



wwPDB EM Validation Summary Report ⓘ

Apr 5, 2026 – 05:37 PM UTC

PDB ID : 9YX2 / pdb_00009yx2
EMDB ID : EMD-73585
Title : Structure of the long chain acyl-CoA carboxylase complex from Mycobacterium smegmatis with ATP, bicarbonate, and propionyl-CoA
Authors : Liang, Y.; Rubinstein, J.L.
Deposited on : 2025-10-26
Resolution : 2.80 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:

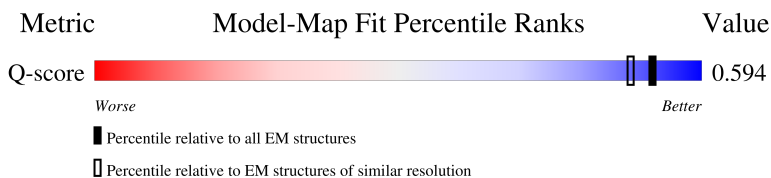
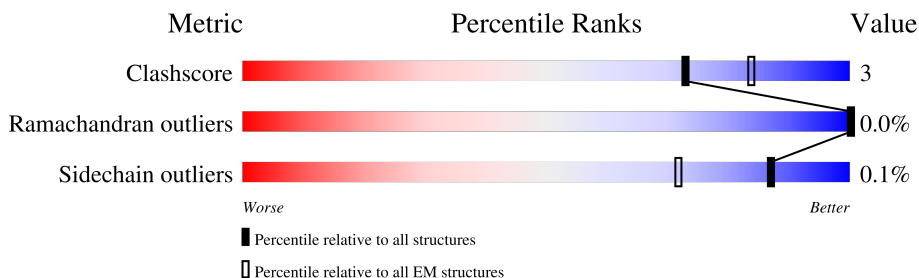
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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:
ELECTRON MICROSCOPY

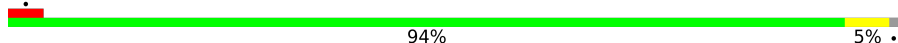
The reported resolution of this entry is 2.80 Å.

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.



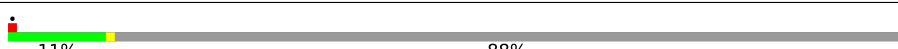
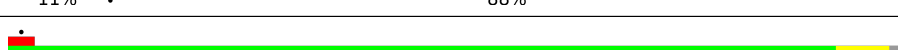
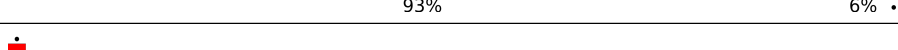
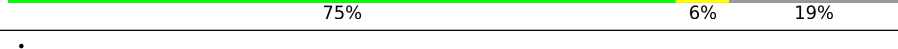
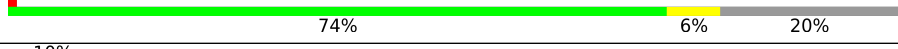
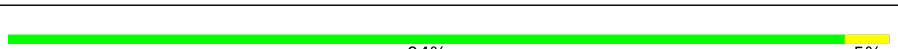
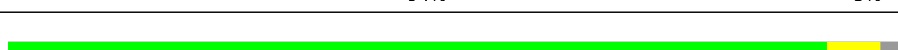
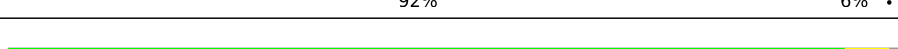
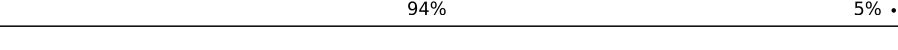
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11806 (2.30 - 3.30)

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 $\leq 5\%$. 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	598	 94% 5%
1	B	598	 75% 6% 19%
1	C	598	 5% 73% 8% 19%
1	D	598	 75% 5% 20%

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Mol	Chain	Length	Quality of chain
1	I	598	
1	J	598	
1	K	598	
1	L	598	
1	Q	598	
1	R	598	
1	S	598	
1	T	598	
2	E	94	
2	P	94	
3	F	517	
3	O	517	
4	G	542	
4	H	542	
4	M	542	
4	N	542	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	BCT	B	603	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 54893 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 Biotin-dependent acyl-coenzyme A carboxylase alpha3 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	592	Total	C	N	O	S	0	0
			4115	2593	748	765	9		
1	B	482	Total	C	N	O	S	0	0
			3423	2173	619	625	6		
1	C	482	Total	C	N	O	S	0	0
			3268	2077	604	583	4		
1	D	481	Total	C	N	O	S	0	0
			3205	2038	596	567	4		
1	I	69	Total	C	N	O	S	0	0
			435	275	75	82	3		
1	J	69	Total	C	N	O	S	0	0
			410	253	75	79	3		
1	K	69	Total	C	N	O	S	0	0
			423	262	75	84	2		
1	L	69	Total	C	N	O	S	0	0
			396	244	72	78	2		
1	Q	592	Total	C	N	O	S	0	0
			4141	2611	754	768	8		
1	R	482	Total	C	N	O	S	0	0
			3348	2119	610	614	5		
1	S	482	Total	C	N	O	S	0	0
			3280	2077	609	590	4		
1	T	478	Total	C	N	O	S	0	0
			3310	2104	606	595	5		

- Molecule 2 is a protein called Acetyl-/propionyl-coenzyme A carboxylase AccE5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	70	Total	C	N	O	S	0	0
			526	332	105	85	4		
2	P	70	Total	C	N	O	S	0	0
			526	332	105	85	4		

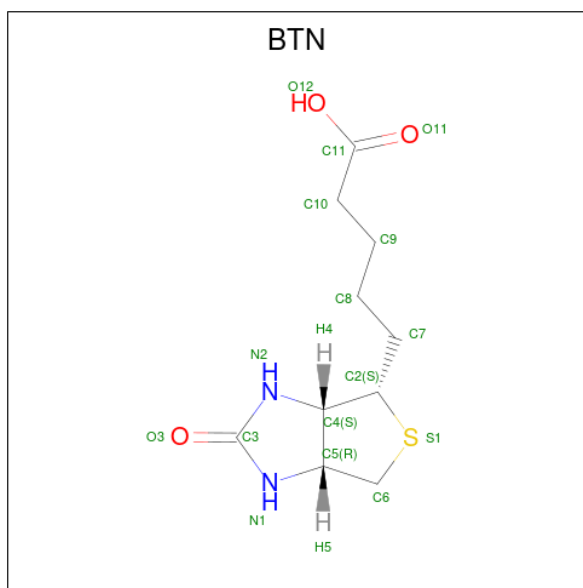
- Molecule 3 is a protein called Propionyl-CoA carboxylase beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	516	Total	C	N	O	S	0	0
			3848	2445	678	709	16		
3	O	515	Total	C	N	O	S	0	0
			3798	2419	670	694	15		

- Molecule 4 is a protein called Propionyl-CoA carboxylase beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	531	Total	C	N	O	S	0	0
			3950	2505	684	746	15		
4	H	539	Total	C	N	O	S	0	0
			3991	2530	694	753	14		
4	M	530	Total	C	N	O	S	0	0
			3939	2499	679	746	15		
4	N	539	Total	C	N	O	S	0	0
			3975	2522	689	749	15		

- Molecule 5 is BIOTIN (CCD ID: BTN) (formula: $C_{10}H_{16}N_2O_3S$) (labeled as "Ligand of Interest" by depositor).



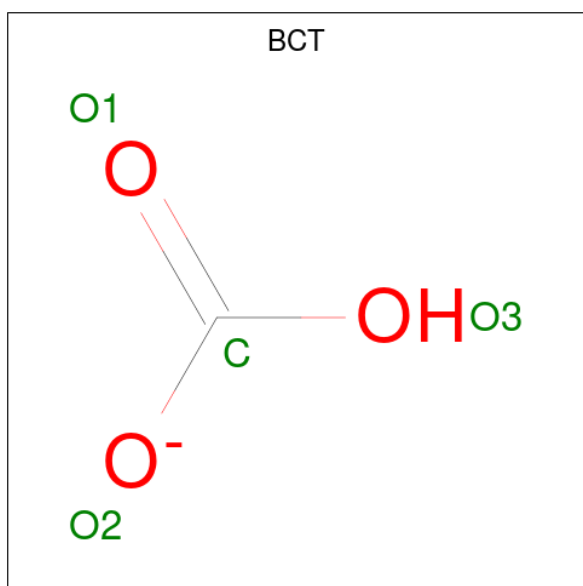
Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	N	O	S	0
			15	10	2	2	1	
5	I	1	Total	C	N	O	S	0
			15	10	2	2	1	
5	J	1	Total	C	N	O	S	0
			15	10	2	2	1	

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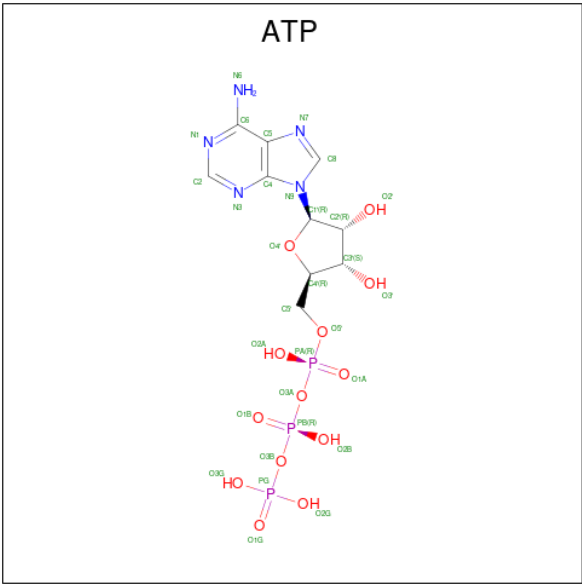
Mol	Chain	Residues	Atoms					AltConf
5	K	1	Total	C	N	O	S	0
			15	10	2	2	1	
5	L	1	Total	C	N	O	S	0
			15	10	2	2	1	
5	Q	1	Total	C	N	O	S	0
			15	10	2	2	1	

- Molecule 6 is BICARBONATE ION (CCD ID: BCT) (formula: CHO_3) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
6	A	1	Total	C	O	0
			4	1	3	
6	B	1	Total	C	O	0
			4	1	3	
6	C	1	Total	C	O	0
			4	1	3	
6	D	1	Total	C	O	0
			4	1	3	
6	Q	1	Total	C	O	0
			4	1	3	
6	R	1	Total	C	O	0
			4	1	3	
6	S	1	Total	C	O	0
			4	1	3	
6	T	1	Total	C	O	0
			4	1	3	

- Molecule 7 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
7	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
7	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
7	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
7	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
7	Q	1	Total	C	N	O	P	0
			31	10	5	13	3	
7	R	1	Total	C	N	O	P	0
			31	10	5	13	3	
7	S	1	Total	C	N	O	P	0
			31	10	5	13	3	
7	T	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 8 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

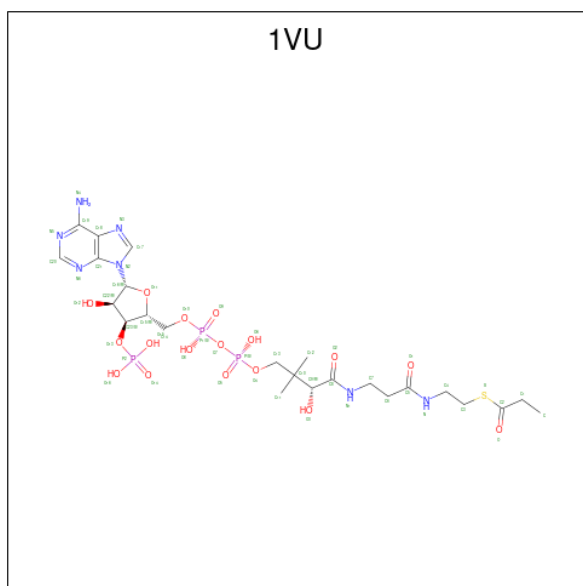
Mol	Chain	Residues	Atoms		AltConf
8	A	1	Total	Mg	0
			1	1	
8	B	1	Total	Mg	0
			1	1	

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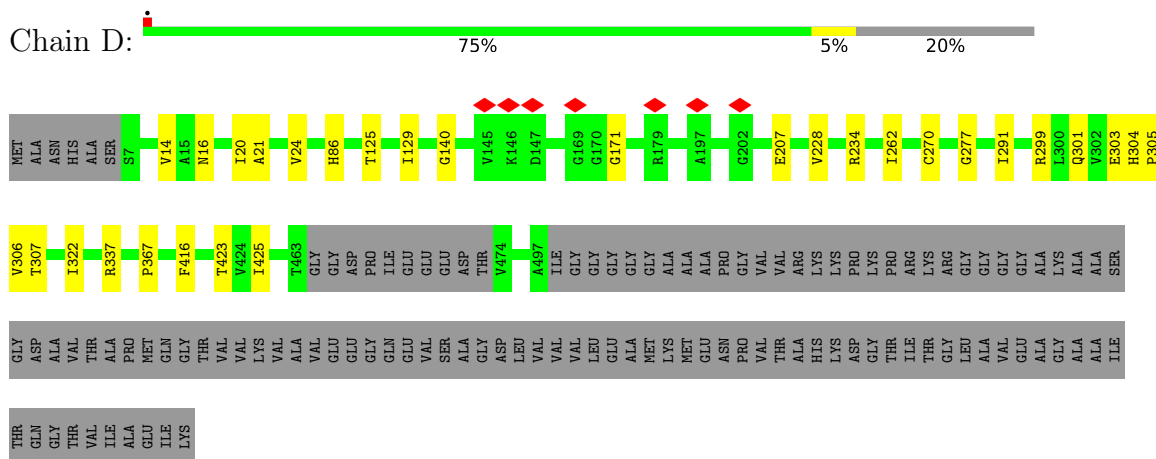
Mol	Chain	Residues	Atoms		AltConf
8	C	1	Total	Mg	0
			1	1	
8	D	1	Total	Mg	0
			1	1	
8	Q	1	Total	Mg	0
			1	1	
8	R	1	Total	Mg	0
			1	1	
8	S	1	Total	Mg	0
			1	1	
8	T	1	Total	Mg	0
			1	1	

- Molecule 9 is propionyl Coenzyme A (CCD ID: 1VU) (formula: $C_{24}H_{40}N_7O_{17}P_3S$) (labeled as "Ligand of Interest" by depositor).

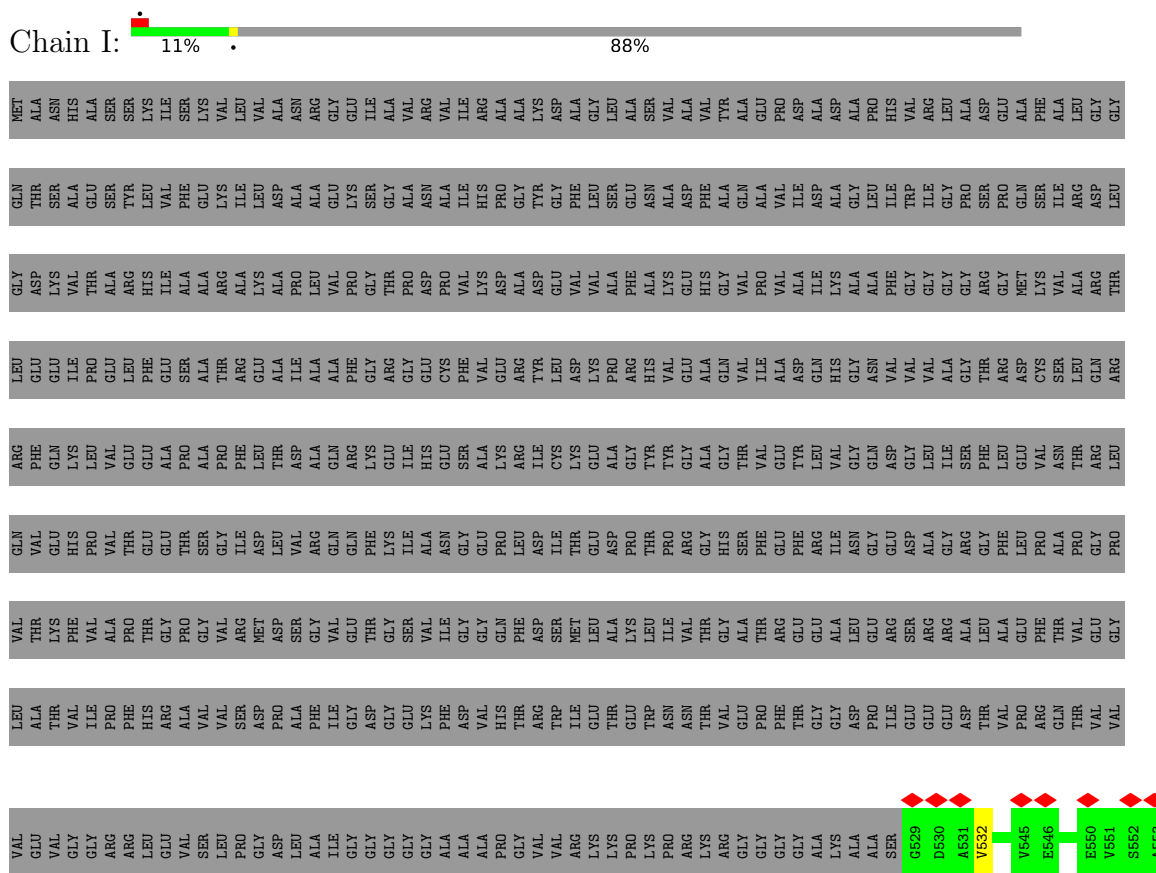


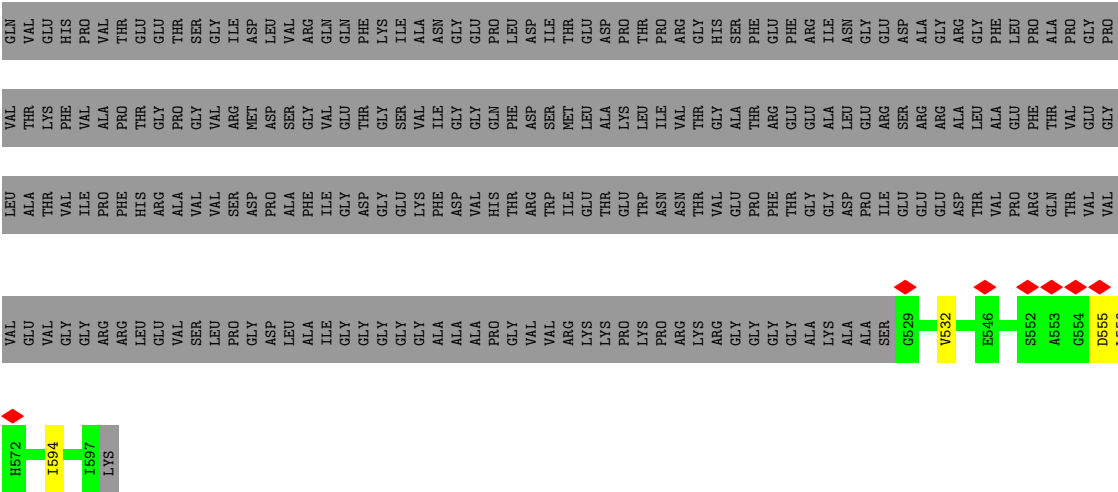
Mol	Chain	Residues	Atoms						AltConf
9	G	1	Total	C	N	O	P	S	0
			52	24	7	17	3	1	
9	G	1	Total	C	N	O	P	S	0
			52	24	7	17	3	1	
9	H	1	Total	C	N	O	P	S	0
			52	24	7	17	3	1	
9	H	1	Total	C	N	O	P	S	0
			52	24	7	17	3	1	

- Molecule 1: Biotin-dependent acyl-coenzyme A carboxylase alpha3 subunit

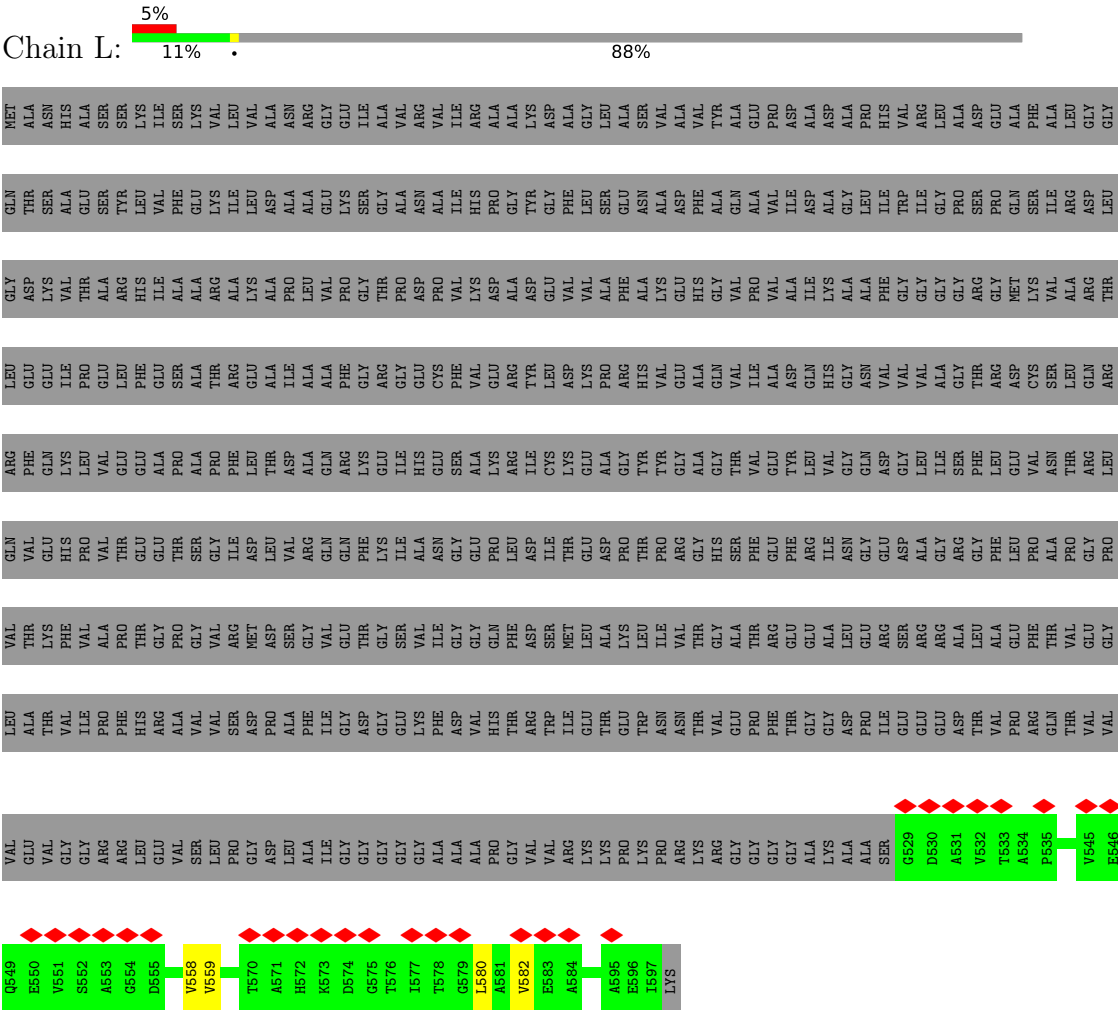


- Molecule 1: Biotin-dependent acyl-coenzyme A carboxylase alpha3 subunit



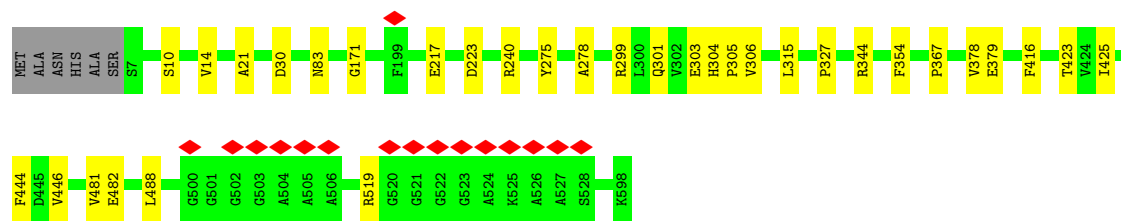


• Molecule 1: Biotin-dependent acyl-coenzyme A carboxylase alpha3 subunit



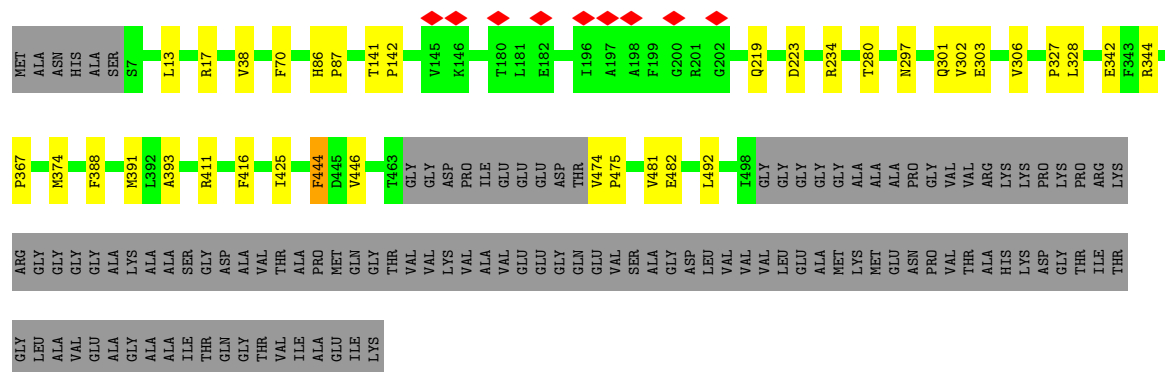
• Molecule 1: Biotin-dependent acyl-coenzyme A carboxylase alpha3 subunit

Chain Q: 93% 6%



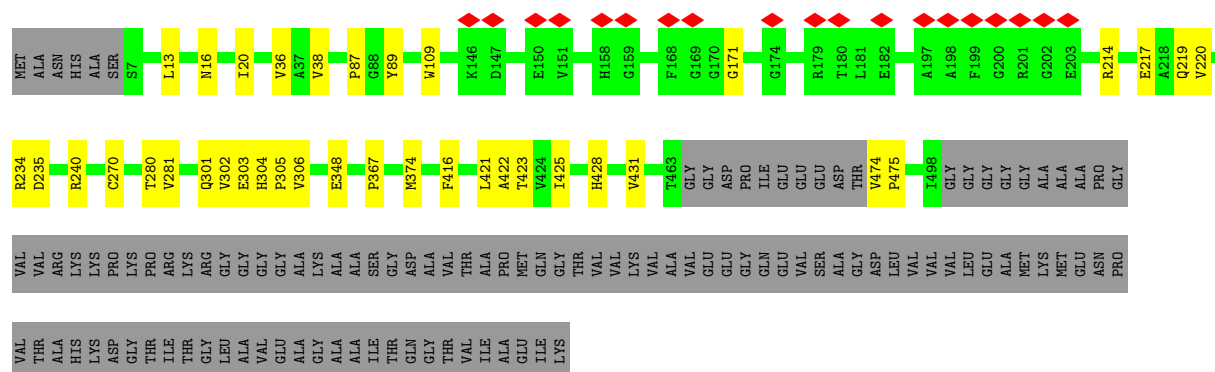
- Molecule 1: Biotin-dependent acyl-coenzyme A carboxylase alpha3 subunit

Chain R:



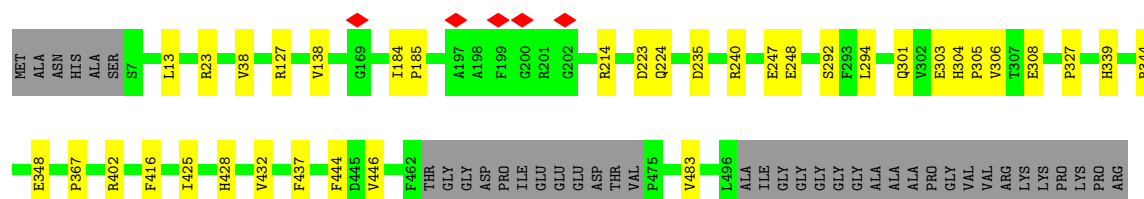
- Molecule 1: Biotin-dependent acyl-coenzyme A carboxylase alpha3 subunit

Chain S:



- Molecule 1: Biotin-dependent acyl-coenzyme A carboxylase alpha3 subunit

Chain T:



LYS	ARG	GLY	GLY	GLY	GLY	ALA	LYS	LYS	ALA	ALA	ALA	SER	SER	GLY	ASP	ALA	VAL	THR	THR	ALA	ALA	PRO	MET	GLN	GLY	THR	THR	VAL	VAL	LYS	VAL	VAL	ALA	ALA	VAL	GLU	GLU	GLY	GLN	GLU	VAL	SER	ALA	GLY	ASP	LEU	VAL	VAL	VAL	LEU	GLU	ALA	MET	MET	LYS	MET	GLU	ASN	PRO	PRO	VAL	THR	THR	ALA	ALA	HIS	LYS	LYS	ASP	GLY	THR	THR	ILE
THR	GLY	LEU	ALA	VAL	GLU	GLY	ALA	ALA	ALA	ALA	ALA	ILE	THR	THR	GLN	GLY	THR	THR	VAL	VAL	ILE	ALA	ALA	GLU	ILE	LYS																																															

- Molecule 2: Acetyl-/propionyl-coenzyme A carboxylase AccE5



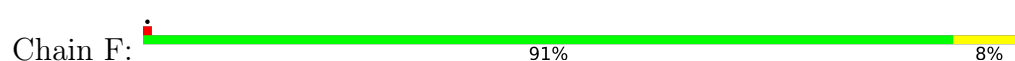
MET	SER	GLY	GLY	ASN	ASP	SER	THR	THR	VAL	SER	SER	ILE	THR	GLY	GLY	VAL	VAL	GLN	ALA	ASP	VAL	THR	ASP	GLU	GLY	ALA	LYS	VAL	ALA	ALA	D25	I30	P37	T38	E41	M42	L45	G54	G55	P56	A57	E58	P59	V60	K61	K62	R94
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- Molecule 2: Acetyl-/propionyl-coenzyme A carboxylase AccE5



MET	SER	GLY	ALA	ASN	ASP	SER	THR	THR	VAL	SER	SER	ILE	THR	GLY	GLY	VAL	VAL	GLN	ALA	ASP	VAL	THR	ASP	GLU	GLY	ALA	LYS	VAL	ALA	ALA	D25	G35	E36	P37	T38	P39	M42	G54	G55	P56	A57	E58	P59	V60	K61	K62	R89	M92	R93	R94
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- Molecule 3: Propionyl-CoA carboxylase beta chain



MET	T2	L19	G25	V29	R41	A42	R43	L48	V88	H91	M117	C120	D127	S128	A129	D135	A136	V137	T138	R154	V157	P158	E159	S174	P175	I192	T193	N247	D250	D278	N279	L330	D340	F358	V359	V360	M366
R379	I387	M410	L415	S416	P424	V430	P445	N448	A449	T469	P470	D480	L515	F516	L517																						

- Molecule 3: Propionyl-CoA carboxylase beta chain



MET	THR	N3	V115	C120	A136	R154	A168	S174	P175	F191	I192	T193	V197	V201	L211	Q235	D239	H285	N336	D340	E371	R379	R400	K401	A402	Y407	R427	V430	Q438	L439	L440	V441	L517
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- Molecule 4: Propionyl-CoA carboxylase beta chain



MET	THR	SER	VAL	THR	GLU	PRO	SER	ALA	GLU	HIS	G12	R28	T32	P86	V112	G147	L179	I180	M181	G186	V189	Y190	S191	P192	V199	F252	T285	E292	M307	R313	V346	A347	L381	V385	Y408	R423	Q450	A459
F462	V463	Y464	D479	L483	I525	E526	R527	K528	I529	G538	L542																											

- Molecule 4: Propionyl-CoA carboxylase beta chain

Chain H:  94% 5%



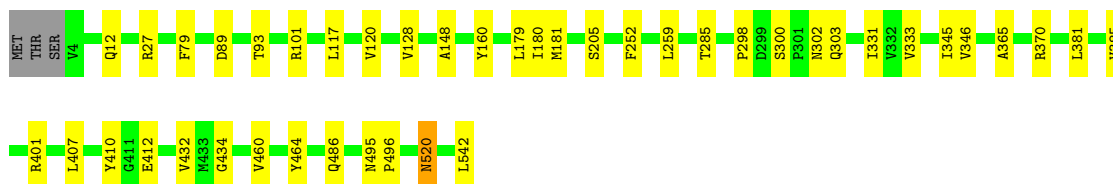
- Molecule 4: Propionyl-CoA carboxylase beta chain

Chain M:  92% 6%



- Molecule 4: Propionyl-CoA carboxylase beta chain

Chain N:  92% 8%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	46806	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	20000	Depositor
Magnification	130000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	1.179	Depositor
Minimum map value	-0.060	Depositor
Average map value	0.013	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.16	Depositor
Map size (Å)	446.4, 446.4, 446.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, BTN, 1VU, BCT, 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	0.33	0/4191	0.34	0/5721
1	B	0.33	0/3494	0.33	0/4772
1	C	0.29	0/3335	0.36	0/4573
1	D	0.28	0/3271	0.33	0/4490
1	I	0.18	0/437	0.29	0/600
1	J	0.19	0/412	0.36	0/566
1	K	0.19	0/425	0.34	0/585
1	L	0.18	0/397	0.32	0/547
1	Q	0.34	0/4219	0.33	0/5761
1	R	0.35	0/3416	0.38	0/4672
1	S	0.32	0/3347	0.33	0/4587
1	T	0.33	0/3380	0.36	0/4624
2	E	0.39	0/540	0.34	0/733
2	P	0.39	0/540	0.36	0/733
3	F	0.44	0/3928	0.40	0/5341
3	O	0.44	0/3878	0.39	0/5279
4	G	0.45	0/4026	0.41	0/5483
4	H	0.44	0/4069	0.41	0/5546
4	M	0.45	0/4015	0.38	0/5469
4	N	0.45	0/4053	0.41	0/5525
All	All	0.38	0/55373	0.37	0/75607

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	4115	0	3930	27	0
1	B	3423	0	3261	28	0
1	C	3268	0	3007	29	0
1	D	3205	0	2913	20	0
1	I	435	0	426	2	0
1	J	410	0	352	1	0
1	K	423	0	380	2	0
1	L	396	0	329	2	0
1	Q	4141	0	3991	25	0
1	R	3348	0	3131	27	0
1	S	3280	0	3016	28	0
1	T	3310	0	3099	24	0
2	E	526	0	509	5	0
2	P	526	0	509	6	0
3	F	3848	0	3797	29	0
3	O	3798	0	3728	16	0
4	G	3950	0	3906	25	0
4	H	3991	0	3927	16	0
4	M	3939	0	3891	22	0
4	N	3975	0	3906	26	0
5	A	15	0	15	0	0
5	I	15	0	15	0	0
5	J	15	0	15	0	0
5	K	15	0	15	0	0
5	L	15	0	15	0	0
5	Q	15	0	15	0	0
6	A	4	0	1	1	0
6	B	4	0	1	2	0
6	C	4	0	1	0	0
6	D	4	0	1	1	0
6	Q	4	0	1	1	0
6	R	4	0	1	1	0
6	S	4	0	1	0	0
6	T	4	0	1	1	0
7	A	31	0	12	1	0
7	B	31	0	12	0	0
7	C	31	0	12	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	D	31	0	12	1	0
7	Q	31	0	12	1	0
7	R	31	0	12	1	0
7	S	31	0	12	1	0
7	T	31	0	12	1	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
8	C	1	0	0	0	0
8	D	1	0	0	0	0
8	Q	1	0	0	0	0
8	R	1	0	0	0	0
8	S	1	0	0	0	0
8	T	1	0	0	0	0
9	G	104	0	76	7	0
9	H	104	0	76	12	0
All	All	54893	0	52354	351	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 3.

The worst 5 of 351 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:B:453:THR:OG1	1:B:454:GLU:OE1	1.84	0.96
1:T:301:GLN:OE1	6:T:602:BCT:O3	1.88	0.90
1:C:337:ARG:HH21	1:D:337:ARG:HB3	1.37	0.90
9:H:602:1VU:H37	4:M:148:ALA:H	1.36	0.90
1:T:127:ARG:NH2	1:T:138:VAL:O	2.09	0.86

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	590/598 (99%)	577 (98%)	13 (2%)	0	100	100
1	B	478/598 (80%)	468 (98%)	10 (2%)	0	100	100
1	C	478/598 (80%)	466 (98%)	11 (2%)	1 (0%)	43	72
1	D	477/598 (80%)	466 (98%)	11 (2%)	0	100	100
1	I	67/598 (11%)	67 (100%)	0	0	100	100
1	J	67/598 (11%)	66 (98%)	1 (2%)	0	100	100
1	K	67/598 (11%)	64 (96%)	3 (4%)	0	100	100
1	L	67/598 (11%)	67 (100%)	0	0	100	100
1	Q	590/598 (99%)	581 (98%)	9 (2%)	0	100	100
1	R	478/598 (80%)	469 (98%)	9 (2%)	0	100	100
1	S	478/598 (80%)	470 (98%)	8 (2%)	0	100	100
1	T	474/598 (79%)	468 (99%)	6 (1%)	0	100	100
2	E	68/94 (72%)	65 (96%)	3 (4%)	0	100	100
2	P	68/94 (72%)	63 (93%)	5 (7%)	0	100	100
3	F	514/517 (99%)	502 (98%)	12 (2%)	0	100	100
3	O	513/517 (99%)	498 (97%)	15 (3%)	0	100	100
4	G	529/542 (98%)	519 (98%)	9 (2%)	1 (0%)	43	72
4	H	537/542 (99%)	525 (98%)	12 (2%)	0	100	100
4	M	528/542 (97%)	516 (98%)	12 (2%)	0	100	100
4	N	537/542 (99%)	526 (98%)	11 (2%)	0	100	100
All	All	7605/10566 (72%)	7443 (98%)	160 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	439	GLY
4	G	462	PHE

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	370/453 (82%)	369 (100%)	1 (0%)	86	95
1	B	314/453 (69%)	314 (100%)	0	100	100
1	C	269/453 (59%)	269 (100%)	0	100	100
1	D	255/453 (56%)	255 (100%)	0	100	100
1	I	37/453 (8%)	37 (100%)	0	100	100
1	J	27/453 (6%)	27 (100%)	0	100	100
1	K	32/453 (7%)	32 (100%)	0	100	100
1	L	23/453 (5%)	23 (100%)	0	100	100
1	Q	380/453 (84%)	380 (100%)	0	100	100
1	R	295/453 (65%)	294 (100%)	1 (0%)	86	95
1	S	273/453 (60%)	273 (100%)	0	100	100
1	T	288/453 (64%)	288 (100%)	0	100	100
2	E	49/76 (64%)	49 (100%)	0	100	100
2	P	49/76 (64%)	49 (100%)	0	100	100
3	F	386/412 (94%)	386 (100%)	0	100	100
3	O	374/412 (91%)	374 (100%)	0	100	100
4	G	405/436 (93%)	404 (100%)	1 (0%)	87	96
4	H	406/436 (93%)	406 (100%)	0	100	100
4	M	404/436 (93%)	404 (100%)	0	100	100
4	N	403/436 (92%)	402 (100%)	1 (0%)	87	96
All	All	5039/8156 (62%)	5035 (100%)	4 (0%)	87	97

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	221	ILE
4	G	462	PHE
4	N	520	ASN
1	R	444	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
3	O	224	HIS
1	R	225	HIS

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Mol	Chain	Res	Type
1	S	456	ASN
1	R	319	GLN
4	H	167	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 34 ligands modelled in this entry, 8 are monoatomic - leaving 26 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	$\# Z > 2$
7	ATP	S	601	8	32,33,33	0.63	1 (3%)	48,52,52	0.71	0
6	BCT	B	603	-	3,3,3	1.15	0	2,3,3	4.20	2 (100%)
9	1VU	H	601	-	52,54,54	0.51	0	73,80,80	0.90	3 (4%)
5	BTN	I	601	1	15,16,17	6.48	11 (73%)	20,21,23	2.71	8 (40%)
7	ATP	A	603	8	32,33,33	0.45	0	48,52,52	0.72	0
6	BCT	A	602	-	3,3,3	1.22	0	2,3,3	4.22	1 (50%)
5	BTN	L	601	1	15,16,17	6.54	11 (73%)	20,21,23	2.75	8 (40%)
5	BTN	A	601	1	15,16,17	6.64	11 (73%)	20,21,23	3.13	10 (50%)
7	ATP	C	601	8	32,33,33	0.43	0	48,52,52	0.81	4 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	BCT	D	603	-	3,3,3	1.12	0	2,3,3	4.25	2 (100%)
9	1VU	G	602	-	52,54,54	0.47	0	73,80,80	0.89	2 (2%)
7	ATP	Q	603	8	32,33,33	0.46	0	48,52,52	0.72	2 (4%)
9	1VU	H	602	-	52,54,54	0.48	0	73,80,80	0.82	1 (1%)
6	BCT	Q	602	-	3,3,3	1.15	0	2,3,3	4.24	2 (100%)
6	BCT	T	602	-	3,3,3	1.13	0	2,3,3	4.10	2 (100%)
7	ATP	D	601	8	32,33,33	0.59	1 (3%)	48,52,52	0.75	2 (4%)
6	BCT	S	603	-	3,3,3	1.13	0	2,3,3	4.18	2 (100%)
5	BTN	Q	601	1	15,16,17	6.52	11 (73%)	20,21,23	2.76	8 (40%)
6	BCT	R	603	-	3,3,3	1.17	0	2,3,3	4.11	2 (100%)
7	ATP	T	601	8	32,33,33	0.42	0	48,52,52	0.72	3 (6%)
7	ATP	B	601	8	32,33,33	0.67	2 (6%)	48,52,52	0.72	1 (2%)
9	1VU	G	601	-	52,54,54	0.49	0	73,80,80	0.91	3 (4%)
5	BTN	K	601	1	15,16,17	6.51	11 (73%)	20,21,23	2.75	8 (40%)
7	ATP	R	601	8	32,33,33	0.91	2 (6%)	48,52,52	0.77	3 (6%)
5	BTN	J	601	1	15,16,17	6.52	11 (73%)	20,21,23	2.70	8 (40%)
6	BCT	C	603	-	3,3,3	1.12	0	2,3,3	4.16	2 (100%)

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
7	ATP	A	603	8	-	2/22/38/38	0/3/3/3
9	1VU	H	602	-	-	16/53/69/69	0/3/3/3
7	ATP	B	601	8	-	9/22/38/38	0/3/3/3
5	BTN	L	601	1	-	3/6/27/28	0/2/2/2
9	1VU	G	601	-	-	12/53/69/69	0/3/3/3
5	BTN	K	601	1	-	1/6/27/28	0/2/2/2
5	BTN	A	601	1	-	1/6/27/28	0/2/2/2
7	ATP	C	601	8	-	8/22/38/38	0/3/3/3
7	ATP	D	601	8	-	3/22/38/38	0/3/3/3
7	ATP	R	601	8	-	4/22/38/38	0/3/3/3
7	ATP	S	601	8	-	3/22/38/38	0/3/3/3
9	1VU	H	601	-	-	12/53/69/69	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BTN	J	601	1	-	2/6/27/28	0/2/2/2
7	ATP	T	601	8	-	9/22/38/38	0/3/3/3
9	1VU	G	602	-	-	10/53/69/69	0/3/3/3
7	ATP	Q	603	8	-	3/22/38/38	0/3/3/3
5	BTN	Q	601	1	-	3/6/27/28	0/2/2/2
5	BTN	I	601	1	-	0/6/27/28	0/2/2/2

The worst 5 of 72 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	601	BTN	C6-S1	-13.65	1.43	1.81
5	I	601	BTN	C6-S1	-13.48	1.43	1.81
5	L	601	BTN	C6-S1	-13.48	1.43	1.81
5	J	601	BTN	C6-S1	-13.41	1.44	1.81
5	K	601	BTN	C6-S1	-13.41	1.44	1.81

The worst 5 of 89 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	601	BTN	C4-C5-N1	7.17	110.40	102.43
5	A	601	BTN	C6-S1-C2	7.17	104.90	89.98
5	L	601	BTN	C6-S1-C2	6.78	104.08	89.98
5	I	601	BTN	C6-S1-C2	6.76	104.05	89.98
5	K	601	BTN	C6-S1-C2	6.43	103.36	89.98

There are no chirality outliers.

5 of 101 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	L	601	BTN	S1-C2-C7-C8
5	L	601	BTN	C4-C2-C7-C8
5	Q	601	BTN	C9-C10-C11-O11
5	Q	601	BTN	S1-C2-C7-C8
5	Q	601	BTN	C4-C2-C7-C8

There are no ring outliers.

17 monomers are involved in 34 short contacts:

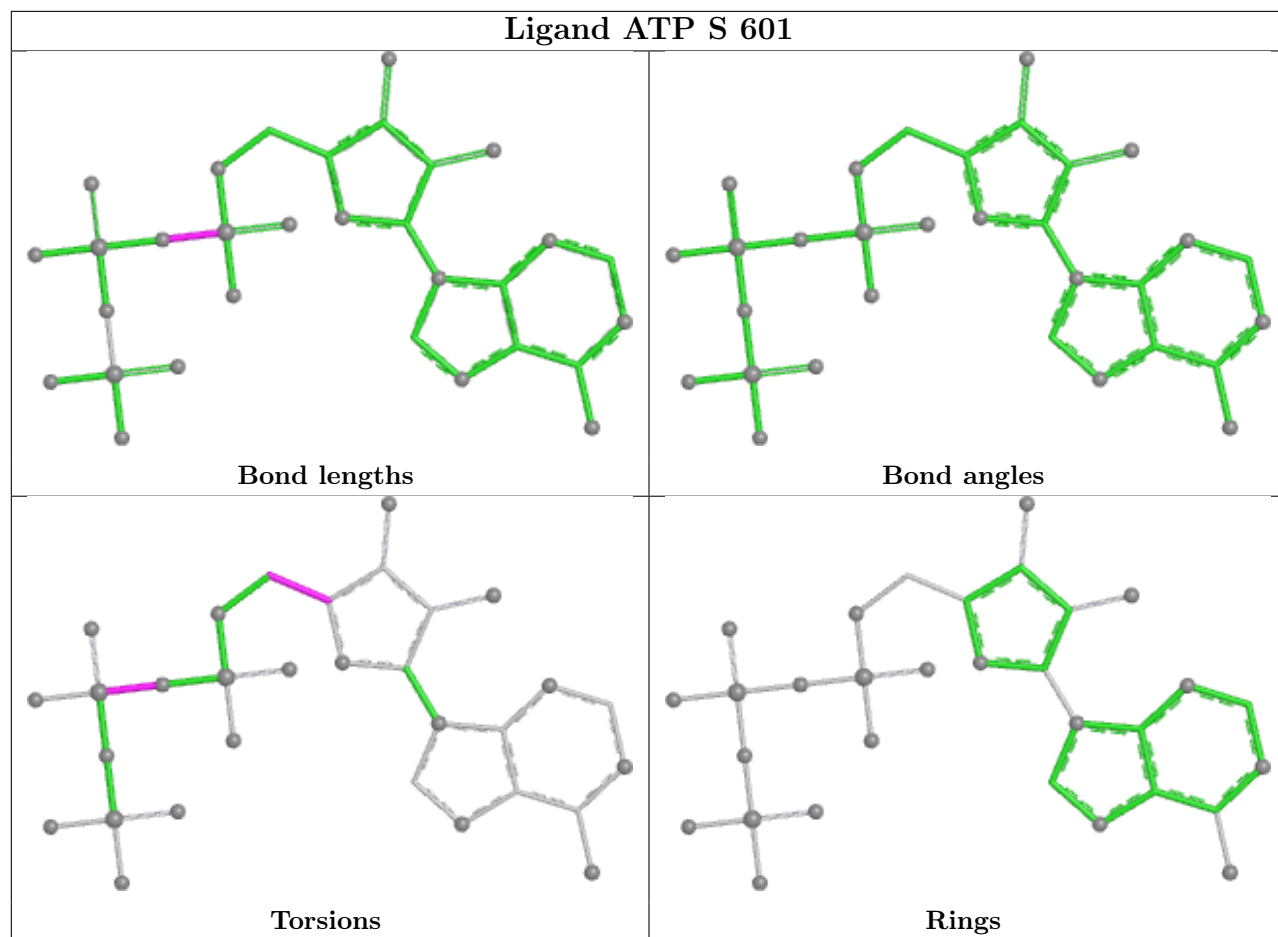
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	S	601	ATP	1	0

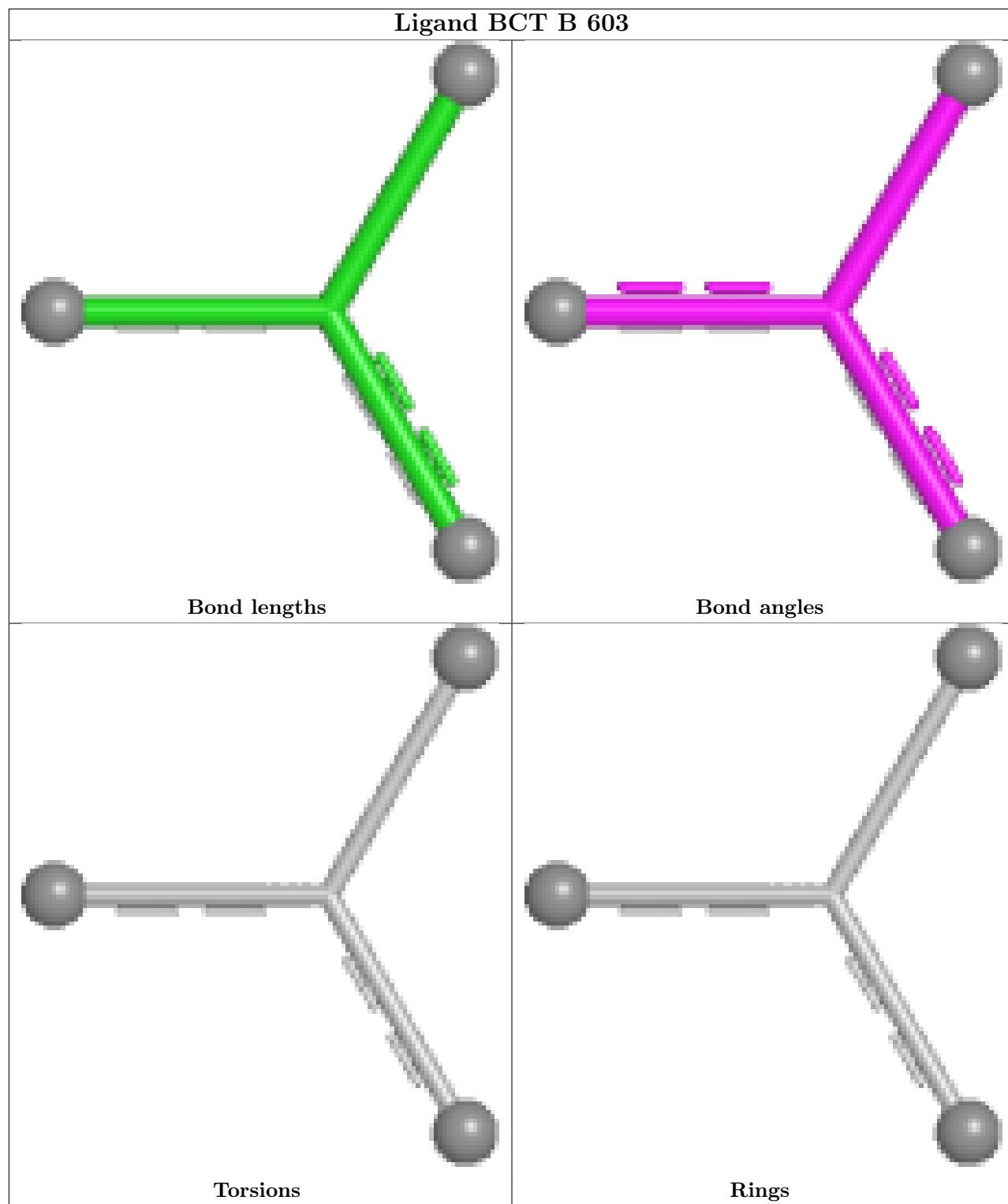
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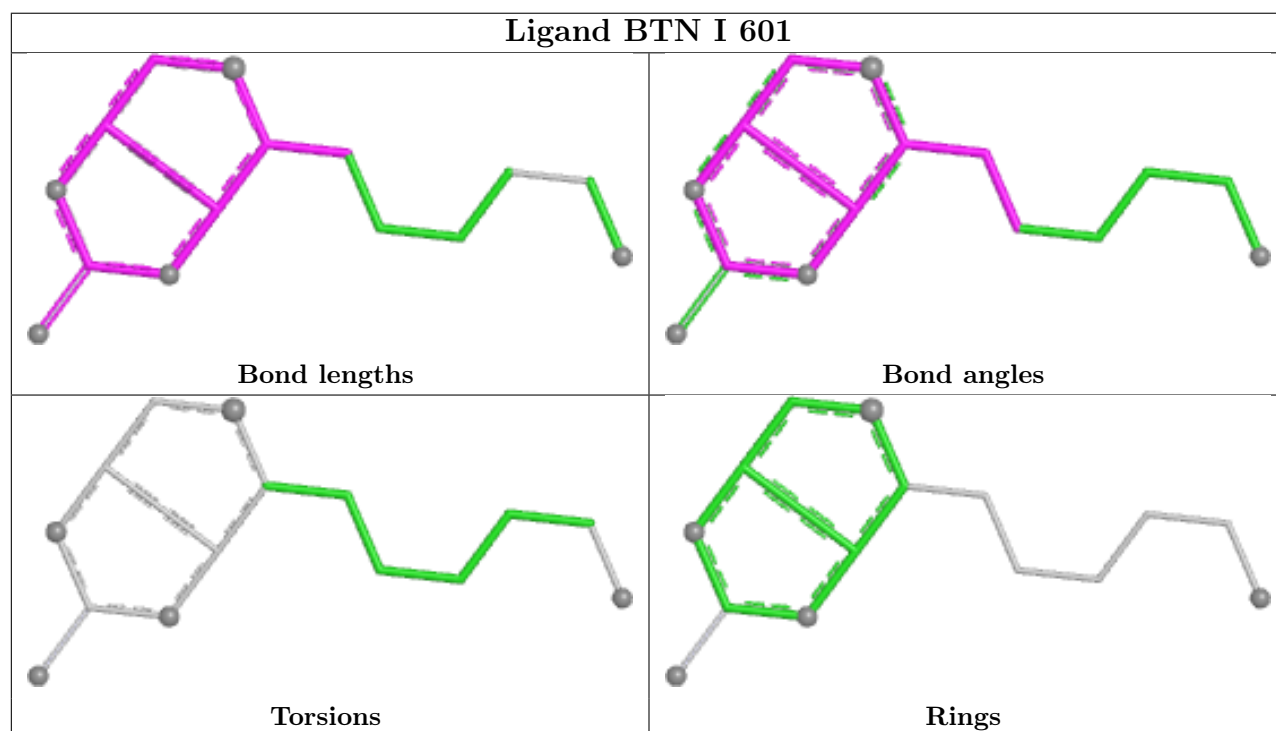
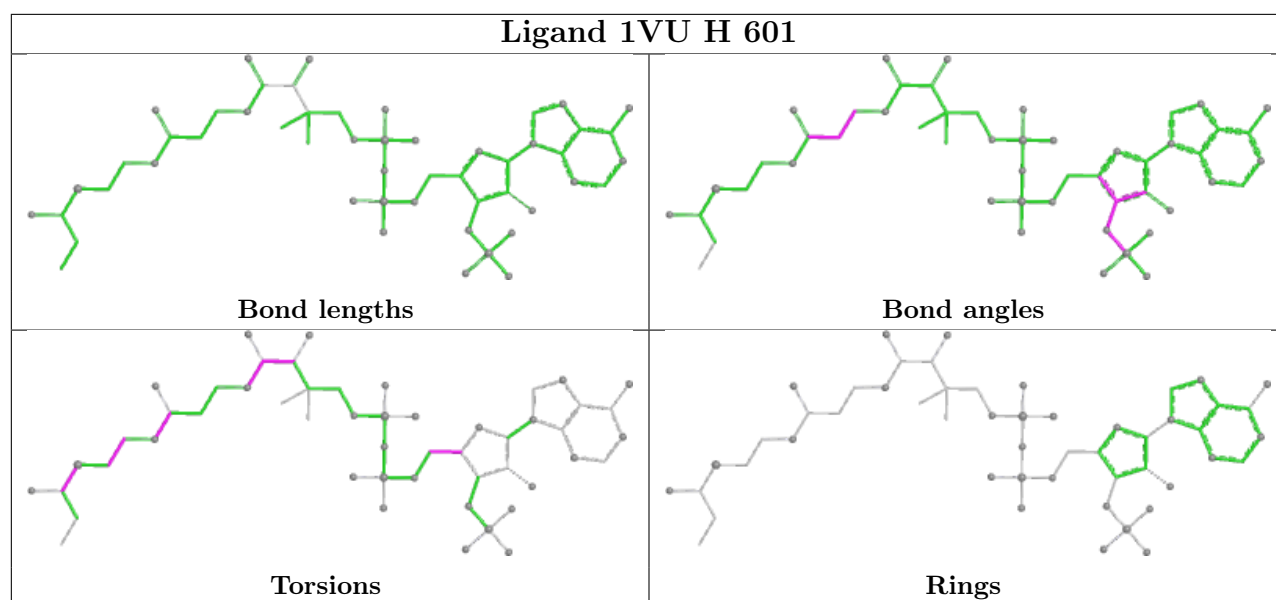
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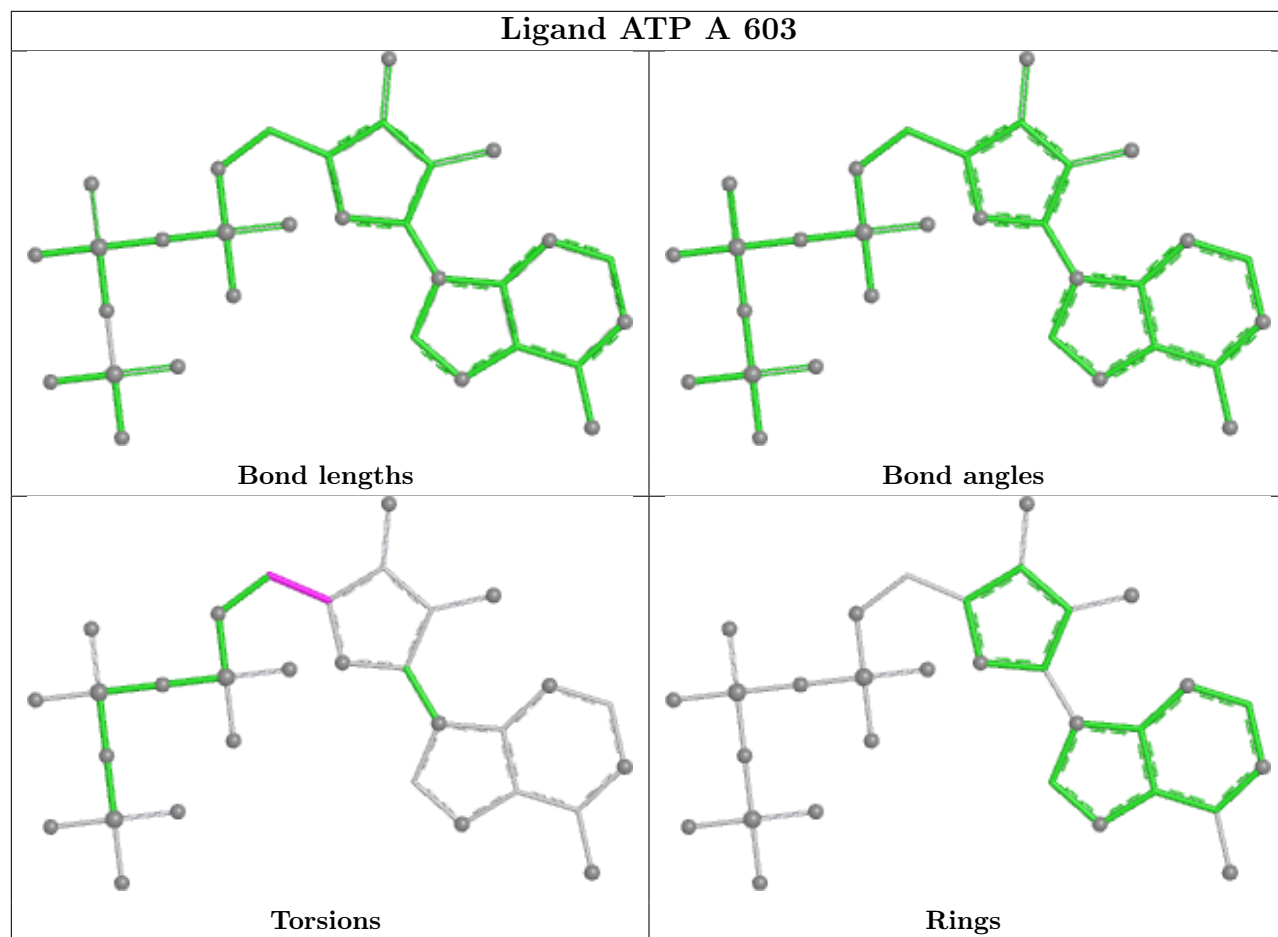
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	603	BCT	2	0
9	H	601	1VU	6	0
7	A	603	ATP	1	0
6	A	602	BCT	1	0
7	C	601	ATP	2	0
6	D	603	BCT	1	0
9	G	602	1VU	3	0
7	Q	603	ATP	1	0
9	H	602	1VU	6	0
6	Q	602	BCT	1	0
6	T	602	BCT	1	0
7	D	601	ATP	1	0
6	R	603	BCT	1	0
7	T	601	ATP	1	0
9	G	601	1VU	4	0
7	R	601	ATP	1	0

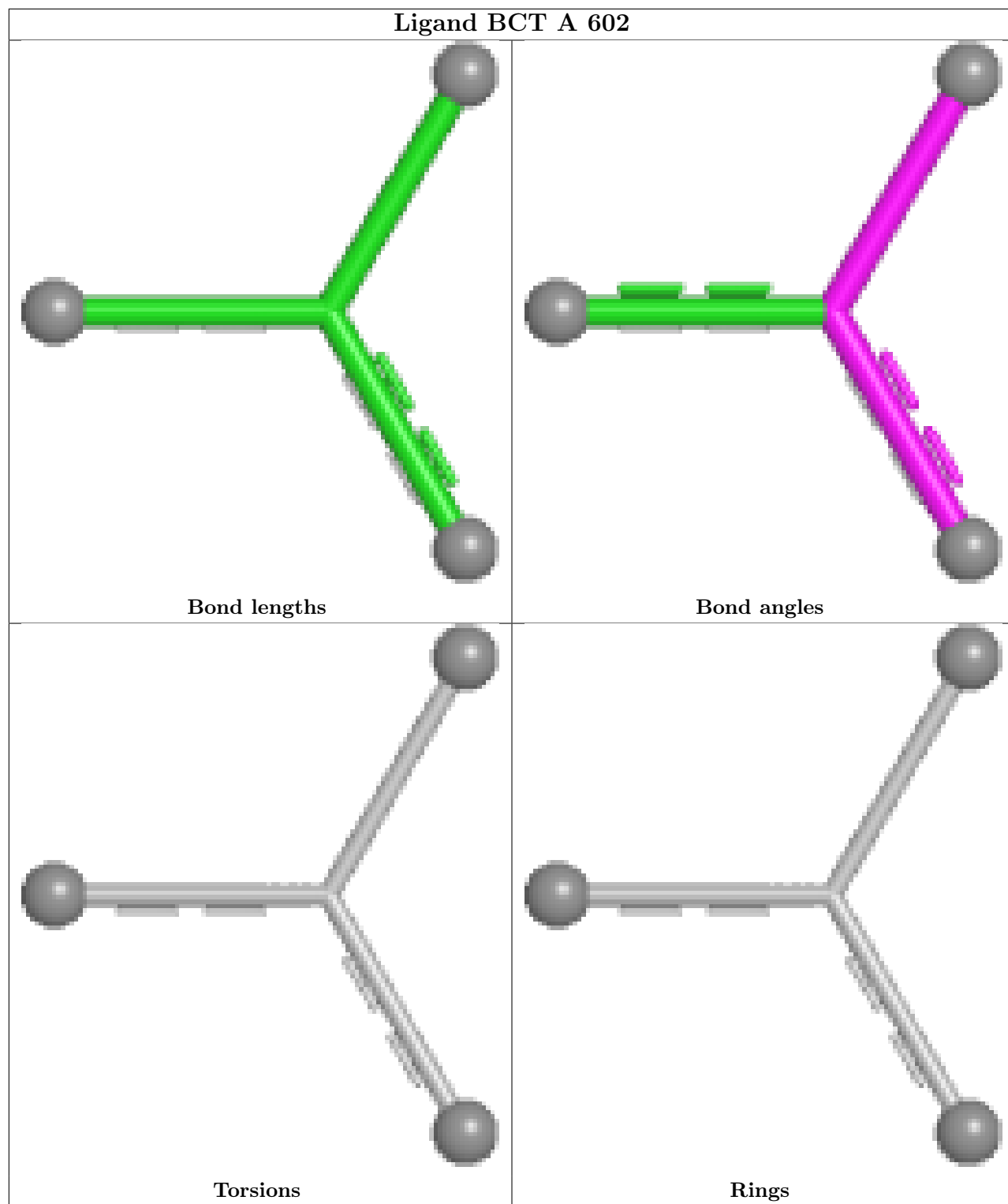
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

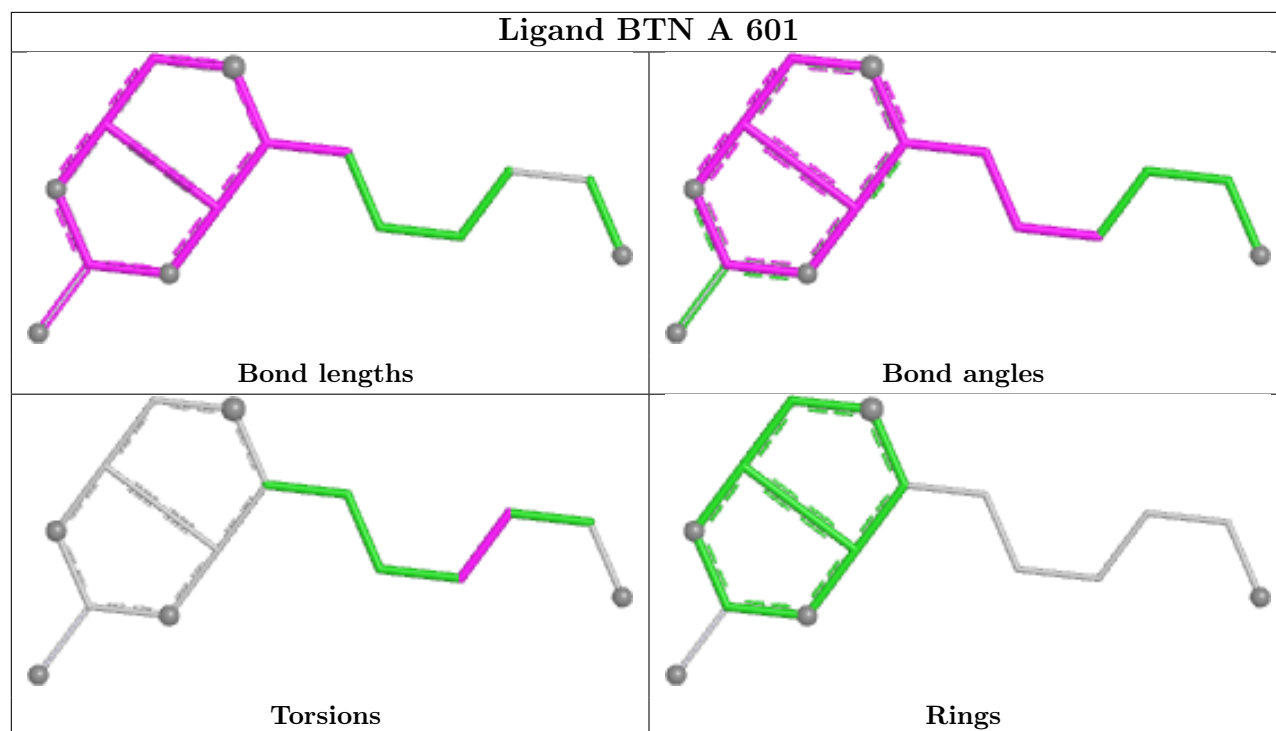
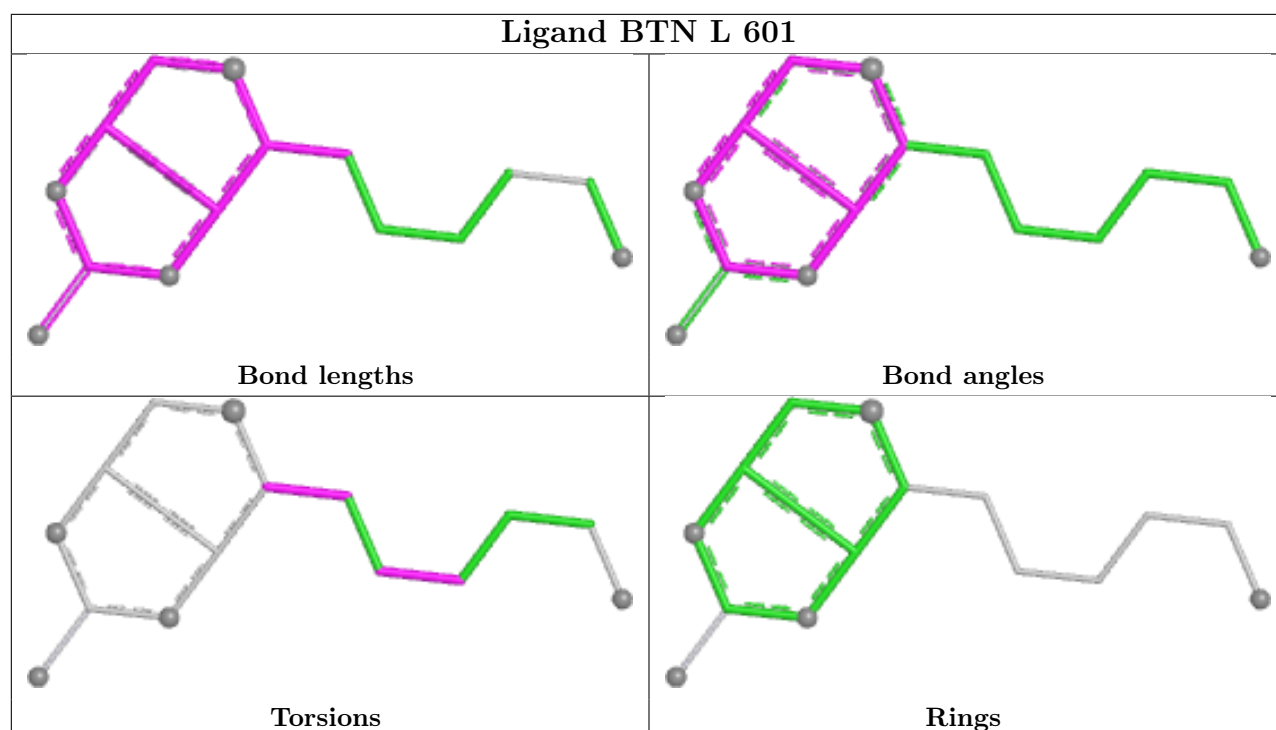


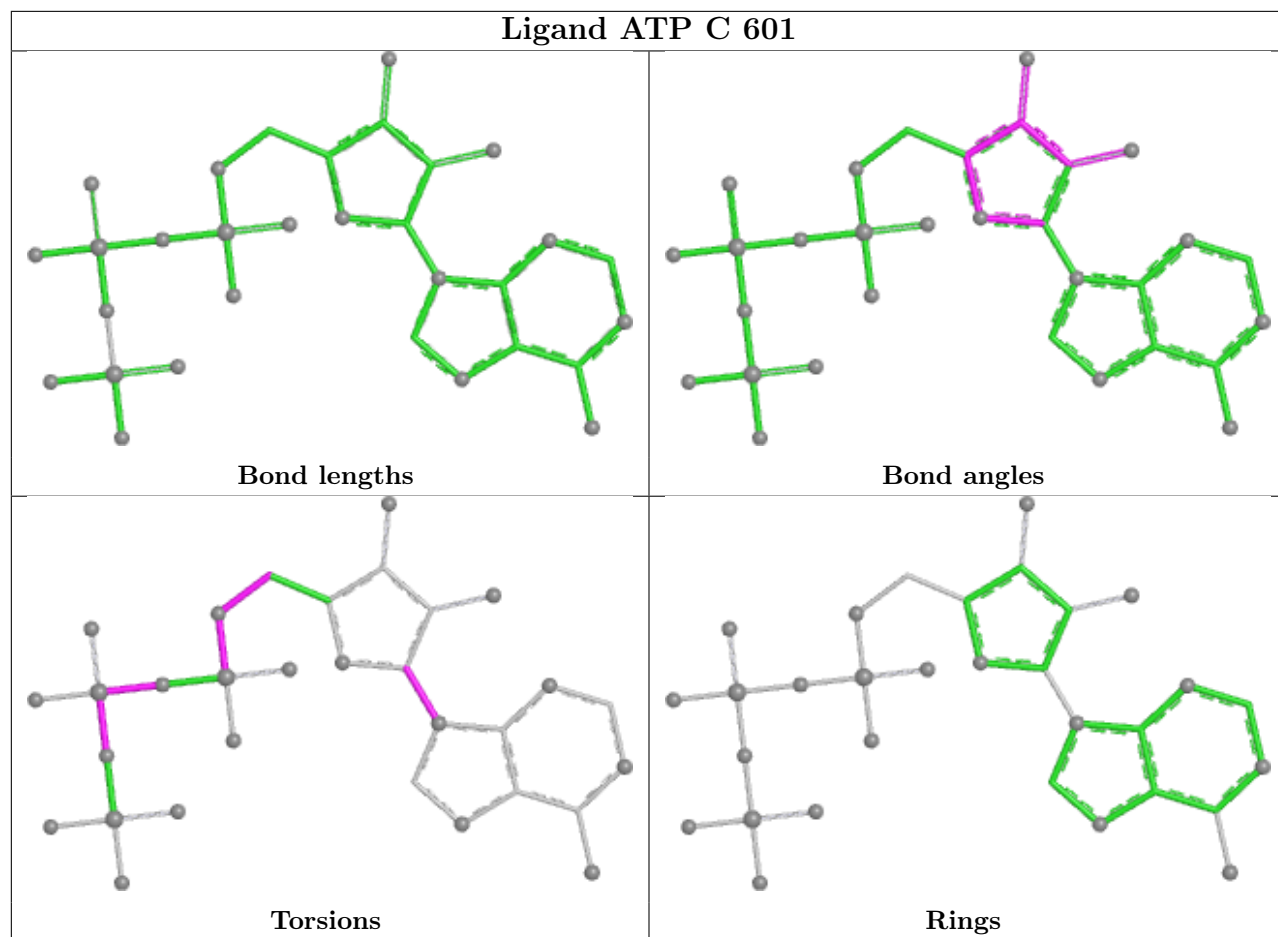


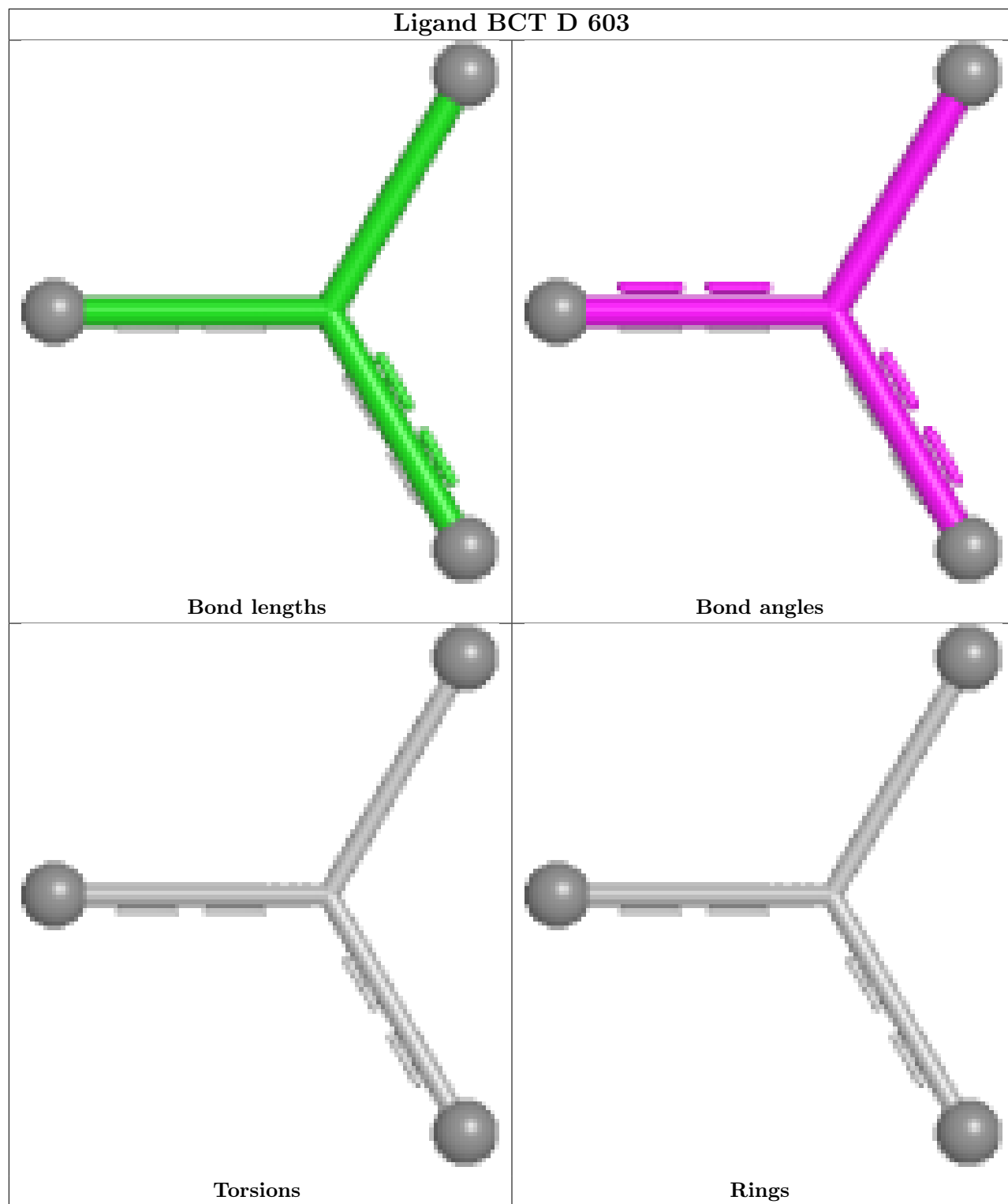


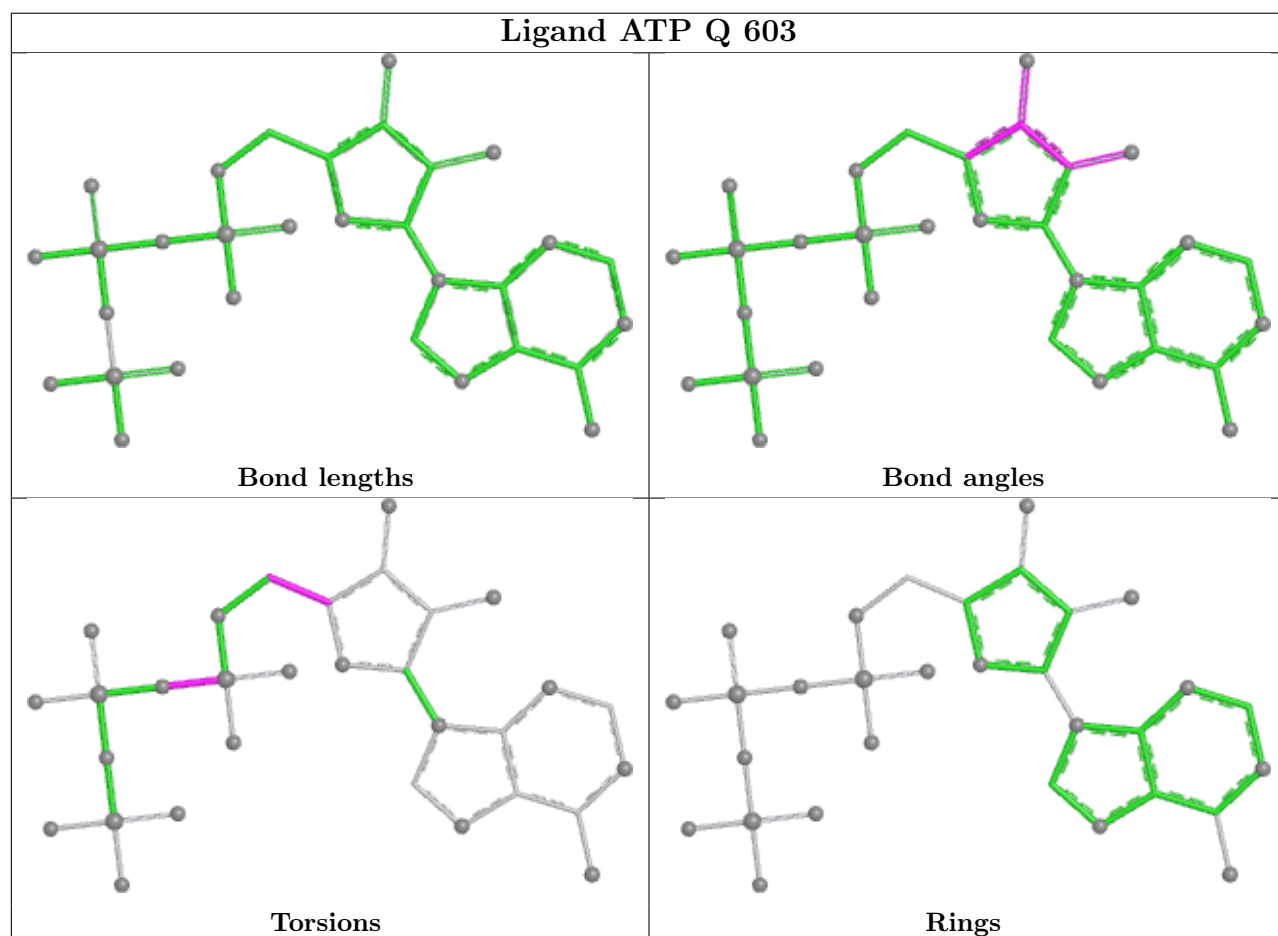
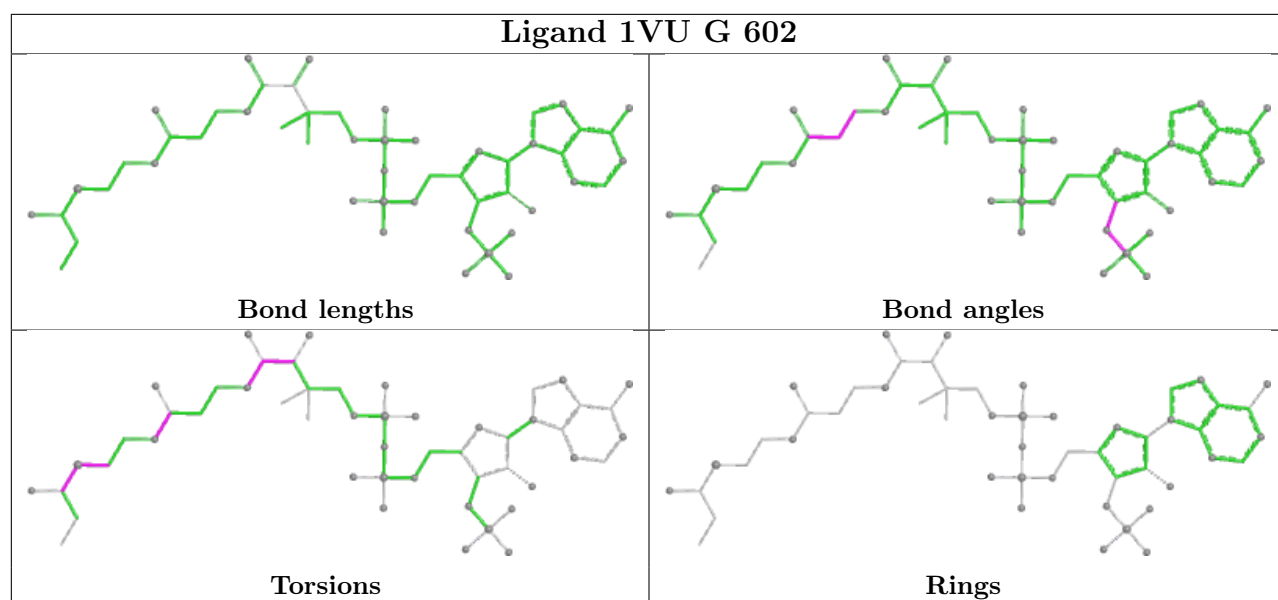


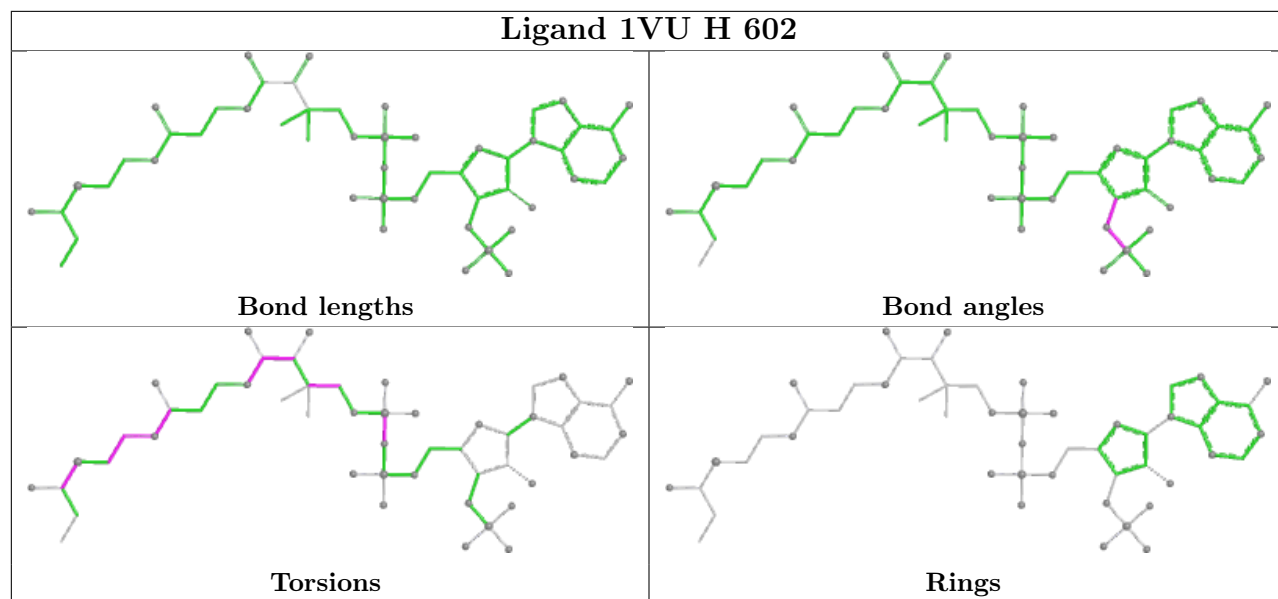


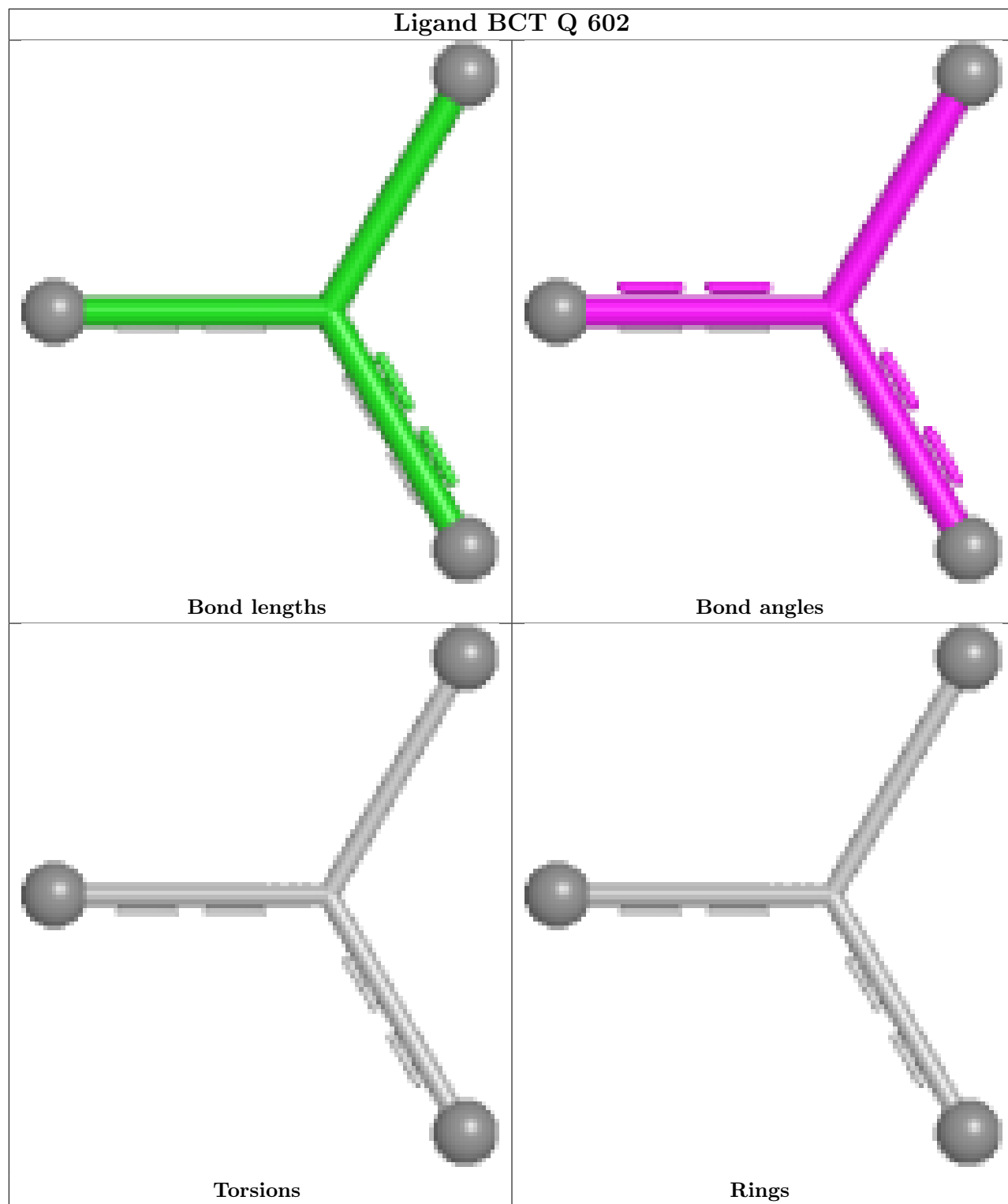


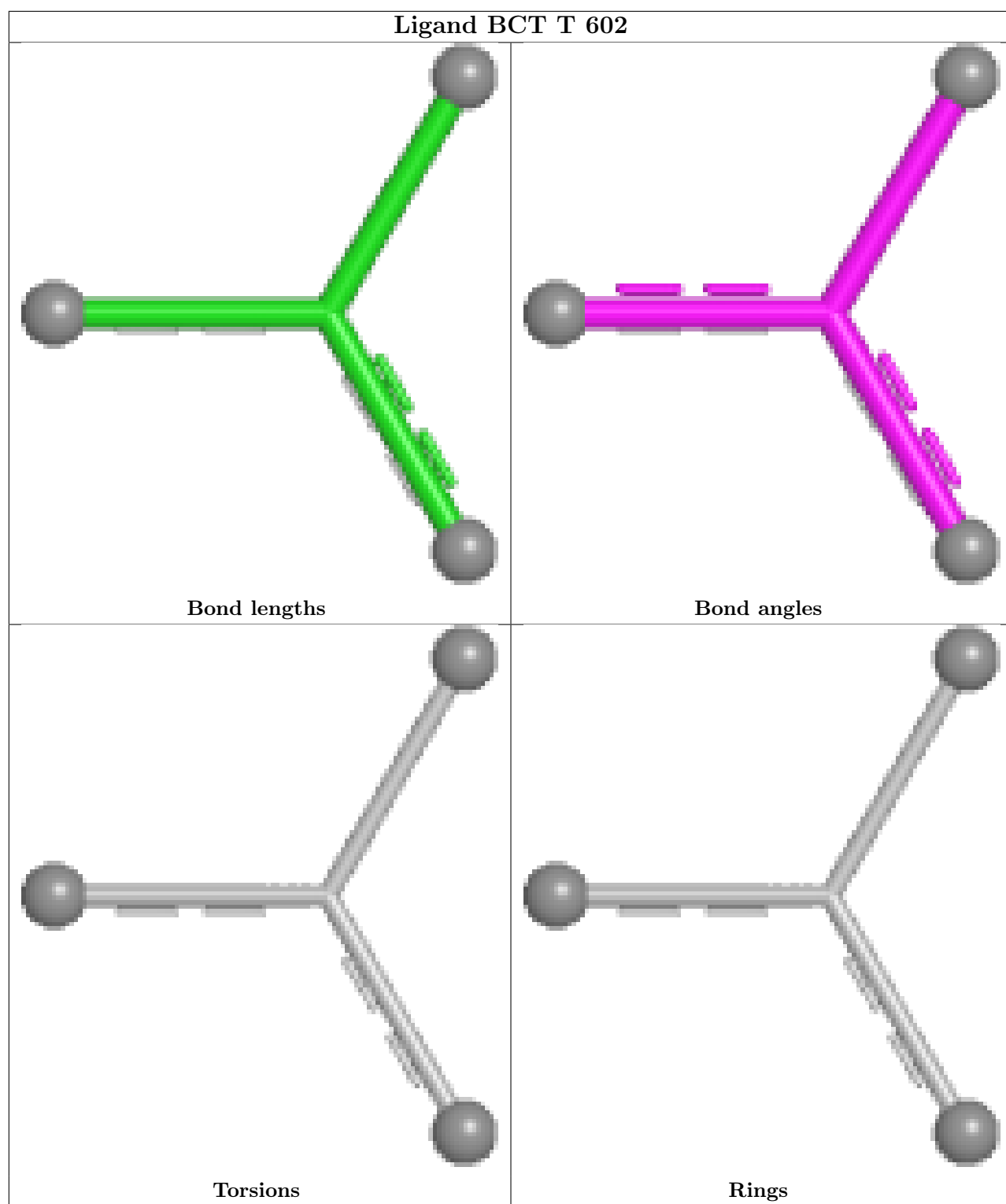


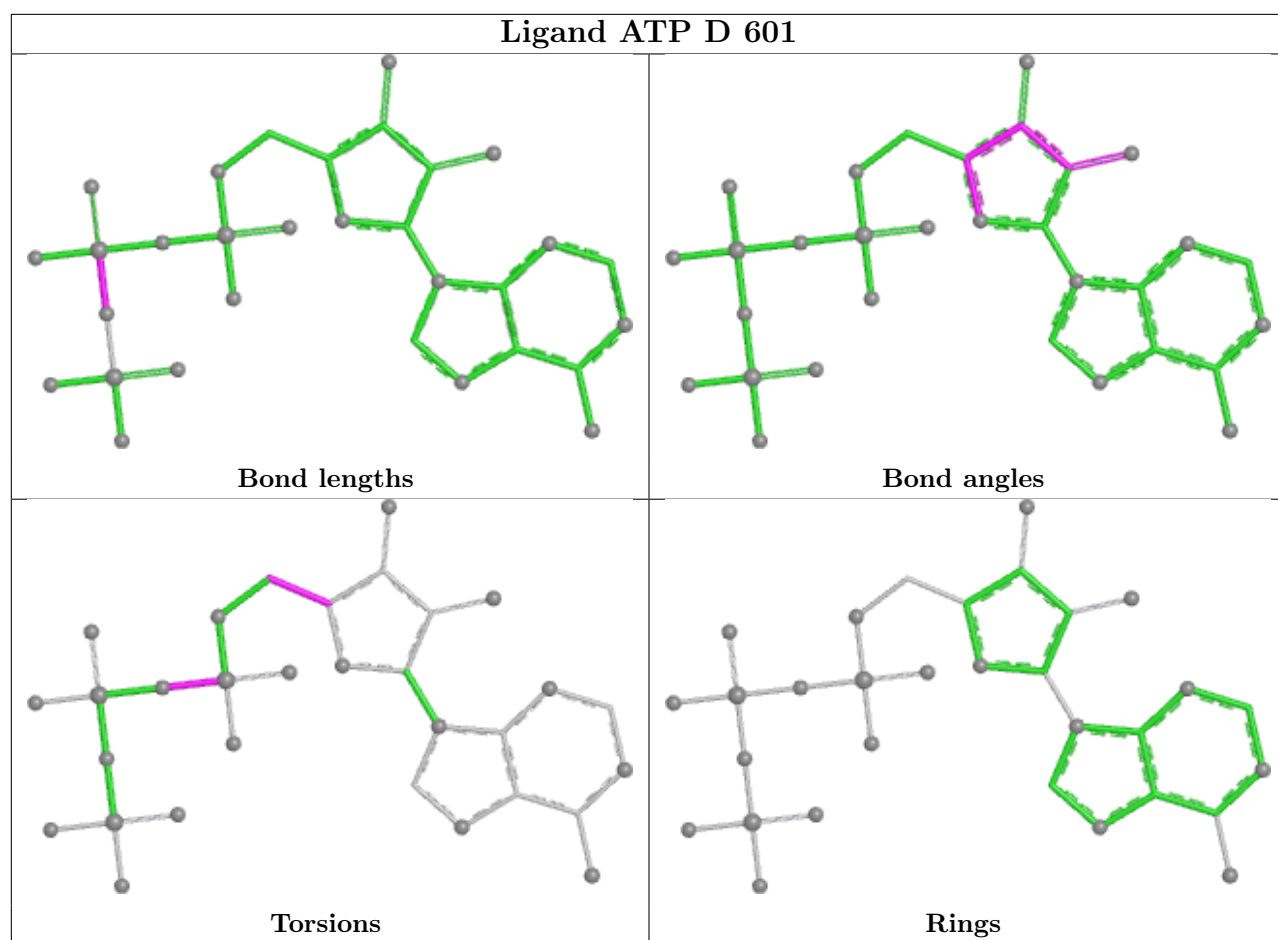


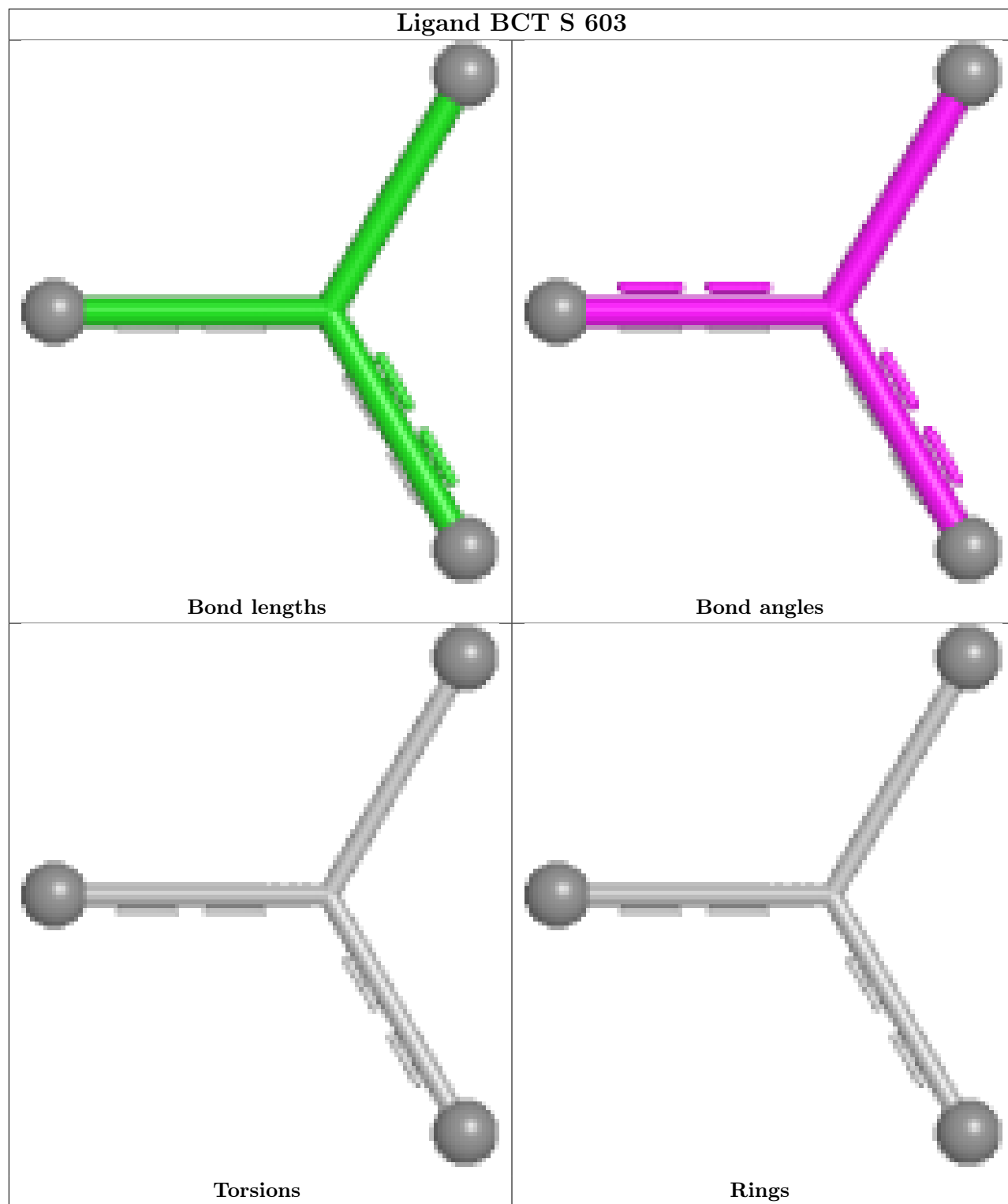


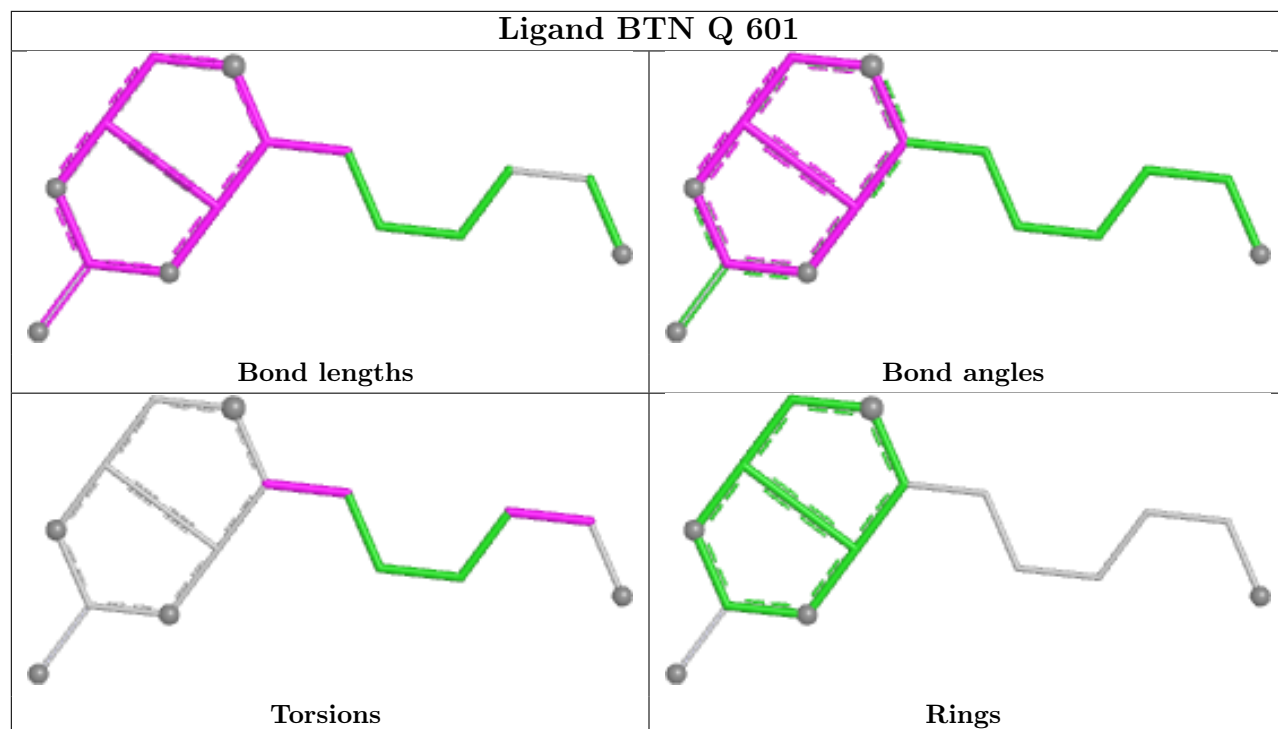


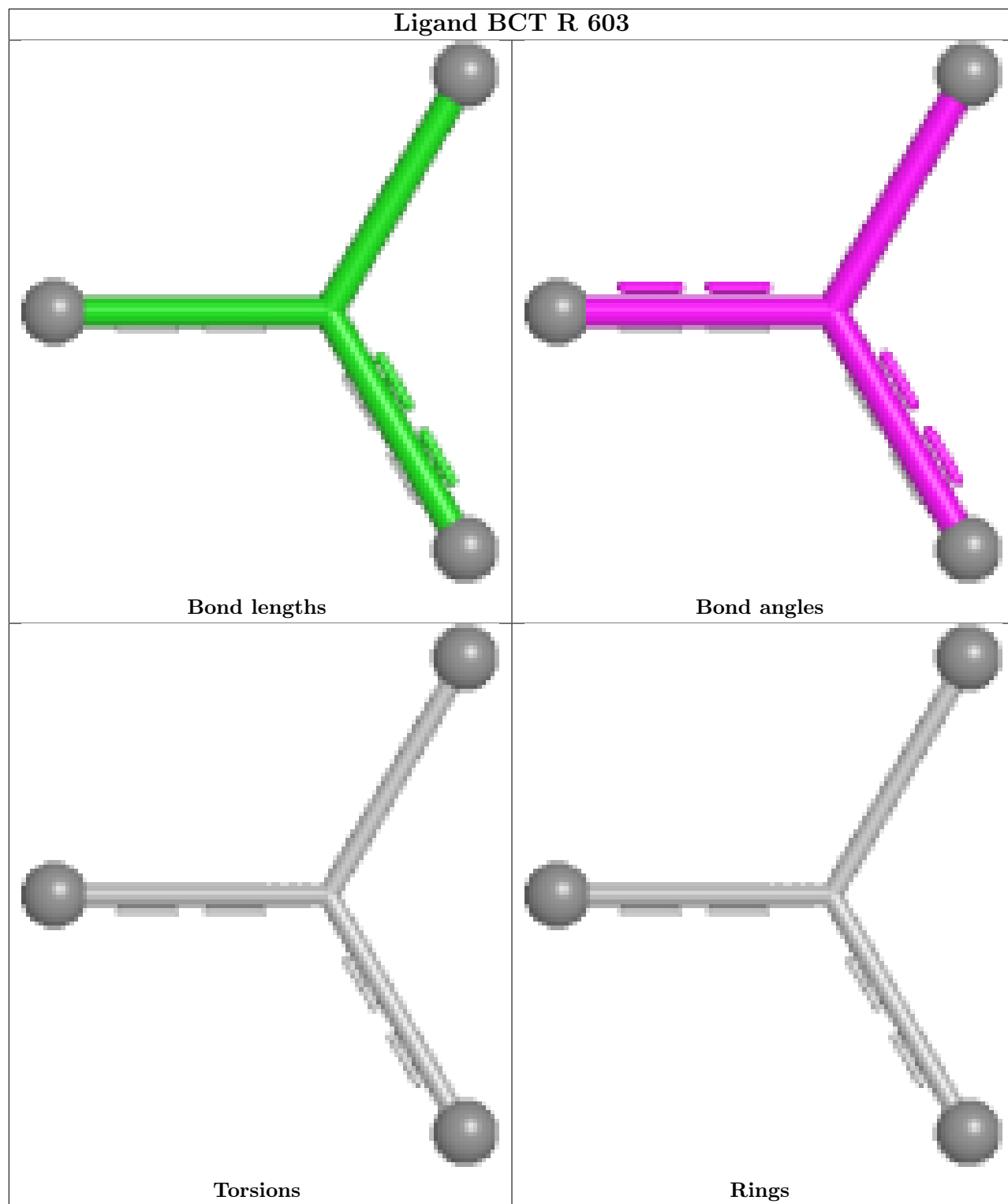


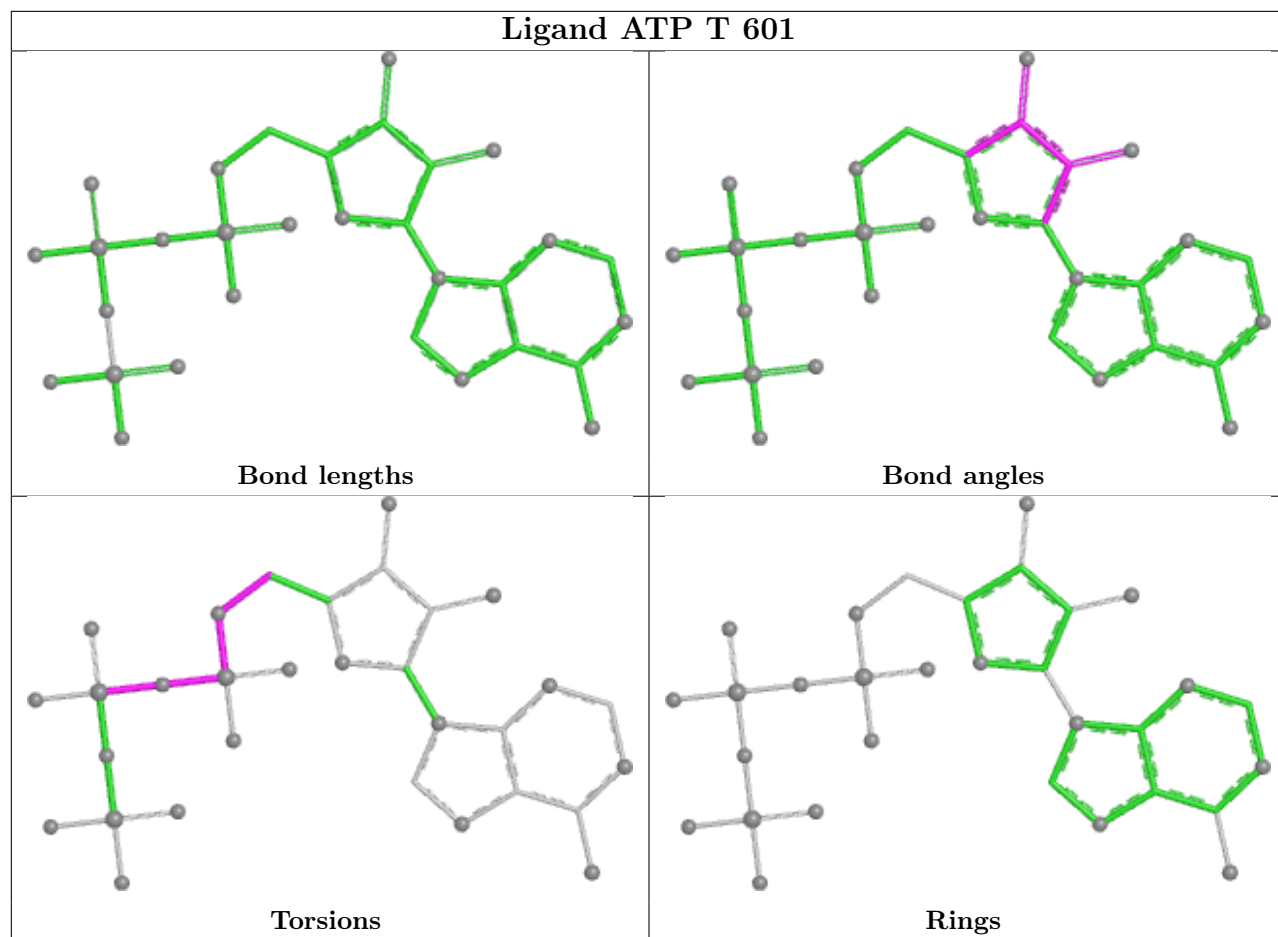


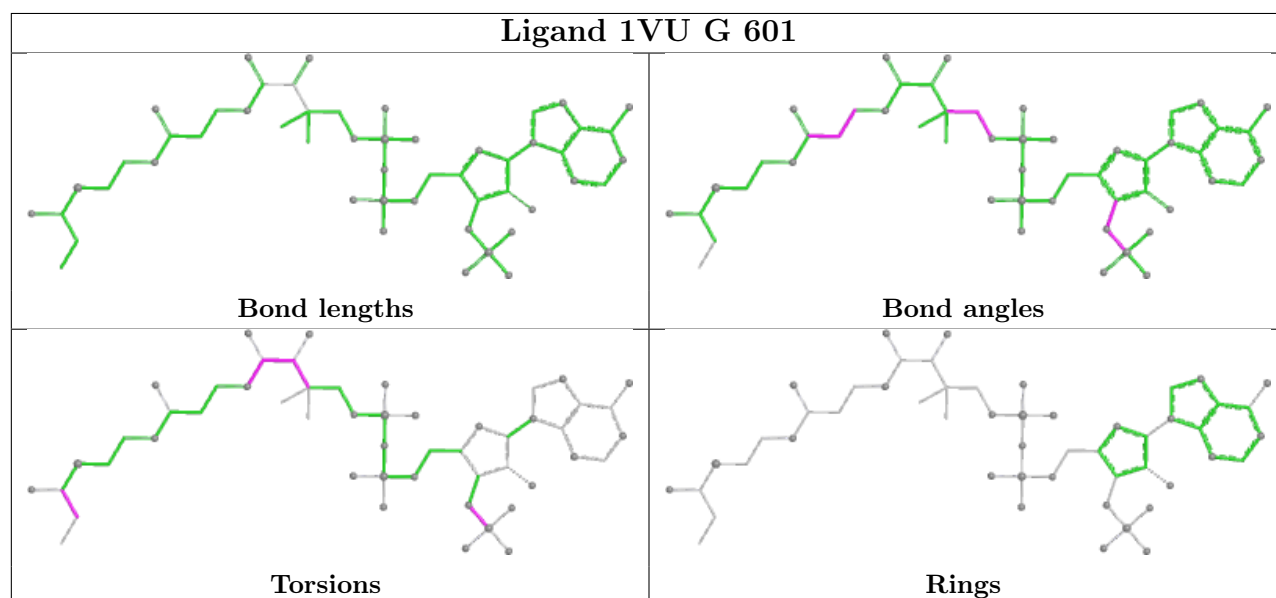
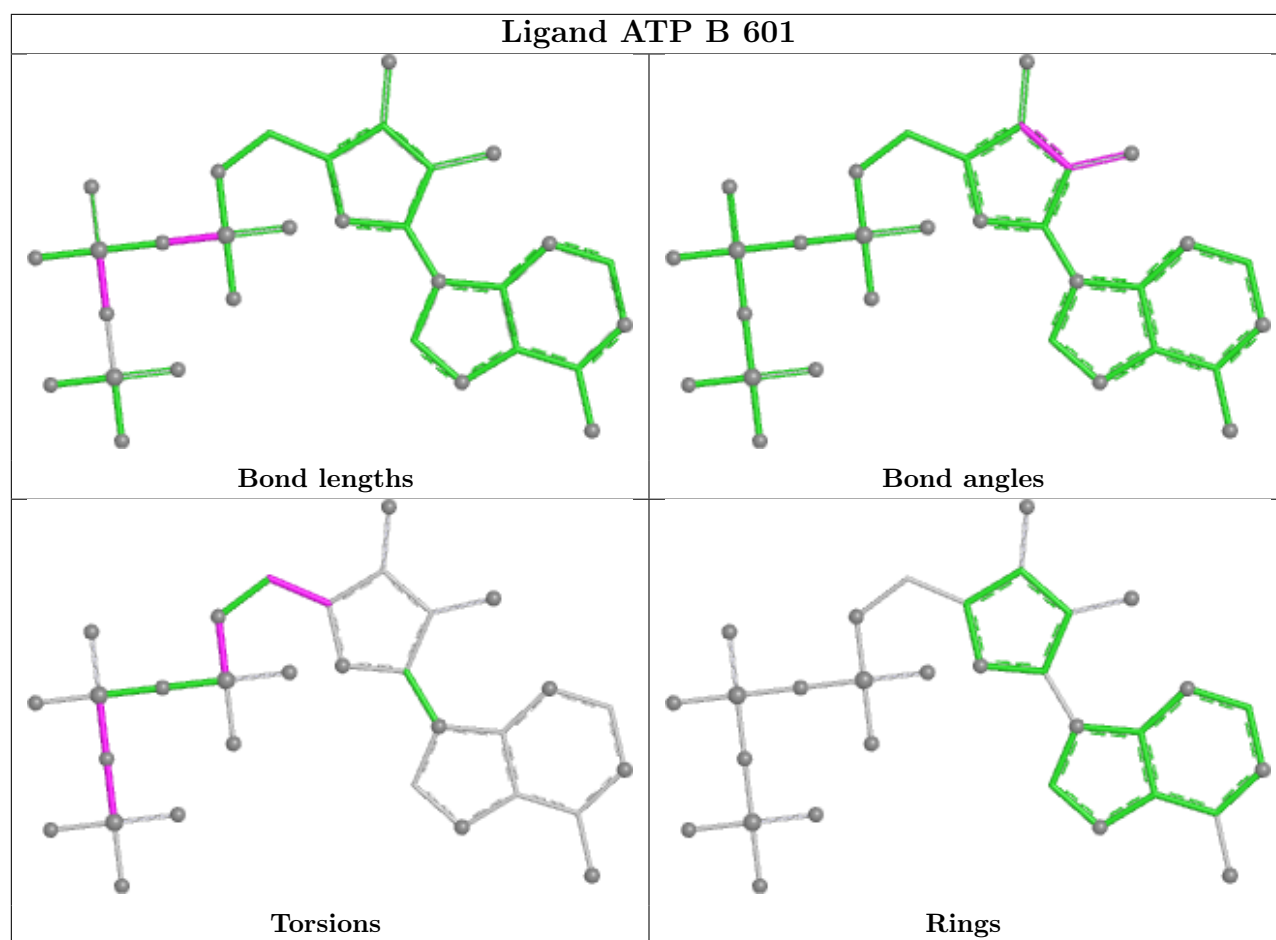


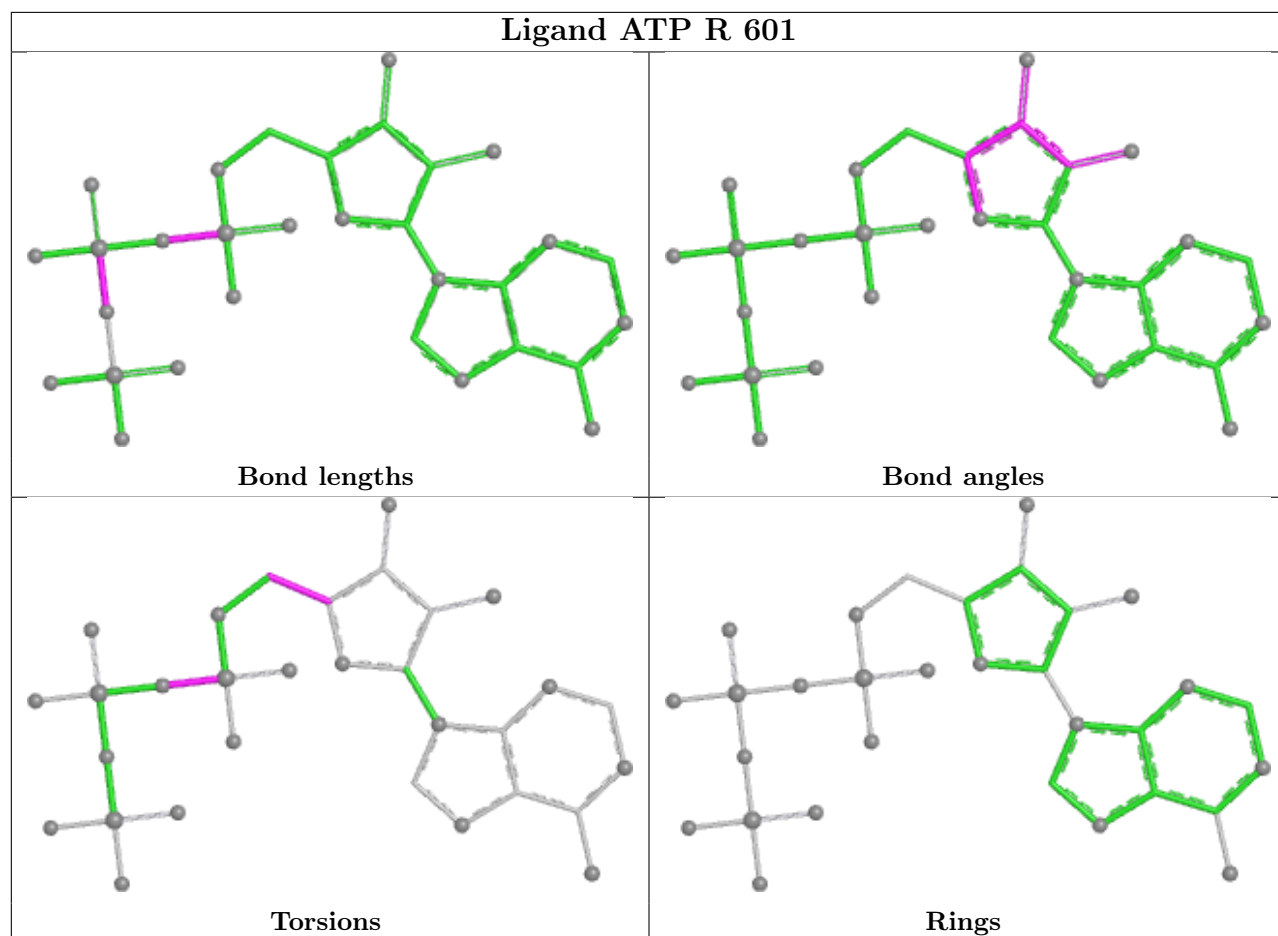
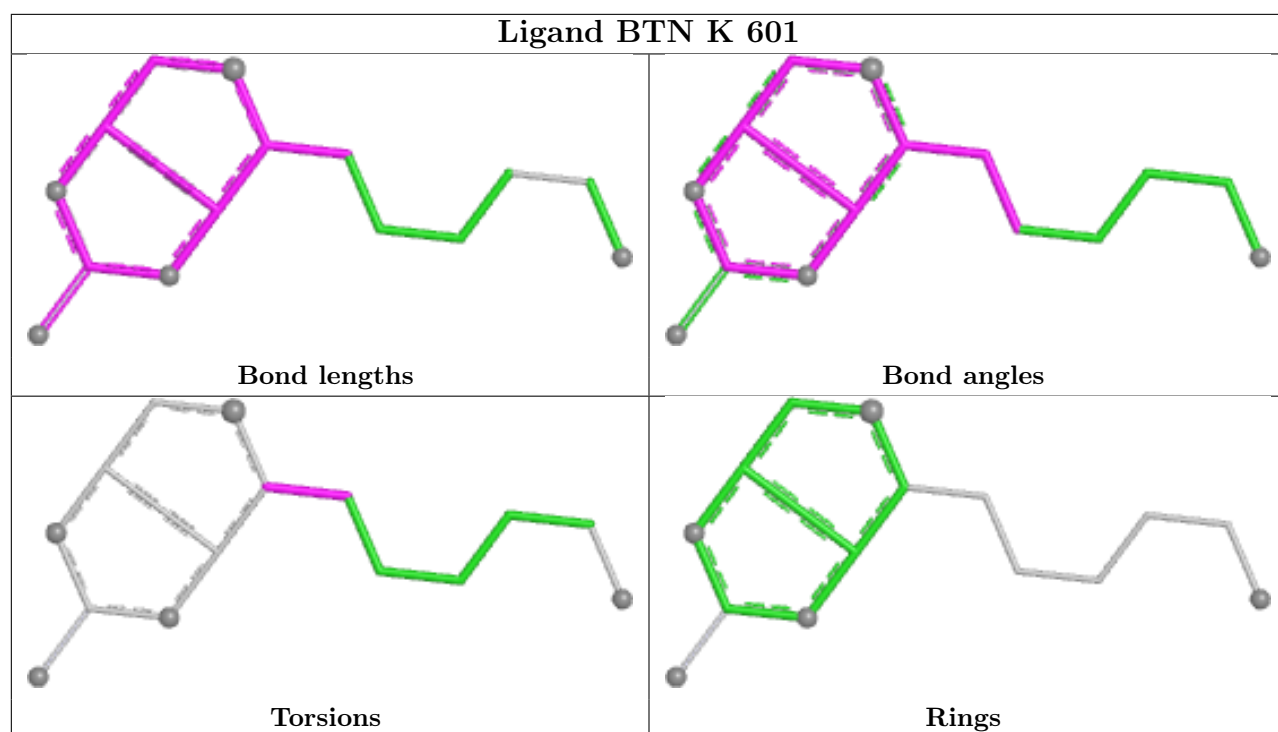


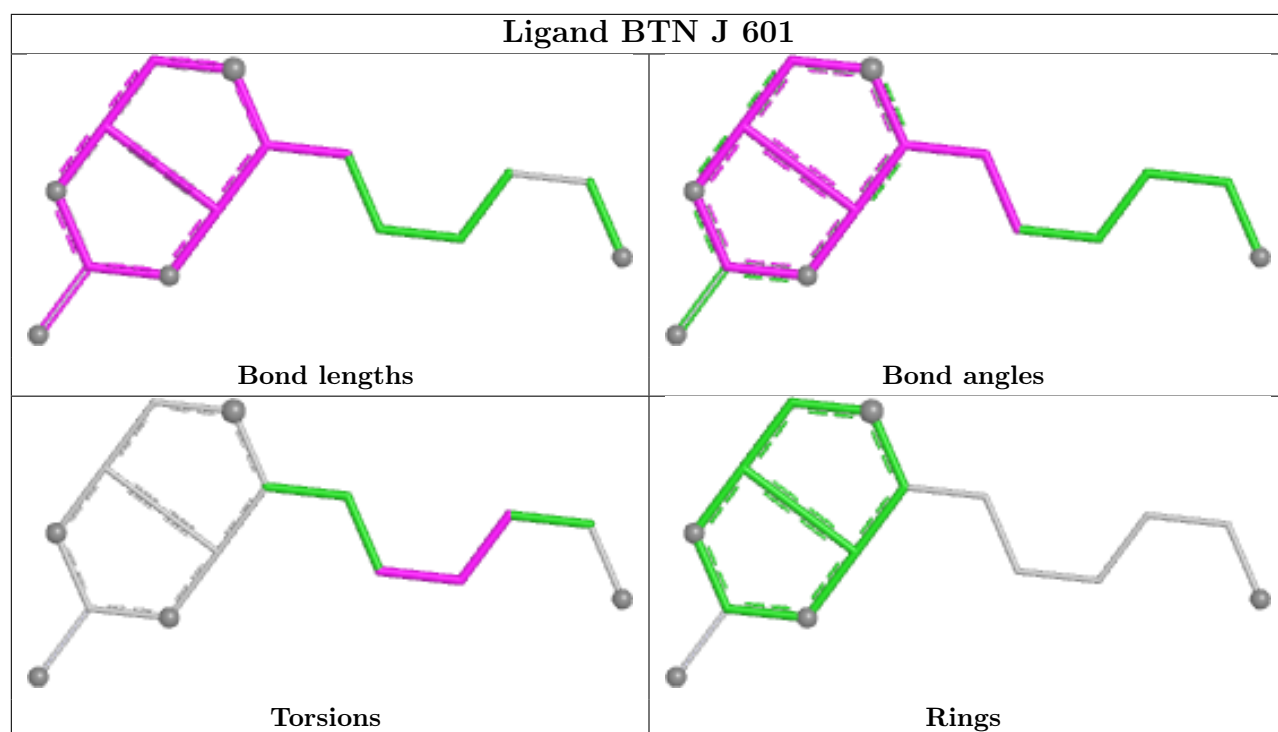


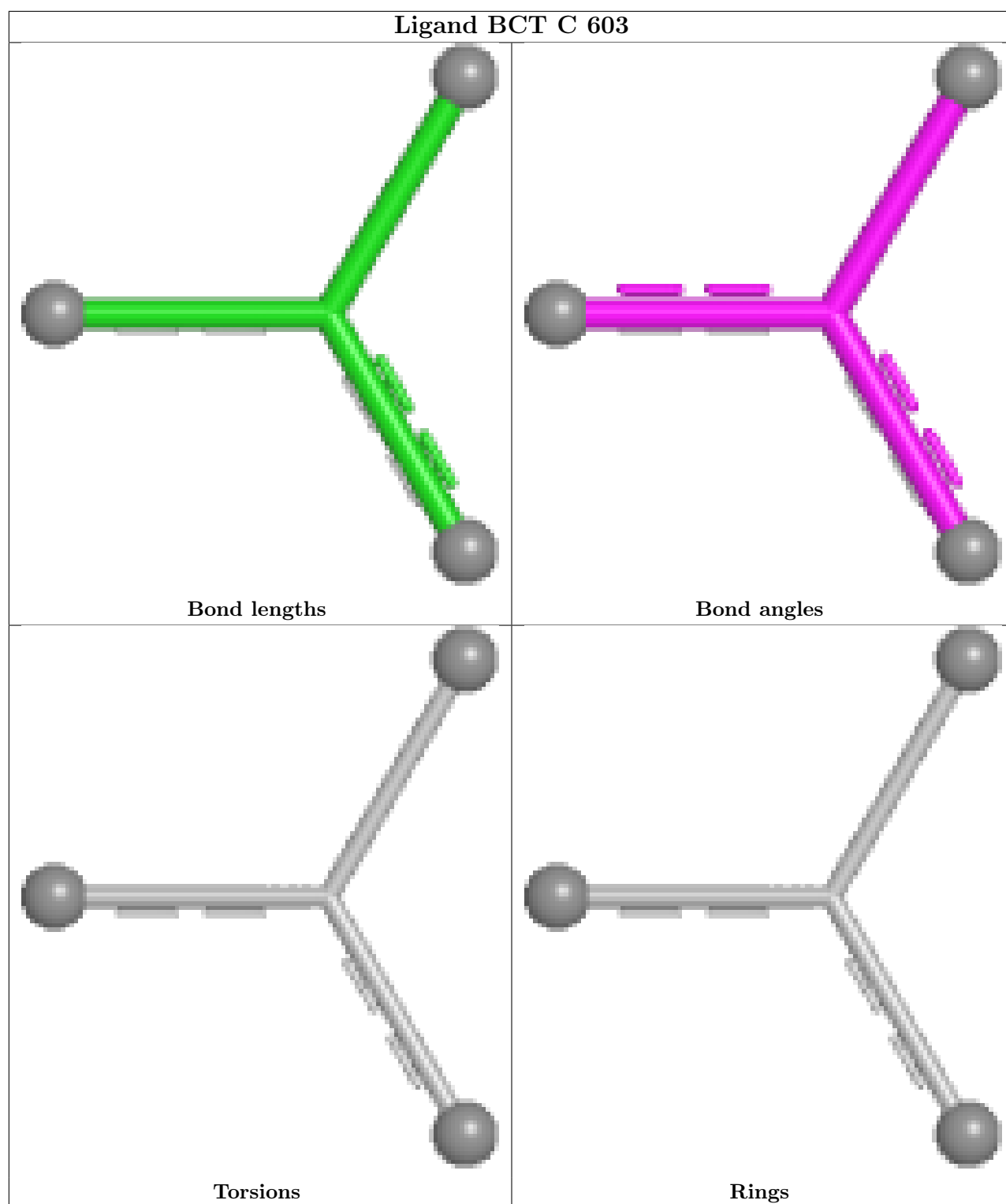












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

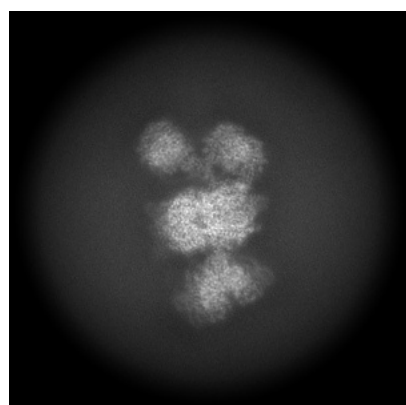
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73585. These allow visual inspection of the internal detail of the map and identification of artifacts.

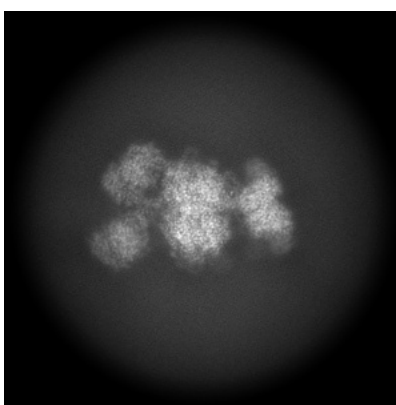
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

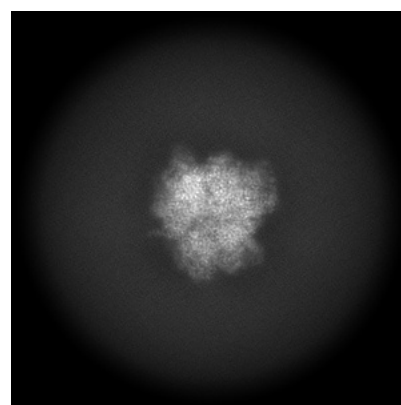
6.1.1 Primary map



X



Y

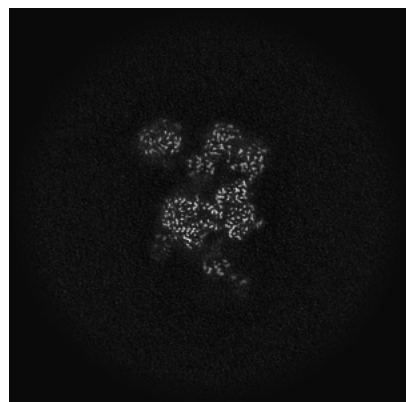


Z

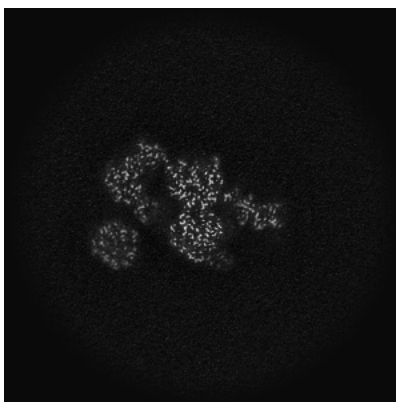
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

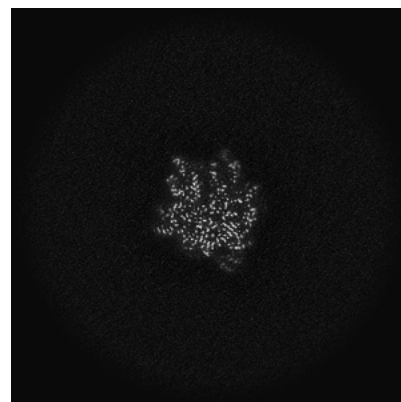
6.2.1 Primary map



X Index: 240



Y Index: 240

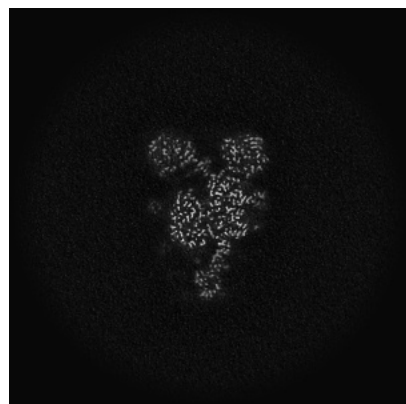


Z Index: 240

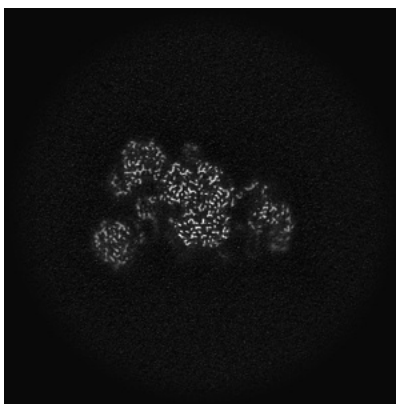
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

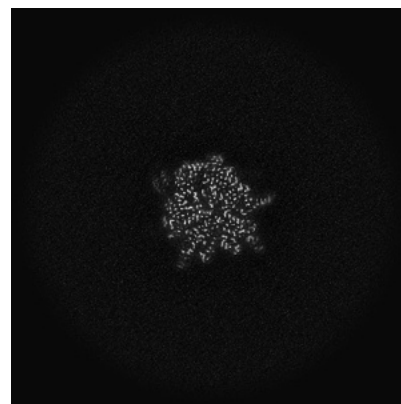
6.3.1 Primary map



X Index: 253



Y Index: 255

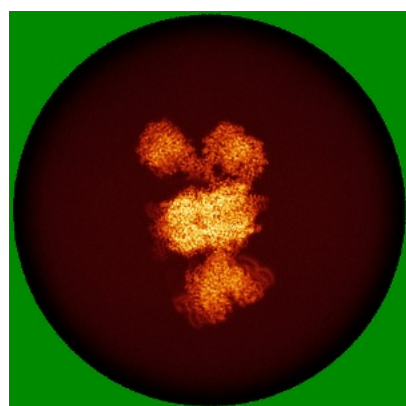


Z Index: 217

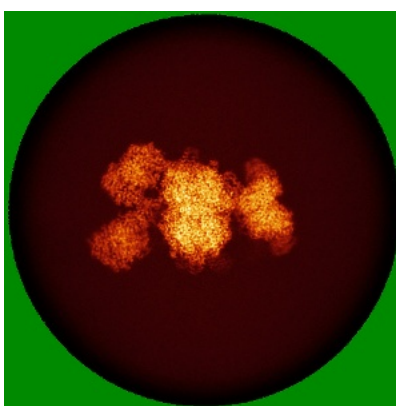
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

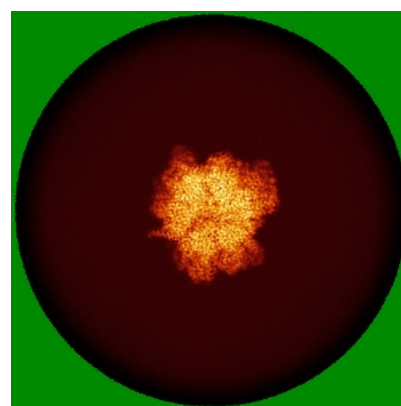
6.4.1 Primary map



X



Y

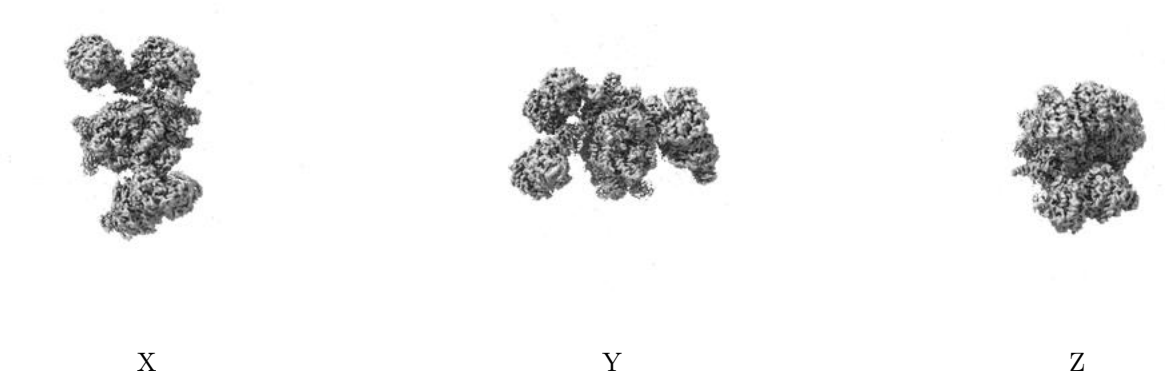


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.16. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

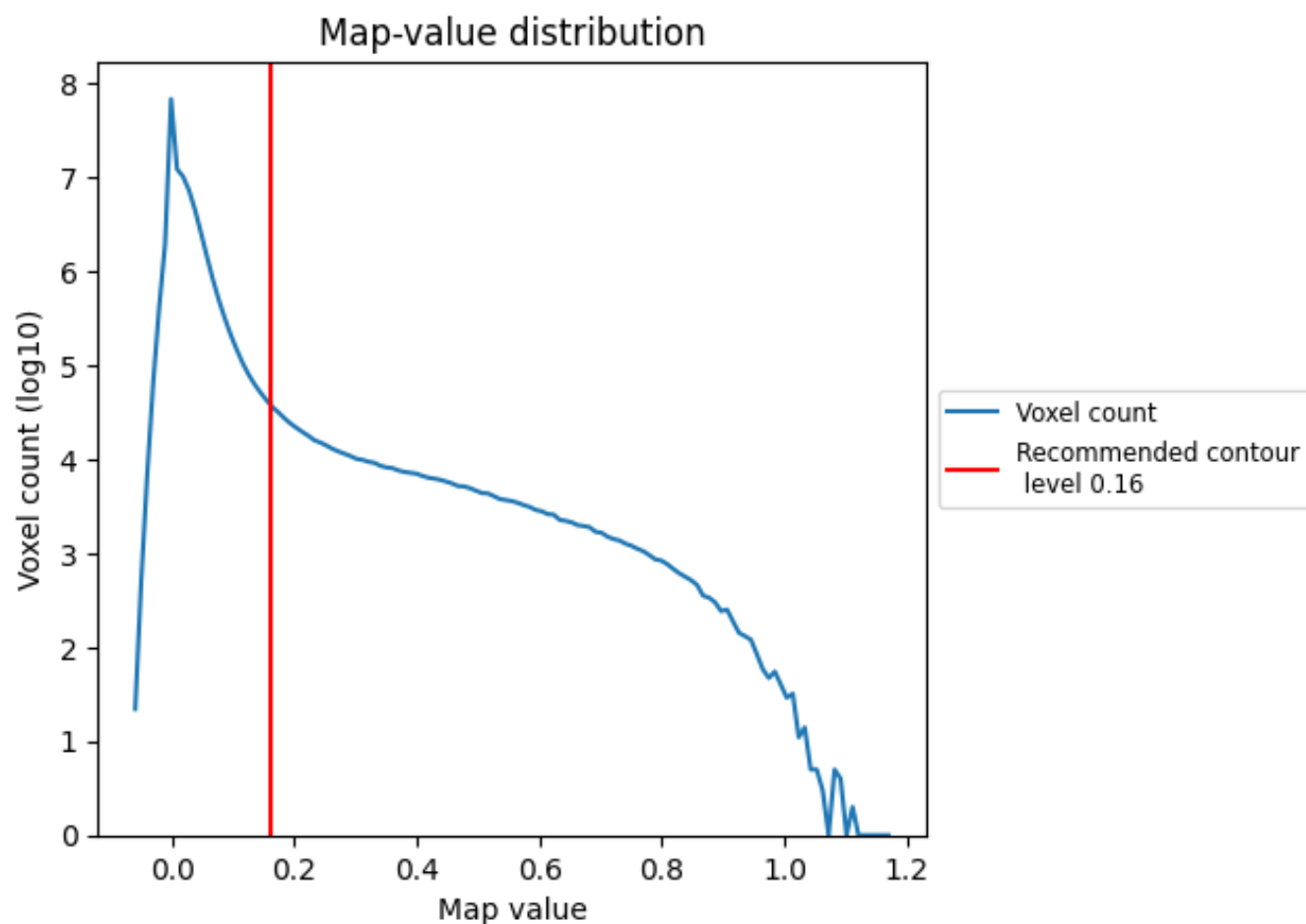
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

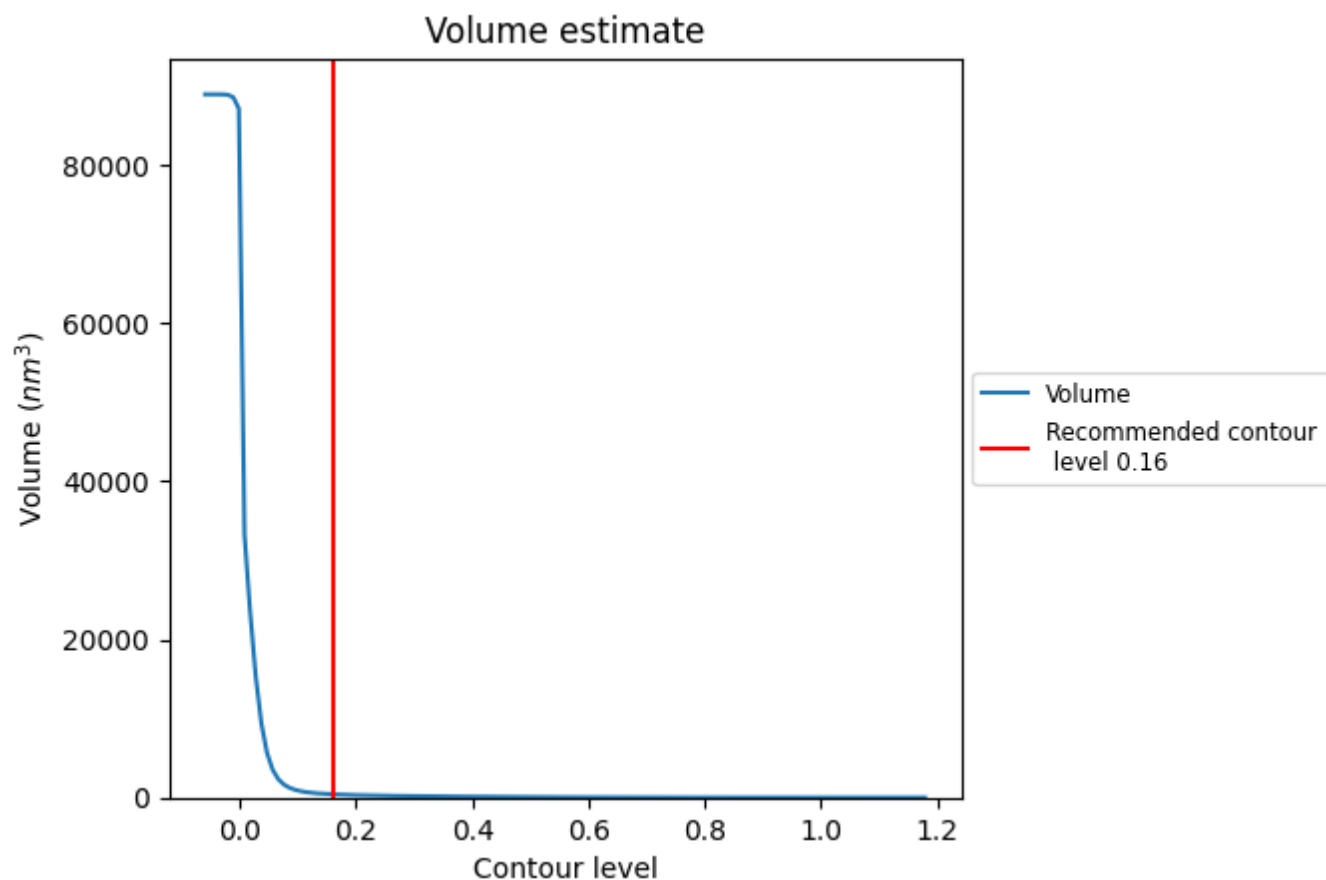
This section contains the results of statistical analysis of the map.

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.

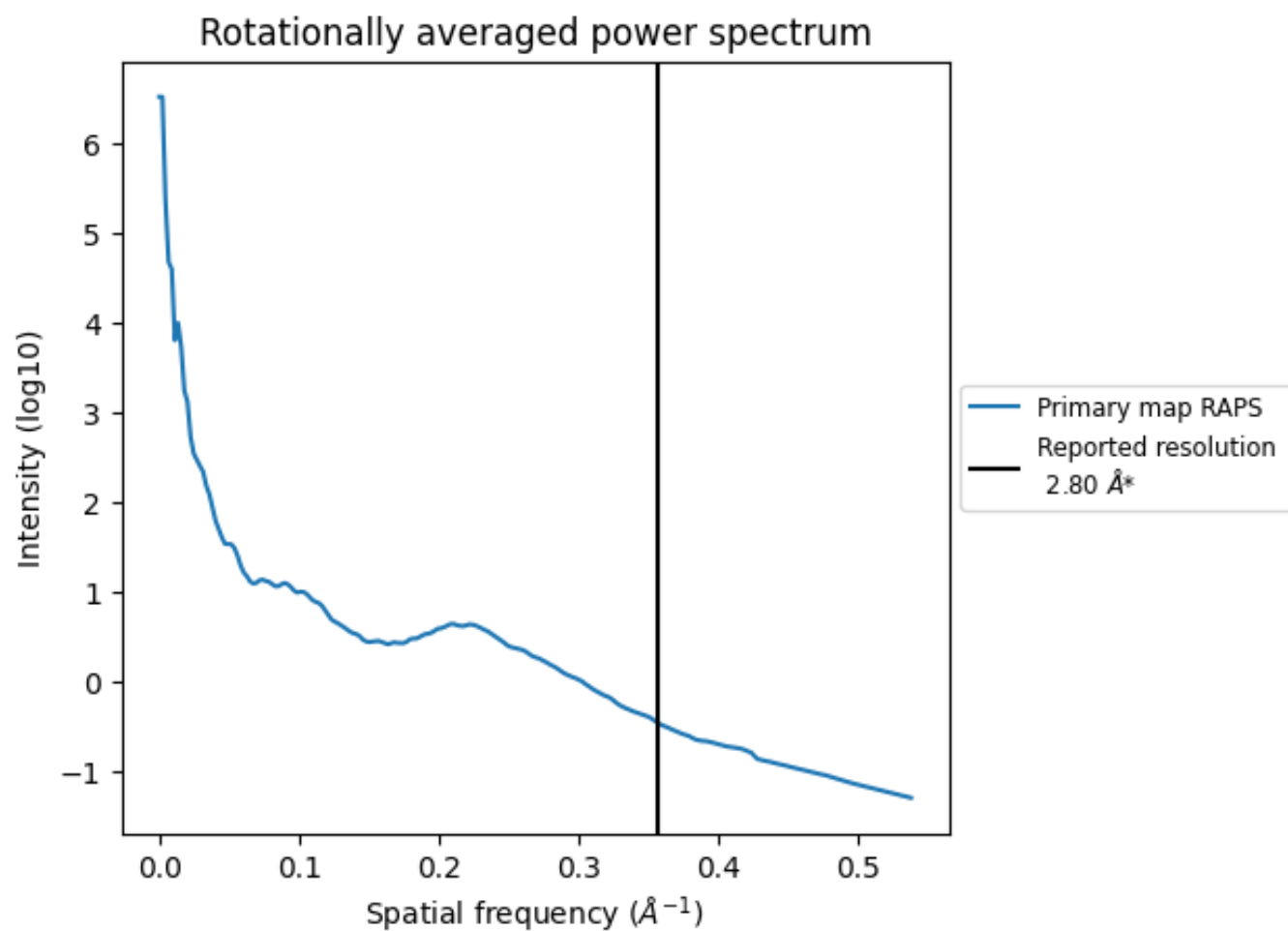
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 413 nm³; this corresponds to an approximate mass of 374 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

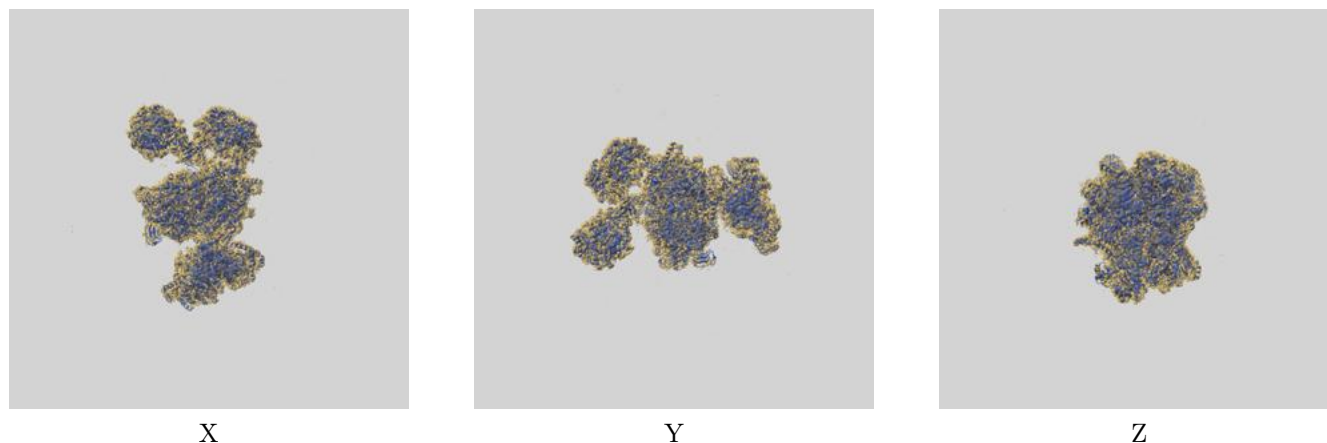
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

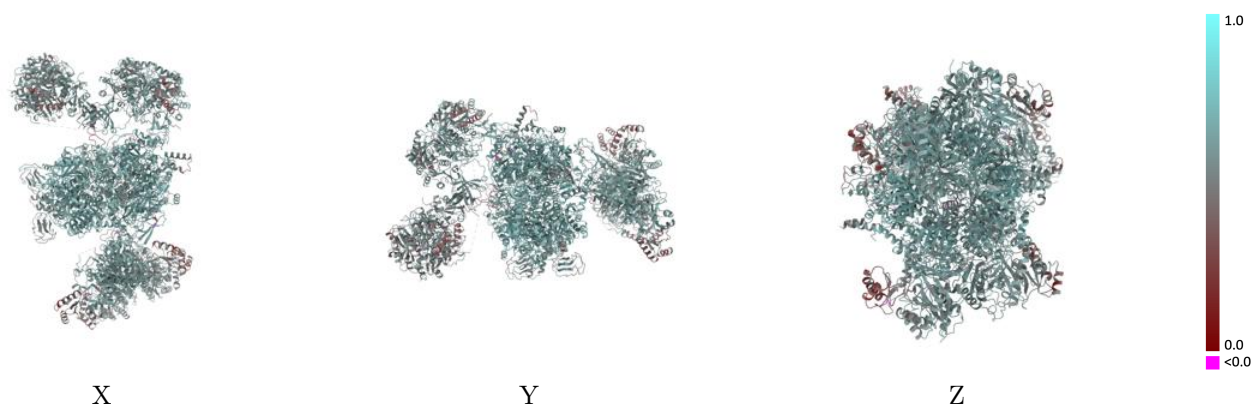
This section contains information regarding the fit between EMDB map EMD-73585 and PDB model 9YX2. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



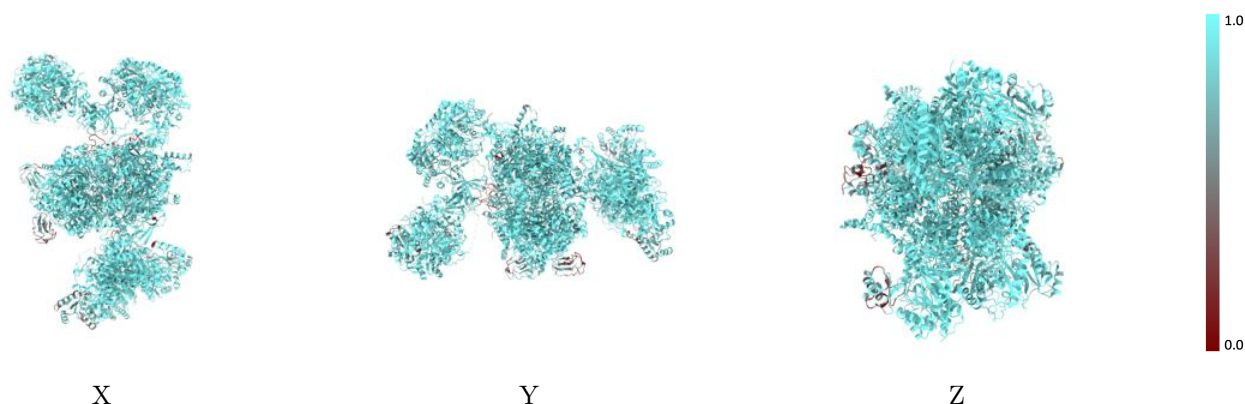
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



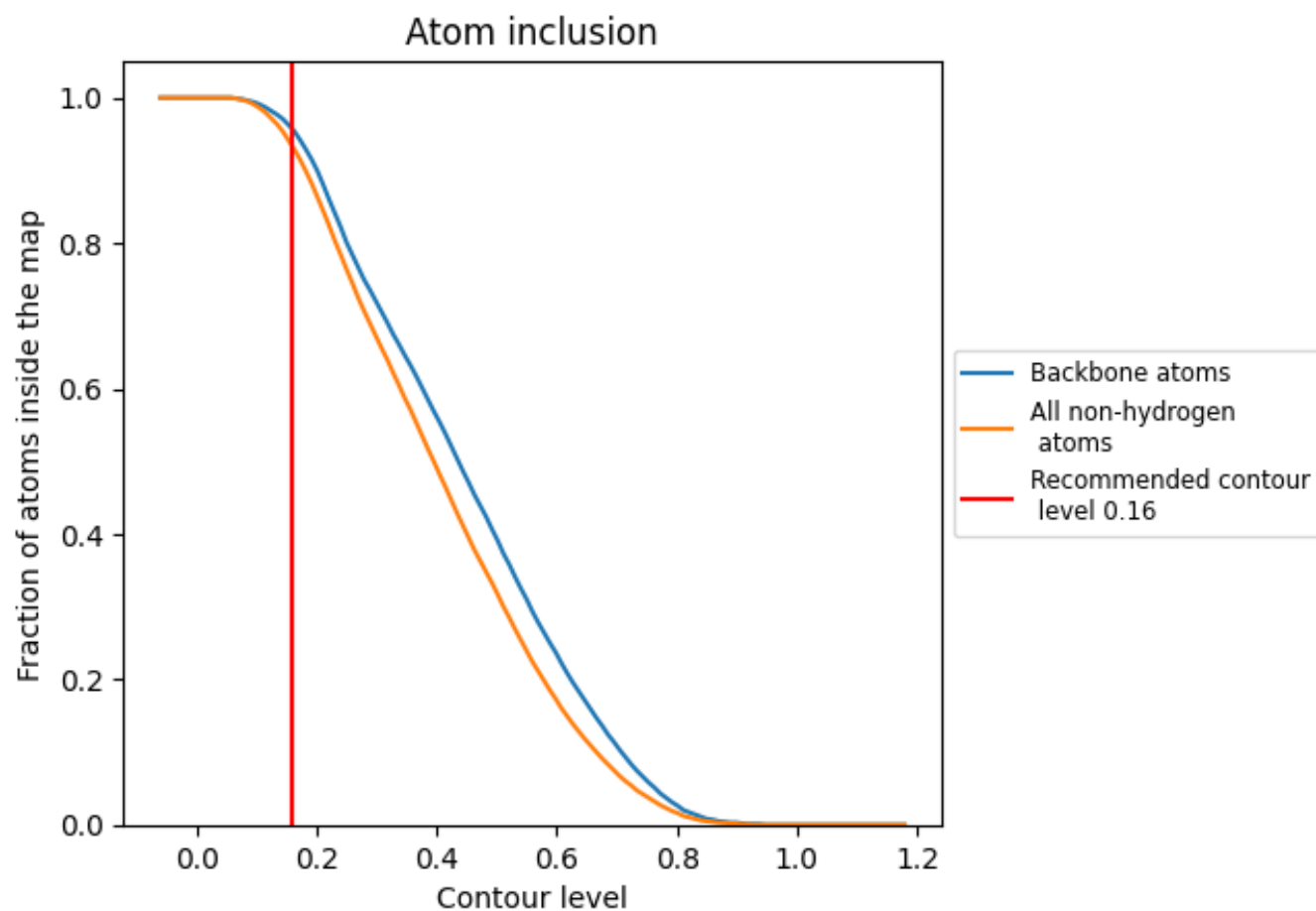
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



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 (0.16).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9330	 0.5940
A	 0.9260	 0.5650
B	 0.9120	 0.5490
C	 0.8510	 0.5060
D	 0.9140	 0.5210
E	 0.8780	 0.5860
F	 0.9720	 0.6530
G	 0.9780	 0.6580
H	 0.9740	 0.6540
I	 0.6640	 0.5440
J	 0.5530	 0.5190
K	 0.7240	 0.5550
L	 0.5380	 0.5230
M	 0.9790	 0.6590
N	 0.9790	 0.6570
O	 0.9760	 0.6520
P	 0.8920	 0.5950
Q	 0.9400	 0.5740
R	 0.9430	 0.5600
S	 0.9120	 0.5370
T	 0.9390	 0.5460

