



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:45 AM UTC

PDB ID : 3WBZ / pdb_00003wbz
Title : Crystal structure of *C. albicans* tRNA(His) guanylyltransferase (Thg1) with ATP
Authors : Nakamura, A.; Nemoto, T.; Sonoda, T.; Yamashita, K.; Tanaka, I.; Yao, M.
Deposited on : 2013-05-24
Resolution : 2.39 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

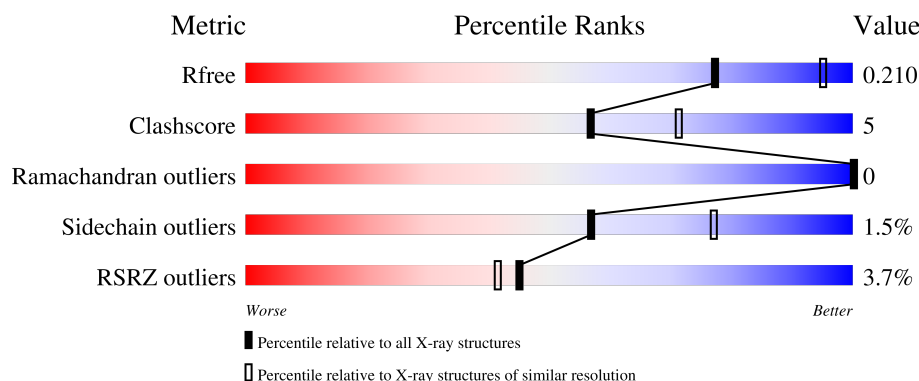
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	271	3% 78% 12% 10%
1	B	271	% 77% 12% 10%
1	C	271	4% 83% 15% .
1	D	271	5% 84% 14% ..
1	E	271	3% 84% 15% .

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Mol	Chain	Length	Quality of chain
1	F	271	 3% 84% 10% 6%
1	G	271	 4% 76% 13% 10%
1	H	271	 5% 80% 15% •

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 18389 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 Likely histidyl tRNA-specific guanylyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	244	Total	C	N	O	S	0	0	0
			2085	1354	339	380	12			
1	B	243	Total	C	N	O	S	0	0	0
			2077	1350	337	378	12			
1	C	265	Total	C	N	O	S	0	1	0
			2277	1470	378	417	12			
1	D	266	Total	C	N	O	S	0	0	0
			2275	1468	377	418	12			
1	E	268	Total	C	N	O	S	0	1	0
			2298	1482	382	421	13			
1	F	255	Total	C	N	O	S	0	0	0
			2186	1417	361	396	12			
1	G	243	Total	C	N	O	S	0	1	0
			2087	1356	340	379	12			
1	H	259	Total	C	N	O	S	0	0	0
			2219	1436	369	402	12			

There are 24 discrepancies between the modelled and reference sequences:

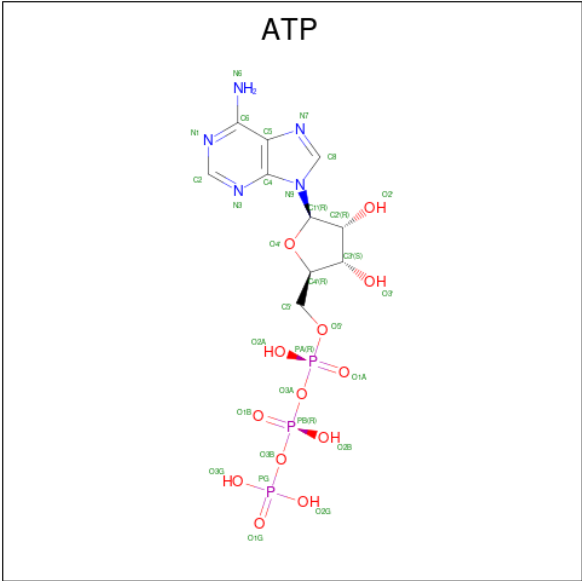
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q5AFK5
A	-1	GLY	-	expression tag	UNP Q5AFK5
A	0	SER	-	expression tag	UNP Q5AFK5
B	-2	GLY	-	expression tag	UNP Q5AFK5
B	-1	GLY	-	expression tag	UNP Q5AFK5
B	0	SER	-	expression tag	UNP Q5AFK5
C	-2	GLY	-	expression tag	UNP Q5AFK5
C	-1	GLY	-	expression tag	UNP Q5AFK5
C	0	SER	-	expression tag	UNP Q5AFK5
D	-2	GLY	-	expression tag	UNP Q5AFK5
D	-1	GLY	-	expression tag	UNP Q5AFK5
D	0	SER	-	expression tag	UNP Q5AFK5
E	-2	GLY	-	expression tag	UNP Q5AFK5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	GLY	-	expression tag	UNP Q5AFK5
E	0	SER	-	expression tag	UNP Q5AFK5
F	-2	GLY	-	expression tag	UNP Q5AFK5
F	-1	GLY	-	expression tag	UNP Q5AFK5
F	0	SER	-	expression tag	UNP Q5AFK5
G	-2	GLY	-	expression tag	UNP Q5AFK5
G	-1	GLY	-	expression tag	UNP Q5AFK5
G	0	SER	-	expression tag	UNP Q5AFK5
H	-2	GLY	-	expression tag	UNP Q5AFK5
H	-1	GLY	-	expression tag	UNP Q5AFK5
H	0	SER	-	expression tag	UNP Q5AFK5

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



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

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	D	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	D	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	G	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	G	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	H	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	H	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

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

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

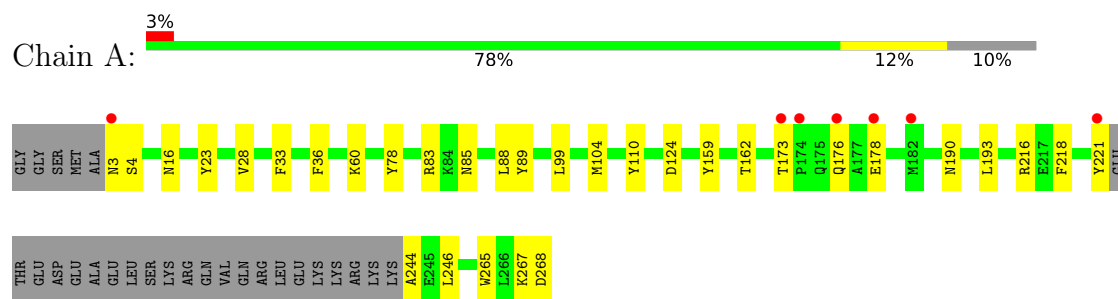
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	59	Total 59	O 59	0	0
4	B	65	Total 65	O 65	0	0
4	C	52	Total 52	O 52	0	0
4	D	47	Total 47	O 47	0	0
4	E	51	Total 51	O 51	0	0
4	F	39	Total 39	O 39	0	0
4	G	23	Total 23	O 23	0	0
4	H	29	Total 29	O 29	0	0

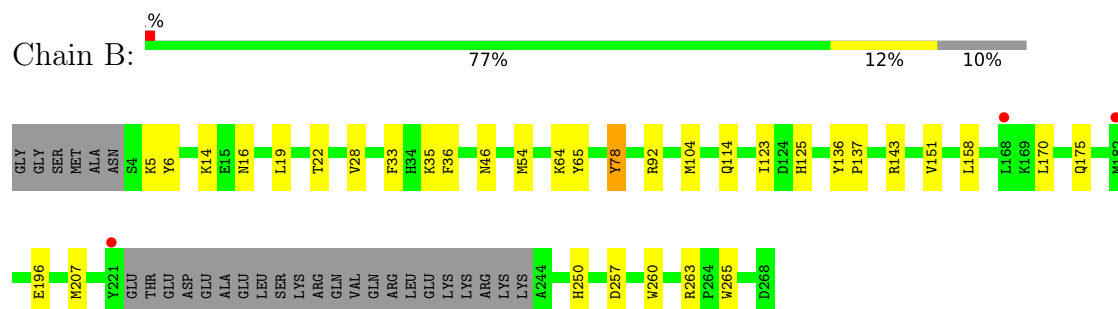
3 Residue-property plots [i](#)

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

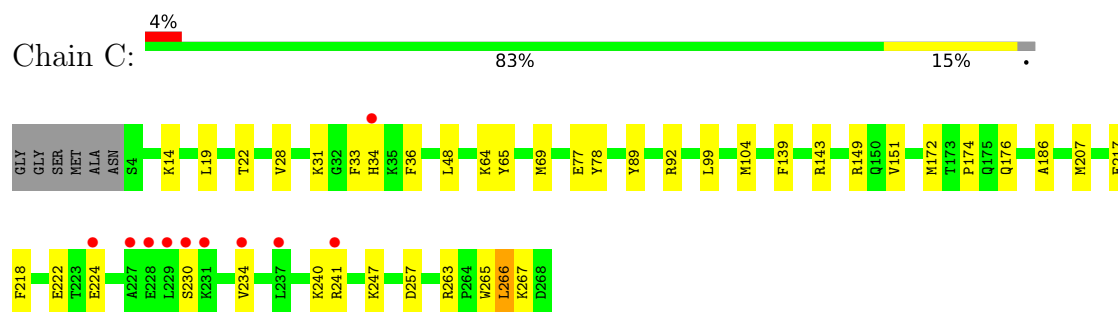
- Molecule 1: Likely histidyl tRNA-specific guanylyltransferase



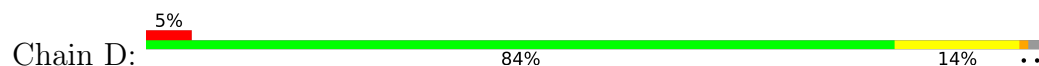
- Molecule 1: Likely histidyl tRNA-specific guanylyltransferase

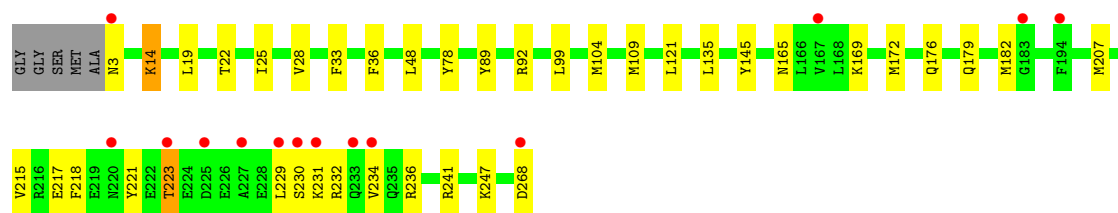


- Molecule 1: Likely histidyl tRNA-specific guanylyltransferase

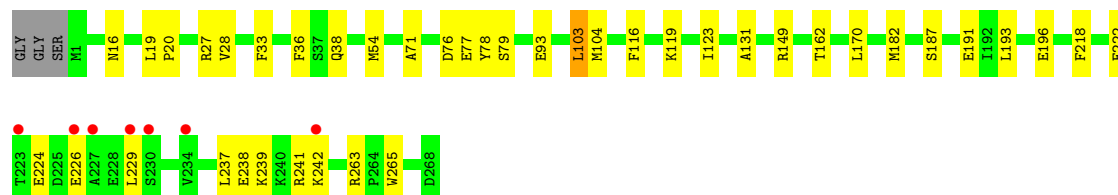
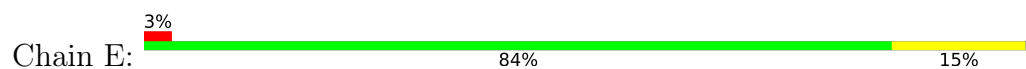


- Molecule 1: Likely histidyl tRNA-specific guanylyltransferase

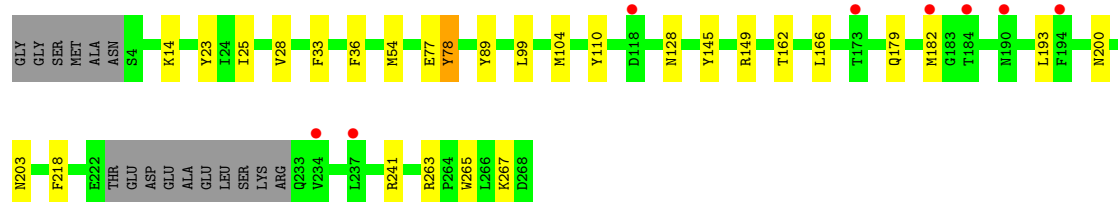
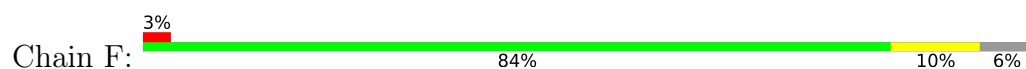




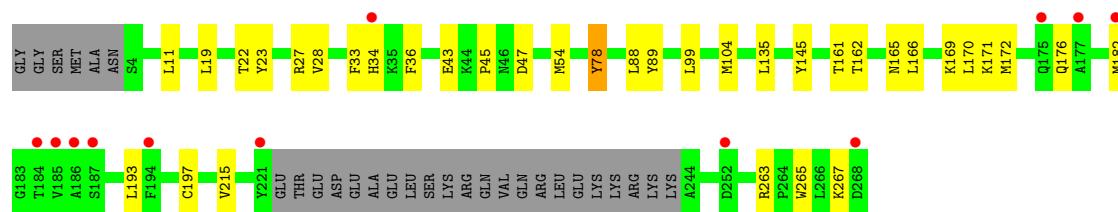
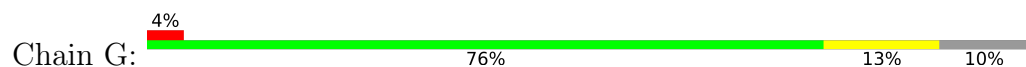
- Molecule 1: Likely histidyl tRNA-specific guanylyltransferase



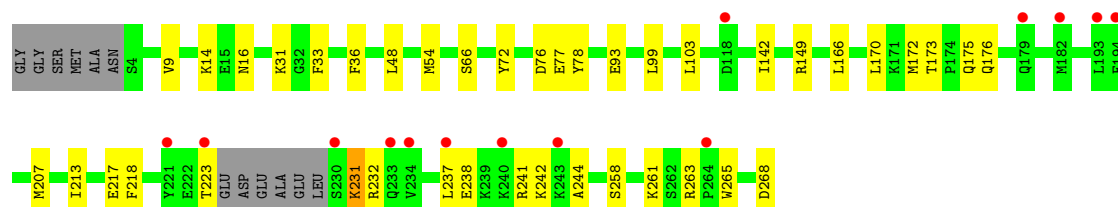
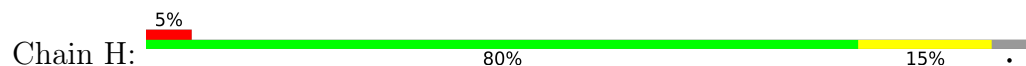
- Molecule 1: Likely histidyl tRNA-specific guanylyltransferase



- Molecule 1: Likely histidyl tRNA-specific guanylyltransferase



- Molecule 1: Likely histidyl tRNA-specific guanylyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.83Å 217.87Å 87.24Å 90.00° 113.68° 90.00°	Depositor
Resolution (Å)	42.26 – 2.39 42.26 – 2.39	Depositor EDS
% Data completeness (in resolution range)	97.3 (42.26-2.39) 97.3 (42.26-2.39)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.53 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.176 , 0.208 0.179 , 0.210	Depositor DCC
R_{free} test set	3528 reflections (3.51%)	wwPDB-VP
Wilson B-factor (Å ²)	46.4	Xtriage
Anisotropy	0.491	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.026 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18389	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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: ATP, 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	0.56	0/2144	0.77	0/2894
1	B	0.62	0/2136	0.83	2/2883 (0.1%)
1	C	0.56	0/2338	0.80	1/3150 (0.0%)
1	D	0.53	0/2335	0.81	1/3146 (0.0%)
1	E	0.55	0/2359	0.79	0/3178
1	F	0.51	0/2245	0.75	0/3024
1	G	0.46	0/2147	0.77	0/2898
1	H	0.48	0/2278	0.81	2/3067 (0.1%)
All	All	0.54	0/17982	0.79	6/24240 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	136	TYR	CA-C-N	6.50	127.06	120.04
1	B	136	TYR	C-N-CA	6.50	127.06	120.04
1	H	231	LYS	CB-CA-C	-5.86	109.83	116.63
1	C	186	ALA	N-CA-C	5.27	116.71	111.07
1	D	223	THR	N-CA-C	5.21	118.89	112.54
1	H	244	ALA	N-CA-C	-5.04	102.72	110.14

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	2085	0	2016	18	0
1	B	2077	0	2010	23	0
1	C	2277	0	2219	27	0
1	D	2275	0	2219	27	0
1	E	2298	0	2242	24	0
1	F	2186	0	2136	14	0
1	G	2087	0	2016	21	0
1	H	2219	0	2174	23	0
2	A	62	0	24	1	0
2	B	62	0	24	0	0
2	C	62	0	24	3	0
2	D	62	0	24	2	0
2	E	62	0	24	0	0
2	F	62	0	24	0	0
2	G	62	0	24	2	0
2	H	62	0	24	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
3	E	3	0	0	0	0
3	F	3	0	0	0	0
3	G	3	0	0	0	0
3	H	3	0	0	0	0
4	A	59	0	0	0	0
4	B	65	0	0	1	0
4	C	52	0	0	1	0
4	D	47	0	0	1	0
4	E	51	0	0	1	0
4	F	39	0	0	0	0
4	G	23	0	0	0	0
4	H	29	0	0	0	0
All	All	18389	0	17224	161	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.

All (161) 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:H:217:GLU:OE2	1:H:263:ARG:NH2	2.15	0.79
1:H:238:GLU:HG2	1:H:242:LYS:HE3	1.63	0.78
1:C:151:VAL:HG11	1:D:3:ASN:HB2	1.68	0.75
1:F:179:GLN:HA	1:F:182:MET:HE2	1.68	0.74
1:G:33:PHE:HA	1:G:36:PHE:HB3	1.71	0.72
1:A:159:TYR:OH	1:A:178:GLU:OE1	2.09	0.69
2:C:402:ATP:O3G	1:D:92:ARG:NH2	2.26	0.68
1:C:92:ARG:NH2	2:D:402:ATP:O3G	2.26	0.68
1:C:19:LEU:HD23	1:C:22:THR:HG21	1.77	0.67
1:C:218:PHE:HD2	1:C:240:LYS:HZ3	1.43	0.66
1:D:221:TYR:OH	1:D:268:ASP:OD2	2.15	0.65
1:A:28:VAL:HG21	1:A:104:MET:HG3	1.79	0.64
1:C:77:GLU:OE1	1:C:149:ARG:HD3	1.98	0.64
1:F:89:TYR:HE2	1:F:99:LEU:HD22	1.64	0.62
1:C:31:LYS:NZ	1:D:89:TYR:OH	2.28	0.62
1:D:179:GLN:HA	1:D:182:MET:HE2	1.80	0.62
1:H:166:LEU:HD23	1:H:170:LEU:HD22	1.82	0.62
1:C:89:TYR:HE2	1:C:99:LEU:HD22	1.64	0.62
1:H:54:MET:HE3	1:H:76:ASP:HA	1.82	0.61
1:D:217:GLU:HG3	1:D:247:LYS:HD2	1.82	0.60
1:B:143:ARG:NH2	1:B:257:ASP:OD1	2.34	0.59
1:E:123:ILE:HD13	1:F:110:TYR:CD2	2.38	0.58
1:A:110:TYR:CD2	1:B:123:ILE:HD13	2.39	0.58
1:A:221:TYR:OH	1:A:268:ASP:OD2	2.22	0.58
1:C:33:PHE:HA	1:C:36:PHE:HB3	1.86	0.56
1:C:143:ARG:NH1	1:C:257:ASP:OD1	2.30	0.56
1:D:19:LEU:HD23	1:D:22:THR:HG21	1.87	0.56
1:G:45:PRO:HG3	1:G:161:THR:HA	1.87	0.56
1:B:46:ASN:ND2	4:B:549:HOH:O	2.37	0.55
1:G:19:LEU:HD23	1:G:22:THR:HG21	1.89	0.55
1:D:33:PHE:HA	1:D:36:PHE:HB3	1.87	0.55
1:B:175:GLN:OE1	1:E:38:GLN:NE2	2.37	0.55
2:C:402:ATP:PG	1:D:92:ARG:HH22	2.31	0.54
1:F:200:ASN:ND2	1:F:203:ASN:OD1	2.39	0.54
1:H:77:GLU:OE2	1:H:149:ARG:HD3	2.07	0.54
1:D:232:ARG:HH12	1:D:236:ARG:HE	1.56	0.54
1:C:263:ARG:HG2	1:C:265:TRP:CZ2	2.44	0.53
1:B:137:PRO:HG3	1:D:22:THR:HG22	1.89	0.53
1:C:28:VAL:HG21	1:C:104:MET:HG3	1.89	0.53
1:C:172:MET:HB3	1:C:176:GLN:HG3	1.90	0.53
1:E:263:ARG:HG2	1:E:265:TRP:CZ2	2.44	0.52
1:G:28:VAL:HG21	1:G:104:MET:HG3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:54:MET:HE3	1:E:76:ASP:HA	1.91	0.52
1:F:263:ARG:HG2	1:F:265:TRP:CZ2	2.44	0.52
1:B:16:ASN:OD1	1:C:14:LYS:NZ	2.42	0.52
1:A:23:TYR:OH	1:A:267:LYS:O	2.27	0.52
1:F:77:GLU:OE2	1:F:149:ARG:HD3	2.10	0.51
1:C:218:PHE:HZ	1:C:241:ARG:HG3	1.74	0.51
1:G:169:LYS:HD2	1:G:197:CYS:HB3	1.91	0.51
1:B:54:MET:HE3	1:B:78:TYR:HD2	1.76	0.50
1:G:99:LEU:HD22	1:H:31:LYS:HD2	1.93	0.50
1:G:165:ASN:O	1:G:169:LYS:HB2	2.11	0.50
1:D:172:MET:HE2	1:D:176:GLN:HG3	1.92	0.50
1:C:92:ARG:HH22	2:D:402:ATP:PG	2.35	0.50
1:H:16:ASN:ND2	1:H:93:GLU:OE1	2.34	0.50
1:E:77:GLU:CD	1:E:149:ARG:HH21	2.19	0.49
1:A:3:ASN:HA	1:B:151:VAL:HG11	1.95	0.49
1:C:217:GLU:HG3	1:C:247:LYS:HD2	1.94	0.49
1:E:162:THR:HA	1:E:193:LEU:HD21	1.93	0.49
1:F:25:ILE:HD13	1:F:145:TYR:CD2	2.47	0.49
1:G:166:LEU:HD23	1:G:170:LEU:HD22	1.94	0.48
1:B:263:ARG:HG2	1:B:265:TRP:CZ2	2.49	0.48
1:D:25:ILE:HD13	1:D:145:TYR:CD2	2.49	0.48
1:F:218:PHE:HZ	1:F:241:ARG:HG3	1.79	0.48
1:C:139:PHE:CG	1:C:267:LYS:HG2	2.48	0.48
1:E:239:LYS:HD3	1:E:242:LYS:HD2	1.95	0.47
2:A:402:ATP:O3G	1:B:92:ARG:NH2	2.43	0.47
1:C:230:SER:HA	1:C:234:VAL:HG23	1.97	0.47
1:A:173:THR:OG1	1:A:176:GLN:HG2	2.14	0.47
1:D:221:TYR:CZ	1:D:223:THR:HA	2.49	0.47
1:B:170:LEU:HD11	1:B:196:GLU:O	2.14	0.47
1:G:34[A]:HIS:CD2	2:G:401:ATP:H4'	2.50	0.47
1:B:207:MET:HE2	1:B:250:HIS:CE1	2.49	0.47
1:C:222:GLU:O	1:C:224:GLU:N	2.44	0.47
1:A:60:LYS:HE3	1:B:123:ILE:HG13	1.97	0.47
1:A:162:THR:HA	1:A:193:LEU:HD21	1.97	0.47
1:D:14:LYS:NZ	4:D:544:HOH:O	2.48	0.47
1:D:218:PHE:HZ	1:D:241:ARG:HG3	1.80	0.46
1:E:33:PHE:HA	1:E:36:PHE:HB3	1.97	0.46
1:E:71:ALA:HA	1:E:79:SER:O	2.15	0.46
1:E:16:ASN:OD1	1:H:14:LYS:NZ	2.42	0.46
1:C:139:PHE:CD2	1:C:267:LYS:HG2	2.51	0.46
1:D:232:ARG:HH12	1:D:236:ARG:NE	2.12	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:263:ARG:HG2	1:G:265:TRP:CZ2	2.51	0.46
1:A:83:ARG:NH1	1:A:85:ASN:HB2	2.31	0.45
1:C:34[A]:HIS:NE2	2:C:401:ATP:O3'	2.43	0.45
1:F:33:PHE:HA	1:F:36:PHE:HB3	1.96	0.45
1:C:263:ARG:HB3	1:C:266:LEU:HD22	1.97	0.45
1:C:31:LYS:HZ3	1:D:89:TYR:HH	1.56	0.45
1:A:33:PHE:HA	1:A:36:PHE:HB3	1.99	0.45
1:B:5:LYS:HE3	1:B:6:TYR:CZ	2.52	0.45
1:C:69:MET:HE1	1:C:218:PHE:HE1	1.82	0.45
1:H:172:MET:HE2	1:H:176:GLN:HG3	1.98	0.45
1:H:223:THR:HG22	1:H:268:ASP:OD2	2.16	0.45
1:A:99:LEU:HD23	1:A:99:LEU:HA	1.85	0.45
1:G:88:LEU:HG	1:G:89:TYR:CD2	2.52	0.45
1:H:231:LYS:HB3	1:H:232:ARG:H	1.46	0.45
1:B:143:ARG:HD3	1:B:260:TRP:CD2	2.52	0.44
1:C:64:LYS:NZ	1:C:65:TYR:OH	2.49	0.44
1:G:27:ARG:HD3	1:G:145:TYR:OH	2.17	0.44
1:B:64:LYS:HB3	1:B:65:TYR:CD1	2.53	0.44
1:G:162:THR:HA	1:G:193:LEU:HD21	2.00	0.44
1:A:218:PHE:CE2	1:A:244:ALA:HB2	2.53	0.44
1:E:218:PHE:HZ	1:E:241:ARG:HG3	1.81	0.44
1:H:66:SER:HB3	1:H:242:LYS:HA	1.99	0.44
1:F:162:THR:HA	1:F:193:LEU:HD21	1.98	0.43
1:E:103:LEU:HD12	1:F:128:ASN:CG	2.42	0.43
1:H:263:ARG:HG2	1:H:265:TRP:CZ2	2.53	0.43
1:B:35:LYS:HE2	1:B:125:HIS:NE2	2.33	0.43
1:E:54:MET:HG2	4:E:523:HOH:O	2.18	0.43
1:G:23:TYR:OH	1:G:267:LYS:O	2.34	0.43
1:F:23:TYR:OH	1:F:267:LYS:O	2.33	0.43
1:H:172:MET:HB3	1:H:176:GLN:HG3	1.99	0.43
1:B:28:VAL:HG21	1:B:104:MET:HG3	2.00	0.43
1:C:174:PRO:HG2	1:H:175:GLN:HG3	2.01	0.43
1:D:109:MET:HG2	1:D:121:LEU:CD1	2.49	0.43
1:E:237:LEU:HD23	1:E:237:LEU:HA	1.82	0.42
1:A:124:ASP:OD1	1:B:64:LYS:HE3	2.20	0.42
1:B:5:LYS:HE3	1:B:6:TYR:OH	2.19	0.42
1:G:172:MET:HB3	1:G:176:GLN:HG3	2.01	0.42
1:D:22:THR:OG1	1:D:135:LEU:HD22	2.19	0.42
1:G:54:MET:HE3	1:G:78:TYR:HD2	1.85	0.42
1:H:33:PHE:HA	1:H:36:PHE:HB3	2.01	0.42
1:D:230:SER:HA	1:D:234:VAL:HG23	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:222:GLU:O	1:E:224:GLU:N	2.49	0.42
1:B:19:LEU:HD23	1:B:22:THR:HG21	2.01	0.42
1:H:173:THR:OG1	1:H:176:GLN:HG2	2.20	0.42
1:H:72:TYR:HD1	1:H:213:ILE:HG13	1.84	0.42
1:H:142:ILE:HD13	1:H:142:ILE:HA	1.89	0.42
1:G:34[A]:HIS:ND1	2:G:401:ATP:O2B	2.52	0.42
1:E:182:MET:HE2	1:E:182:MET:HB2	1.89	0.41
1:H:238:GLU:O	1:H:242:LYS:HG3	2.19	0.41
1:D:109:MET:HG2	1:D:121:LEU:HD13	2.01	0.41
1:E:116:PHE:HB3	1:E:119:LYS:HB2	2.01	0.41
1:G:43:GLU:HB2	1:G:47:ASP:HA	2.01	0.41
1:B:14:LYS:HE2	4:C:507:HOH:O	2.20	0.41
1:D:28:VAL:HG21	1:D:104:MET:HG3	2.01	0.41
1:H:218:PHE:HZ	1:H:241:ARG:HG3	1.85	0.41
1:E:16:ASN:ND2	1:E:93:GLU:OE1	2.43	0.41
1:E:19:LEU:HA	1:E:20:PRO:HD3	1.93	0.41
1:F:28:VAL:HG21	1:F:104:MET:HG3	2.01	0.41
1:H:48:LEU:HD12	1:H:207:MET:HE1	2.02	0.41
1:E:187:SER:O	1:E:191:GLU:HG3	2.20	0.41
1:E:238:GLU:HB3	1:E:242:LYS:HE3	2.03	0.41
1:G:182:MET:HE2	1:G:182:MET:HB2	1.93	0.41
1:A:3:ASN:HB3	1:A:4:SER:H	1.62	0.41
1:F:54:MET:HE3	1:F:78:TYR:HD2	1.85	0.41
1:G:22:THR:OG1	1:G:135:LEU:HD22	2.21	0.41
1:C:48:LEU:HD12	1:C:207:MET:HE1	2.03	0.41
1:D:48:LEU:HD12	1:D:207:MET:HE1	2.02	0.41
1:G:99:LEU:HD23	1:G:99:LEU:HA	1.98	0.41
1:A:16:ASN:OD1	1:D:14:LYS:HE2	2.21	0.41
1:A:88:LEU:HG	1:A:89:TYR:CD2	2.55	0.41
1:E:27:ARG:O	1:E:131:ALA:HA	2.21	0.41
1:E:28:VAL:HG21	1:E:104:MET:HG3	2.03	0.41
1:A:216:ARG:O	1:A:265:TRP:NE1	2.49	0.40
1:D:165:ASN:O	1:D:169:LYS:HB2	2.22	0.40
1:E:170:LEU:HD11	1:E:196:GLU:O	2.21	0.40
1:D:231:LYS:HD3	1:D:231:LYS:HA	1.88	0.40
1:H:258:SER:HA	1:H:261:LYS:HB3	2.02	0.40
1:B:33:PHE:HA	1:B:36:PHE:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	240/271 (89%)	235 (98%)	5 (2%)	0	100	100
1	B	239/271 (88%)	233 (98%)	6 (2%)	0	100	100
1	C	264/271 (97%)	256 (97%)	8 (3%)	0	100	100
1	D	264/271 (97%)	255 (97%)	9 (3%)	0	100	100
1	E	267/271 (98%)	259 (97%)	8 (3%)	0	100	100
1	F	251/271 (93%)	243 (97%)	8 (3%)	0	100	100
1	G	240/271 (89%)	234 (98%)	6 (2%)	0	100	100
1	H	255/271 (94%)	246 (96%)	9 (4%)	0	100	100
All	All	2020/2168 (93%)	1961 (97%)	59 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	229/252 (91%)	226 (99%)	3 (1%)	61	80
1	B	228/252 (90%)	225 (99%)	3 (1%)	61	80
1	C	250/252 (99%)	248 (99%)	2 (1%)	73	86
1	D	250/252 (99%)	245 (98%)	5 (2%)	48	70
1	E	252/252 (100%)	248 (98%)	4 (2%)	55	76
1	F	240/252 (95%)	237 (99%)	3 (1%)	61	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	229/252 (91%)	225 (98%)	4 (2%)	53	74
1	H	244/252 (97%)	239 (98%)	5 (2%)	48	70
All	All	1922/2016 (95%)	1893 (98%)	29 (2%)	57	77

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	TYR
1	A	190	ASN
1	A	246	LEU
1	B	78	TYR
1	B	114	GLN
1	B	158	LEU
1	C	78	TYR
1	C	266	LEU
1	D	14	LYS
1	D	78	TYR
1	D	99	LEU
1	D	215	VAL
1	D	229	LEU
1	E	78	TYR
1	E	103	LEU
1	E	226	GLU
1	E	229	LEU
1	F	14	LYS
1	F	78	TYR
1	F	166	LEU
1	G	11	LEU
1	G	78	TYR
1	G	171	LYS
1	G	215	VAL
1	H	9	VAL
1	H	78	TYR
1	H	99	LEU
1	H	103	LEU
1	H	237	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	GLN
1	A	46	ASN
1	A	157	ASN
1	B	34	HIS
1	B	46	ASN
1	B	157	ASN
1	C	85	ASN
1	C	87	GLN
1	C	179	GLN
1	C	233	GLN
1	C	235	GLN
1	D	34	HIS
1	D	85	ASN
1	E	46	ASN
1	E	157	ASN
1	E	165	ASN
1	E	175	GLN
1	E	203	ASN
1	F	34	HIS
1	F	125	HIS
1	F	200	ASN
1	F	202	ASN
1	G	125	HIS
1	H	34	HIS
1	H	46	ASN
1	H	154	HIS
1	H	156	ASN
1	H	157	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 40 ligands modelled in this entry, 24 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	ATP	A	401	3	32,33,33	1.48	6 (18%)	48,52,52	1.88	12 (25%)
2	ATP	D	402	3	32,33,33	1.49	6 (18%)	48,52,52	1.85	9 (18%)
2	ATP	E	402	3	32,33,33	1.41	4 (12%)	48,52,52	2.00	13 (27%)
2	ATP	C	402	3	32,33,33	1.47	4 (12%)	48,52,52	1.73	10 (20%)
2	ATP	H	402	3	32,33,33	1.68	8 (25%)	48,52,52	1.75	10 (20%)
2	ATP	G	402	3	32,33,33	1.52	7 (21%)	48,52,52	1.74	9 (18%)
2	ATP	D	401	3	32,33,33	1.46	5 (15%)	48,52,52	1.86	13 (27%)
2	ATP	A	402	3	32,33,33	1.61	7 (21%)	48,52,52	1.89	11 (22%)
2	ATP	E	401	3	32,33,33	1.59	6 (18%)	48,52,52	1.97	12 (25%)
2	ATP	C	401	3	32,33,33	1.45	4 (12%)	48,52,52	1.78	9 (18%)
2	ATP	B	402	3	32,33,33	1.60	6 (18%)	48,52,52	1.78	9 (18%)
2	ATP	H	401	3	32,33,33	1.64	6 (18%)	48,52,52	1.74	11 (22%)
2	ATP	G	401	3	32,33,33	1.39	5 (15%)	48,52,52	1.74	8 (16%)
2	ATP	F	401	3	32,33,33	1.56	5 (15%)	48,52,52	1.78	11 (22%)
2	ATP	B	401	3	32,33,33	1.34	6 (18%)	48,52,52	1.74	10 (20%)
2	ATP	F	402	3	32,33,33	1.52	6 (18%)	48,52,52	1.85	10 (20%)

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	ATP	A	401	3	-	4/22/38/38	0/3/3/3
2	ATP	D	402	3	-	7/22/38/38	0/3/3/3
2	ATP	E	402	3	-	12/22/38/38	0/3/3/3
2	ATP	C	402	3	-	6/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ATP	H	402	3	-	6/22/38/38	0/3/3/3
2	ATP	G	402	3	-	8/22/38/38	0/3/3/3
2	ATP	D	401	3	-	4/22/38/38	0/3/3/3
2	ATP	A	402	3	-	12/22/38/38	0/3/3/3
2	ATP	E	401	3	-	4/22/38/38	0/3/3/3
2	ATP	C	401	3	-	4/22/38/38	0/3/3/3
2	ATP	B	402	3	-	9/22/38/38	0/3/3/3
2	ATP	H	401	3	-	8/22/38/38	0/3/3/3
2	ATP	G	401	3	-	7/22/38/38	0/3/3/3
2	ATP	F	401	3	-	5/22/38/38	0/3/3/3
2	ATP	B	401	3	-	5/22/38/38	0/3/3/3
2	ATP	F	402	3	-	13/22/38/38	0/3/3/3

All (91) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	401	ATP	C5-C4	4.96	1.47	1.39
2	B	402	ATP	C5-C4	4.95	1.47	1.39
2	D	401	ATP	C5-C4	4.86	1.47	1.39
2	F	401	ATP	C5-C4	4.79	1.47	1.39
2	G	401	ATP	C5-C4	4.74	1.47	1.39
2	C	402	ATP	C5-C4	4.74	1.47	1.39
2	D	402	ATP	C5-C4	4.71	1.47	1.39
2	A	402	ATP	C5-C4	4.63	1.47	1.39
2	H	402	ATP	C5-C4	4.62	1.47	1.39
2	C	401	ATP	C5-C4	4.60	1.47	1.39
2	E	402	ATP	C5-C4	4.59	1.47	1.39
2	G	402	ATP	C5-C4	4.58	1.47	1.39
2	F	402	ATP	C5-C4	4.56	1.47	1.39
2	E	401	ATP	C5-C4	4.48	1.47	1.39
2	B	401	ATP	C5-C4	4.35	1.46	1.39
2	B	402	ATP	PA-O3A	4.04	1.63	1.59
2	F	401	ATP	PB-O3A	3.95	1.63	1.59
2	H	402	ATP	PA-O3A	3.86	1.63	1.59
2	E	401	ATP	PB-O3A	3.80	1.63	1.59
2	A	401	ATP	PB-O3A	3.73	1.63	1.59
2	H	401	ATP	PA-O3A	3.58	1.63	1.59
2	A	401	ATP	C5-C4	3.58	1.45	1.39
2	A	402	ATP	PA-O3A	3.57	1.63	1.59
2	H	402	ATP	PB-O3A	3.47	1.63	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	402	ATP	PB-O3B	3.46	1.63	1.59
2	F	402	ATP	PB-O3B	3.42	1.63	1.59
2	G	402	ATP	PA-O3A	3.18	1.62	1.59
2	H	401	ATP	PB-O3A	3.13	1.62	1.59
2	C	402	ATP	C5-C6	3.05	1.49	1.41
2	E	401	ATP	C5-C6	3.05	1.49	1.41
2	A	402	ATP	PB-O3A	3.03	1.62	1.59
2	A	402	ATP	PB-O3B	3.02	1.62	1.59
2	H	401	ATP	C5-C6	3.01	1.49	1.41
2	G	402	ATP	C5-C6	2.98	1.49	1.41
2	E	402	ATP	C5-C6	2.98	1.49	1.41
2	A	401	ATP	PA-O3A	2.90	1.62	1.59
2	F	402	ATP	C5-C6	2.90	1.49	1.41
2	D	402	ATP	C5-C6	2.90	1.49	1.41
2	F	401	ATP	C5-C6	2.83	1.48	1.41
2	D	402	ATP	PB-O3A	2.83	1.62	1.59
2	C	401	ATP	C5-N7	-2.82	1.33	1.39
2	B	402	ATP	PB-O3A	2.80	1.62	1.59
2	H	401	ATP	PB-O3B	2.78	1.62	1.59
2	B	402	ATP	C5-C6	2.77	1.48	1.41
2	H	402	ATP	C5-C6	2.73	1.48	1.41
2	C	401	ATP	C5-C6	2.67	1.48	1.41
2	A	402	ATP	C5-C6	2.66	1.48	1.41
2	G	401	ATP	C5-C6	2.64	1.48	1.41
2	F	401	ATP	C8-N7	2.59	1.36	1.31
2	E	402	ATP	PB-O3B	2.57	1.62	1.59
2	B	402	ATP	C8-N7	2.54	1.36	1.31
2	A	401	ATP	C5-C6	2.52	1.48	1.41
2	F	402	ATP	C8-N7	2.50	1.36	1.31
2	C	402	ATP	PA-O3A	2.50	1.62	1.59
2	A	401	ATP	C5-N7	-2.50	1.34	1.39
2	B	401	ATP	C5-N7	-2.50	1.34	1.39
2	E	401	ATP	PA-O3A	2.49	1.62	1.59
2	H	401	ATP	C8-N7	2.49	1.36	1.31
2	D	402	ATP	C8-N7	2.47	1.36	1.31
2	D	401	ATP	PB-O3B	2.46	1.62	1.59
2	G	401	ATP	C5-N7	-2.43	1.34	1.39
2	D	401	ATP	C8-N7	2.43	1.36	1.31
2	D	401	ATP	C5-C6	2.42	1.47	1.41
2	B	401	ATP	C5-C6	2.36	1.47	1.41
2	A	402	ATP	C5-N7	-2.36	1.34	1.39
2	E	401	ATP	C5-N7	-2.35	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	402	ATP	PB-O3B	2.35	1.62	1.59
2	F	402	ATP	PA-O3A	2.34	1.62	1.59
2	D	402	ATP	PA-O3A	2.33	1.62	1.59
2	E	402	ATP	C8-N7	2.33	1.36	1.31
2	B	401	ATP	C4-N9	-2.29	1.32	1.37
2	H	402	ATP	C8-N7	2.28	1.36	1.31
2	A	401	ATP	C8-N9	-2.24	1.33	1.37
2	B	401	ATP	PB-O3B	2.22	1.61	1.59
2	C	402	ATP	PB-O3B	2.22	1.61	1.59
2	G	402	ATP	C8-N7	2.22	1.36	1.31
2	G	401	ATP	PB-O3B	2.21	1.61	1.59
2	E	401	ATP	PB-O3B	2.20	1.61	1.59
2	G	401	ATP	C8-N7	2.20	1.35	1.31
2	A	402	ATP	C8-N7	2.19	1.35	1.31
2	G	402	ATP	PB-O3B	2.19	1.61	1.59
2	F	401	ATP	PA-O3A	2.16	1.61	1.59
2	G	402	ATP	PB-O3A	2.12	1.61	1.59
2	G	402	ATP	C5-N7	-2.12	1.35	1.39
2	D	401	ATP	C4-N9	-2.09	1.33	1.37
2	B	401	ATP	C8-N9	-2.05	1.34	1.37
2	B	402	ATP	C5-N7	-2.05	1.35	1.39
2	H	402	ATP	C5-N7	-2.05	1.35	1.39
2	F	402	ATP	C5-N7	-2.04	1.35	1.39
2	C	401	ATP	C8-N9	-2.04	1.34	1.37
2	H	402	ATP	C4-N9	-2.03	1.33	1.37

All (167) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	ATP	C5-C4-N3	-6.17	118.22	126.72
2	E	401	ATP	C5-C4-N3	-6.13	118.27	126.72
2	A	402	ATP	C5-C4-N3	-5.94	118.54	126.72
2	D	402	ATP	C5-C4-N3	-5.85	118.66	126.72
2	G	401	ATP	C5-C4-N3	-5.78	118.76	126.72
2	F	401	ATP	C5-C4-N3	-5.77	118.78	126.72
2	B	402	ATP	C5-C4-N3	-5.74	118.82	126.72
2	G	402	ATP	C5-C4-N3	-5.67	118.91	126.72
2	C	401	ATP	C5-C4-N3	-5.65	118.93	126.72
2	E	402	ATP	C5-C4-N3	-5.65	118.94	126.72
2	D	401	ATP	C5-C4-N3	-5.60	119.00	126.72
2	C	402	ATP	C5-C4-N3	-5.57	119.05	126.72
2	F	402	ATP	C5-C4-N3	-5.53	119.10	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	402	ATP	C5-C4-N3	-5.39	119.30	126.72
2	B	401	ATP	C5-C4-N3	-5.33	119.37	126.72
2	E	401	ATP	N3-C4-N9	5.21	136.03	127.17
2	A	401	ATP	N3-C4-N9	5.11	135.85	127.17
2	H	401	ATP	C5-C4-N3	-5.02	119.81	126.72
2	C	401	ATP	N3-C4-N9	4.94	135.57	127.17
2	A	402	ATP	N3-C4-N9	4.92	135.54	127.17
2	G	401	ATP	N3-C4-N9	4.69	135.14	127.17
2	C	402	ATP	N3-C4-N9	4.66	135.09	127.17
2	D	402	ATP	N3-C4-N9	4.65	135.08	127.17
2	E	402	ATP	N3-C4-N9	4.65	135.07	127.17
2	G	402	ATP	N3-C4-N9	4.60	134.99	127.17
2	B	402	ATP	N3-C4-N9	4.59	134.97	127.17
2	D	401	ATP	N3-C4-N9	4.56	134.93	127.17
2	F	401	ATP	N3-C4-N9	4.50	134.81	127.17
2	H	402	ATP	N3-C4-N9	4.44	134.72	127.17
2	F	402	ATP	N3-C4-N9	4.39	134.63	127.17
2	B	401	ATP	N3-C4-N9	4.29	134.47	127.17
2	H	401	ATP	N3-C4-N9	3.96	133.90	127.17
2	E	401	ATP	C2-N3-C4	3.94	121.45	111.83
2	D	402	ATP	C4-C5-N7	-3.93	106.09	110.58
2	F	401	ATP	C4-C5-N7	-3.91	106.11	110.58
2	B	401	ATP	C4-C5-N7	-3.86	106.17	110.58
2	E	402	ATP	C2-N3-C4	3.85	121.24	111.83
2	D	402	ATP	C2-N3-C4	3.85	121.23	111.83
2	F	402	ATP	C4-C5-N7	-3.83	106.21	110.58
2	E	402	ATP	C4-C5-N7	-3.81	106.22	110.58
2	D	401	ATP	C2-N3-C4	3.80	121.11	111.83
2	D	401	ATP	N3-C2-N1	-3.74	122.93	128.58
2	G	402	ATP	C2-N3-C4	3.73	120.93	111.83
2	A	402	ATP	C2-N3-C4	3.71	120.90	111.83
2	B	402	ATP	C2-N3-C4	3.70	120.88	111.83
2	H	401	ATP	N3-C2-N1	-3.69	123.00	128.58
2	A	401	ATP	C2-N3-C4	3.68	120.81	111.83
2	E	402	ATP	C4-N9-C8	3.66	109.58	105.74
2	C	402	ATP	C2-N3-C4	3.63	120.70	111.83
2	F	402	ATP	C2-N3-C4	3.63	120.69	111.83
2	E	402	ATP	N3-C2-N1	-3.61	123.11	128.58
2	H	401	ATP	C2-N3-C4	3.61	120.64	111.83
2	E	401	ATP	C4-C5-N7	-3.61	106.46	110.58
2	H	402	ATP	C2-N3-C4	3.59	120.60	111.83
2	F	401	ATP	C2-N3-C4	3.56	120.53	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	401	ATP	C2-N3-C4	3.52	120.42	111.83
2	G	402	ATP	C4-C5-N7	-3.50	106.58	110.58
2	C	401	ATP	C2-N3-C4	3.48	120.33	111.83
2	C	402	ATP	C4-C5-N7	-3.45	106.64	110.58
2	D	401	ATP	C4-C5-N7	-3.43	106.66	110.58
2	B	402	ATP	C4-C5-N7	-3.42	106.67	110.58
2	D	402	ATP	N3-C2-N1	-3.42	123.41	128.58
2	H	402	ATP	C4-C5-N7	-3.39	106.70	110.58
2	B	402	ATP	N3-C2-N1	-3.39	123.45	128.58
2	A	402	ATP	C4-C5-N7	-3.33	106.77	110.58
2	B	401	ATP	C2-N3-C4	3.33	119.95	111.83
2	E	401	ATP	N3-C2-N1	-3.32	123.55	128.58
2	F	402	ATP	C4-N9-C8	3.30	109.20	105.74
2	H	401	ATP	C4-C5-N7	-3.29	106.81	110.58
2	B	401	ATP	C4-N9-C8	3.29	109.19	105.74
2	D	402	ATP	C4-N9-C8	3.28	109.19	105.74
2	F	402	ATP	N3-C2-N1	-3.28	123.61	128.58
2	H	402	ATP	C4-N9-C8	3.28	109.18	105.74
2	H	402	ATP	N3-C2-N1	-3.26	123.64	128.58
2	A	401	ATP	C4-C5-N7	-3.24	106.88	110.58
2	G	401	ATP	C4-C5-N7	-3.23	106.89	110.58
2	G	402	ATP	N3-C2-N1	-3.20	123.74	128.58
2	A	402	ATP	N3-C2-N1	-3.20	123.75	128.58
2	C	401	ATP	N3-C2-N1	-3.18	123.78	128.58
2	E	401	ATP	C2'-C1'-N9	-3.17	105.42	113.30
2	E	401	ATP	C4-N9-C8	3.17	109.07	105.74
2	C	401	ATP	C4-C5-N7	-3.14	106.99	110.58
2	D	401	ATP	C4-N9-C8	3.13	109.03	105.74
2	C	402	ATP	C4-N9-C8	3.10	109.00	105.74
2	C	402	ATP	N3-C2-N1	-3.09	123.91	128.58
2	G	402	ATP	C4-N9-C8	3.04	108.93	105.74
2	A	401	ATP	N3-C2-N1	-3.04	123.98	128.58
2	D	402	ATP	C5-N7-C8	2.99	108.15	103.45
2	E	402	ATP	C5-N7-C8	2.97	108.12	103.45
2	E	401	ATP	C5-N7-C8	2.96	108.10	103.45
2	F	401	ATP	N3-C2-N1	-2.95	124.12	128.58
2	G	401	ATP	N3-C2-N1	-2.93	124.14	128.58
2	B	401	ATP	C5-N7-C8	2.90	108.01	103.45
2	C	401	ATP	C4-N9-C8	2.88	108.76	105.74
2	F	402	ATP	C5-N7-C8	2.85	107.94	103.45
2	F	401	ATP	C5-N7-C8	2.83	107.90	103.45
2	F	401	ATP	C4-N9-C8	2.82	108.70	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	ATP	N3-C2-N1	-2.80	124.35	128.58
2	H	401	ATP	C2-N1-C6	2.79	123.31	118.73
2	A	401	ATP	C4-N9-C8	2.78	108.65	105.74
2	A	402	ATP	C4-N9-C8	2.76	108.64	105.74
2	H	401	ATP	C4-N9-C8	2.72	108.60	105.74
2	E	402	ATP	N9-C8-N7	-2.72	110.08	113.94
2	A	402	ATP	C5-N7-C8	2.71	107.71	103.45
2	B	402	ATP	C4-N9-C8	2.66	108.53	105.74
2	C	401	ATP	C2'-C1'-N9	-2.66	106.71	113.30
2	E	402	ATP	C6-C5-N7	2.65	137.19	132.09
2	A	401	ATP	C5-N7-C8	2.64	107.60	103.45
2	G	402	ATP	C5-N7-C8	2.62	107.57	103.45
2	D	401	ATP	O2B-PB-O3B	2.58	114.24	107.27
2	H	402	ATP	C5-N7-C8	2.57	107.49	103.45
2	H	401	ATP	C6-C5-N7	2.56	137.03	132.09
2	D	402	ATP	N9-C8-N7	-2.55	110.31	113.94
2	B	402	ATP	C5-N7-C8	2.55	107.46	103.45
2	G	401	ATP	C4-N9-C8	2.54	108.41	105.74
2	C	402	ATP	C5-N7-C8	2.53	107.43	103.45
2	F	402	ATP	N9-C8-N7	-2.51	110.38	113.94
2	C	401	ATP	C5-N7-C8	2.50	107.38	103.45
2	B	401	ATP	N9-C8-N7	-2.44	110.48	113.94
2	D	402	ATP	C6-C5-N7	2.42	136.75	132.09
2	F	401	ATP	C6-C5-N7	2.40	136.72	132.09
2	F	402	ATP	C6-C5-N7	2.39	136.70	132.09
2	A	401	ATP	O2'-C2'-C3'	-2.39	104.15	111.82
2	E	402	ATP	O3A-PB-O1B	-2.38	103.55	110.70
2	E	402	ATP	O4'-C1'-N9	-2.36	103.56	108.09
2	G	401	ATP	C5-N7-C8	2.34	107.12	103.45
2	H	402	ATP	N9-C8-N7	-2.32	110.64	113.94
2	D	401	ATP	C5-N7-C8	2.32	107.09	103.45
2	D	401	ATP	C6-C5-N7	2.31	136.54	132.09
2	F	401	ATP	C3'-C2'-C1'	2.30	105.82	101.46
2	E	401	ATP	N9-C8-N7	-2.30	110.67	113.94
2	B	401	ATP	C6-C5-N7	2.29	136.51	132.09
2	F	401	ATP	O3G-PG-O2G	2.29	116.38	107.80
2	H	402	ATP	C6-C5-N7	2.29	136.50	132.09
2	E	401	ATP	O5'-PA-O1A	-2.27	99.93	108.94
2	H	402	ATP	O3G-PG-O2G	2.24	116.19	107.80
2	G	402	ATP	C6-C5-N7	2.23	136.38	132.09
2	E	402	ATP	O2B-PB-O3B	2.21	113.25	107.27
2	A	402	ATP	O2A-PA-O3A	2.20	113.22	107.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	402	ATP	N9-C8-N7	-2.19	110.83	113.94
2	B	402	ATP	O3B-PG-O1G	-2.19	99.53	111.04
2	B	402	ATP	C6-C5-N7	2.17	136.28	132.09
2	E	401	ATP	O3G-PG-O2G	2.17	115.94	107.80
2	E	402	ATP	O3B-PG-O1G	-2.17	99.64	111.04
2	A	401	ATP	O3G-PG-O2G	2.16	115.90	107.80
2	D	401	ATP	O3A-PB-O1B	-2.16	104.22	110.70
2	F	401	ATP	N9-C8-N7	-2.15	110.88	113.94
2	D	401	ATP	O2B-PB-O3A	2.14	113.07	107.27
2	H	401	ATP	O3B-PB-O1B	-2.14	104.28	110.70
2	A	401	ATP	N9-C8-N7	-2.13	110.91	113.94
2	D	401	ATP	C2-N1-C6	2.13	122.22	118.73
2	E	401	ATP	C6-C5-N7	2.11	136.17	132.09
2	F	402	ATP	O3A-PB-O1B	-2.11	104.36	110.70
2	H	401	ATP	C5-N7-C8	2.11	106.76	103.45
2	A	402	ATP	N9-C8-N7	-2.09	110.97	113.94
2	C	402	ATP	C6-C5-N7	2.08	136.10	132.09
2	A	402	ATP	O3G-PG-O2G	2.05	115.50	107.80
2	G	401	ATP	C3'-C2'-C1'	2.05	105.34	101.46
2	A	401	ATP	O2B-PB-O3B	2.04	112.80	107.27
2	H	401	ATP	O2B-PB-O3B	2.04	112.79	107.27
2	B	401	ATP	O2A-PA-O1A	2.03	121.90	112.44
2	A	402	ATP	O2B-PB-O3A	2.03	112.77	107.27
2	D	401	ATP	O2A-PA-O1A	2.03	121.89	112.44
2	C	401	ATP	C2-N1-C6	2.03	122.06	118.73
2	C	402	ATP	N9-C8-N7	-2.02	111.08	113.94
2	C	402	ATP	O3'-C3'-C4'	-2.00	105.33	111.08
2	A	401	ATP	C3'-C2'-C1'	2.00	105.25	101.46

There are no chirality outliers.

All (114) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	ATP	PB-O3B-PG-O2G
2	A	402	ATP	PB-O3B-PG-O2G
2	A	402	ATP	C5'-O5'-PA-O1A
2	A	402	ATP	C5'-O5'-PA-O2A
2	A	402	ATP	C5'-O5'-PA-O3A
2	B	402	ATP	C5'-O5'-PA-O1A
2	B	402	ATP	C5'-O5'-PA-O3A
2	C	401	ATP	PB-O3B-PG-O2G
2	C	401	ATP	PB-O3B-PG-O3G

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Mol	Chain	Res	Type	Atoms
2	C	402	ATP	C5'-O5'-PA-O1A
2	C	402	ATP	C5'-O5'-PA-O2A
2	C	402	ATP	C5'-O5'-PA-O3A
2	D	402	ATP	PB-O3B-PG-O3G
2	D	402	ATP	C5'-O5'-PA-O1A
2	D	402	ATP	C5'-O5'-PA-O2A
2	D	402	ATP	C5'-O5'-PA-O3A
2	E	401	ATP	PB-O3B-PG-O2G
2	E	402	ATP	PB-O3B-PG-O2G
2	E	402	ATP	C5'-O5'-PA-O1A
2	E	402	ATP	C5'-O5'-PA-O3A
2	F	401	ATP	PB-O3B-PG-O2G
2	F	402	ATP	PB-O3B-PG-O2G
2	F	402	ATP	C5'-O5'-PA-O1A
2	F	402	ATP	C5'-O5'-PA-O3A
2	G	401	ATP	PB-O3B-PG-O2G
2	G	401	ATP	PB-O3A-PA-O5'
2	G	401	ATP	C3'-C4'-C5'-O5'
2	G	402	ATP	C5'-O5'-PA-O1A
2	G	402	ATP	C5'-O5'-PA-O2A
2	G	402	ATP	C5'-O5'-PA-O3A
2	H	401	ATP	PB-O3B-PG-O2G
2	H	401	ATP	C5'-O5'-PA-O1A
2	H	401	ATP	C5'-O5'-PA-O3A
2	F	402	ATP	C3'-C4'-C5'-O5'
2	H	402	ATP	O4'-C4'-C5'-O5'
2	B	402	ATP	O4'-C4'-C5'-O5'
2	B	402	ATP	C3'-C4'-C5'-O5'
2	F	402	ATP	O4'-C4'-C5'-O5'
2	G	401	ATP	O4'-C4'-C5'-O5'
2	H	402	ATP	C3'-C4'-C5'-O5'
2	G	402	ATP	O4'-C4'-C5'-O5'
2	E	402	ATP	O4'-C4'-C5'-O5'
2	G	402	ATP	C3'-C4'-C5'-O5'
2	A	402	ATP	PB-O3A-PA-O1A
2	E	402	ATP	C3'-C4'-C5'-O5'
2	H	401	ATP	O4'-C4'-C5'-O5'
2	C	402	ATP	PB-O3B-PG-O3G
2	H	402	ATP	PB-O3B-PG-O3G
2	C	402	ATP	C2'-C1'-N9-C8
2	F	402	ATP	C2'-C1'-N9-C8
2	A	401	ATP	PA-O3A-PB-O2B

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Mol	Chain	Res	Type	Atoms
2	B	401	ATP	PB-O3A-PA-O1A
2	B	402	ATP	PG-O3B-PB-O2B
2	C	401	ATP	PA-O3A-PB-O1B
2	D	402	ATP	PA-O3A-PB-O1B
2	F	401	ATP	PA-O3A-PB-O1B
2	F	402	ATP	PB-O3A-PA-O2A
2	H	402	ATP	PB-O3A-PA-O1A
2	B	402	ATP	C5'-O5'-PA-O2A
2	E	402	ATP	C5'-O5'-PA-O2A
2	F	402	ATP	C5'-O5'-PA-O2A
2	G	401	ATP	C5'-O5'-PA-O1A
2	H	401	ATP	C5'-O5'-PA-O2A
2	A	402	ATP	PB-O3A-PA-O2A
2	B	401	ATP	PB-O3A-PA-O2A
2	D	401	ATP	PA-O3A-PB-O2B
2	E	401	ATP	PA-O3A-PB-O2B
2	E	402	ATP	PA-O3A-PB-O1B
2	H	401	ATP	PA-O3A-PB-O2B
2	G	402	ATP	C2'-C1'-N9-C8
2	A	401	ATP	PB-O3B-PG-O1G
2	B	402	ATP	PB-O3B-PG-O1G
2	E	401	ATP	PB-O3B-PG-O1G
2	E	401	ATP	O4'-C4'-C5'-O5'
2	A	402	ATP	PA-O3A-PB-O1B
2	B	401	ATP	PG-O3B-PB-O1B
2	D	401	ATP	PG-O3B-PB-O2B
2	D	401	ATP	PA-O3A-PB-O1B
2	E	402	ATP	PB-O3A-PA-O1A
2	G	402	ATP	PA-O3A-PB-O1B
2	F	402	ATP	O4'-C1'-N9-C8
2	F	401	ATP	PB-O3B-PG-O1G
2	F	402	ATP	PB-O3B-PG-O1G
2	A	402	ATP	PB-O3B-PG-O3G
2	E	402	ATP	PB-O3B-PG-O3G
2	F	401	ATP	PB-O3B-PG-O3G
2	F	402	ATP	PB-O3B-PG-O3G
2	G	401	ATP	PB-O3B-PG-O3G
2	H	401	ATP	PB-O3B-PG-O3G
2	A	402	ATP	C2'-C1'-N9-C8
2	H	402	ATP	C2'-C1'-N9-C8
2	F	402	ATP	C2'-C1'-N9-C4
2	A	402	ATP	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	E	402	ATP	C2'-C1'-N9-C8
2	B	402	ATP	PG-O3B-PB-O1B
2	C	401	ATP	PA-O3A-PB-O2B
2	D	402	ATP	PA-O3A-PB-O2B
2	E	402	ATP	PA-O3A-PB-O2B
2	E	402	ATP	PB-O3A-PA-O2A
2	F	401	ATP	PA-O3A-PB-O2B
2	F	402	ATP	PB-O3A-PA-O1A
2	H	402	ATP	PB-O3A-PA-O2A
2	H	401	ATP	C3'-C4'-C5'-O5'
2	D	402	ATP	C2'-C1'-N9-C8
2	G	401	ATP	PB-O3B-PG-O1G
2	A	402	ATP	O4'-C4'-C5'-O5'
2	B	401	ATP	O4'-C4'-C5'-O5'
2	A	401	ATP	PA-O3A-PB-O1B
2	A	402	ATP	PA-O3A-PB-O2B
2	B	401	ATP	PG-O3B-PB-O2B
2	B	402	ATP	PB-O3A-PA-O1A
2	C	402	ATP	PA-O3A-PB-O2B
2	G	402	ATP	PA-O3A-PB-O2B
2	D	401	ATP	O4'-C4'-C5'-O5'

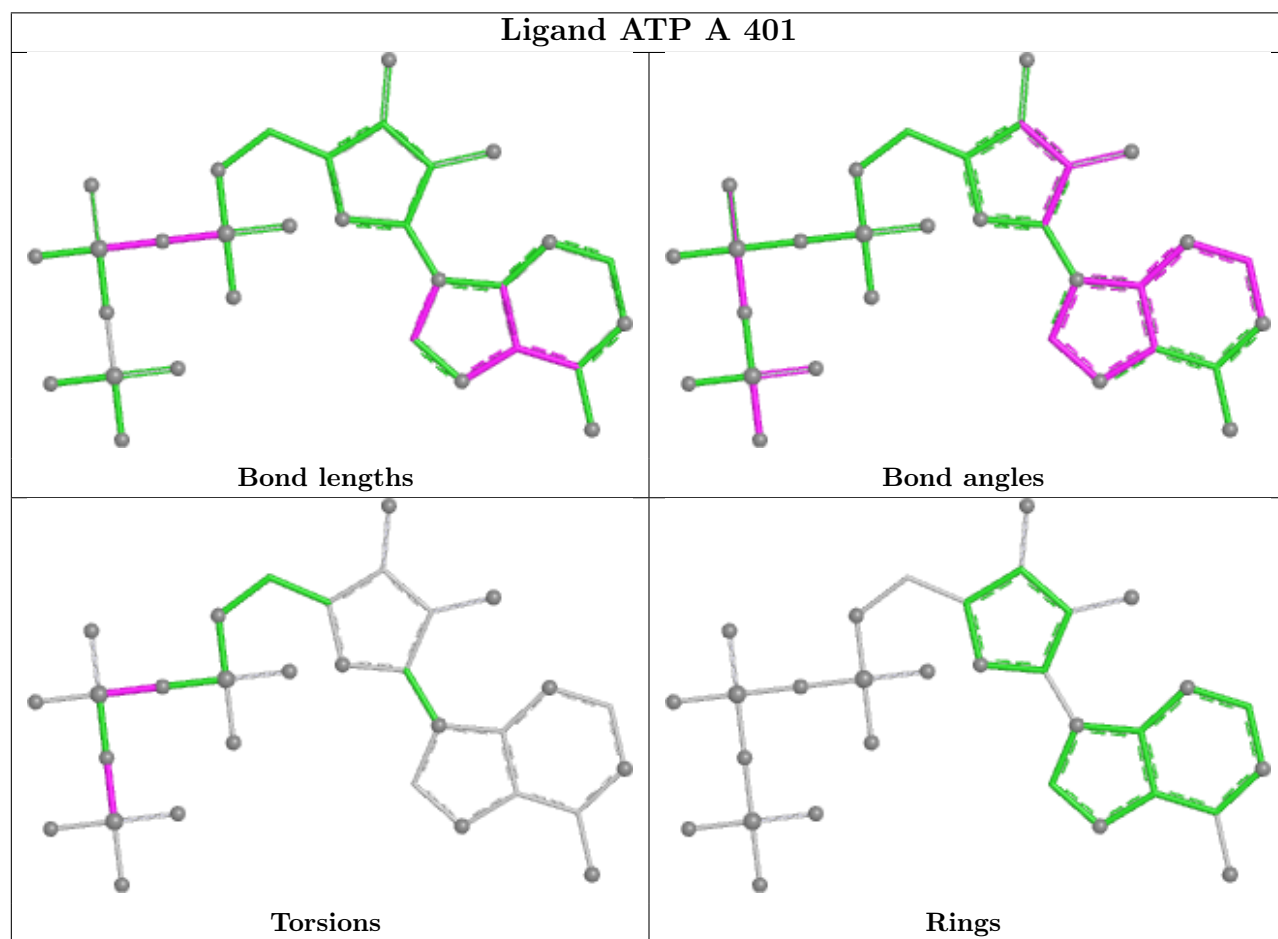
There are no ring outliers.

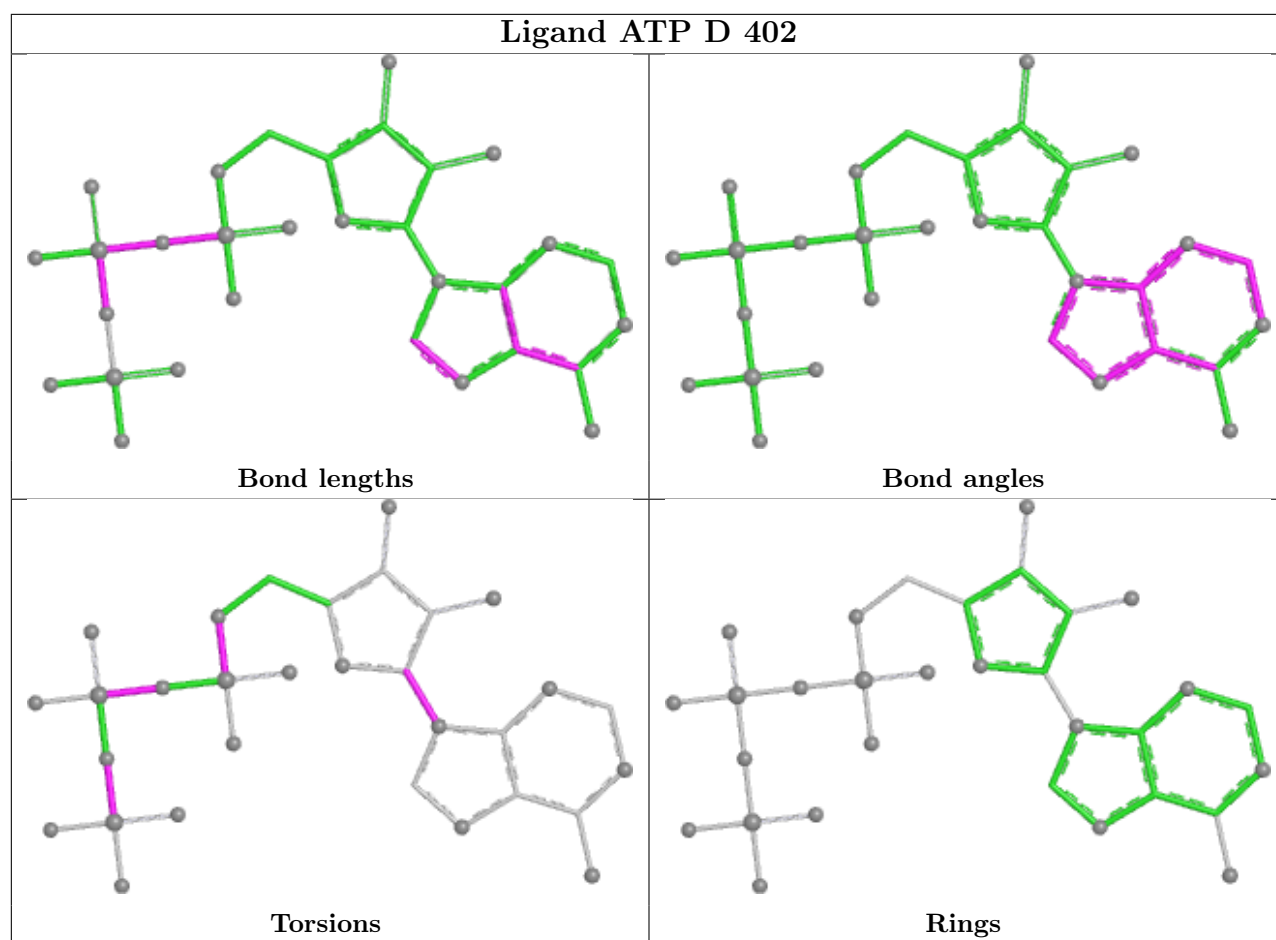
5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	402	ATP	2	0
2	C	402	ATP	2	0
2	A	402	ATP	1	0
2	C	401	ATP	1	0
2	G	401	ATP	2	0

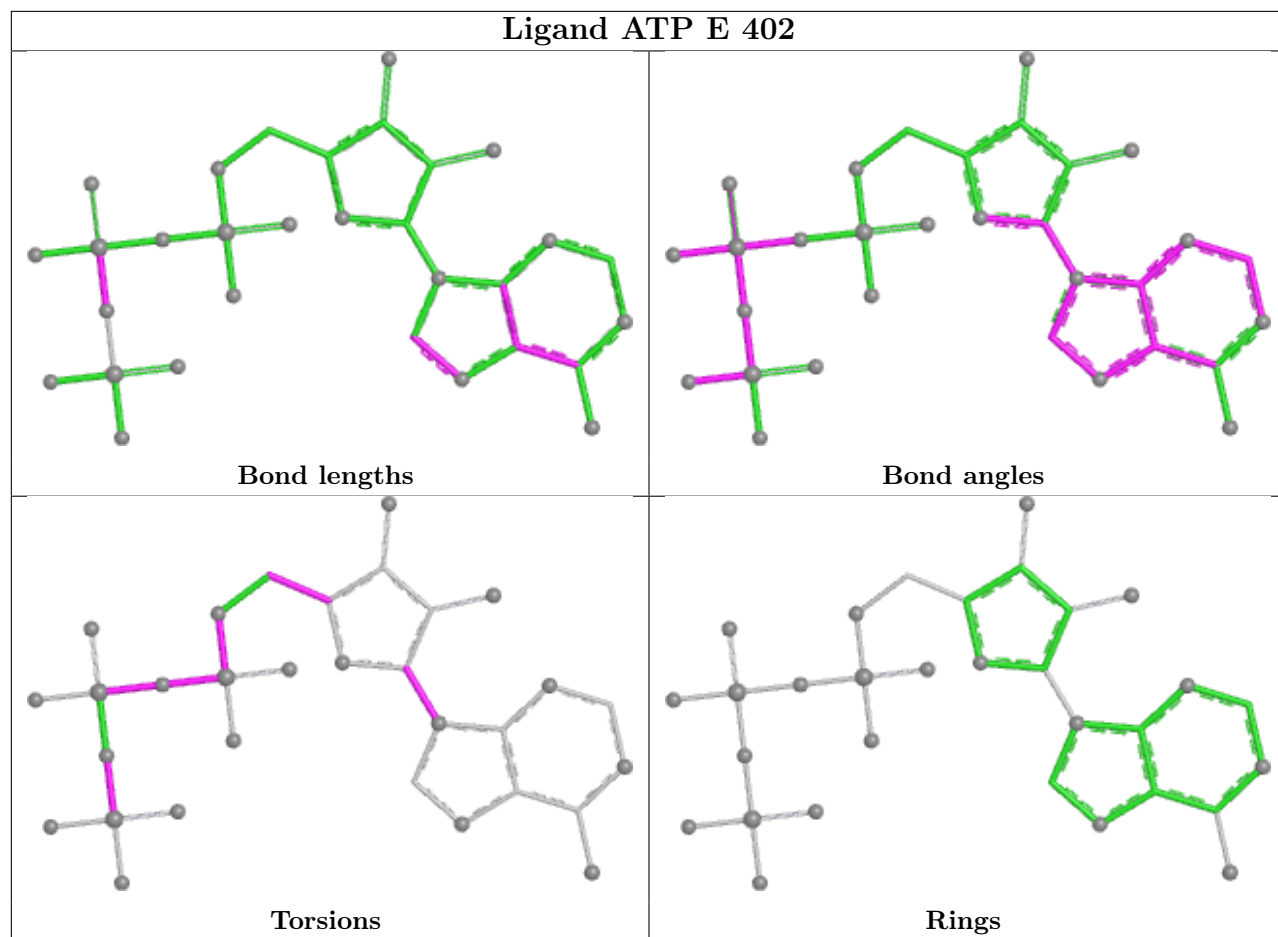
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

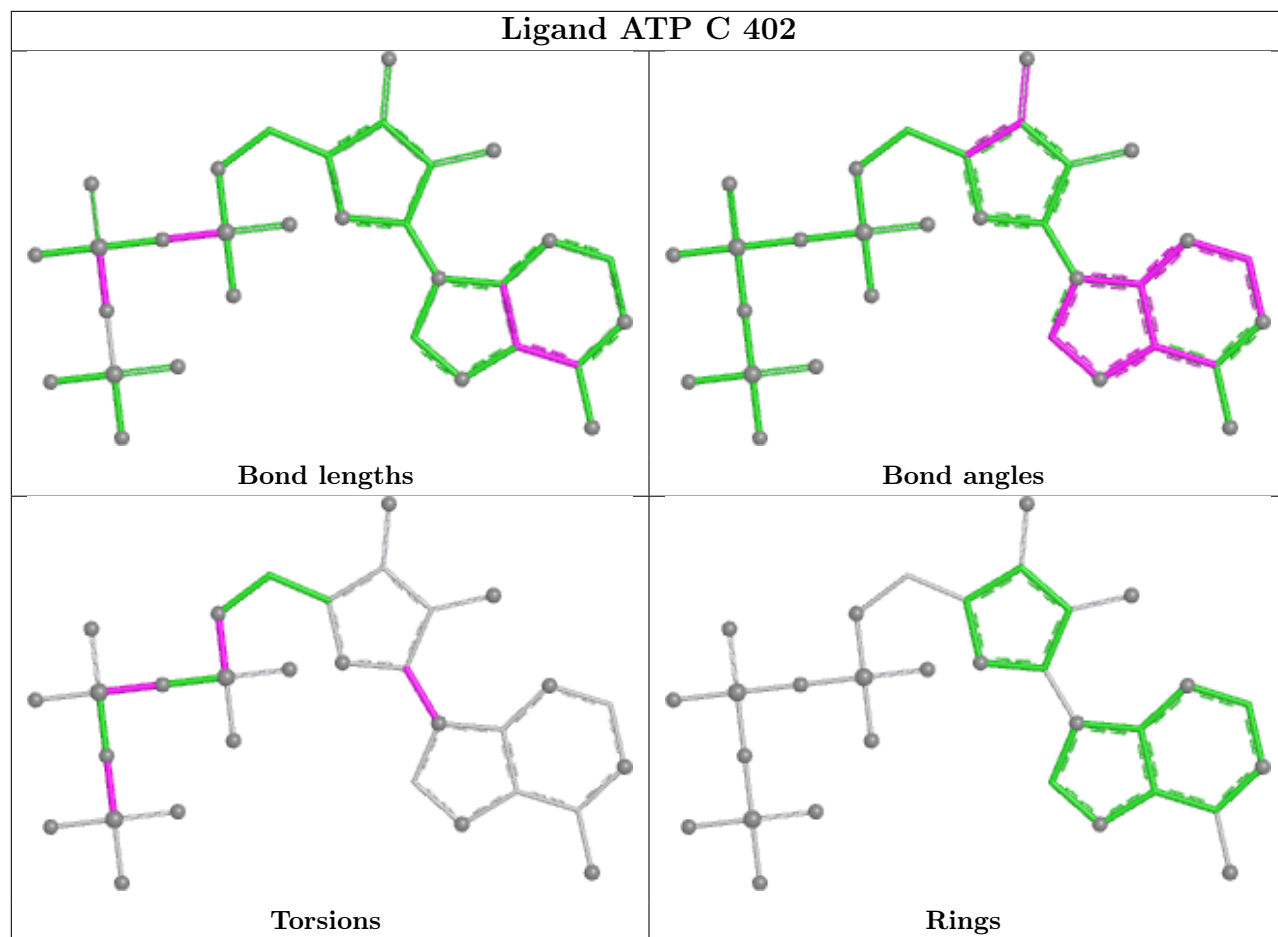
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

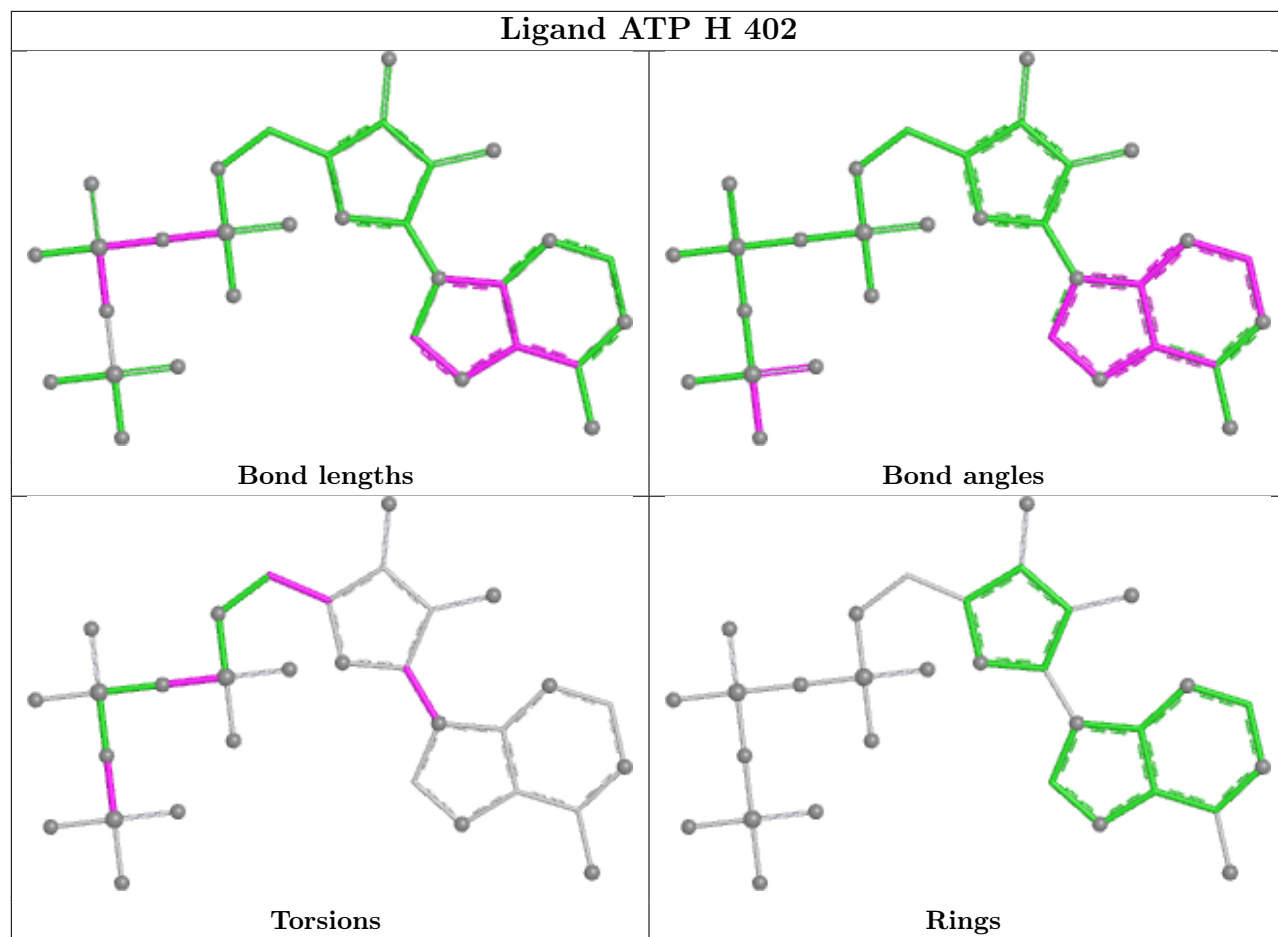


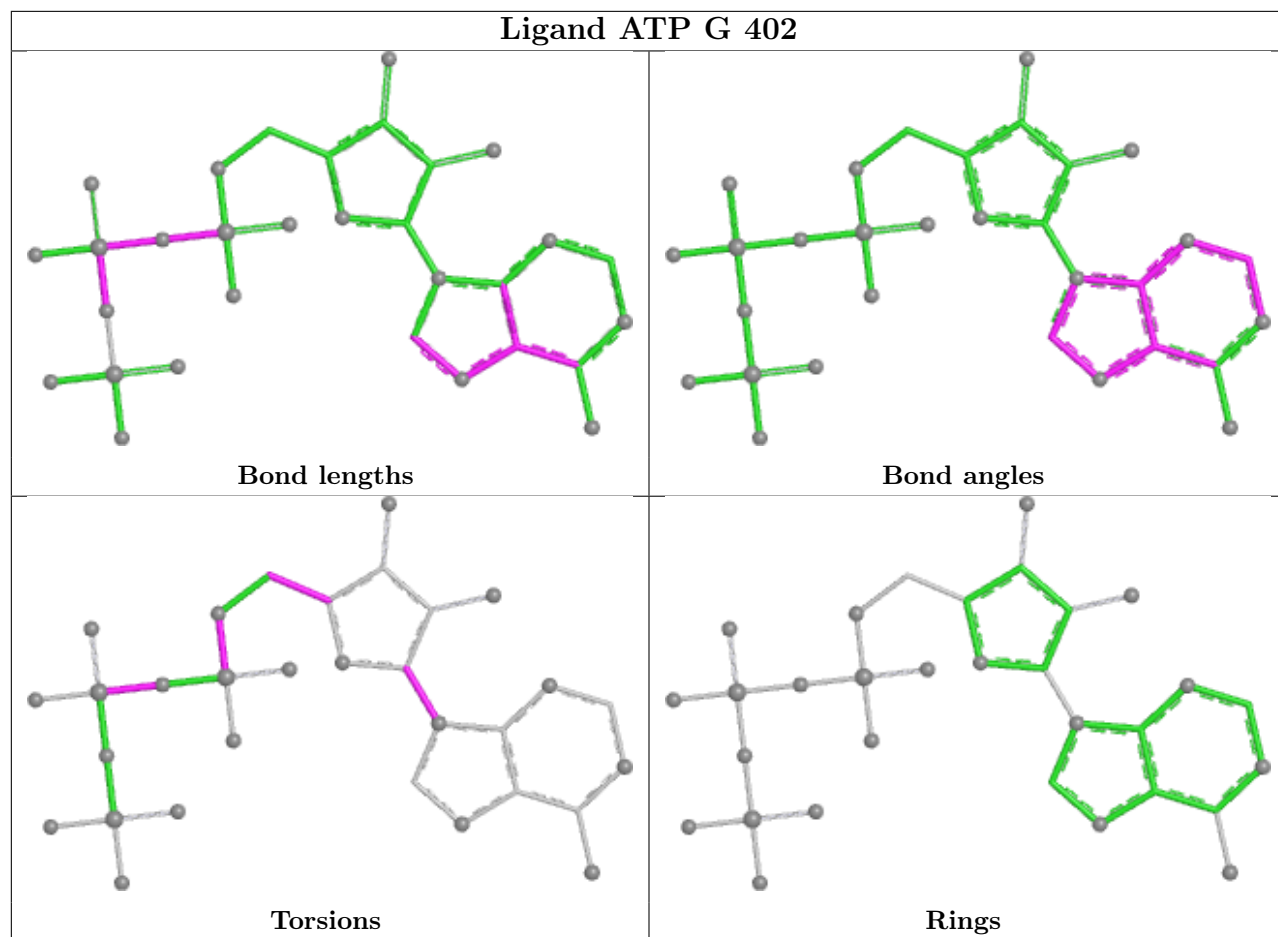


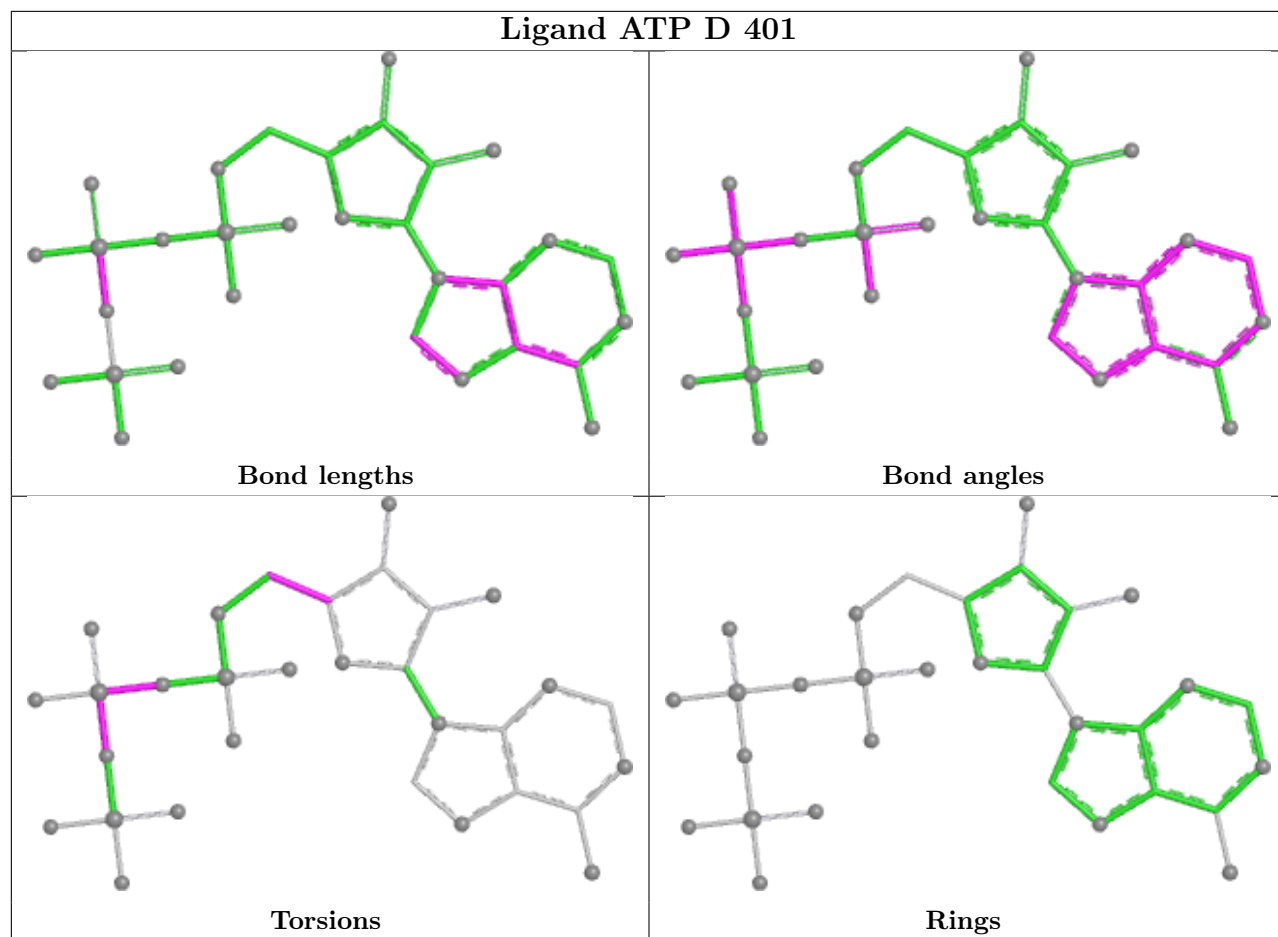
Ligand ATP E 402

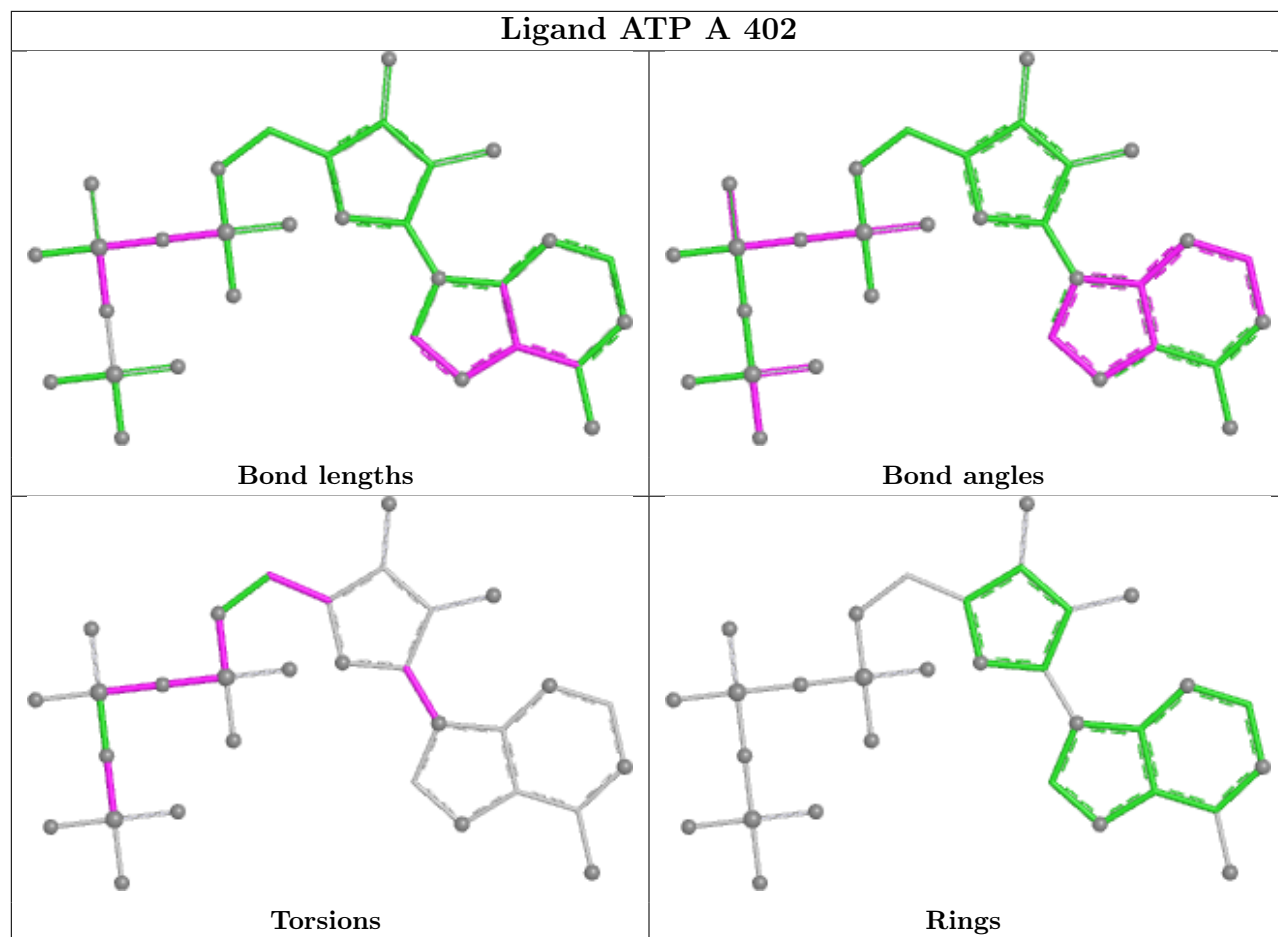


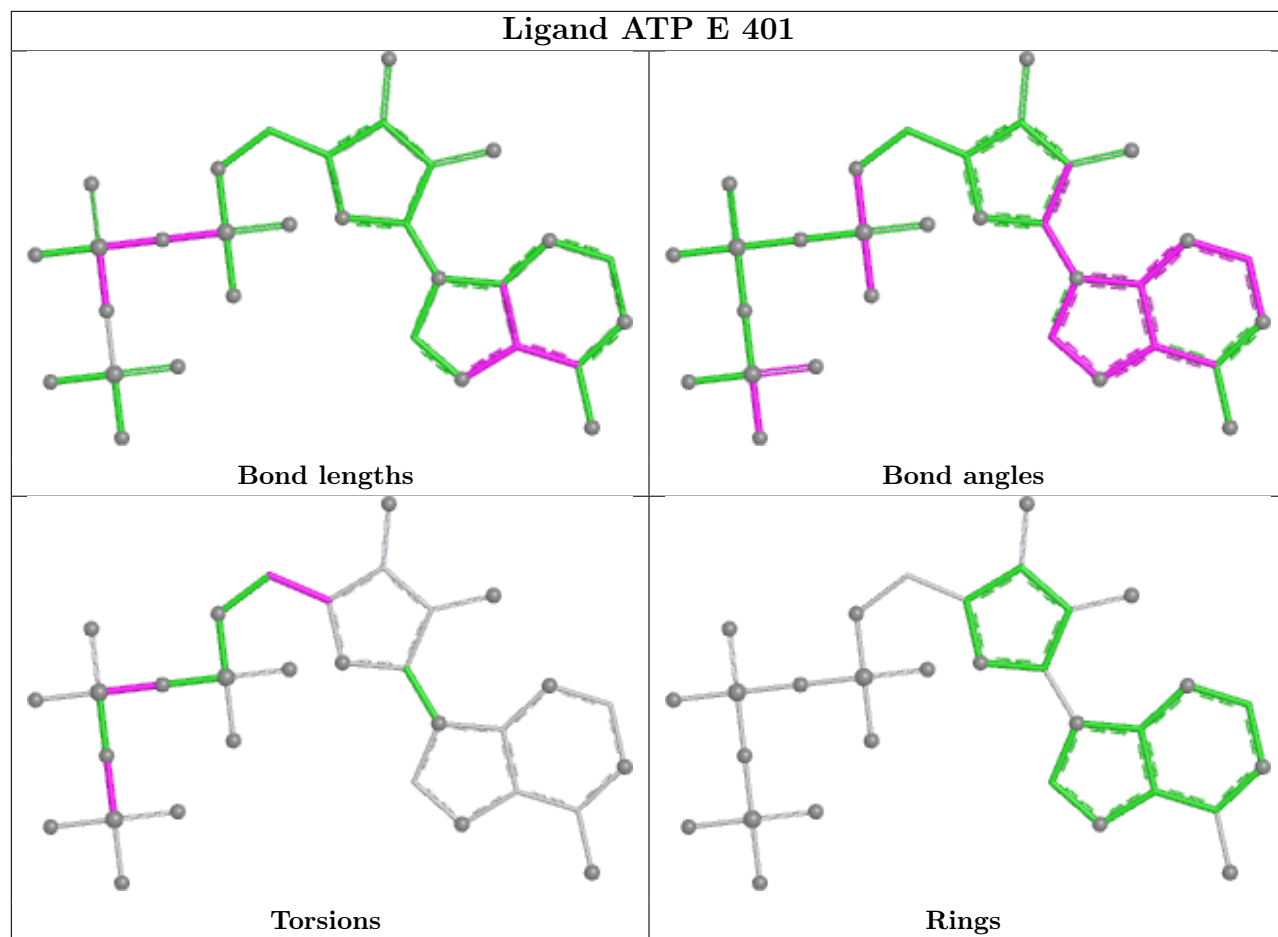


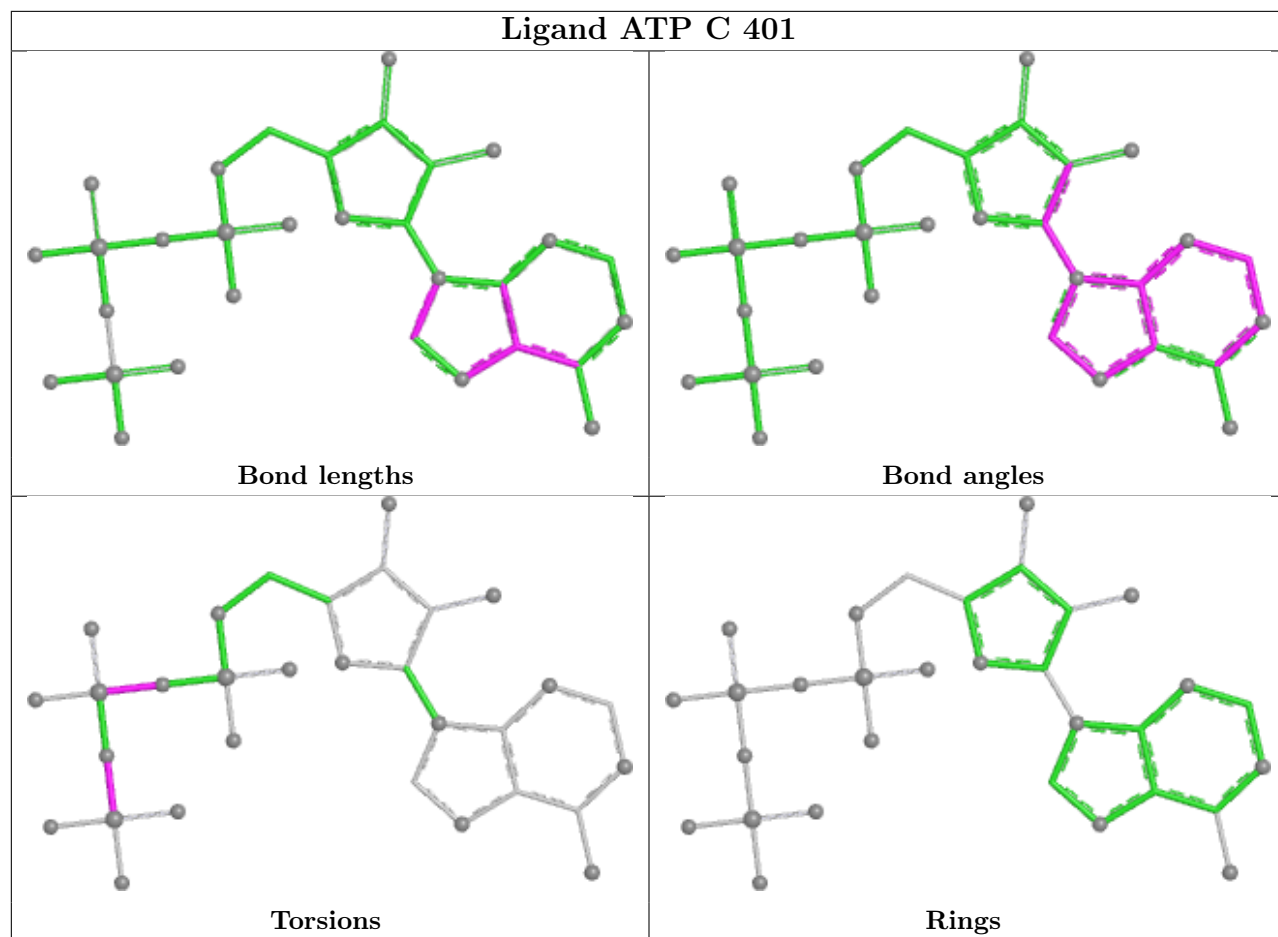


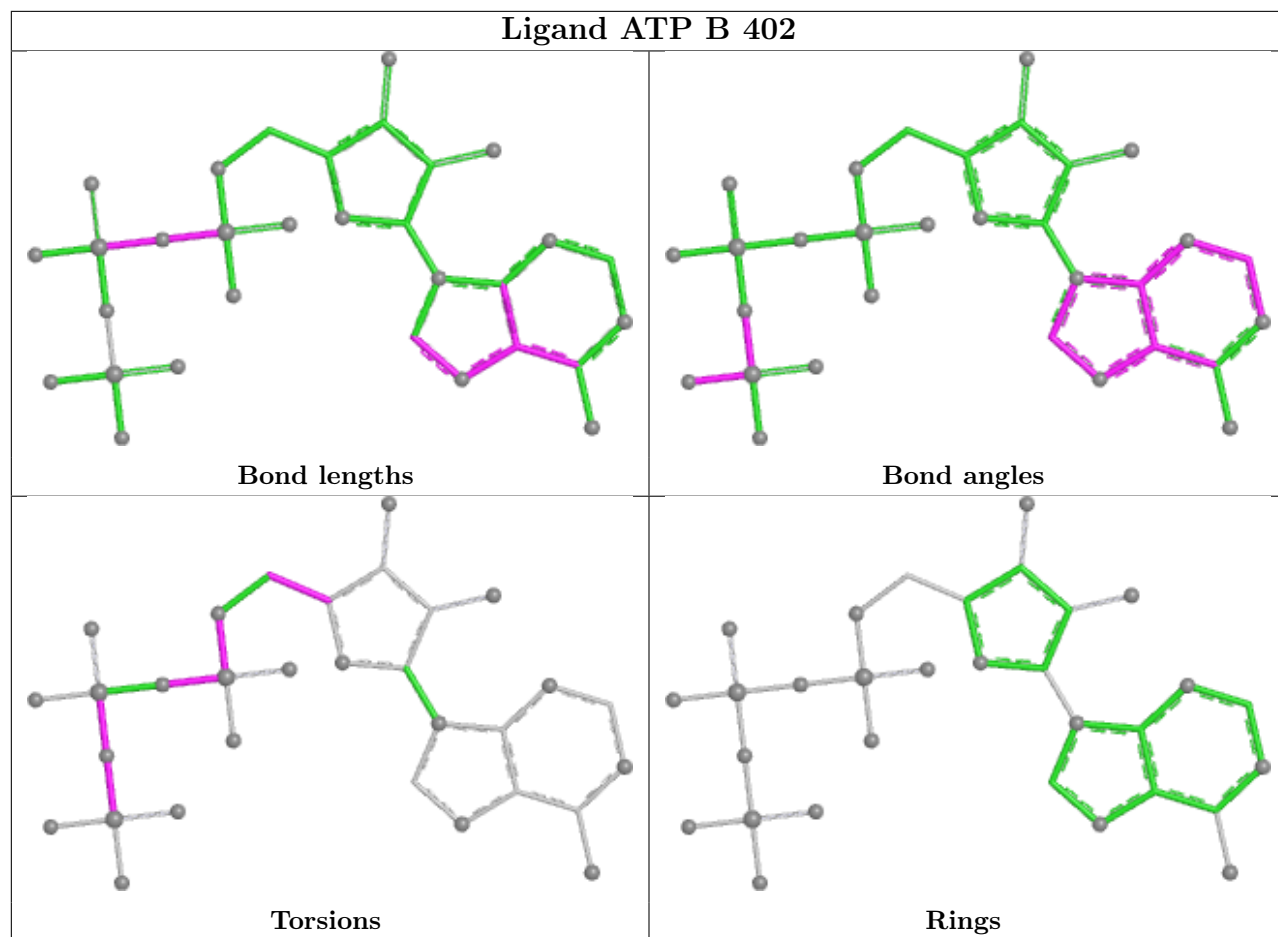


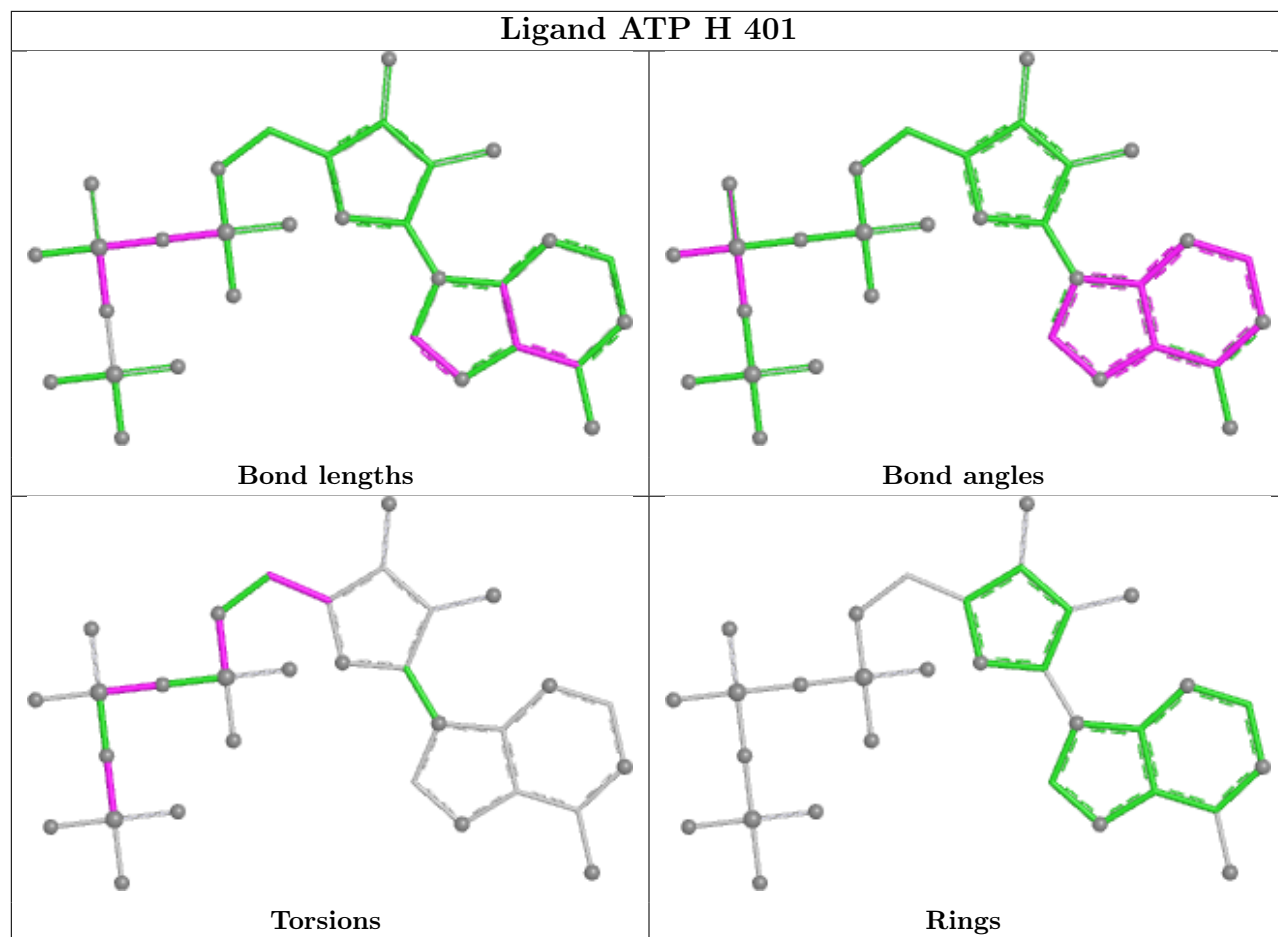


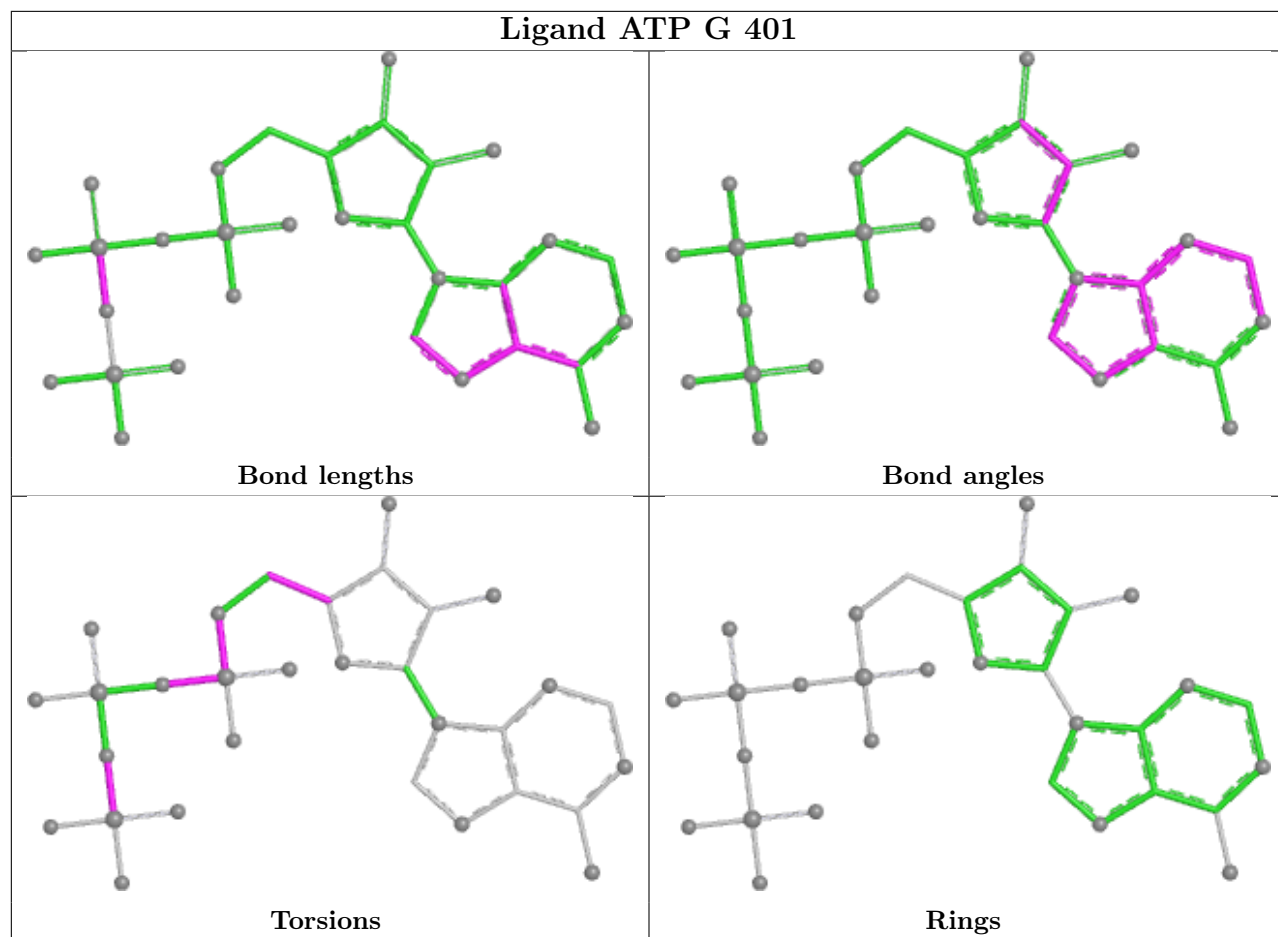




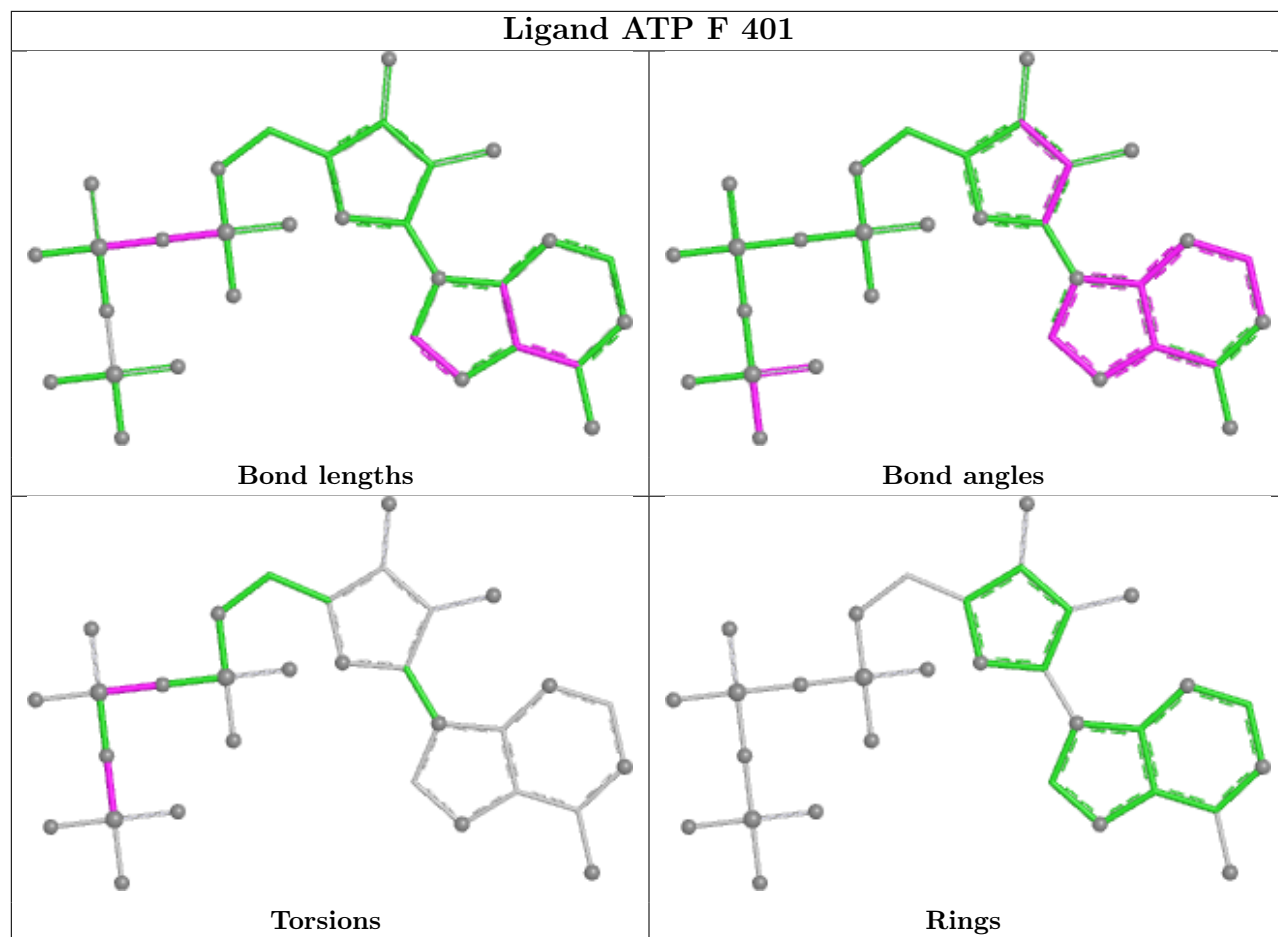


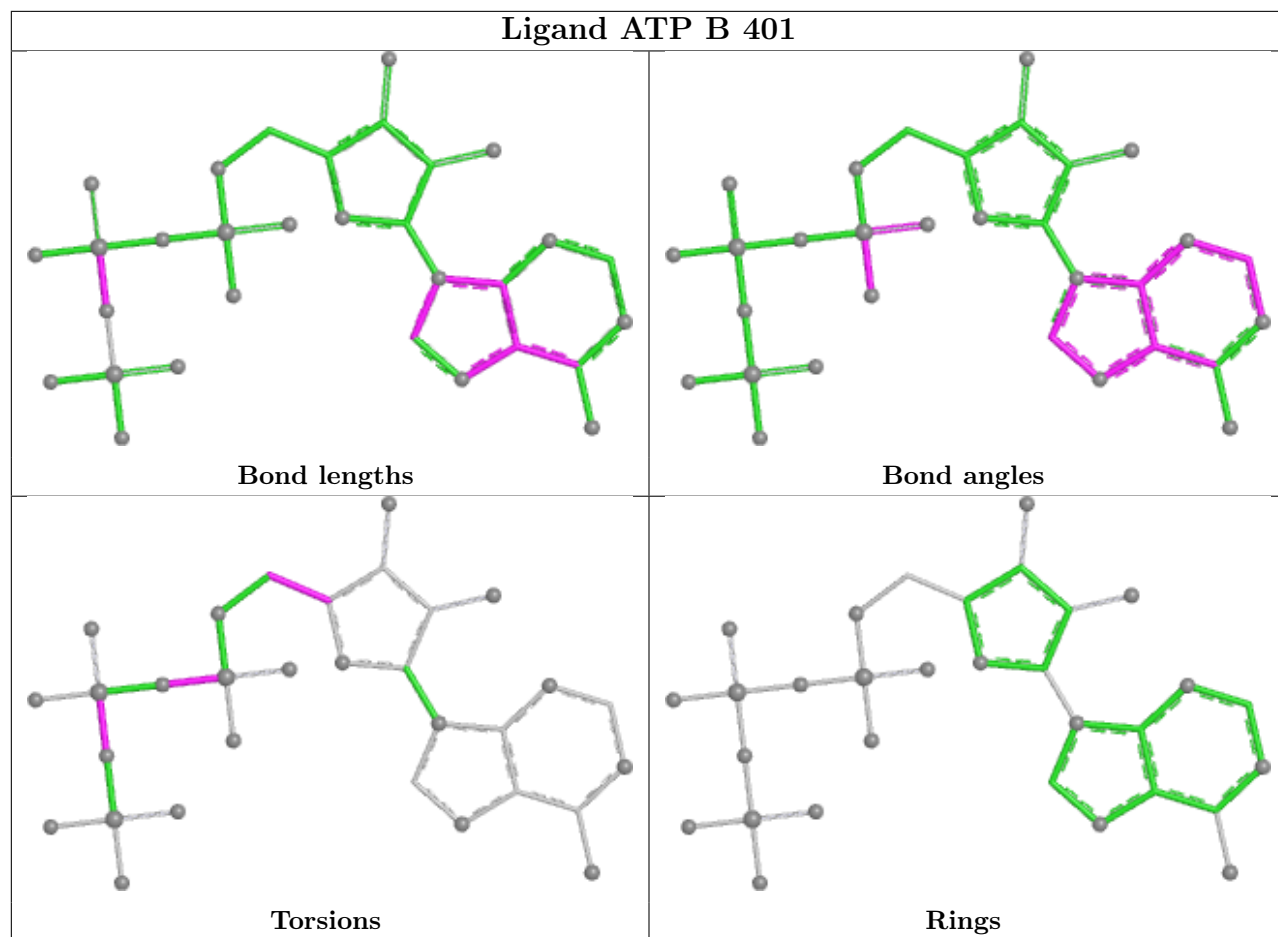


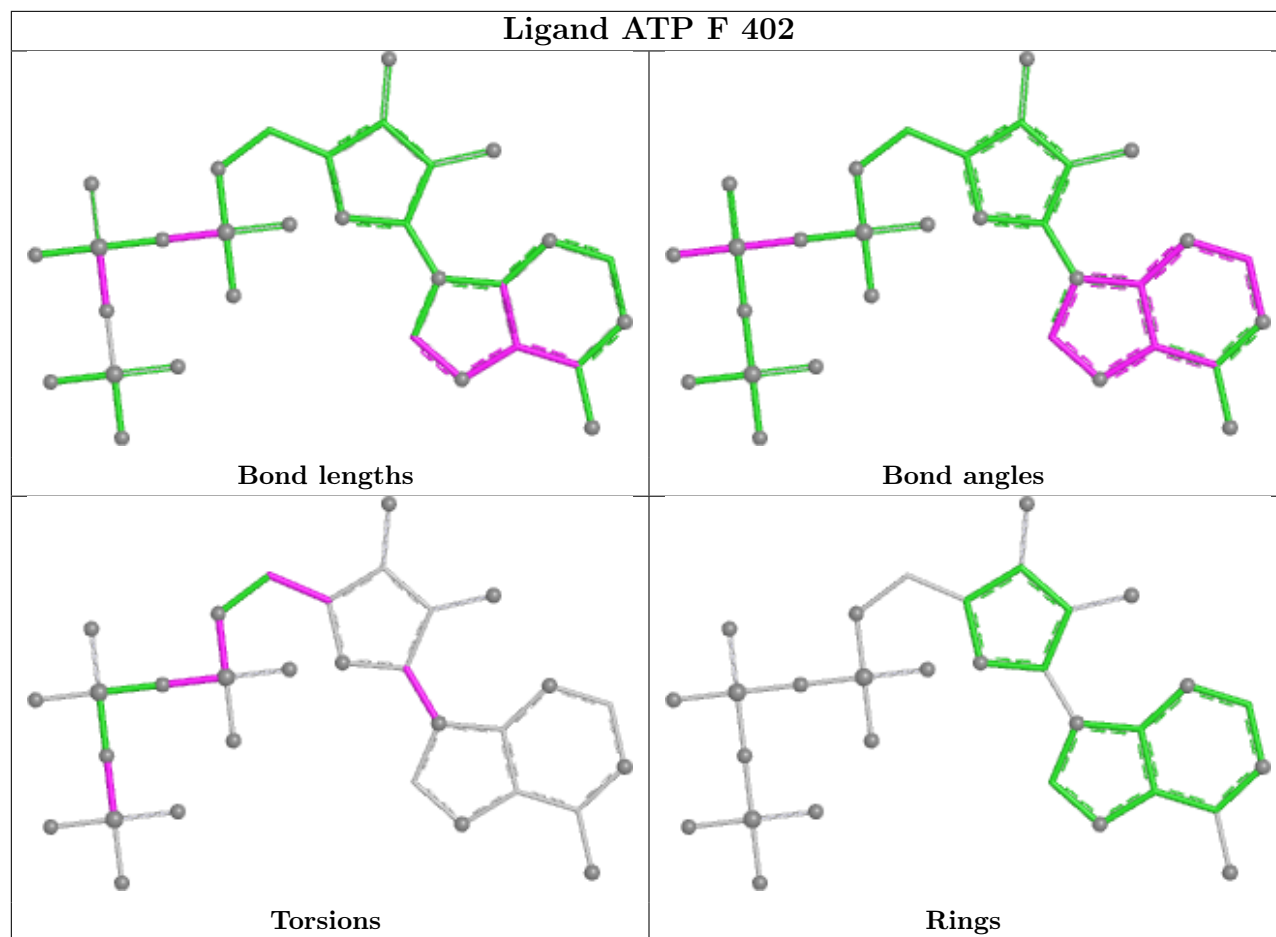




Ligand ATP F 401







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	244/271 (90%)	-0.15	7 (2%) 53 50	19, 37, 65, 88	0
1	B	243/271 (89%)	-0.21	3 (1%) 76 73	20, 34, 50, 83	0
1	C	265/271 (97%)	0.04	10 (3%) 44 40	21, 43, 84, 114	1 (0%)
1	D	266/271 (98%)	0.22	14 (5%) 32 28	23, 46, 95, 118	0
1	E	268/271 (98%)	0.05	7 (2%) 57 53	19, 41, 88, 114	1 (0%)
1	F	255/271 (94%)	0.20	8 (3%) 51 47	26, 50, 93, 109	0
1	G	243/271 (89%)	0.46	12 (4%) 35 31	31, 58, 101, 114	1 (0%)
1	H	259/271 (95%)	0.42	14 (5%) 31 28	32, 57, 99, 118	0
All	All	2043/2168 (94%)	0.13	75 (3%) 45 41	19, 45, 92, 118	3 (0%)

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	34[A]	HIS	8.4
1	F	234	VAL	6.0
1	E	229	LEU	5.9
1	C	229	LEU	5.0
1	G	186	ALA	4.8
1	F	194	PHE	4.4
1	C	227	ALA	4.2
1	D	229	LEU	4.2
1	E	230	SER	4.1
1	G	185	VAL	4.1
1	A	221	TYR	4.0
1	D	234	VAL	4.0
1	A	182	MET	4.0
1	G	194	PHE	3.9
1	G	187	SER	3.8
1	D	227	ALA	3.8

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Mol	Chain	Res	Type	RSRZ
1	H	223	THR	3.8
1	D	167	VAL	3.8
1	D	233	GLN	3.6
1	E	227	ALA	3.6
1	C	34[A]	HIS	3.5
1	D	223	THR	3.5
1	D	230	SER	3.4
1	D	183	GLY	3.2
1	H	230	SER	3.1
1	D	225	ASP	3.1
1	H	179	GLN	3.0
1	C	224	GLU	3.0
1	F	237	LEU	3.0
1	A	173	THR	2.9
1	C	230	SER	2.9
1	G	182	MET	2.9
1	E	234	VAL	2.8
1	C	241	ARG	2.8
1	F	182	MET	2.8
1	G	221	TYR	2.8
1	H	264	PRO	2.7
1	H	237	LEU	2.7
1	H	234	VAL	2.7
1	A	3	ASN	2.7
1	D	231	LYS	2.6
1	H	240	LYS	2.6
1	D	220	ASN	2.5
1	A	176	GLN	2.5
1	D	3	ASN	2.5
1	C	234	VAL	2.5
1	H	221	TYR	2.5
1	E	242	LYS	2.5
1	D	268	ASP	2.5
1	B	221	TYR	2.4
1	F	184	THR	2.4
1	H	194	PHE	2.4
1	F	118	ASP	2.4
1	H	233	GLN	2.4
1	F	190	ASN	2.3
1	C	237	LEU	2.3
1	E	226	GLU	2.2
1	A	178	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	175	GLN	2.2
1	B	168	LEU	2.2
1	H	118	ASP	2.2
1	C	231	LYS	2.2
1	F	173	THR	2.2
1	G	177	ALA	2.2
1	H	243	LYS	2.1
1	E	223	THR	2.1
1	B	182	MET	2.1
1	H	182	MET	2.1
1	G	252	ASP	2.1
1	H	193	LEU	2.1
1	G	268	ASP	2.1
1	D	194	PHE	2.1
1	A	174	PRO	2.0
1	C	228	GLU	2.0
1	G	184	THR	2.0

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($\text{\AA}^2$)	Q<0.9
2	ATP	B	402	31/31	0.93	0.13	21,104,107,109	0
2	ATP	G	401	31/31	0.94	0.12	42,79,81,82	0
3	MG	H	403	1/1	0.94	0.10	43,43,43,43	0
3	MG	F	403	1/1	0.95	0.07	39,39,39,39	0
3	MG	G	404	1/1	0.95	0.05	38,38,38,38	0
2	ATP	G	402	31/31	0.95	0.09	34,61,70,72	0

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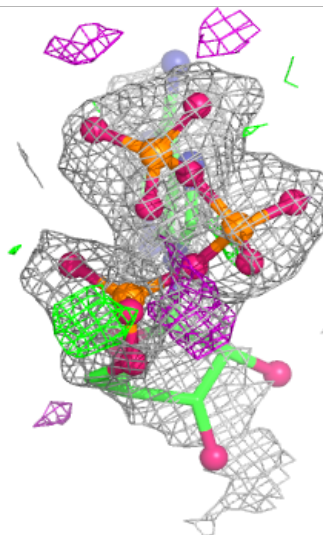
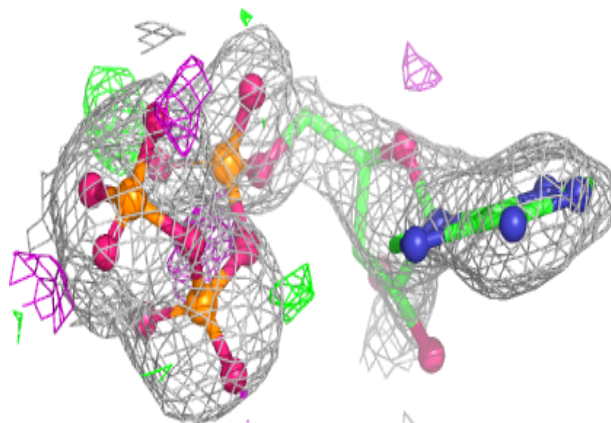
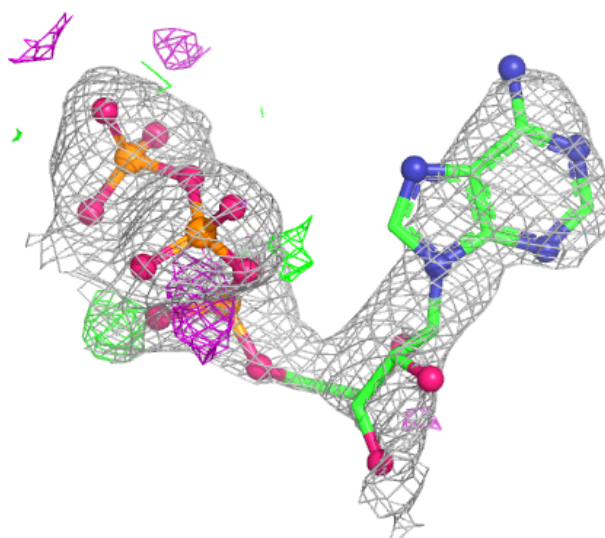
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	G	403	1/1	0.96	0.06	45,45,45,45	0
2	ATP	H	401	31/31	0.96	0.08	32,47,55,57	0
2	ATP	F	401	31/31	0.96	0.09	22,41,53,57	0
2	ATP	H	402	31/31	0.97	0.08	27,66,72,74	0
3	MG	E	403	1/1	0.97	0.04	31,31,31,31	0
2	ATP	F	402	31/31	0.97	0.08	24,57,61,66	0
2	ATP	C	402	31/31	0.97	0.07	24,50,54,55	0
2	ATP	D	402	31/31	0.97	0.07	23,50,55,56	0
2	ATP	C	401	31/31	0.97	0.07	22,40,46,47	0
2	ATP	E	402	31/31	0.98	0.07	19,44,51,57	0
3	MG	A	403	1/1	0.98	0.04	33,33,33,33	0
3	MG	B	405	1/1	0.98	0.04	27,27,27,27	0
3	MG	D	403	1/1	0.98	0.05	39,39,39,39	0
2	ATP	A	402	31/31	0.98	0.07	21,54,62,65	0
3	MG	E	404	1/1	0.98	0.04	26,26,26,26	0
2	ATP	B	401	31/31	0.98	0.05	15,27,34,35	0
2	ATP	D	401	31/31	0.98	0.06	26,34,40,43	0
2	ATP	A	401	31/31	0.98	0.06	20,27,36,38	0
3	MG	G	405	1/1	0.98	0.03	43,43,43,43	0
2	ATP	E	401	31/31	0.98	0.06	25,36,40,41	0
3	MG	B	404	1/1	0.99	0.04	22,22,22,22	0
3	MG	A	404	1/1	0.99	0.04	24,24,24,24	0
3	MG	E	405	1/1	0.99	0.02	22,22,22,22	0
3	MG	C	403	1/1	0.99	0.03	33,33,33,33	0
3	MG	F	404	1/1	0.99	0.04	31,31,31,31	0
3	MG	F	405	1/1	0.99	0.03	30,30,30,30	0
3	MG	C	405	1/1	0.99	0.03	24,24,24,24	0
3	MG	A	405	1/1	0.99	0.03	20,20,20,20	0
3	MG	D	404	1/1	0.99	0.03	28,28,28,28	0
3	MG	D	405	1/1	0.99	0.05	30,30,30,30	0
3	MG	H	405	1/1	0.99	0.04	29,29,29,29	0
3	MG	C	404	1/1	1.00	0.06	32,32,32,32	0
3	MG	H	404	1/1	1.00	0.02	33,33,33,33	0
3	MG	B	403	1/1	1.00	0.02	33,33,33,33	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.

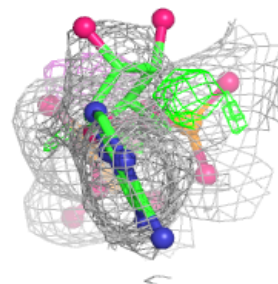
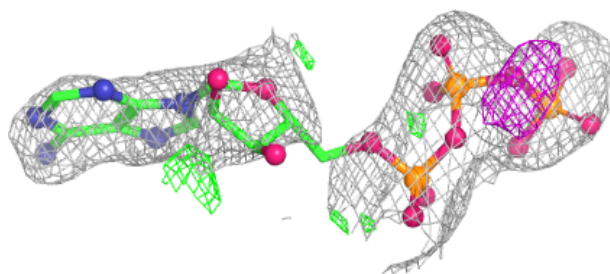
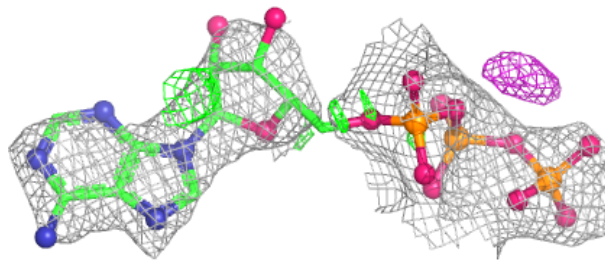
Electron density around ATP B 402:

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



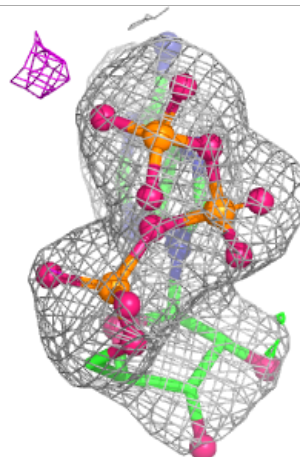
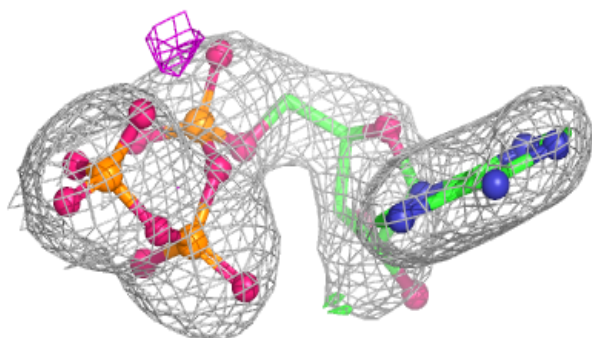
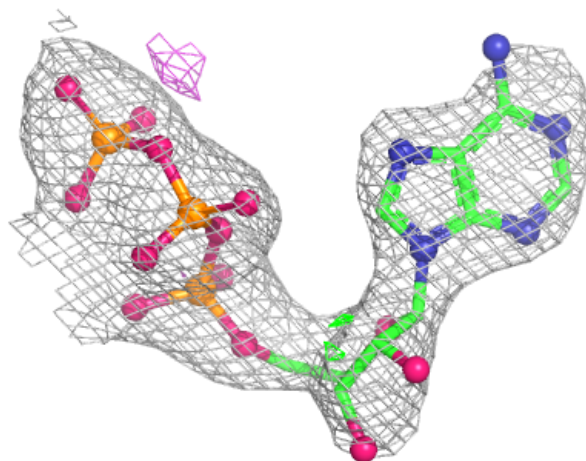
Electron density around ATP G 401:

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



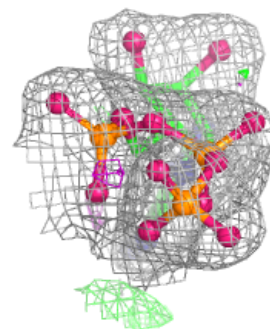
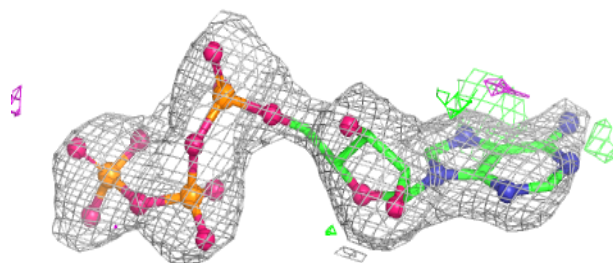
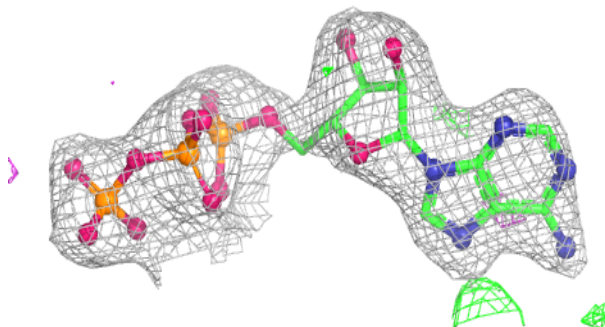
Electron density around ATP G 402:

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and green (positive)

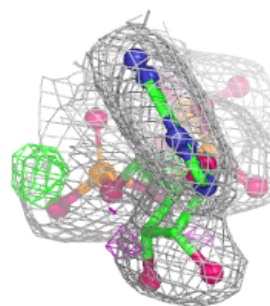
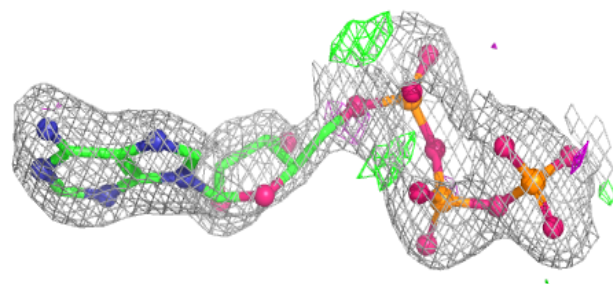
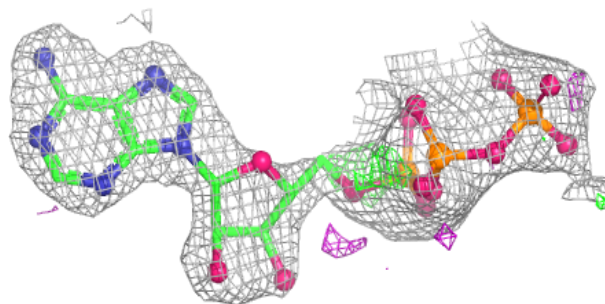


Electron density around ATP H 401:

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and green (positive)

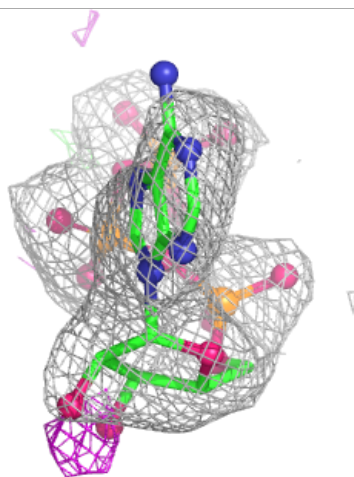
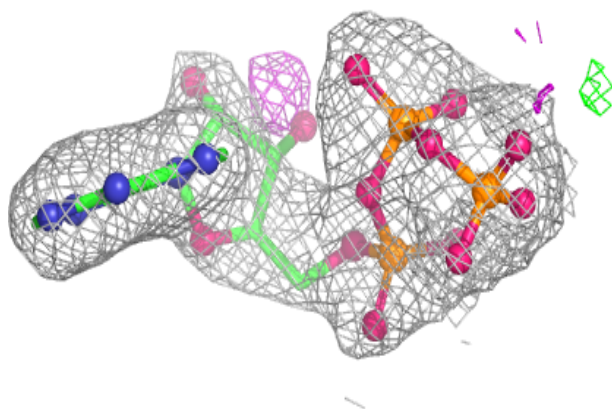
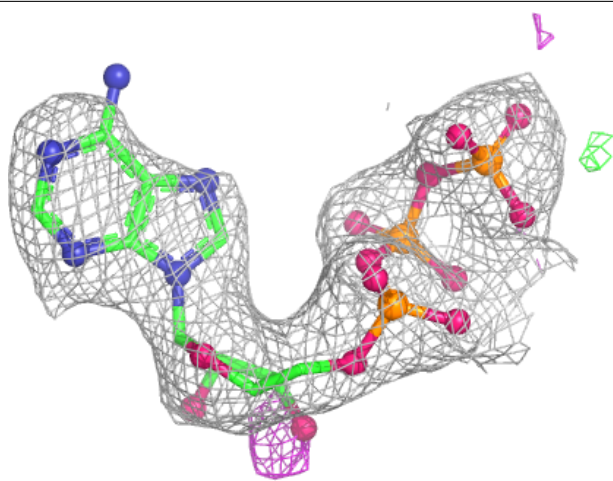
**Electron density around ATP F 401:**

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



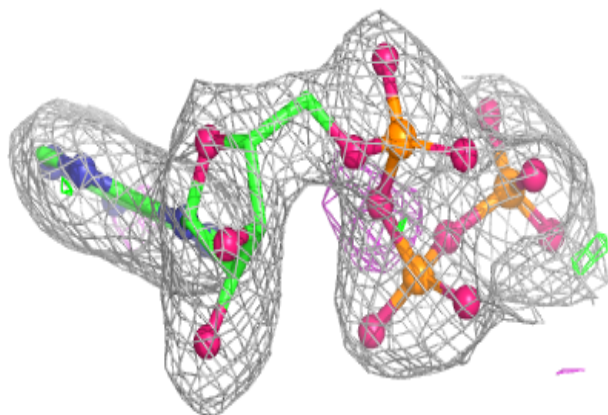
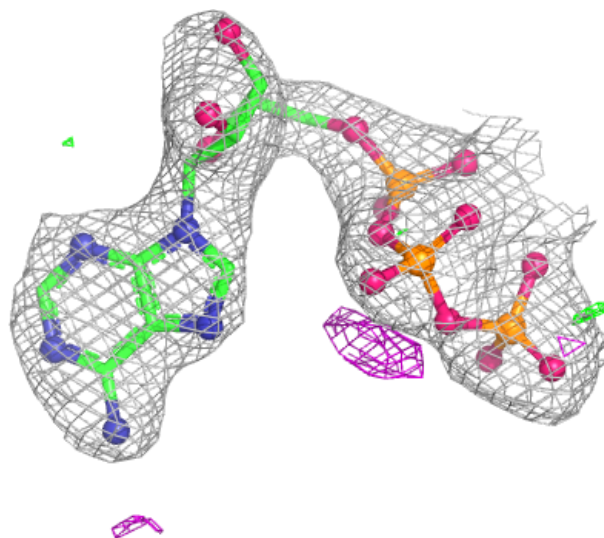
Electron density around ATP H 402:

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



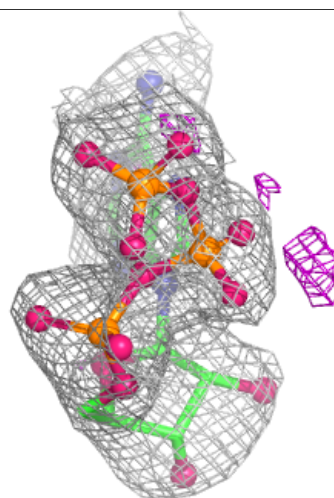
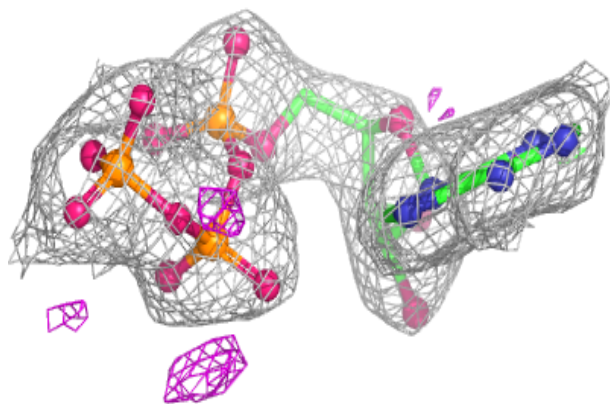
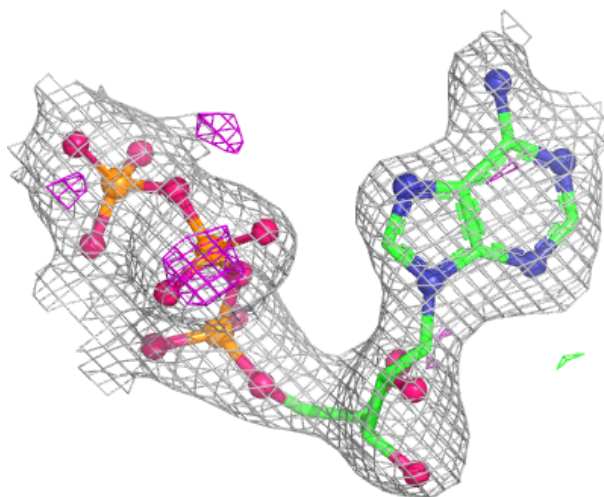
Electron density around ATP F 402:

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



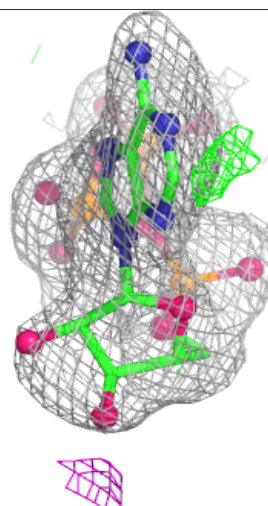
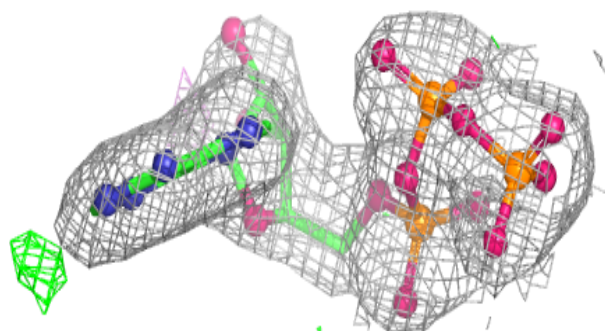
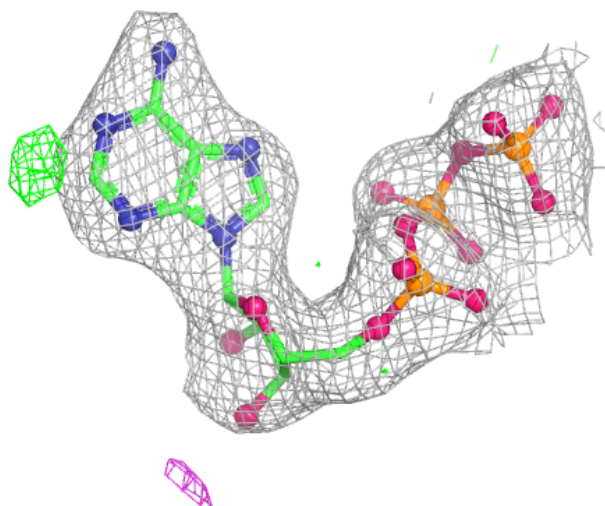
Electron density around ATP C 402:

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



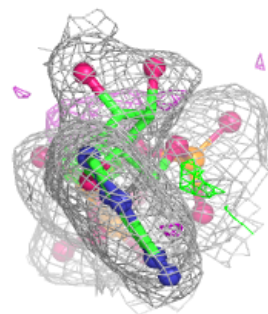
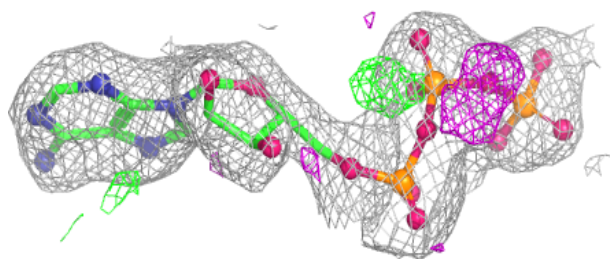
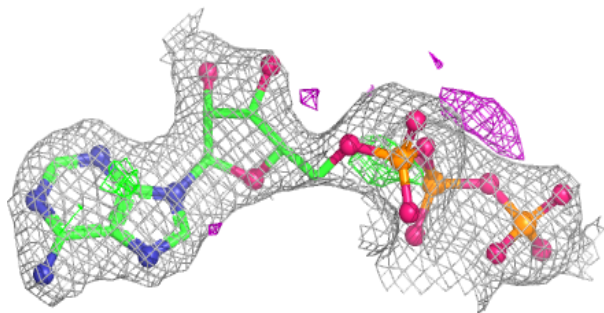
Electron density around ATP D 402:

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



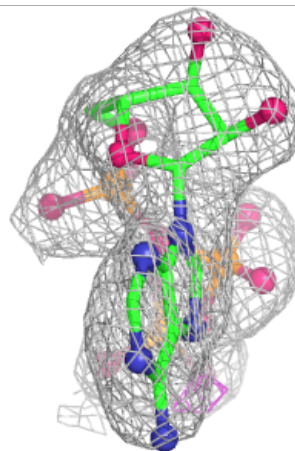
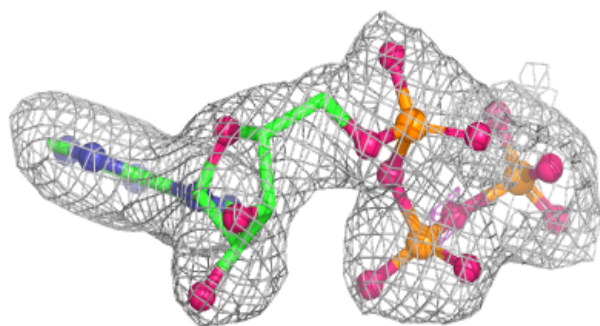
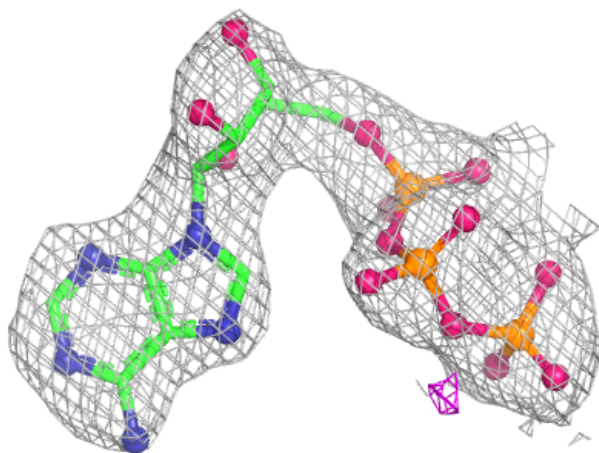
Electron density around ATP C 401:

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



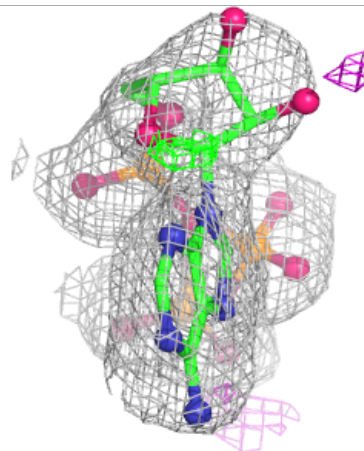
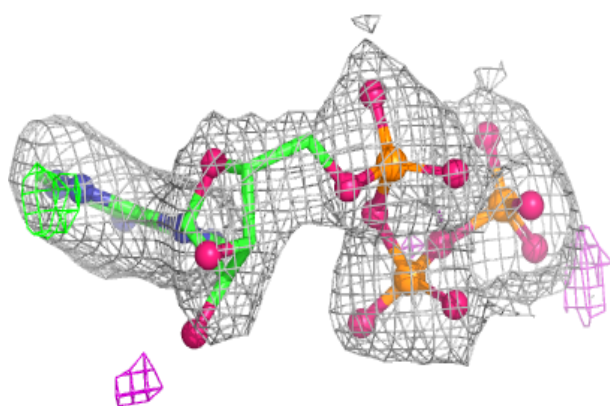
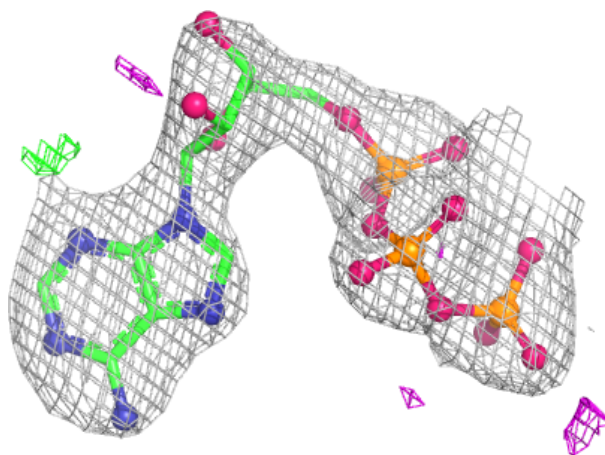
Electron density around ATP E 402:

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



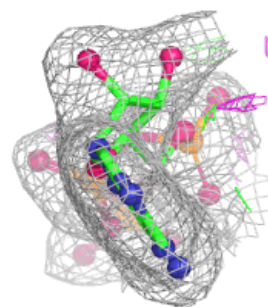
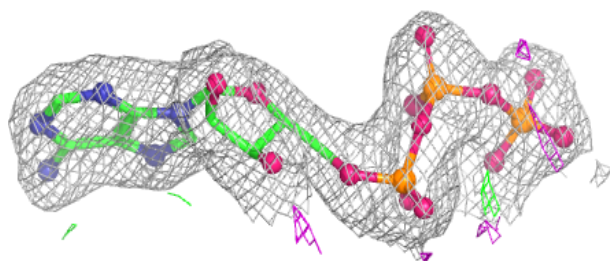
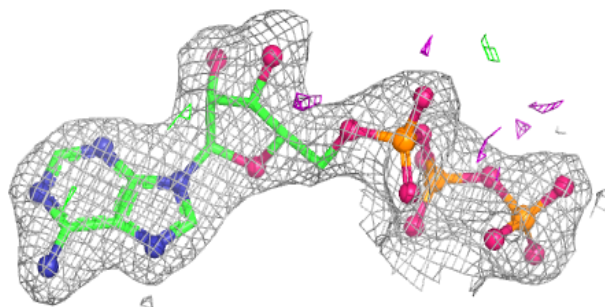
Electron density around ATP A 402:

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

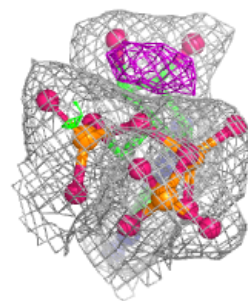
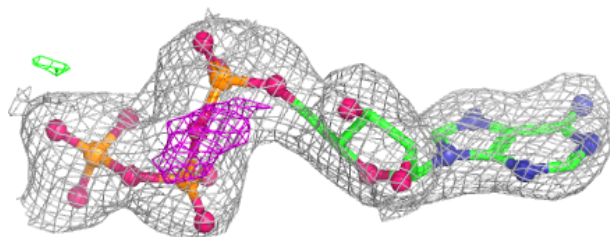
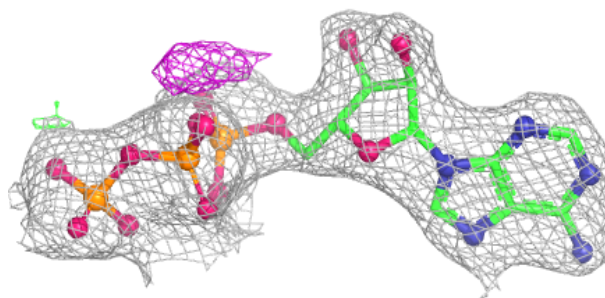


Electron density around ATP B 401:

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

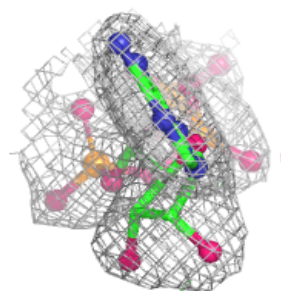
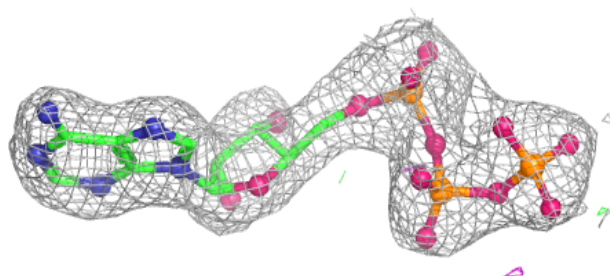
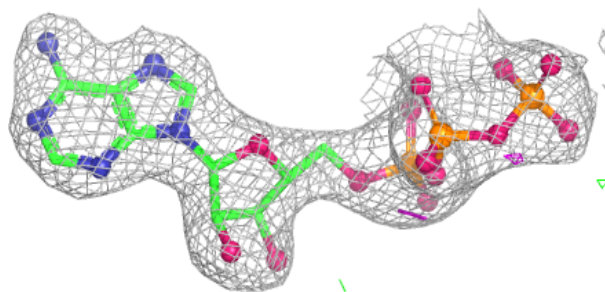
**Electron density around ATP D 401:**

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

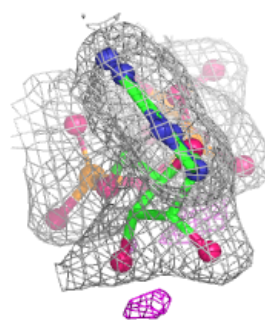
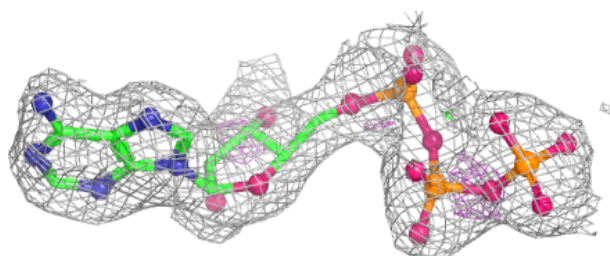
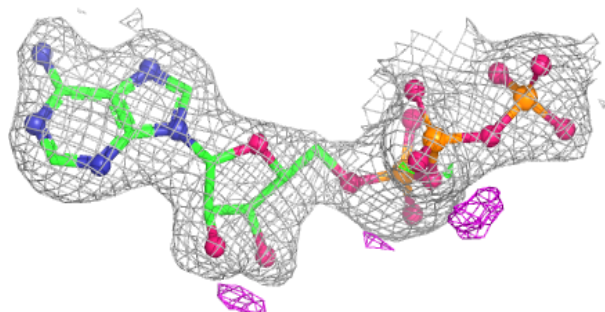


Electron density around ATP A 401:

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

**Electron density around ATP E 401:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.