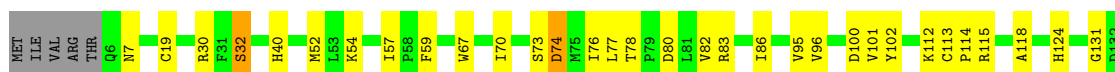
- Molecule 1: Glutamine synthetase

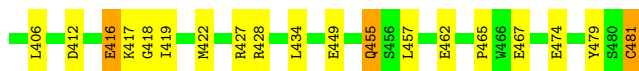


- Molecule 1: Glutamine synthetase

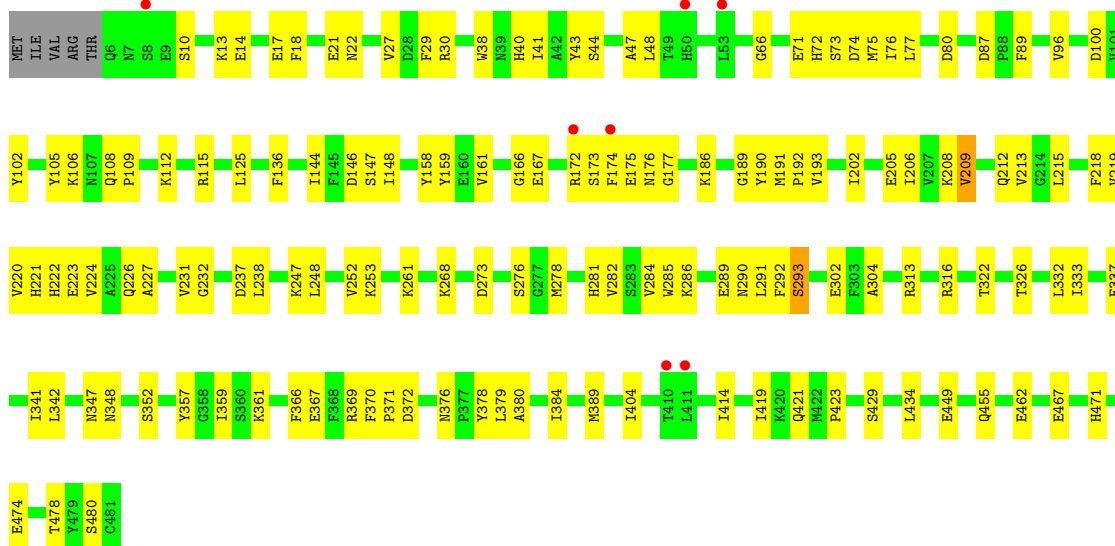


- Molecule 1: Glutamine synthetase

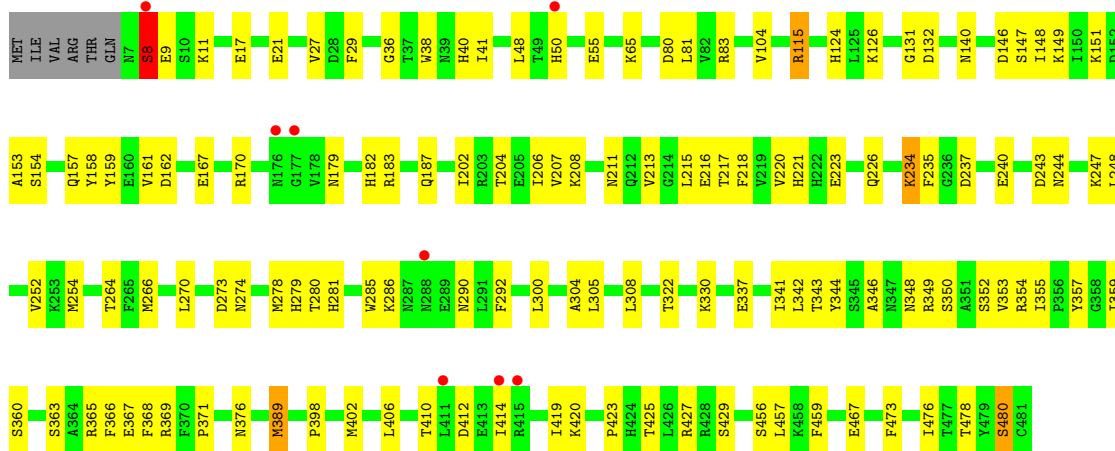




● Molecule 1: Glutamine synthetase



● Molecule 1: Glutamine synthetase



4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	234.41Å 135.17Å 203.08Å 90.00° 91.61° 90.00°	Depositor
Resolution (Å)	47.26 – 2.93 48.43 – 2.93	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.26-2.93) 100.0 (48.43-2.93)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	29.52 (at 2.91Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.168 , 0.246 0.168 , 0.245	Depositor DCC
R_{free} test set	6740 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	40.9	Xtrriage
Anisotropy	0.158	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.058 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.067 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.018 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.038 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.019 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	46003	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.94% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: P3P, ATP, ADP, PPQ, 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	0.58	4/3882 (0.1%)	0.66	1/5247 (0.0%)
1	B	0.51	0/3869	0.65	0/5230
1	C	0.49	0/3868	0.63	0/5227
1	D	0.56	2/3882 (0.1%)	0.66	1/5246 (0.0%)
1	E	0.51	0/3853	0.64	0/5207
1	F	0.52	0/3863	0.64	1/5222 (0.0%)
1	G	0.57	0/3877	0.66	0/5239
1	H	0.57	0/3863	0.67	0/5222
1	I	0.58	0/3866	0.68	0/5226
1	J	0.57	0/3889	0.68	2/5257 (0.0%)
1	K	0.58	0/3869	0.68	0/5229
1	L	0.55	0/3874	0.70	1/5237 (0.0%)
All	All	0.55	6/46455 (0.0%)	0.66	6/62789 (0.0%)

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	B	0	1
1	H	0	1
1	I	0	1
All	All	0	4

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	17	GLU	CD-OE2	-7.78	1.17	1.25
1	A	17	GLU	CD-OE1	-7.21	1.17	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	17	GLU	CG-CD	-7.07	1.41	1.51
1	A	9	GLU	CD-OE1	-5.16	1.20	1.25
1	D	38	TRP	NE1-CE2	-5.15	1.30	1.37

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	457	LEU	CB-CG-CD2	-10.37	93.38	111.00
1	J	248	LEU	CA-CB-CG	7.38	132.26	115.30
1	D	258	LEU	CA-CB-CG	7.05	131.51	115.30
1	J	30	ARG	NE-CZ-NH1	-5.47	117.56	120.30
1	A	354	ARG	NE-CZ-NH2	5.06	122.83	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	185	GLY	Peptide
1	B	225	ALA	Peptide
1	H	55	GLU	Peptide
1	I	55	GLU	Peptide

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	3782	0	3618	99	0
1	B	3769	0	3604	108	0
1	C	3768	0	3611	116	0
1	D	3782	0	3623	109	0
1	E	3753	0	3595	106	0
1	F	3763	0	3595	131	0
1	G	3777	0	3609	104	0
1	H	3763	0	3595	79	0
1	I	3766	0	3597	103	0
1	J	3789	0	3619	91	0
1	K	3769	0	3611	97	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L	3774	0	3608	99	0
2	A	31	0	12	0	0
2	B	31	0	12	1	0
2	C	31	0	12	0	0
2	F	31	0	12	2	0
2	G	31	0	12	0	0
2	K	31	0	12	3	0
3	D	27	0	12	0	0
3	E	27	0	12	0	0
3	H	27	0	12	0	0
3	I	27	0	12	2	0
3	J	27	0	12	2	0
3	L	27	0	12	2	0
4	I	11	0	10	3	0
4	J	11	0	10	0	0
4	K	11	0	10	3	0
5	I	1	0	0	0	0
5	J	1	0	0	0	0
5	L	2	0	0	0	0
6	L	15	0	10	0	0
7	A	25	0	0	0	0
7	B	20	0	0	1	0
7	C	17	0	0	0	0
7	D	26	0	0	2	0
7	E	26	0	0	0	0
7	F	19	0	0	0	0
7	G	42	0	0	0	0
7	H	27	0	0	2	0
7	I	28	0	0	1	0
7	J	40	0	0	0	0
7	K	36	0	0	2	0
7	L	42	0	0	3	0
All	All	46003	0	43469	1110	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 12.

The worst 5 of 1110 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:F:281:HIS:ND1	1:F:365:ARG:NH1	1.97	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:39:ASN:HD22	1:D:191:MET:H	1.14	0.96
1:F:480:SER:HG	1:I:182:HIS:HD1	1.15	0.95
1:J:179:ASN:OD1	1:J:183:ARG:NH2	2.02	0.93
1:G:376:ASN:HD22	1:G:379:LEU:H	1.17	0.92

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	474/481 (98%)	427 (90%)	44 (9%)	3 (1%)	25	56
1	B	473/481 (98%)	431 (91%)	33 (7%)	9 (2%)	8	26
1	C	472/481 (98%)	428 (91%)	38 (8%)	6 (1%)	12	35
1	D	474/481 (98%)	427 (90%)	44 (9%)	3 (1%)	25	56
1	E	471/481 (98%)	423 (90%)	46 (10%)	2 (0%)	34	64
1	F	473/481 (98%)	428 (90%)	40 (8%)	5 (1%)	14	40
1	G	474/481 (98%)	438 (92%)	36 (8%)	0	100	100
1	H	473/481 (98%)	445 (94%)	26 (6%)	2 (0%)	34	64
1	I	473/481 (98%)	437 (92%)	35 (7%)	1 (0%)	47	76
1	J	476/481 (99%)	449 (94%)	27 (6%)	0	100	100
1	K	473/481 (98%)	438 (93%)	34 (7%)	1 (0%)	47	76
1	L	474/481 (98%)	435 (92%)	37 (8%)	2 (0%)	34	64
All	All	5680/5772 (98%)	5206 (92%)	440 (8%)	34 (1%)	25	56

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	298	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	9	GLU
1	L	417	LYS
1	I	8	SER
1	A	218	PHE

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	404/415 (97%)	397 (98%)	7 (2%)	60	83
1	B	402/415 (97%)	394 (98%)	8 (2%)	55	80
1	C	403/415 (97%)	391 (97%)	12 (3%)	41	72
1	D	404/415 (97%)	394 (98%)	10 (2%)	47	76
1	E	399/415 (96%)	387 (97%)	12 (3%)	41	72
1	F	400/415 (96%)	386 (96%)	14 (4%)	36	67
1	G	402/415 (97%)	390 (97%)	12 (3%)	41	72
1	H	400/415 (96%)	394 (98%)	6 (2%)	65	85
1	I	401/415 (97%)	388 (97%)	13 (3%)	39	70
1	J	403/415 (97%)	396 (98%)	7 (2%)	60	83
1	K	402/415 (97%)	389 (97%)	13 (3%)	39	70
1	L	402/415 (97%)	397 (99%)	5 (1%)	71	89
All	All	4822/4980 (97%)	4703 (98%)	119 (2%)	47	76

5 of 119 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	220	VAL
1	I	234	LYS
1	J	372	ASP
1	I	154	SER
1	I	480	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	7	ASN
1	K	444	GLN
1	I	50	HIS
1	G	376	ASN
1	D	50	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 4 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
3	ADP	I	501	-	24,29,29	1.23	3 (12%)	29,45,45	2.18	9 (31%)
2	ATP	K	501	-	26,33,33	1.08	2 (7%)	31,52,52	1.47	6 (19%)
3	ADP	L	503	5	24,29,29	1.42	5 (20%)	29,45,45	2.36	10 (34%)
2	ATP	B	501	-	26,33,33	1.20	3 (11%)	31,52,52	1.58	8 (25%)
3	ADP	H	501	-	24,29,29	1.34	4 (16%)	29,45,45	2.08	9 (31%)
3	ADP	J	501	-	24,29,29	1.25	2 (8%)	29,45,45	2.31	8 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ATP	C	501	-	26,33,33	1.24	2 (7%)	31,52,52	1.68	6 (19%)
4	PPQ	J	502	5	7,10,10	2.75	2 (28%)	7,14,14	2.02	2 (28%)
6	P3P	L	501	5	9,14,14	2.40	3 (33%)	13,21,21	1.71	1 (7%)
3	ADP	E	501	-	24,29,29	1.34	4 (16%)	29,45,45	2.06	7 (24%)
3	ADP	D	501	-	24,29,29	1.49	5 (20%)	29,45,45	2.27	10 (34%)
4	PPQ	K	502	-	7,10,10	2.73	2 (28%)	7,14,14	1.65	2 (28%)
2	ATP	F	501	-	26,33,33	1.17	3 (11%)	31,52,52	1.52	9 (29%)
2	ATP	A	501	-	26,33,33	1.22	3 (11%)	31,52,52	1.64	7 (22%)
4	PPQ	I	502	5	7,10,10	3.48	3 (42%)	7,14,14	2.21	3 (42%)
2	ATP	G	501	-	26,33,33	1.08	2 (7%)	31,52,52	1.66	8 (25%)

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	ADP	I	501	-	-	6/12/32/32	0/3/3/3
2	ATP	K	501	-	-	1/18/38/38	0/3/3/3
3	ADP	L	503	5	-	3/12/32/32	0/3/3/3
2	ATP	B	501	-	-	5/18/38/38	0/3/3/3
3	ADP	H	501	-	-	1/12/32/32	0/3/3/3
3	ADP	J	501	-	-	2/12/32/32	0/3/3/3
2	ATP	C	501	-	-	6/18/38/38	0/3/3/3
4	PPQ	J	502	5	-	7/10/10/10	-
6	P3P	L	501	5	-	11/12/16/16	-
3	ADP	E	501	-	-	0/12/32/32	0/3/3/3
3	ADP	D	501	-	-	2/12/32/32	0/3/3/3
4	PPQ	K	502	-	-	9/10/10/10	-
2	ATP	F	501	-	-	2/18/38/38	0/3/3/3
2	ATP	A	501	-	-	4/18/38/38	0/3/3/3
4	PPQ	I	502	5	-	8/10/10/10	-
2	ATP	G	501	-	-	4/18/38/38	0/3/3/3

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	I	502	PPQ	PDP-CGP	8.20	1.87	1.79
4	K	502	PPQ	PDP-CGP	6.53	1.85	1.79
4	J	502	PPQ	PDP-CGP	6.43	1.85	1.79
6	L	501	P3P	PDP-CGP	5.45	1.84	1.79
2	C	501	ATP	O4'-C1'	3.27	1.45	1.41

The worst 5 of 105 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	503	ADP	N3-C2-N1	-6.80	118.05	128.68
3	J	501	ADP	N3-C2-N1	-6.62	118.33	128.68
3	D	501	ADP	N3-C2-N1	-6.46	118.58	128.68
3	E	501	ADP	C4-C5-N7	-6.12	103.02	109.40
3	I	501	ADP	N3-C2-N1	-6.02	119.27	128.68

There are no chirality outliers.

5 of 71 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	ATP	C5'-O5'-PA-O1A
2	A	501	ATP	C5'-O5'-PA-O2A
2	B	501	ATP	C5'-O5'-PA-O3A
2	C	501	ATP	O4'-C4'-C5'-O5'
2	C	501	ATP	C3'-C4'-C5'-O5'

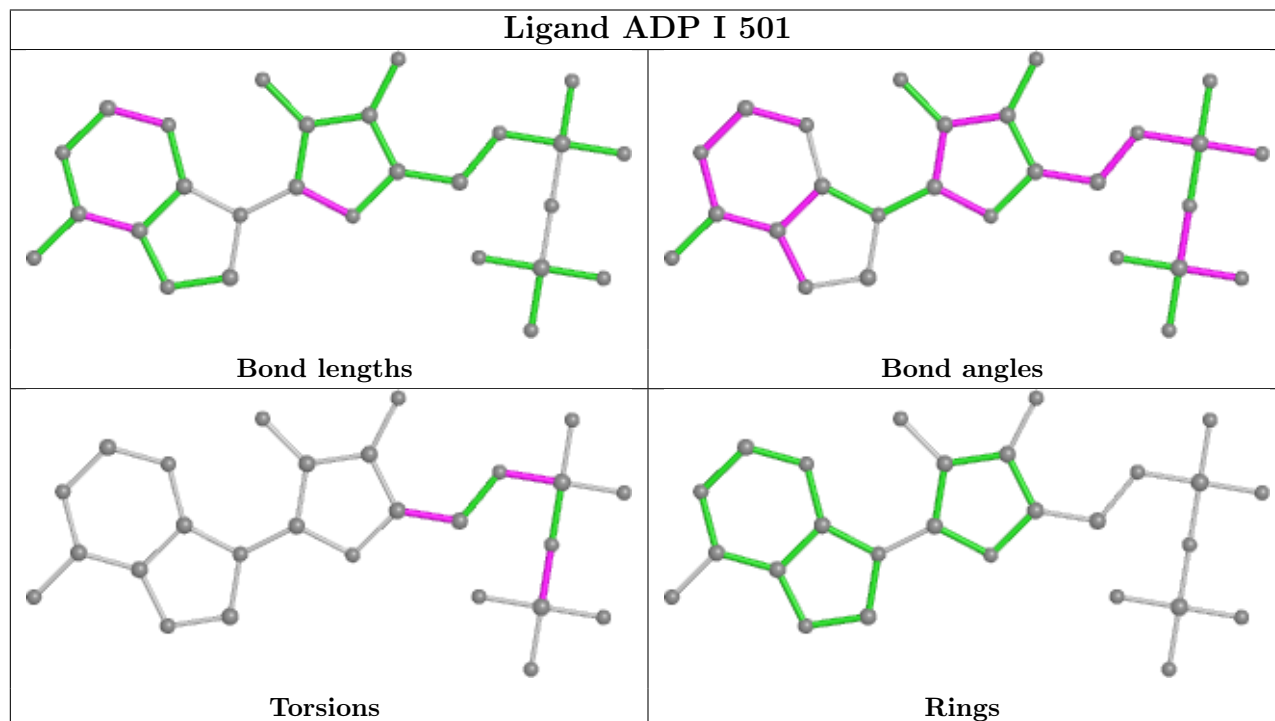
There are no ring outliers.

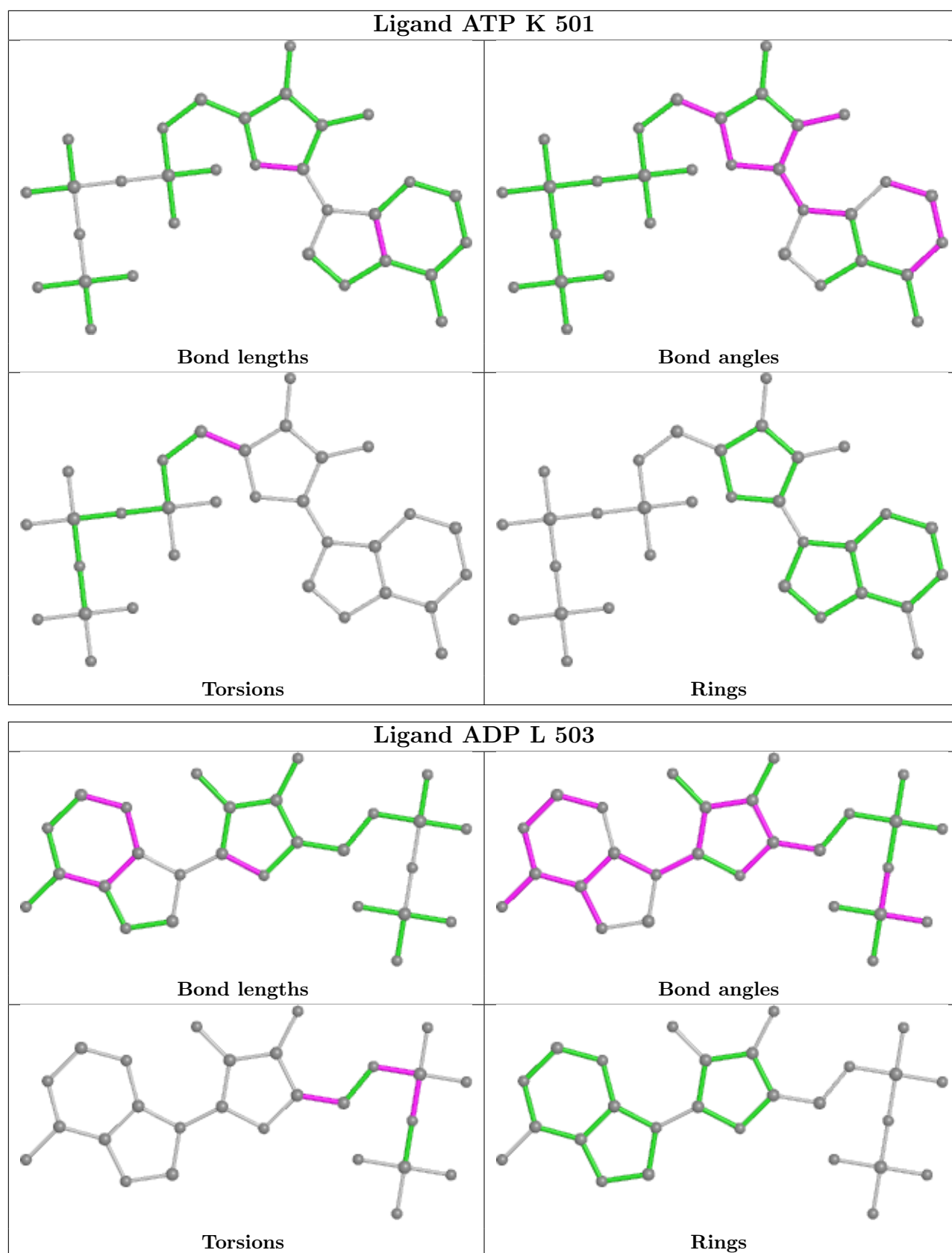
8 monomers are involved in 18 short contacts:

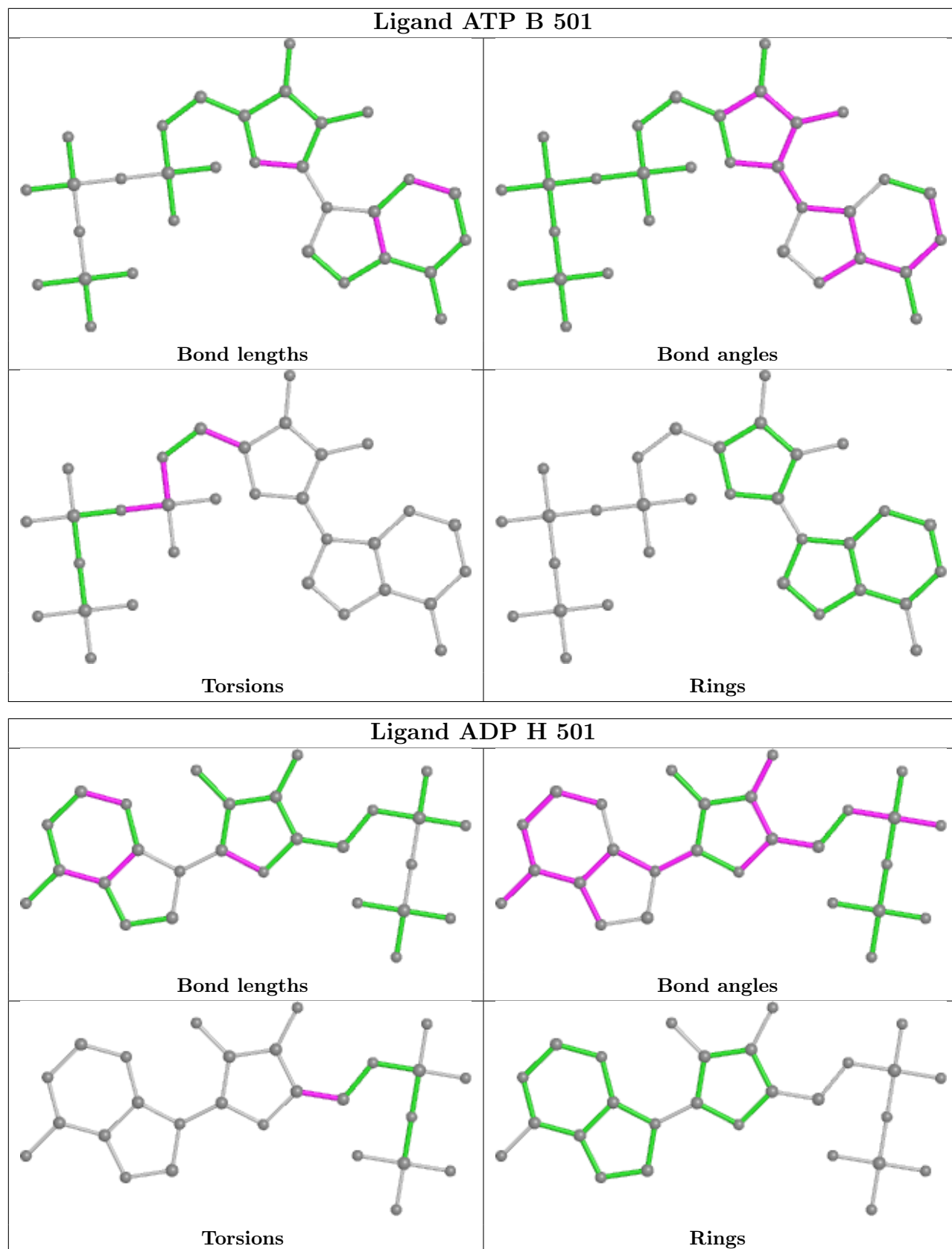
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	501	ADP	2	0
2	K	501	ATP	3	0
3	L	503	ADP	2	0
2	B	501	ATP	1	0
3	J	501	ADP	2	0
4	K	502	PPQ	3	0
2	F	501	ATP	2	0
4	I	502	PPQ	3	0

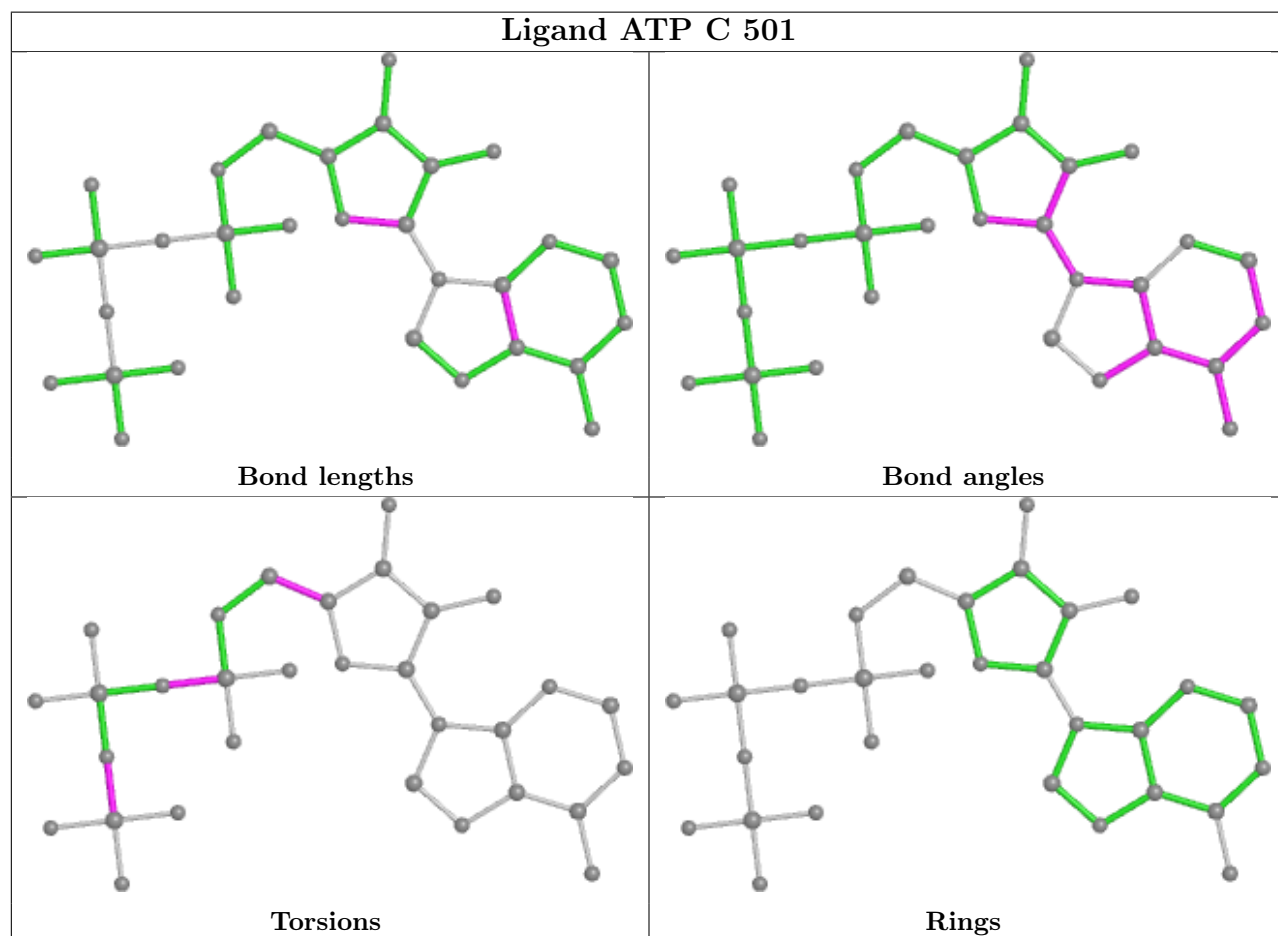
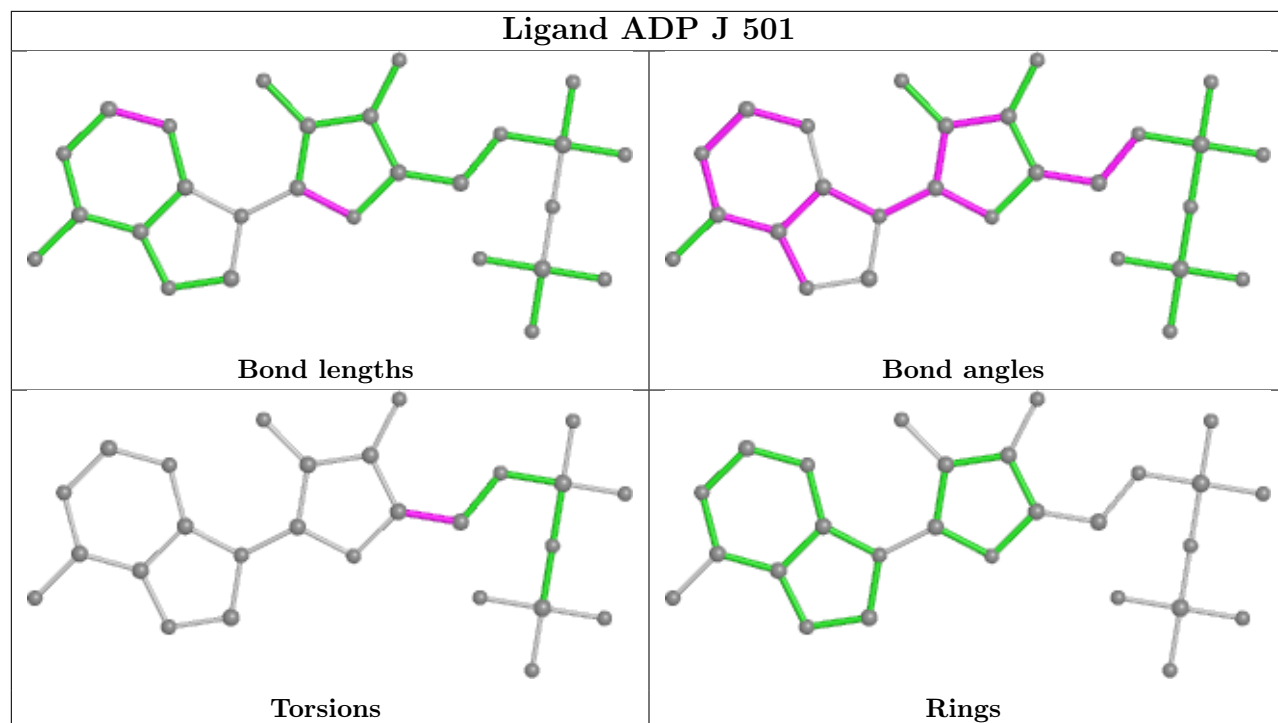
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

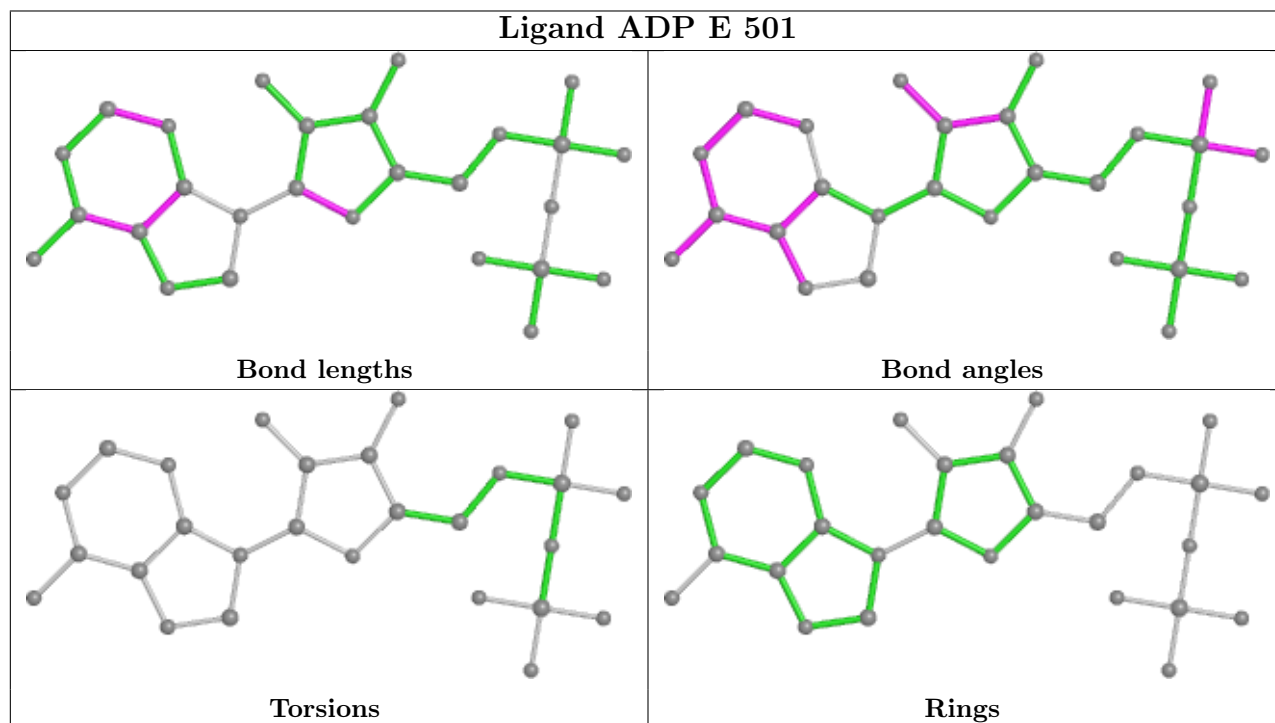
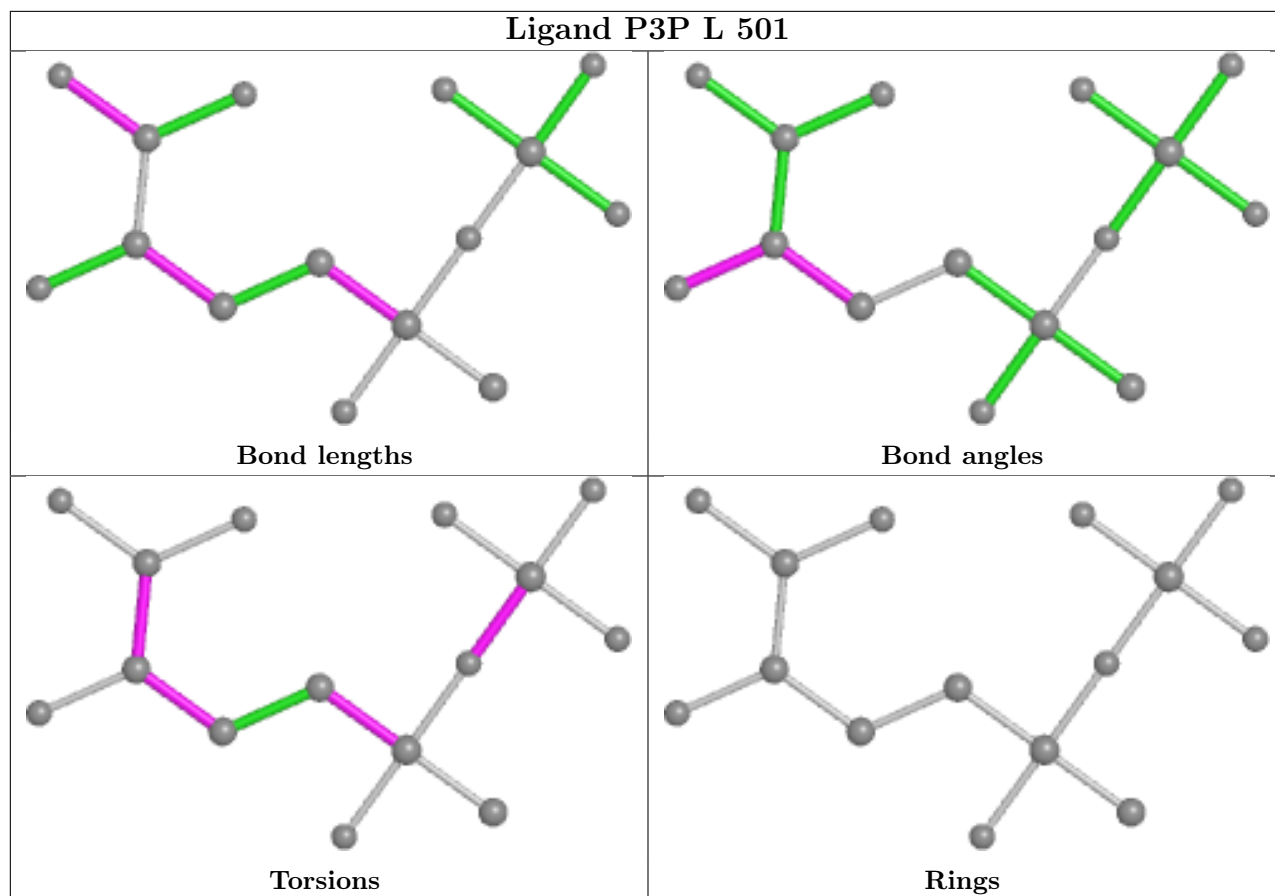
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

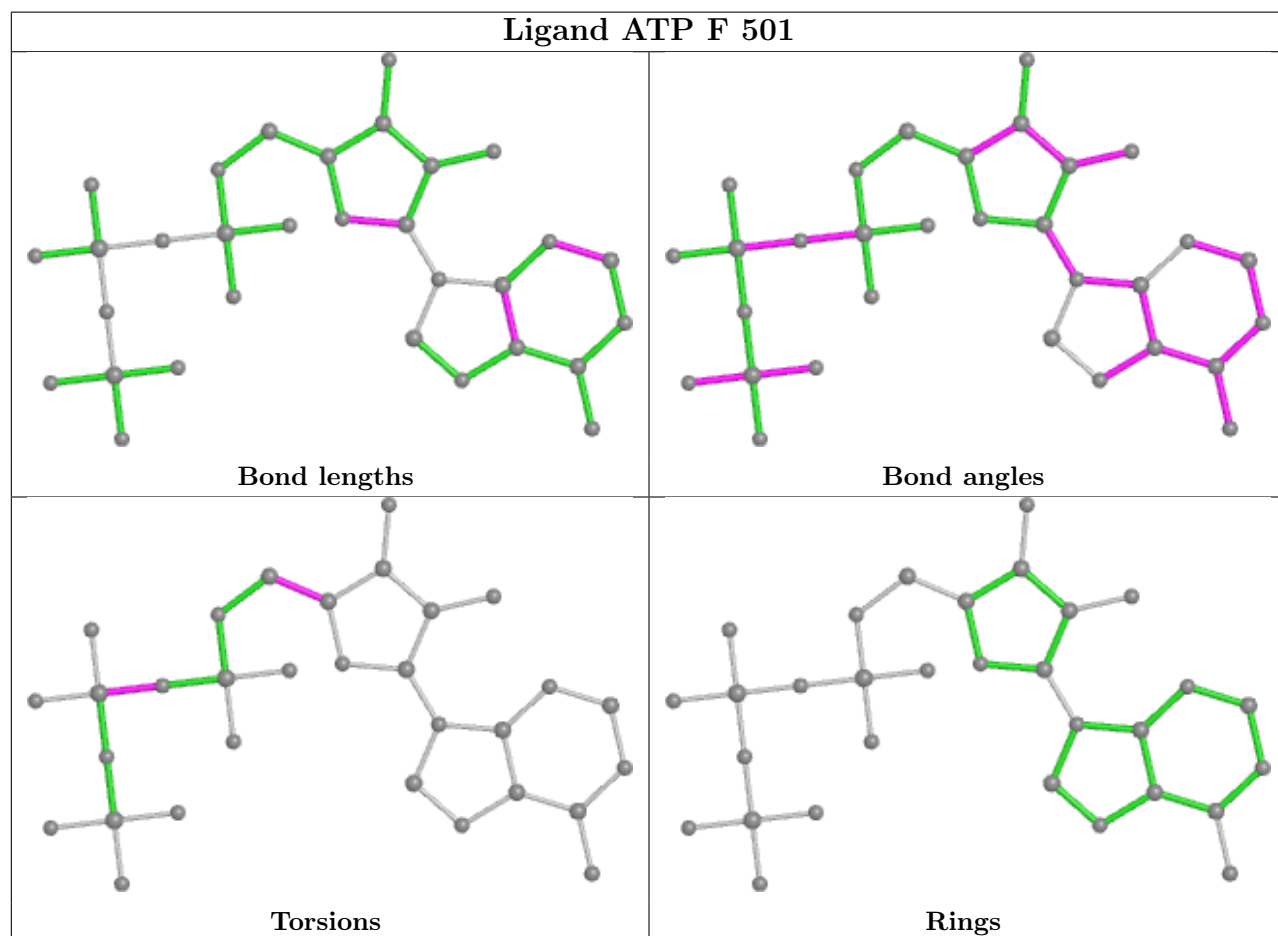
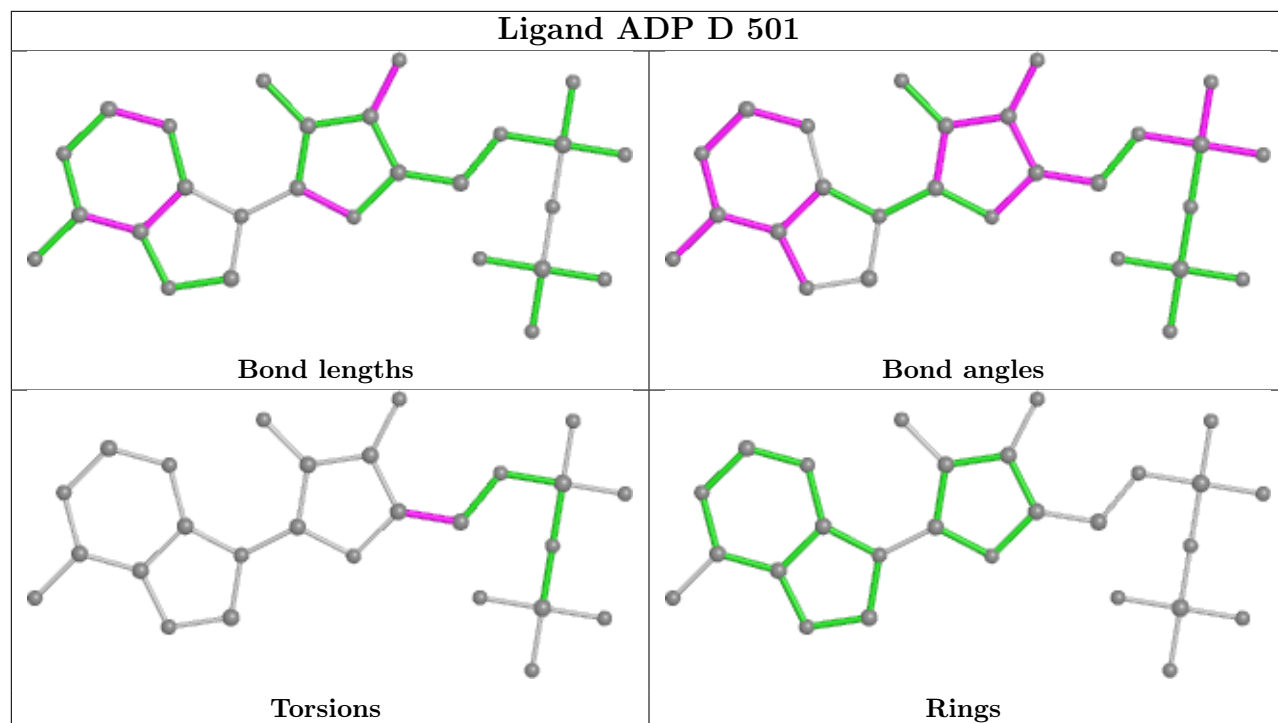


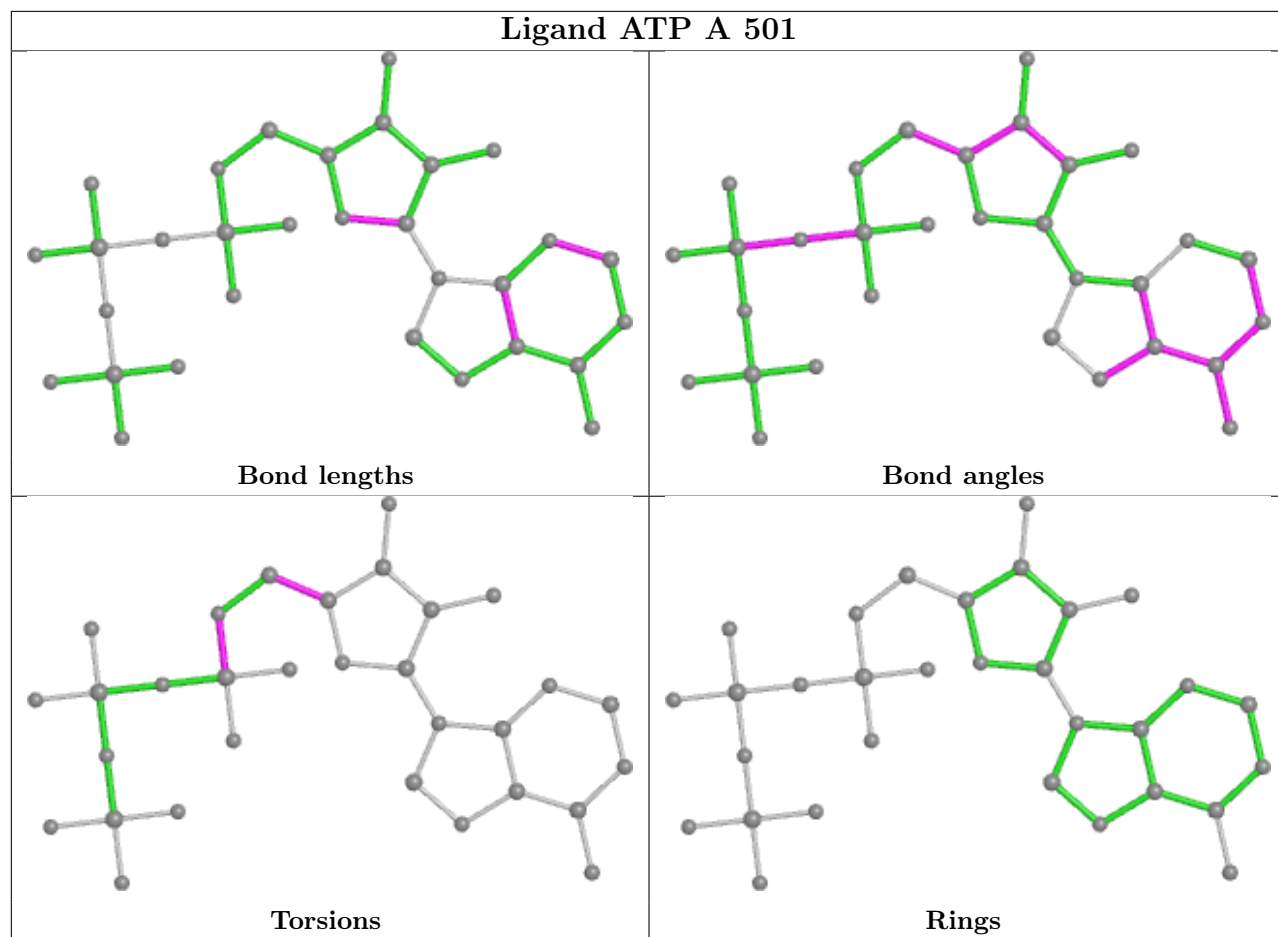


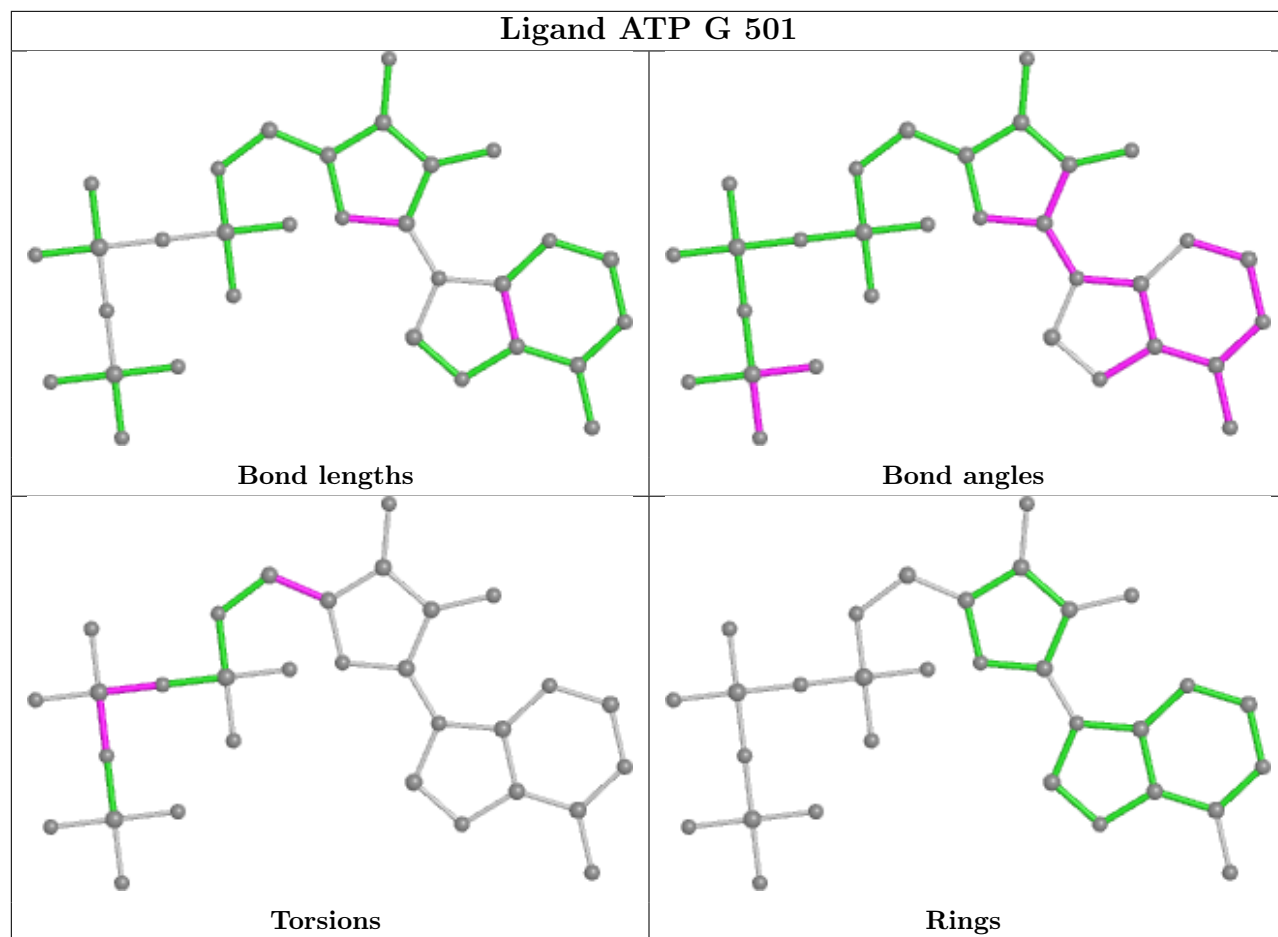












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	476/481 (98%)	-0.01	15 (3%) 47 46	14, 33, 61, 89	0
1	B	475/481 (98%)	-0.07	16 (3%) 45 43	17, 34, 55, 76	0
1	C	474/481 (98%)	-0.03	14 (2%) 50 49	15, 32, 59, 90	0
1	D	476/481 (98%)	-0.09	10 (2%) 63 64	14, 32, 55, 71	0
1	E	473/481 (98%)	-0.06	16 (3%) 45 43	16, 33, 56, 76	0
1	F	475/481 (98%)	-0.07	11 (2%) 60 61	12, 33, 56, 79	0
1	G	476/481 (98%)	-0.26	7 (1%) 73 75	10, 22, 43, 85	0
1	H	475/481 (98%)	-0.28	11 (2%) 60 61	10, 22, 44, 79	0
1	I	475/481 (98%)	-0.29	8 (1%) 70 71	9, 20, 39, 73	0
1	J	478/481 (99%)	-0.23	8 (1%) 70 71	10, 21, 42, 88	0
1	K	475/481 (98%)	-0.26	3 (0%) 89 90	10, 21, 43, 75	0
1	L	476/481 (98%)	-0.31	1 (0%) 95 95	10, 22, 38, 60	0
All	All	5704/5772 (98%)	-0.16	120 (2%) 63 64	9, 27, 52, 90	0

The worst 5 of 120 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	412	ASP	4.2
1	E	414	ILE	4.0
1	D	16	PHE	3.8
1	B	414	ILE	3.6
1	H	411	LEU	3.4

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 monosaccharides in this entry.

6.4 Ligands [i](#)

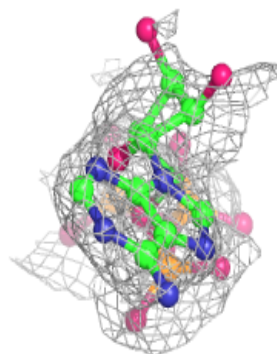
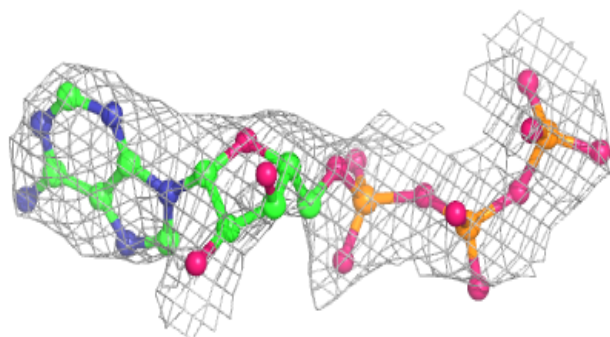
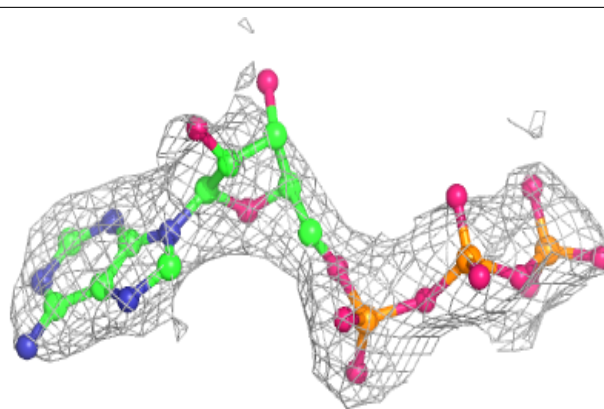
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	MG	J	503	1/1	0.79	0.46	41,41,41,41	0
5	MG	L	504	1/1	0.81	0.31	53,53,53,53	0
4	PPQ	I	502	11/11	0.85	0.25	28,36,51,58	0
2	ATP	A	501	31/31	0.85	0.24	42,63,115,116	0
3	ADP	E	501	27/27	0.85	0.25	40,56,78,102	0
2	ATP	B	501	31/31	0.87	0.20	38,55,90,96	0
2	ATP	C	501	31/31	0.87	0.21	48,60,91,94	0
2	ATP	F	501	31/31	0.88	0.20	45,57,95,104	0
3	ADP	D	501	27/27	0.88	0.24	46,53,95,113	0
5	MG	I	503	1/1	0.88	0.25	44,44,44,44	0
3	ADP	H	501	27/27	0.89	0.23	29,39,81,100	0
3	ADP	L	503	27/27	0.89	0.18	24,38,77,85	0
2	ATP	K	501	31/31	0.90	0.22	23,40,96,99	0
6	P3P	L	501	15/15	0.90	0.21	24,41,68,78	0
3	ADP	I	501	27/27	0.91	0.20	25,34,79,106	0
4	PPQ	J	502	11/11	0.92	0.20	25,29,37,45	11
2	ATP	G	501	31/31	0.92	0.18	22,35,83,98	0
3	ADP	J	501	27/27	0.93	0.18	26,35,83,102	0
5	MG	L	502	1/1	0.95	0.11	48,48,48,48	0
4	PPQ	K	502	11/11	0.95	0.19	22,28,41,43	11

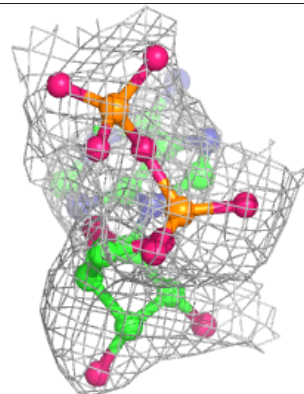
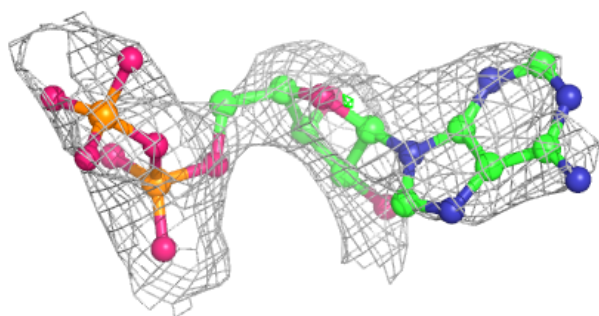
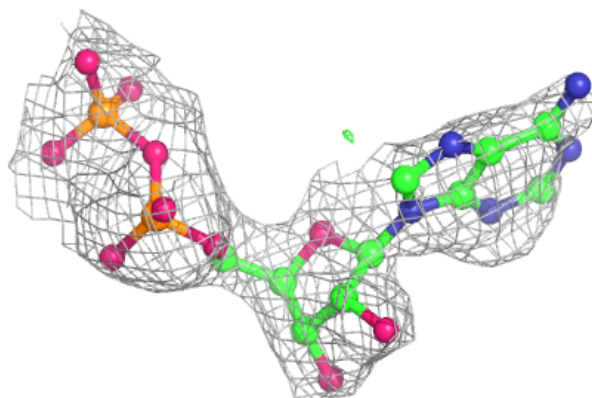
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ATP A 501:

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

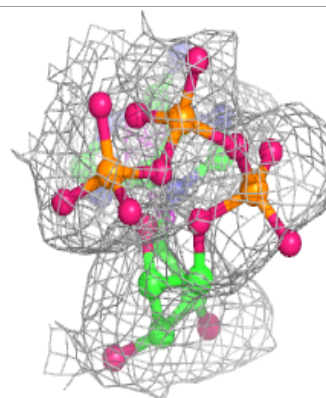
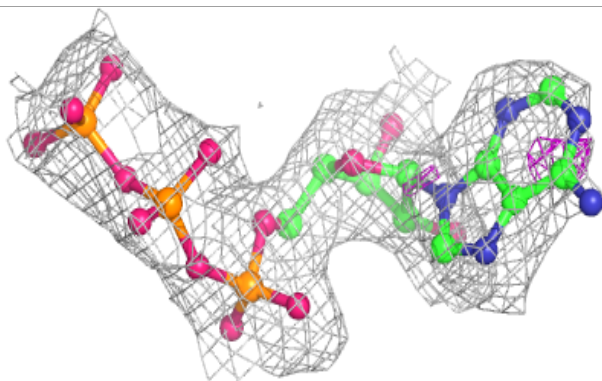
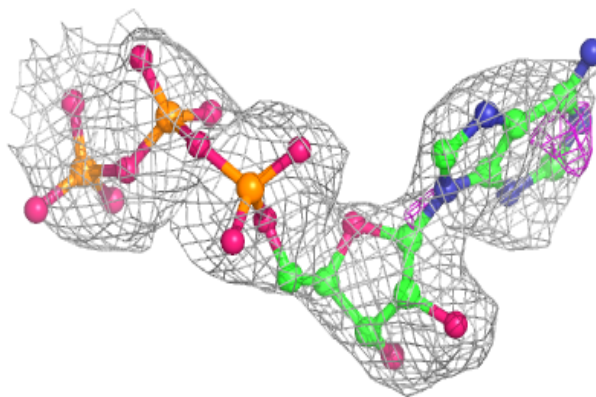
**Electron density around ADP E 501:**

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

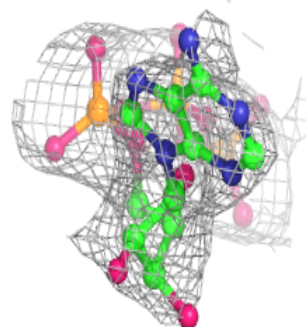
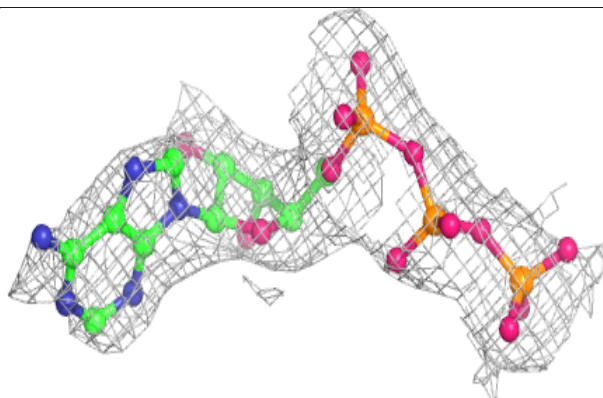
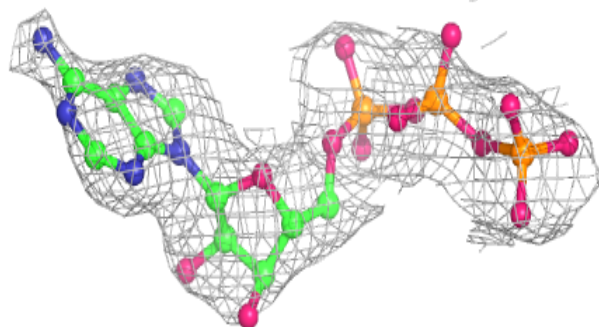


Electron density around ATP B 501:

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

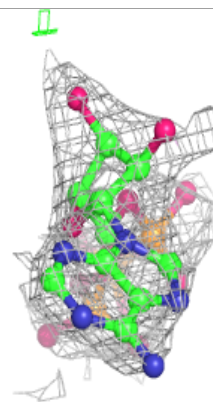
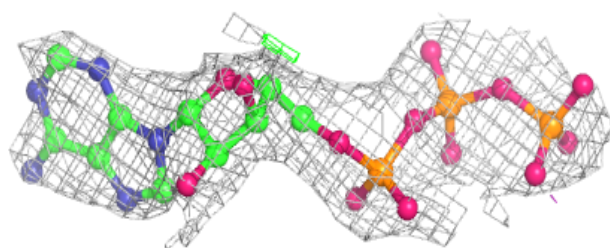
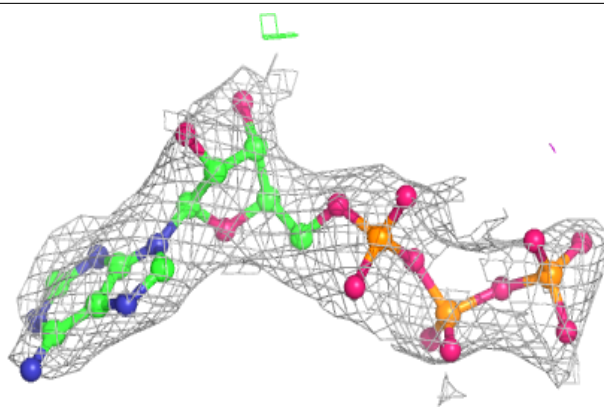
**Electron density around ATP C 501:**

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

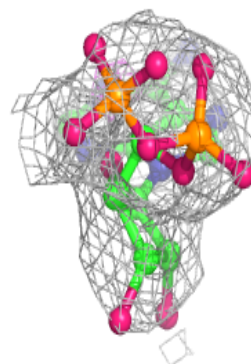
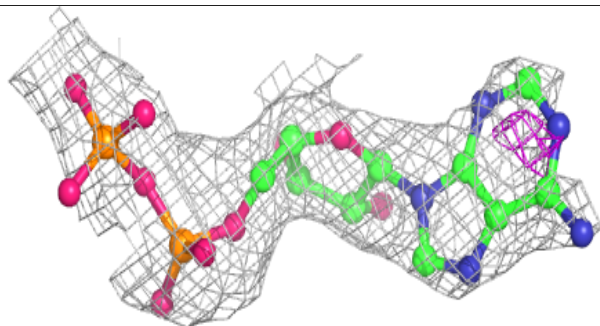
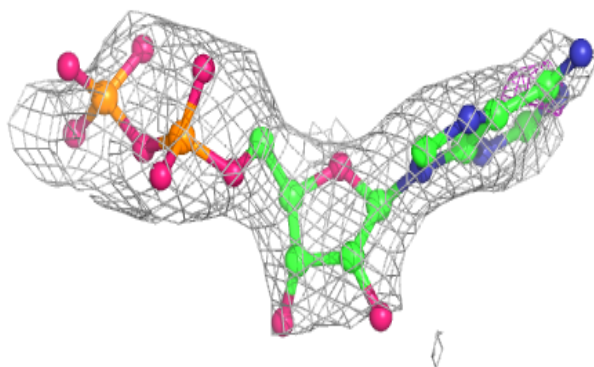


Electron density around ATP F 501:

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and green (positive)

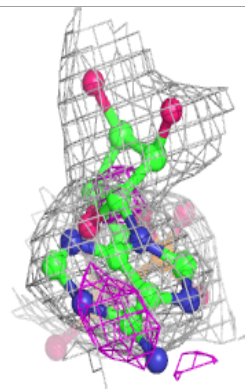
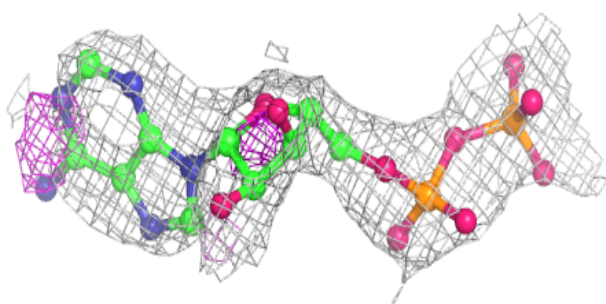
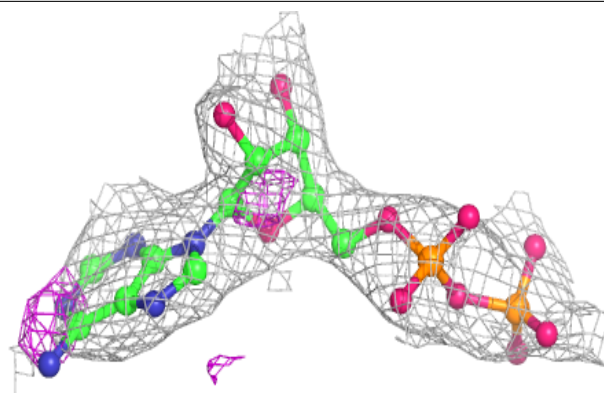
**Electron density around ADP D 501:**

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

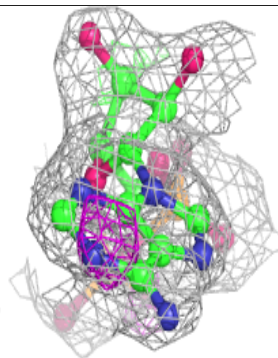
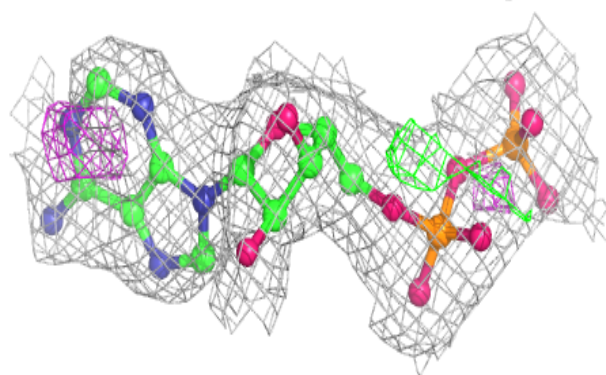
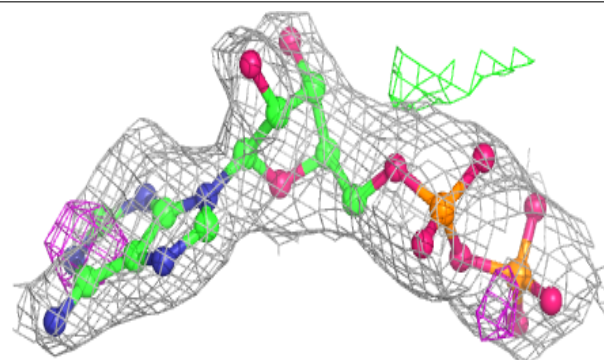


Electron density around ADP H 501:

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

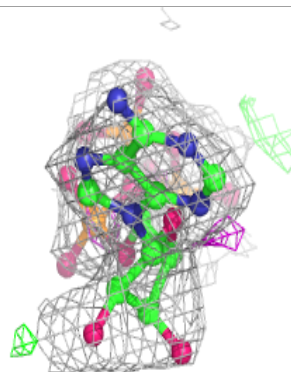
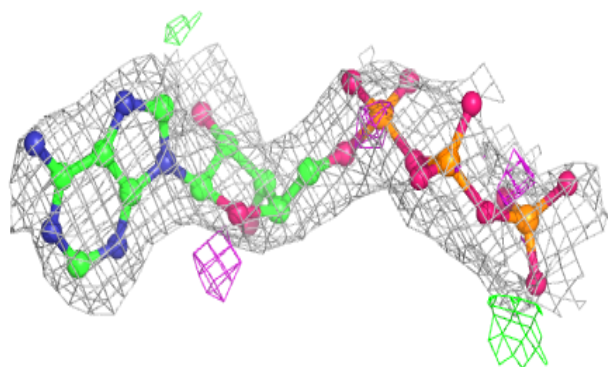
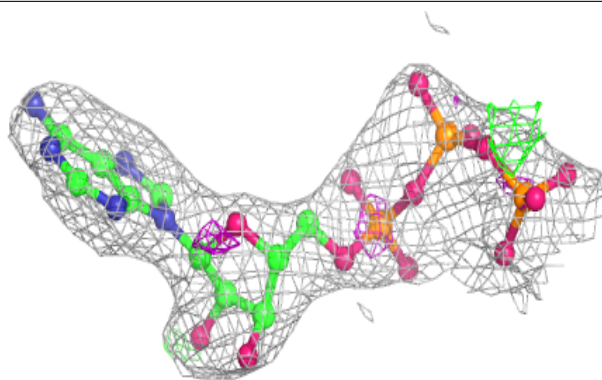
**Electron density around ADP L 503:**

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

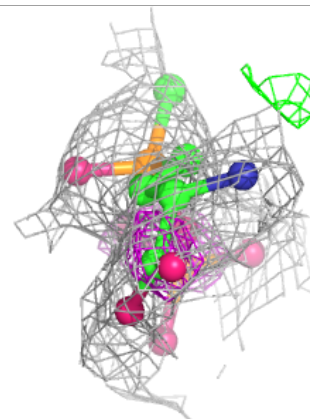
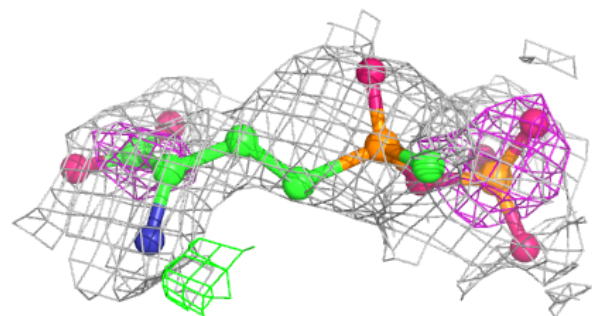
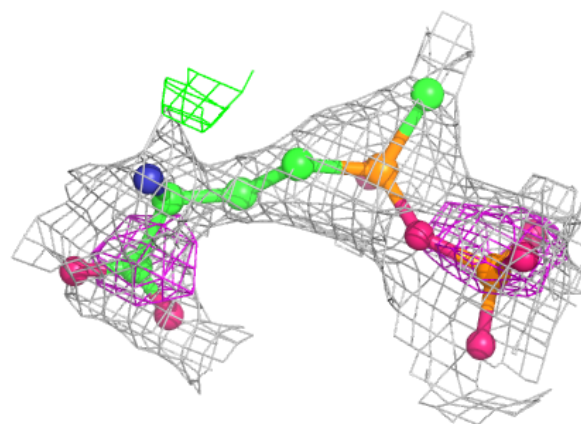


Electron density around ATP K 501:

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

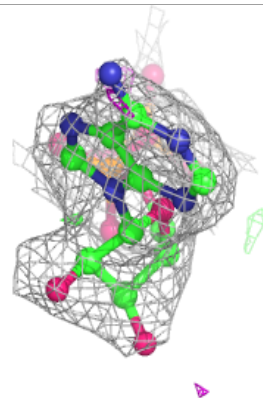
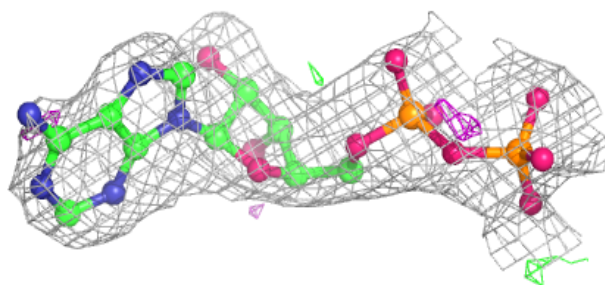
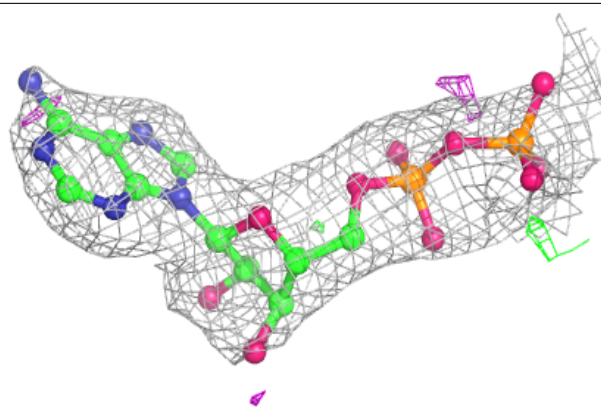
**Electron density around P3P L 501:**

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

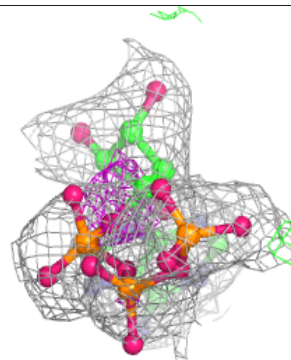
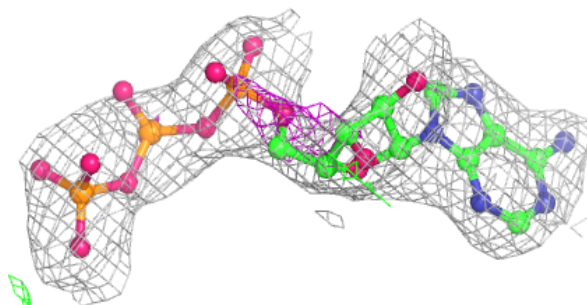
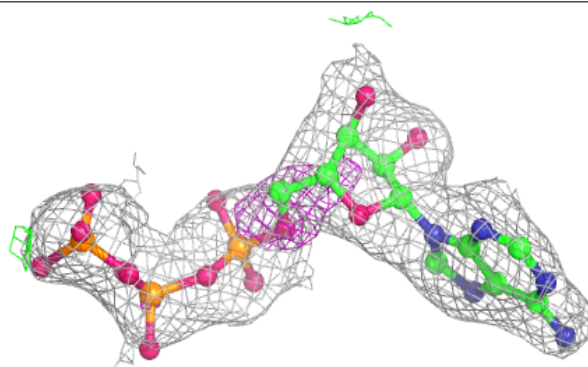


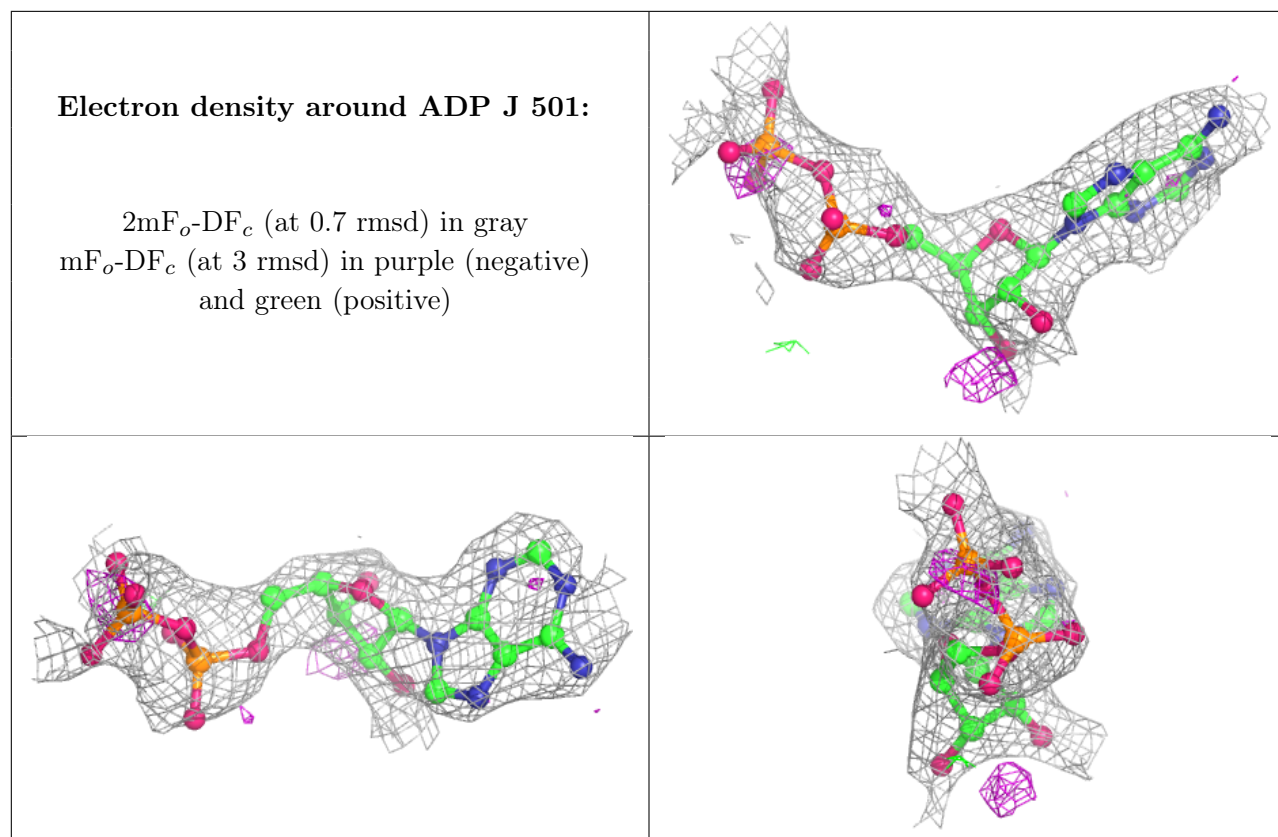
Electron density around ADP I 501:

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

**Electron density around ATP G 501:**

$2mF_o-DF_c$ (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.