wwPDB EM Validation Summary Report (i)

Nov 8, 2022 – 07:40 AM EST

PDB ID	:	6OIF
EMDB ID	:	EMD-20076
Title	:	Cryo-EM structure of human TorsinA filament
Authors	:	Zheng, W.; Demircioglu, F.E.; Schwartz, T.U.; Egelman, E.H.
Deposited on	:	2019-04-09
Resolution	:	4.40 Å(reported)
Based on initial model	:	5J1S

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 (i) 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 (1)) were used in the production of this report:

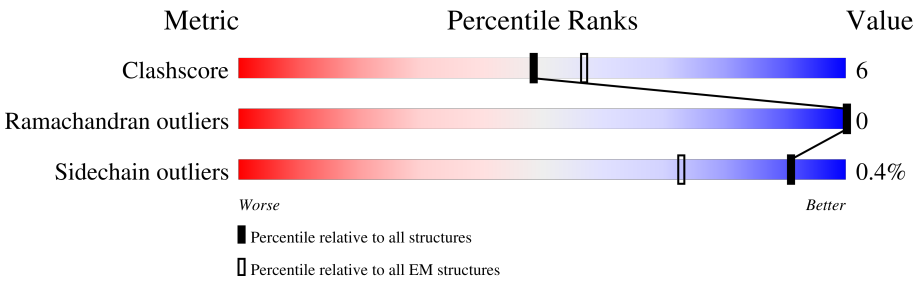
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	282	28% / 83% / 17%
1	B	282	28% / 82% / 18%
1	C	282	29% / 83% / 17%
1	D	282	29% / 83% / 17%
1	E	282	31% / 83% / 17%
1	F	282	30% / 83% / 17%
1	G	282	32% / 83% / 17%
1	H	282	30% / 82% / 18%

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Mol	Chain	Length	Quality of chain
1	I	282	32% 82% 18%
1	J	282	33% 82% 18%
1	K	282	31% 83% 17%
1	L	282	33% 82% 18%
1	M	282	33% 83% 17%
1	N	282	35% 83% 17%
1	O	282	34% 83% 17%
1	P	282	37% 83% 17%
1	Q	282	34% 83% 17%
1	R	282	40% 83% 17%
1	S	282	38% 83% 17%
1	T	282	41% 83% 17%
1	U	282	38% 83% 17%
1	V	282	47% 83% 17%
1	W	282	39% 83% 17%
1	X	282	48% 82% 18%
1	Y	282	42% 83% 17%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 115325 atoms, of which 57050 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 Torsin-1A.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	282	4570	1485	2270	385	421	9	0	0
1	B	282	4570	1485	2270	385	421	9	0	0
1	C	282	4570	1485	2270	385	421	9	0	0
1	D	282	4570	1485	2270	385	421	9	0	0
1	E	282	4570	1485	2270	385	421	9	0	0
1	F	282	4570	1485	2270	385	421	9	0	0
1	G	282	4570	1485	2270	385	421	9	0	0
1	H	282	4570	1485	2270	385	421	9	0	0
1	I	282	4570	1485	2270	385	421	9	0	0
1	J	282	4570	1485	2270	385	421	9	0	0
1	K	282	4570	1485	2270	385	421	9	0	0
1	L	282	4570	1485	2270	385	421	9	0	0
1	M	282	4570	1485	2270	385	421	9	0	0
1	N	282	4570	1485	2270	385	421	9	0	0
1	O	282	4570	1485	2270	385	421	9	0	0
1	P	282	4570	1485	2270	385	421	9	0	0
1	Q	282	4570	1485	2270	385	421	9	0	0

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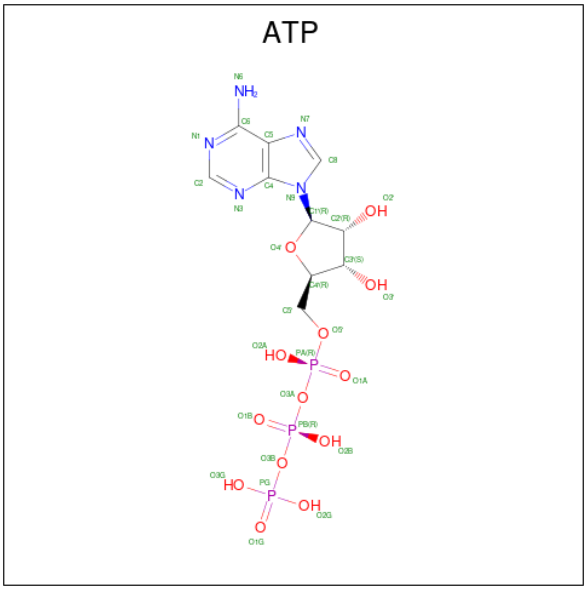
Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	R	282	4570	1485	2270	385	421	9	0	0
1	S	282	4570	1485	2270	385	421	9	0	0
1	T	282	4570	1485	2270	385	421	9	0	0
1	U	282	4570	1485	2270	385	421	9	0	0
1	V	282	4570	1485	2270	385	421	9	0	0
1	W	282	4570	1485	2270	385	421	9	0	0
1	X	282	4570	1485	2270	385	421	9	0	0
1	Y	282	4570	1485	2270	385	421	9	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						AltConf
			Total	C	H	N	O	P	
2	A	1	43	10	12	5	13	3	0
2	B	1	43	10	12	5	13	3	0
2	C	1	43	10	12	5	13	3	0

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Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
2	D	1	43	10	12	5	13	3	0
2	E	1	43	10	12	5	13	3	0
2	F	1	43	10	12	5	13	3	0
2	G	1	43	10	12	5	13	3	0
2	H	1	43	10	12	5	13	3	0
2	I	1	43	10	12	5	13	3	0
2	J	1	43	10	12	5	13	3	0
2	K	1	43	10	12	5	13	3	0
2	L	1	43	10	12	5	13	3	0
2	M	1	43	10	12	5	13	3	0
2	N	1	43	10	12	5	13	3	0
2	O	1	43	10	12	5	13	3	0
2	P	1	43	10	12	5	13	3	0
2	Q	1	43	10	12	5	13	3	0
2	R	1	43	10	12	5	13	3	0
2	S	1	43	10	12	5	13	3	0
2	T	1	43	10	12	5	13	3	0
2	U	1	43	10	12	5	13	3	0
2	V	1	43	10	12	5	13	3	0
2	W	1	43	10	12	5	13	3	0
2	X	1	86	20	24	10	26	6	0

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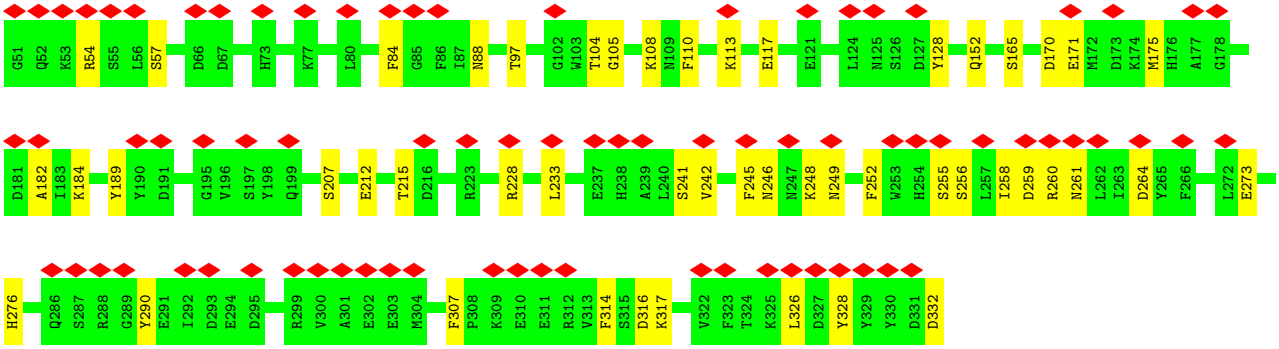
Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
2	X	1	86	20	24	10	26	6	0

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

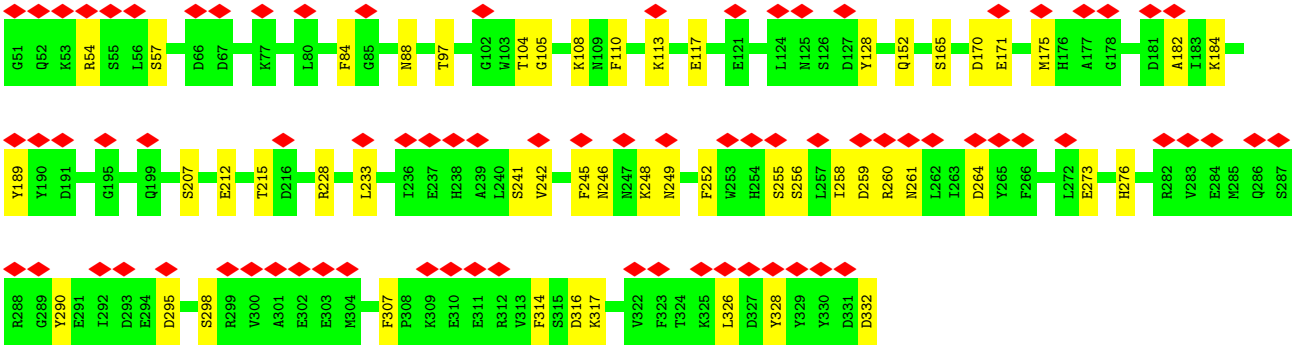
- Molecule 1: Torsin-1A

Chain A:



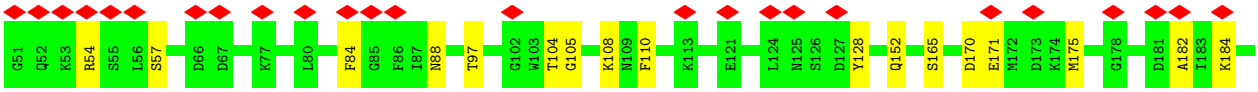
- Molecule 1: Torsin-1A

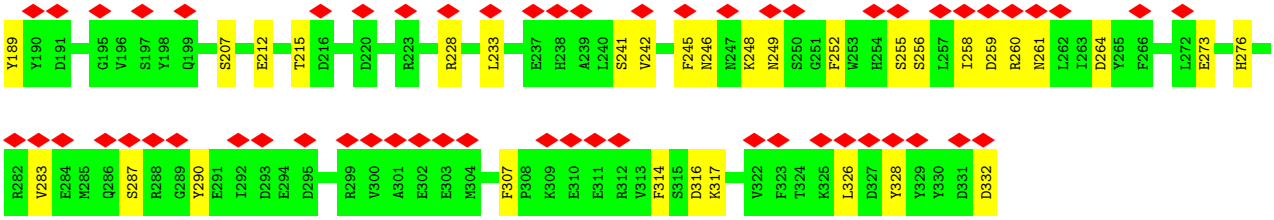
Chain B:



- Molecule 1: Torsin-1A

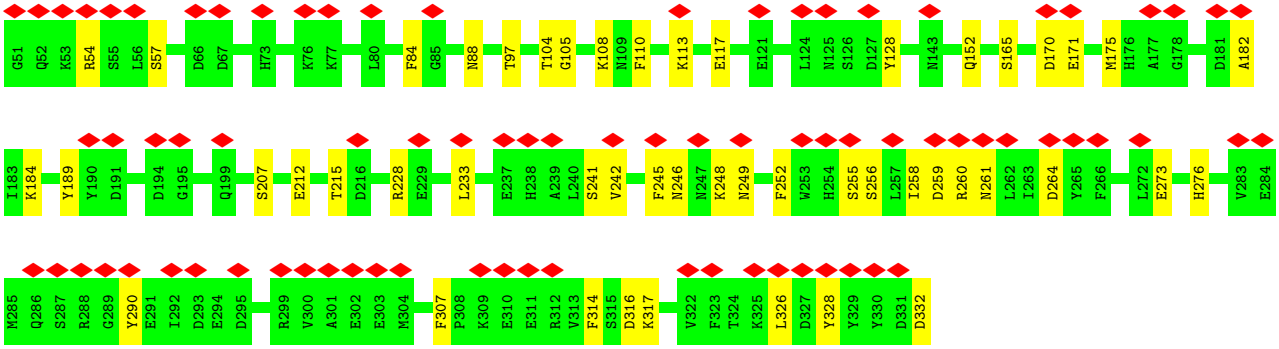
Chain C:





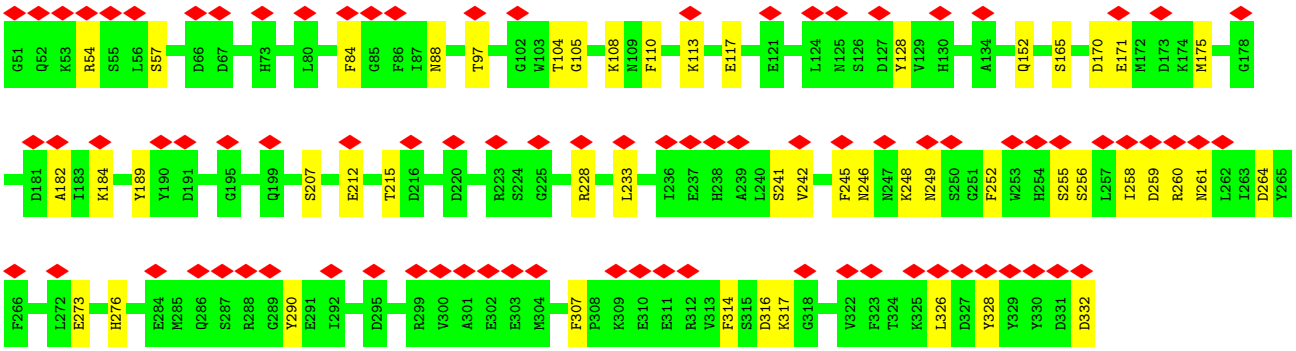
- Molecule 1: Torsin-1A

Chain D:



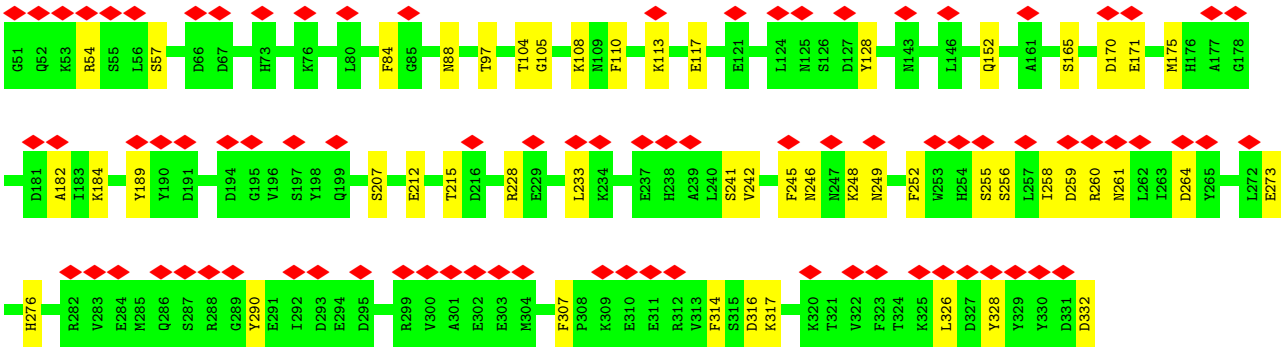
- Molecule 1: Torsin-1A

Chain E:



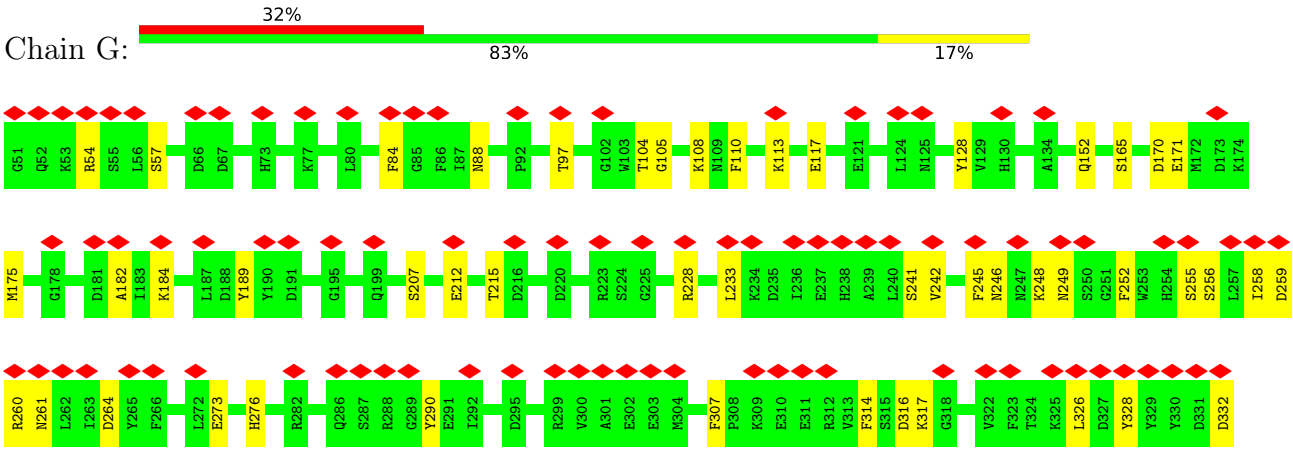
- Molecule 1: Torsin-1A

Chain F:



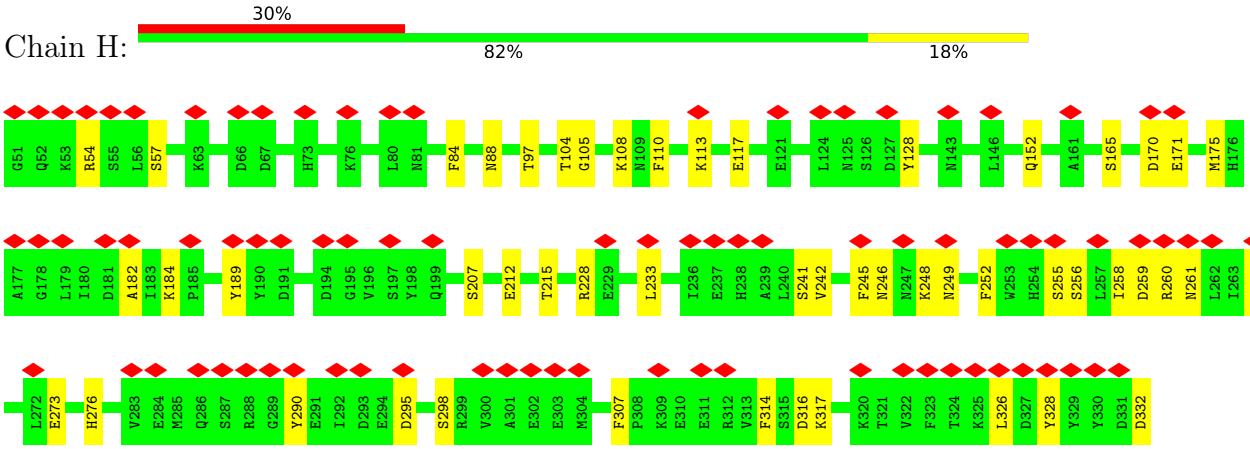
- Molecule 1: Torsin-1A

Chain G:



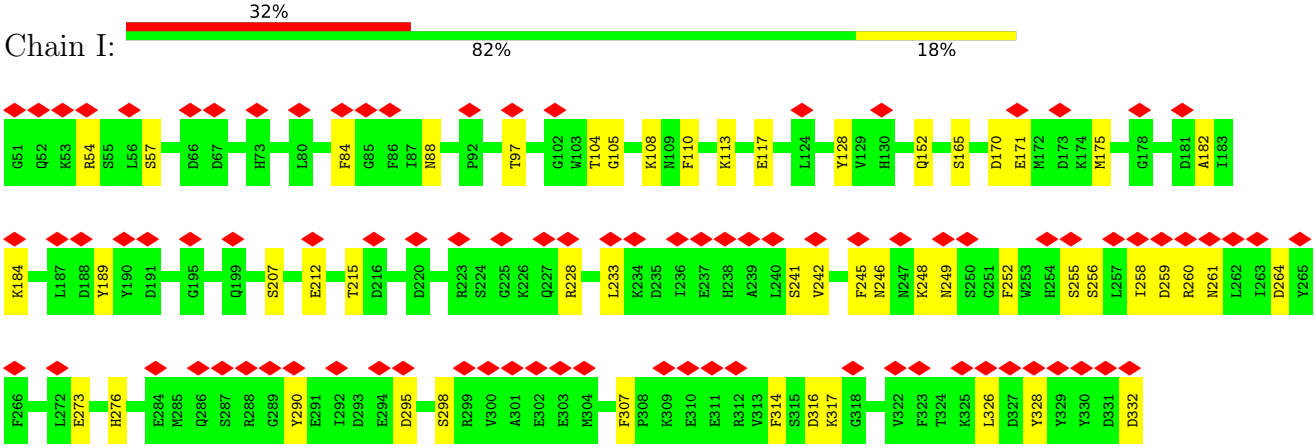
- Molecule 1: Torsin-1A

Chain H:



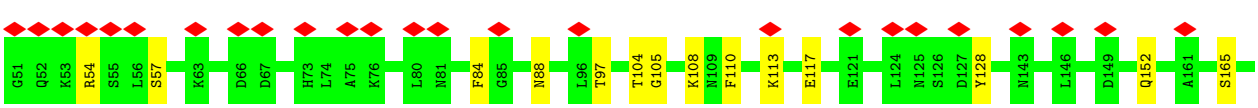
- Molecule 1: Torsin-1A

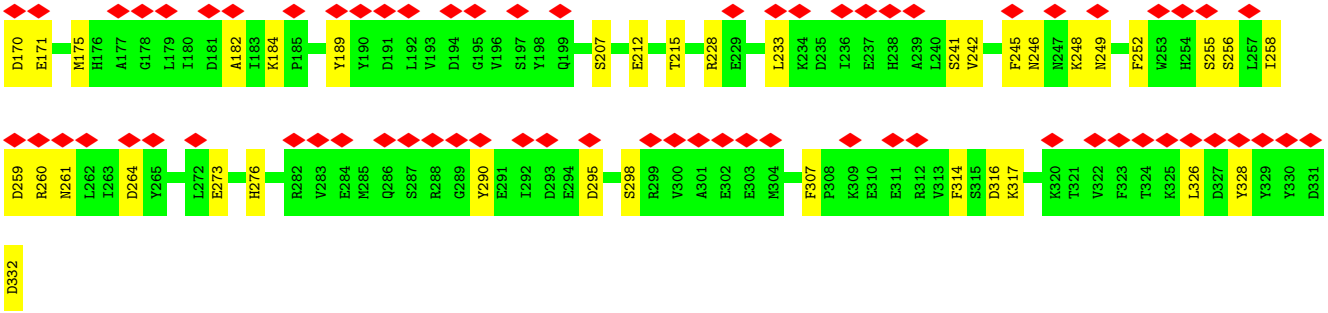
Chain I:



- Molecule 1: Torsin-1A

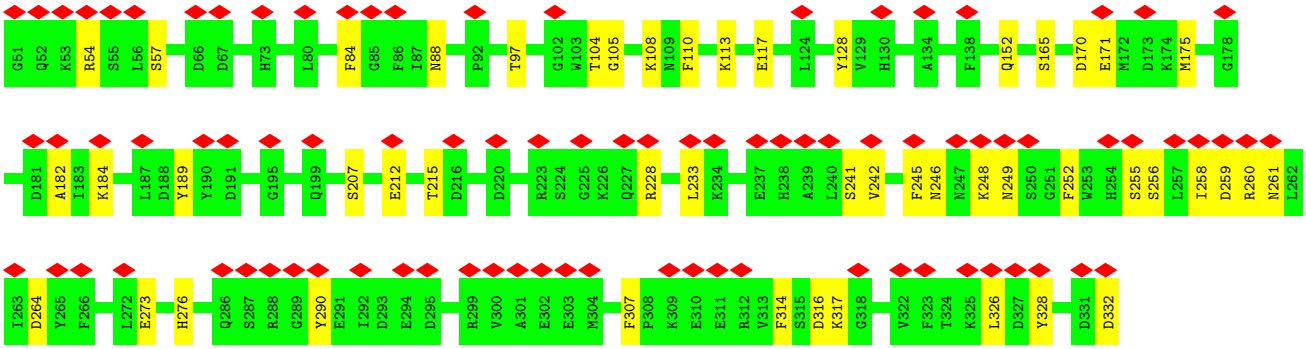
Chain J:





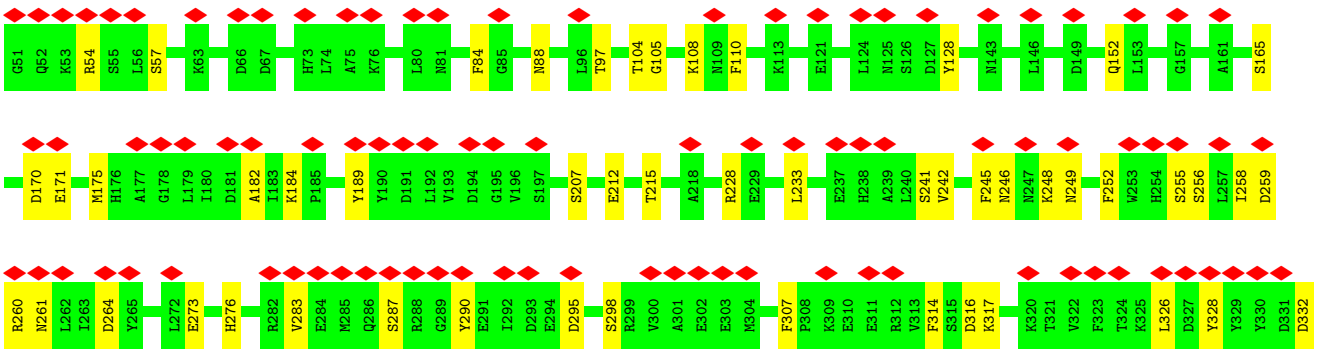
- Molecule 1: Torsin-1A

Chain K:



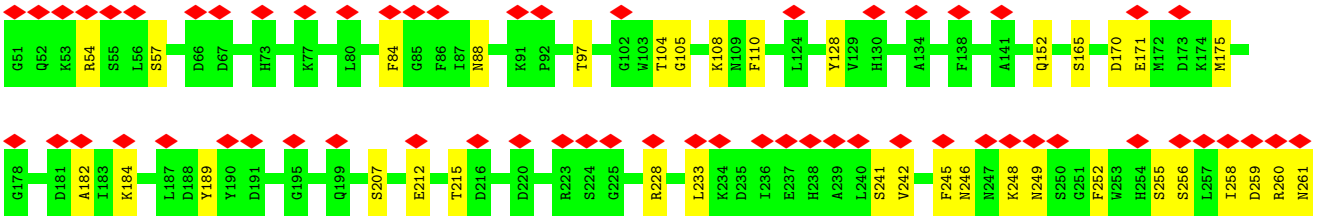
- Molecule 1: Torsin-1A

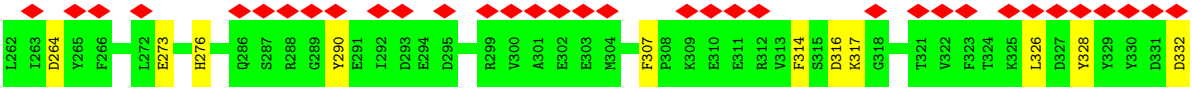
Chain L:



- Molecule 1: Torsin-1A

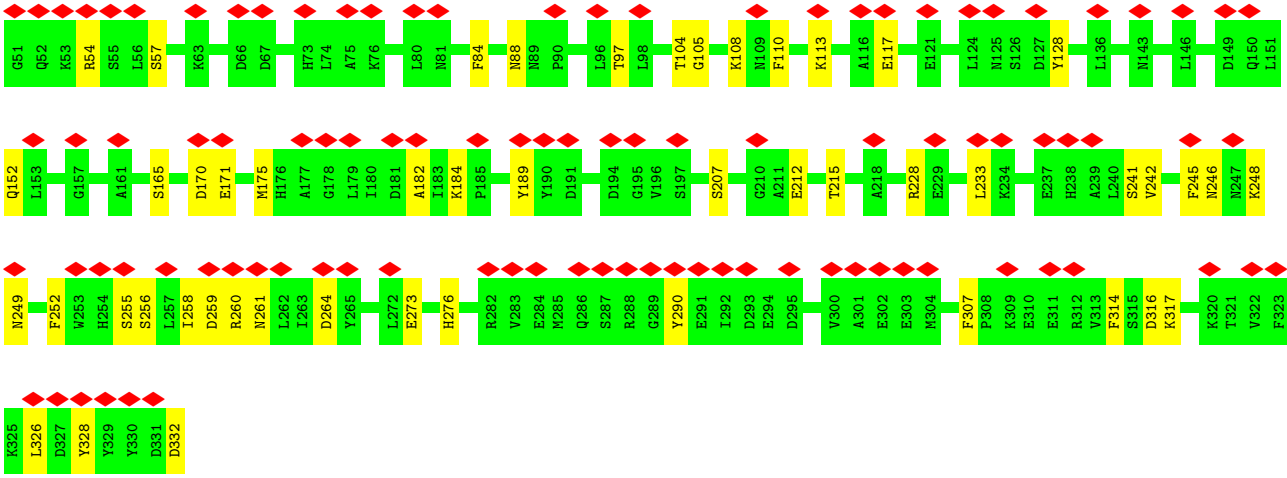
Chain M:





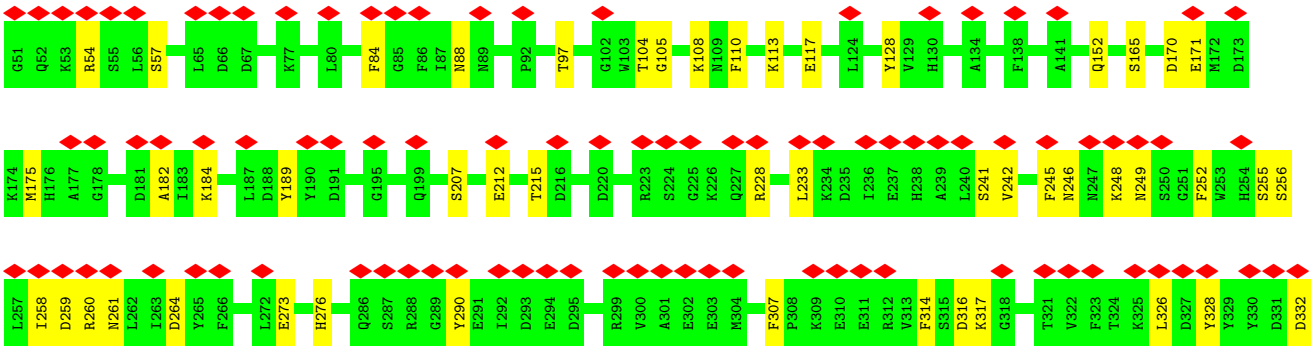
- Molecule 1: Torsin-1A

Chain N:



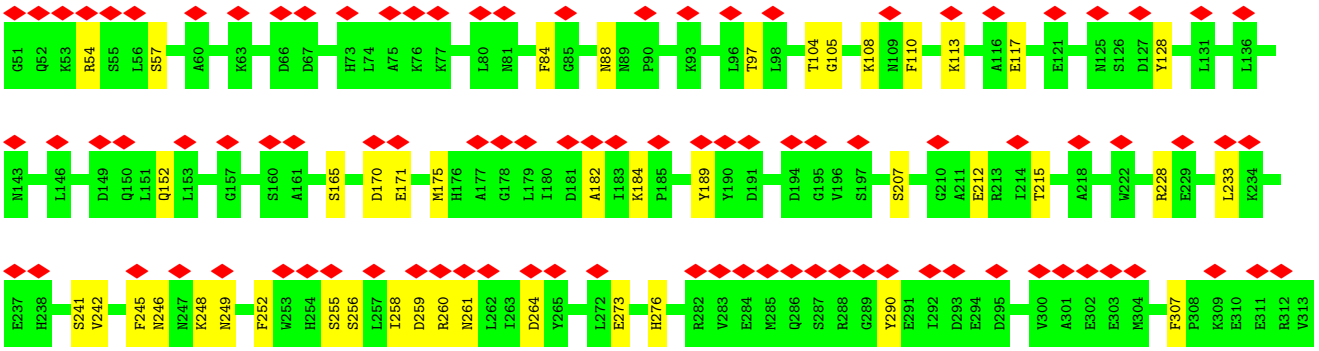
- Molecule 1: Torsin-1A

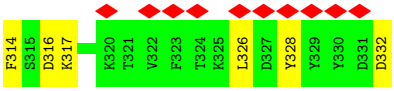
Chain O:



- Molecule 1: Torsin-1A

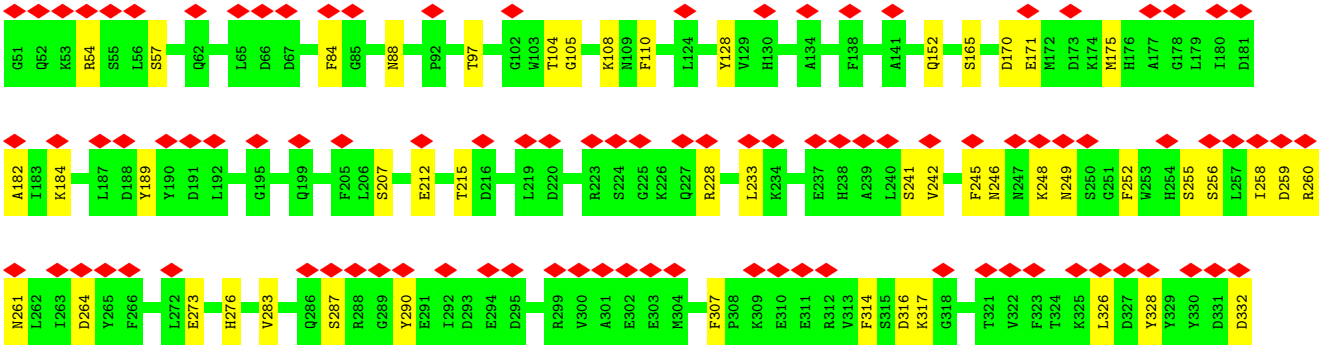
Chain P:





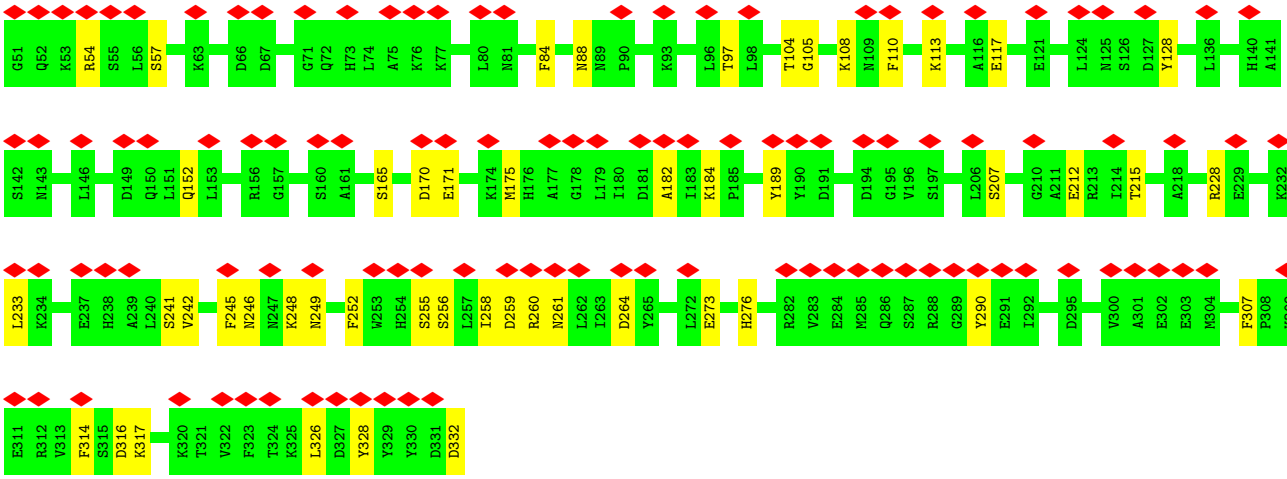
- Molecule 1: Torsin-1A

Chain Q:



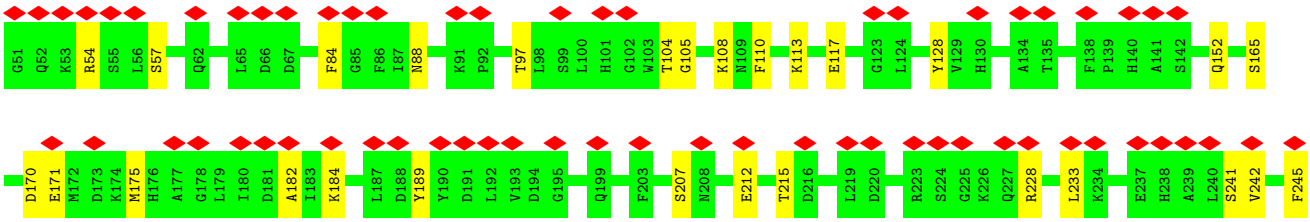
- Molecule 1: Torsin-1A

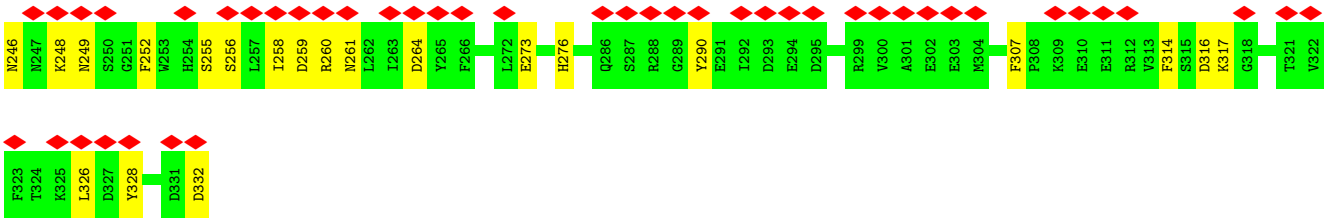
Chain R:



- Molecule 1: Torsin-1A

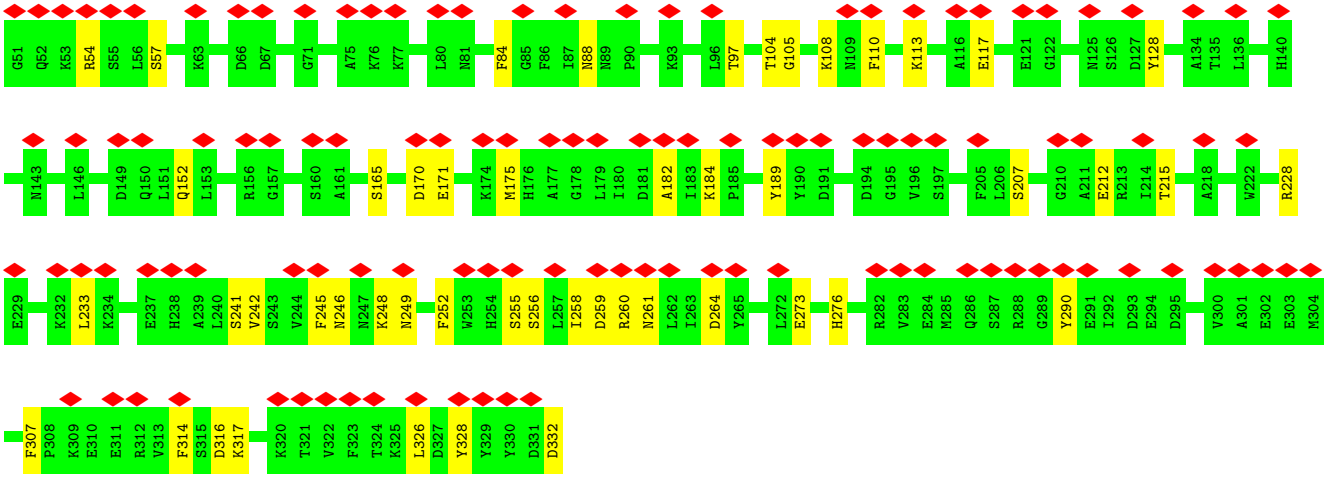
Chain S:





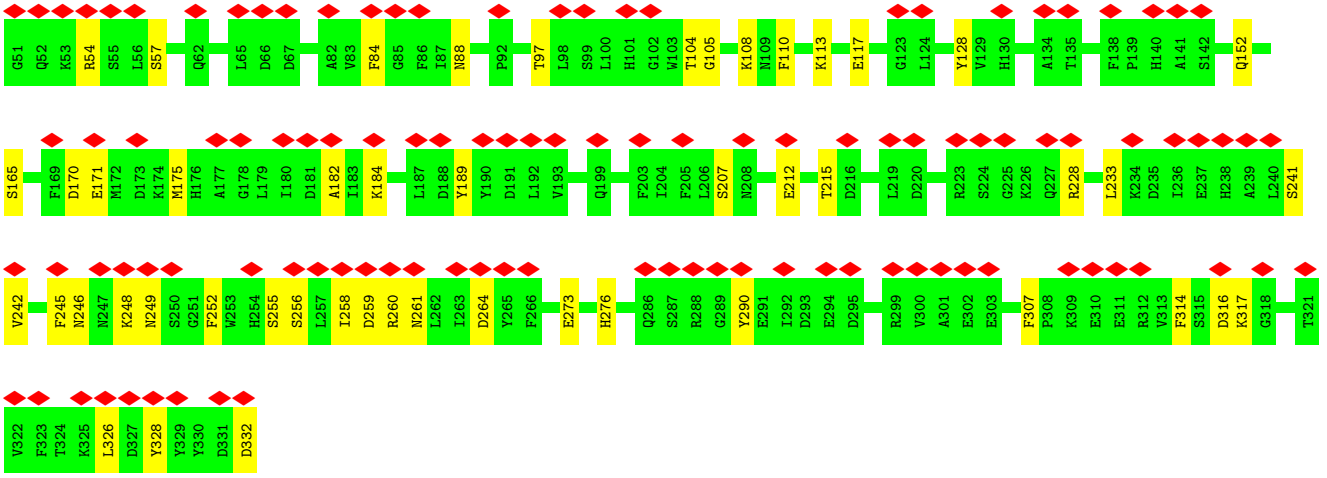
• Molecule 1: Torsin-1A

Chain T:



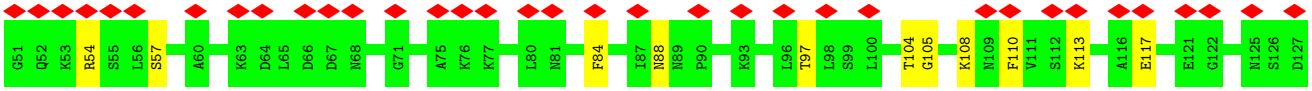
• Molecule 1: Torsin-1A

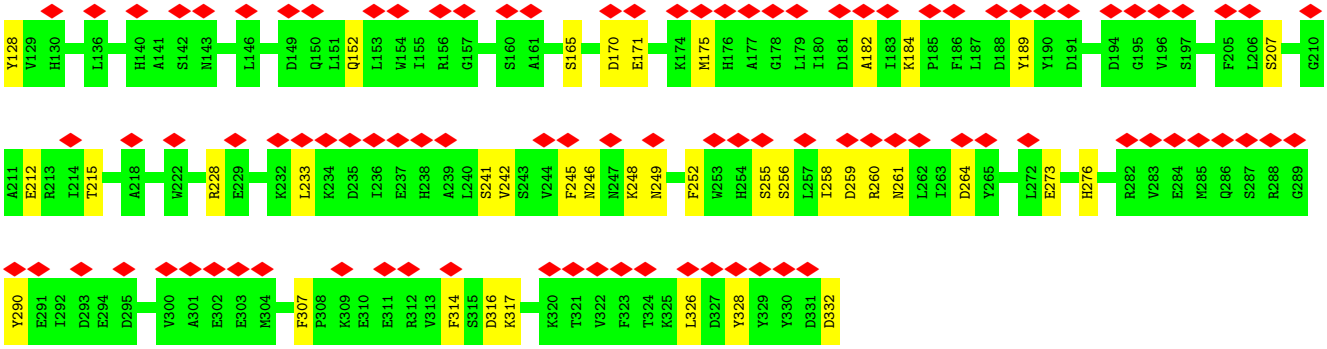
Chain U:



• Molecule 1: Torsin-1A

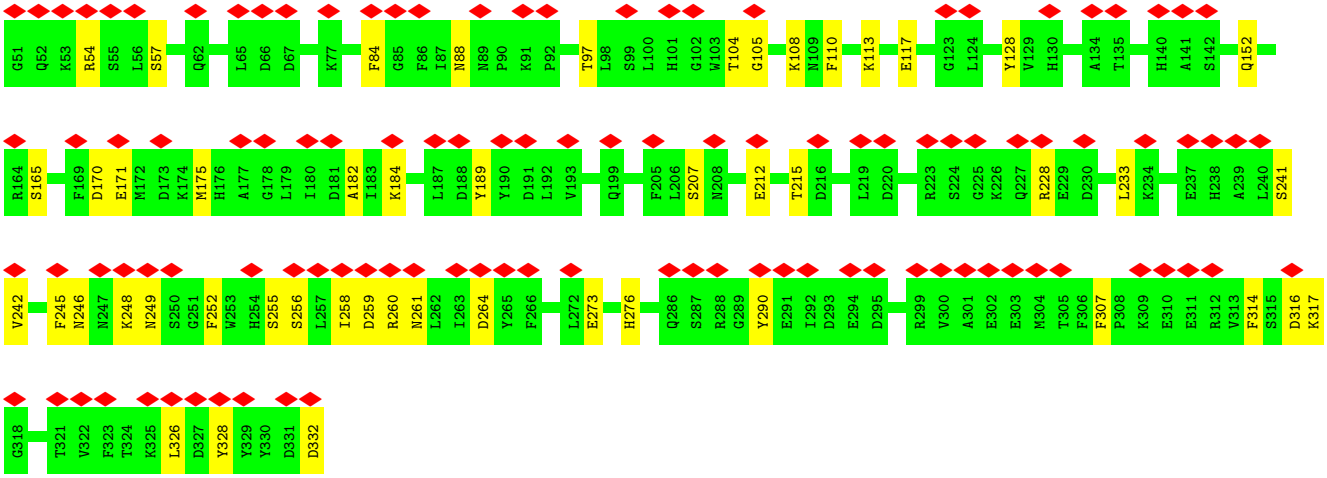
Chain V:





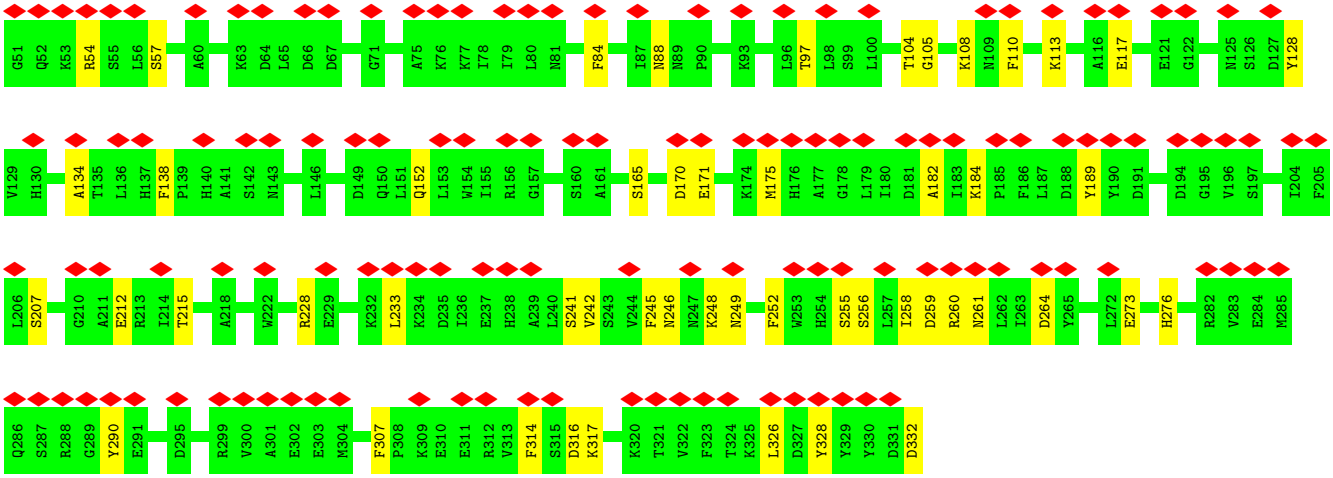
- Molecule 1: Torsin-1A

Chain W:



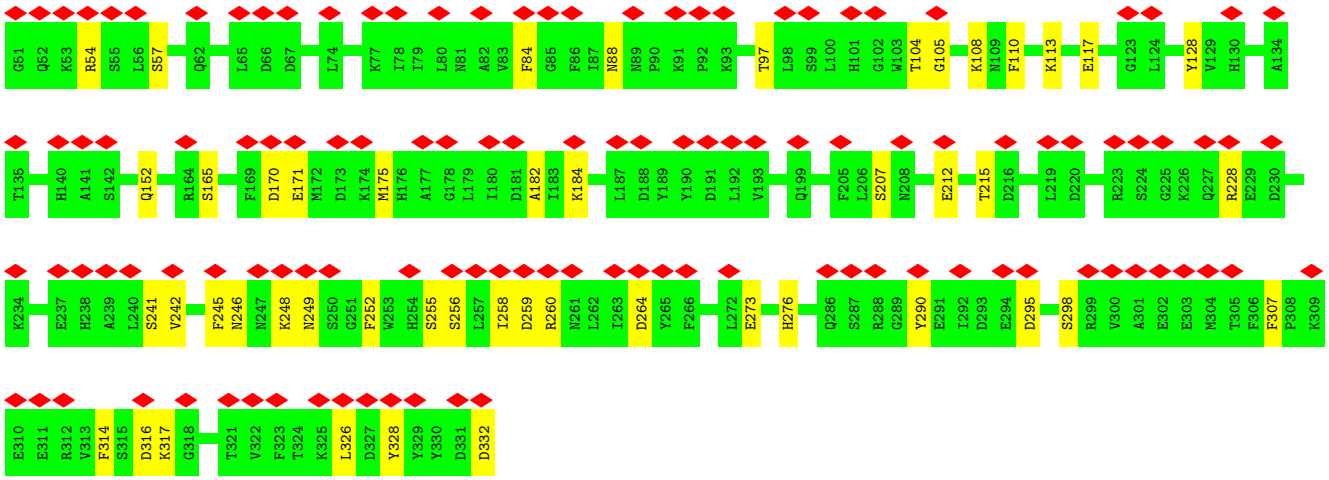
- Molecule 1: Torsin-1A

Chain X:



- Molecule 1: Torsin-1A

Chain Y:


G51 Q52 K53 R54 S55 L56 S57 Q62 L65 D66 D67 L74 K77 I78 I79 L80 N81 A82 V83 F84 G85 F86 I87 N88 N89 P90 K91 P92 K93 T97 L98 S99 L100 H101 G102 W103 T104 G105 K108 N109 F110 K113 E117 G123 L124 Y128 V129 H130 A134
T135 H140 A141 S142 Q152 R164 S165 F169 D170 E171 M172 D173 K174 M175 H176 A177 G178 L179 I180 D181 A182 I183 K184 L187 D188 Y189 Y190 D191 L192 V193 Q199 F205 L206 S207 N208 E212 T215 D216 L219 D220 R223 S224 G225 K226 Q227 R228 E229 D230
K234 E237 H238 A239 L240 S241 V242 F245 N246 N247 K248 N249 S250 G251 F252 W253 H254 S255 S256 L257 I258 D259 R260 N261 L262 I263 D264 Y265 F266 L272 E273 H276 Q286 S287 R288 G289 Y290 E291 I292 D293 E294 D295 S298 R299 V300 A301 E302 E303 M304 T305 F306 F307 P308 K309
E310 E311 R312 V313 F314 S315 D316 K317 G318 T321 V322 F323 T324 K325 L326 D327 Y328 Y329 Y330 D331 D332

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=42.51°, rise=5.53 Å, axial sym=C1	Depositor
Number of segments used	75909	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.722	Depositor
Minimum map value	-0.246	Depositor
Average map value	0.028	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.247	Depositor
Map size (Å)	224.448, 224.448, 224.448	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.169, 1.169, 1.169	Depositor

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

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	0.39	0/2356	0.65	0/3177
1	B	0.39	0/2356	0.65	0/3177
1	C	0.39	0/2356	0.65	0/3177
1	D	0.39	0/2356	0.65	0/3177
1	E	0.39	0/2356	0.65	0/3177
1	F	0.39	0/2356	0.65	0/3177
1	G	0.39	0/2356	0.65	0/3177
1	H	0.39	0/2356	0.65	0/3177
1	I	0.39	0/2356	0.65	0/3177
1	J	0.39	0/2356	0.65	0/3177
1	K	0.39	0/2356	0.65	0/3177
1	L	0.39	0/2356	0.65	0/3177
1	M	0.39	0/2356	0.65	0/3177
1	N	0.39	0/2356	0.65	0/3177
1	O	0.39	0/2356	0.65	0/3177
1	P	0.39	0/2356	0.65	0/3177
1	Q	0.39	0/2356	0.65	0/3177
1	R	0.39	0/2356	0.65	0/3177
1	S	0.39	0/2356	0.65	0/3177
1	T	0.39	0/2356	0.65	0/3177
1	U	0.39	0/2356	0.65	0/3177
1	V	0.39	0/2356	0.65	0/3177
1	W	0.39	0/2356	0.65	0/3177
1	X	0.39	0/2356	0.65	0/3177
1	Y	0.39	0/2356	0.65	0/3177
All	All	0.39	0/58900	0.65	0/79425

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 (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	2300	2270	2266	32	0
1	B	2300	2270	2266	31	0
1	C	2300	2270	2266	31	0
1	D	2300	2270	2266	30	0
1	E	2300	2270	2266	31	0
1	F	2300	2270	2266	30	0
1	G	2300	2270	2266	30	0
1	H	2300	2270	2266	31	0
1	I	2300	2270	2266	31	0
1	J	2300	2270	2266	31	0
1	K	2300	2270	2266	30	0
1	L	2300	2270	2266	32	0
1	M	2300	2270	2266	29	0
1	N	2300	2270	2266	30	0
1	O	2300	2270	2266	30	0
1	P	2300	2270	2266	32	0
1	Q	2300	2270	2266	32	0
1	R	2300	2270	2266	31	0
1	S	2300	2270	2266	31	0
1	T	2300	2270	2266	30	0
1	U	2300	2270	2266	30	0
1	V	2300	2270	2266	30	0
1	W	2300	2270	2266	30	0
1	X	2300	2270	2266	29	0
1	Y	2300	2270	2267	26	0
2	A	31	12	12	4	0
2	B	31	12	12	5	0
2	C	31	12	12	4	0
2	D	31	12	12	4	0
2	E	31	12	12	4	0
2	F	31	12	12	4	0
2	G	31	12	12	4	0
2	H	31	12	12	4	0
2	I	31	12	12	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	31	12	12	4	0
2	K	31	12	12	4	0
2	L	31	12	12	4	0
2	M	31	12	12	4	0
2	N	31	12	12	4	0
2	O	31	12	12	5	0
2	P	31	12	12	4	0
2	Q	31	12	12	5	0
2	R	31	12	12	5	0
2	S	31	12	12	4	0
2	T	31	12	12	5	0
2	U	31	12	12	4	0
2	V	31	12	12	4	0
2	W	31	12	12	4	0
2	X	62	24	24	5	0
All	All	58275	57050	56951	712	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 6.

The worst 5 of 712 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:189:TYR:CE1	2:C:401:ATP:O2A	1.91	1.10
1:I:189:TYR:CE1	2:I:401:ATP:O2A	1.91	1.09
1:T:189:TYR:CE1	2:T:401:ATP:O2A	1.91	1.08
1:F:189:TYR:CE1	2:F:401:ATP:O2A	1.91	1.07
1:L:189:TYR:CE1	2:L:401:ATP:O2A	1.91	1.06

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	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	B	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	C	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	D	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	E	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	F	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	G	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	H	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	I	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	J	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	K	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	L	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	M	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	N	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	O	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	P	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	Q	280/282 (99%)	247 (88%)	33 (12%)	0	100	100
1	R	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	S	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	T	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	U	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	V	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	W	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	X	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
1	Y	280/282 (99%)	248 (89%)	32 (11%)	0	100	100
All	All	7000/7050 (99%)	6199 (89%)	801 (11%)	0	100	100

There are no Ramachandran outliers to report.

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 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	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	B	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	C	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	D	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	E	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	F	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	G	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	H	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	I	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	J	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	K	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	L	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	M	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	N	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	O	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	P	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	Q	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	R	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	S	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	T	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	U	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	V	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	W	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	X	250/250 (100%)	249 (100%)	1 (0%)	91	94
1	Y	250/250 (100%)	249 (100%)	1 (0%)	91	94
All	All	6250/6250 (100%)	6225 (100%)	25 (0%)	91	94

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	228	ARG
1	R	228	ARG

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Mol	Chain	Res	Type
1	Y	228	ARG
1	Q	228	ARG
1	S	228	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
1	T	72	GLN
1	X	158	ASN
1	T	158	ASN
1	V	158	ASN
1	I	72	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

25 ligands are modelled in this entry.

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	W	401	-	26,33,33	0.90	1 (3%)	31,52,52	1.72	6 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	ATP	M	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.72	6 (19%)
2	ATP	E	401	-	26,33,33	0.90	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	X	402	-	26,33,33	0.90	1 (3%)	31,52,52	1.72	6 (19%)
2	ATP	R	401	-	26,33,33	0.90	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	T	401	-	26,33,33	0.90	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	H	401	-	26,33,33	0.90	1 (3%)	31,52,52	1.72	6 (19%)
2	ATP	X	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	B	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	P	401	-	26,33,33	0.90	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	C	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.72	6 (19%)
2	ATP	J	401	-	26,33,33	0.90	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	U	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	S	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	G	401	-	26,33,33	0.90	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	K	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	A	401	-	26,33,33	0.90	1 (3%)	31,52,52	1.72	6 (19%)
2	ATP	O	401	-	26,33,33	0.90	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	I	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	D	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	F	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	V	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	Q	401	-	26,33,33	0.90	1 (3%)	31,52,52	1.72	6 (19%)
2	ATP	N	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.73	6 (19%)
2	ATP	L	401	-	26,33,33	0.91	1 (3%)	31,52,52	1.73	6 (19%)

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	W	401	-	-	1/18/38/38	0/3/3/3
2	ATP	M	401	-	-	1/18/38/38	0/3/3/3
2	ATP	E	401	-	-	1/18/38/38	0/3/3/3
2	ATP	X	402	-	-	1/18/38/38	0/3/3/3
2	ATP	R	401	-	-	1/18/38/38	0/3/3/3
2	ATP	T	401	-	-	1/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ATP	H	401	-	-	1/18/38/38	0/3/3/3
2	ATP	X	401	-	-	1/18/38/38	0/3/3/3
2	ATP	B	401	-	-	1/18/38/38	0/3/3/3
2	ATP	P	401	-	-	1/18/38/38	0/3/3/3
2	ATP	C	401	-	-	1/18/38/38	0/3/3/3
2	ATP	J	401	-	-	1/18/38/38	0/3/3/3
2	ATP	U	401	-	-	1/18/38/38	0/3/3/3
2	ATP	S	401	-	-	1/18/38/38	0/3/3/3
2	ATP	G	401	-	-	1/18/38/38	0/3/3/3
2	ATP	K	401	-	-	1/18/38/38	0/3/3/3
2	ATP	A	401	-	-	1/18/38/38	0/3/3/3
2	ATP	O	401	-	-	1/18/38/38	0/3/3/3
2	ATP	I	401	-	-	1/18/38/38	0/3/3/3
2	ATP	D	401	-	-	1/18/38/38	0/3/3/3
2	ATP	F	401	-	-	1/18/38/38	0/3/3/3
2	ATP	V	401	-	-	1/18/38/38	0/3/3/3
2	ATP	Q	401	-	-	1/18/38/38	0/3/3/3
2	ATP	N	401	-	-	1/18/38/38	0/3/3/3
2	ATP	L	401	-	-	1/18/38/38	0/3/3/3

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	S	401	ATP	C5-C4	2.20	1.46	1.40
2	M	401	ATP	C5-C4	2.19	1.46	1.40
2	O	401	ATP	C5-C4	2.19	1.46	1.40
2	I	401	ATP	C5-C4	2.19	1.46	1.40
2	G	401	ATP	C5-C4	2.19	1.46	1.40

The worst 5 of 150 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	401	ATP	PA-O3A-PB	-4.74	116.55	132.83
2	C	401	ATP	PA-O3A-PB	-4.74	116.55	132.83
2	U	401	ATP	PA-O3A-PB	-4.74	116.56	132.83
2	N	401	ATP	PA-O3A-PB	-4.74	116.57	132.83
2	P	401	ATP	PA-O3A-PB	-4.74	116.57	132.83

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	ATP	PA-O3A-PB-O2B
2	B	401	ATP	PA-O3A-PB-O2B
2	C	401	ATP	PA-O3A-PB-O2B
2	D	401	ATP	PA-O3A-PB-O2B
2	E	401	ATP	PA-O3A-PB-O2B

There are no ring outliers.

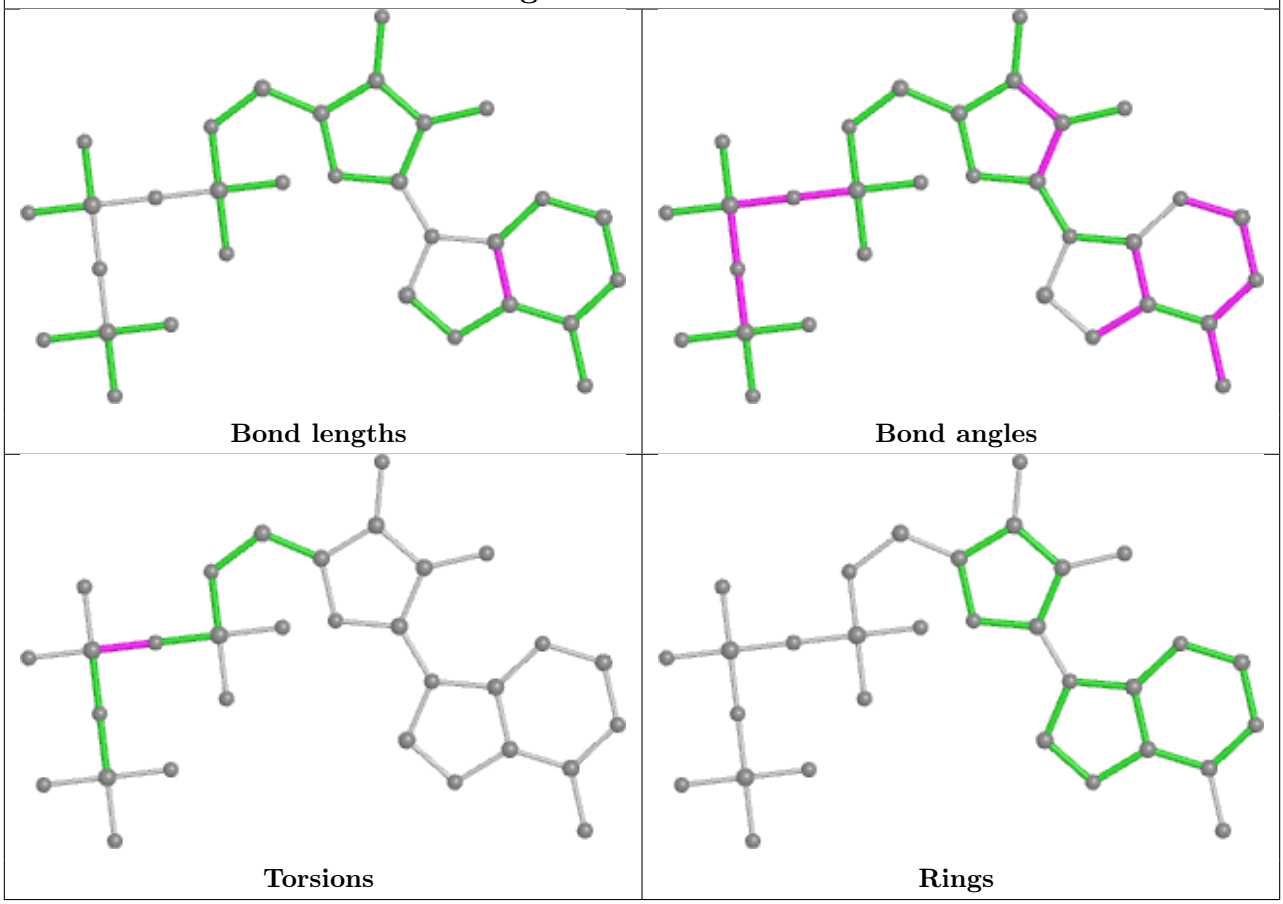
25 monomers are involved in 102 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	W	401	ATP	4	0
2	M	401	ATP	4	0
2	E	401	ATP	4	0
2	X	402	ATP	1	0
2	R	401	ATP	5	0
2	T	401	ATP	5	0
2	H	401	ATP	4	0
2	X	401	ATP	4	0
2	B	401	ATP	5	0
2	P	401	ATP	4	0
2	C	401	ATP	4	0
2	J	401	ATP	4	0
2	U	401	ATP	4	0
2	S	401	ATP	4	0
2	G	401	ATP	4	0
2	K	401	ATP	4	0
2	A	401	ATP	4	0
2	O	401	ATP	5	0
2	I	401	ATP	4	0
2	D	401	ATP	4	0
2	F	401	ATP	4	0
2	V	401	ATP	4	0
2	Q	401	ATP	5	0
2	N	401	ATP	4	0
2	L	401	ATP	4	0

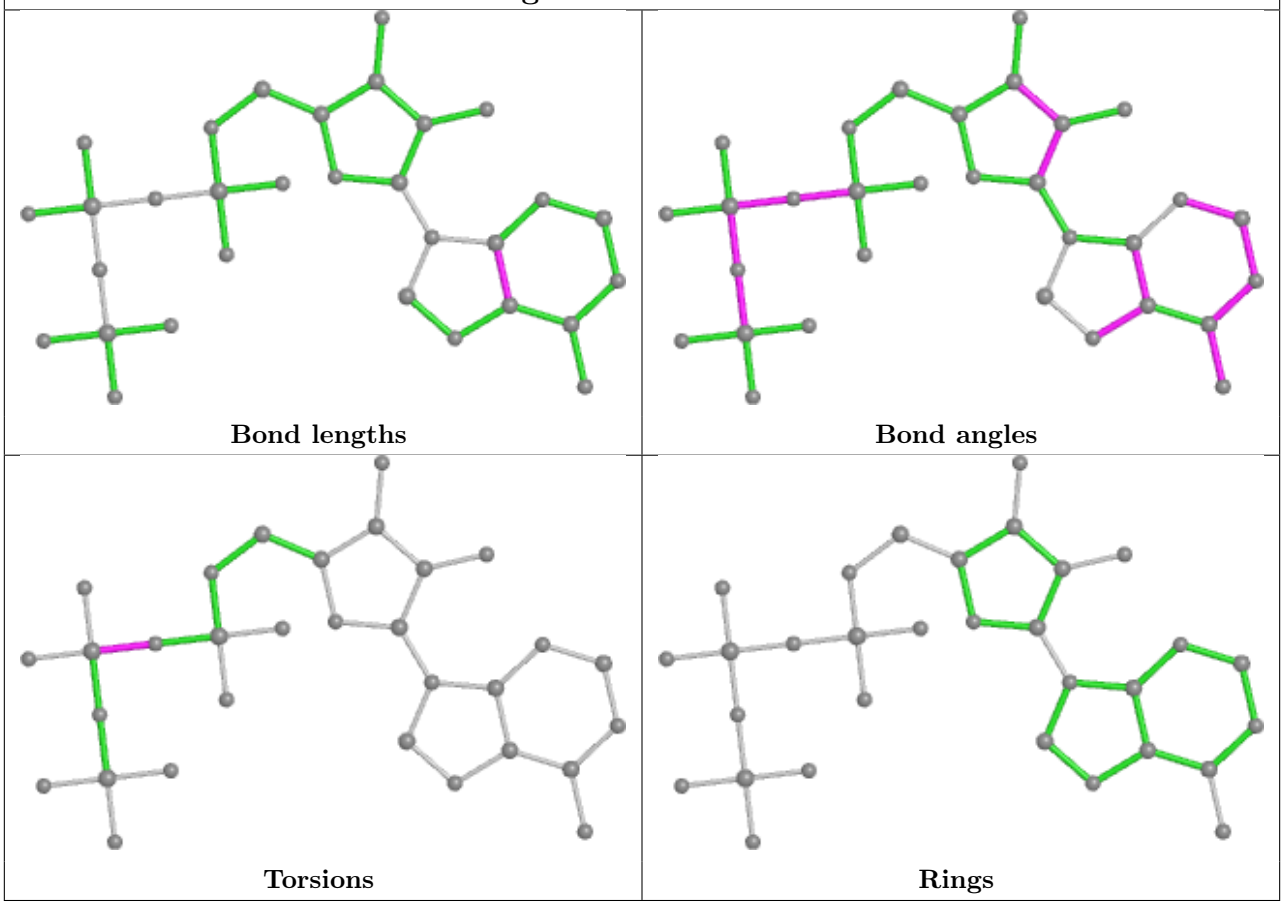
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

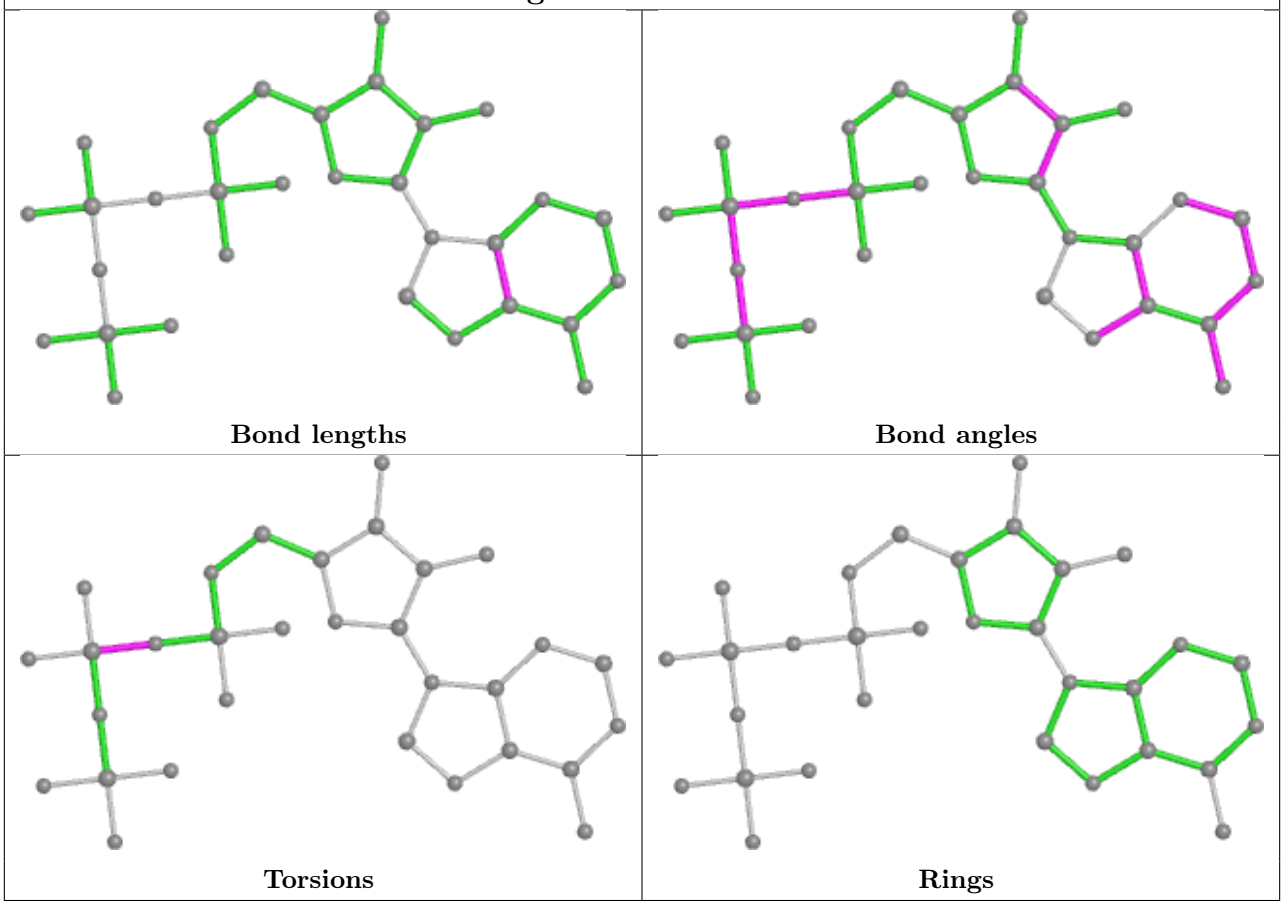
Ligand ATP W 401



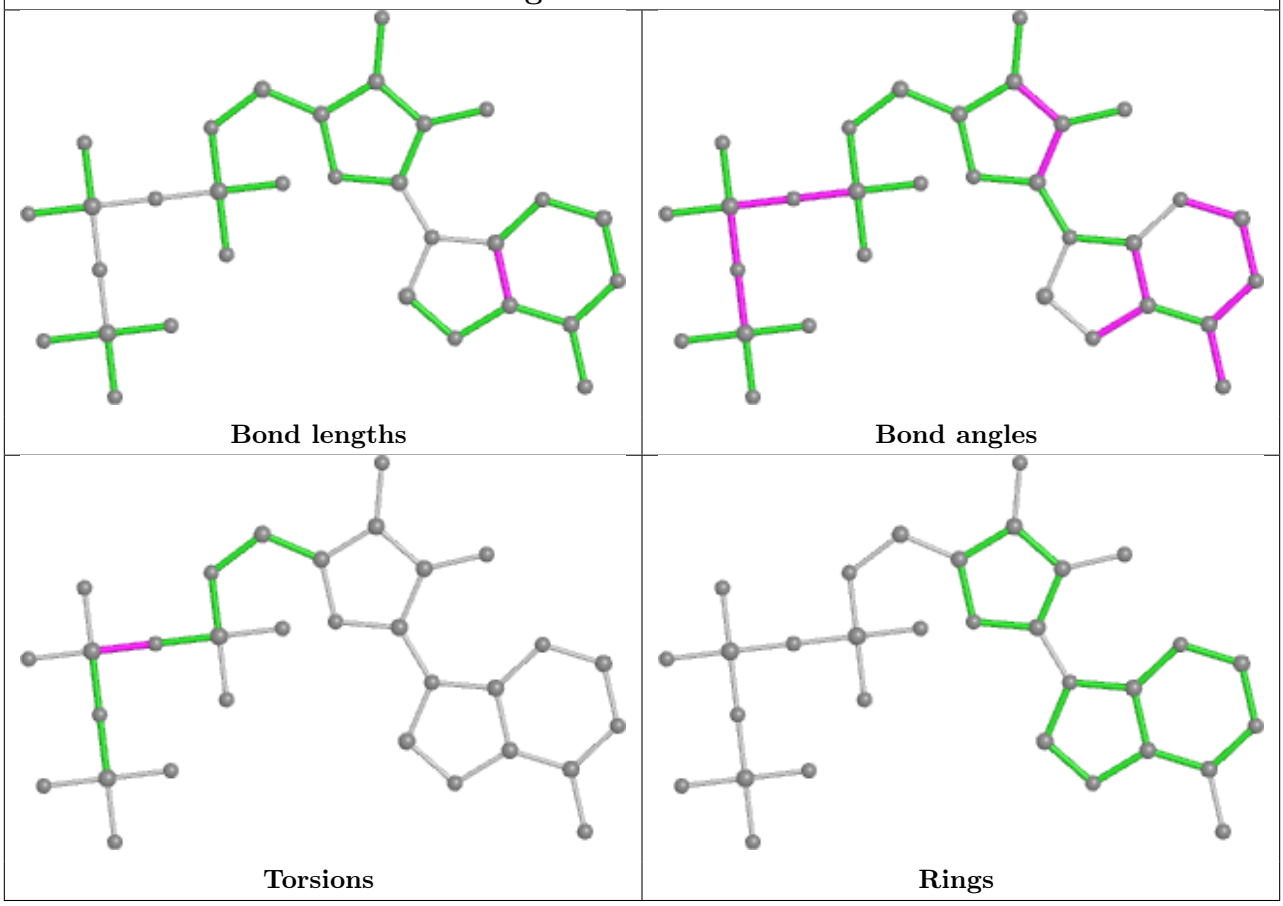
Ligand ATP M 401



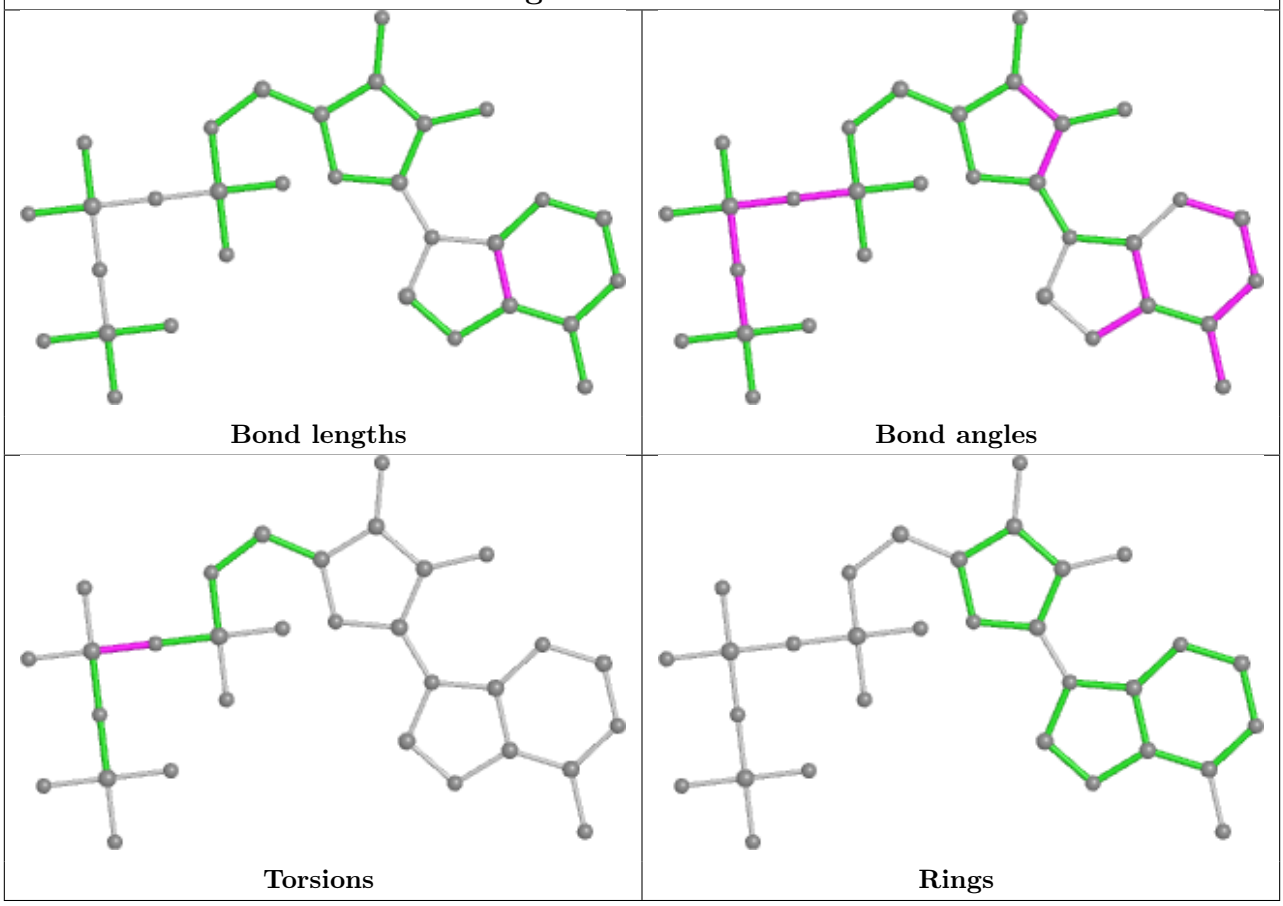
Ligand ATP E 401



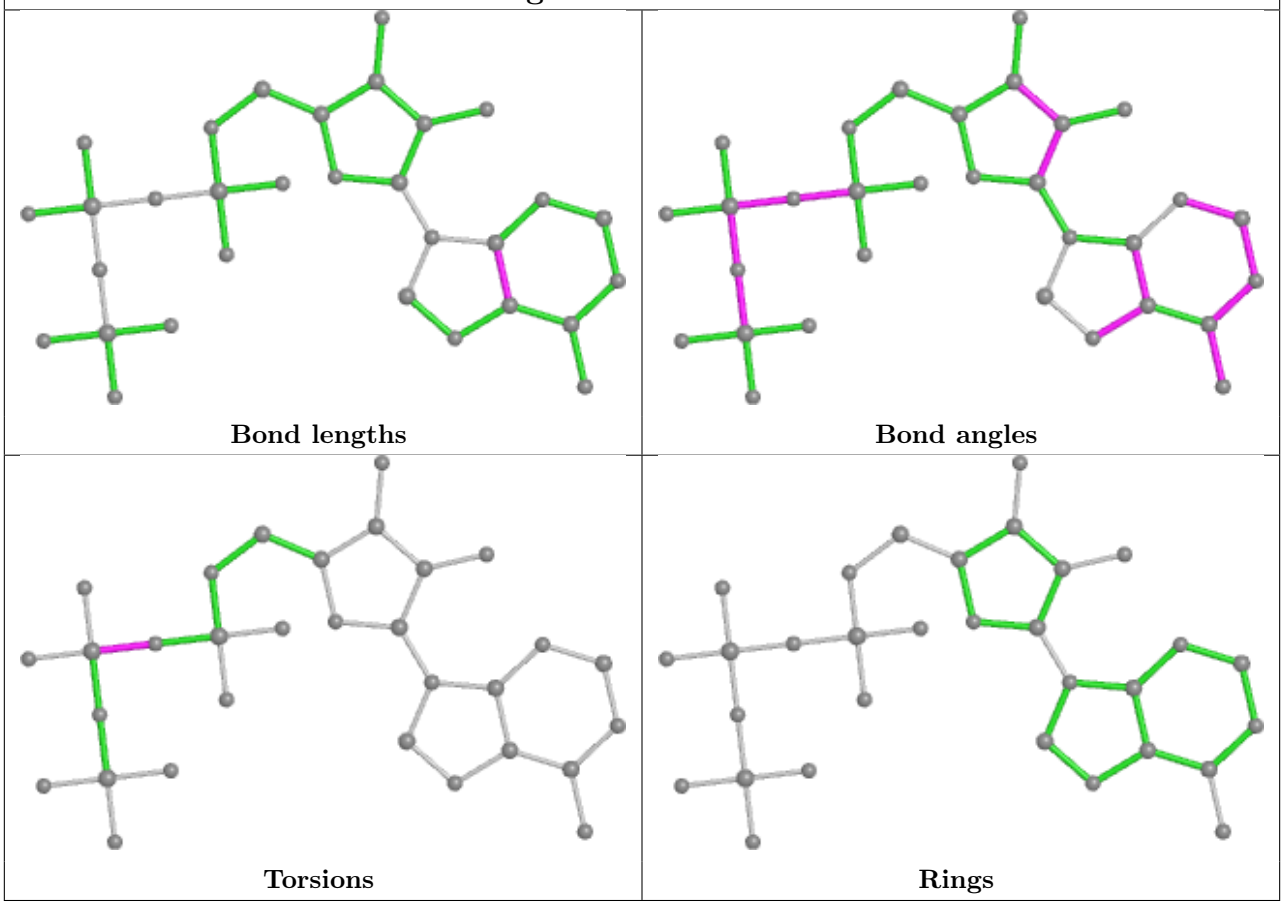
Ligand ATP X 402



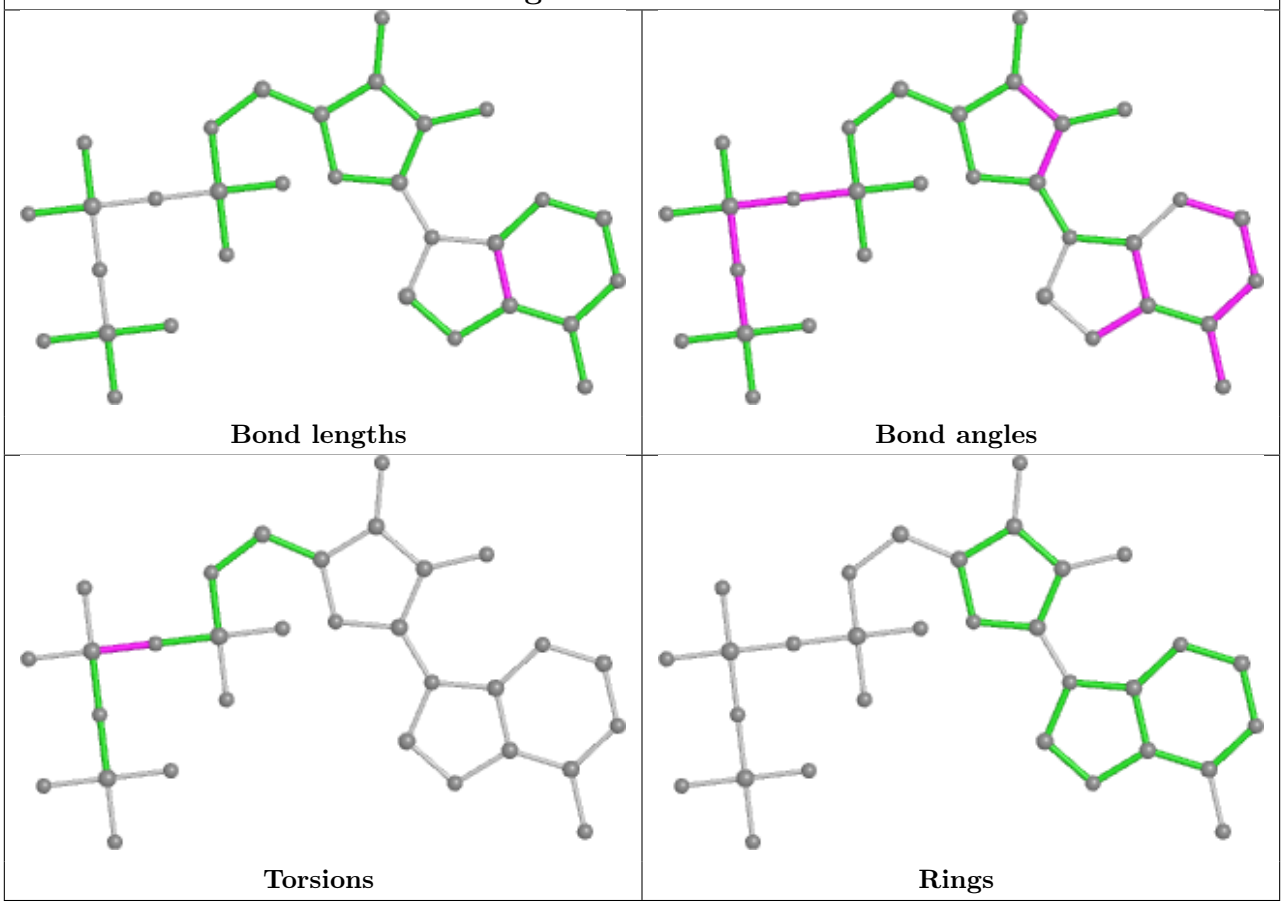
Ligand ATP R 401



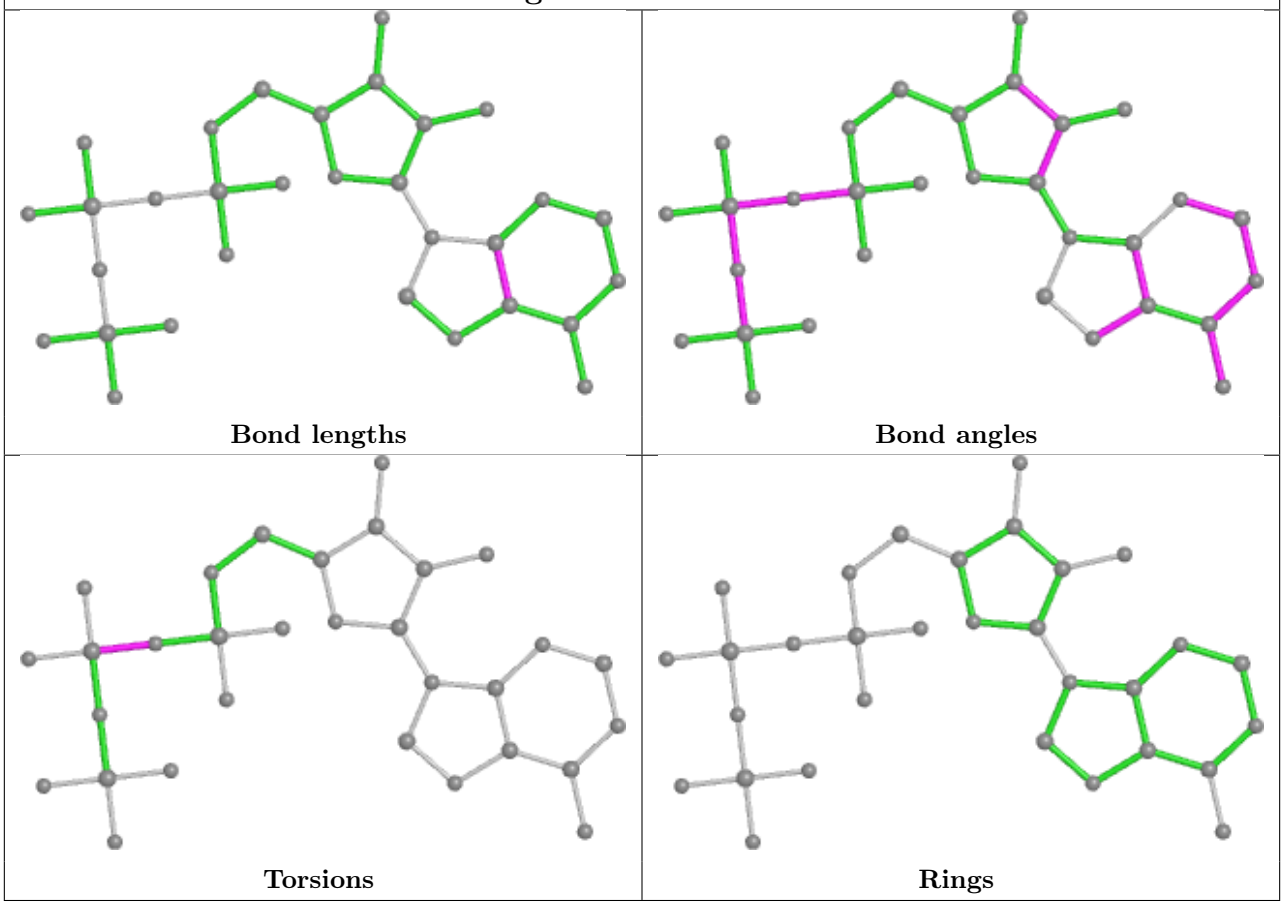
Ligand ATP T 401



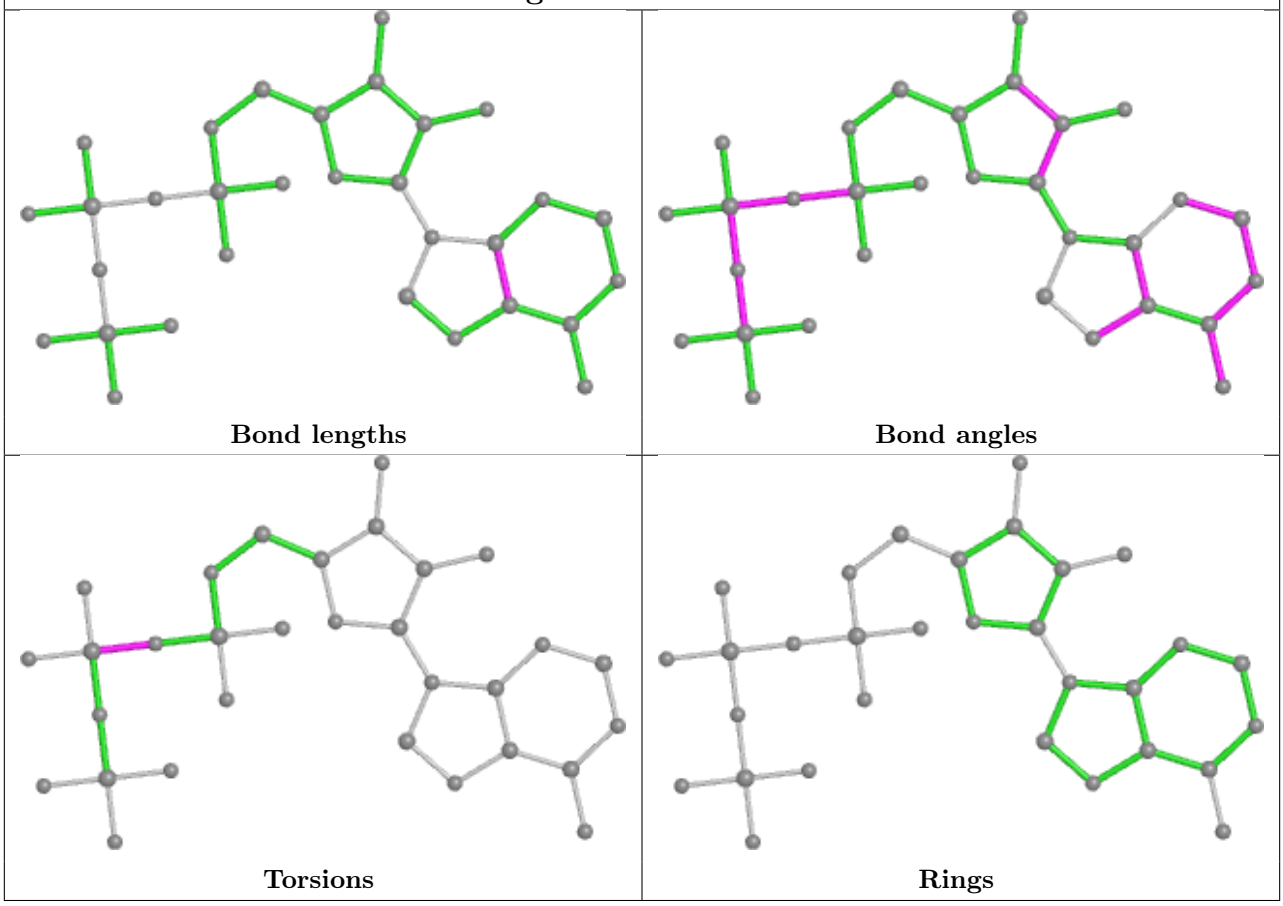
Ligand ATP H 401



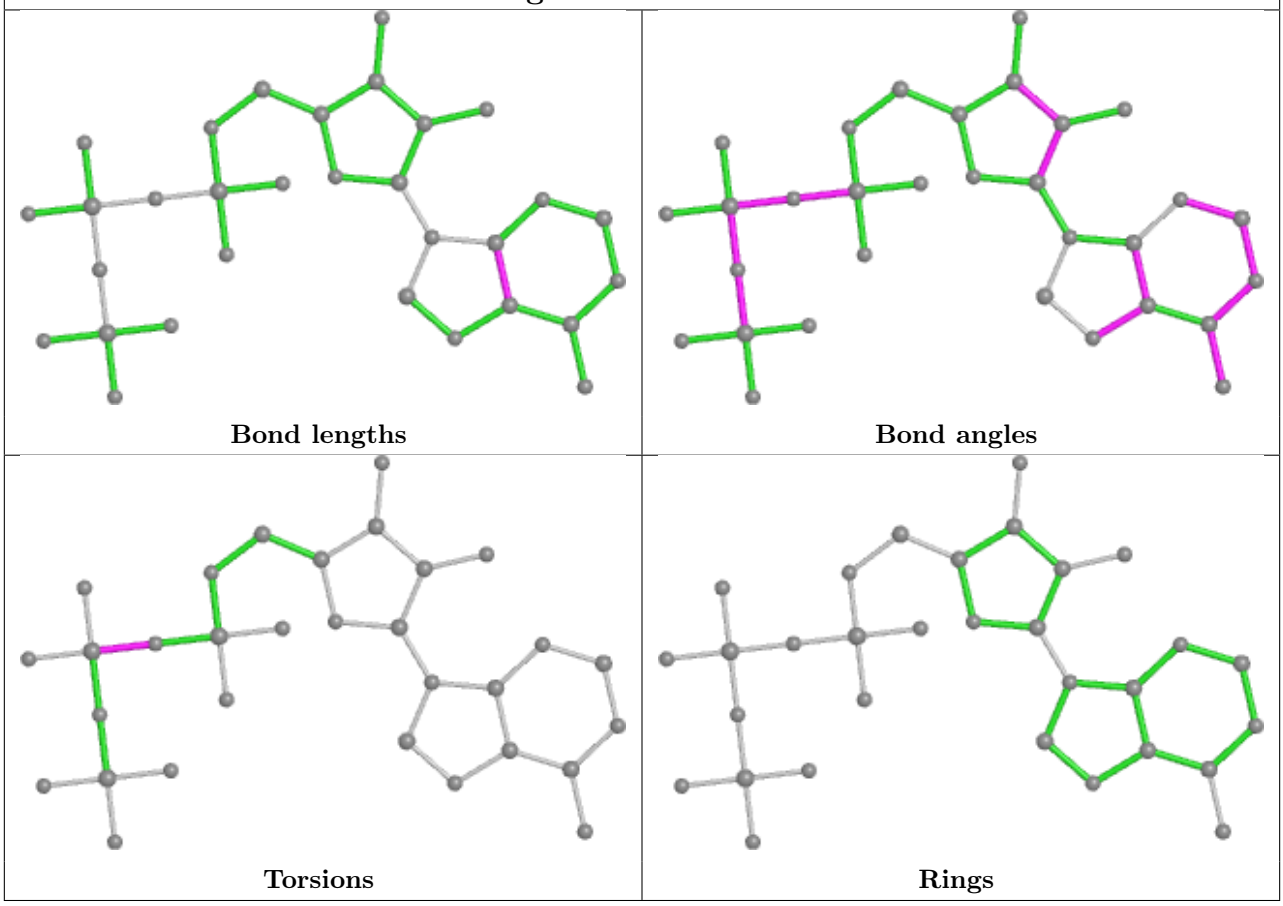
Ligand ATP X 401



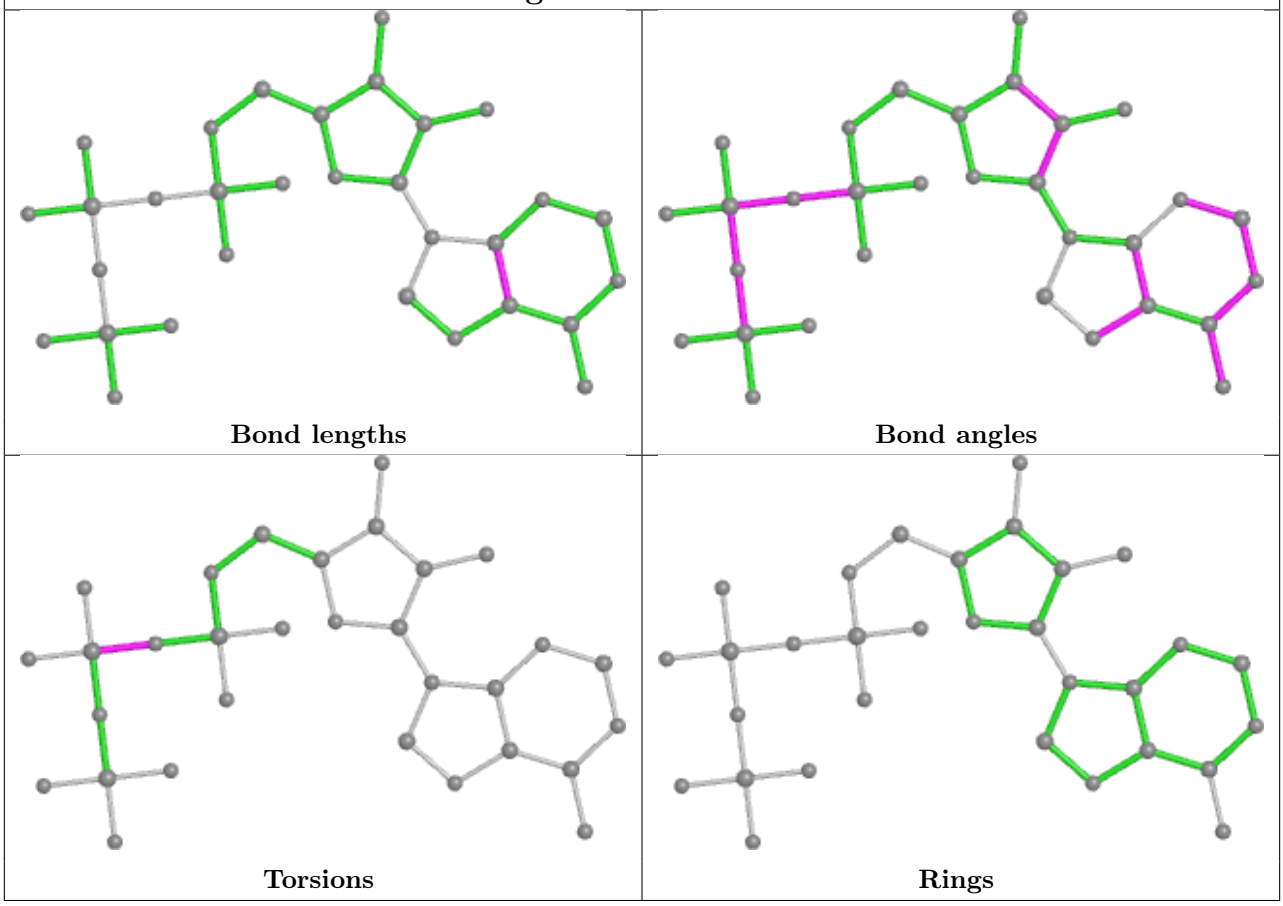
Ligand ATP B 401



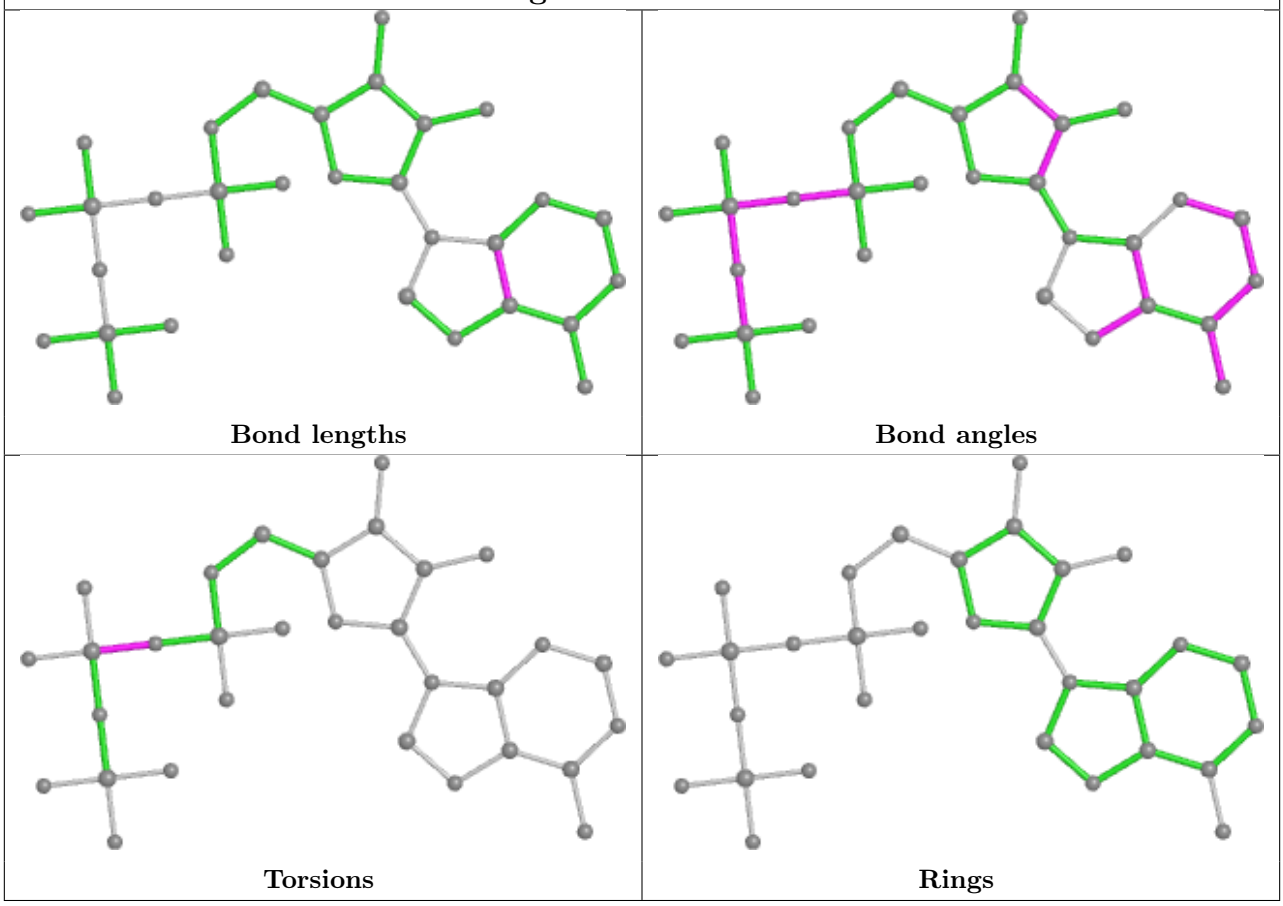
Ligand ATP P 401



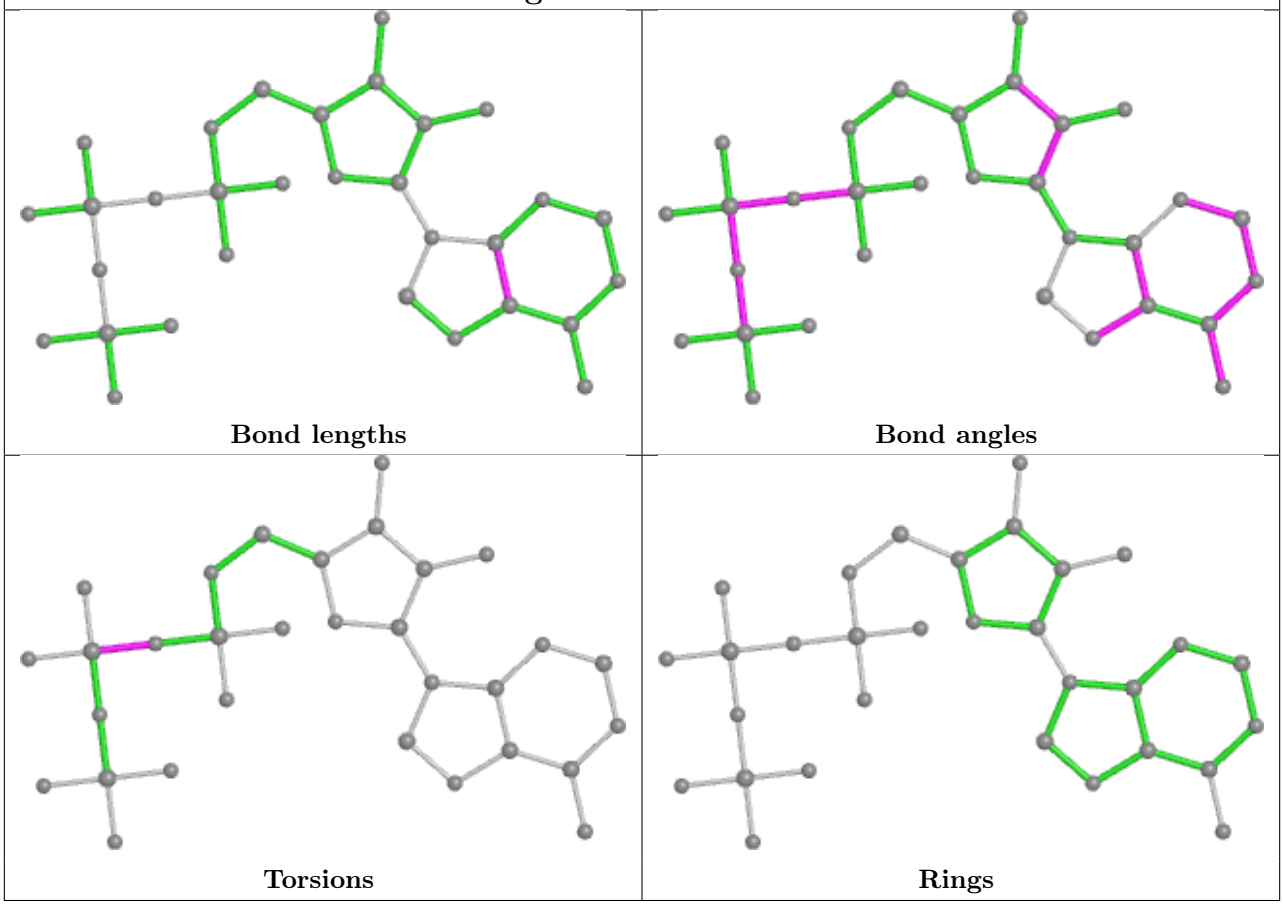
Ligand ATP C 401



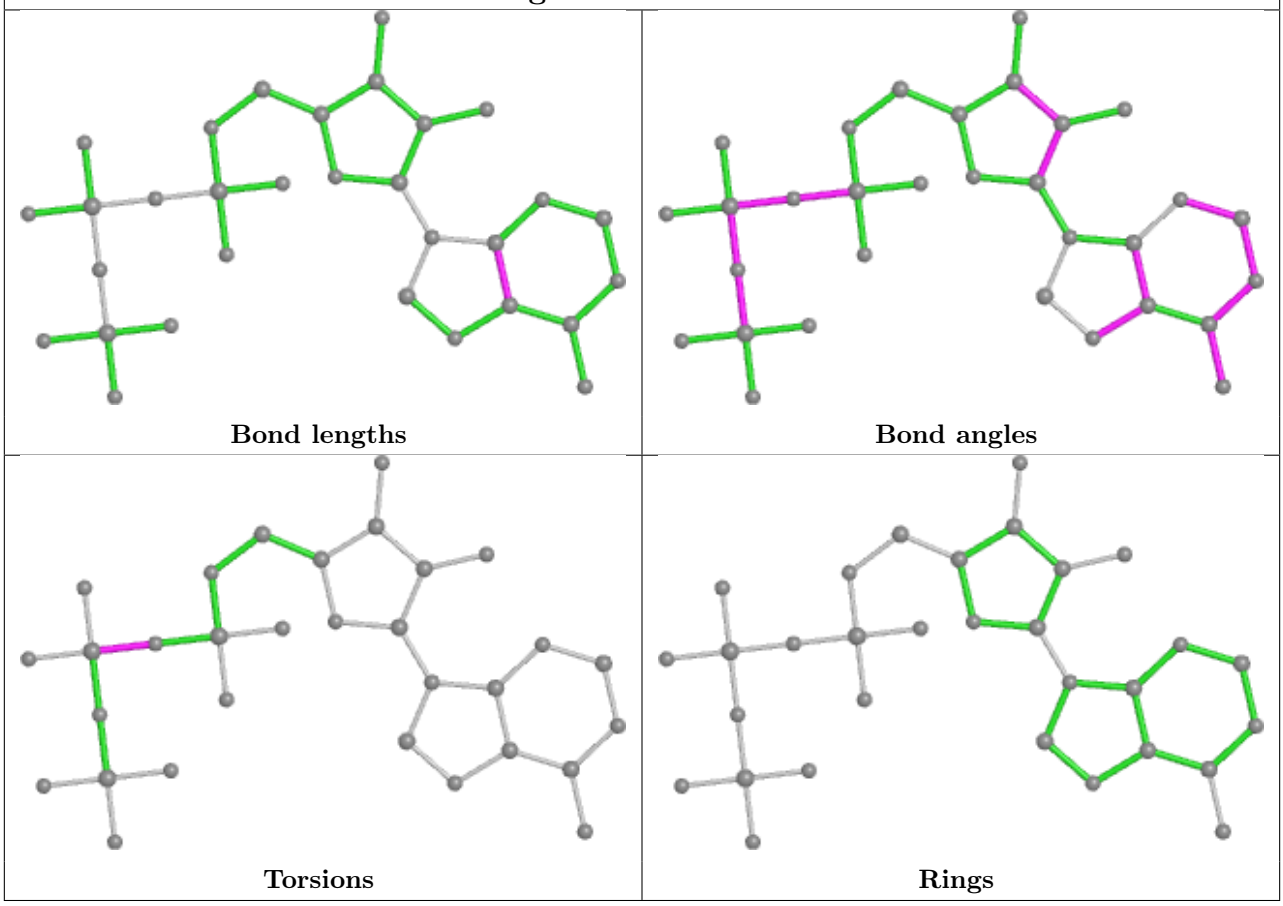
Ligand ATP J 401



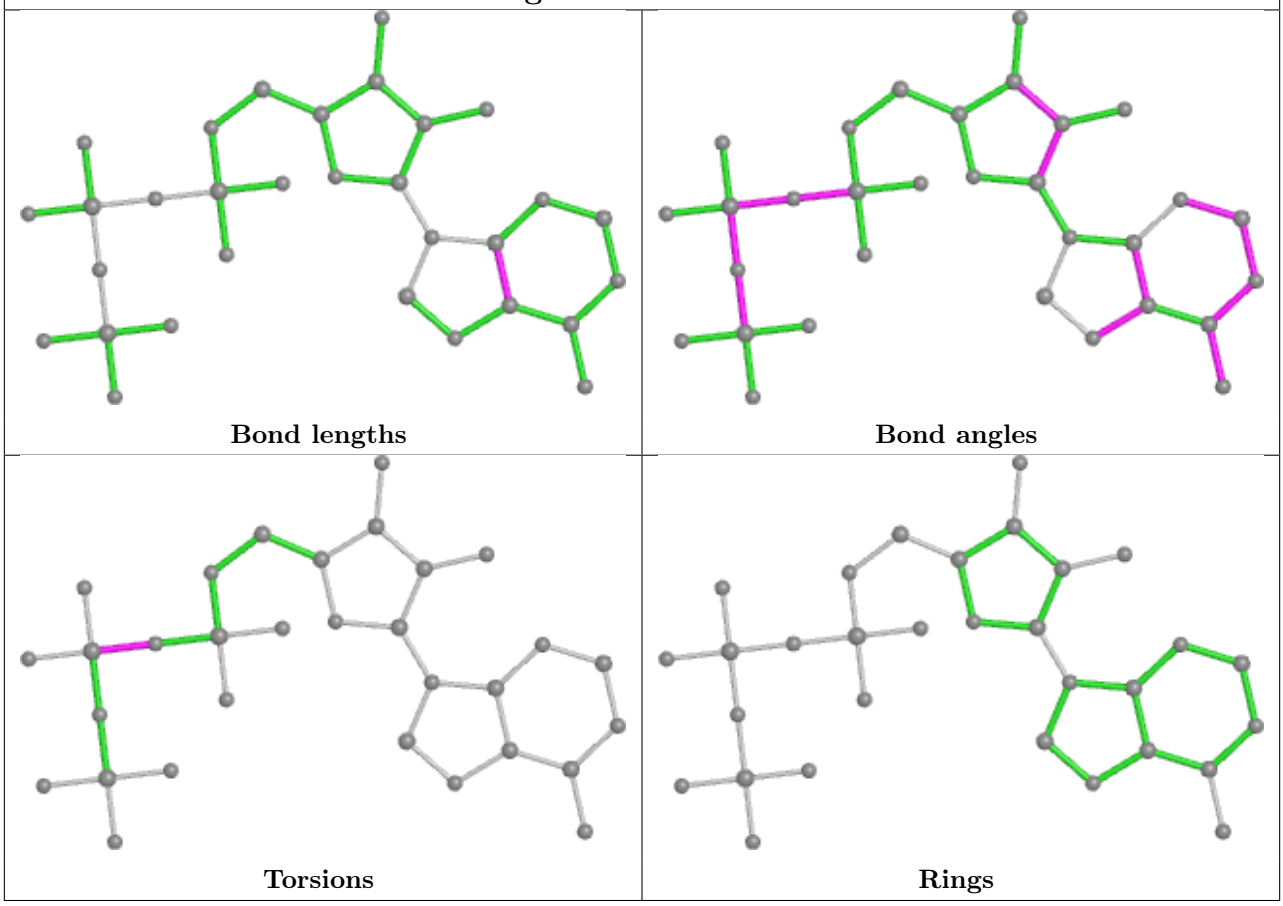
Ligand ATP U 401



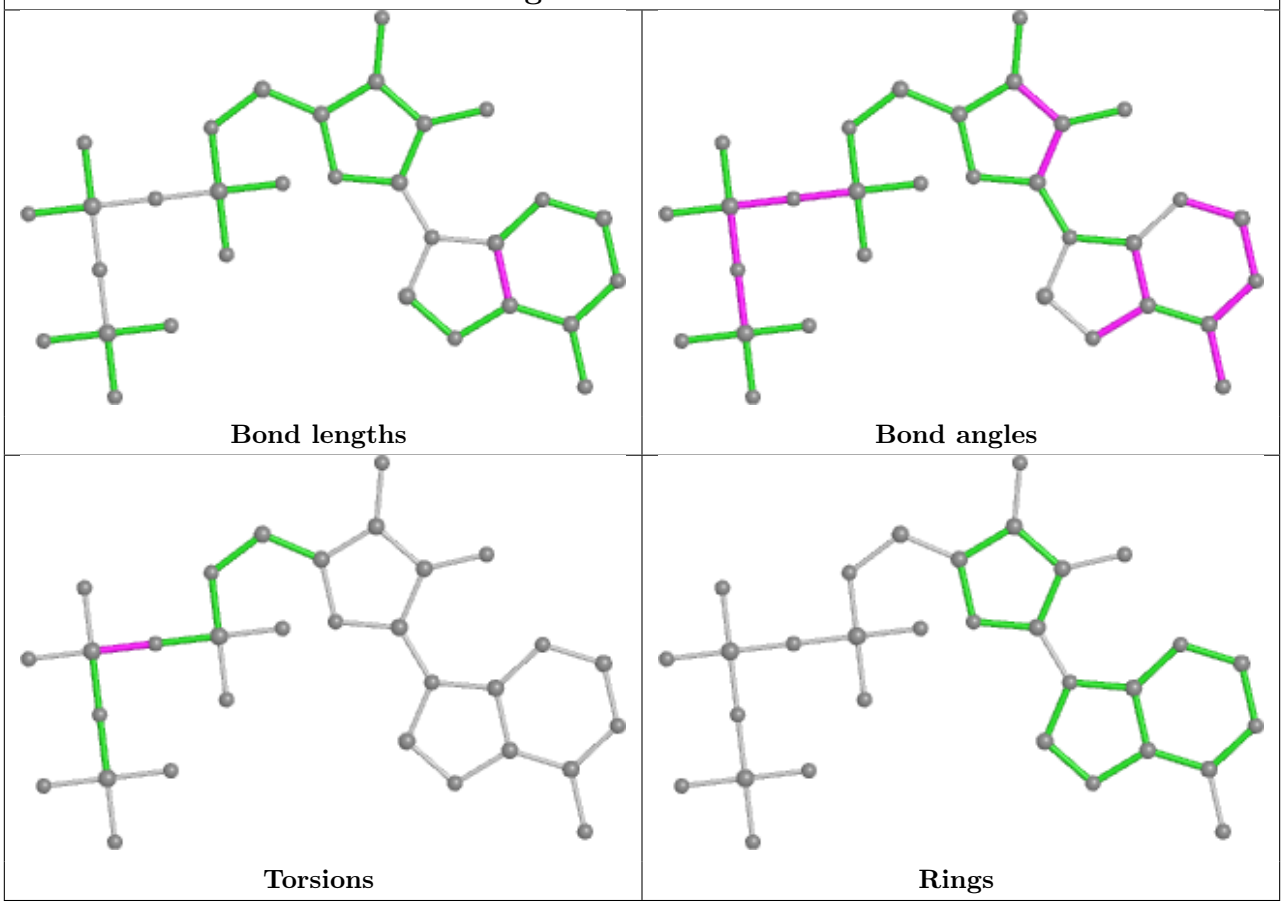
Ligand ATP S 401



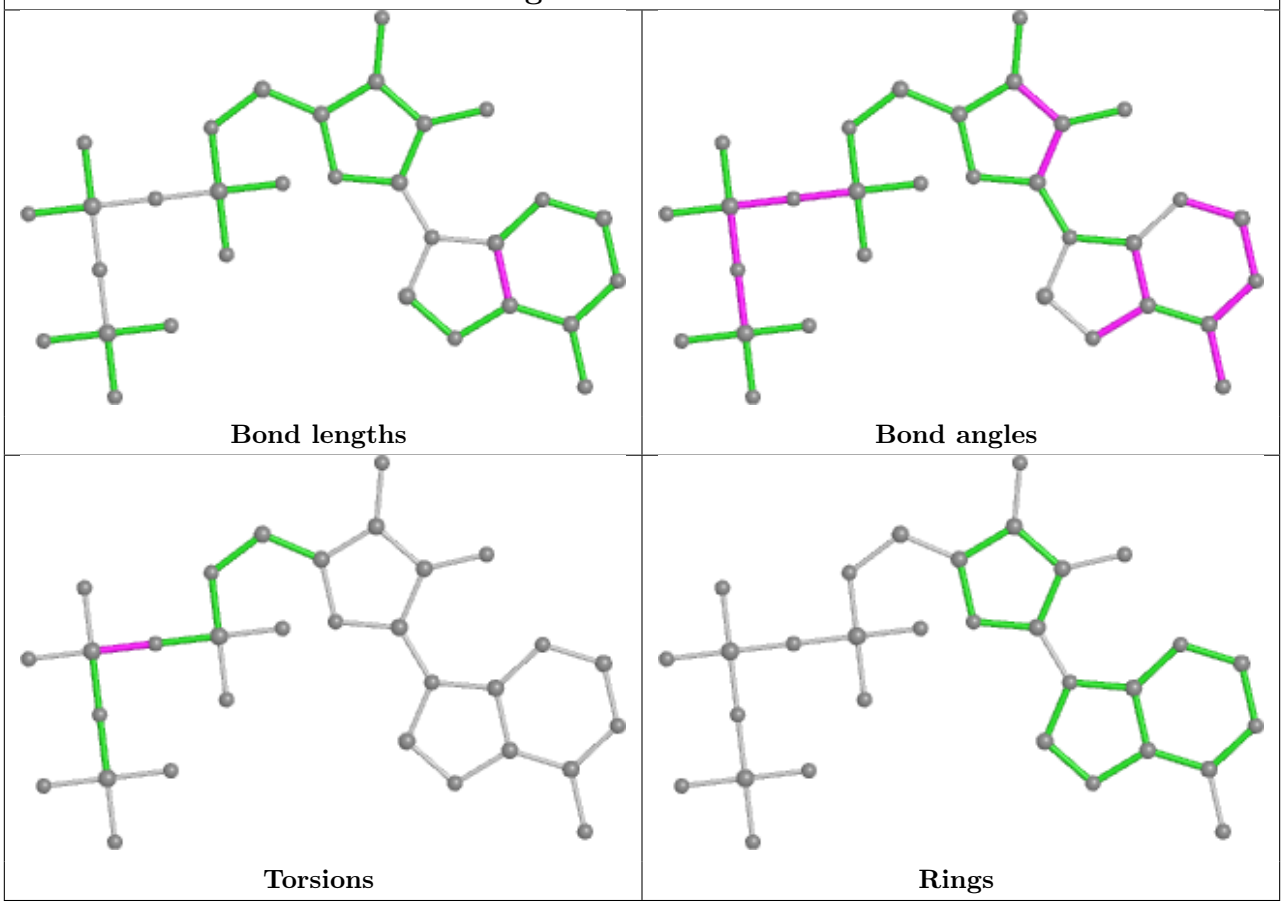
Ligand ATP G 401



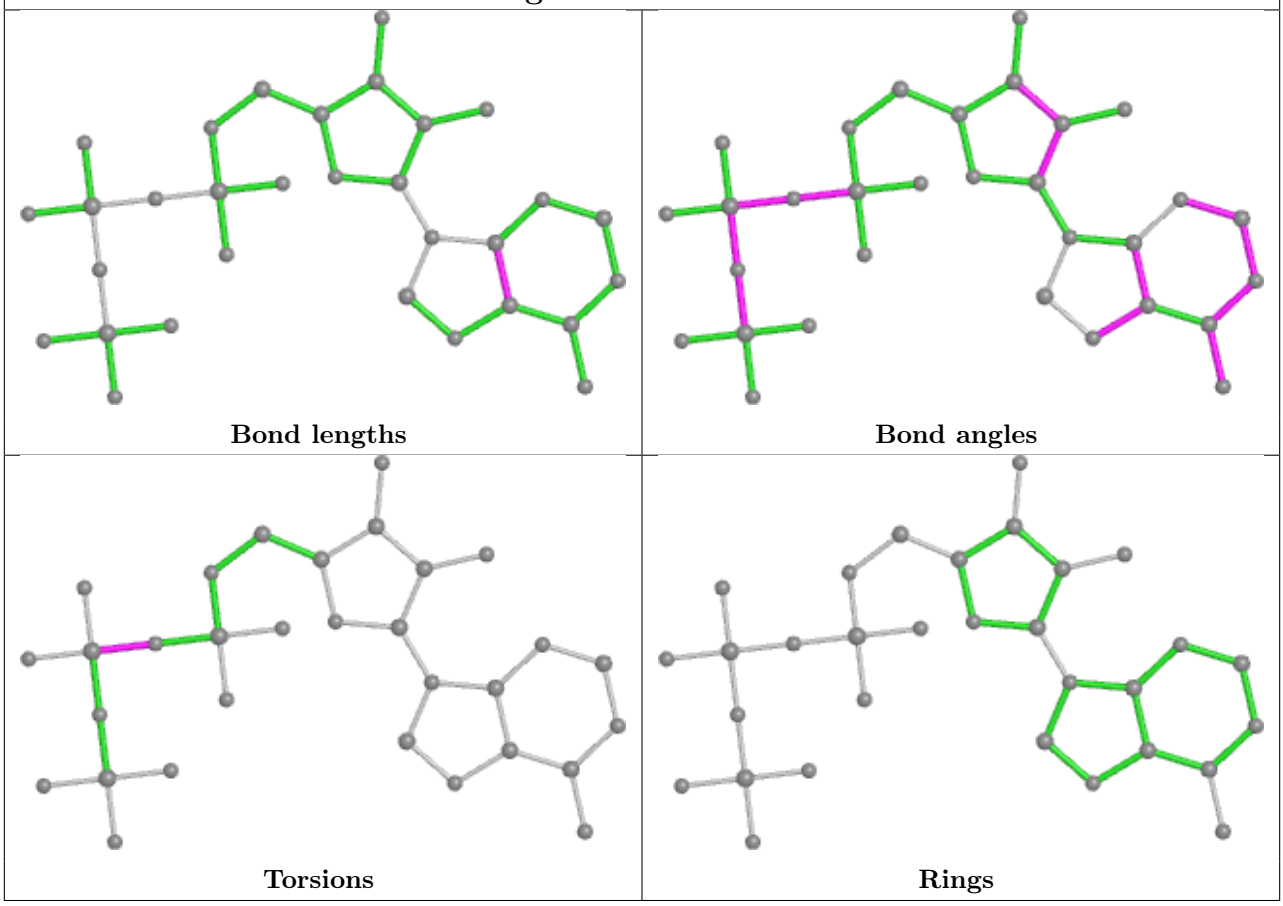
Ligand ATP K 401



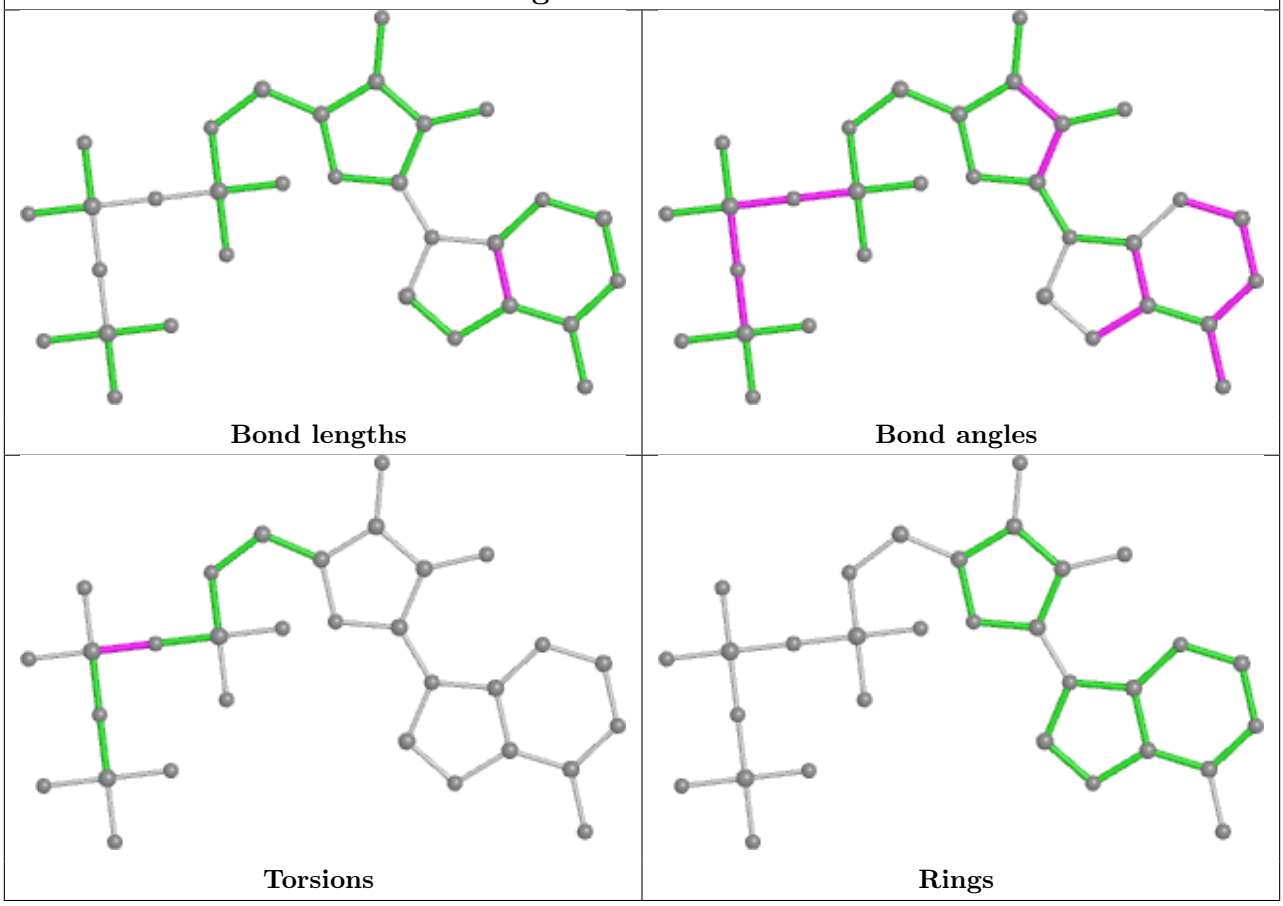
Ligand ATP A 401



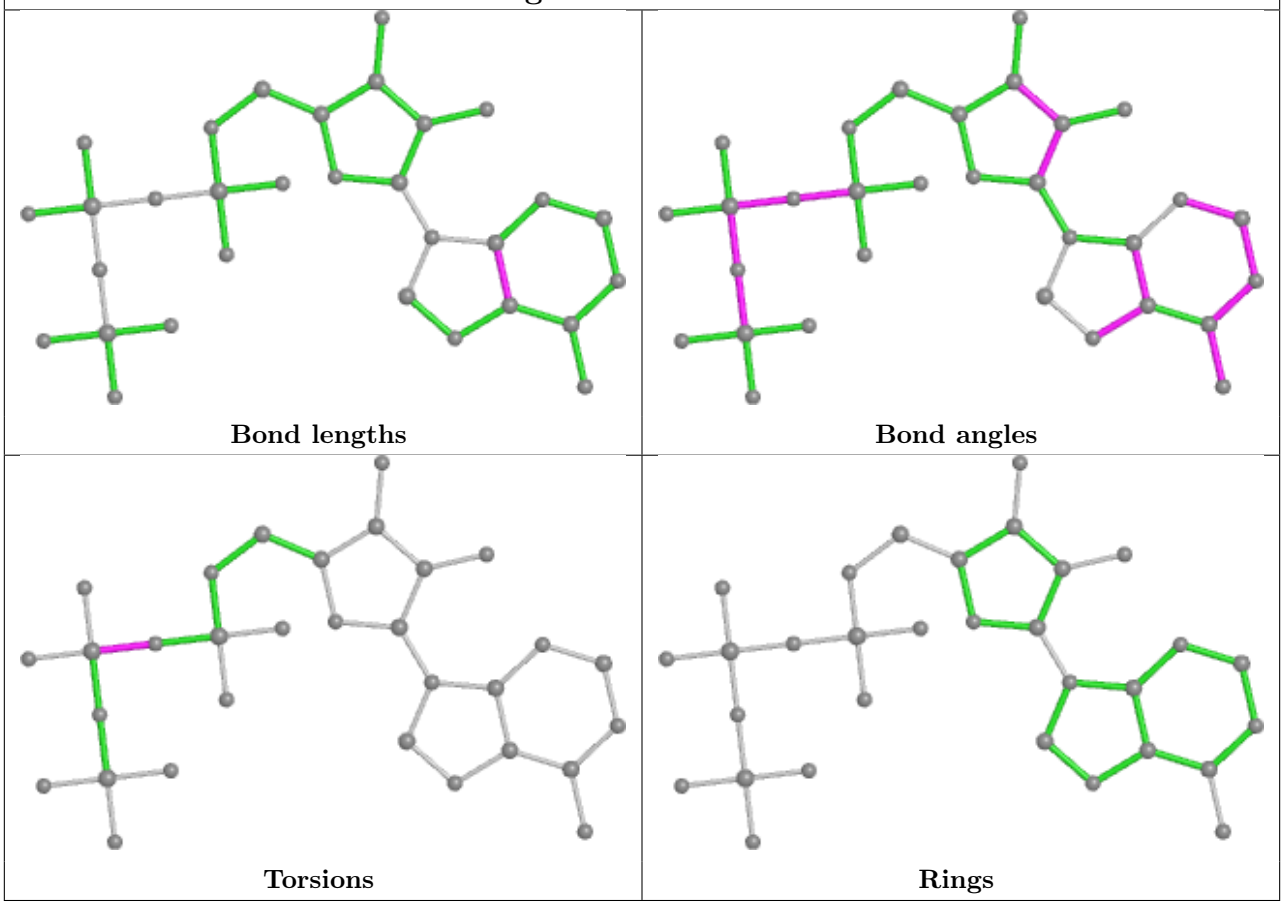
Ligand ATP O 401



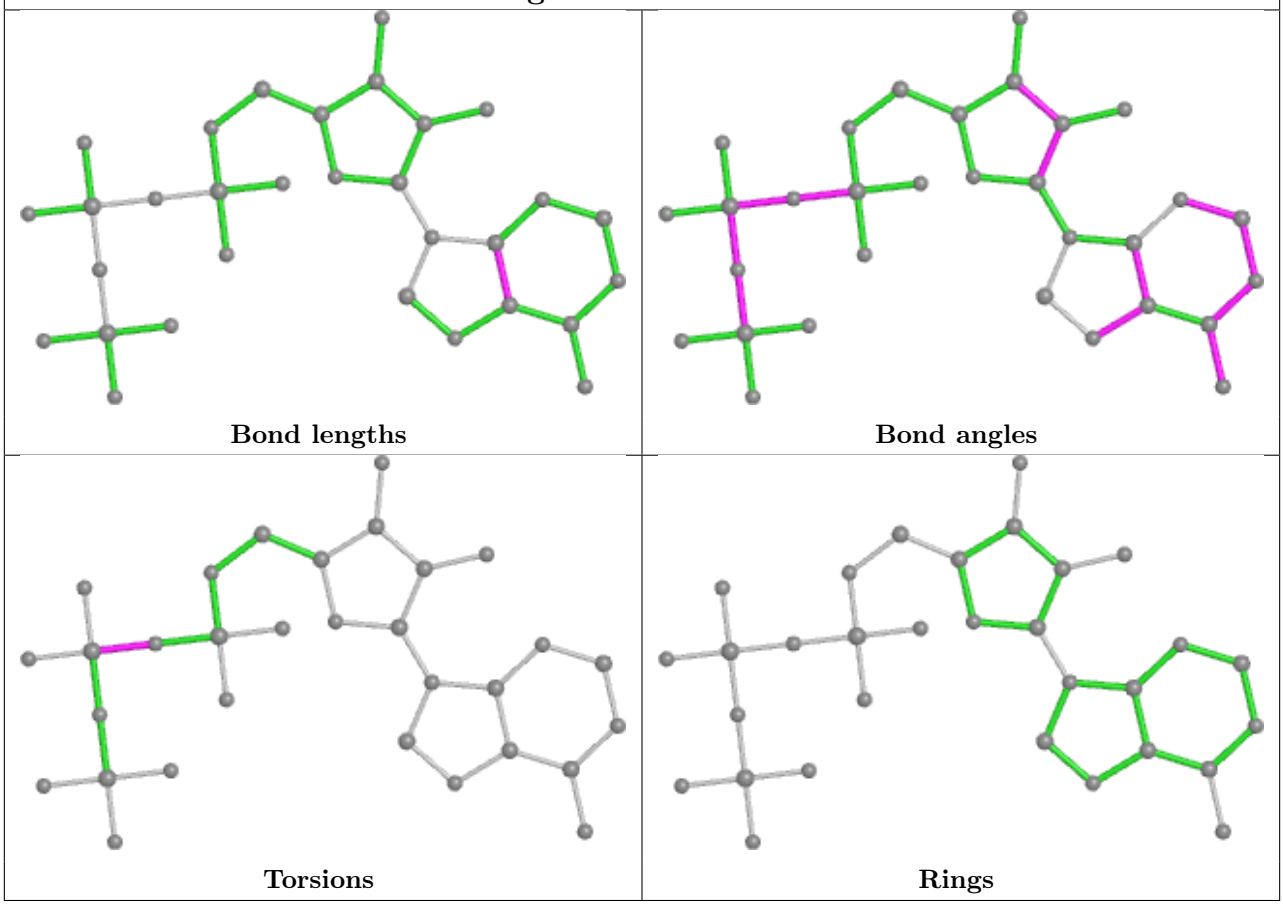
Ligand ATP I 401



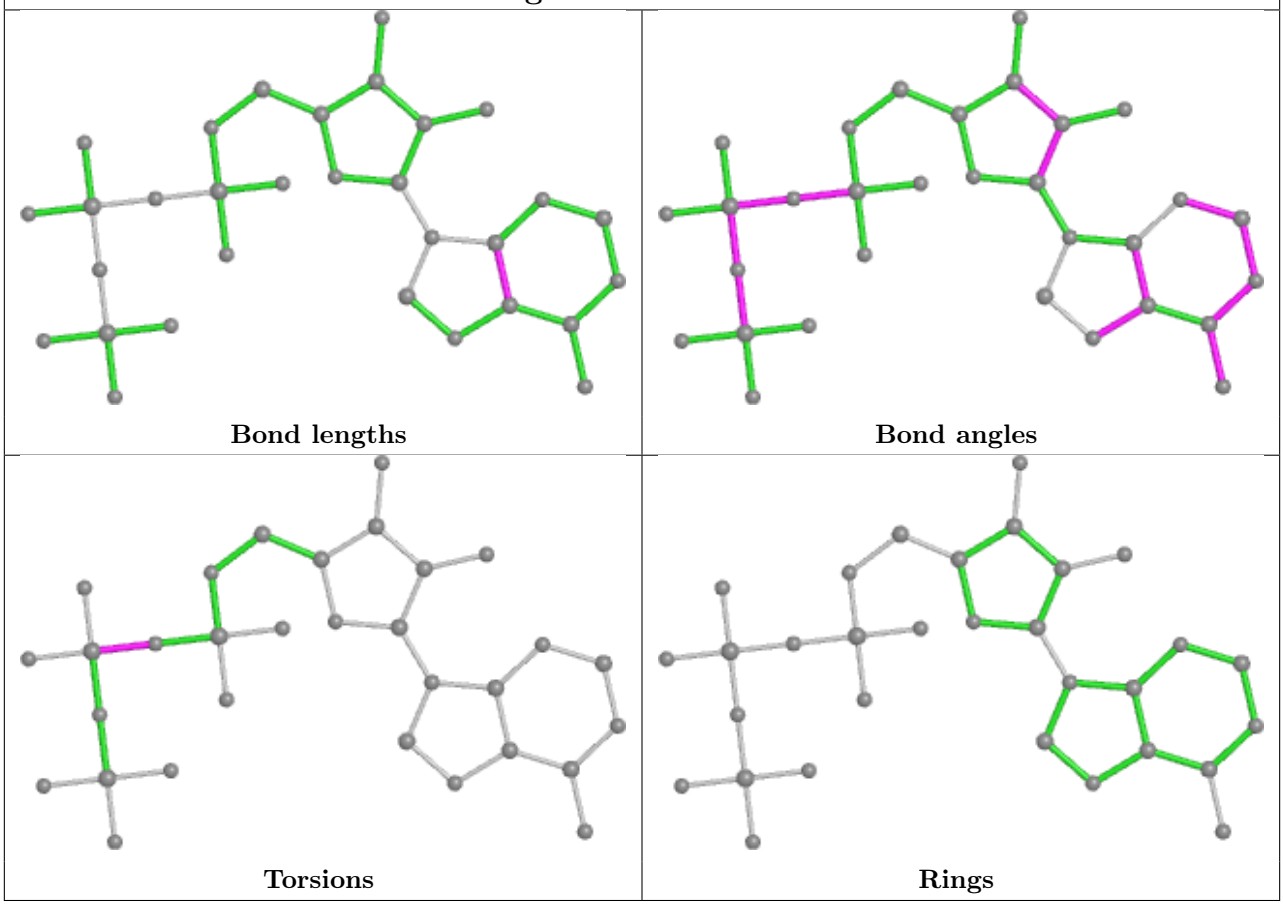
Ligand ATP D 401



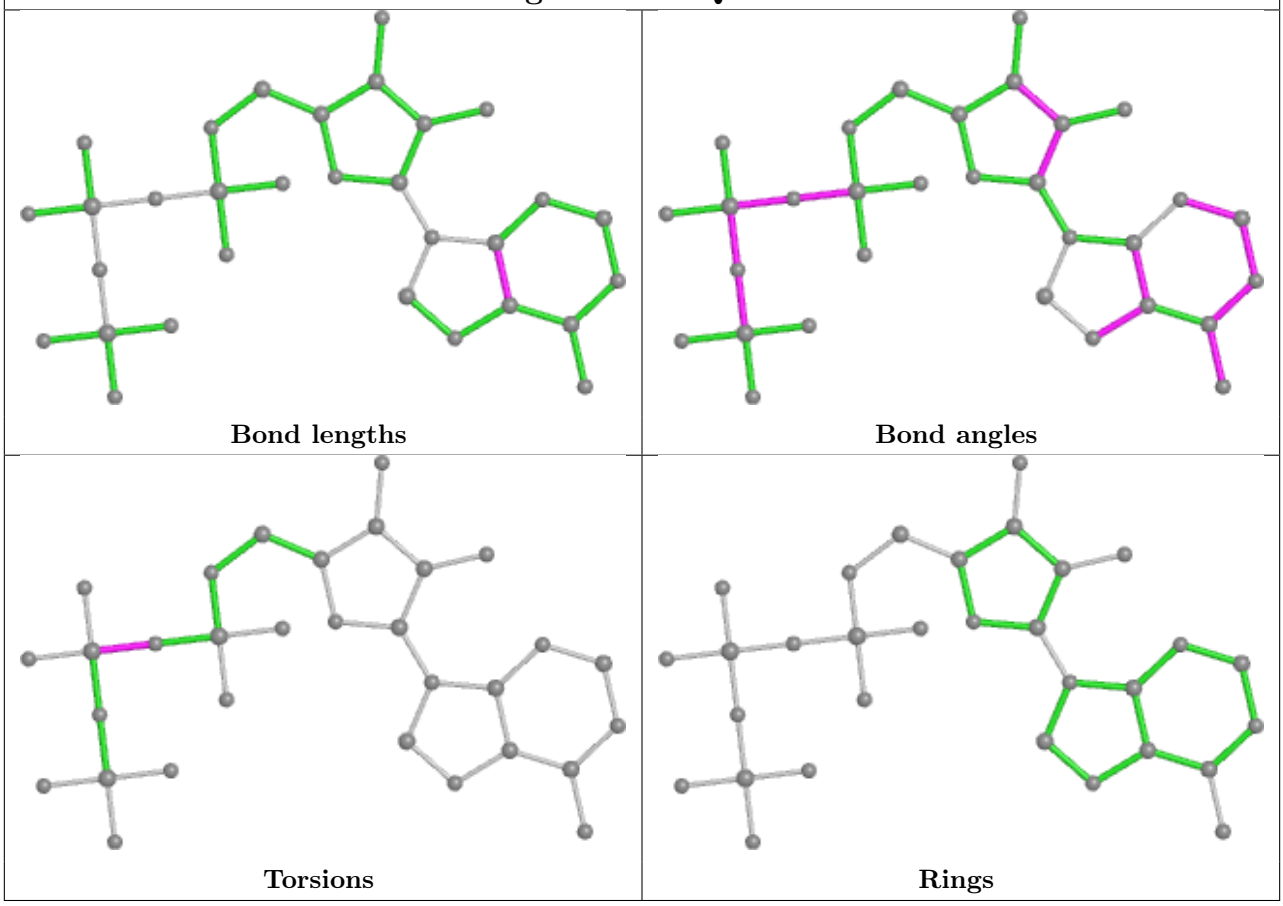
Ligand ATP F 401



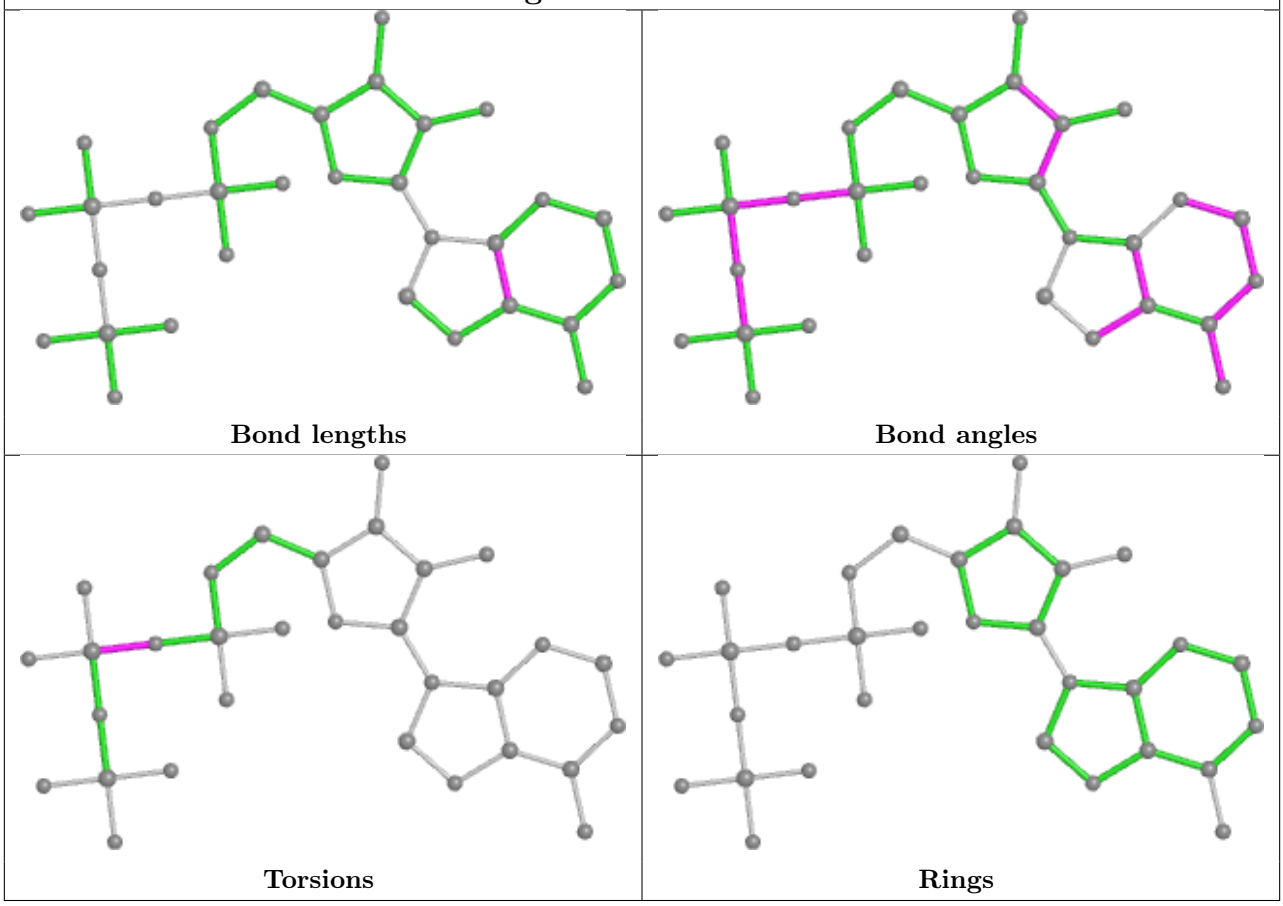
Ligand ATP V 401



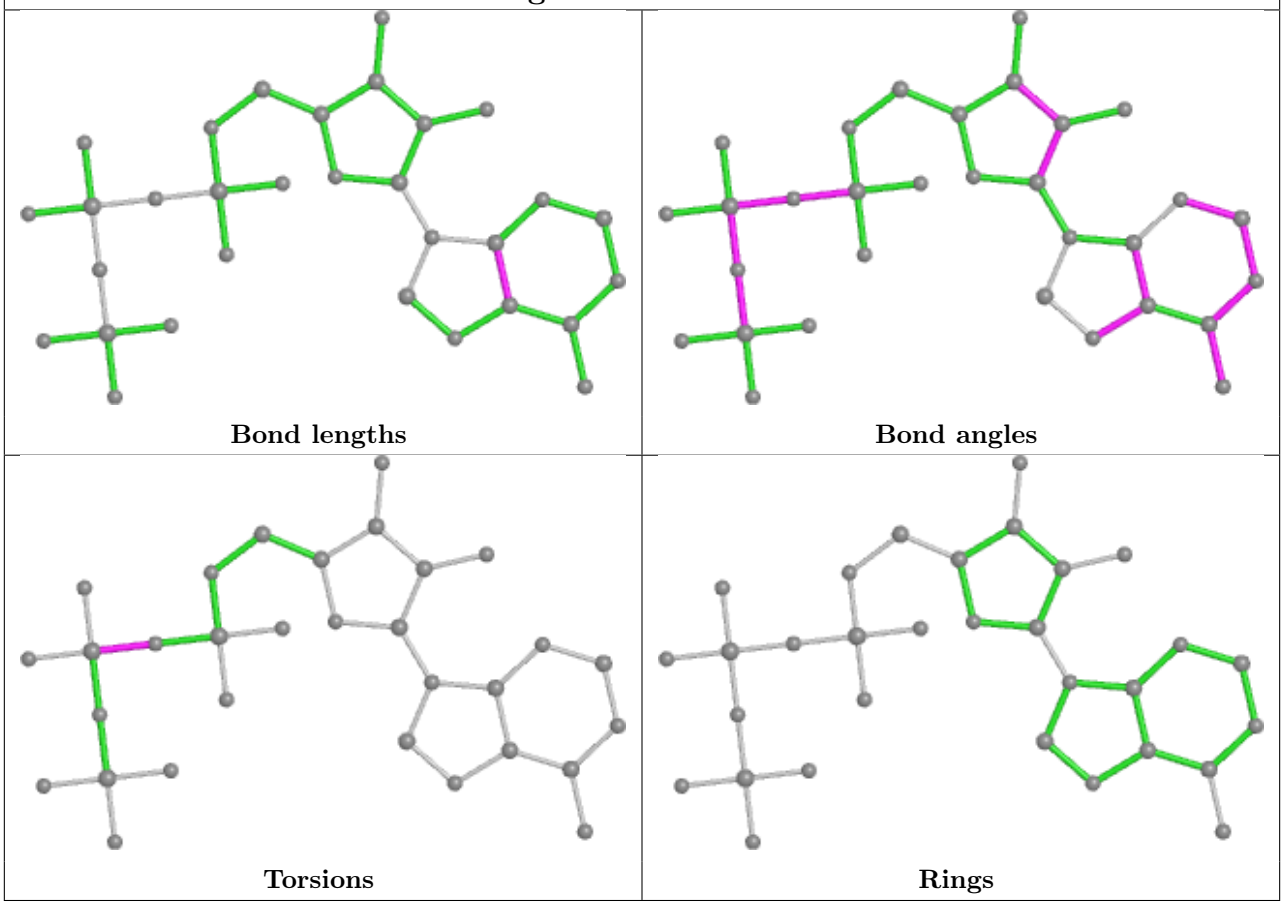
Ligand ATP Q 401



Ligand ATP N 401



Ligand ATP L 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.

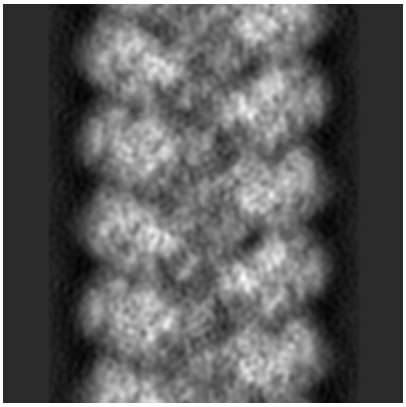
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-20076. These allow visual inspection of the internal detail of the map and identification of artifacts.

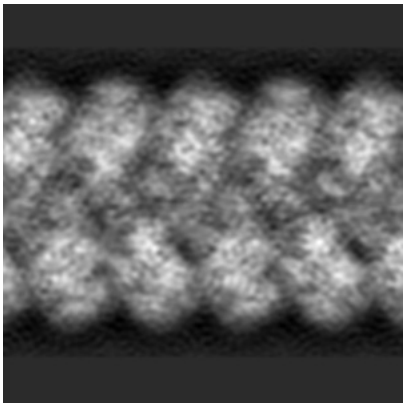
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

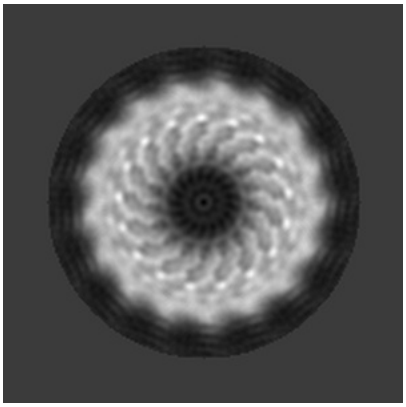
6.1.1 Primary map



X



Y

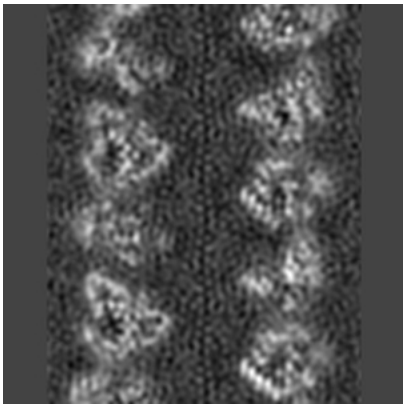


Z

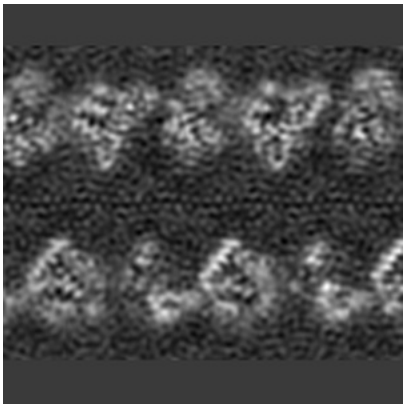
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

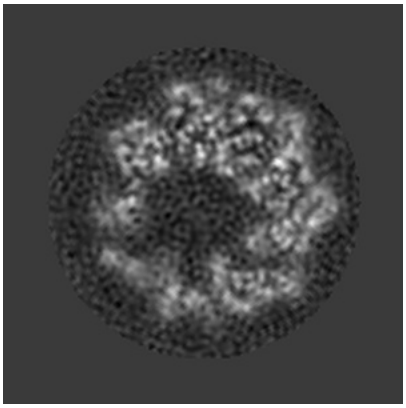
6.2.1 Primary map



X Index: 96



Y Index: 96

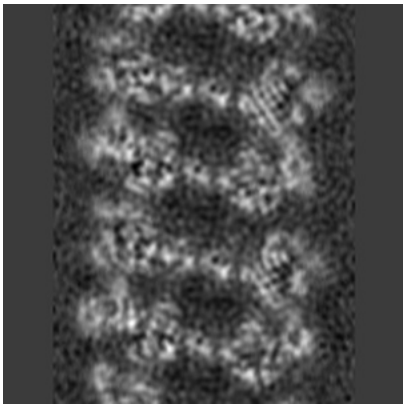


Z Index: 96

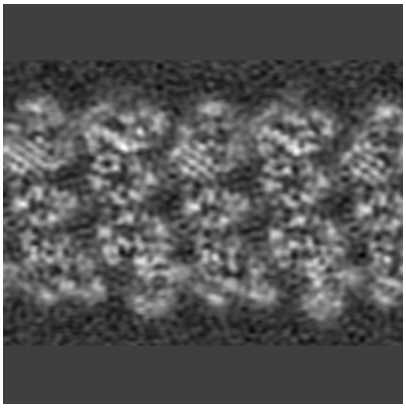
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

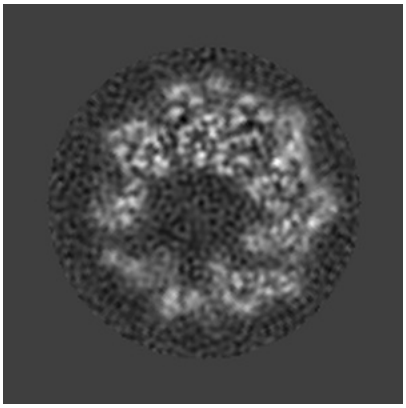
6.3.1 Primary map



X Index: 75



Y Index: 127

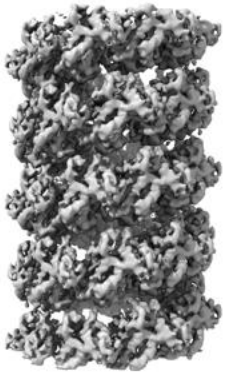


Z Index: 97

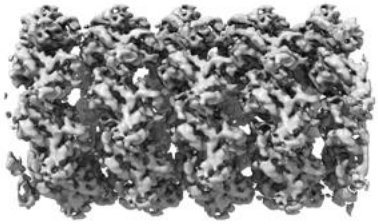
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

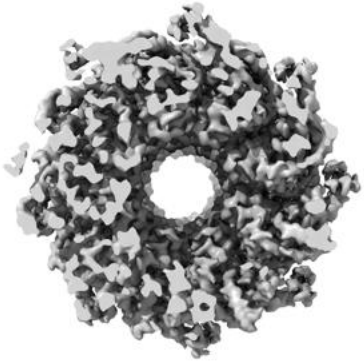
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.247. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

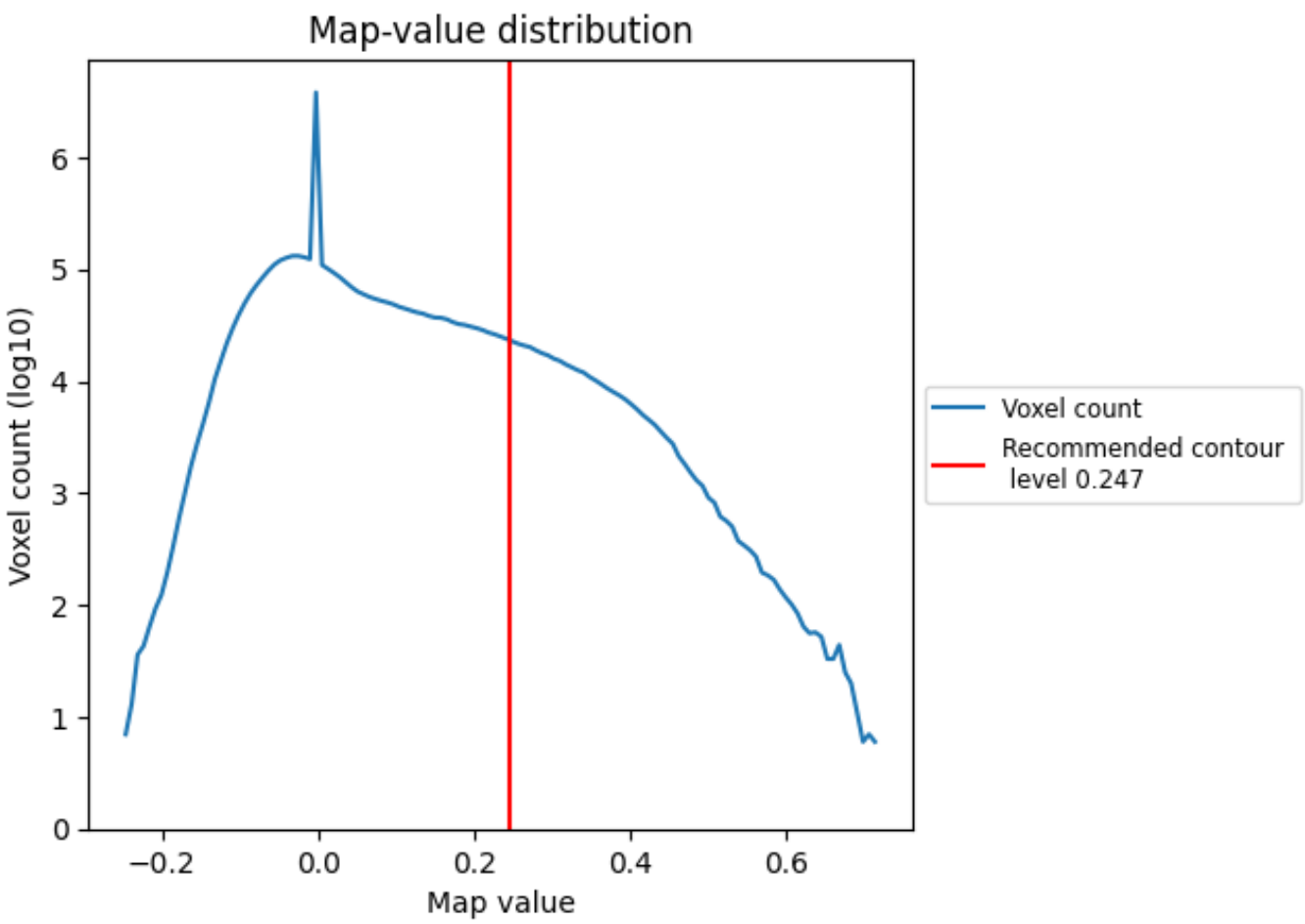
6.5 Mask visualisation (i)

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

7 Map analysis (i)

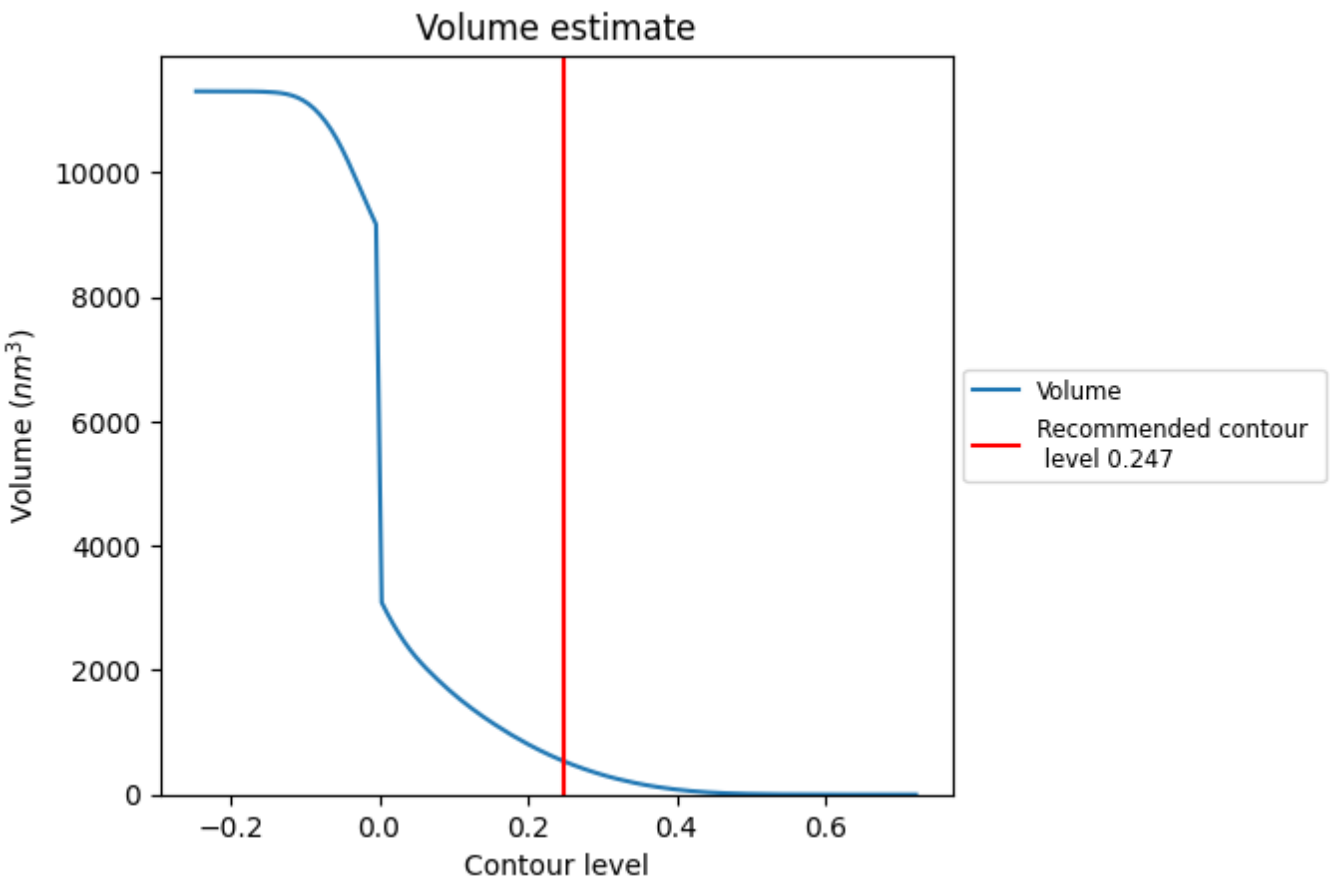
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

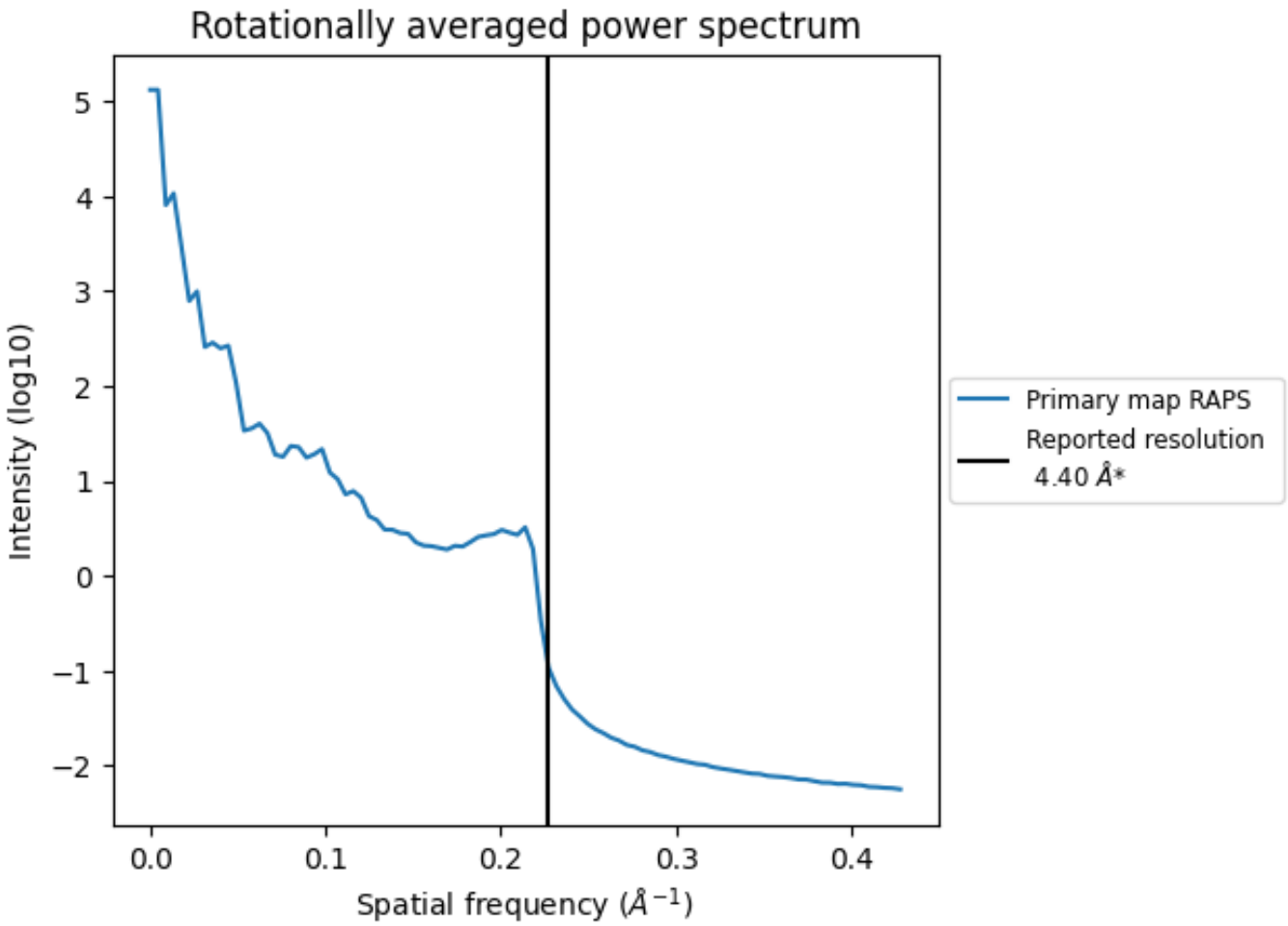
7.2 Volume estimate (i)



The volume at the recommended contour level is 543 nm^3; this corresponds to an approximate mass of 491 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.227 Å^{-1}

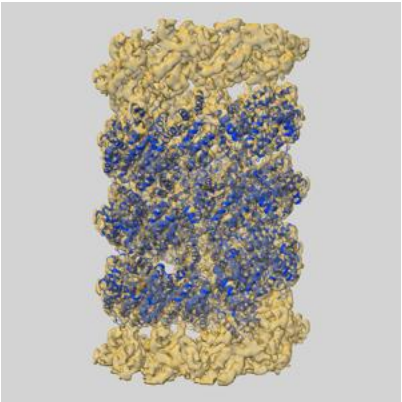
8 Fourier-Shell correlation (i)

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

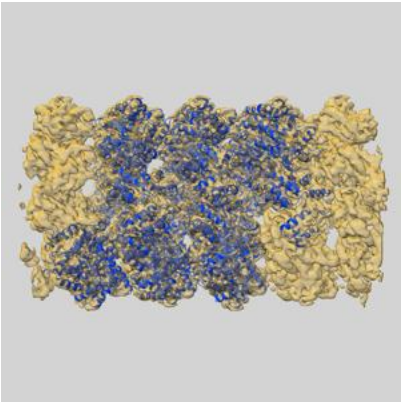
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-20076 and PDB model 6OIF. Per-residue inclusion information can be found in section 3 on page 8.

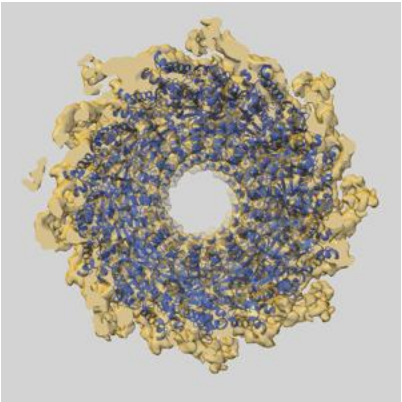
9.1 Map-model overlay (i)



X



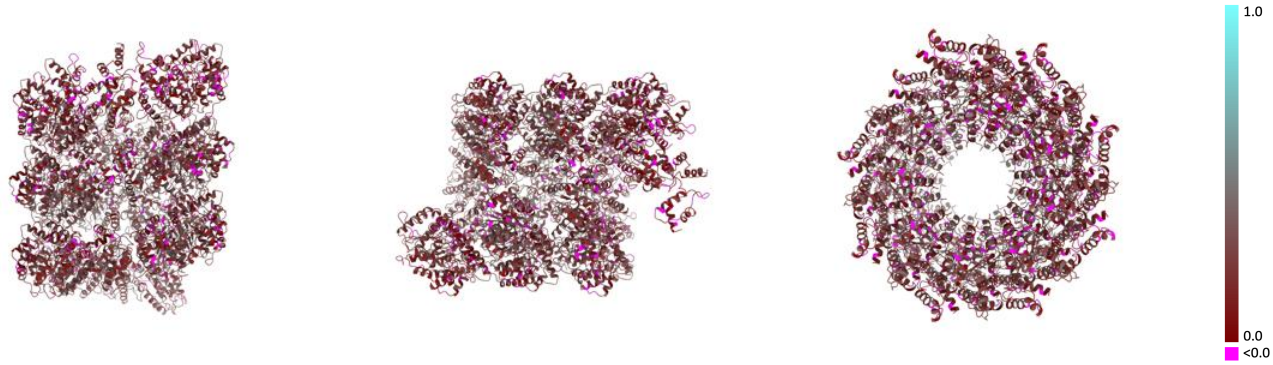
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.247 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

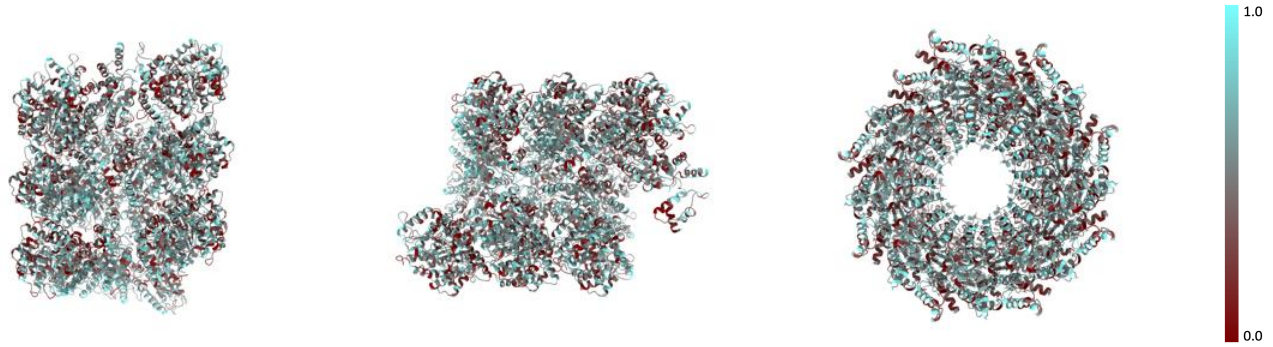
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

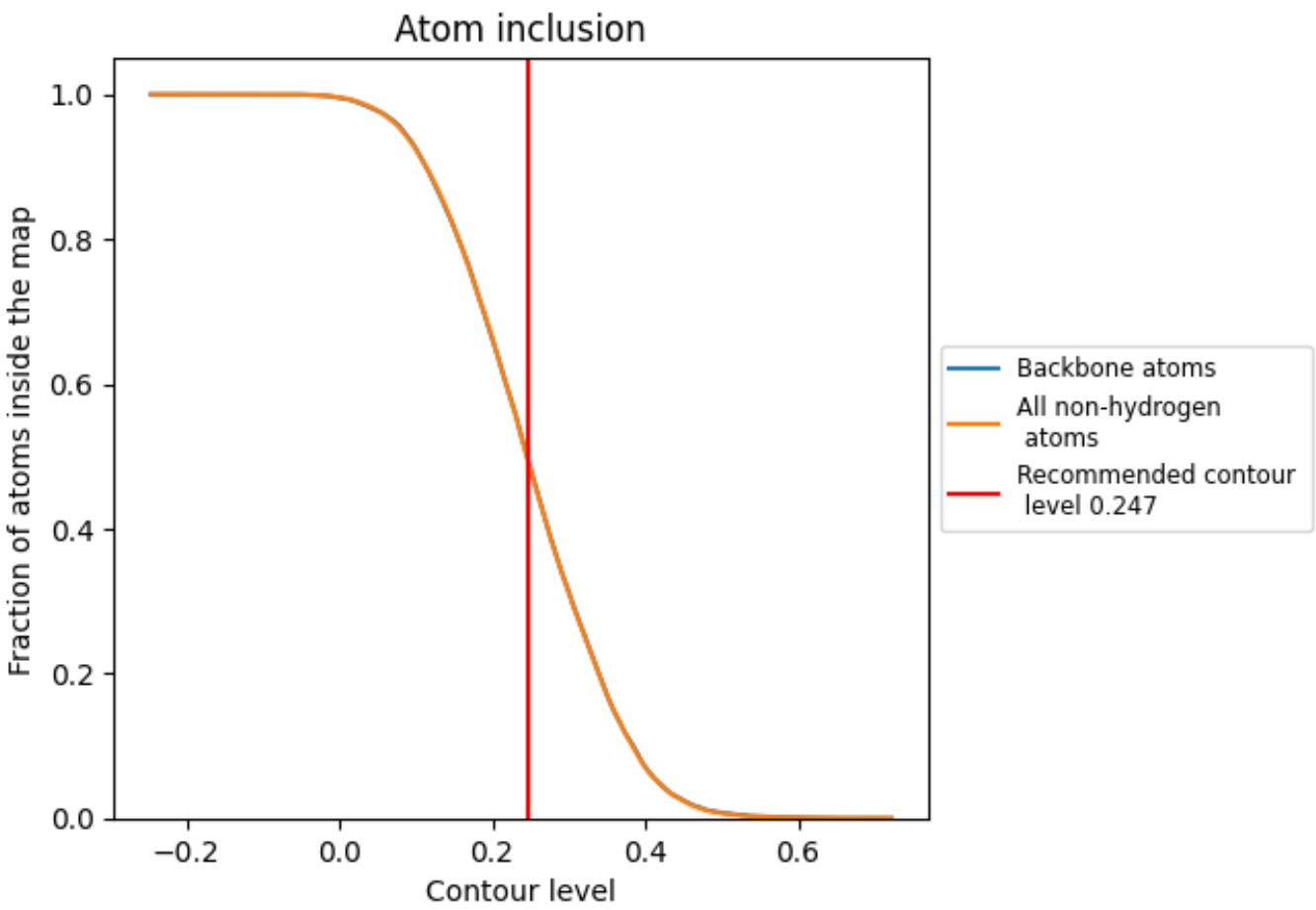
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.247).

9.4 Atom inclusion (i)



At the recommended contour level, 50% of all backbone atoms, 49% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.247) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4934	0.2210
A	0.5395	0.2600
B	0.5382	0.2550
C	0.5399	0.2560
D	0.5330	0.2530
E	0.5351	0.2550
F	0.5212	0.2460
G	0.5286	0.2550
H	0.5207	0.2430
I	0.5273	0.2490
J	0.5068	0.2340
K	0.5229	0.2440
L	0.5076	0.2240
M	0.5124	0.2400
N	0.5063	0.2140
O	0.5081	0.2290
P	0.4967	0.2020
Q	0.4989	0.2200
R	0.4793	0.1890
S	0.4858	0.2090
T	0.4732	0.1800
U	0.4819	0.1990
V	0.4526	0.1650
W	0.4749	0.1880
X	0.4440	0.1510
Y	0.4465	0.1730