



wwPDB EM Validation Summary Report ⓘ

Apr 1, 2025 – 07:38 pm BST

PDB ID : 6RIQ / pdb_00006riq
EMDB ID : EMD-4897
Title : MinCD filament from Pseudomonas aeruginosa
Authors : Szewczak-Harris, A.; Wagstaff, J.; Lowe, J.
Deposited on : 2019-04-24
Resolution : 3.10 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

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:

EMDB validation analysis : 0.0.1.dev117
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

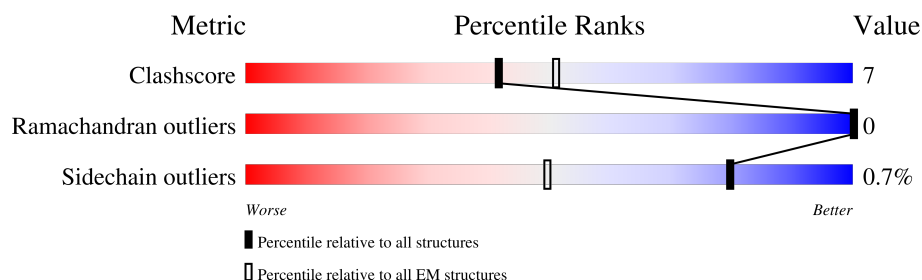
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.













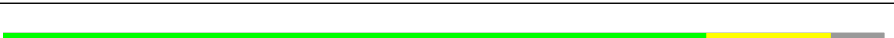
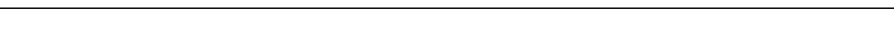
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	144	60% 14% 26%
1	B	144	63% 11% 26%
1	E	144	58% 16% 26%
1	F	144	62% 12% 26%
1	H	144	60% 15% 26%
1	I	144	63% 11% 26%
1	L	144	62% 12% 26%
1	O	144	59% 15% 26%
1	P	144	62% 12% 26%

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Mol	Chain	Length	Quality of chain
1	S	144	
1	T	144	
2	C	271	
2	D	271	
2	G	271	
2	J	271	
2	K	271	
2	M	271	
2	N	271	
2	Q	271	
2	R	271	
2	U	271	
2	V	271	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 30327 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 MinC.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	107	Total	C	N	O	S	0	0
			784	494	145	142	3		
1	B	107	Total	C	N	O	S	0	0
			784	494	145	142	3		
1	E	107	Total	C	N	O	S	0	0
			784	494	145	142	3		
1	F	107	Total	C	N	O	S	0	0
			784	494	145	142	3		
1	H	107	Total	C	N	O	S	0	0
			784	494	145	142	3		
1	I	107	Total	C	N	O	S	0	0
			784	494	145	142	3		
1	L	107	Total	C	N	O	S	0	0
			784	494	145	142	3		
1	O	107	Total	C	N	O	S	0	0
			784	494	145	142	3		
1	P	107	Total	C	N	O	S	0	0
			784	494	145	142	3		
1	S	107	Total	C	N	O	S	0	0
			784	494	145	142	3		
1	T	107	Total	C	N	O	S	0	0
			784	494	145	142	3		

- Molecule 2 is a protein called Site-determining protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	254	Total	C	N	O	S	0	0
			1941	1218	338	378	7		
2	D	254	Total	C	N	O	S	0	0
			1941	1218	338	378	7		
2	G	254	Total	C	N	O	S	0	0
			1941	1218	338	378	7		
2	J	254	Total	C	N	O	S	0	0
			1941	1218	338	378	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	K	254	Total 1941	C 1218	N 338	O 378	S 7	0	0
2	M	254	Total 1941	C 1218	N 338	O 378	S 7	0	0
2	N	254	Total 1941	C 1218	N 338	O 378	S 7	0	0
2	Q	254	Total 1941	C 1218	N 338	O 378	S 7	0	0
2	R	254	Total 1941	C 1218	N 338	O 378	S 7	0	0
2	U	254	Total 1941	C 1218	N 338	O 378	S 7	0	0
2	V	254	Total 1941	C 1218	N 338	O 378	S 7	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	194	SER	GLY	conflict	UNP A0A071KWM5
D	194	SER	GLY	conflict	UNP A0A071KWM5
G	194	SER	GLY	conflict	UNP A0A071KWM5
J	194	SER	GLY	conflict	UNP A0A071KWM5
K	194	SER	GLY	conflict	UNP A0A071KWM5
M	194	SER	GLY	conflict	UNP A0A071KWM5
N	194	SER	GLY	conflict	UNP A0A071KWM5
Q	194	SER	GLY	conflict	UNP A0A071KWM5
R	194	SER	GLY	conflict	UNP A0A071KWM5
U	194	SER	GLY	conflict	UNP A0A071KWM5
V	194	SER	GLY	conflict	UNP A0A071KWM5

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

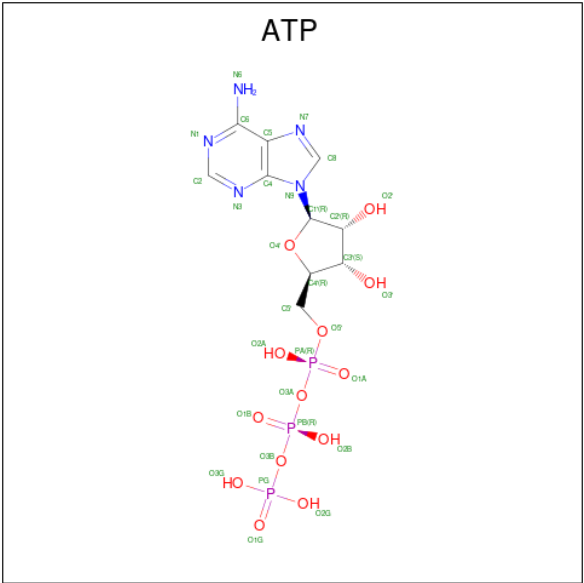
Mol	Chain	Residues	Atoms		AltConf
3	C	1	Total 1	Mg 1	0
3	D	1	Total 1	Mg 1	0
3	G	1	Total 1	Mg 1	0
3	J	1	Total 1	Mg 1	0

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Mol	Chain	Residues	Atoms		AltConf
3	K	1	Total	Mg	0
			1	1	
3	M	1	Total	Mg	0
			1	1	
3	N	1	Total	Mg	0
			1	1	
3	Q	1	Total	Mg	0
			1	1	
3	R	1	Total	Mg	0
			1	1	
3	U	1	Total	Mg	0
			1	1	
3	V	1	Total	Mg	0
			1	1	

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					AltConf
4	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	G	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	J	1	Total	C	N	O	P	0
			31	10	5	13	3	

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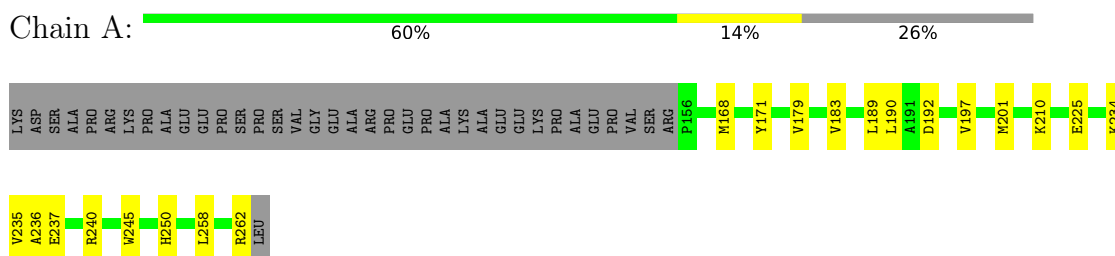
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Mol	Chain	Residues	Atoms					AltConf
4	K	1	Total 31	C 10	N 5	O 13	P 3	0
4	M	1	Total 31	C 10	N 5	O 13	P 3	0
4	N	1	Total 31	C 10	N 5	O 13	P 3	0
4	Q	1	Total 31	C 10	N 5	O 13	P 3	0
4	R	1	Total 31	C 10	N 5	O 13	P 3	0
4	U	1	Total 31	C 10	N 5	O 13	P 3	0
4	V	1	Total 31	C 10	N 5	O 13	P 3	0

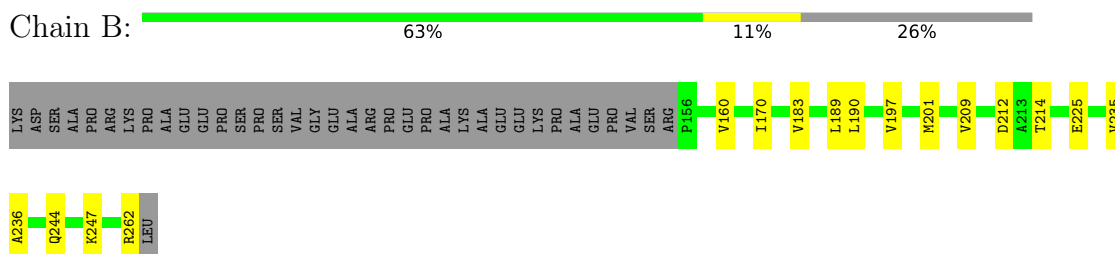
3 Residue-property plots [i](#)

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. 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. 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.

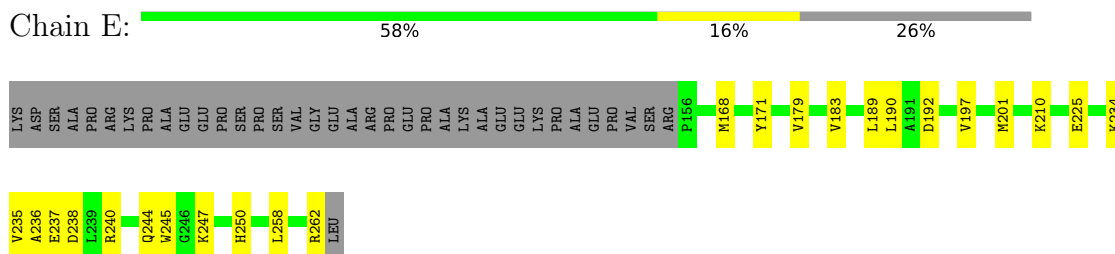
- Molecule 1: MinC



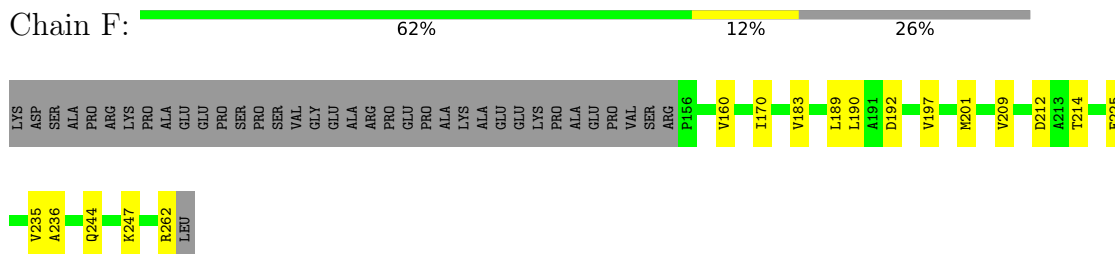
- Molecule 1: MinC



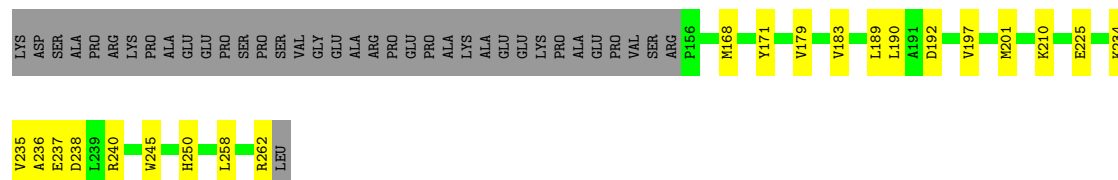
- Molecule 1: MinC



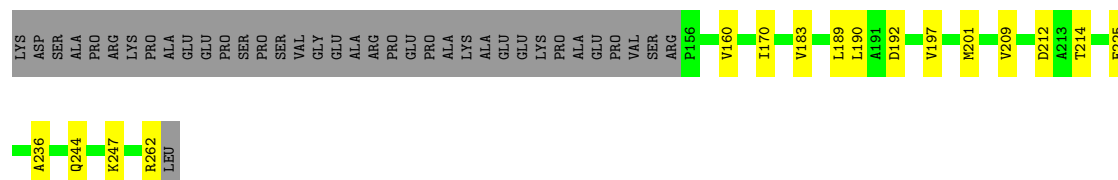
- Molecule 1: MinC



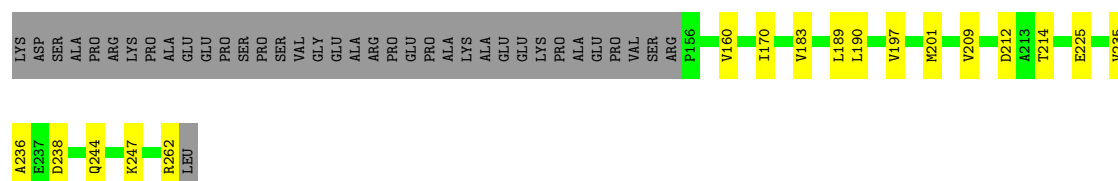
● Molecule 1: MinC

Chain H:  60% 15% 26%

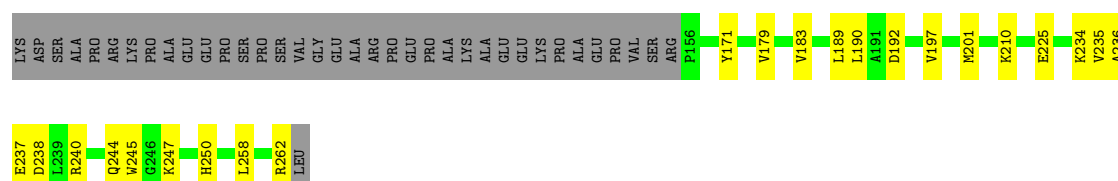
● Molecule 1: MinC

Chain I:  63% 11% 26%

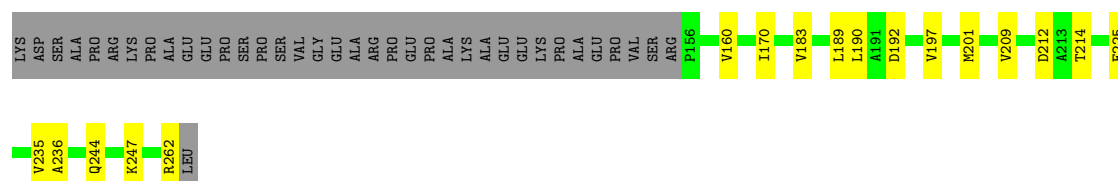
● Molecule 1: MinC

Chain L:  62% 12% 26%

● Molecule 1: MinC

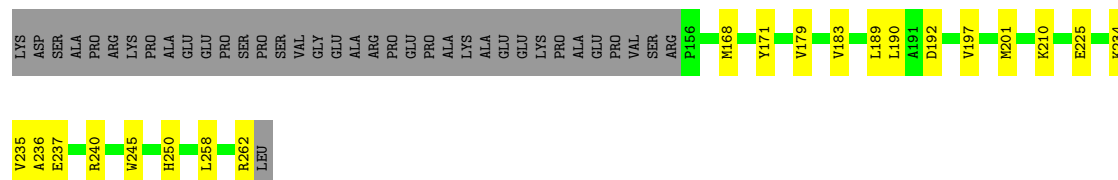
Chain O:  59% 15% 26%

● Molecule 1: MinC

Chain P:  62% 12% 26%

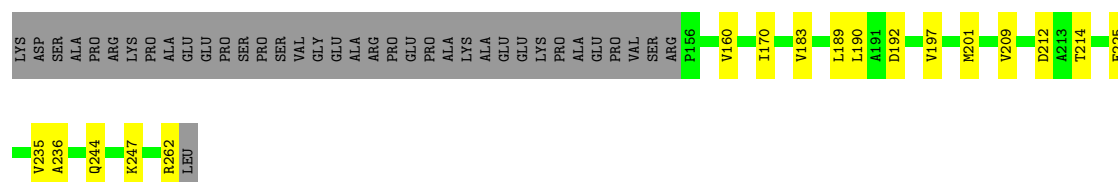
- Molecule 1: MinC

Chain S: 




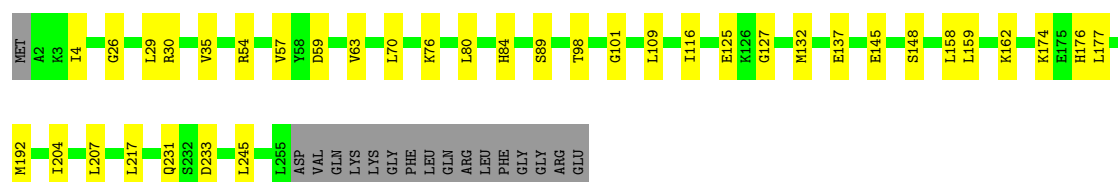
- Molecule 1: MinC

Chain T: 




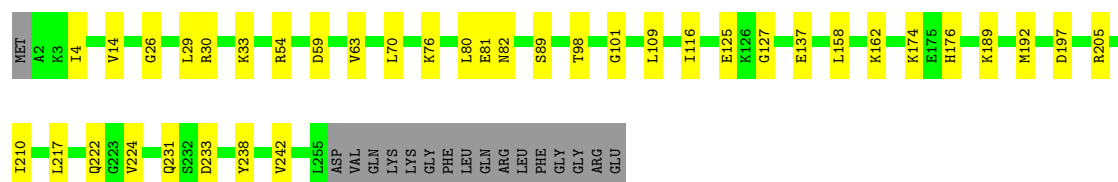
- Molecule 2: Site-determining protein

Chain C: 




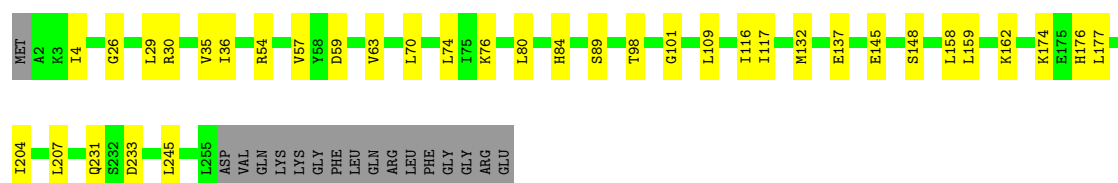
- Molecule 2: Site-determining protein

Chain D: 

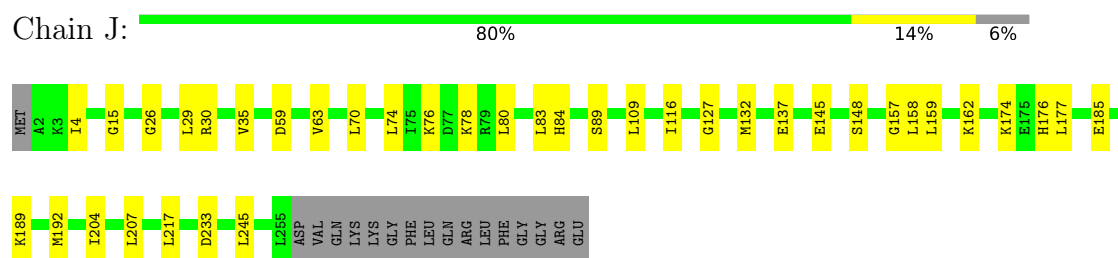


- Molecule 2: Site-determining protein

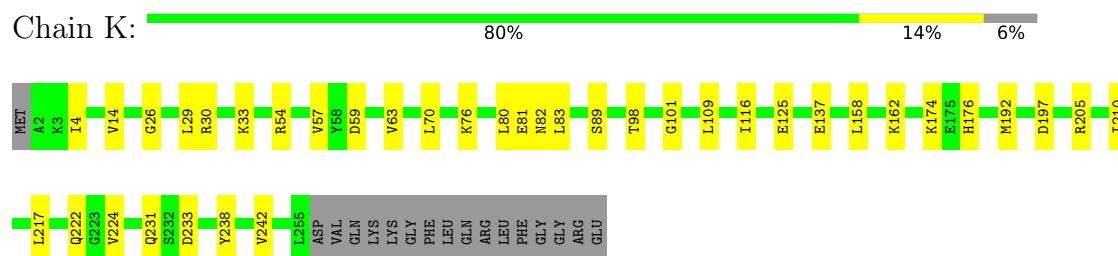
Chain G: 



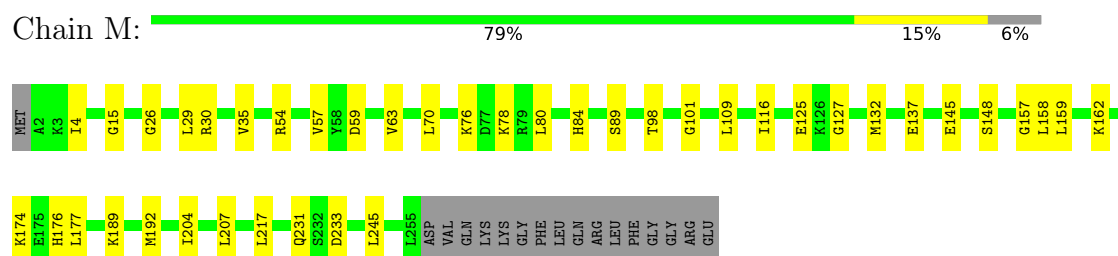
- Molecule 2: Site-determining protein



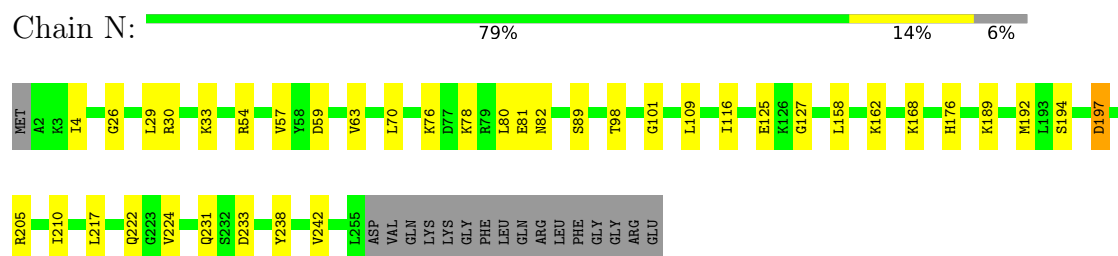
- Molecule 2: Site-determining protein



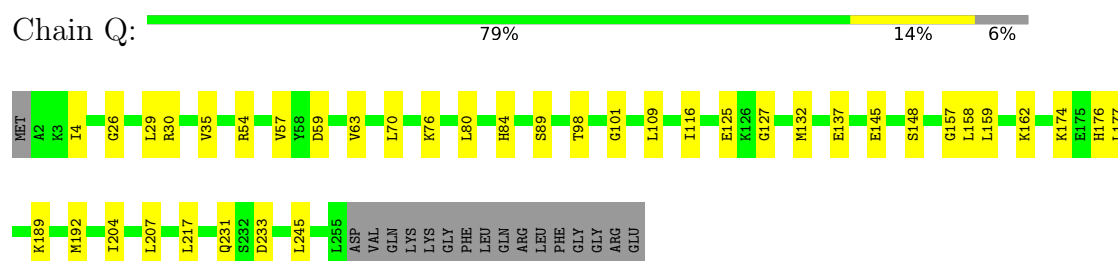
- Molecule 2: Site-determining protein




- Molecule 2: Site-determining protein

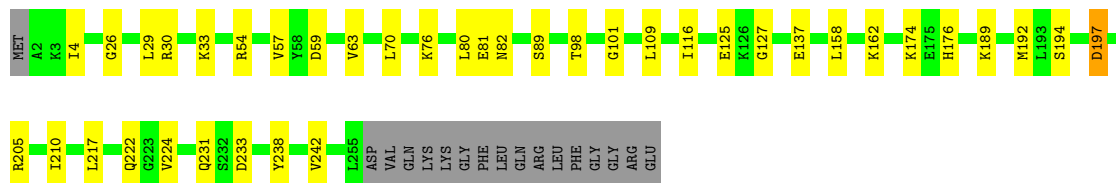


- Molecule 2: Site-determining protein




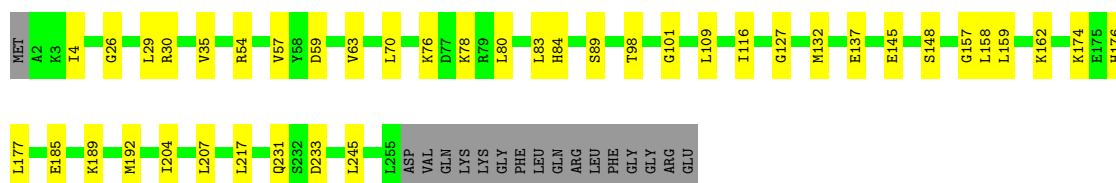
- Molecule 2: Site-determining protein

Chain R:  79% 14% 6%




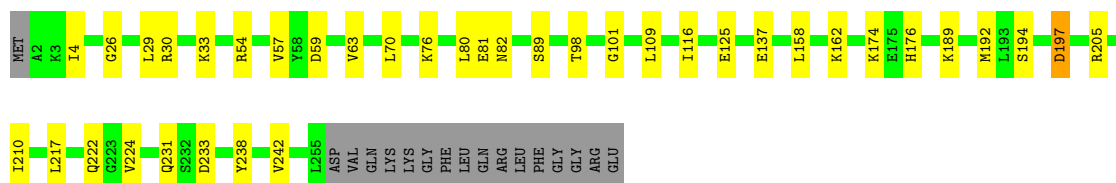
- Molecule 2: Site-determining protein

Chain U:  79% 15% 6%



- Molecule 2: Site-determining protein

Chain V:  80% 14% 6%



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=116.265°, rise=24.998 Å, axial sym=C1	Depositor
Number of segments used	118659	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	38	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ATP

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	0.30	0/796	0.54	0/1078
1	B	0.31	0/796	0.54	0/1078
1	E	0.30	0/796	0.54	0/1078
1	F	0.31	0/796	0.54	0/1078
1	H	0.30	0/796	0.54	0/1078
1	I	0.31	0/796	0.54	0/1078
1	L	0.31	0/796	0.54	0/1078
1	O	0.30	0/796	0.54	0/1078
1	P	0.31	0/796	0.54	0/1078
1	S	0.30	0/796	0.54	0/1078
1	T	0.31	0/796	0.54	0/1078
2	C	0.30	0/1962	0.50	0/2648
2	D	0.31	0/1962	0.50	0/2648
2	G	0.30	0/1962	0.50	0/2648
2	J	0.30	0/1962	0.50	0/2648
2	K	0.31	0/1962	0.50	0/2648
2	M	0.30	0/1962	0.50	0/2648
2	N	0.31	0/1962	0.50	0/2648
2	Q	0.30	0/1962	0.50	0/2648
2	R	0.31	0/1962	0.50	0/2648
2	U	0.30	0/1962	0.50	0/2648
2	V	0.31	0/1962	0.50	0/2648
All	All	0.31	0/30338	0.51	0/40986

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	784	0	813	13	0
1	B	784	0	813	8	0
1	E	784	0	813	14	0
1	F	784	0	813	9	0
1	H	784	0	813	13	0
1	I	784	0	813	8	0
1	L	784	0	813	9	0
1	O	784	0	813	12	0
1	P	784	0	813	9	0
1	S	784	0	813	13	0
1	T	784	0	813	9	0
2	C	1941	0	1994	32	0
2	D	1941	0	1994	33	0
2	G	1941	0	1994	29	0
2	J	1941	0	1994	29	0
2	K	1941	0	1994	33	0
2	M	1941	0	1994	38	0
2	N	1941	0	1994	36	0
2	Q	1941	0	1994	37	0
2	R	1941	0	1994	35	0
2	U	1941	0	1994	38	0
2	V	1941	0	1994	33	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	G	1	0	0	0	0
3	J	1	0	0	0	0
3	K	1	0	0	0	0
3	M	1	0	0	0	0
3	N	1	0	0	0	0
3	Q	1	0	0	0	0
3	R	1	0	0	0	0
3	U	1	0	0	0	0
3	V	1	0	0	0	0
4	C	31	0	12	0	0
4	D	31	0	12	0	0
4	G	31	0	12	0	0
4	J	31	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	K	31	0	12	0	0
4	M	31	0	12	1	0
4	N	31	0	12	0	0
4	Q	31	0	12	0	0
4	R	31	0	12	0	0
4	U	31	0	12	0	0
4	V	31	0	12	0	0
All	All	30327	0	31009	406	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 7.

The worst 5 of 406 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:231:GLN:CD	2:U:54:ARG:HH22	1.72	0.93
2:D:231:GLN:CD	2:G:54:ARG:HH22	1.72	0.93
2:K:231:GLN:CD	2:M:54:ARG:HH22	1.72	0.93
2:N:231:GLN:CD	2:Q:54:ARG:HH22	1.72	0.92
2:C:54:ARG:HH22	2:V:231:GLN:CD	1.72	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 PDB entries followed by that with respect to all EM entries.

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	105/144 (73%)	95 (90%)	10 (10%)	0	100	100
1	B	105/144 (73%)	95 (90%)	10 (10%)	0	100	100
1	E	105/144 (73%)	95 (90%)	10 (10%)	0	100	100
1	F	105/144 (73%)	95 (90%)	10 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	105/144 (73%)	95 (90%)	10 (10%)	0	100	100
1	I	105/144 (73%)	95 (90%)	10 (10%)	0	100	100
1	L	105/144 (73%)	95 (90%)	10 (10%)	0	100	100
1	O	105/144 (73%)	95 (90%)	10 (10%)	0	100	100
1	P	105/144 (73%)	95 (90%)	10 (10%)	0	100	100
1	S	105/144 (73%)	95 (90%)	10 (10%)	0	100	100
1	T	105/144 (73%)	95 (90%)	10 (10%)	0	100	100
2	C	252/271 (93%)	244 (97%)	8 (3%)	0	100	100
2	D	252/271 (93%)	243 (96%)	9 (4%)	0	100	100
2	G	252/271 (93%)	244 (97%)	8 (3%)	0	100	100
2	J	252/271 (93%)	244 (97%)	8 (3%)	0	100	100
2	K	252/271 (93%)	243 (96%)	9 (4%)	0	100	100
2	M	252/271 (93%)	244 (97%)	8 (3%)	0	100	100
2	N	252/271 (93%)	243 (96%)	9 (4%)	0	100	100
2	Q	252/271 (93%)	244 (97%)	8 (3%)	0	100	100
2	R	252/271 (93%)	243 (96%)	9 (4%)	0	100	100
2	U	252/271 (93%)	244 (97%)	8 (3%)	0	100	100
2	V	252/271 (93%)	243 (96%)	9 (4%)	0	100	100
All	All	3927/4565 (86%)	3724 (95%)	203 (5%)	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 PDB entries followed by that with respect to all EM entries.

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	79/109 (72%)	77 (98%)	2 (2%)	42	69
1	B	79/109 (72%)	78 (99%)	1 (1%)	65	82
1	E	79/109 (72%)	77 (98%)	2 (2%)	42	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	79/109 (72%)	78 (99%)	1 (1%)	65	82
1	H	79/109 (72%)	77 (98%)	2 (2%)	42	69
1	I	79/109 (72%)	78 (99%)	1 (1%)	65	82
1	L	79/109 (72%)	78 (99%)	1 (1%)	65	82
1	O	79/109 (72%)	77 (98%)	2 (2%)	42	69
1	P	79/109 (72%)	78 (99%)	1 (1%)	65	82
1	S	79/109 (72%)	77 (98%)	2 (2%)	42	69
1	T	79/109 (72%)	78 (99%)	1 (1%)	65	82
2	C	211/225 (94%)	211 (100%)	0	100	100
2	D	211/225 (94%)	210 (100%)	1 (0%)	86	92
2	G	211/225 (94%)	211 (100%)	0	100	100
2	J	211/225 (94%)	211 (100%)	0	100	100
2	K	211/225 (94%)	210 (100%)	1 (0%)	86	92
2	M	211/225 (94%)	211 (100%)	0	100	100
2	N	211/225 (94%)	210 (100%)	1 (0%)	86	92
2	Q	211/225 (94%)	211 (100%)	0	100	100
2	R	211/225 (94%)	210 (100%)	1 (0%)	86	92
2	U	211/225 (94%)	211 (100%)	0	100	100
2	V	211/225 (94%)	210 (100%)	1 (0%)	86	92
All	All	3190/3674 (87%)	3169 (99%)	21 (1%)	80	90

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	262	ARG
1	S	250	HIS
2	V	197	ASP
1	S	262	ARG
2	R	197	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	220	GLN

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Mol	Chain	Res	Type
1	F	220	GLN
1	I	220	GLN
1	O	220	GLN
1	T	220	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 11 are monoatomic - leaving 11 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$
4	ATP	Q	302	2,3	26,33,33	0.89	1 (3%)	31,52,52	1.60	5 (16%)
4	ATP	D	302	2,3	26,33,33	0.90	1 (3%)	31,52,52	1.64	5 (16%)
4	ATP	M	302	2,3	26,33,33	0.90	1 (3%)	31,52,52	1.60	5 (16%)
4	ATP	R	302	2,3	26,33,33	0.91	1 (3%)	31,52,52	1.64	5 (16%)
4	ATP	K	302	2,3	26,33,33	0.90	1 (3%)	31,52,52	1.64	5 (16%)
4	ATP	C	302	2,3	26,33,33	0.89	1 (3%)	31,52,52	1.60	5 (16%)
4	ATP	U	302	2,3	26,33,33	0.89	1 (3%)	31,52,52	1.60	5 (16%)
4	ATP	N	302	2,3	26,33,33	0.90	1 (3%)	31,52,52	1.63	5 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	ATP	V	302	2,3	26,33,33	0.90	1 (3%)	31,52,52	1.64	5 (16%)
4	ATP	J	302	2,3	26,33,33	0.89	1 (3%)	31,52,52	1.60	5 (16%)
4	ATP	G	302	2,3	26,33,33	0.89	1 (3%)	31,52,52	1.60	5 (16%)

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
4	ATP	Q	302	2,3	-	1/18/38/38	0/3/3/3
4	ATP	D	302	2,3	-	2/18/38/38	0/3/3/3
4	ATP	M	302	2,3	-	1/18/38/38	0/3/3/3
4	ATP	R	302	2,3	-	2/18/38/38	0/3/3/3
4	ATP	K	302	2,3	-	2/18/38/38	0/3/3/3
4	ATP	C	302	2,3	-	1/18/38/38	0/3/3/3
4	ATP	U	302	2,3	-	1/18/38/38	0/3/3/3
4	ATP	N	302	2,3	-	2/18/38/38	0/3/3/3
4	ATP	V	302	2,3	-	2/18/38/38	0/3/3/3
4	ATP	J	302	2,3	-	1/18/38/38	0/3/3/3
4	ATP	G	302	2,3	-	1/18/38/38	0/3/3/3

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	302	ATP	C5-C4	2.43	1.47	1.40
4	R	302	ATP	C5-C4	2.42	1.47	1.40
4	K	302	ATP	C5-C4	2.42	1.47	1.40
4	V	302	ATP	C5-C4	2.41	1.47	1.40
4	N	302	ATP	C5-C4	2.40	1.47	1.40

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	302	ATP	PA-O3A-PB	-4.16	118.53	132.83
4	G	302	ATP	PA-O3A-PB	-4.16	118.55	132.83
4	U	302	ATP	PA-O3A-PB	-4.16	118.55	132.83
4	M	302	ATP	PA-O3A-PB	-4.16	118.57	132.83
4	Q	302	ATP	PA-O3A-PB	-4.15	118.58	132.83

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

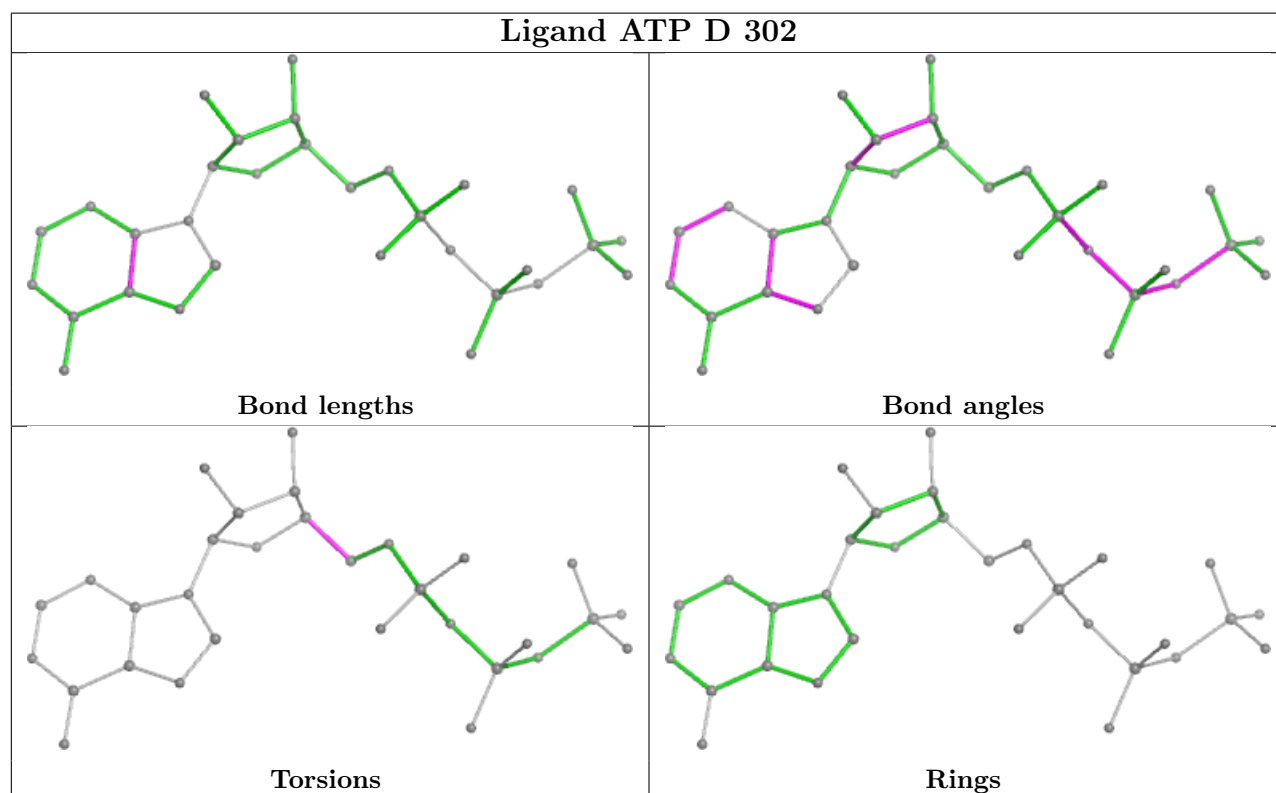
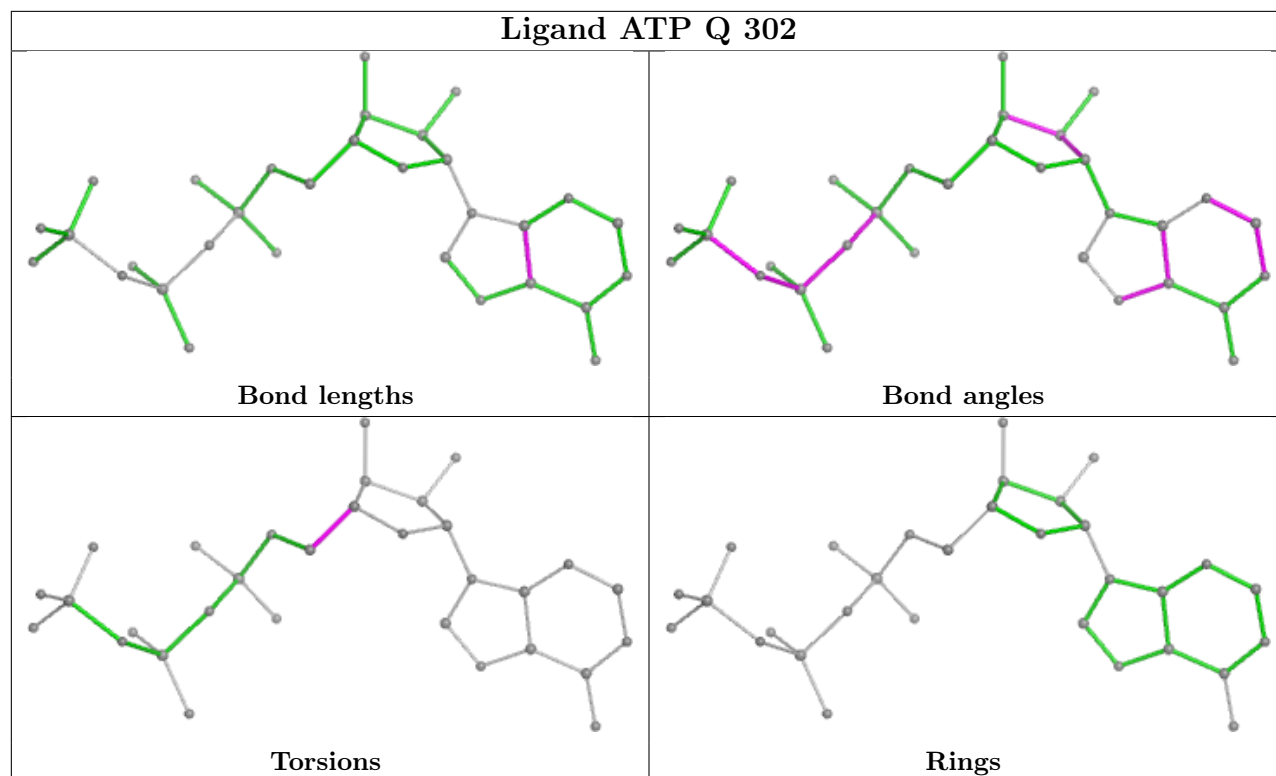
Mol	Chain	Res	Type	Atoms
4	C	302	ATP	O4'-C4'-C5'-O5'
4	G	302	ATP	O4'-C4'-C5'-O5'
4	J	302	ATP	O4'-C4'-C5'-O5'
4	M	302	ATP	O4'-C4'-C5'-O5'
4	Q	302	ATP	O4'-C4'-C5'-O5'

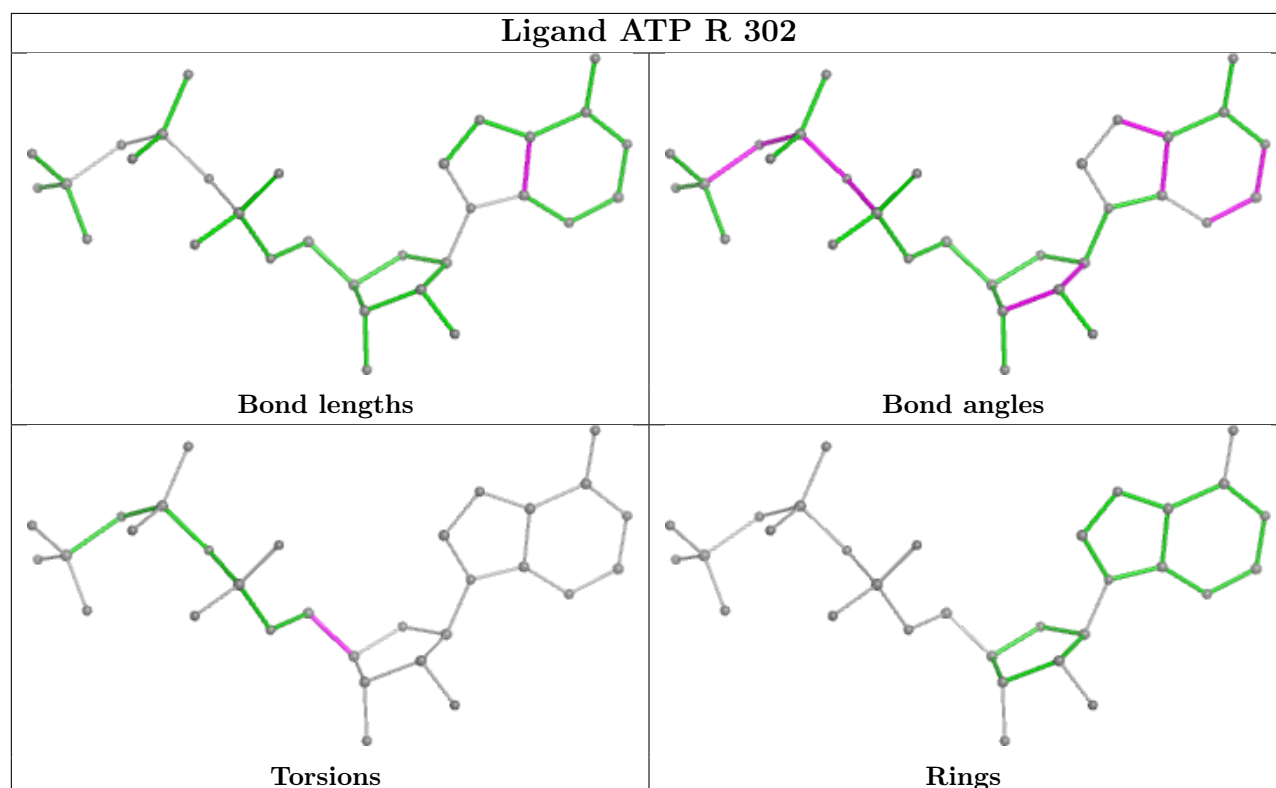
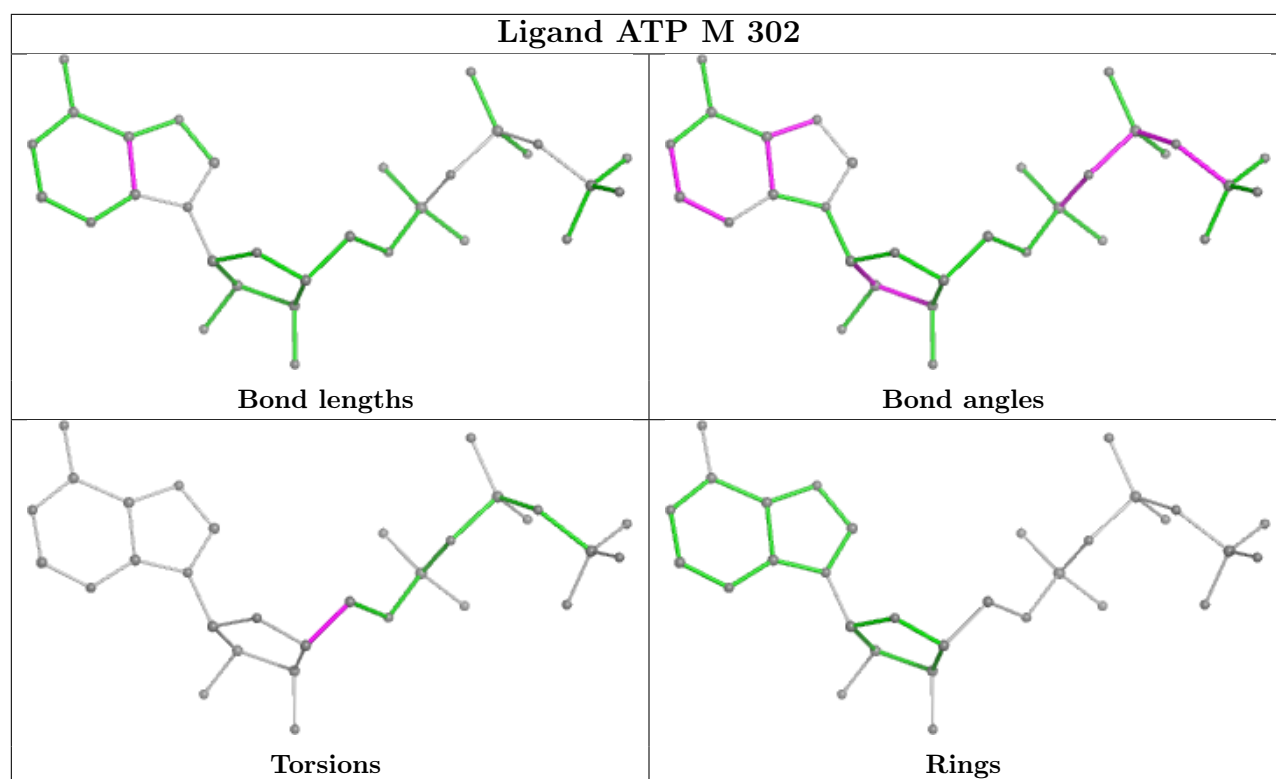
There are no ring outliers.

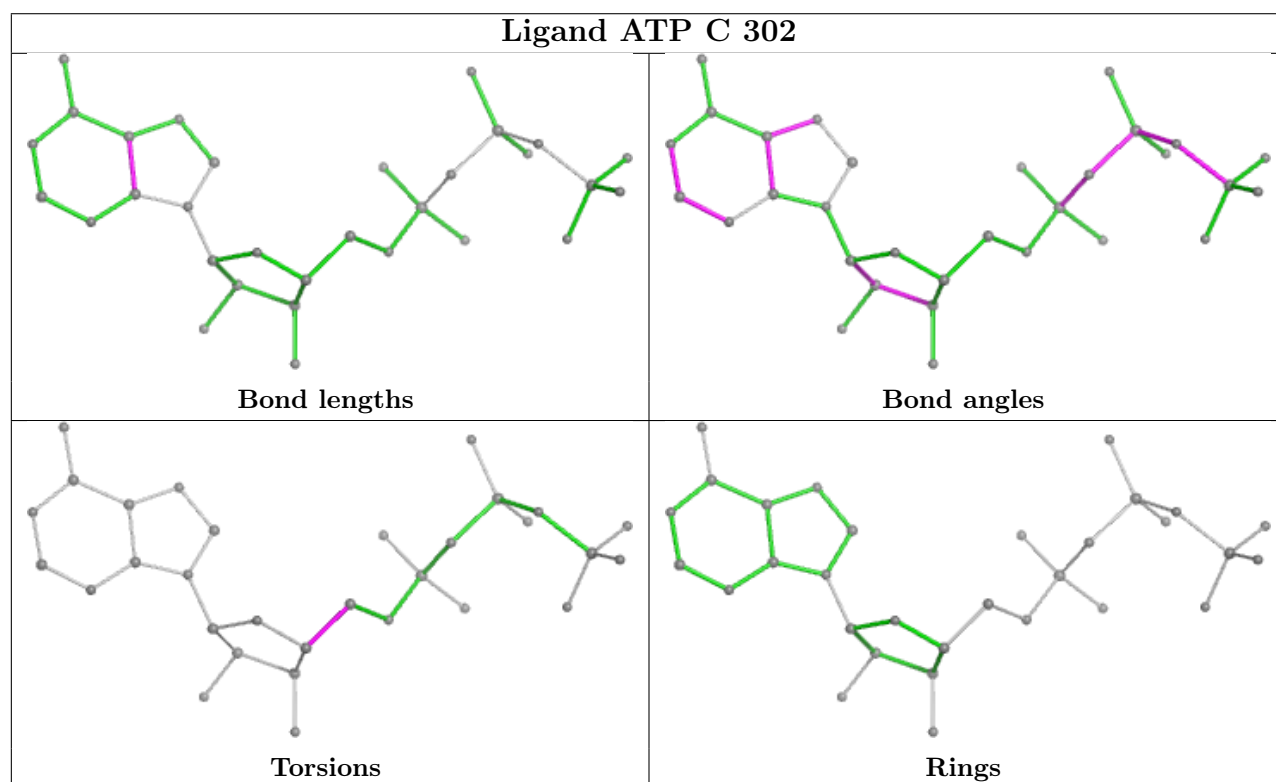
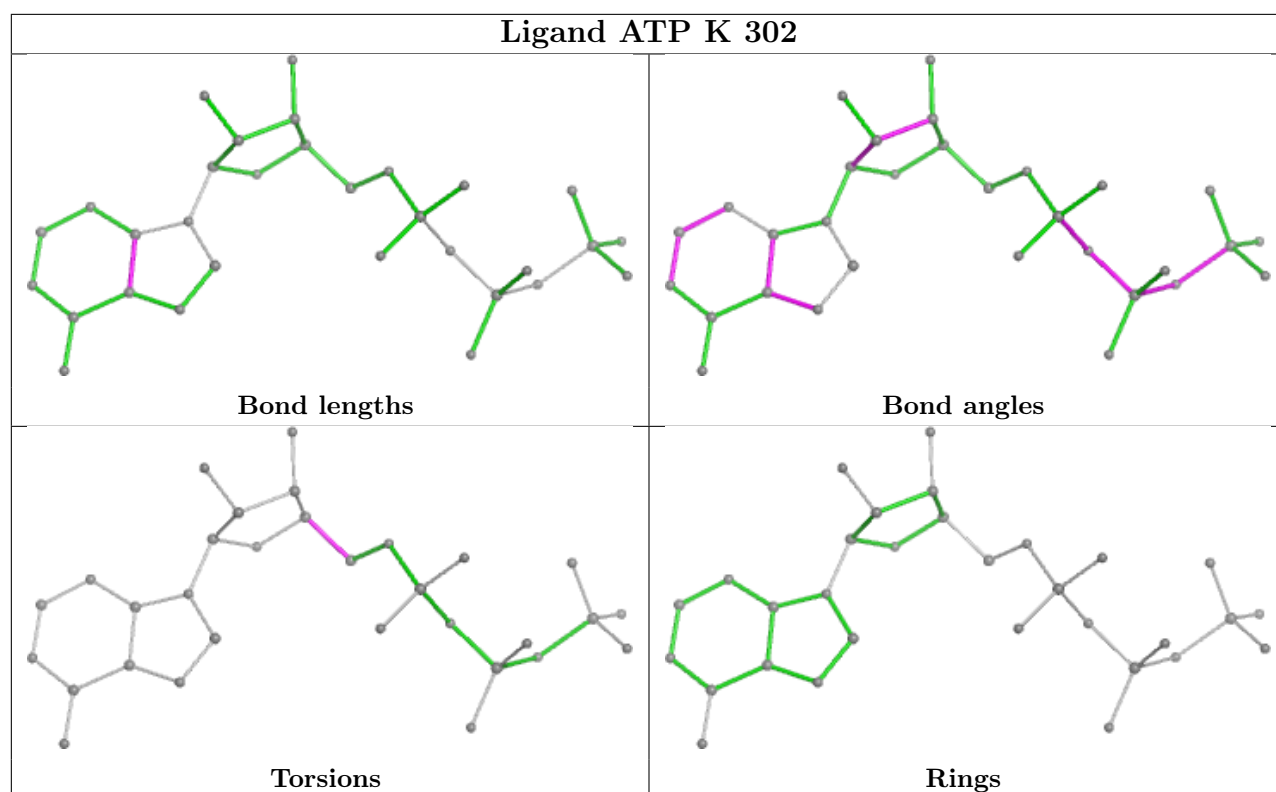
2 monomers are involved in 2 short contacts:

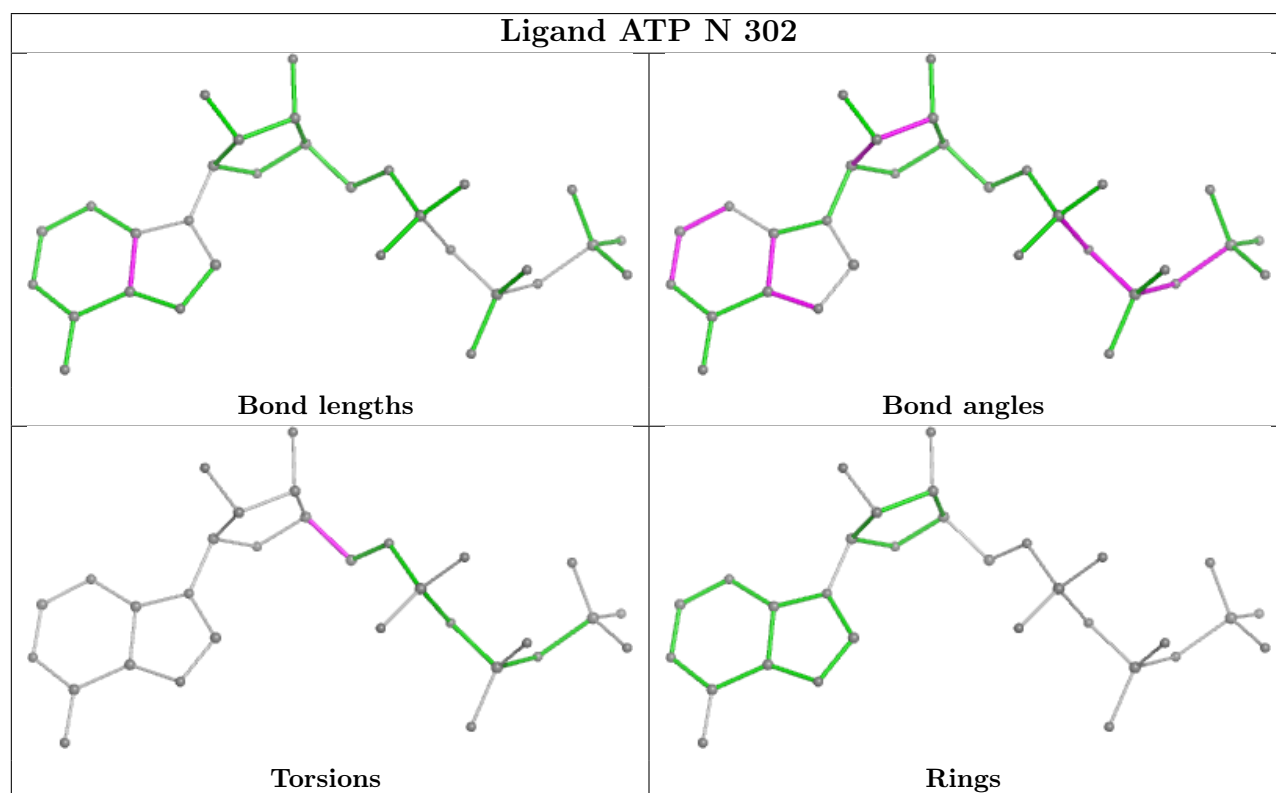
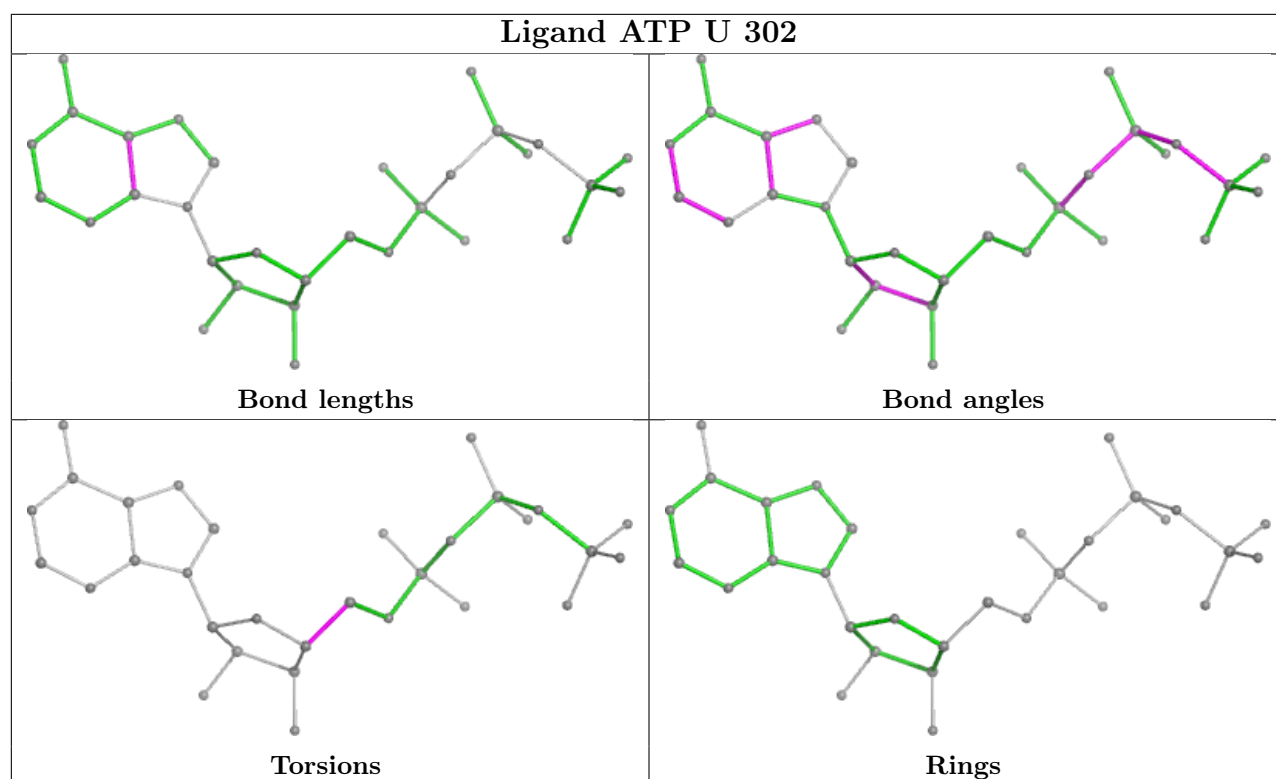
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	M	302	ATP	1	0
4	J	302	ATP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

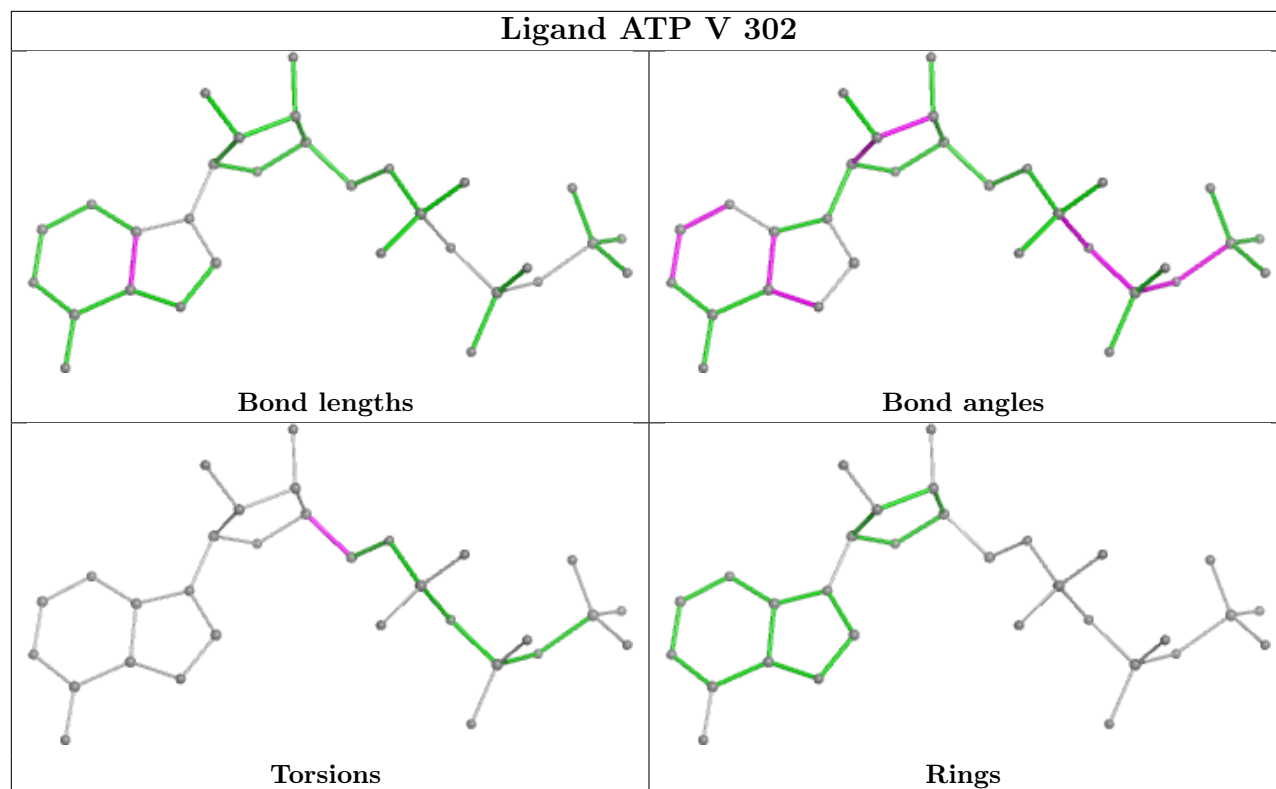




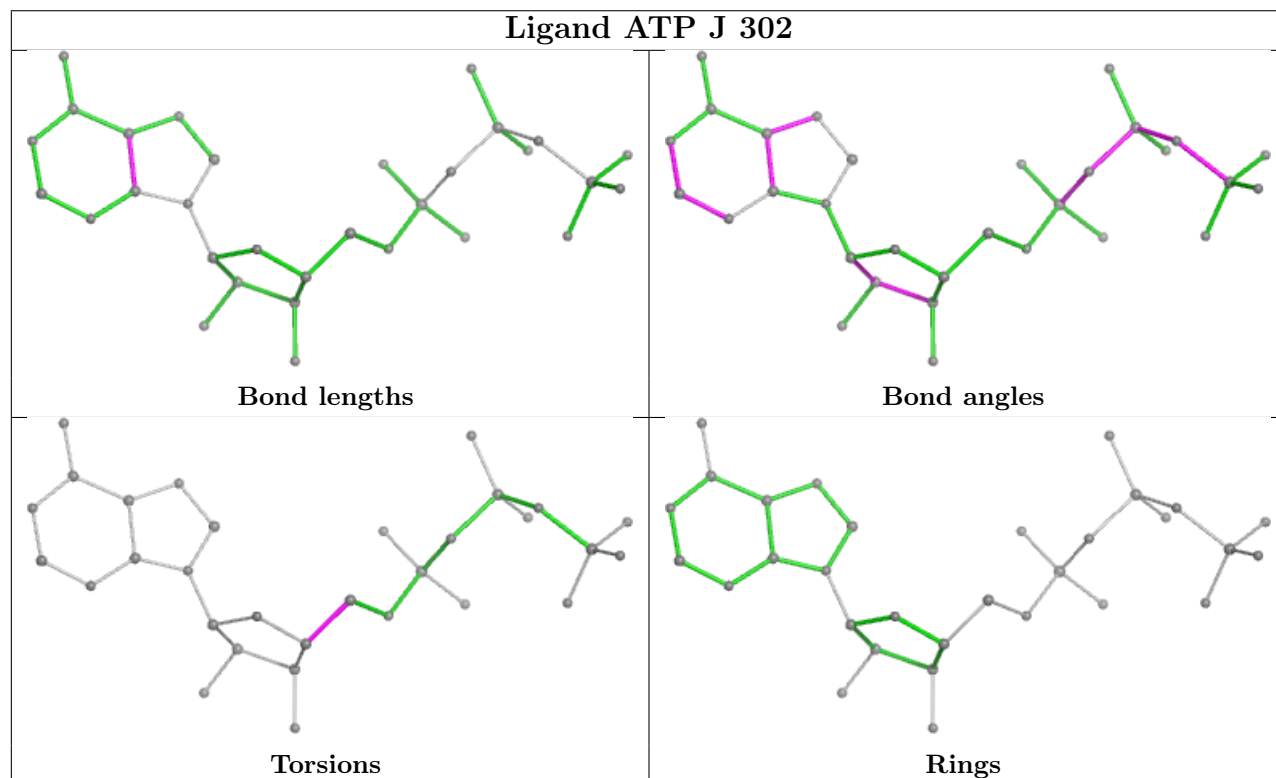


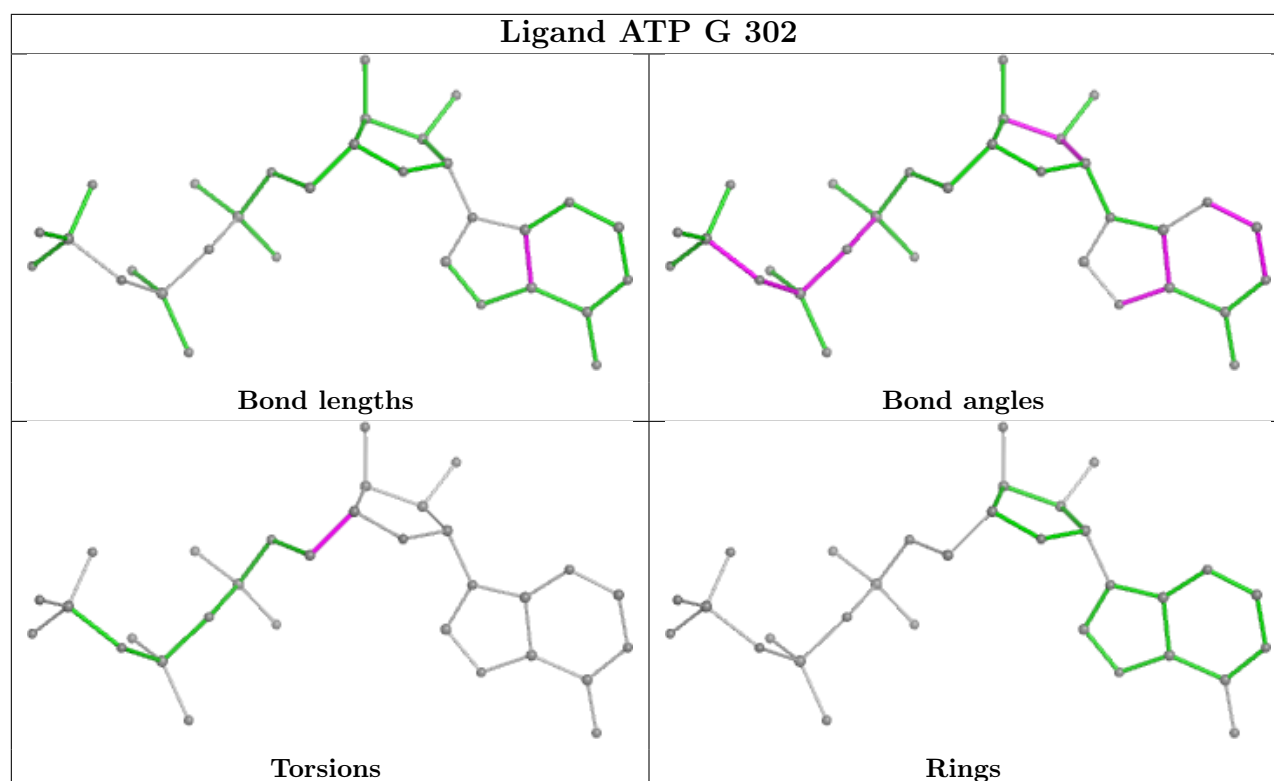


Ligand ATP V 302



Ligand ATP J 302





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 Map visualisation

This section contains visualisations of the EMDB entry EMD-4897. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.