



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 03:48 PM UTC

PDB ID : 7O37 / pdb_00007o37
EMDB ID : EMD-12702
Title : Murine supercomplex CIII2CIV in the assembled locked conformation
Authors : Vercellino, I.; Sazanov, L.A.
Deposited on : 2021-04-01
Resolution : 3.20 Å (reported)
Based on initial models : 1NTZ, 5IY5, 3L75, 5Z62

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

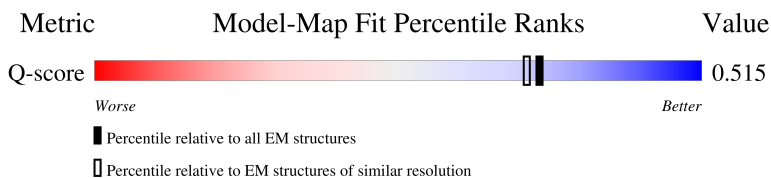
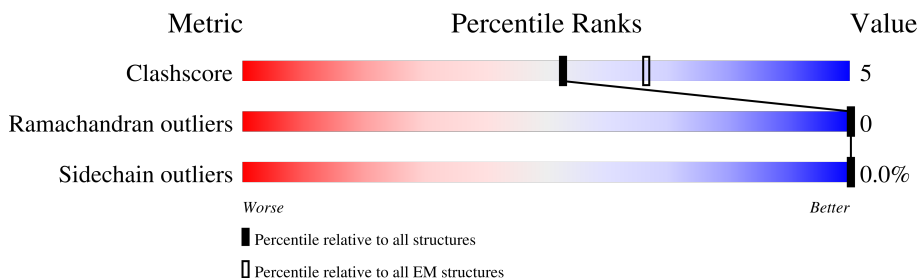
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	446	
1	L	446	
2	B	439	
2	M	439	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	C	381	
3	N	381	
4	D	241	
4	O	241	
5	E	196	
5	P	196	
6	F	110	
6	Q	110	
7	G	81	
7	R	81	
8	H	76	
8	S	76	
9	J	63	
9	U	63	
10	K	56	
10	V	56	
11	T	78	
12	I	113	
13	a	514	
14	b	227	
15	c	261	
16	d	147	
17	e	109	
18	f	99	
19	g	85	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
20	h	85	14% 82% 11% 7%
21	i	75	87% 9%
22	k	56	5% 77% 11% 12%
23	l	47	81% 17%
24	m	46	7% 83% 11% 7%

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 48610 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 Cytochrome b-c1 complex subunit 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	446	Total	C	N	O	S	0	0
			3466	2167	611	671	17		
1	L	445	Total	C	N	O	S	0	0
			3460	2163	610	670	17		

- Molecule 2 is a protein called Cytochrome b-c1 complex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	420	Total	C	N	O	S	0	0
			3154	1980	555	610	9		
2	M	420	Total	C	N	O	S	0	0
			3154	1980	555	610	9		

- Molecule 3 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	380	Total	C	N	O	S	0	0
			3045	2052	473	499	21		
3	N	380	Total	C	N	O	S	0	0
			3046	2052	473	499	22		

- Molecule 4 is a protein called Cytochrome c1, heme protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	241	Total	C	N	O	S	0	0
			1919	1224	329	352	14		
4	O	240	Total	C	N	O	S	0	0
			1909	1218	327	350	14		

- Molecule 5 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	196	Total	C	N	O	S	0	0
			1512	952	263	290	7		
5	P	196	Total	C	N	O	S	0	0
			1512	952	263	290	7		

- Molecule 6 is a protein called Cytochrome b-c1 complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	102	Total	C	N	O	S	0	0
			900	575	160	162	3		
6	Q	101	Total	C	N	O	S	0	0
			894	572	159	160	3		

- Molecule 7 is a protein called Cytochrome b-c1 complex subunit 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	G	74	Total	C	N	O	0	0
			624	404	117	103		
7	R	72	Total	C	N	O	0	0
			609	396	112	101		

- Molecule 8 is a protein called Cytochrome b-c1 complex subunit 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	68	Total	C	N	O	S	0	0
			563	343	103	112	5		
8	S	68	Total	C	N	O	S	0	0
			563	343	103	112	5		

- Molecule 9 is a protein called Cytochrome b-c1 complex subunit 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	J	60	Total	C	N	O	0	0
			495	323	86	86		
9	U	60	Total	C	N	O	0	0
			495	323	86	86		

- Molecule 10 is a protein called Cytochrome b-c1 complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	52	Total	C	N	O	S	0	0
			429	286	75	66	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
10	V	53	Total	C	N	O	S	0	0
			438	292	77	67	2		

- Molecule 11 is a protein called Cytochrome b-c1 complex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	T	78	Total	C	N	O	S	0	0
			554	352	103	97	2		

- Molecule 12 is a protein called Cox7a2l protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	111	Total	C	N	O	S	0	0
			828	539	138	146	5		

- Molecule 13 is a protein called Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	a	514	Total	C	N	O	S	0	0
			4021	2691	623	675	32		

- Molecule 14 is a protein called Cytochrome c oxidase subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	b	227	Total	C	N	O	S	0	0
			1817	1180	282	336	19		

- Molecule 15 is a protein called Cytochrome c oxidase subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	c	259	Total	C	N	O	S	0	0
			2111	1414	338	349	10		

- Molecule 16 is a protein called Cytochrome c oxidase subunit 4 isoform 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	d	144	Total	C	N	O	S	0	0
			1195	770	199	219	7		

- Molecule 17 is a protein called Cytochrome c oxidase subunit 5A, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	e	104	Total	C	N	O	S	0	0
			842	538	141	161	2		

- Molecule 18 is a protein called Cytochrome c oxidase subunit 5B, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	f	95	Total	C	N	O	S	0	0
			727	452	127	140	8		

- Molecule 19 is a protein called Cytochrome c oxidase subunit 6A2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	g	75	Total	C	N	O	S	0	0
			605	392	114	96	3		

- Molecule 20 is a protein called Cytochrome c oxidase subunit 6B1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	h	79	Total	C	N	O	S	0	0
			654	416	116	117	5		

- Molecule 21 is a protein called Cytochrome c oxidase subunit 6C.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	i	72	Total	C	N	O	S	0	0
			572	372	103	94	3		

- Molecule 22 is a protein called Cytochrome c oxidase subunit 7B, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	k	49	Total	C	N	O	S	0	0
			383	248	65	68	2		

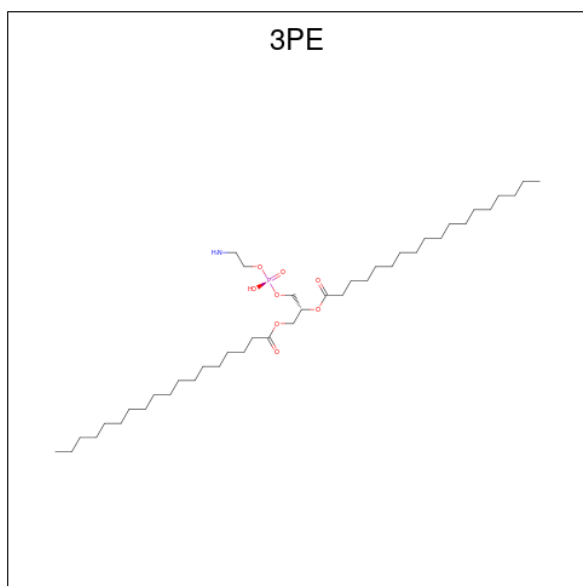
- Molecule 23 is a protein called Cytochrome c oxidase subunit 7C, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	l	46	Total	C	N	O	S	0	0
			380	253	64	61	2		

- Molecule 24 is a protein called Cytochrome c oxidase subunit 8B, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	m	43	Total	C	N	O	S	0	0
			311	203	51	56	1		

- Molecule 25 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$).



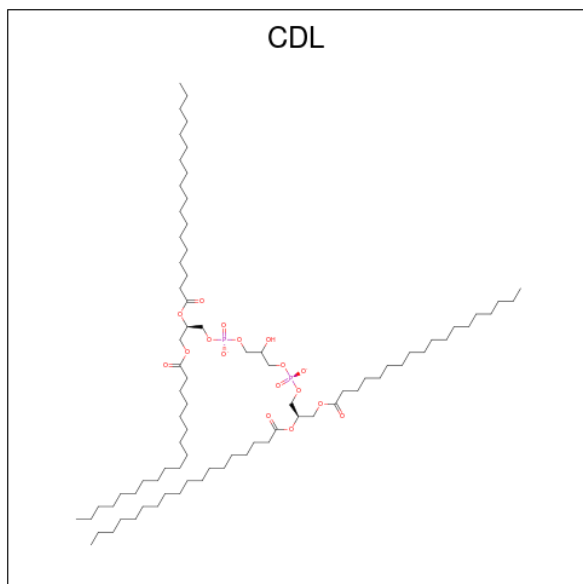
Mol	Chain	Residues	Atoms					AltConf
25	A	1	Total	C	N	O	P	0
			23	13	1	8	1	
25	C	1	Total	C	N	O	P	0
			35	25	1	8	1	
25	D	1	Total	C	N	O	P	0
			32	22	1	8	1	
25	F	1	Total	C	N	O	P	0
			37	27	1	8	1	
25	G	1	Total	C	N	O	P	0
			42	32	1	8	1	
25	L	1	Total	C	N	O	P	0
			23	13	1	8	1	
25	N	1	Total	C	N	O	P	0
			37	27	1	8	1	
25	O	1	Total	C	N	O	P	0
			23	13	1	8	1	
25	R	1	Total	C	N	O	P	0
			51	41	1	8	1	
25	a	1	Total	C	N	O	P	0
			34	24	1	8	1	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf
25	a	1	Total	C	N	O	P	0
			28	18	1	8	1	
25	b	1	Total	C	N	O	P	0
			29	19	1	8	1	
25	b	1	Total	C	N	O	P	0
			28	18	1	8	1	
25	c	1	Total	C	N	O	P	0
			45	35	1	8	1	
25	g	1	Total	C	N	O	P	0
			25	15	1	8	1	
25	k	1	Total	C	N	O	P	0
			27	17	1	8	1	

- Molecule 26 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



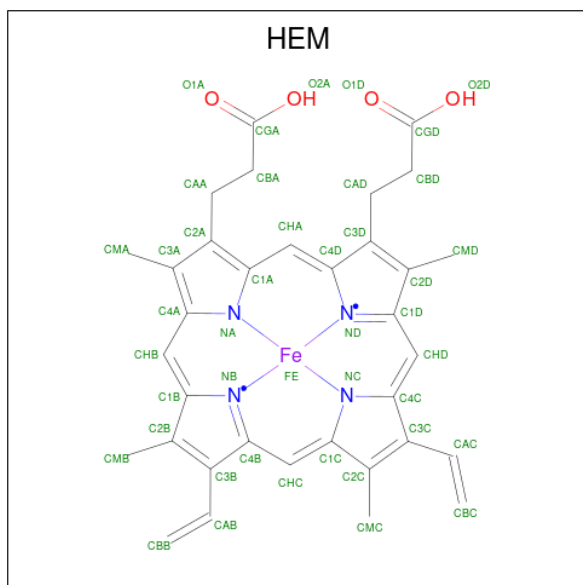
Mol	Chain	Residues	Atoms				AltConf
26	A	1	Total	C	O	P	0
			46	27	17	2	
26	D	1	Total	C	O	P	0
			56	37	17	2	
26	G	1	Total	C	O	P	0
			42	23	17	2	
26	L	1	Total	C	O	P	0
			46	27	17	2	
26	O	1	Total	C	O	P	0
			57	38	17	2	

Continued on next page...

Continued from previous page...

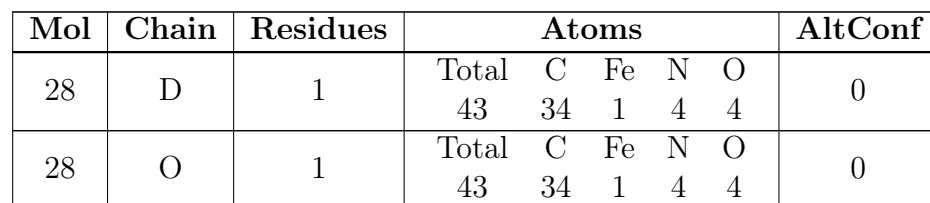
Mol	Chain	Residues	Atoms				AltConf
26	R	1	Total	C	O	P	0
			41	22	17	2	

- Molecule 27 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms					AltConf
27	C	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
27	C	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
27	N	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
27	N	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

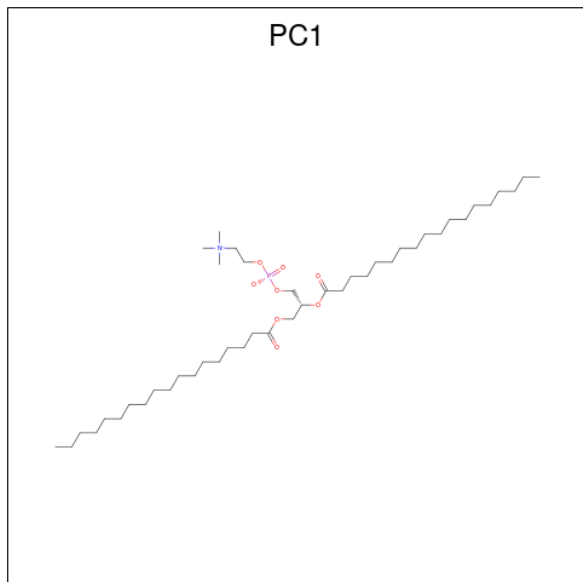
- Molecule 28 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



-
- Diagram illustrating the structure of a ferredoxin (FES) molecule, showing a square planar arrangement of two iron (Fe) and two sulfur (S) atoms. The atoms are labeled S1, S2, FE1, and FE2. The bonds between S1-Fe2, Fe1-S2, and S1-S2 are yellow, while the bond between Fe1-Fe2 is purple.

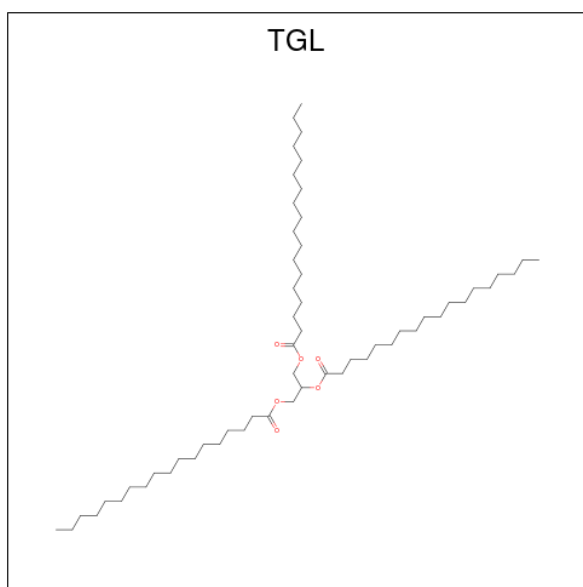
Mol	Chain	Residues	Atoms			AltConf
29	E	1	Total 4	Fe 2	S 2	0
29	P	1	Total 4	Fe 2	S 2	0

- Molecule 30 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$).



Mol	Chain	Residues	Atoms					AltConf
30	E	1	Total	C	N	O	P	0
			35	25	1	8	1	
30	G	1	Total	C	N	O	P	0
			35	25	1	8	1	
30	G	1	Total	C	N	O	P	0
			43	33	1	8	1	
30	U	1	Total	C	N	O	P	0
			24	14	1	8	1	
30	a	1	Total	C	N	O	P	0
			43	33	1	8	1	

- Molecule 31 is TRISTEAROYLGLYCEROL (CCD ID: TGL) (formula: $C_{57}H_{110}O_6$).



Mol	Chain	Residues	Atoms			AltConf
31	G	1	Total	C	O	0
			44	38	6	

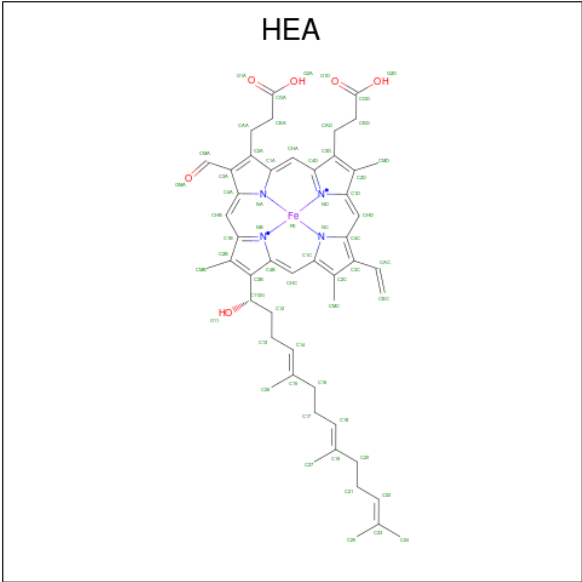
- Molecule 32 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		AltConf
32	a	1	Total	Cu	0
			1	1	

- Molecule 33 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
33	a	1	Total	Na	0
			1	1	

- Molecule 34 is HEME-A (CCD ID: HEA) (formula: C₄₉H₅₆FeN₄O₆).

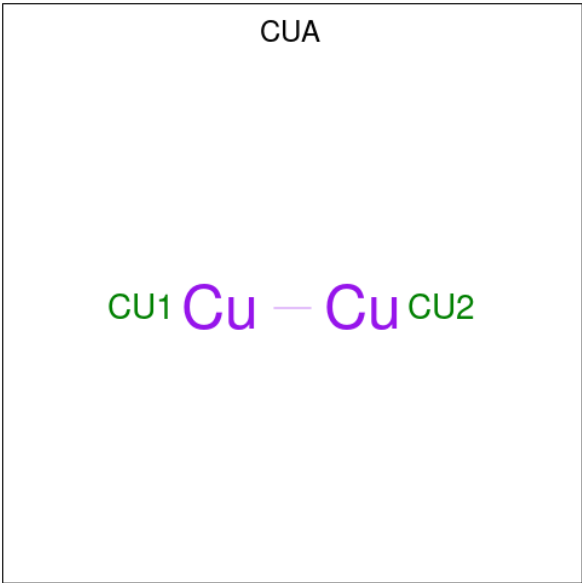


Mol	Chain	Residues	Atoms					AltConf
34	a	1	Total 60	C 49	Fe 1	N 4	O 6	0
34	a	1	Total 60	C 49	Fe 1	N 4	O 6	0

- Molecule 35 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
35	b	1	Total	Mg	0
			1	1	

- Molecule 36 is DINUCLEAR COPPER ION (CCD ID: CUA) (formula: Cu₂).



Mol	Chain	Residues	Atoms		AltConf
36	b	1	Total	Cu	0
			2	2	

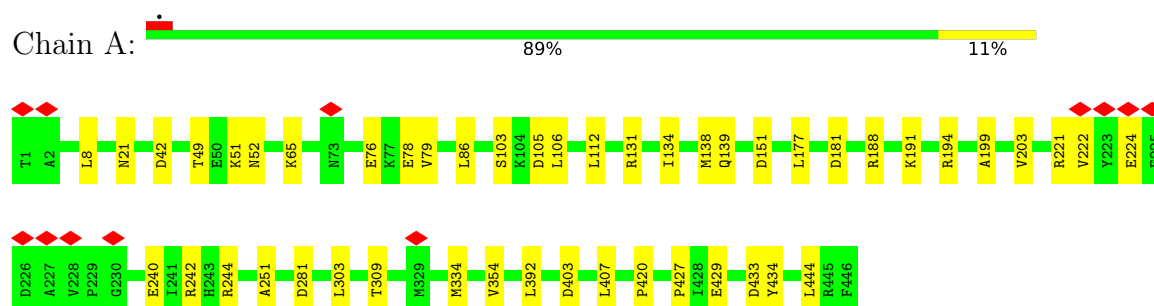
- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
37	f	1	Total	Zn	0
			1	1	

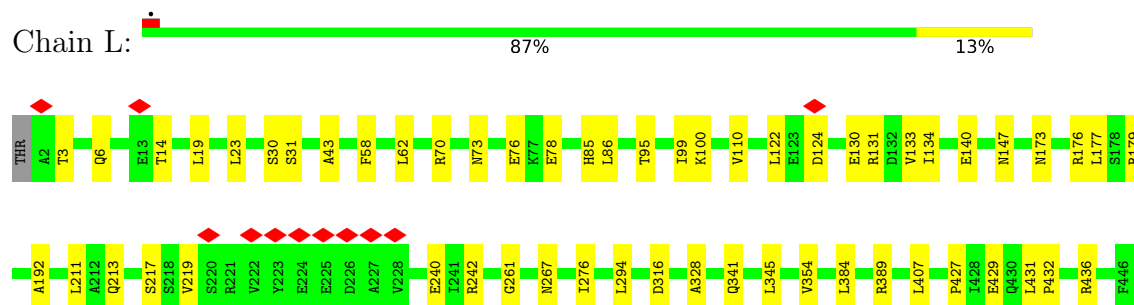
3 Residue-property plots

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: Cytochrome b-c1 complex subunit 1, mitochondrial



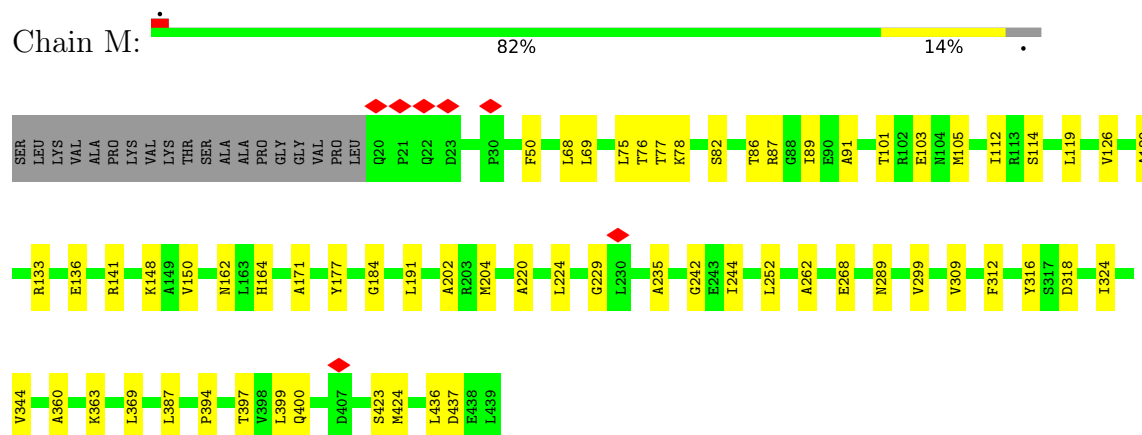
- Molecule 1: Cytochrome b-c1 complex subunit 1, mitochondrial



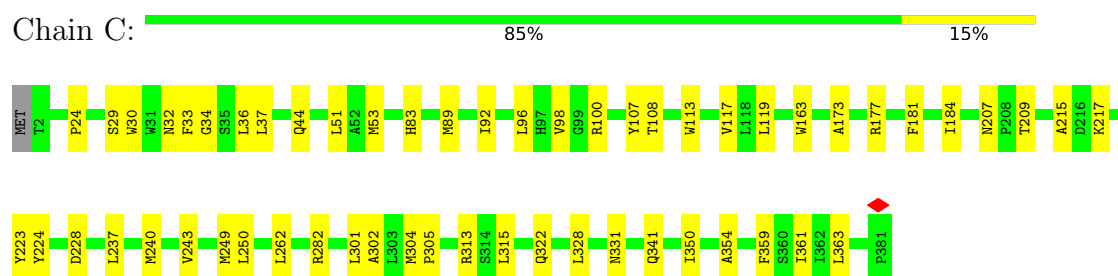
- Molecule 2: Cytochrome b-c1 complex subunit 2, mitochondrial



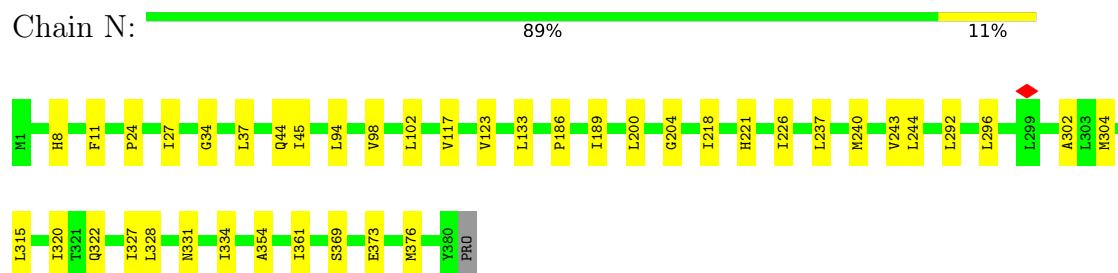
- Molecule 2: Cytochrome b-c1 complex subunit 2, mitochondrial



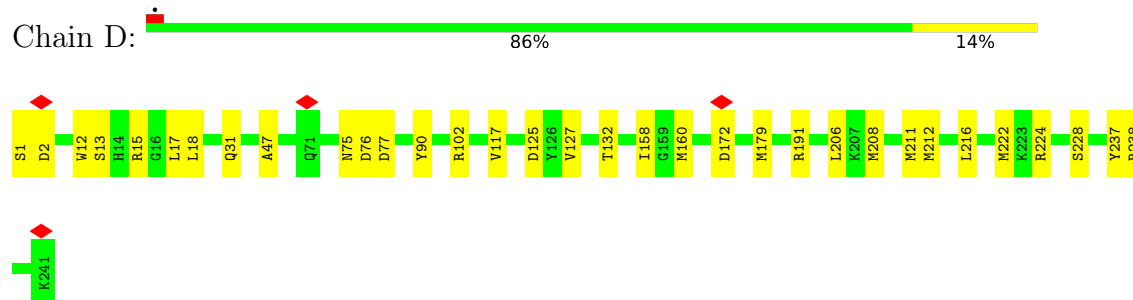
- Molecule 3: Cytochrome b



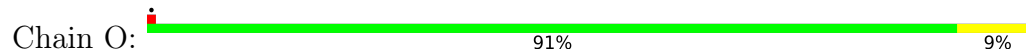
- Molecule 3: Cytochrome b



- Molecule 4: Cytochrome c1, heme protein, mitochondrial

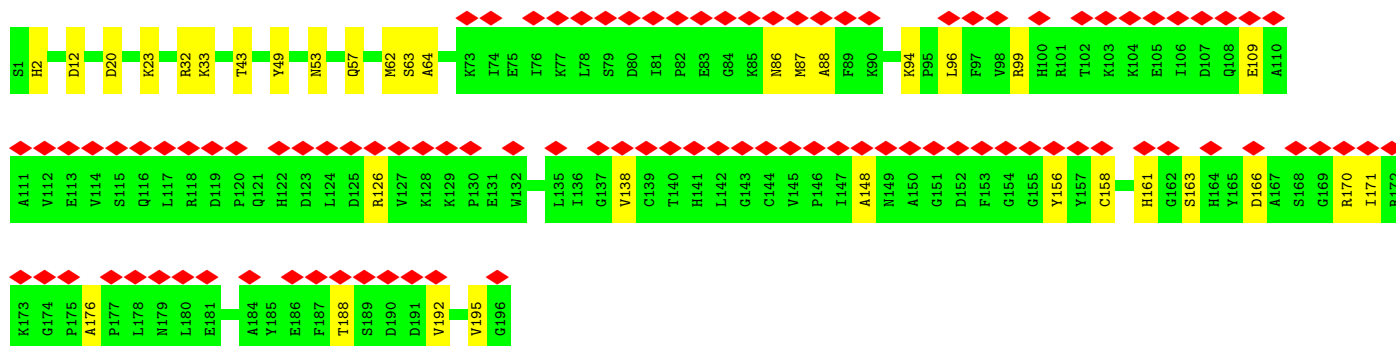
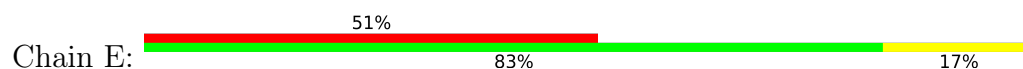


- Molecule 4: Cytochrome c1, heme protein, mitochondrial

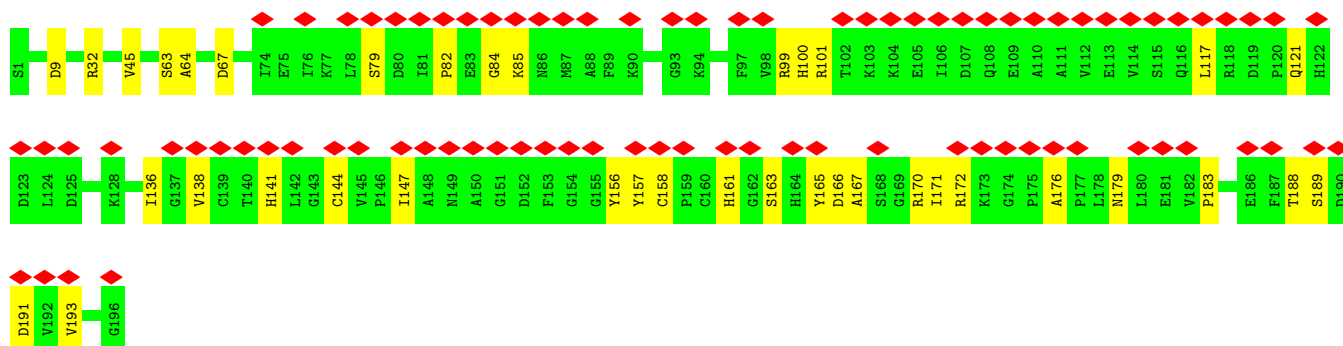
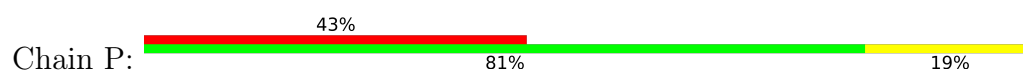




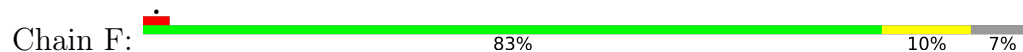
- Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial



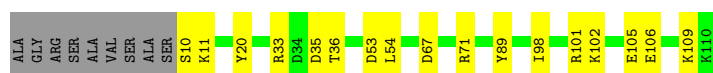
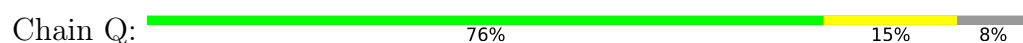
- Molecule 5: Cytochrome b-c1 complex subunit Rieske, mitochondrial



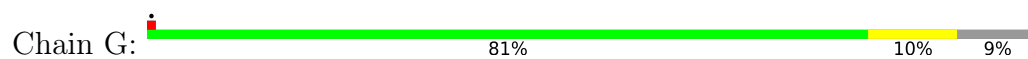
- Molecule 6: Cytochrome b-c1 complex subunit 7



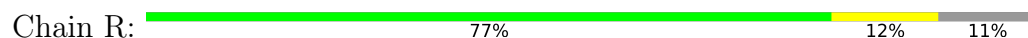
- Molecule 6: Cytochrome b-c1 complex subunit 7



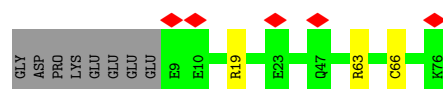
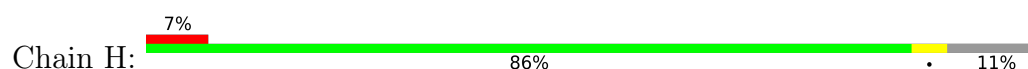
- Molecule 7: Cytochrome b-c1 complex subunit 8



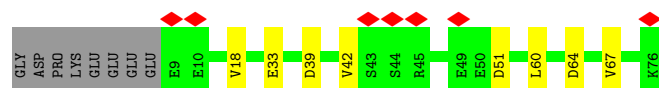
- Molecule 7: Cytochrome b-c1 complex subunit 8



- Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial



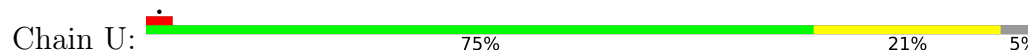
- Molecule 8: Cytochrome b-c1 complex subunit 6, mitochondrial



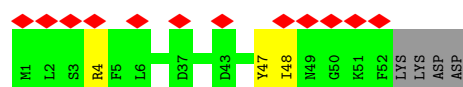
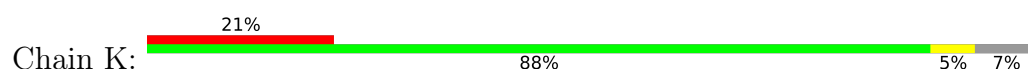
- Molecule 9: Cytochrome b-c1 complex subunit 9



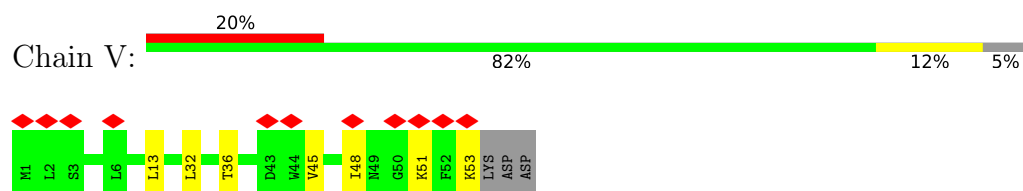
- Molecule 9: Cytochrome b-c1 complex subunit 9



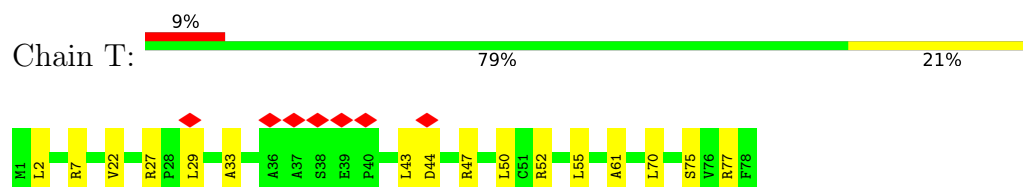
- Molecule 10: Cytochrome b-c1 complex subunit 10



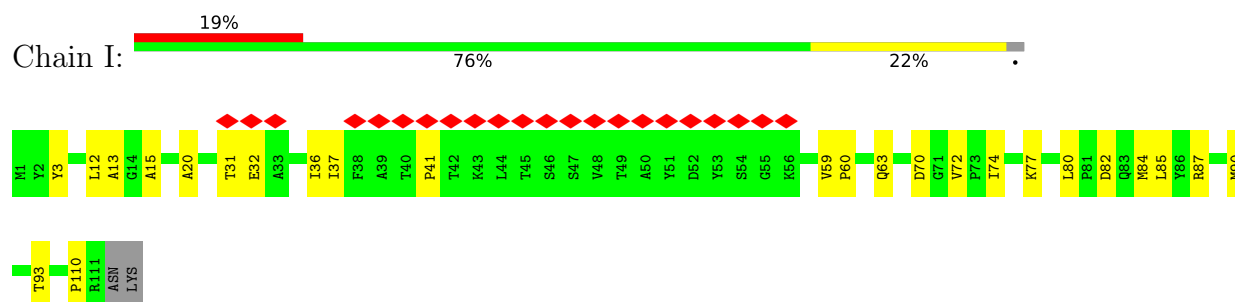
- Molecule 10: Cytochrome b-c1 complex subunit 10



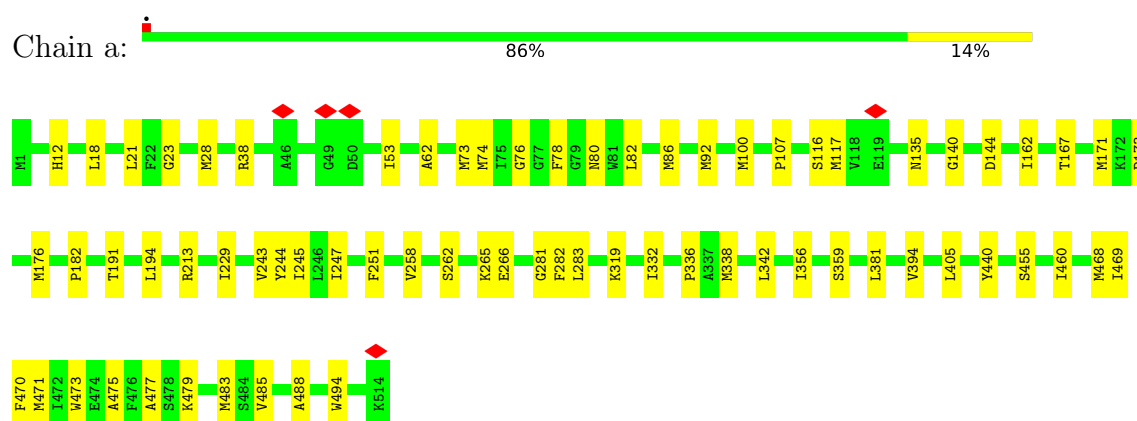
- Molecule 11: Cytochrome b-c1 complex subunit 9



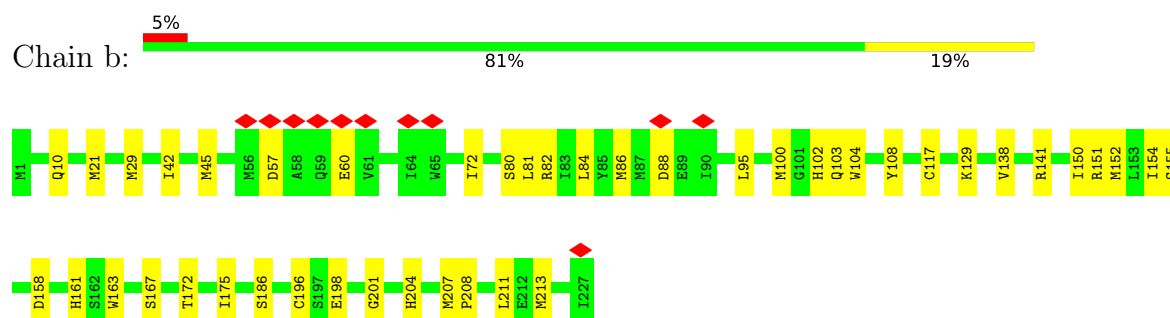
- Molecule 12: Cox7a2l protein



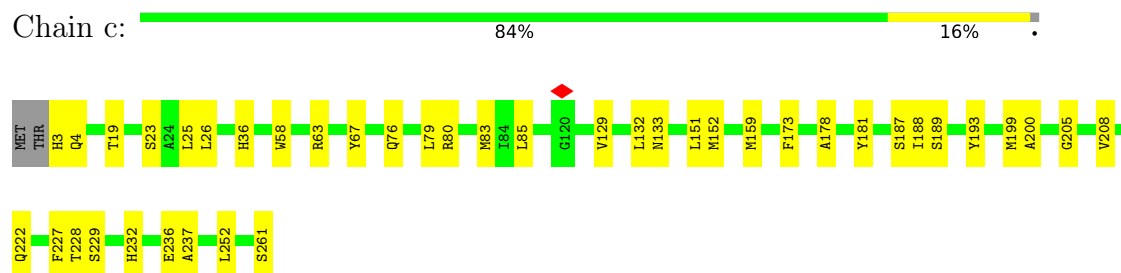
- Molecule 13: Cytochrome c oxidase subunit 1



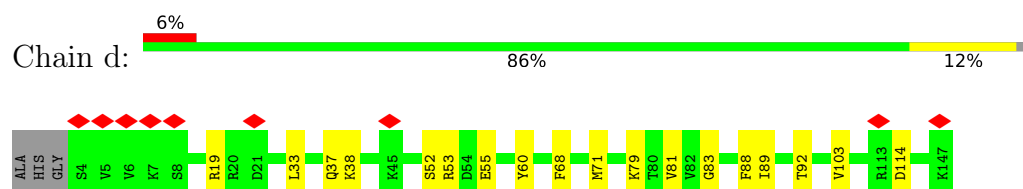
- Molecule 14: Cytochrome c oxidase subunit 2



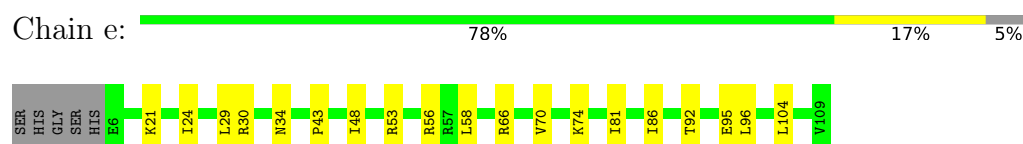
- Molecule 15: Cytochrome c oxidase subunit 3



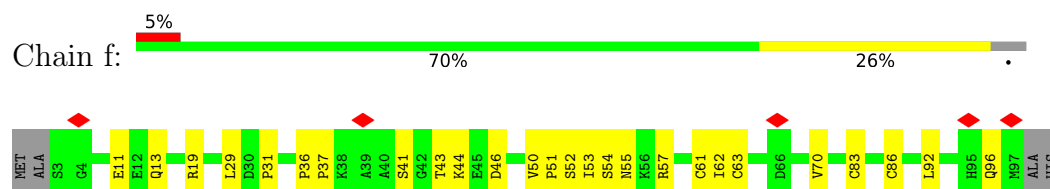
- Molecule 16: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial



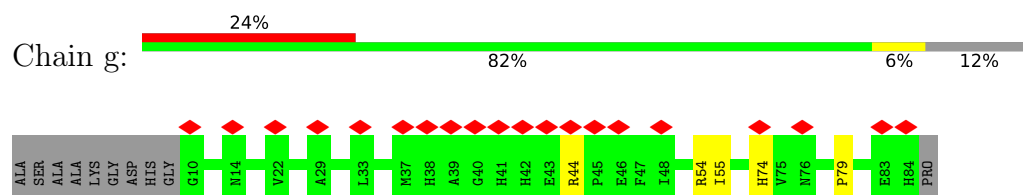
- Molecule 17: Cytochrome c oxidase subunit 5A, mitochondrial



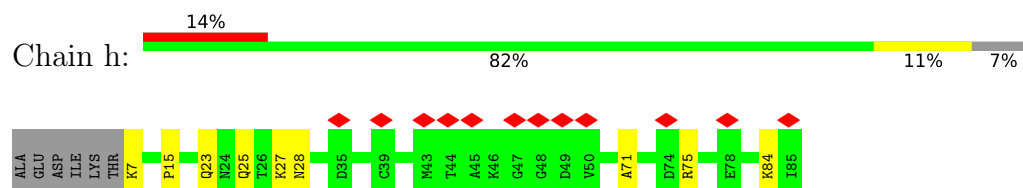
- Molecule 18: Cytochrome c oxidase subunit 5B, mitochondrial



- Molecule 19: Cytochrome c oxidase subunit 6A2, mitochondrial



- Molecule 20: Cytochrome c oxidase subunit 6B1



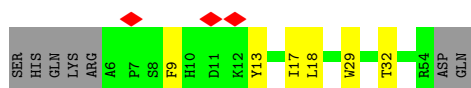
- Molecule 21: Cytochrome c oxidase subunit 6C

Chain i:  87% 9% .



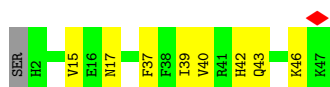
- Molecule 22: Cytochrome c oxidase subunit 7B, mitochondrial

Chain k:  5% 77% 11% 12%



- Molecule 23: Cytochrome c oxidase subunit 7C, mitochondrial

Chain l:  81% 17% .



- Molecule 24: Cytochrome c oxidase subunit 8B, mitochondrial

Chain m:  7% 83% 11% 7%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided, Not provided, Not provided, C1, Not provided, Not provided, Not provided	Depositor
Number of particles used	14851	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	90.66	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.332	Depositor
Minimum map value	-0.028	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	165.98401, 217.056, 176.62401	wwPDB
Map dimensions	166, 204, 156	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.064, 1.064, 1.064	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CDL, CUA, HEM, 3PE, HEC, HEA, ZN, FES, PC1, CU, MG, TGL, NA

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	0.22	0/3536	0.49	0/4803
1	L	0.23	0/3530	0.50	1/4793 (0.0%)
2	B	0.19	0/3205	0.43	0/4332
2	M	0.19	0/3205	0.42	0/4332
3	C	0.25	0/3147	0.53	0/4299
3	N	0.24	0/3147	0.52	0/4297
4	D	0.21	0/1978	0.45	0/2685
4	O	0.18	0/1968	0.40	0/2674
5	E	0.19	0/1545	0.45	0/2091
5	P	0.19	0/1545	0.46	0/2091
6	F	0.18	0/922	0.38	0/1234
6	Q	0.20	0/916	0.43	0/1226
7	G	0.27	0/642	0.54	0/867
7	R	0.26	0/627	0.57	0/848
8	H	0.25	0/570	0.58	1/763 (0.1%)
8	S	0.26	0/570	0.69	1/763 (0.1%)
9	J	0.23	0/509	0.54	0/687
9	U	0.24	0/509	0.55	0/687
10	K	0.20	0/445	0.46	0/608
10	V	0.24	0/454	0.55	0/619
11	T	0.22	0/565	0.50	0/772
12	I	0.28	0/849	0.69	1/1153 (0.1%)
13	a	0.31	0/4162	0.63	1/5686 (0.0%)
14	b	0.31	0/1863	0.68	4/2542 (0.2%)
15	c	0.27	0/2195	0.54	0/3000
16	d	0.25	0/1229	0.55	0/1659
17	e	0.28	0/860	0.59	0/1167
18	f	0.27	0/744	0.64	0/1009
19	g	0.20	0/632	0.50	0/866
20	h	0.26	0/674	0.66	0/910
21	i	0.26	0/584	0.56	0/778
22	k	0.29	0/396	0.62	0/541

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
23	l	0.28	0/393	0.48	0/527
24	m	0.26	0/318	0.57	0/433
All	All	0.24	0/48434	0.52	9/65742 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
18	f	0	1

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	I	41	PRO	N-CA-CB	7.48	110.30	103.34
14	b	45	MET	CB-CG-SD	-6.57	93.00	112.70
8	S	33	GLU	N-CA-CB	5.71	119.70	110.40
14	b	103	GLN	CA-C-N	5.67	132.37	121.54
14	b	103	GLN	C-N-CA	5.67	132.37	121.54

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
18	f	61	CYS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3466	0	3377	32	0
1	L	3460	0	3367	31	0
2	B	3154	0	3158	43	0
2	M	3154	0	3158	37	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	3045	0	3107	41	0
3	N	3046	0	3112	27	0
4	D	1919	0	1867	24	0
4	O	1909	0	1854	16	0
5	E	1512	0	1495	24	0
5	P	1512	0	1495	25	0
6	F	900	0	887	6	0
6	Q	894	0	882	10	0
7	G	624	0	633	9	0
7	R	609	0	614	8	0
8	H	563	0	541	1	0
8	S	563	0	541	5	0
9	J	495	0	489	9	0
9	U	495	0	489	8	0
10	K	429	0	430	3	0
10	V	438	0	443	4	0
11	T	554	0	590	15	0
12	I	828	0	807	18	0
13	a	4021	0	3997	52	0
14	b	1817	0	1822	30	0
15	c	2111	0	2047	28	0
16	d	1195	0	1161	16	0
17	e	842	0	838	12	0
18	f	727	0	703	16	0
19	g	605	0	570	3	0
20	h	654	0	622	7	0
21	i	572	0	596	5	0
22	k	383	0	367	4	0
23	l	380	0	378	9	0
24	m	311	0	329	6	0
25	A	23	0	20	1	0
25	C	35	0	44	0	0
25	D	32	0	38	1	0
25	F	37	0	48	2	0
25	G	42	0	61	0	0
25	L	23	0	20	1	0
25	N	37	0	48	0	0
25	O	23	0	20	0	0
25	R	51	0	82	2	0
25	a	62	0	72	3	0
25	b	57	0	62	1	0
25	c	45	0	67	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	g	25	0	24	2	0
25	k	27	0	28	0	0
26	A	46	0	36	1	0
26	D	56	0	56	1	0
26	G	42	0	28	2	0
26	L	46	0	36	1	0
26	O	57	0	58	0	0
26	R	41	0	26	0	0
27	C	86	0	60	5	0
27	N	86	0	60	3	0
28	D	43	0	30	0	0
28	O	43	0	30	1	0
29	E	4	0	0	0	0
29	P	4	0	0	0	0
30	E	35	0	44	1	0
30	G	78	0	104	4	0
30	U	24	0	22	0	0
30	a	43	0	60	0	0
31	G	44	0	63	1	0
32	a	1	0	0	0	0
33	a	1	0	0	0	0
34	a	120	0	108	6	0
35	b	1	0	0	0	0
36	b	2	0	0	0	0
37	f	1	0	0	0	0
All	All	48610	0	48221	512	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 512 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)
5:P:156:TYR:HB2	5:P:165:TYR:HB2	1.69	0.74
3:C:100:ARG:HH12	27:C:402:HEM:HBD1	1.58	0.68
17:e:70:VAL:O	17:e:74:LYS:HB2	1.94	0.67
23:l:37:PHE:HB3	24:m:33:VAL:HG11	1.76	0.67
13:a:194:LEU:HB2	13:a:245:ILE:HD11	1.78	0.65

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	444/446 (100%)	426 (96%)	18 (4%)	0	100	100
1	L	443/446 (99%)	428 (97%)	15 (3%)	0	100	100
2	B	418/439 (95%)	403 (96%)	15 (4%)	0	100	100
2	M	418/439 (95%)	402 (96%)	16 (4%)	0	100	100
3	C	378/381 (99%)	367 (97%)	11 (3%)	0	100	100
3	N	378/381 (99%)	368 (97%)	10 (3%)	0	100	100
4	D	239/241 (99%)	237 (99%)	2 (1%)	0	100	100
4	O	238/241 (99%)	234 (98%)	4 (2%)	0	100	100
5	E	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
5	P	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
6	F	100/110 (91%)	100 (100%)	0	0	100	100
6	Q	99/110 (90%)	98 (99%)	1 (1%)	0	100	100
7	G	72/81 (89%)	66 (92%)	6 (8%)	0	100	100
7	R	70/81 (86%)	67 (96%)	3 (4%)	0	100	100
8	H	66/76 (87%)	64 (97%)	2 (3%)	0	100	100
8	S	66/76 (87%)	64 (97%)	2 (3%)	0	100	100
9	J	58/63 (92%)	56 (97%)	2 (3%)	0	100	100
9	U	58/63 (92%)	56 (97%)	2 (3%)	0	100	100
10	K	50/56 (89%)	48 (96%)	2 (4%)	0	100	100
10	V	51/56 (91%)	48 (94%)	3 (6%)	0	100	100
11	T	76/78 (97%)	67 (88%)	9 (12%)	0	100	100
12	I	109/113 (96%)	99 (91%)	10 (9%)	0	100	100
13	a	512/514 (100%)	498 (97%)	14 (3%)	0	100	100
14	b	225/227 (99%)	209 (93%)	16 (7%)	0	100	100
15	c	257/261 (98%)	248 (96%)	9 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	d	142/147 (97%)	133 (94%)	9 (6%)	0	100	100
17	e	102/109 (94%)	99 (97%)	3 (3%)	0	100	100
18	f	93/99 (94%)	85 (91%)	8 (9%)	0	100	100
19	g	73/85 (86%)	68 (93%)	5 (7%)	0	100	100
20	h	77/85 (91%)	74 (96%)	3 (4%)	0	100	100
21	i	70/75 (93%)	68 (97%)	2 (3%)	0	100	100
22	k	47/56 (84%)	45 (96%)	2 (4%)	0	100	100
23	l	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
24	m	41/46 (89%)	39 (95%)	2 (5%)	0	100	100
All	All	5902/6120 (96%)	5682 (96%)	220 (4%)	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	373/373 (100%)	372 (100%)	1 (0%)	86	88
1	L	372/373 (100%)	372 (100%)	0	100	100
2	B	330/344 (96%)	329 (100%)	1 (0%)	86	88
2	M	330/344 (96%)	330 (100%)	0	100	100
3	C	332/333 (100%)	332 (100%)	0	100	100
3	N	332/333 (100%)	332 (100%)	0	100	100
4	D	206/206 (100%)	206 (100%)	0	100	100
4	O	205/206 (100%)	205 (100%)	0	100	100
5	E	166/166 (100%)	166 (100%)	0	100	100
5	P	166/166 (100%)	166 (100%)	0	100	100
6	F	94/98 (96%)	94 (100%)	0	100	100
6	Q	93/98 (95%)	93 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	G	67/73 (92%)	67 (100%)	0	100	100
7	R	66/73 (90%)	66 (100%)	0	100	100
8	H	65/72 (90%)	65 (100%)	0	100	100
8	S	65/72 (90%)	65 (100%)	0	100	100
9	J	51/54 (94%)	51 (100%)	0	100	100
9	U	51/54 (94%)	51 (100%)	0	100	100
10	K	42/46 (91%)	42 (100%)	0	100	100
10	V	43/46 (94%)	43 (100%)	0	100	100
11	T	58/58 (100%)	58 (100%)	0	100	100
12	I	79/95 (83%)	79 (100%)	0	100	100
13	a	425/425 (100%)	425 (100%)	0	100	100
14	b	210/210 (100%)	210 (100%)	0	100	100
15	c	225/227 (99%)	225 (100%)	0	100	100
16	d	127/128 (99%)	127 (100%)	0	100	100
17	e	91/95 (96%)	91 (100%)	0	100	100
18	f	81/83 (98%)	81 (100%)	0	100	100
19	g	62/67 (92%)	62 (100%)	0	100	100
20	h	70/75 (93%)	70 (100%)	0	100	100
21	i	54/56 (96%)	54 (100%)	0	100	100
22	k	39/46 (85%)	39 (100%)	0	100	100
23	l	39/40 (98%)	39 (100%)	0	100	100
24	m	33/34 (97%)	33 (100%)	0	100	100
All	All	5042/5169 (98%)	5040 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	139	GLN
2	B	289	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
3	N	85	ASN
13	a	55	ASN
22	k	35	GLN
3	N	263	ASN
7	R	64	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 43 ligands modelled in this entry, 4 are monoatomic - leaving 39 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	$\# Z > 2$
26	CDL	G	101	-	41,41,99	0.44	0	47,53,111	0.37	0
29	FES	P	201	5	0,4,4	-	-	-		
25	3PE	F	201	-	36,36,50	0.35	0	39,41,55	0.32	0
30	PC1	E	202	-	34,34,53	0.35	0	40,42,61	0.36	0
36	CUA	b	303	14	0,1,1	-	-	-		
27	HEM	N	402	3	50,50,50	1.34	6 (12%)	67,82,82	1.58	15 (22%)
25	3PE	N	403	-	36,36,50	0.35	0	39,41,55	0.32	0
30	PC1	G	103	-	34,34,53	0.36	0	40,42,61	0.72	1 (2%)
27	HEM	C	401	3	50,50,50	1.32	8 (16%)	67,82,82	1.66	12 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	3PE	C	403	-	34,34,50	0.36	0	37,39,55	0.36	0
26	CDL	O	301	-	56,56,99	0.38	0	62,68,111	0.33	0
28	HEC	D	303	4	46,50,50	1.82	5 (10%)	58,82,82	1.95	5 (8%)
31	TGL	G	104	-	43,43,62	0.20	0	46,46,65	0.25	0
25	3PE	L	501	-	22,22,50	0.44	0	25,27,55	0.45	0
34	HEA	a	603	13	67,67,67	1.35	8 (11%)	81,103,103	2.28	28 (34%)
25	3PE	b	304	-	27,27,50	0.39	0	30,32,55	0.42	0
30	PC1	G	105	-	42,42,53	0.32	0	48,50,61	0.32	0
34	HEA	a	604	13	67,67,67	1.37	7 (10%)	81,103,103	2.19	29 (35%)
28	HEC	O	303	4	46,50,50	1.83	5 (10%)	58,82,82	1.99	5 (8%)
25	3PE	A	501	-	22,22,50	0.46	0	25,27,55	0.74	1 (4%)
26	CDL	A	502	-	45,45,99	0.43	0	51,57,111	0.40	0
26	CDL	D	301	-	55,55,99	0.39	0	61,67,111	0.35	0
27	HEM	C	402	3	50,50,50	1.35	7 (14%)	67,82,82	1.60	14 (20%)
27	HEM	N	401	3	50,50,50	1.32	7 (14%)	67,82,82	1.61	12 (17%)
25	3PE	a	605	-	33,33,50	0.38	0	36,38,55	0.62	2 (5%)
25	3PE	c	301	-	44,44,50	0.32	0	47,49,55	0.34	0
25	3PE	b	302	-	28,28,50	0.40	0	31,33,55	0.36	0
25	3PE	k	101	-	26,26,50	0.41	0	29,31,55	0.39	0
26	CDL	R	101	-	40,40,99	0.47	0	46,52,111	0.61	1 (2%)
25	3PE	R	102	-	50,50,50	0.31	0	53,55,55	0.31	0
30	PC1	a	606	-	42,42,53	0.33	0	48,50,61	0.36	0
25	3PE	D	302	-	31,31,50	0.38	0	34,36,55	0.36	0
25	3PE	g	101	-	24,24,50	0.45	0	27,29,55	0.72	1 (3%)
29	FES	E	201	5	0,4,4	-	-	-	-	-
25	3PE	G	102	-	41,41,50	0.33	0	44,46,55	0.32	0
25	3PE	a	607	-	27,27,50	0.41	0	30,32,55	0.49	0
30	PC1	U	101	-	23,23,53	0.45	0	29,31,61	0.71	1 (3%)
25	3PE	O	302	-	22,22,50	0.44	0	25,27,55	0.45	0
26	CDL	L	502	-	45,45,99	0.44	0	51,57,111	0.58	1 (1%)

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
26	CDL	G	101	-	-	14/52/52/110	-
29	FES	P	201	5	-	-	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	3PE	F	201	-	-	12/40/40/54	-
30	PC1	E	202	-	-	11/38/38/57	-
27	HEM	N	402	3	-	8/14/54/54	-
25	3PE	N	403	-	-	8/40/40/54	-
30	PC1	G	103	-	-	9/37/37/57	-
27	HEM	C	401	3	-	7/14/54/54	-
25	3PE	C	403	-	-	1/38/38/54	-
26	CDL	O	301	-	-	17/67/67/110	-
28	HEC	D	303	4	-	4/14/54/54	-
31	TGL	G	104	-	-	6/46/46/65	-
25	3PE	L	501	-	-	7/26/26/54	-
34	HEA	a	603	13	-	13/36/76/76	-
25	3PE	b	304	-	-	12/31/31/54	-
30	PC1	G	105	-	-	13/46/46/57	-
34	HEA	a	604	13	-	12/36/76/76	-
28	HEC	O	303	4	-	8/14/54/54	-
25	3PE	A	501	-	-	7/26/26/54	-
26	CDL	A	502	-	-	16/56/56/110	-
26	CDL	D	301	-	-	16/66/66/110	-
27	HEM	C	402	3	-	7/14/54/54	-
27	HEM	N	401	3	-	9/14/54/54	-
25	3PE	a	605	-	-	7/37/37/54	-
25	3PE	c	301	-	-	10/48/48/54	-
25	3PE	b	302	-	-	8/32/32/54	-
25	3PE	k	101	-	-	9/30/30/54	-
26	CDL	R	101	-	-	12/51/51/110	-
25	3PE	R	102	-	-	13/54/54/54	-
30	PC1	a	606	-	-	9/46/46/57	-
25	3PE	D	302	-	-	10/35/35/54	-
25	3PE	g	101	-	-	9/28/28/54	-
30	PC1	U	101	-	-	10/27/27/57	-
25	3PE	G	102	-	-	10/45/45/54	-
25	3PE	a	607	-	-	11/31/31/54	-
29	FES	E	201	5	-	-	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	3PE	O	302	-	-	5/26/26/54	-
26	CDL	L	502	-	-	21/56/56/110	-

The worst 5 of 53 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	D	303	HEC	CAB-C3B	6.11	1.54	1.35
28	O	303	HEC	CAC-C3C	6.05	1.54	1.35
28	D	303	HEC	CAC-C3C	6.02	1.54	1.35
28	O	303	HEC	CAB-C3B	5.98	1.54	1.35
28	O	303	HEC	C3D-C2D	5.61	1.53	1.38

The worst 5 of 128 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	D	303	HEC	CBC-CAC-C3C	-9.10	109.25	127.43
28	O	303	HEC	CBC-CAC-C3C	-8.93	109.59	127.43
28	O	303	HEC	CBB-CAB-C3B	-8.55	110.35	127.43
28	D	303	HEC	CBB-CAB-C3B	-8.09	111.27	127.43
34	a	603	HEA	C3A-C2A-C1A	-7.38	100.06	107.05

There are no chirality outliers.

5 of 361 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	A	501	3PE	C1-O11-P-O12
25	A	501	3PE	O13-C11-C12-N
25	C	403	3PE	C11-O13-P-O14
25	D	302	3PE	C1-O11-P-O12
25	D	302	3PE	C1-O11-P-O13

There are no ring outliers.

25 monomers are involved in 39 short contacts:

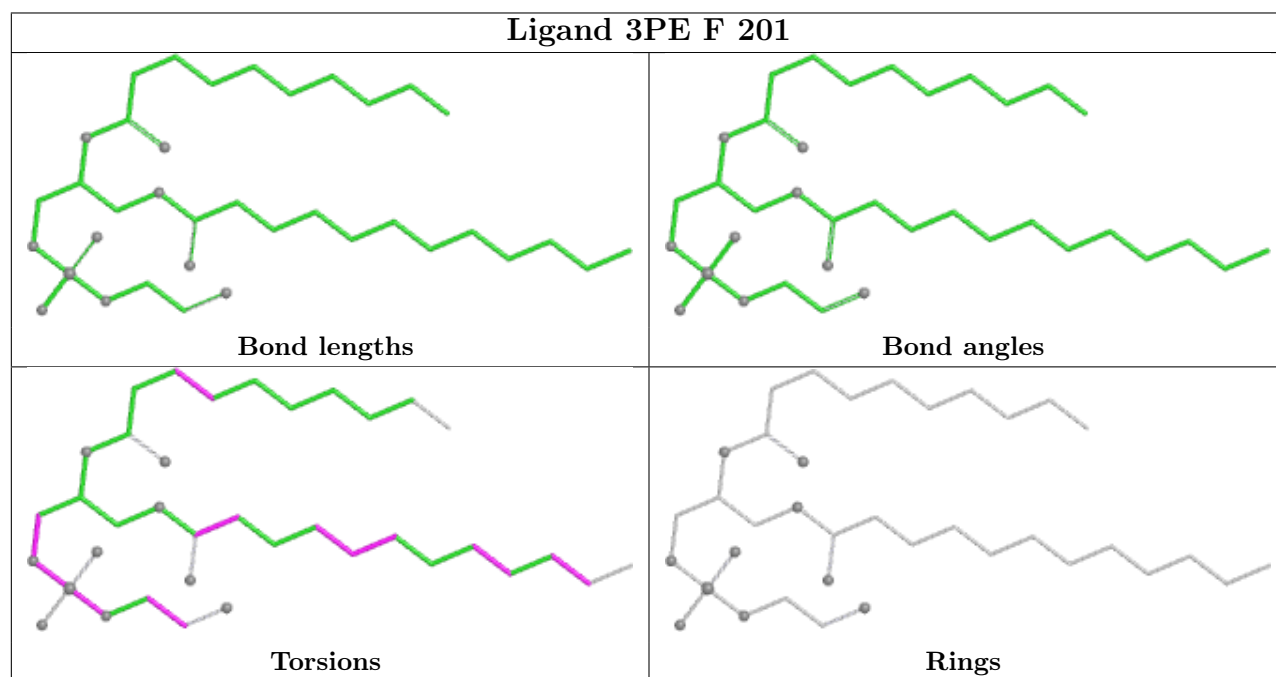
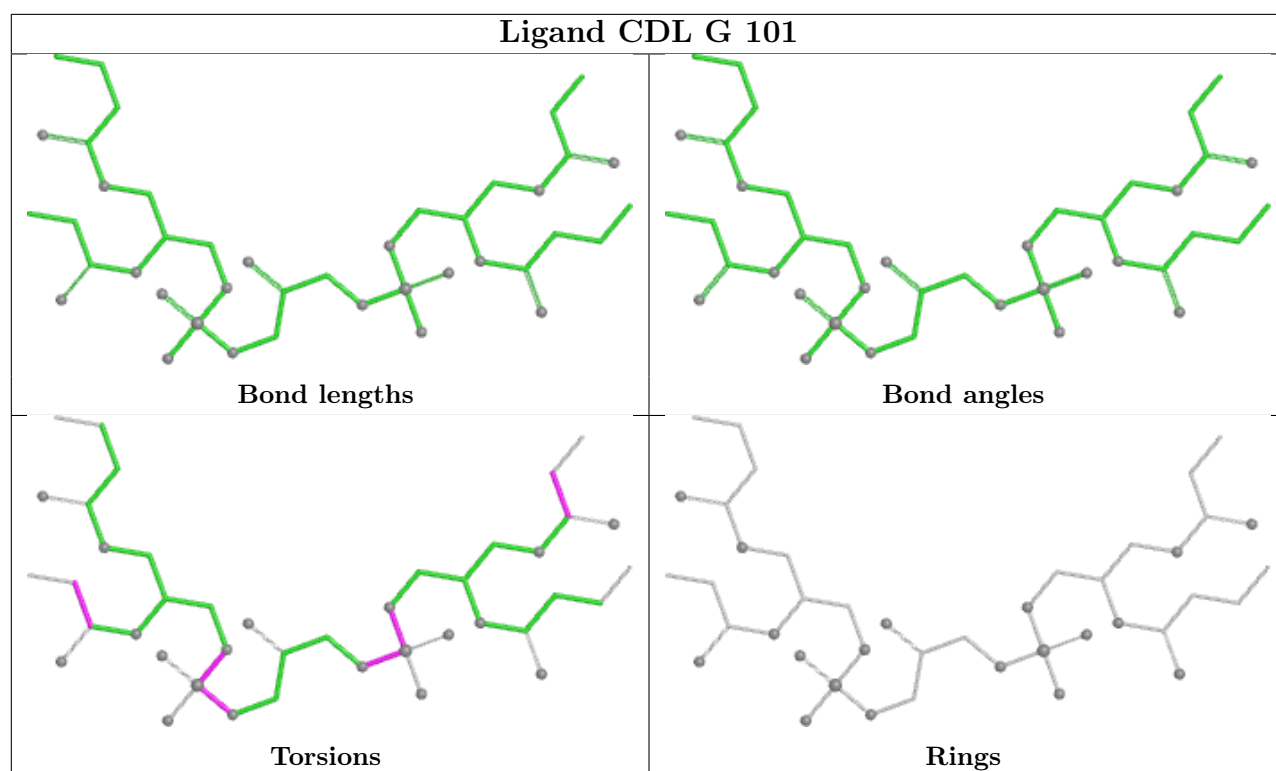
Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	G	101	CDL	2	0
25	F	201	3PE	2	0
30	E	202	PC1	1	0
27	N	402	HEM	1	0
30	G	103	PC1	1	0

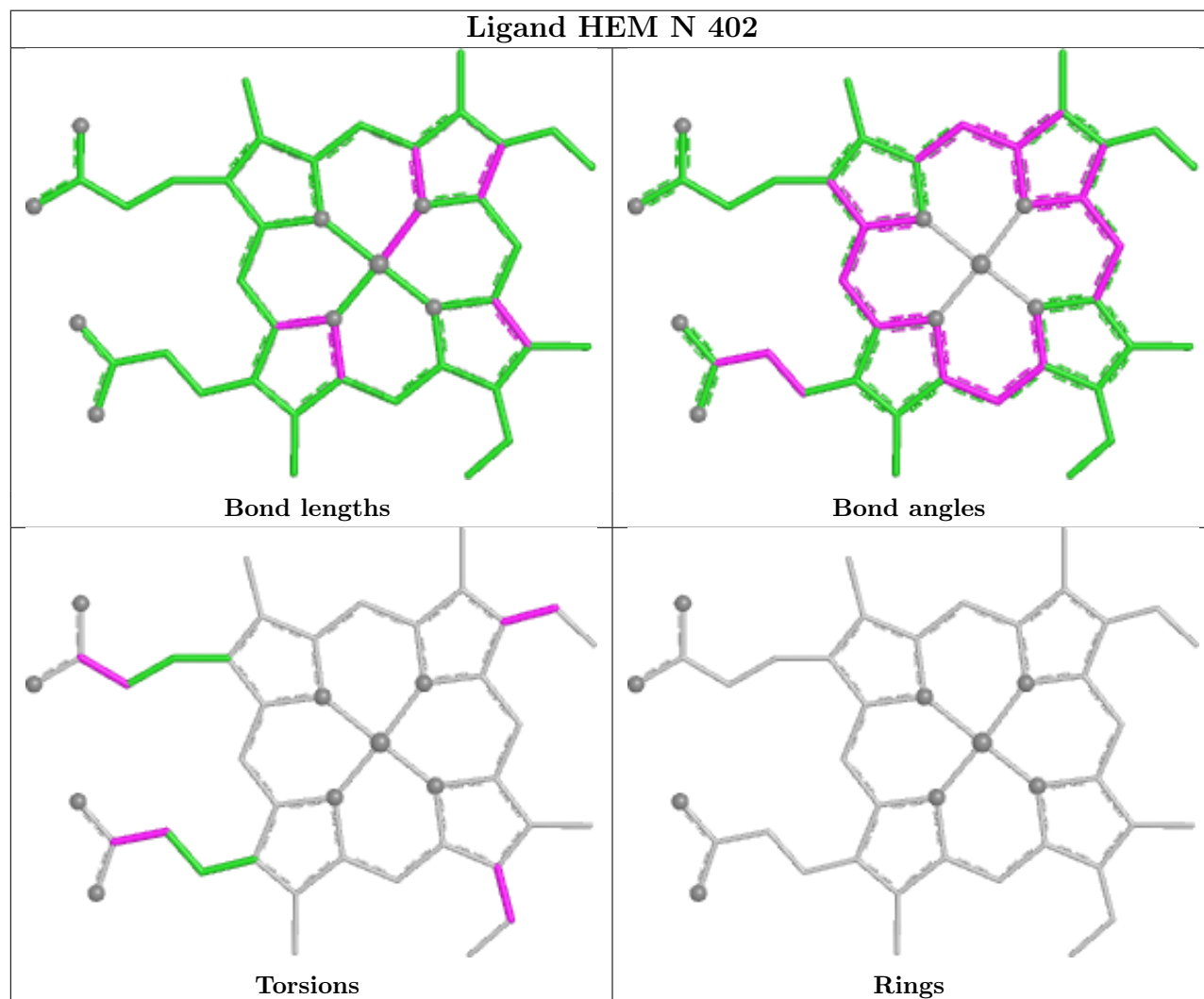
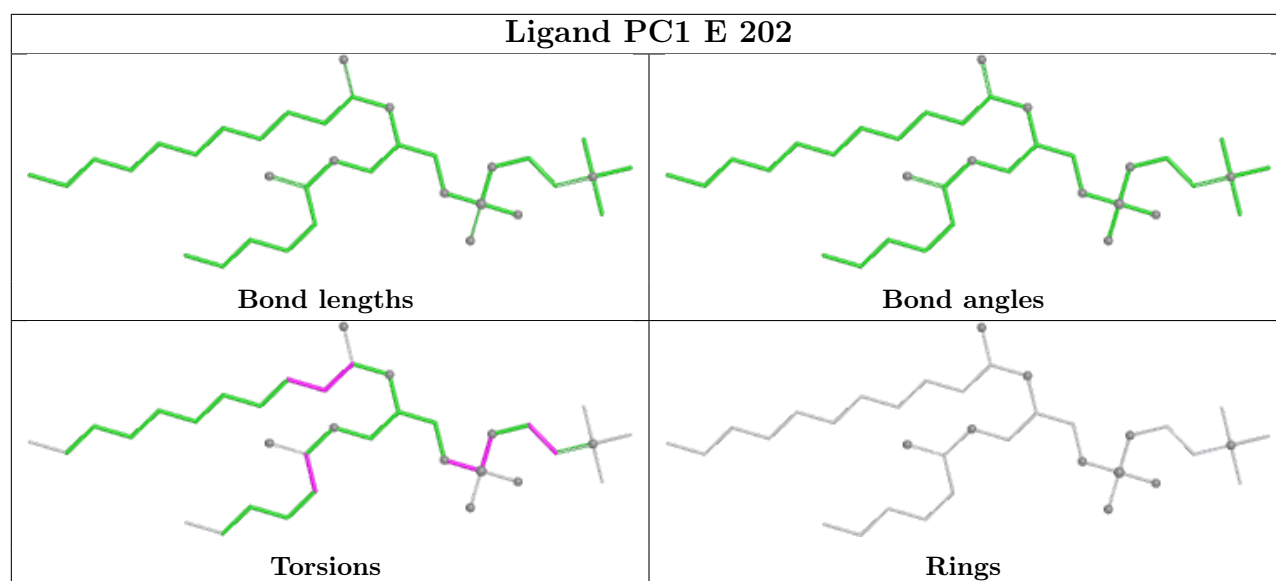
Continued on next page...

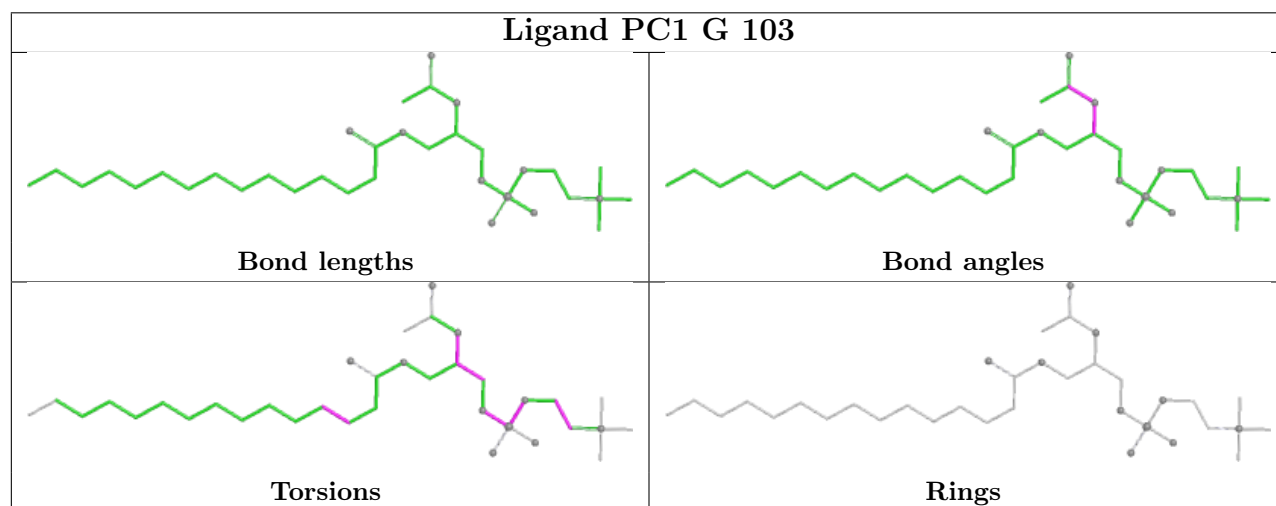
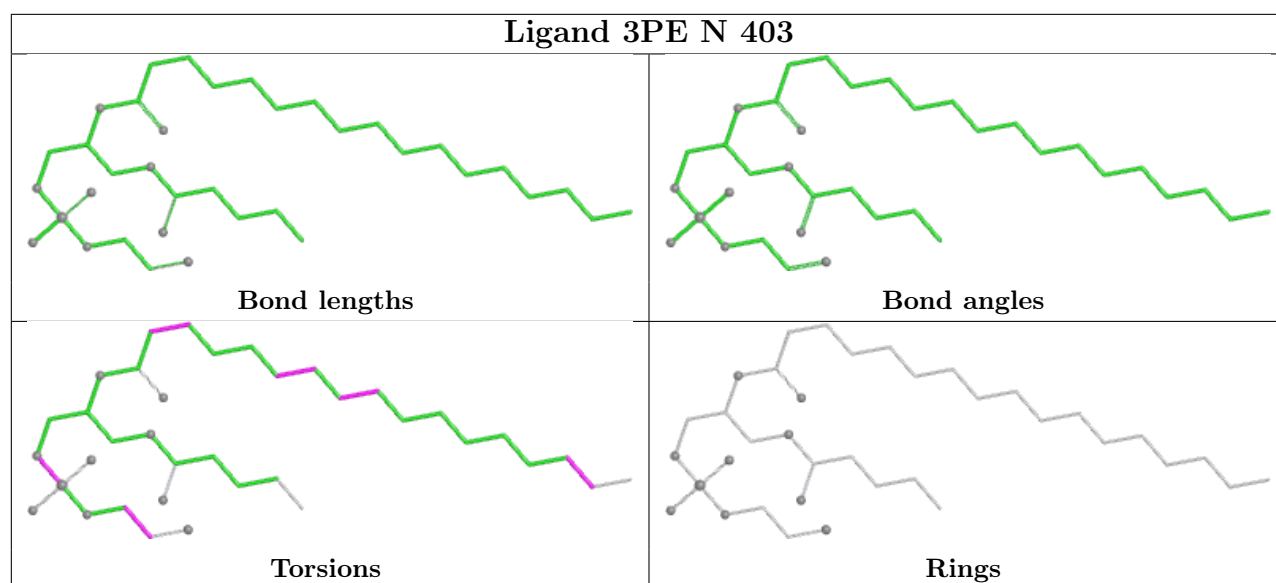
Continued from previous page...

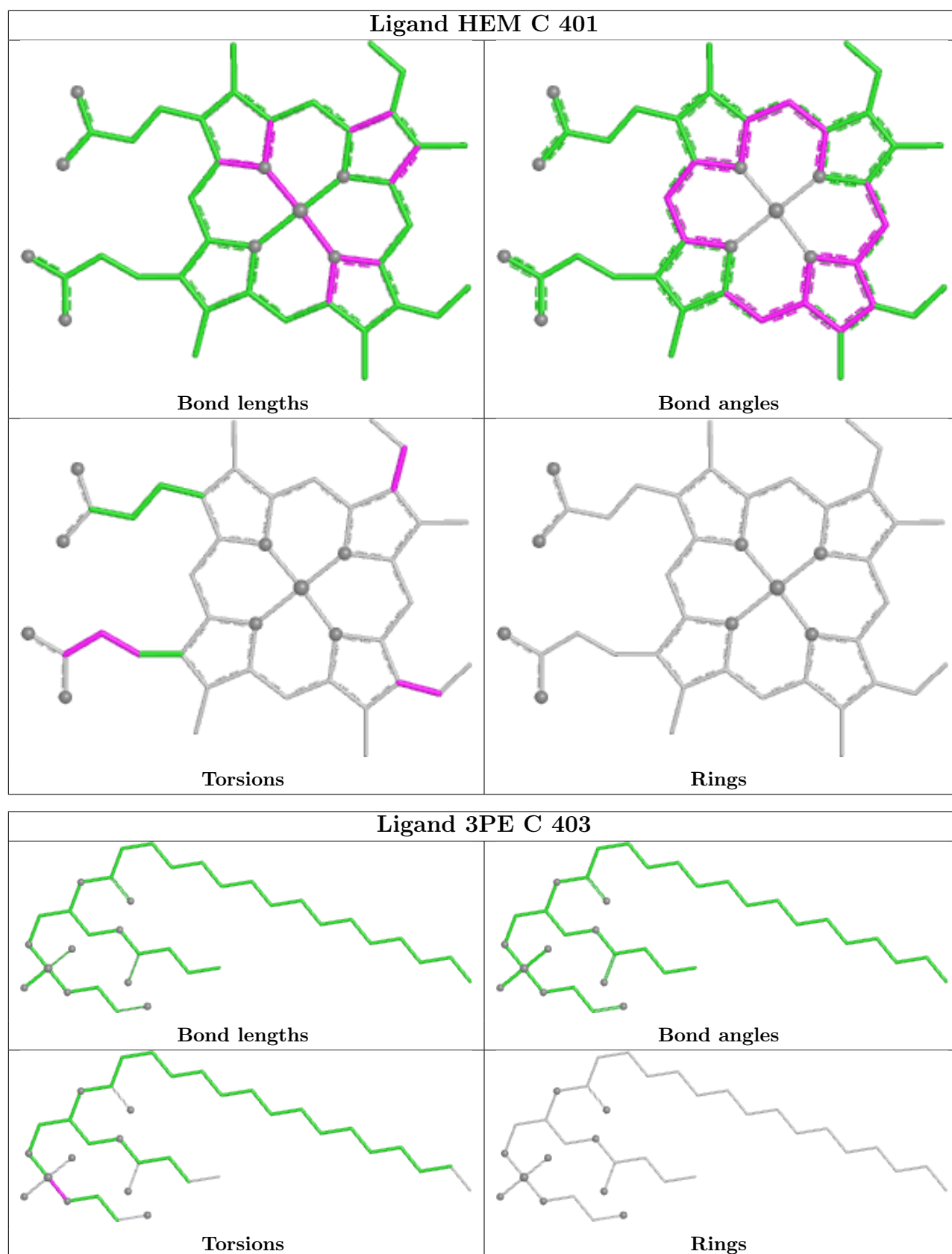
Mol	Chain	Res	Type	Clashes	Symm-Clashes
27	C	401	HEM	2	0
31	G	104	TGL	1	0
25	L	501	3PE	1	0
34	a	603	HEA	2	0
25	b	304	3PE	1	0
30	G	105	PC1	3	0
34	a	604	HEA	4	0
28	O	303	HEC	1	0
25	A	501	3PE	1	0
26	A	502	CDL	1	0
26	D	301	CDL	1	0
27	C	402	HEM	3	0
27	N	401	HEM	2	0
25	a	605	3PE	2	0
25	c	301	3PE	1	0
25	R	102	3PE	2	0
25	D	302	3PE	1	0
25	g	101	3PE	2	0
25	a	607	3PE	1	0
26	L	502	CDL	1	0

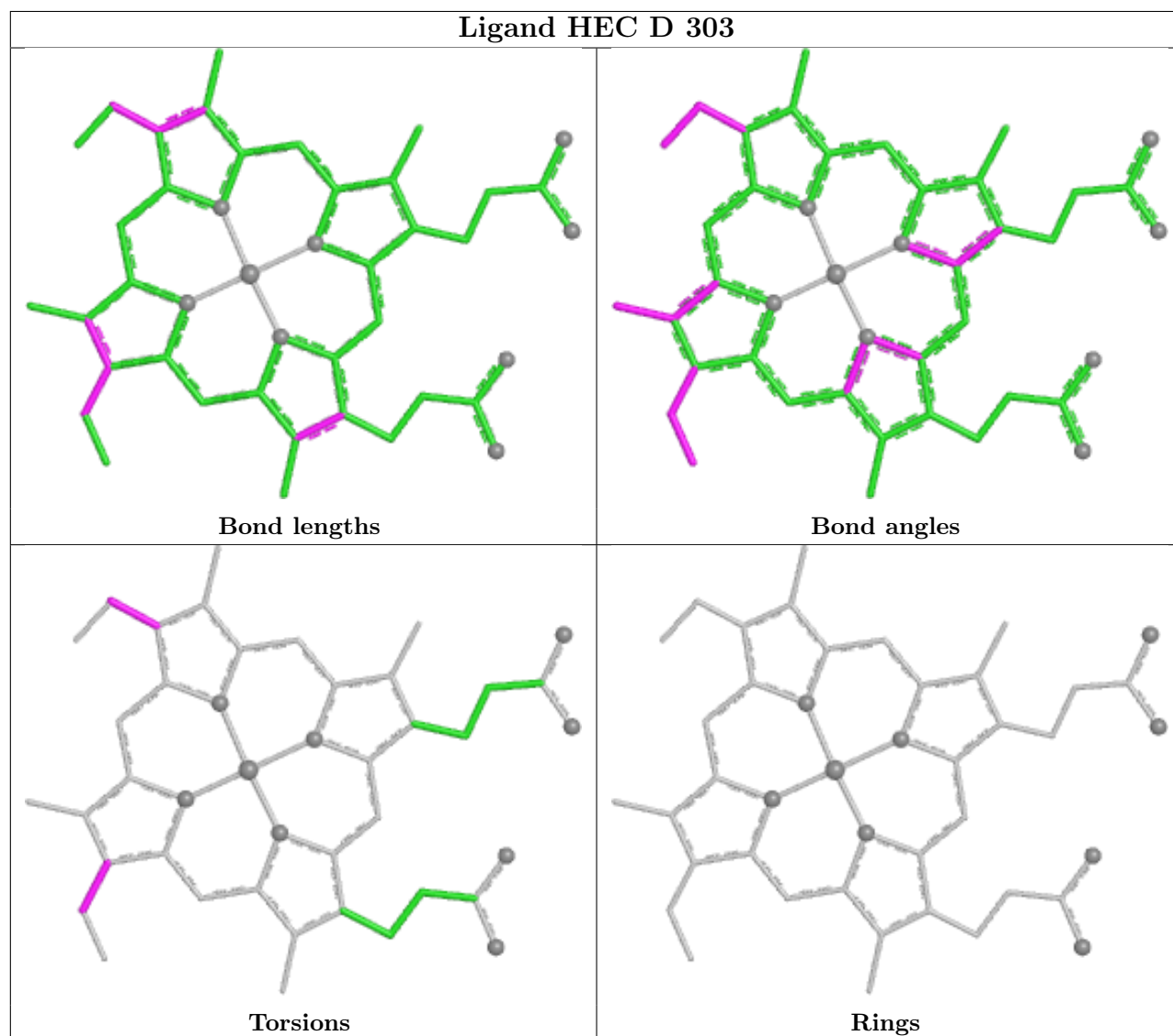
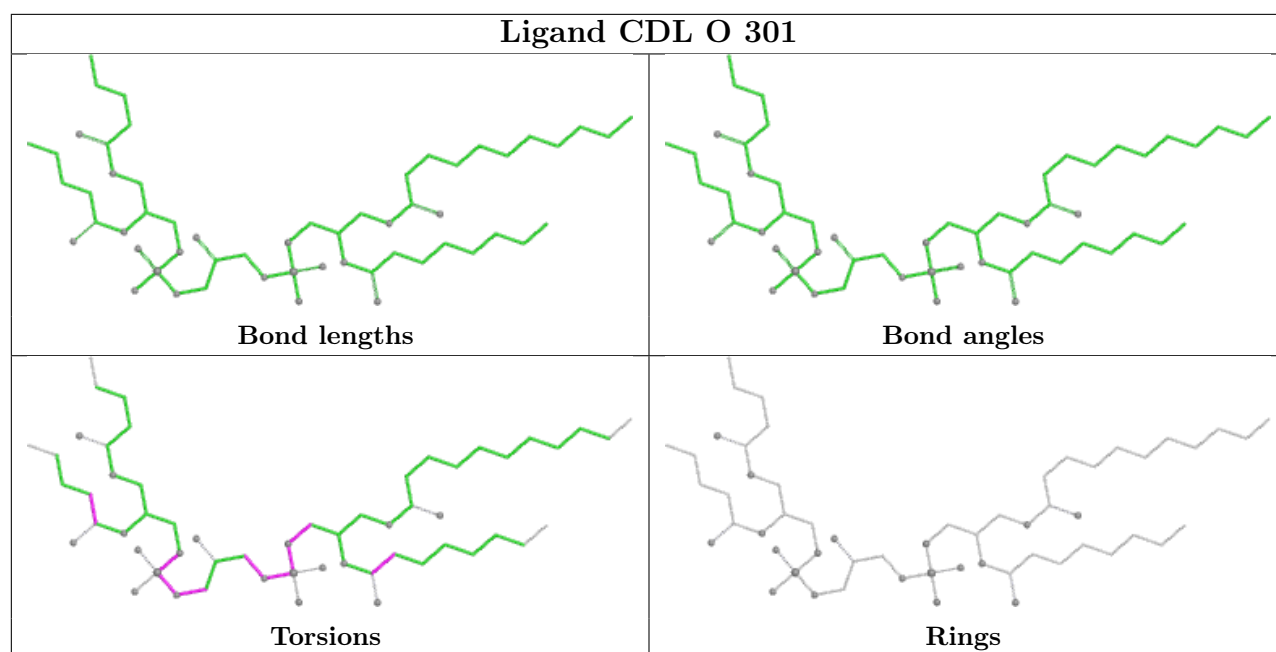
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

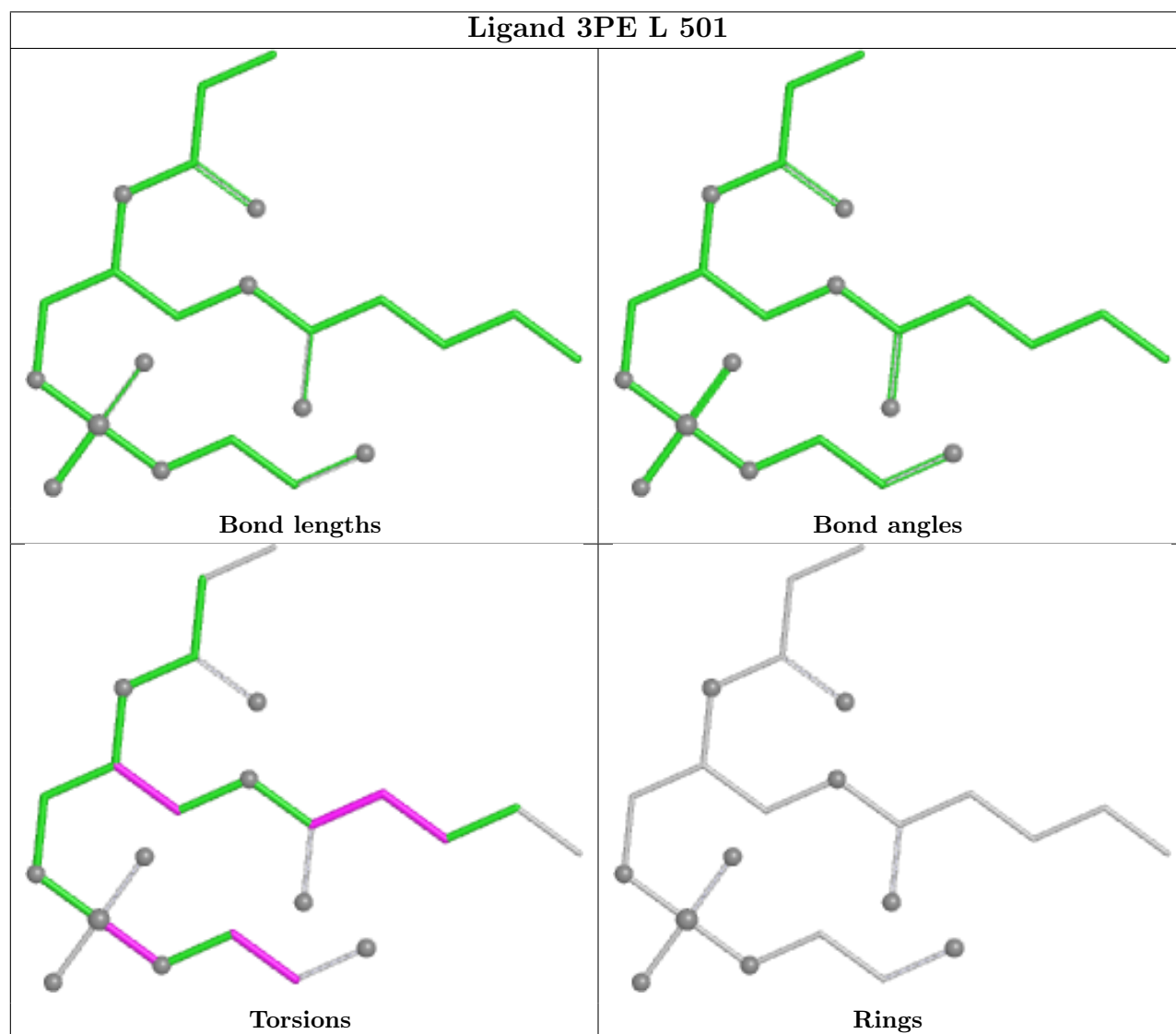
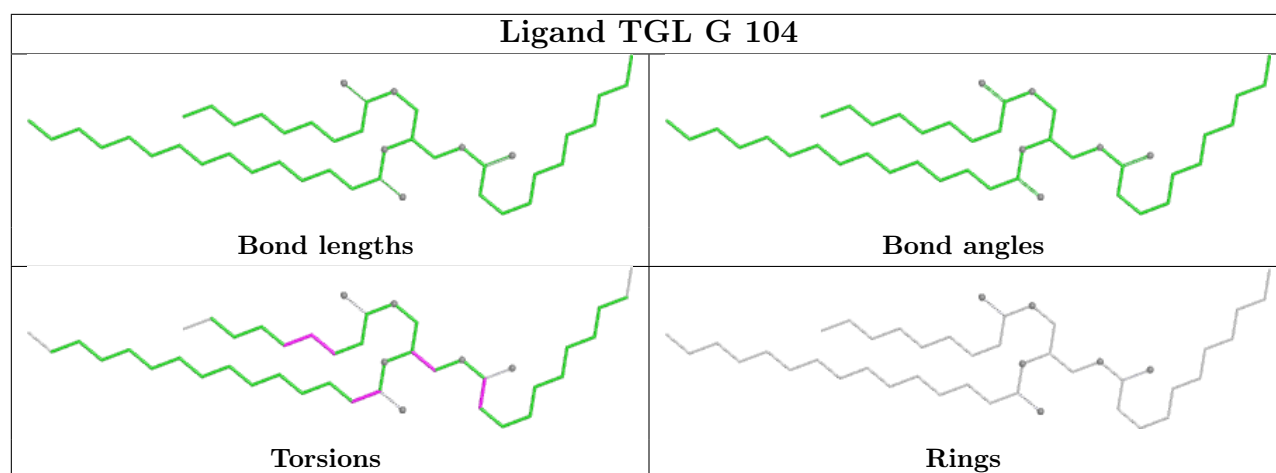


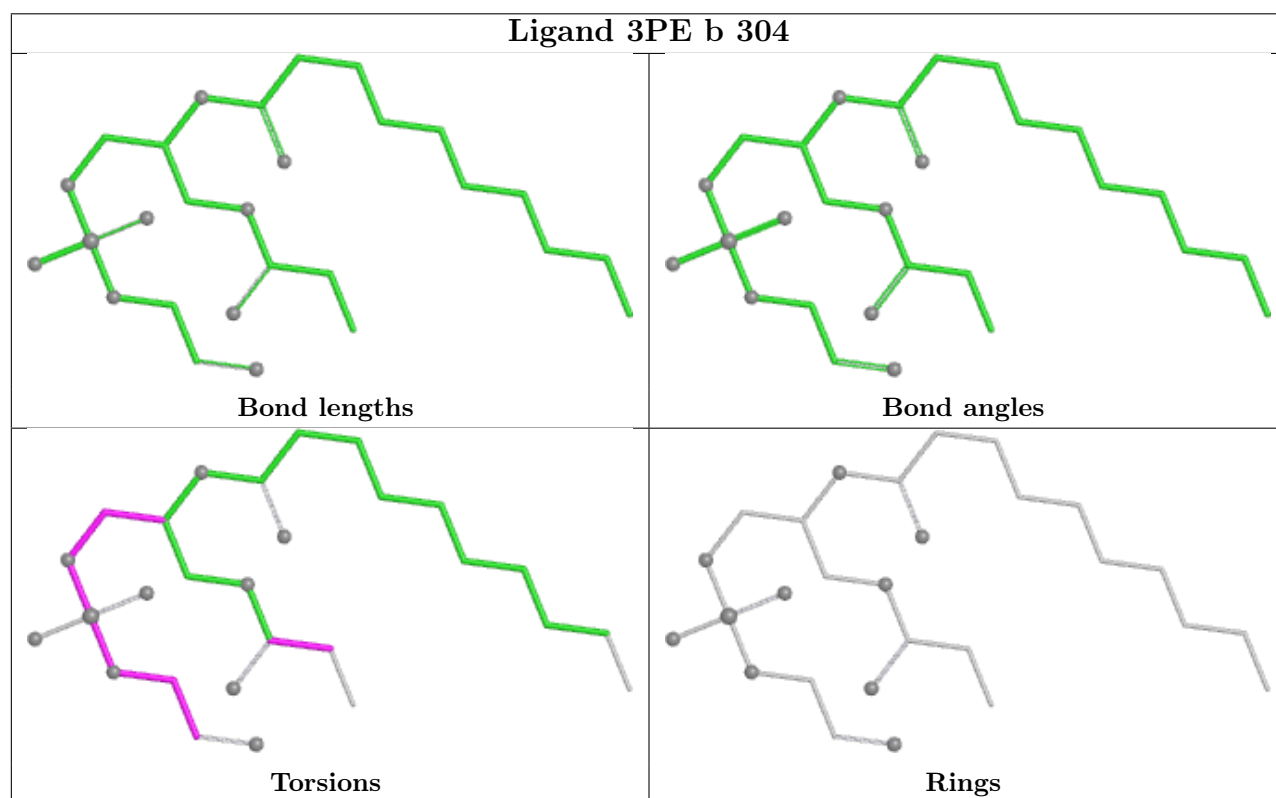
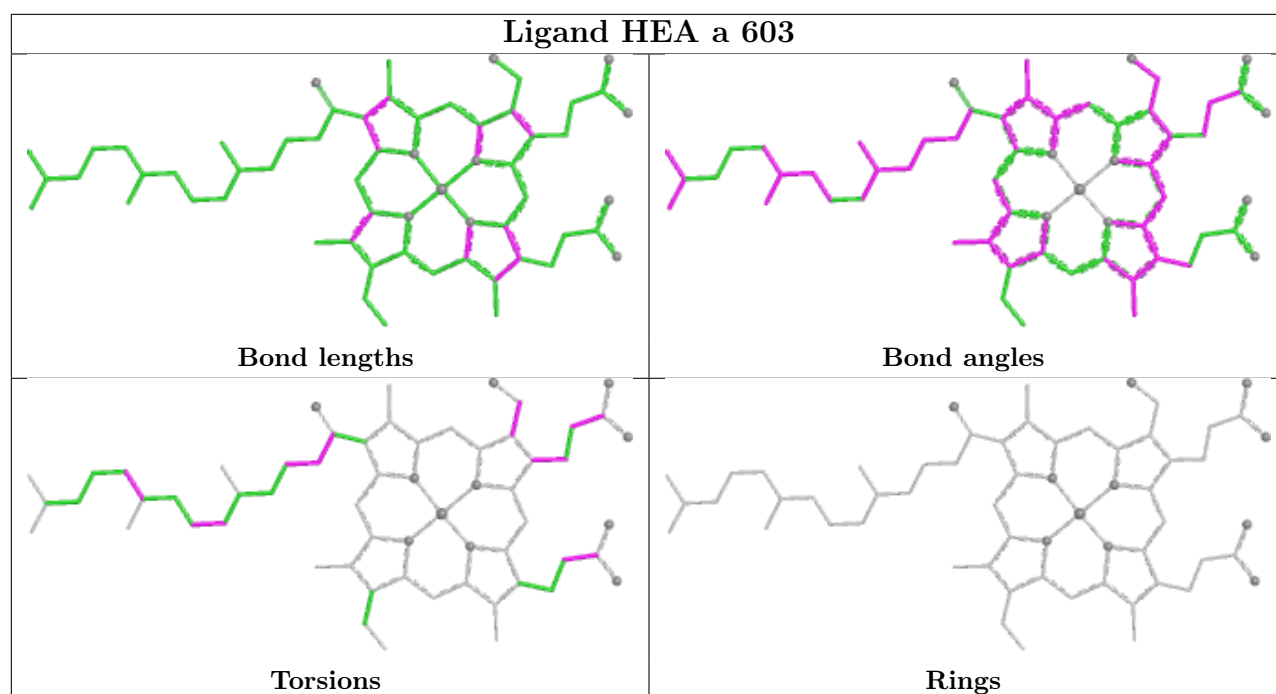


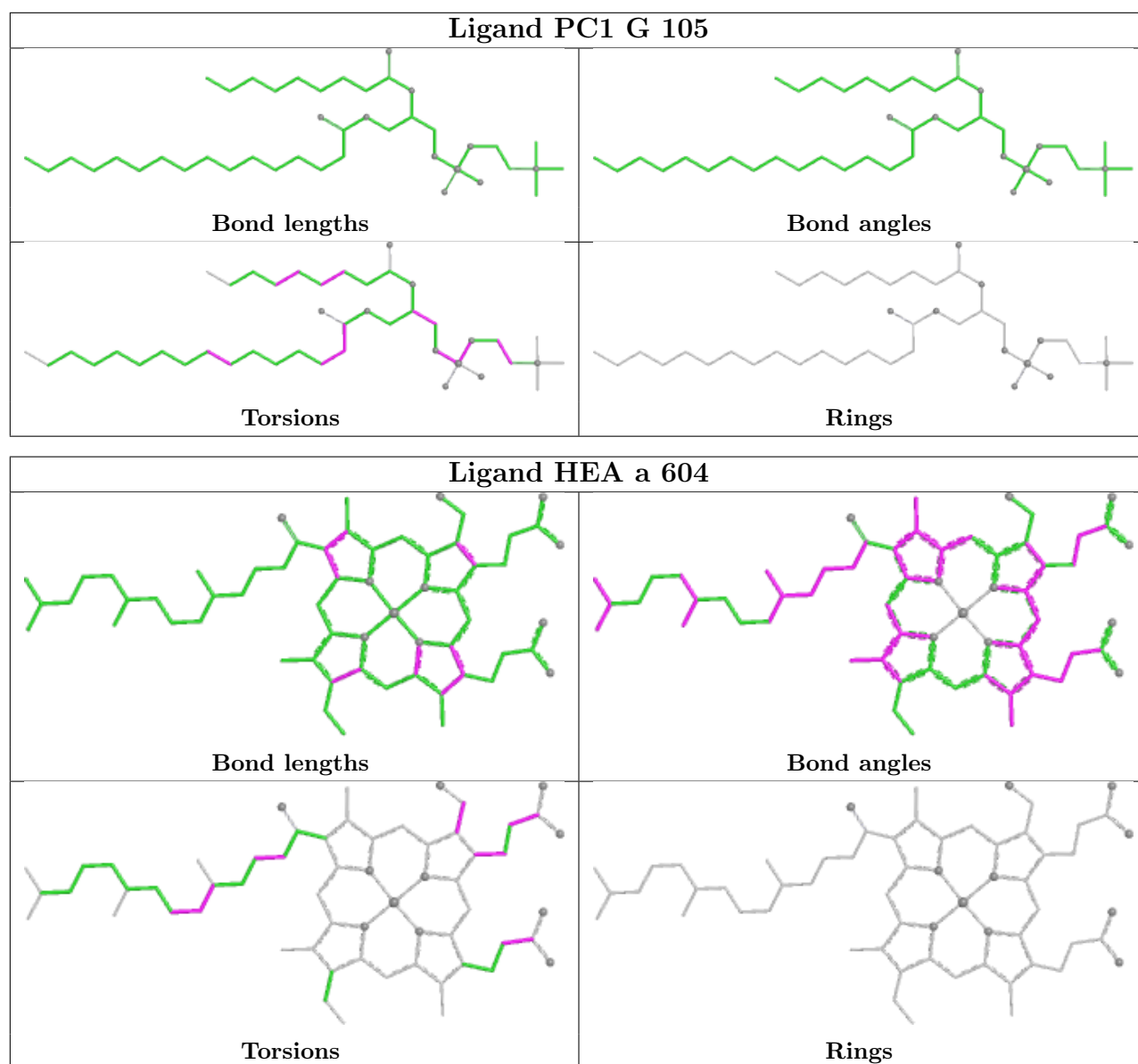


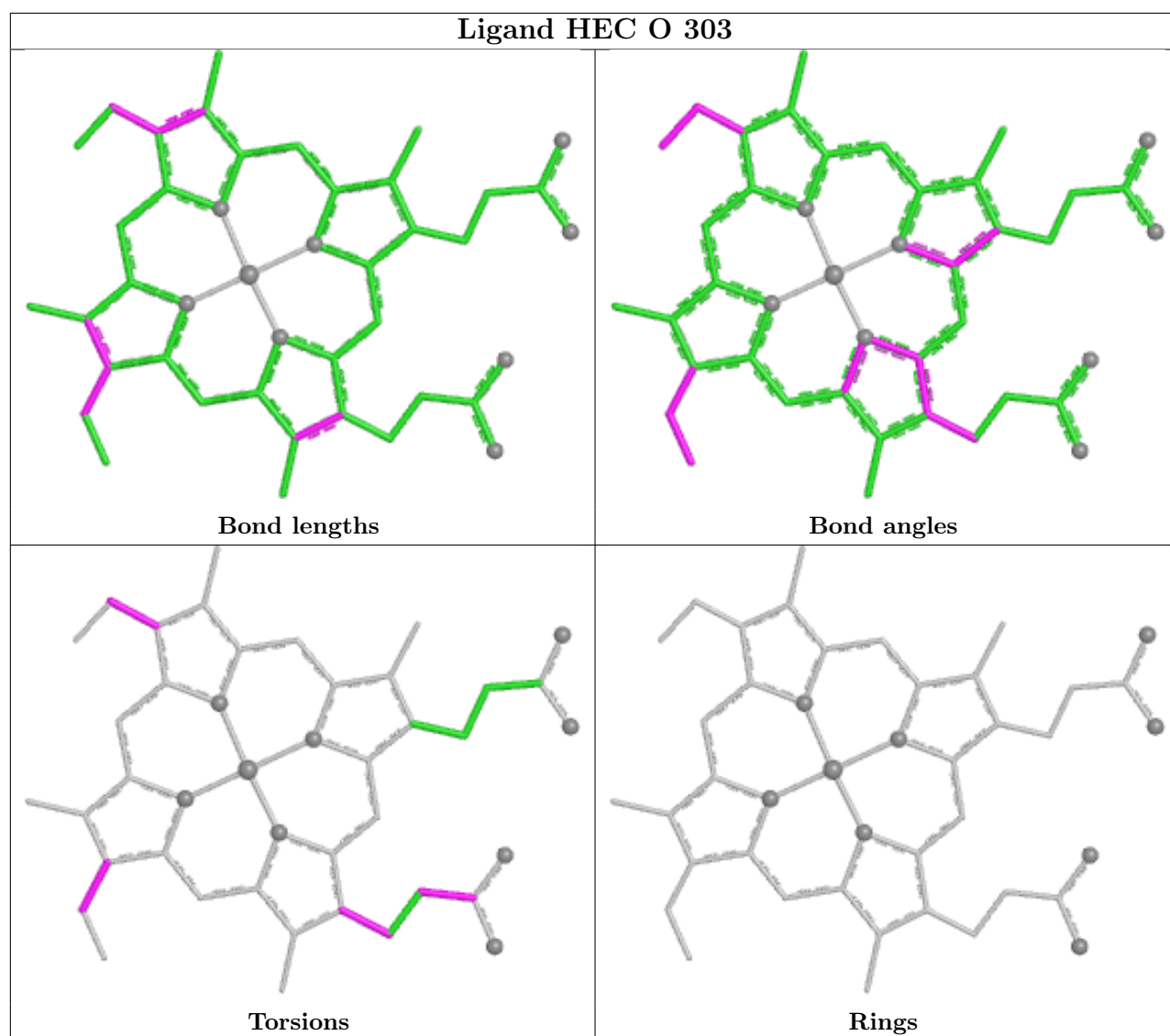




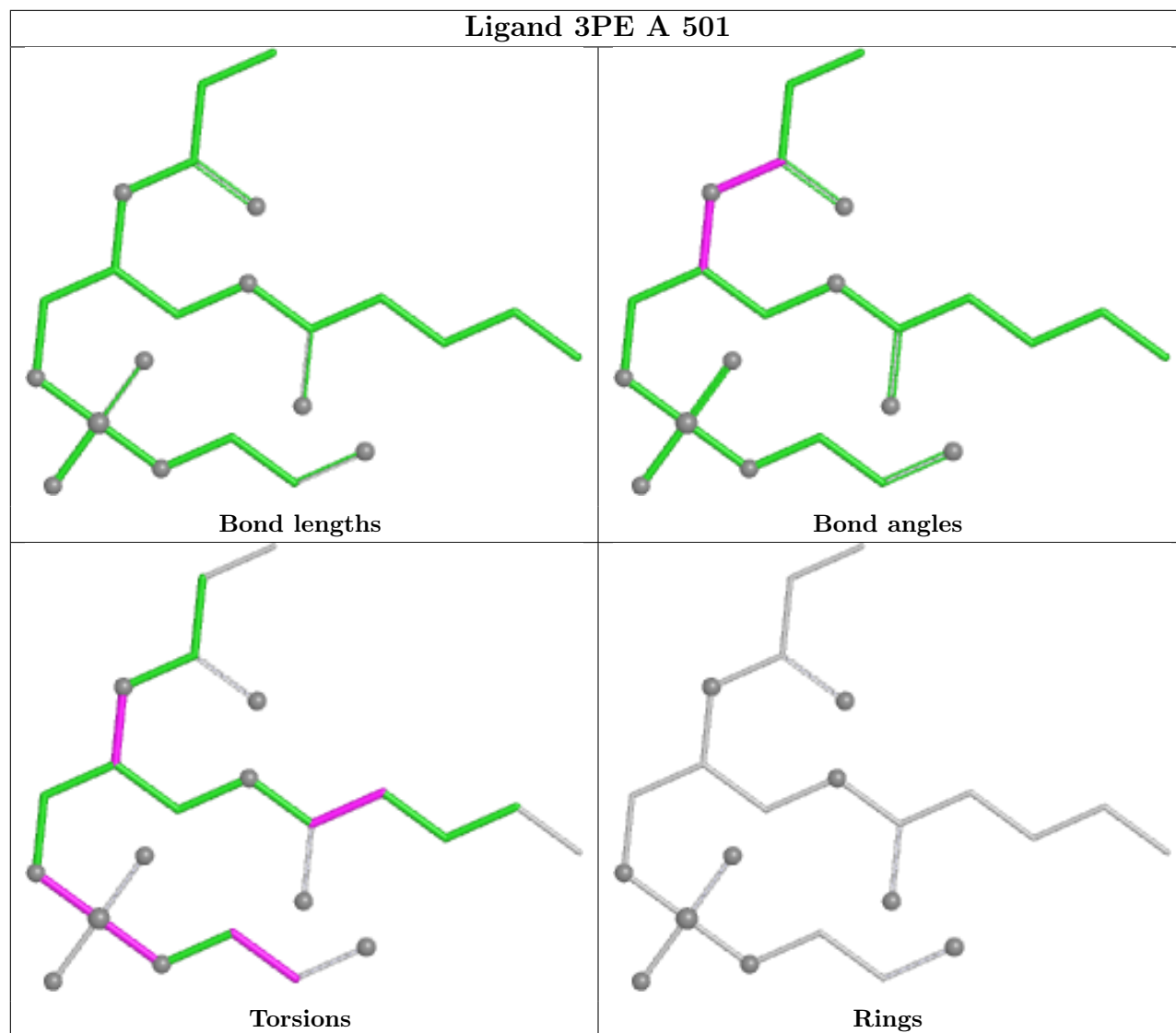


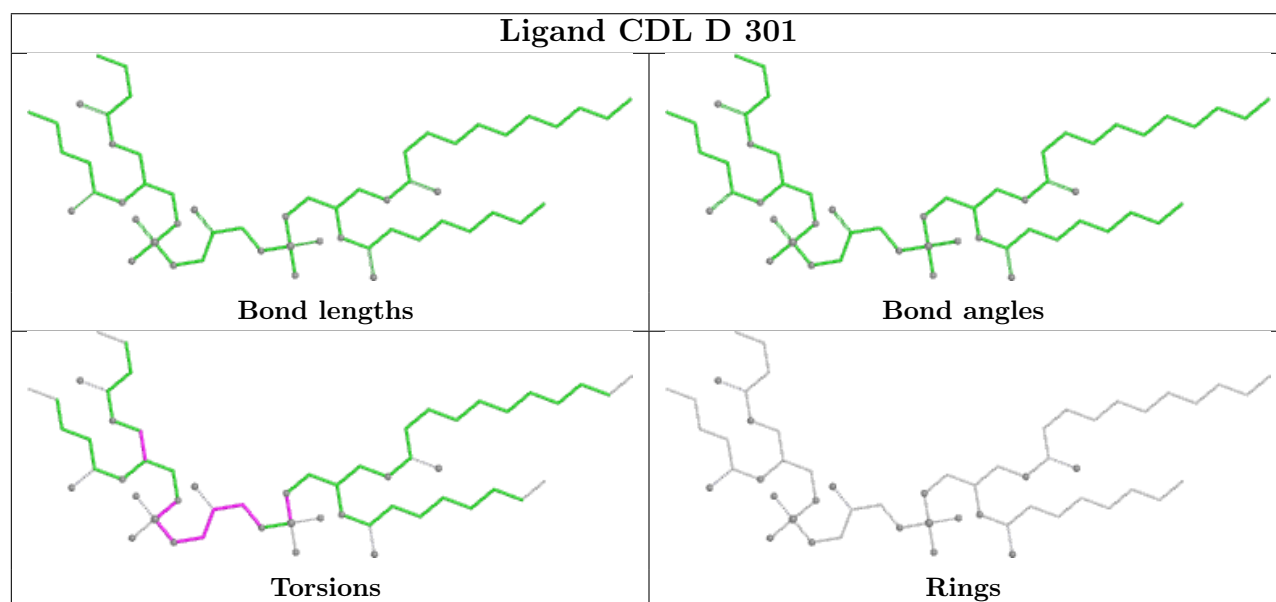
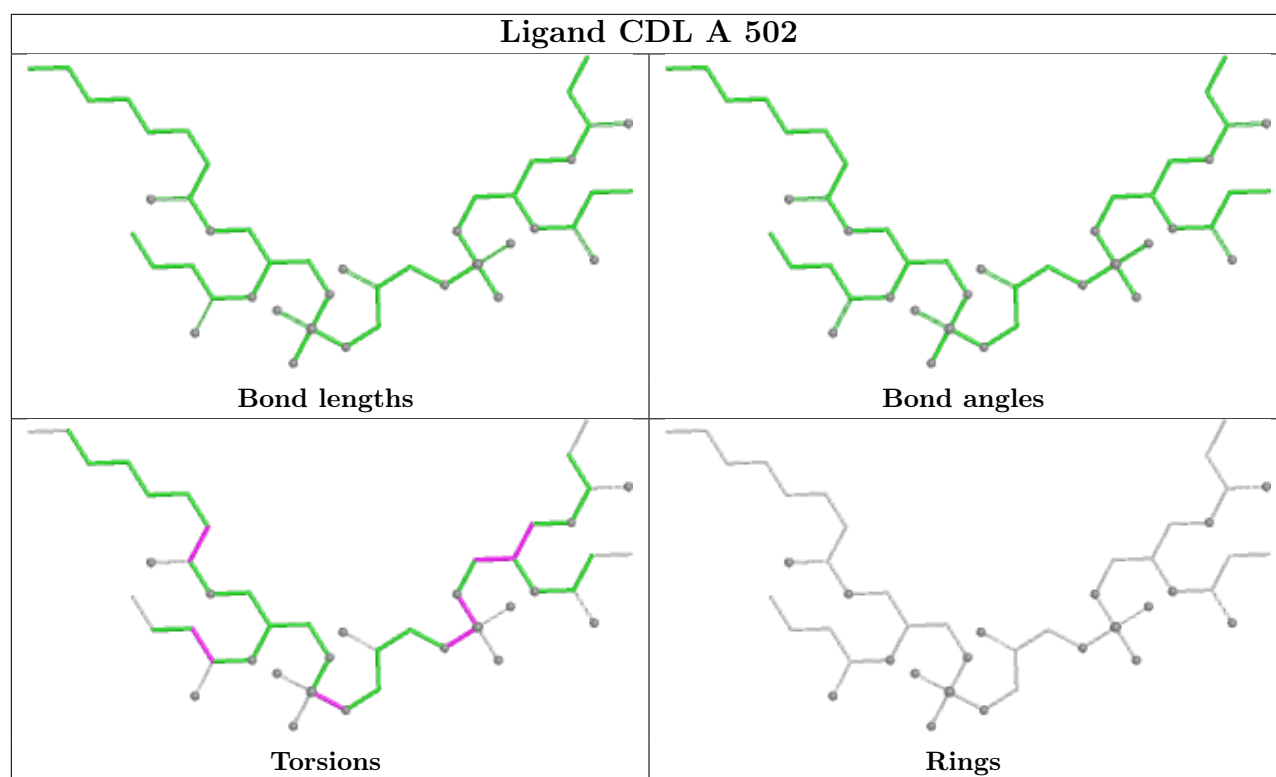


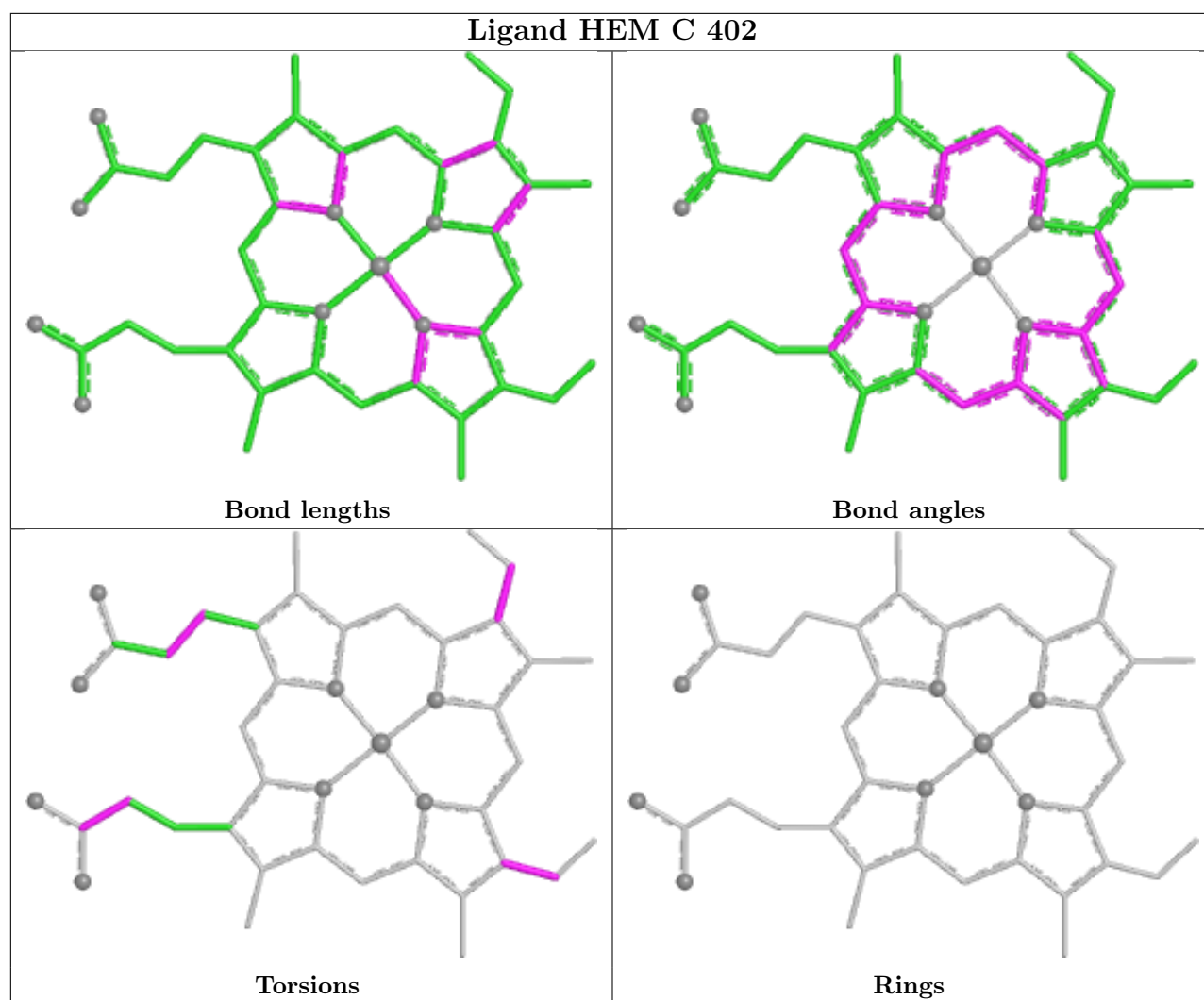


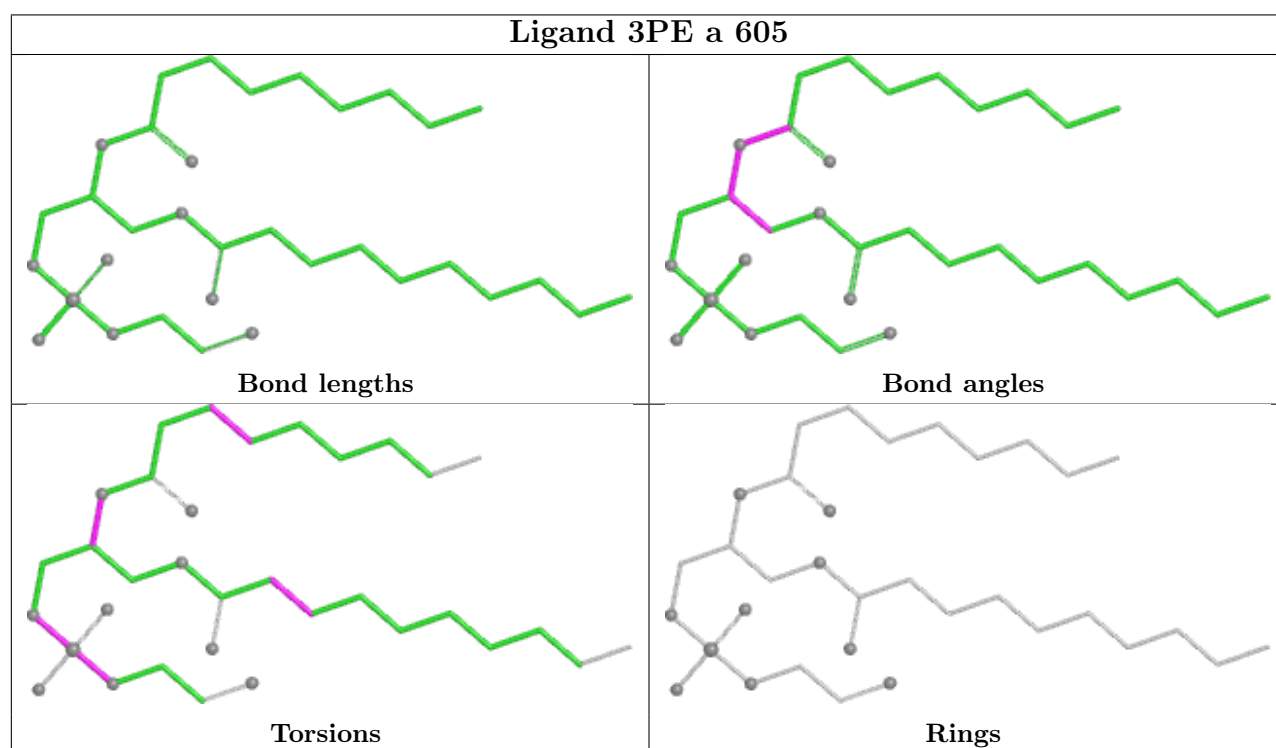
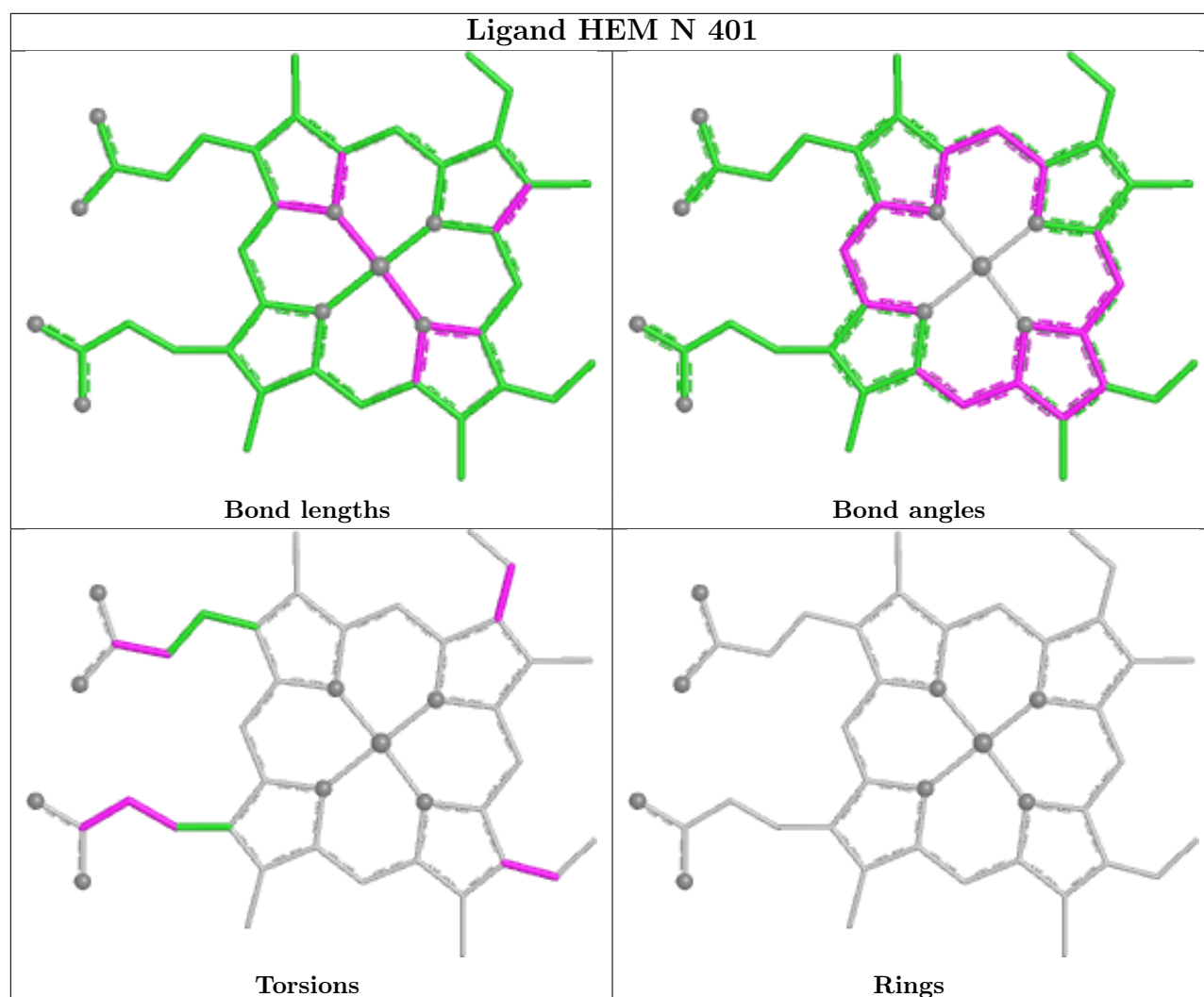


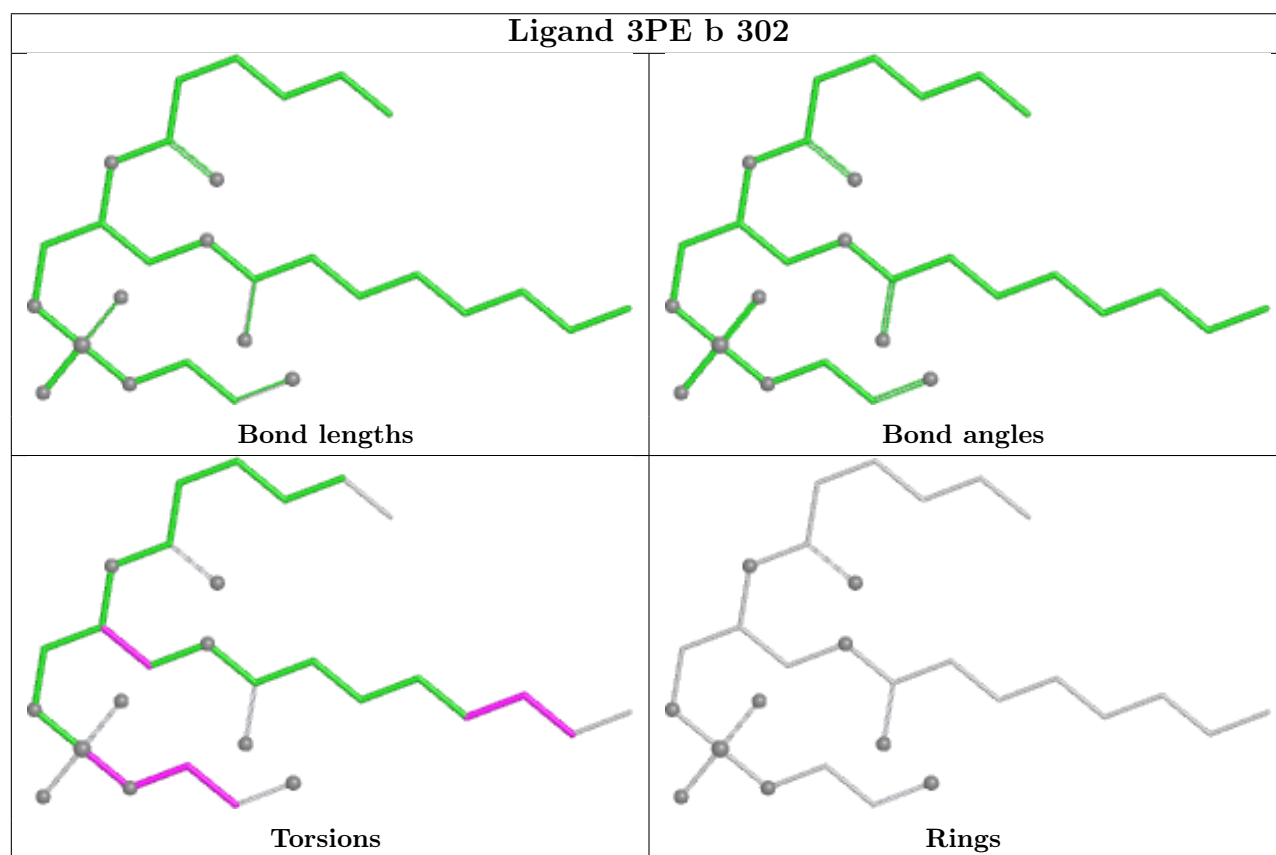
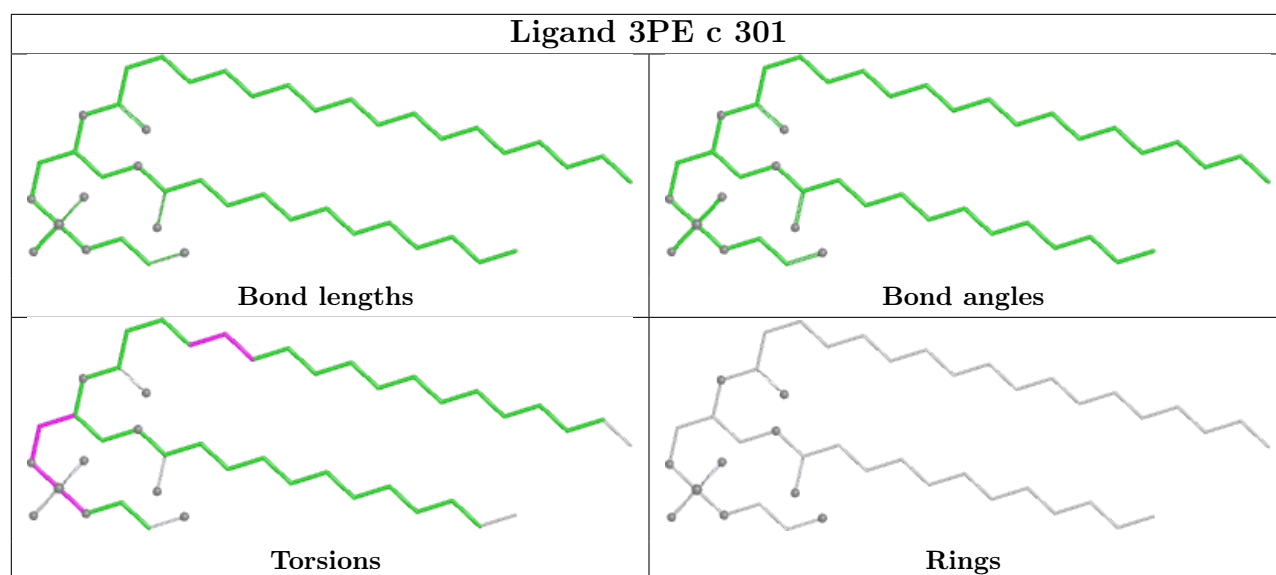
Ligand 3PE A 501

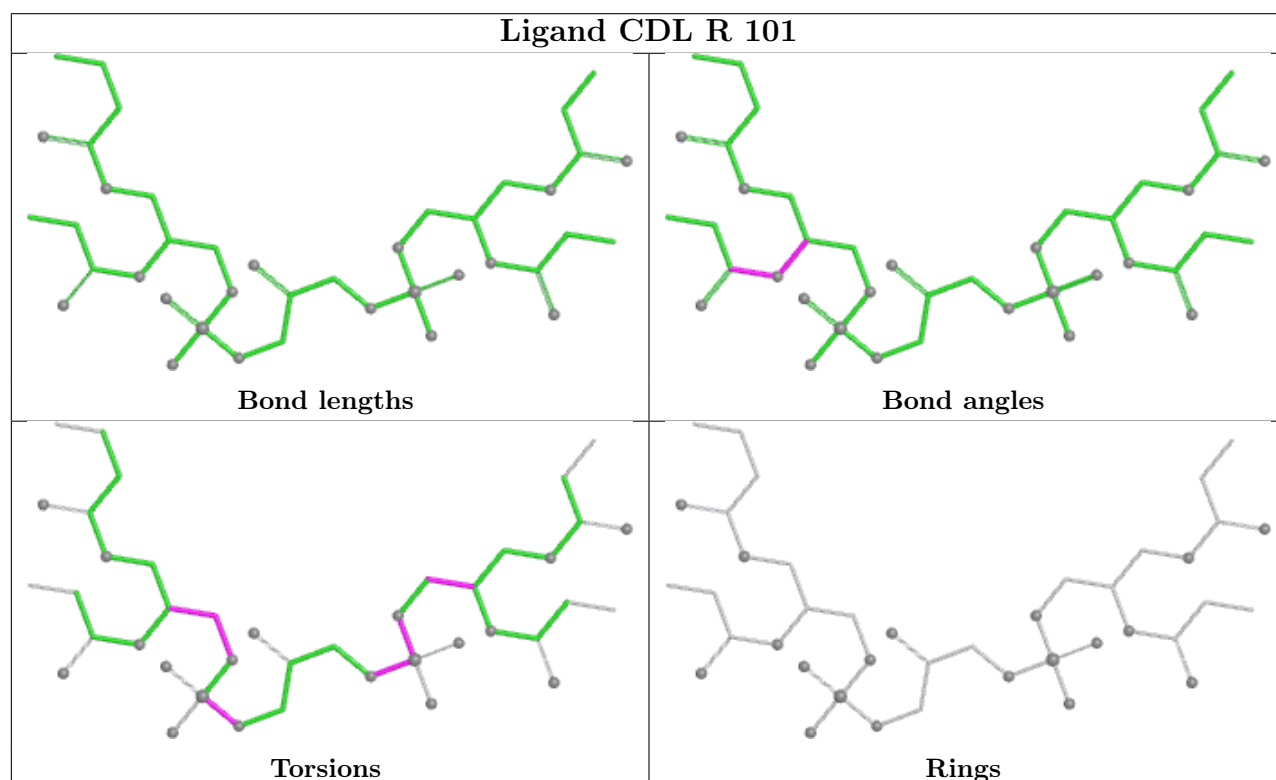
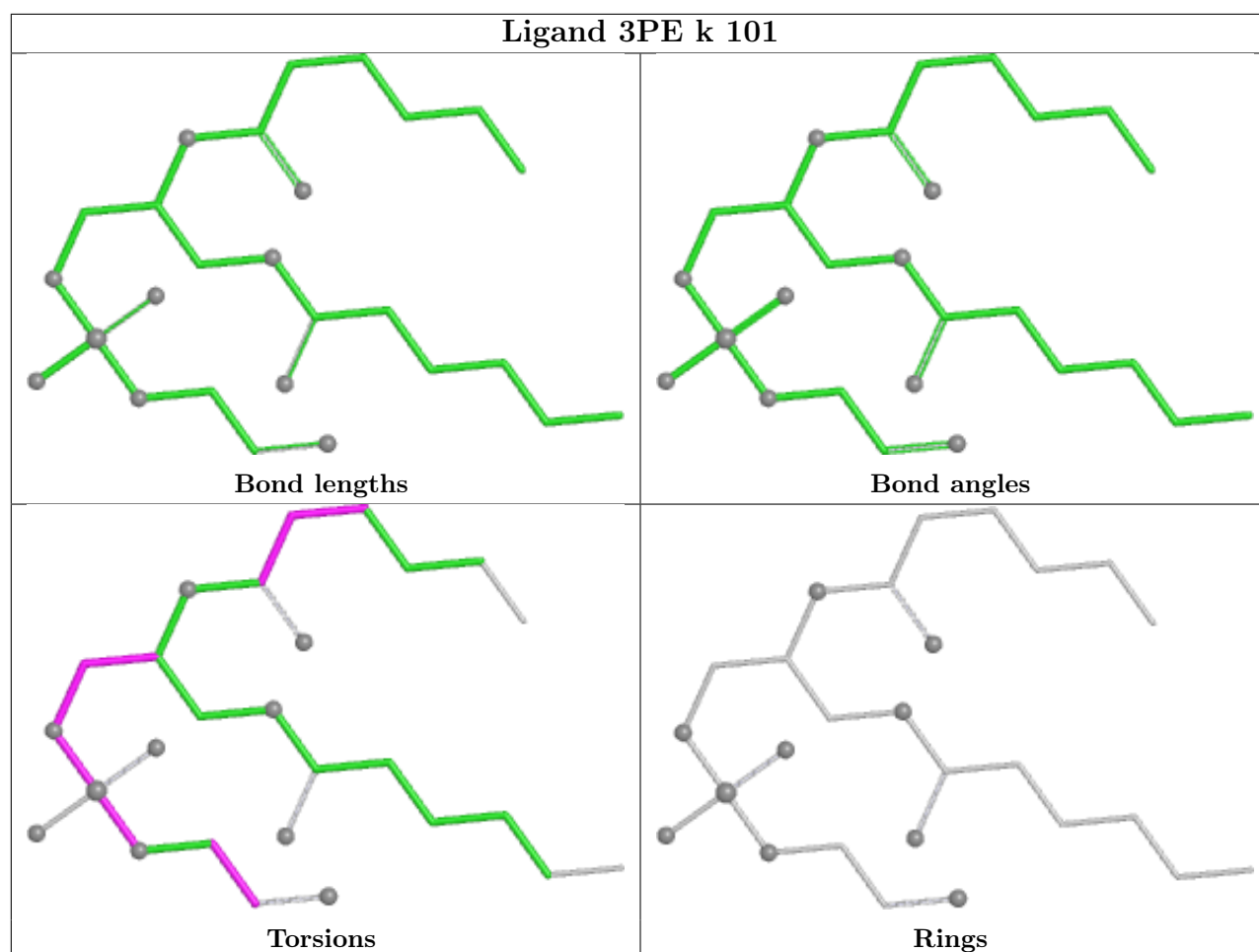


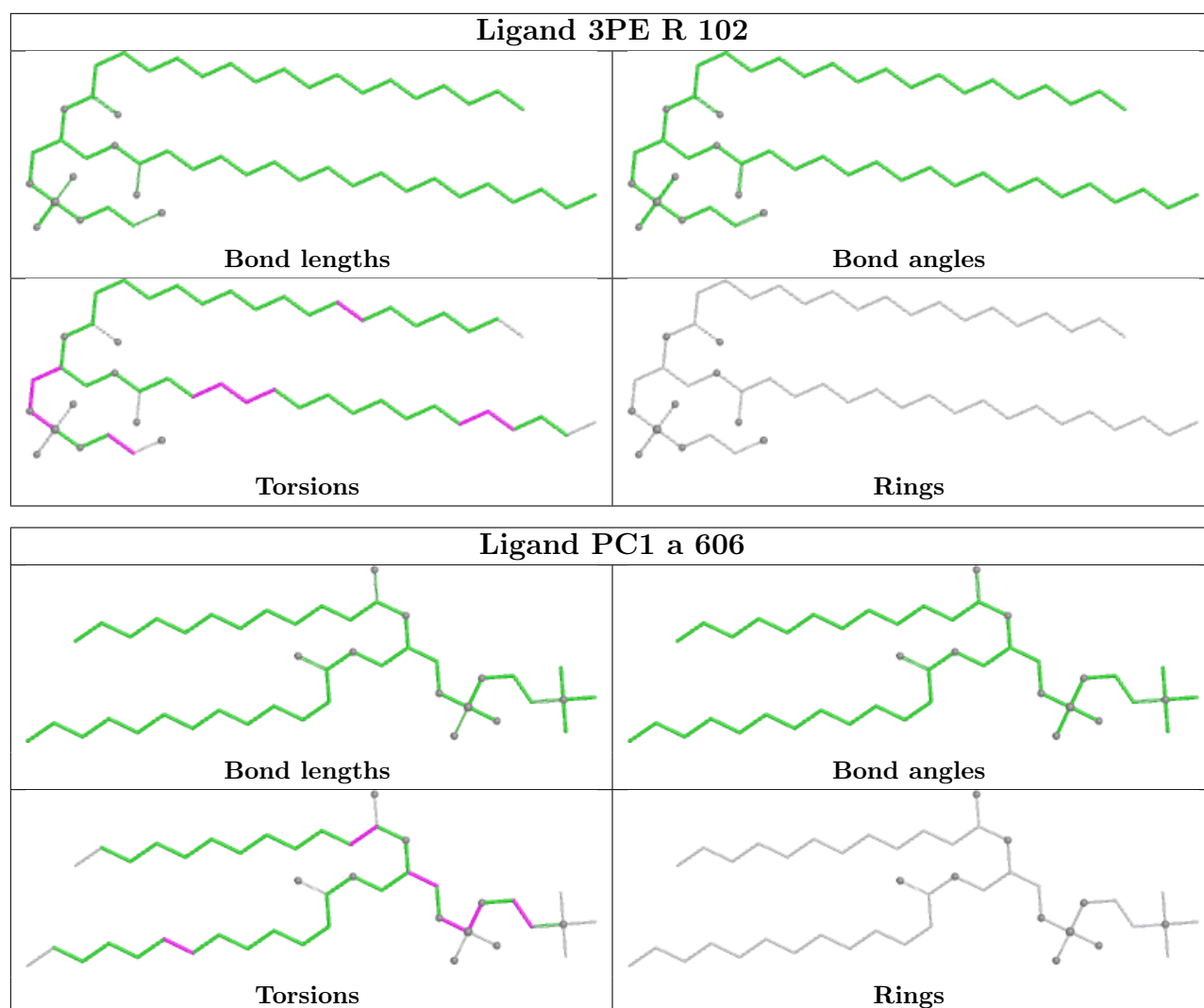


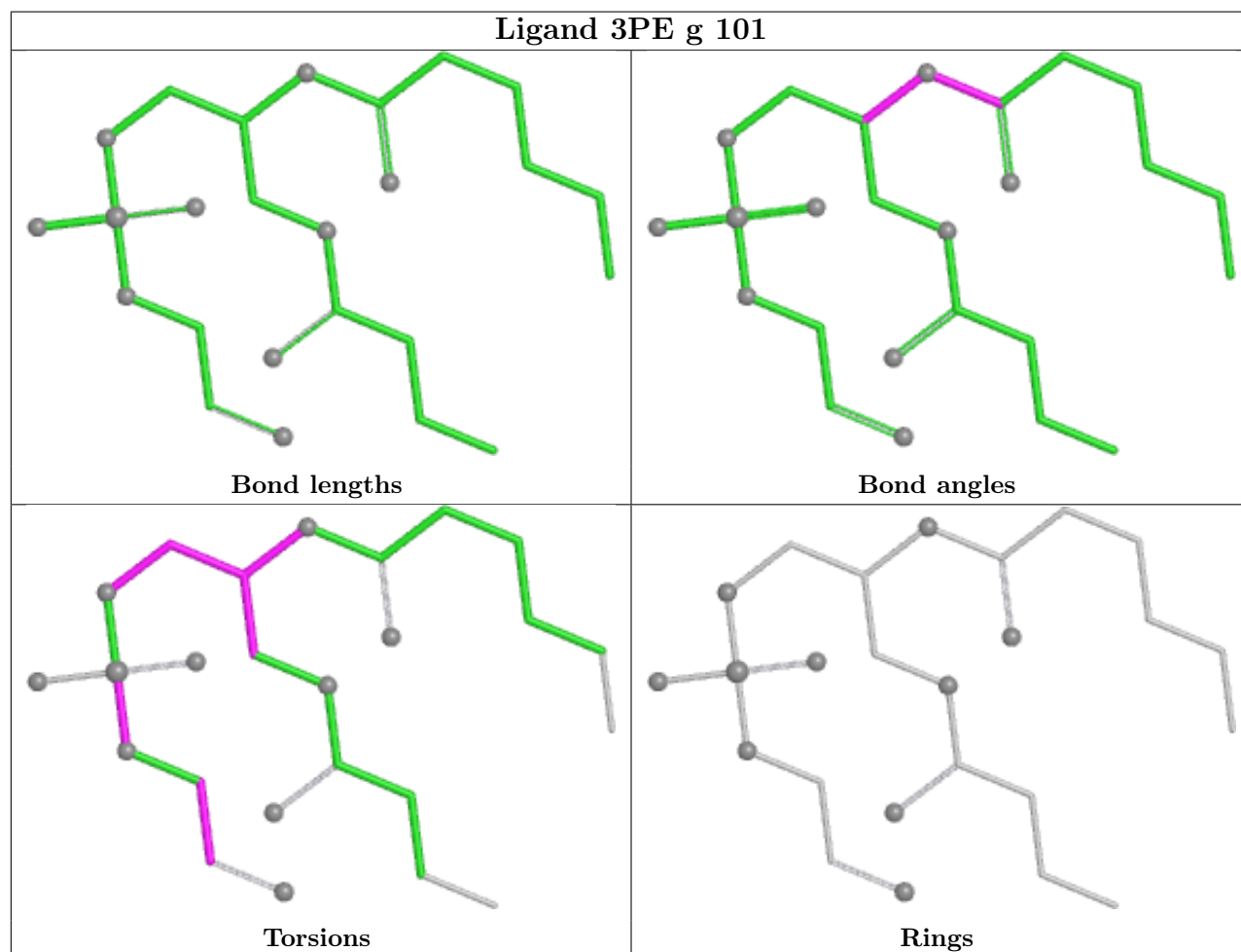
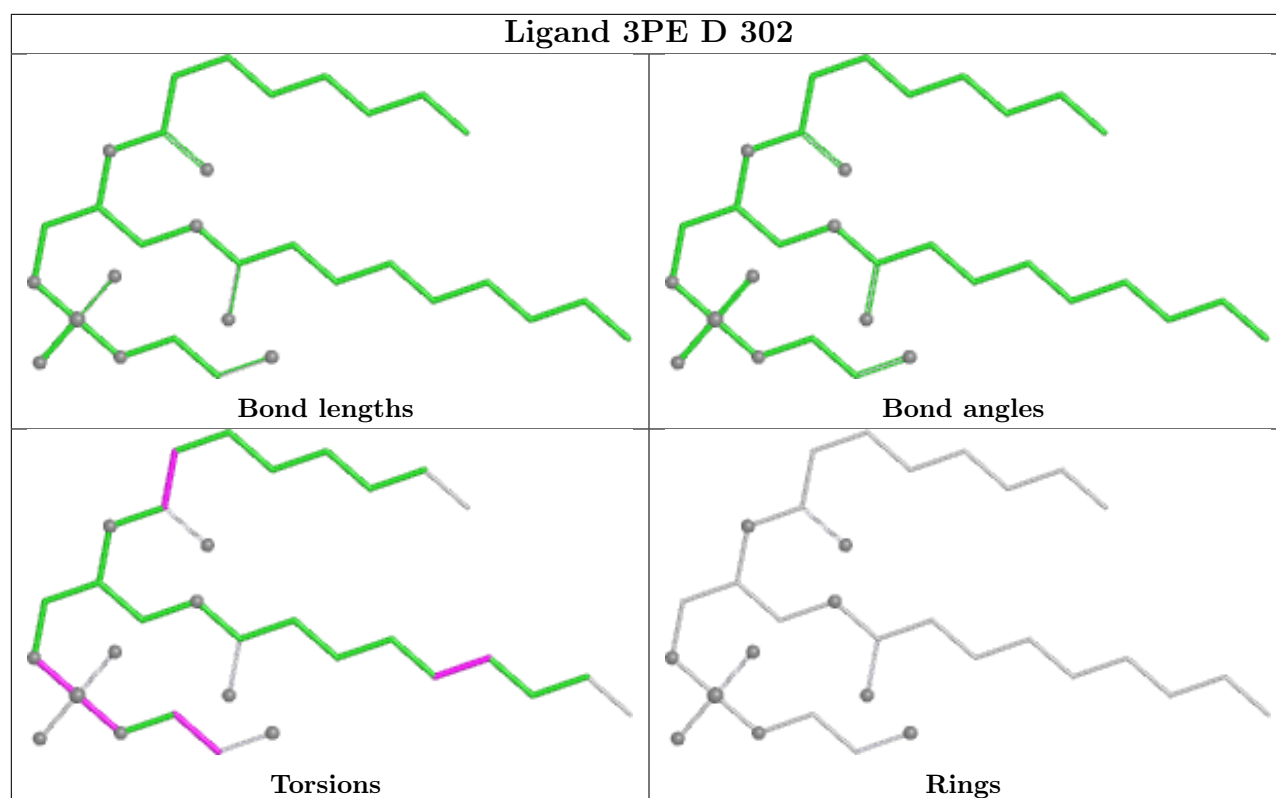


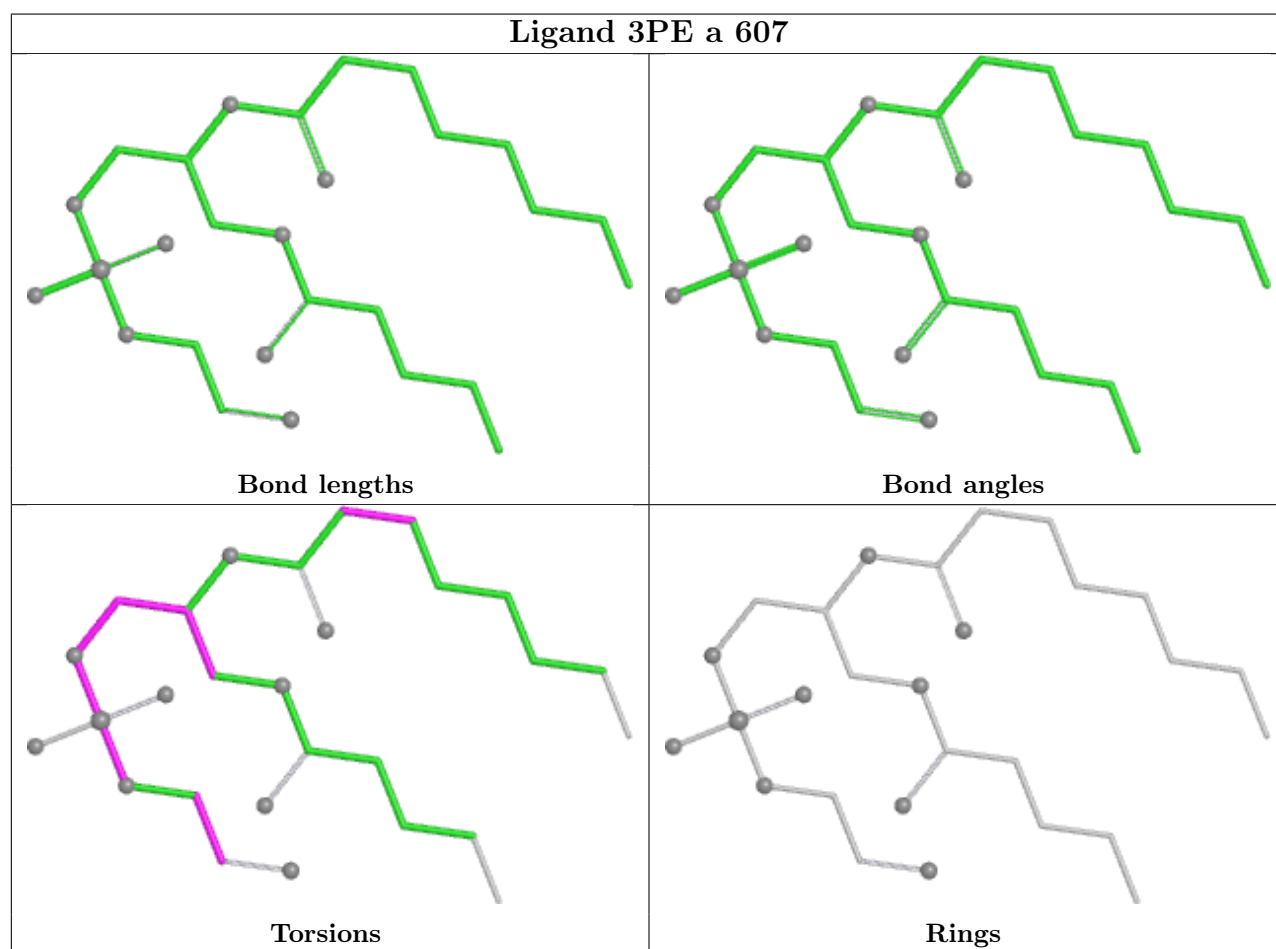
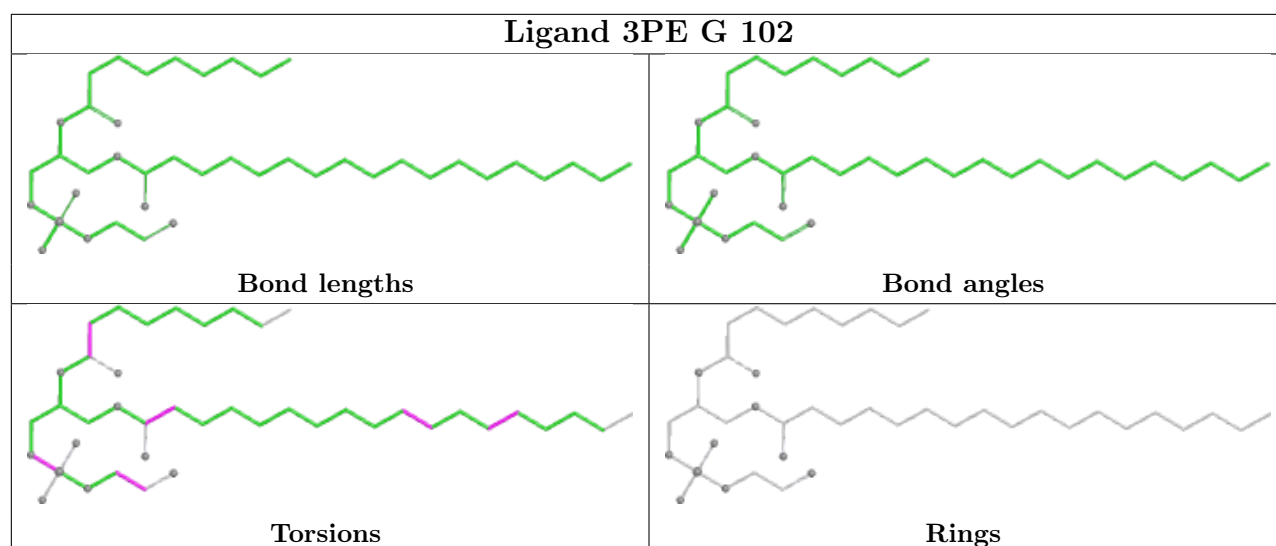


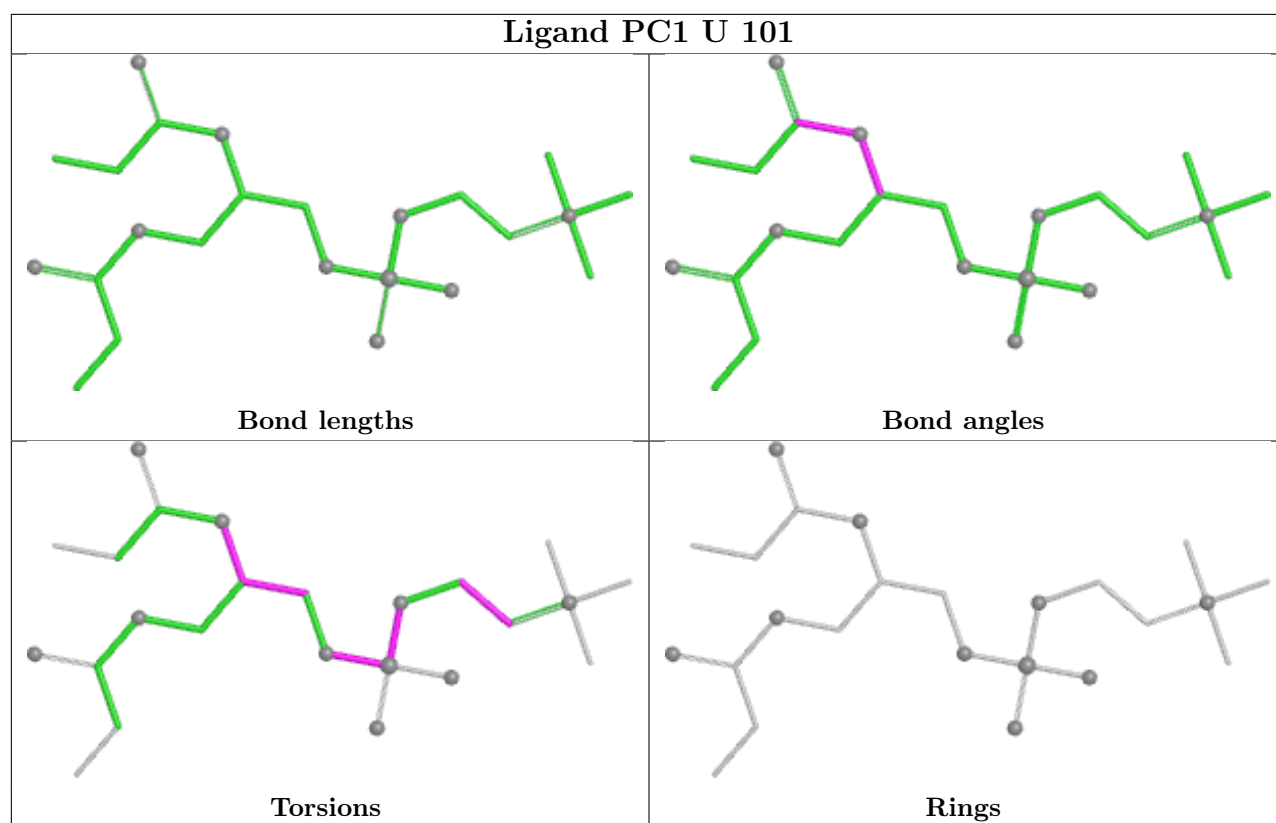


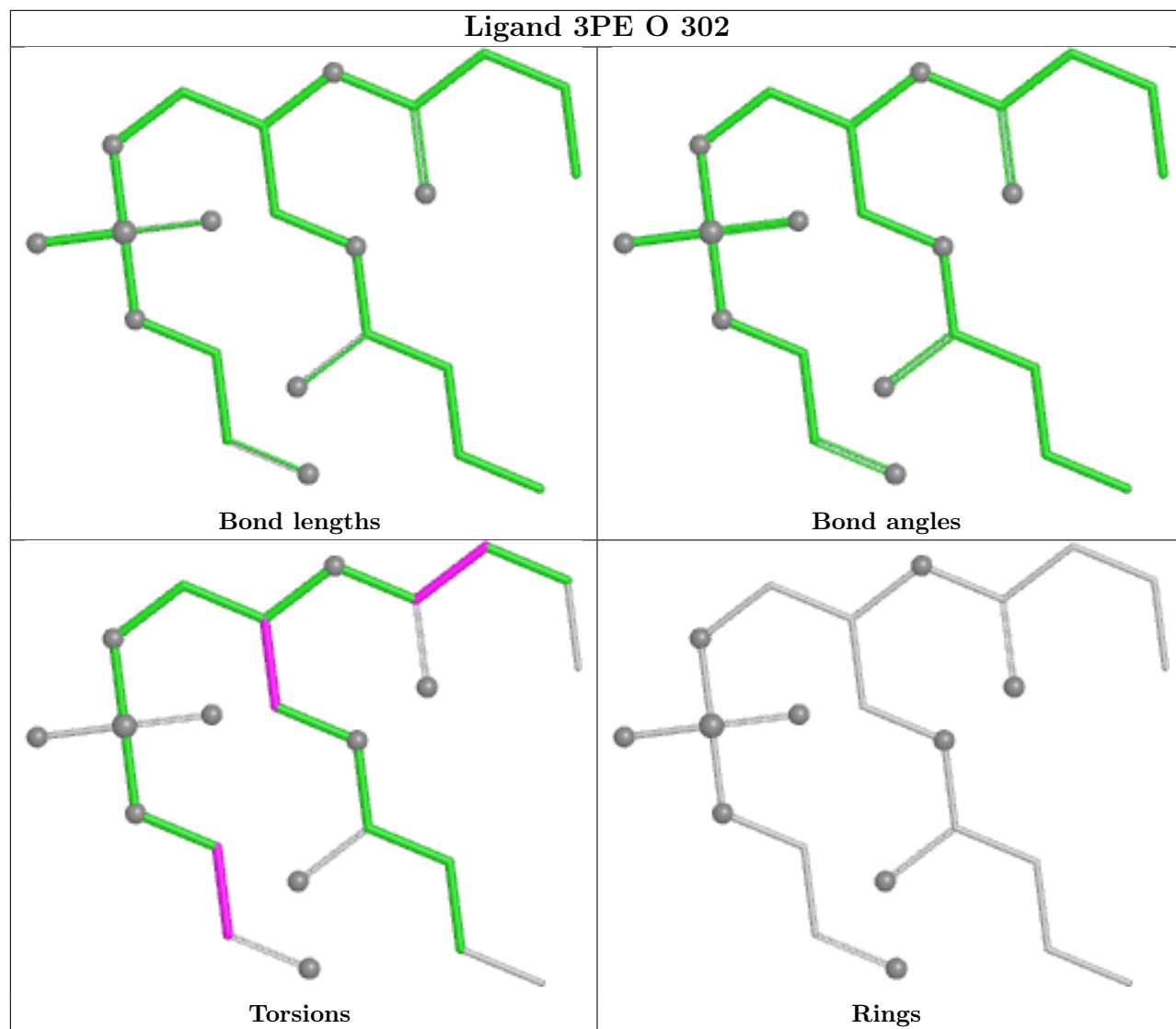


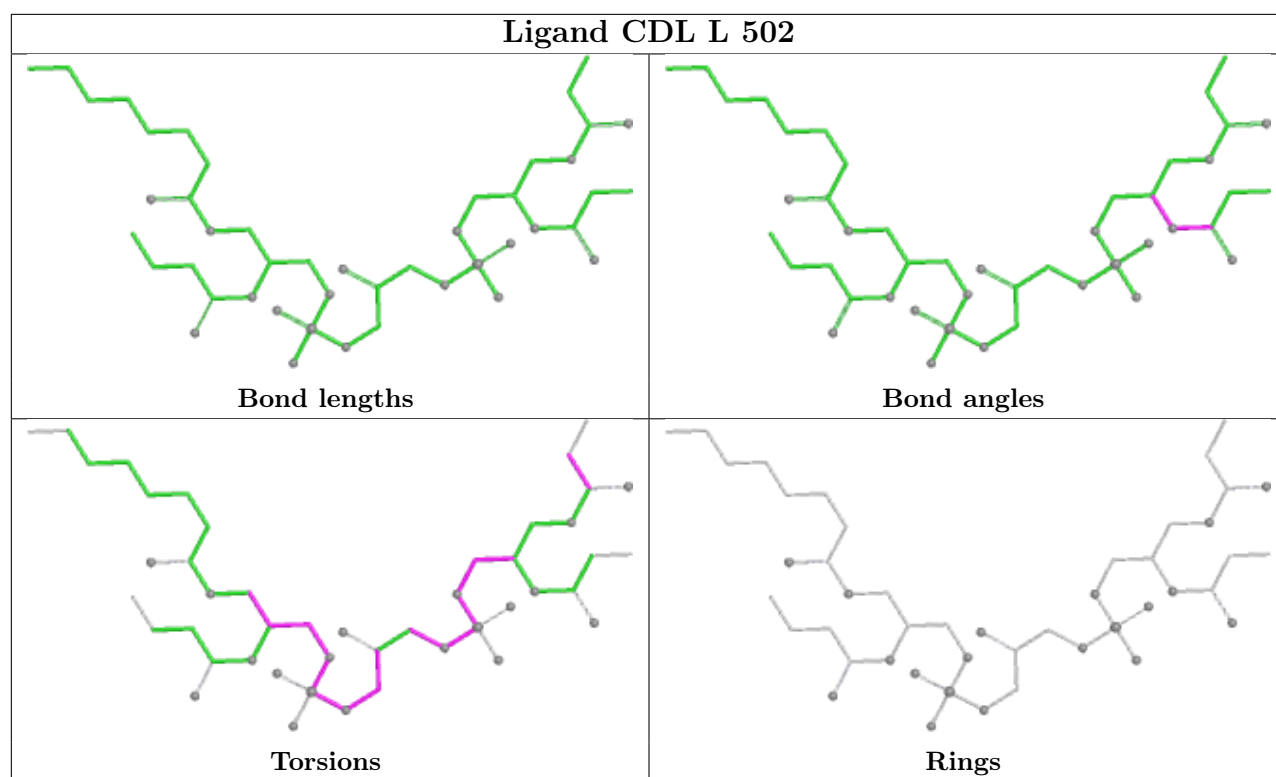












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

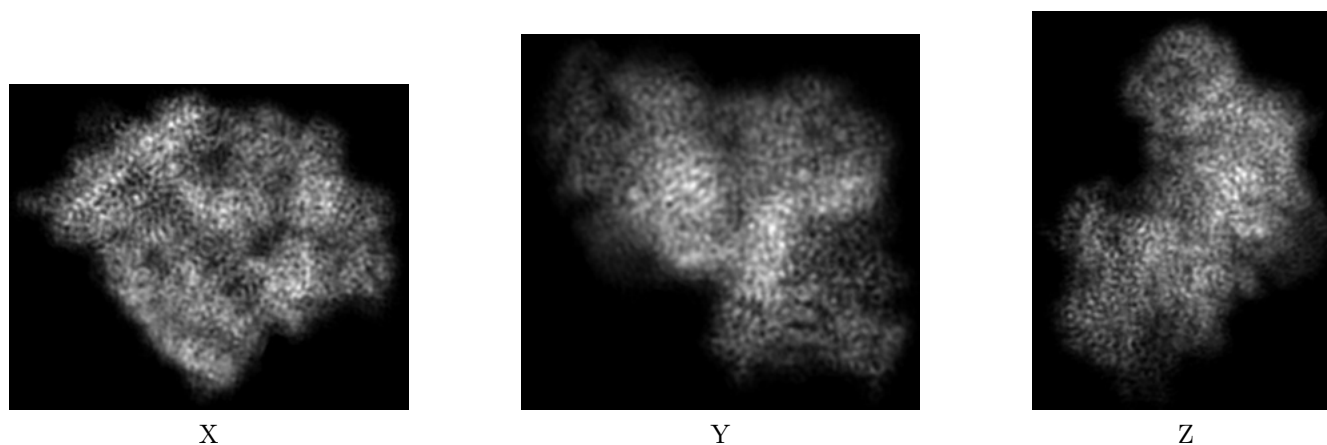
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12702. 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](#)

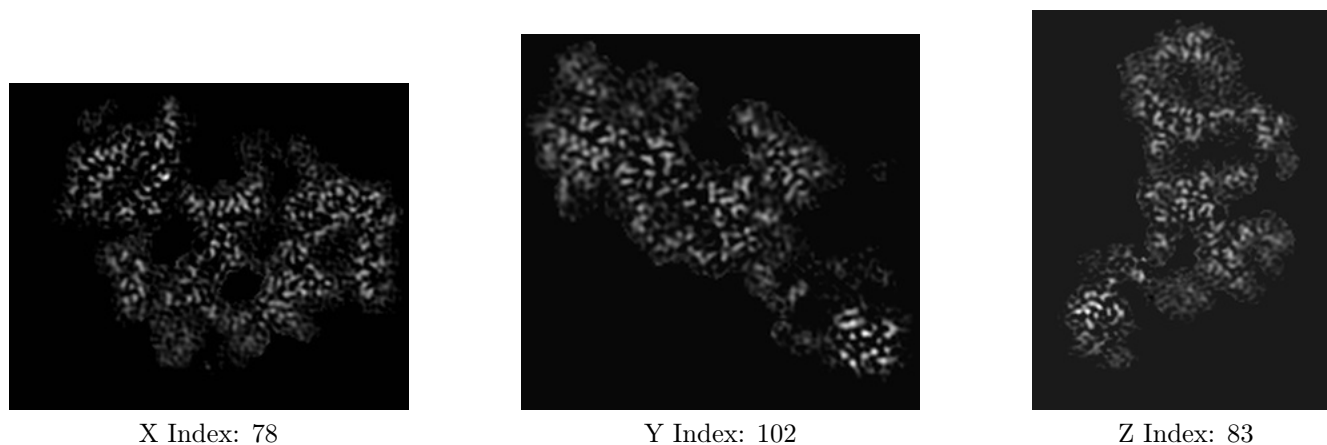
6.1.1 Primary map



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

6.2 Central slices [i](#)

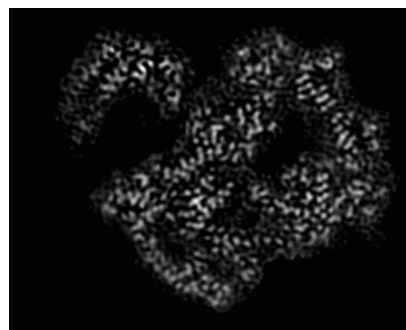
6.2.1 Primary map



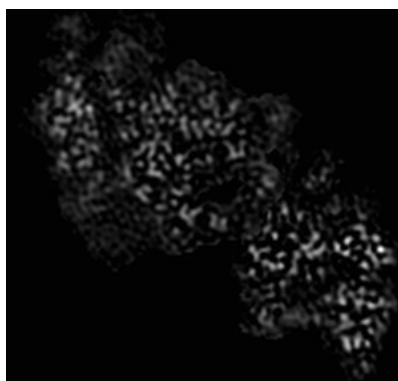
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 92



Y Index: 91

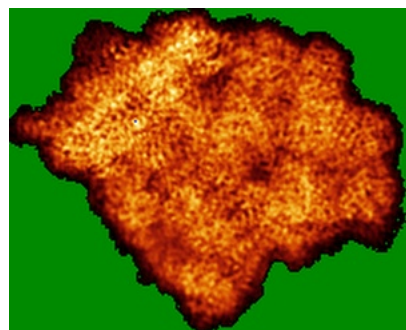


Z Index: 104

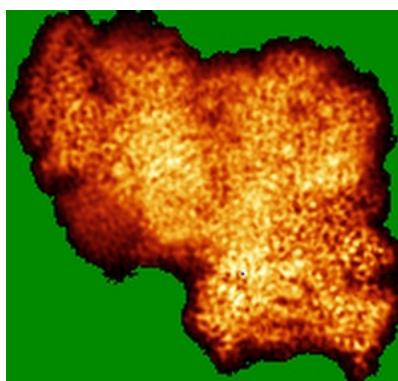
The images above show the largest variance slices of the map in three orthogonal directions.

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

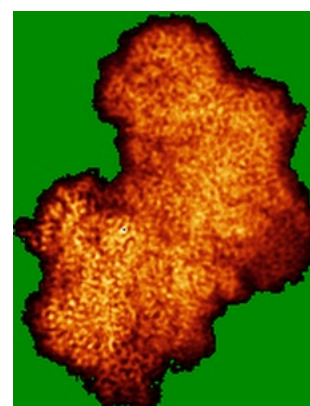
6.4.1 Primary map



X



Y

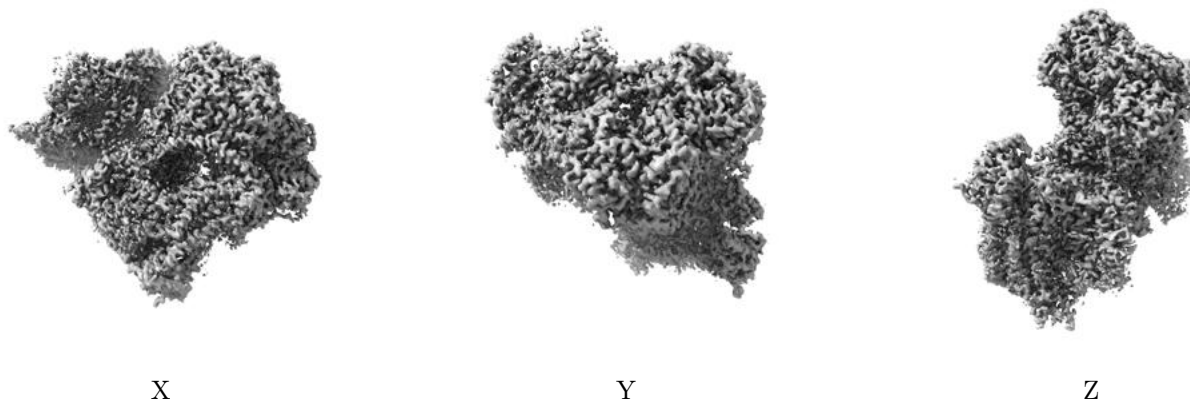


Z

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 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

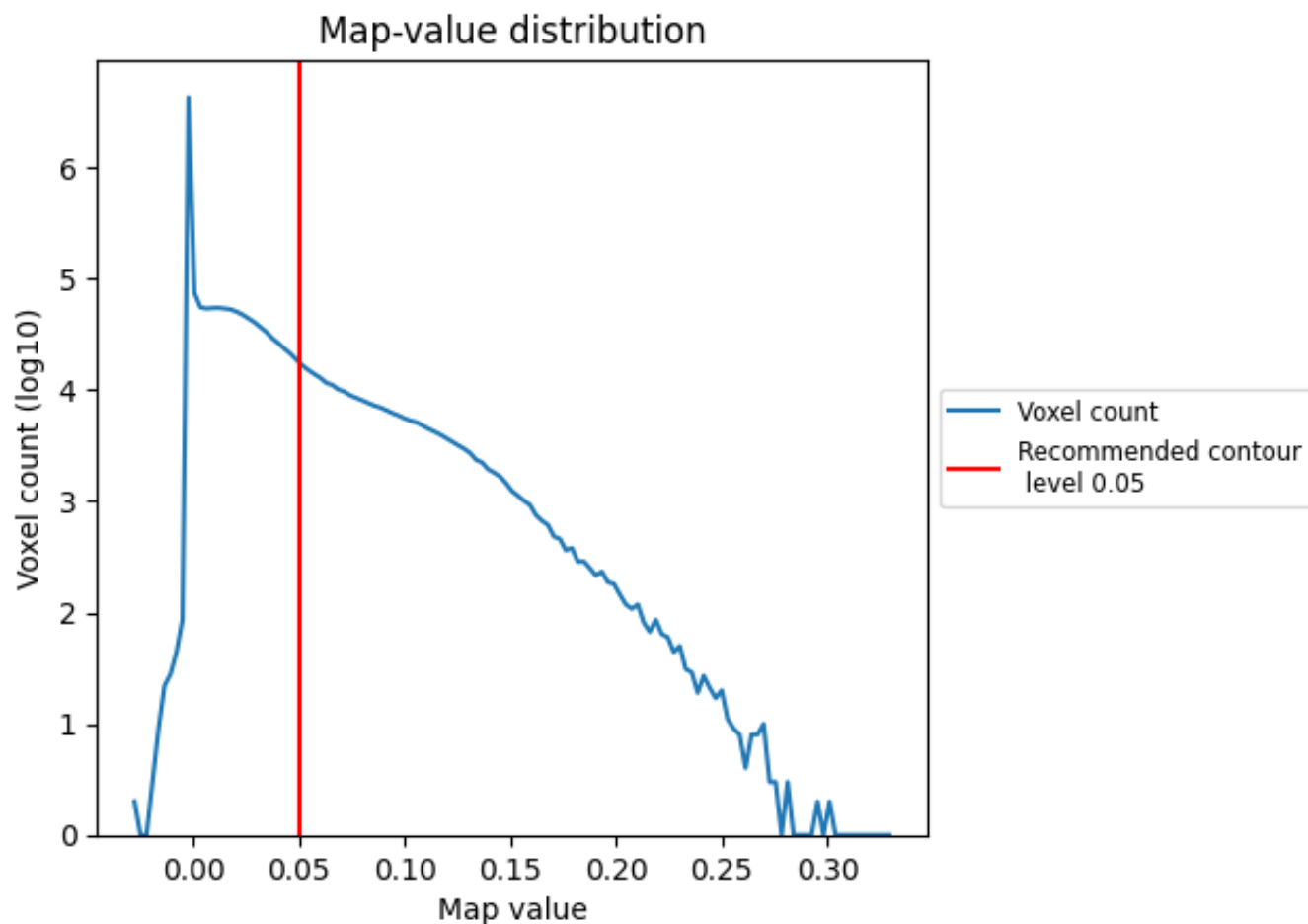
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

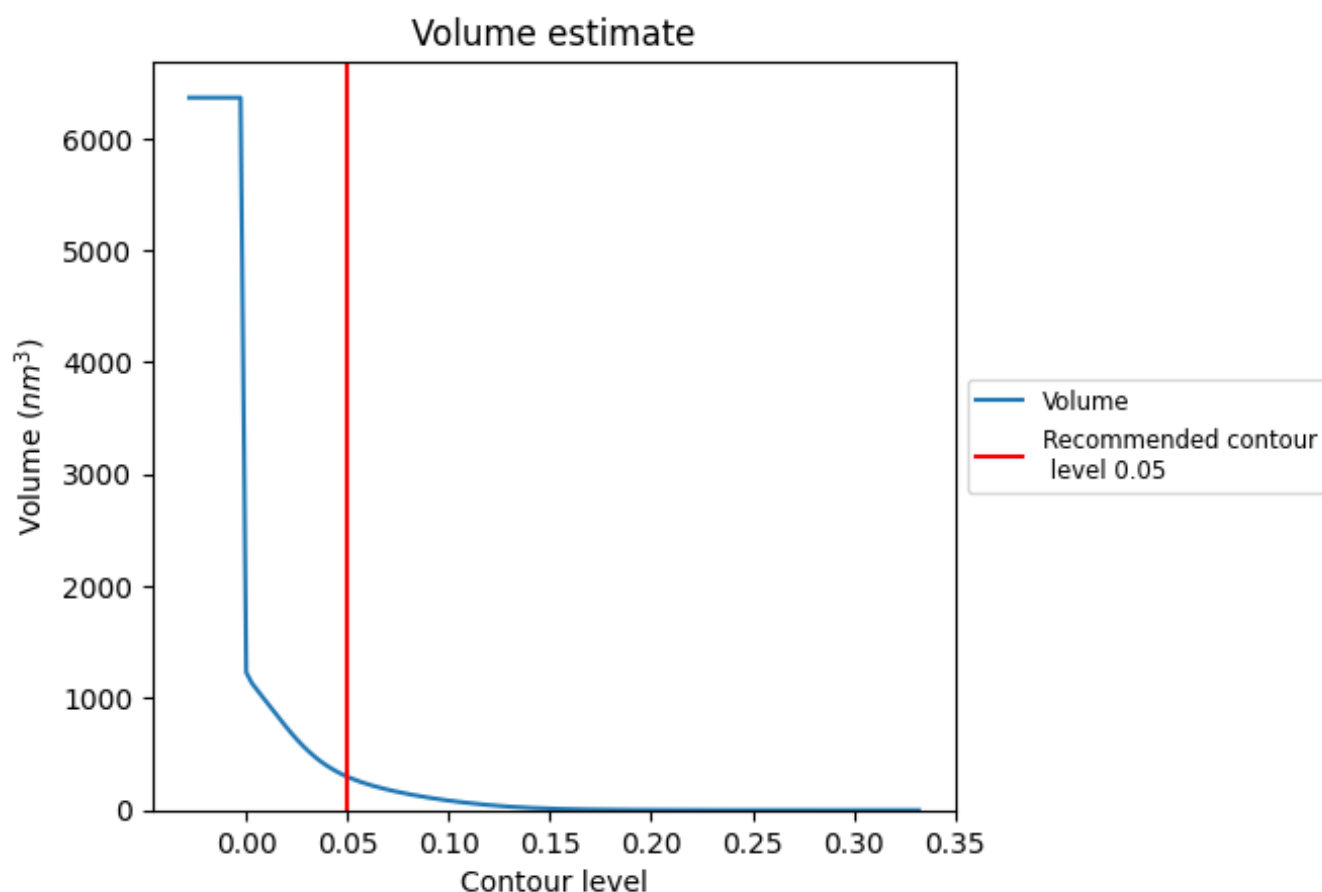
This section contains the results of statistical analysis of the map.

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 299 nm³; this corresponds to an approximate mass of 270 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.

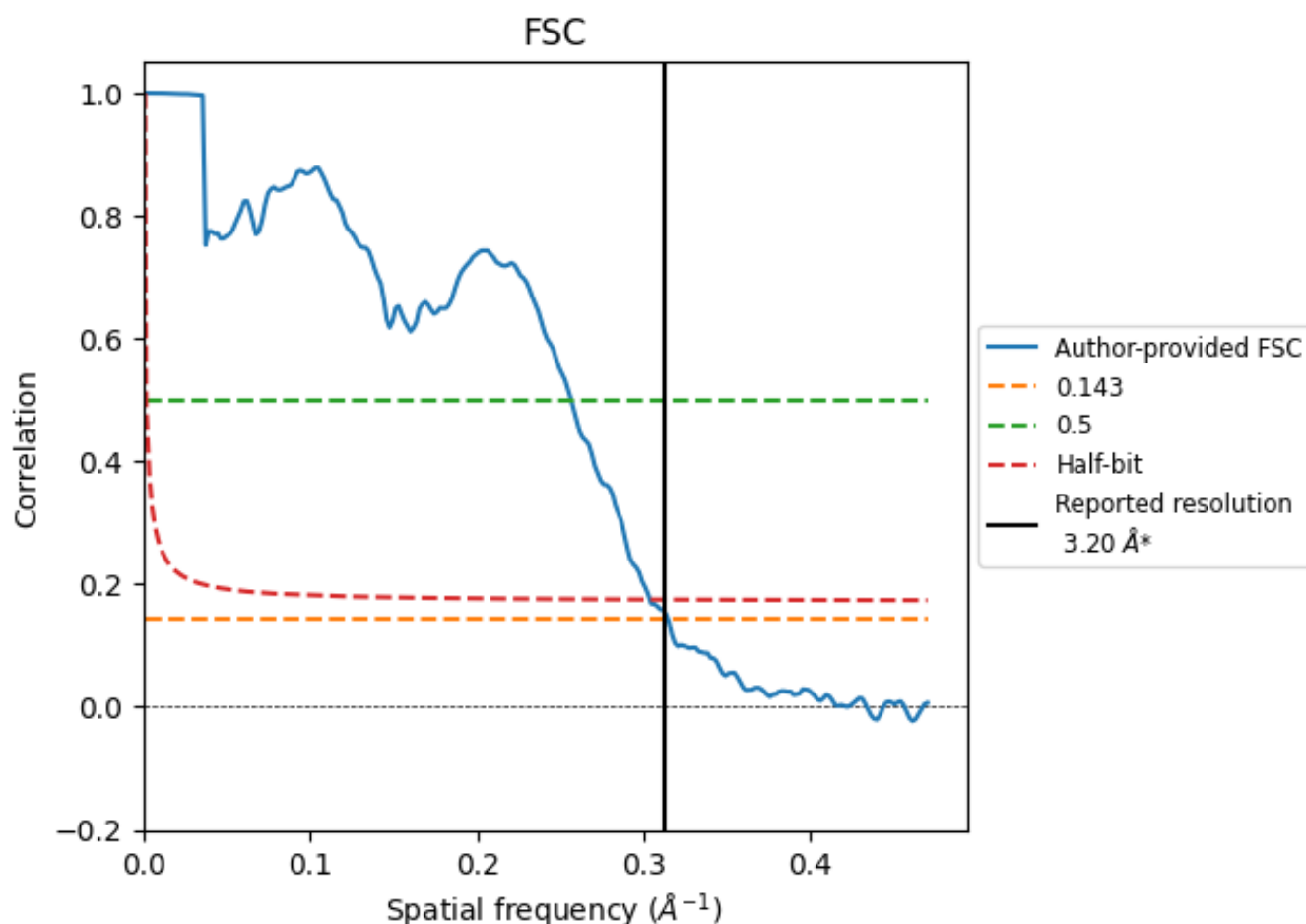
7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

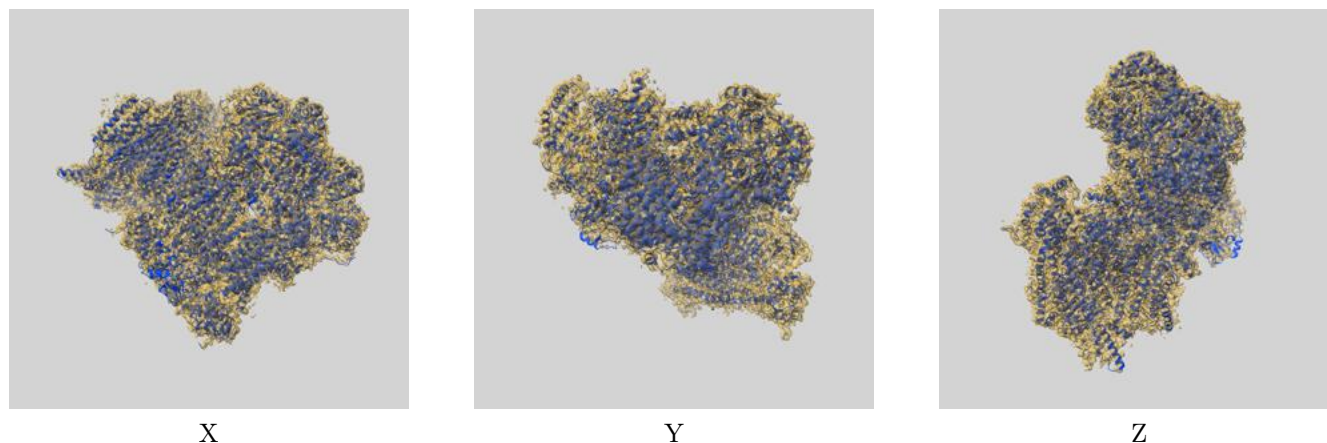
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.18	3.90	3.29
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

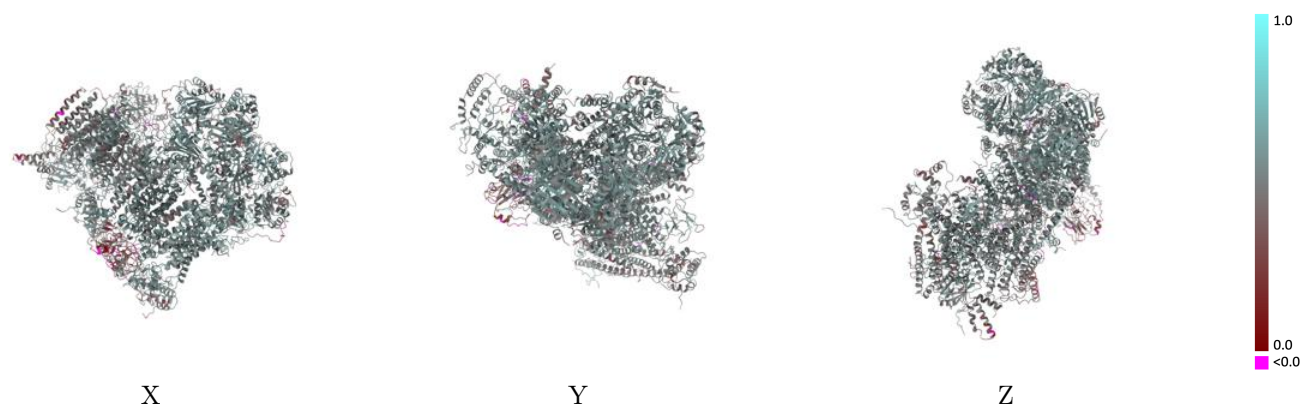
This section contains information regarding the fit between EMDB map EMD-12702 and PDB model 7O37. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



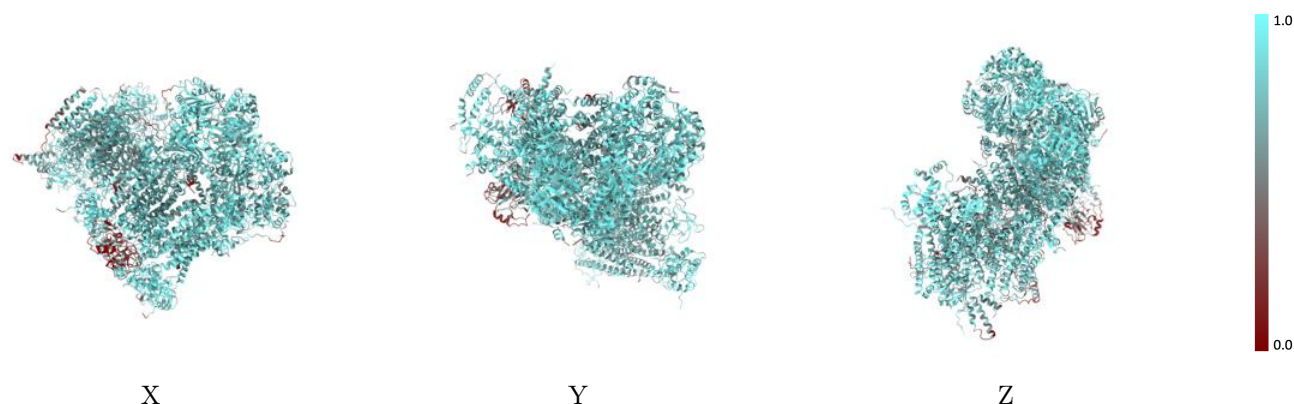
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



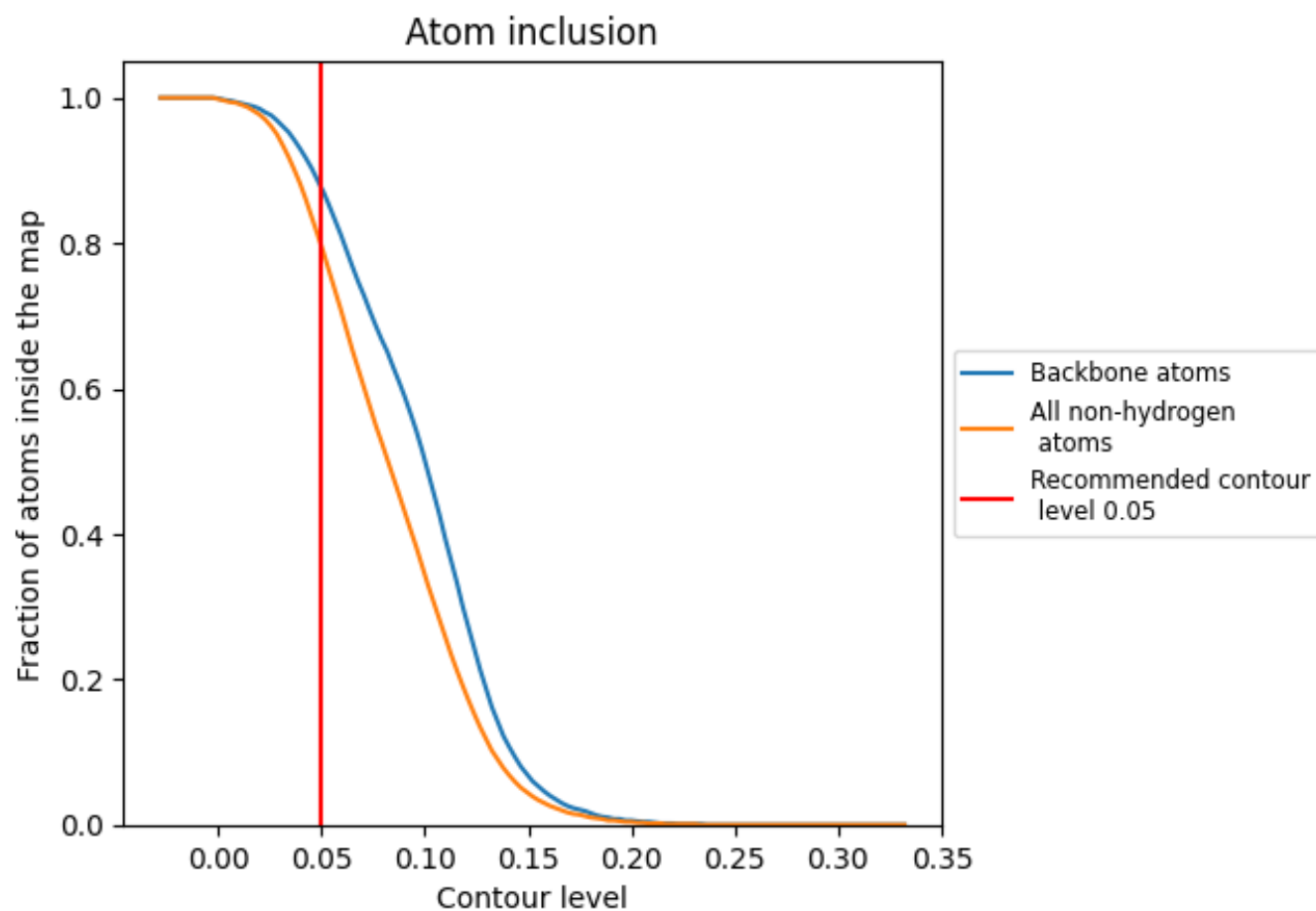
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 80% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7950	 0.5150
A	 0.8480	 0.5470
B	 0.8570	 0.5410
C	 0.8510	 0.5520
D	 0.8610	 0.5460
E	 0.4380	 0.3650
F	 0.8070	 0.5410
G	 0.7430	 0.5310
H	 0.7460	 0.4880
I	 0.6450	 0.4260
J	 0.8470	 0.5370
K	 0.6260	 0.4860
L	 0.8290	 0.5360
M	 0.8410	 0.5400
N	 0.8580	 0.5530
O	 0.8690	 0.5440
P	 0.4810	 0.3750
Q	 0.8360	 0.5380
R	 0.8430	 0.5500
S	 0.7480	 0.4710
T	 0.7740	 0.4970
U	 0.8190	 0.5230
V	 0.6030	 0.4490
a	 0.8350	 0.5400
b	 0.8170	 0.5040
c	 0.7850	 0.4900
d	 0.7960	 0.4750
e	 0.8540	 0.4820
f	 0.7980	 0.5060
g	 0.5480	 0.4310
h	 0.6780	 0.4300
i	 0.8260	 0.4810
k	 0.7630	 0.4850
l	 0.8180	 0.5430
m	 0.6930	 0.4510

