



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:53 AM UTC

PDB ID : 6T15 / pdb_00006t15
EMDB ID : EMD-10318
Title : The III2-IV(5B)1 respiratory supercomplex from *S. cerevisiae*
Authors : Marechal, A.; Pinotsis, N.; Hartley, A.
Deposited on : 2019-10-03
Resolution : 3.29 Å (reported)
Based on initial model : 6HU9

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

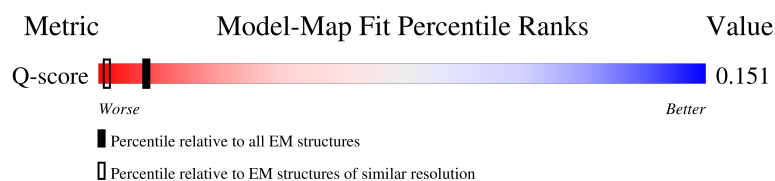
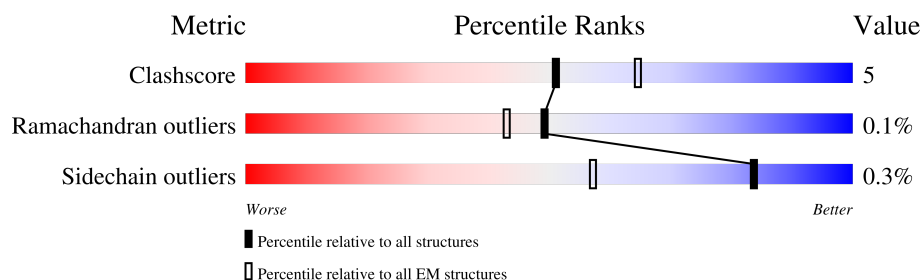
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.29 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	13997 (2.91 - 3.91)

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	431	
1	L	431	
2	B	352	
2	M	352	

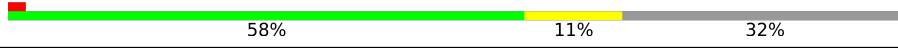
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	C	385	
3	N	385	
4	D	248	
4	O	248	
5	E	185	
5	P	185	
6	F	147	
6	Q	147	
7	G	127	
7	R	127	
8	H	94	
8	S	94	
9	I	66	
9	T	66	
10	J	77	
10	U	77	
11	a	534	
12	b	236	
13	c	269	
14	d	130	
15	e	134	
16	f	108	
17	g	59	
18	h	51	
19	i	55	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
20	j	82	
21	k	131	
22	l	66	
23	m	224	

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 48966 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; SYNONYM: COMPLEX III SUBUNIT 1, CORE PROTEIN I, UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	431	Total	C	N	O	S	0	0
			3345	2110	576	653	6		
1	L	431	Total	C	N	O	S	0	0
			3345	2110	576	653	6		

- Molecule 2 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 2, MITOCHONDRIAL; SYNONYM: COMPLEX III SUBUNIT 2, CORE PROTEIN II, UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	352	Total	C	N	O	S	0	0
			2735	1747	453	534	1		
2	M	352	Total	C	N	O	S	0	0
			2735	1747	453	534	1		

- Molecule 3 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 2, MITOCHONDRIAL; SYNONYM: COMPLEX III SUBUNIT 2, CORE PROTEIN II, UBIQUINOL-CYTOCHROME-C COMPLEX CORE PROTEIN 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	385	Total	C	N	O	S	0	0
			3090	2082	484	503	21		
3	N	385	Total	C	N	O	S	0	0
			3090	2082	484	503	21		

- Molecule 4 is a protein called CYTOCHROME C1, HEME PROTEIN, MITOCHONDRIAL; SYNONYM: COMPLEX III SUBUNIT 4, COMPLEX III SUBUNIT IV, CYTOCHROME B-C1 COMPLEX SUBUNIT 4, UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CYTOCHROME C1 SUBUNIT, CYTOCHROME C-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	247	Total	C	N	O	S	0	0
			1951	1243	338	361	9		
4	O	247	Total	C	N	O	S	0	0
			1951	1243	338	361	9		

- Molecule 5 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT RIESKE, MITOCHONDRIAL; SYNONYM: COMPLEX III SUBUNIT 5, RIESKE IRON-SULFUR PROTEIN, RISP, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	185	Total	C	N	O	S	0	0
			1411	893	242	266	10		
5	P	185	Total	C	N	O	S	0	0
			1411	893	242	266	10		

- Molecule 6 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 6; SYNONYM: COMPLEX III SUBUNIT 6, COMPLEX III SUBUNIT VI, CYTOCHROME C1 NON-HEME 17 KDA PROTEIN, MITOCHONDRIAL HINGE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 17 KDA PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	75	Total	C	N	O	S	0	0
			633	396	109	126	2		
6	Q	75	Total	C	N	O	S	0	0
			633	396	109	126	2		

- Molecule 7 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 7; SYNONYM: COMPLEX III SUBUNIT 7, COMPLEX III SUBUNIT VII, UBIQUINOL-CYTOCHROME C REDUCTASE C REDUCTASE COMPLEX 14 KDA PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	126	Total	C	N	O	S	0	0
			1019	653	173	191	2		
7	R	126	Total	C	N	O	S	0	0
			1019	653	173	191	2		

- Molecule 8 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 8; SYNONYM: COMPLEX III SUBUNIT 8, COMPLEX III SUBUNIT VII, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 11 KDA PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	93	Total	C	N	O	S	0	0
			773	510	131	130	2		
8	S	93	Total	C	N	O	S	0	0
			773	510	131	130	2		

- Molecule 9 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 9; SYNONYM: COMPLEX III SUBUNIT 9, COMPLEX III SUBUNIT X, CYTOCHROME C1 NON-HEME 7.3 KDA PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.3 KDA PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	57	Total	C	N	O		0	0
			465	310	77	78			
9	T	57	Total	C	N	O		0	0
			465	310	77	78			

- Molecule 10 is a protein called CYTOCHROME B-C1 COMPLEX SUBUNIT 10; SYNONYM: COMPLEX III SUBUNIT 10, COMPLEX III SUBUNIT XI, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.5 KDA PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	76	Total	C	N	O	S	0	0
			599	391	98	108	2		
10	U	76	Total	C	N	O	S	0	0
			599	391	98	108	2		

- Molecule 11 is a protein called CYTOCHROME C OXIDASE SUBUNIT 1; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE I, COX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	a	534	Total	C	N	O	S	0	0
			4162	2778	649	713	22		

- Molecule 12 is a protein called CYTOCHROME C OXIDASE SUBUNIT 2; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE II, COX2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	b	236	Total	C	N	O	S	0	0
			1889	1242	286	351	10		

- Molecule 13 is a protein called CYTOCHROME C OXIDASE SUBUNIT 3; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE III, COX3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	c	269	Total	C	N	O	S	0	0
			2146	1430	344	357	15		

- Molecule 14 is a protein called CYTOCHROME C OXIDASE SUBUNIT 4, MITOCHONDRIAL; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE IV, COX4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	d	121	Total	C	N	O	S	0	0
			913	576	151	181	5		

- Molecule 15 is a protein called CYTOCHROME C OXIDASE POLYPEPTIDE 5B, MITOCHONDRIAL; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE VB, COX5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	e	134	Total	C	N	O	S	0	0
			1083	694	188	199	2		

- Molecule 16 is a protein called CYTOCHROME C OXIDASE SUBUNIT 6, MITOCHONDRIAL; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE VI, COX6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	f	104	Total	C	N	O	S	0	0
			866	554	141	170	1		

- Molecule 17 is a protein called CYTOCHROME C OXIDASE SUBUNIT 7; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE VII, COX7.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	g	59	Total	C	N	O	0	0
			484	328	83	73		

- Molecule 18 is a protein called Cytochrome c oxidase polypeptide VIII, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	h	51	Total	C	N	O	S	0	0
			409	278	66	64	1		

- Molecule 19 is a protein called CYTOCHROME C OXIDASE SUBUNIT 7A; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE VIIA, COX9.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	i	55	Total	C	N	O	S	0	0
			456	300	79	74	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	j	77	Total	C	N	O	S	0	0
			642	410	109	118	5		

- Molecule 21 is a protein called CYTOCHROME C OXIDASE SUBUNIT 6A, MITOCHONDRIAL; CYTOCHROME C OXIDASE POLYPEPTIDE VIA, COX13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	k	118	Total	C	N	O	S	0	0
			967	626	167	171	3		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	130	GLY	-	expression tag	UNP P32799
k	131	ALA	-	expression tag	UNP P32799
k	132	ARG	-	expression tag	UNP P32799
k	133	GLY	-	expression tag	UNP P32799
k	134	SER	-	expression tag	UNP P32799
k	135	HIS	-	expression tag	UNP P32799
k	136	HIS	-	expression tag	UNP P32799
k	137	HIS	-	expression tag	UNP P32799
k	138	HIS	-	expression tag	UNP P32799
k	139	HIS	-	expression tag	UNP P32799
k	140	HIS	-	expression tag	UNP P32799

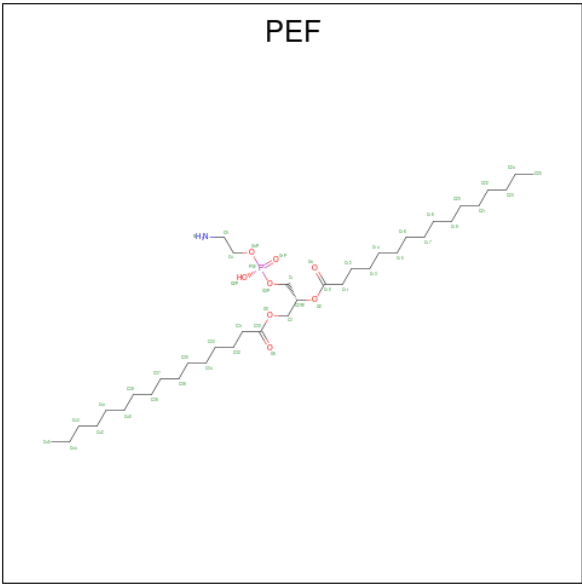
- Molecule 22 is a protein called COX26; SYNONYM: Uncharacterized protein YDR119W-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	l	45	Total	C	N	O	S	0	0
			361	238	63	59	1		

- Molecule 23 is a protein called RCF2; SYNONYM: Respiratory supercomplex factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	m	99	Total	C	N	O	S	0	0
			799	511	140	144	4		

- Molecule 24 is DI-PALMITOYL-3-SN-PHOSPHATIDYLETHANOLAMINE (CCD ID: PEF) (formula: C₃₇H₇₄NO₈P).



Mol	Chain	Residues	Atoms					AltConf
24	A	1	Total	C	N	O	P	0
			31	21	1	8	1	
24	C	1	Total	C	N	O	P	0
			40	30	1	8	1	
24	C	1	Total	C	N	O	P	0
			43	33	1	8	1	
24	E	1	Total	C	N	O	P	0
			43	33	1	8	1	
24	H	1	Total	C	N	O	P	0
			32	22	1	8	1	
24	J	1	Total	C	N	O	P	0
			29	19	1	8	1	
24	L	1	Total	C	N	O	P	0
			36	26	1	8	1	
24	N	1	Total	C	N	O	P	0
			44	34	1	8	1	
24	N	1	Total	C	N	O	P	0
			39	29	1	8	1	
24	P	1	Total	C	N	O	P	0
			42	32	1	8	1	
24	S	1	Total	C	N	O	P	0
			36	26	1	8	1	
24	U	1	Total	C	N	O	P	0
			47	37	1	8	1	

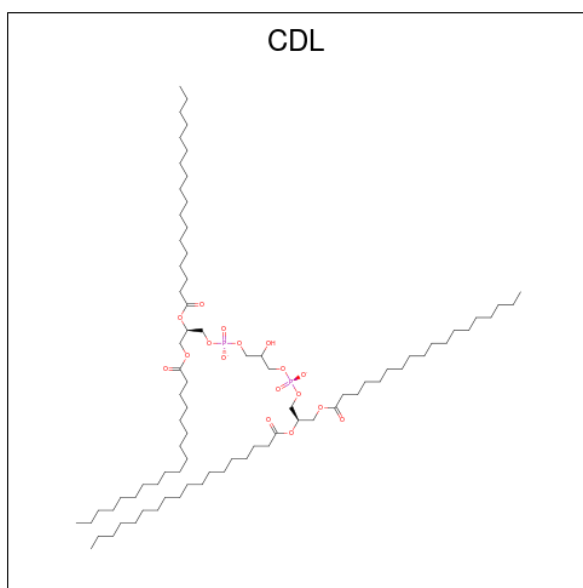
Continued on next page...

Mol	Chain	Residues	Atoms					AltConf
24	a	1	Total 33	C 23	N 1	O 8	P 1	0
24	b	1	Total 40	C 30	N 1	O 8	P 1	0
24	b	1	Total 33	C 23	N 1	O 8	P 1	0
24	c	1	Total 36	C 26	N 1	O 8	P 1	0
24	c	1	Total 41	C 31	N 1	O 8	P 1	0
24	e	1	Total 42	C 32	N 1	O 8	P 1	0

- # HEM

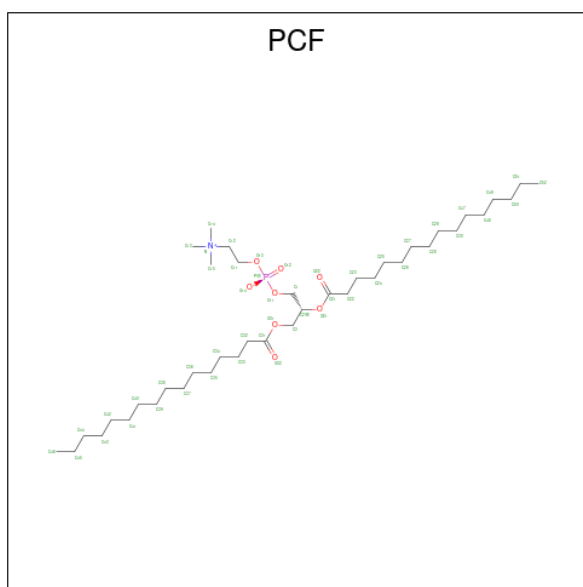
- Molecule 26 is CARDIOLIPIN (CCD ID: CDL) (formula: $\text{C}_{81}\text{H}_{156}\text{O}_{17}\text{P}_2$) (labeled as "Ligand

of Interest" by depositor).



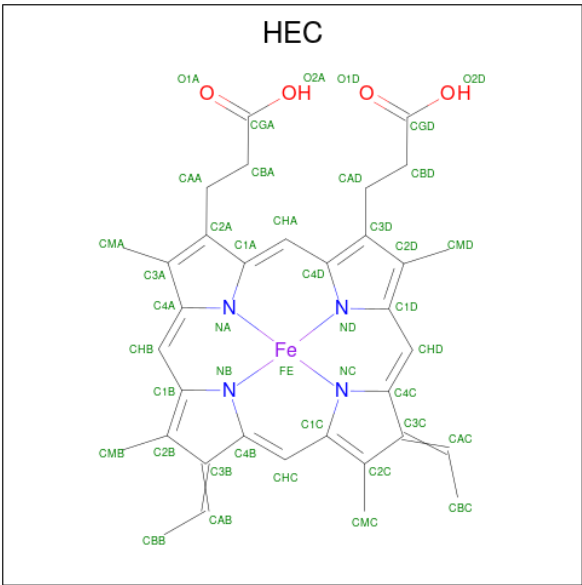
Mol	Chain	Residues	Atoms				AltConf
26	C	1	Total	C	O	P	0
			55	36	17	2	
26	D	1	Total	C	O	P	0
			67	48	17	2	
26	H	1	Total	C	O	P	0
			53	34	17	2	
26	L	1	Total	C	O	P	0
			58	39	17	2	
26	N	1	Total	C	O	P	0
			66	47	17	2	
26	O	1	Total	C	O	P	0
			71	52	17	2	
26	S	1	Total	C	O	P	0
			53	34	17	2	

- Molecule 27 is 1,2-DIACYL-SN-GLYCERO-3-PHOSHOCHOLINE (CCD ID: PCF) (formula: C₄₀H₈₀NO₈P).



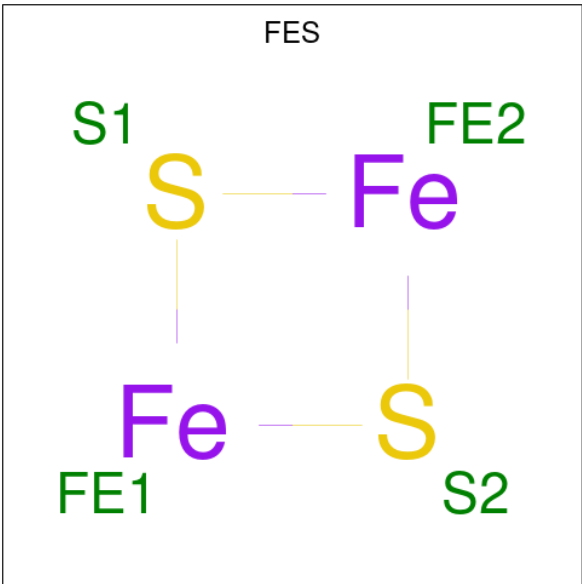
Mol	Chain	Residues	Atoms					AltConf
27	C	1	Total	C	N	O	P	0
			50	40	1	8	1	
27	I	1	Total	C	N	O	P	0
			39	29	1	8	1	
27	N	1	Total	C	N	O	P	0
			39	29	1	8	1	
27	S	1	Total	C	N	O	P	0
			32	22	1	8	1	
27	T	1	Total	C	N	O	P	0
			50	40	1	8	1	
27	e	1	Total	C	N	O	P	0
			36	26	1	8	1	

- Molecule 28 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 29 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2) (labeled as "Ligand of Interest" by depositor).



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

Continued on next page...

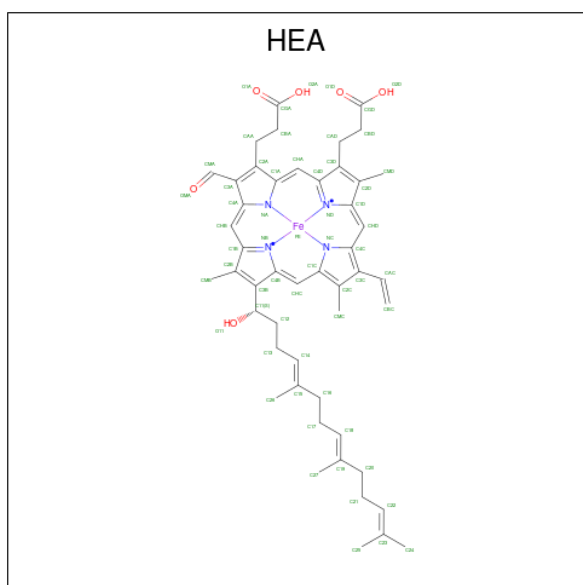
Continued from previous page...

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

- Molecule 30 is COPPER (II) ION (CCD ID: CU) (formula: Cu) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 31 is HEME-A (CCD ID: HEA) (formula: C₄₉H₅₆FeN₄O₆) (labeled as "Ligand of Interest" by depositor).

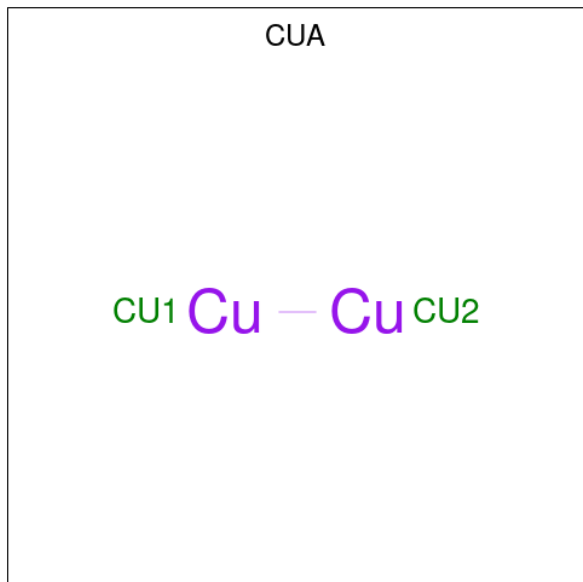


Mol	Chain	Residues	Atoms					AltConf
31	a	1	Total	C	Fe	N	O	0
			60	49	1	4	6	
31	a	1	Total	C	Fe	N	O	0
			60	49	1	4	6	

- Molecule 32 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 33 is DINUCLEAR COPPER ION (CCD ID: CUA) (formula: Cu_2) (labeled as "Ligand of Interest" by depositor).



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

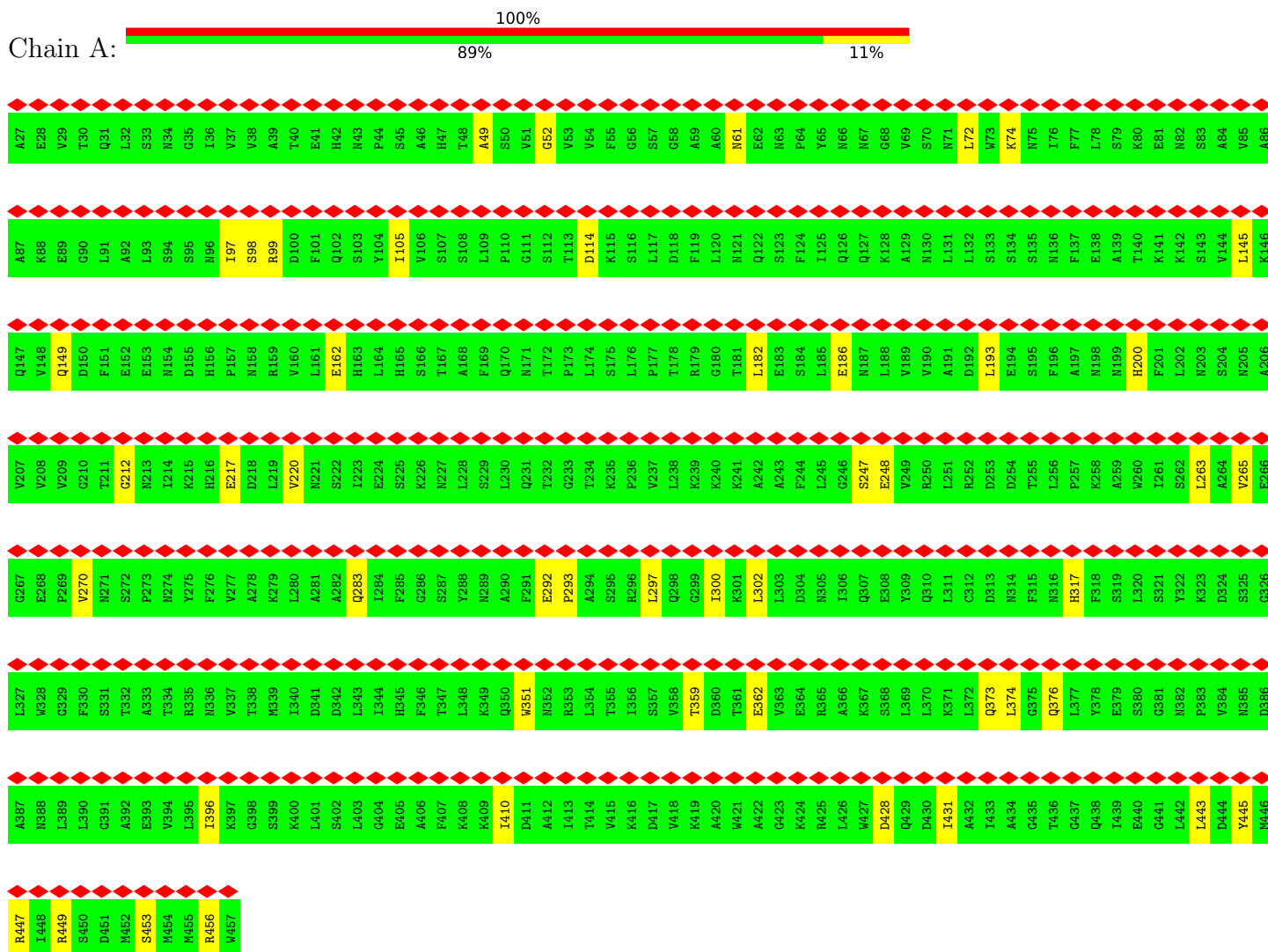
- Molecule 34 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
34	d	1	Total	Zn	0
			1	1	

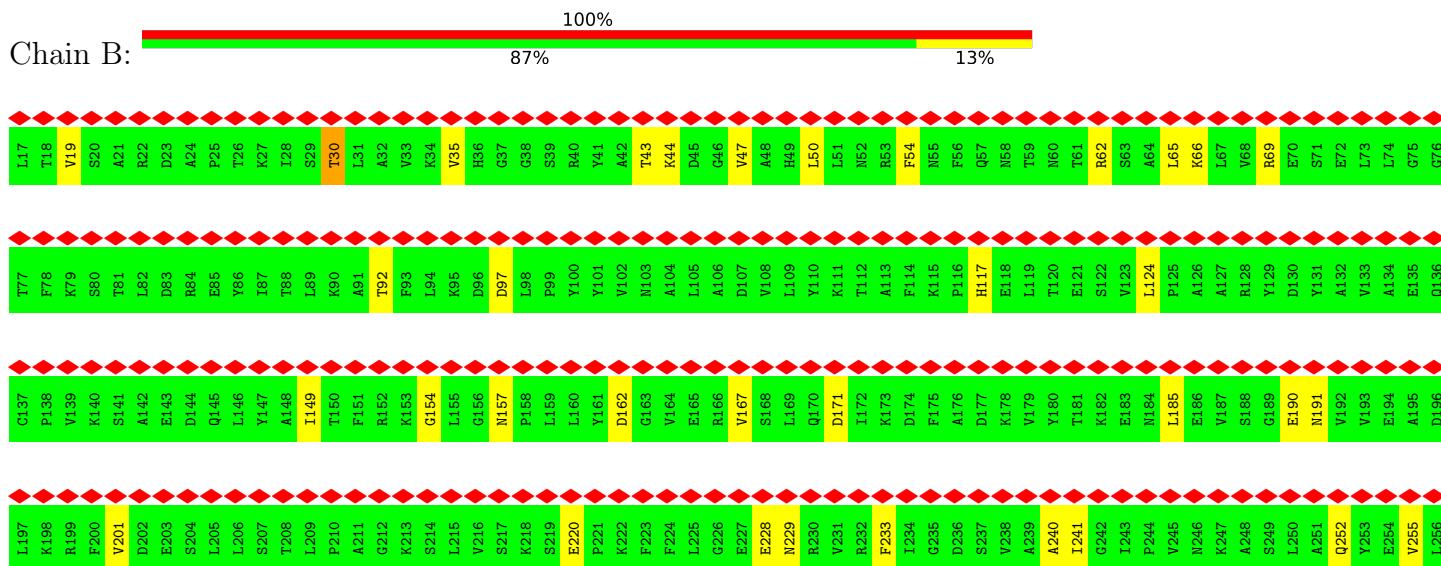
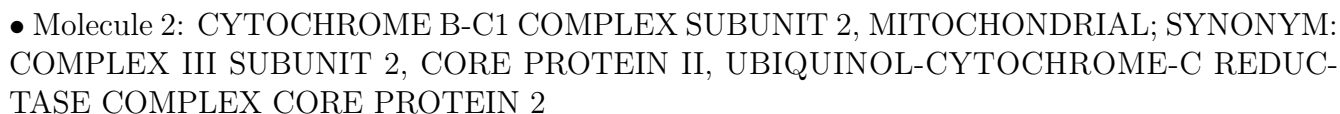
3 Residue-property plots

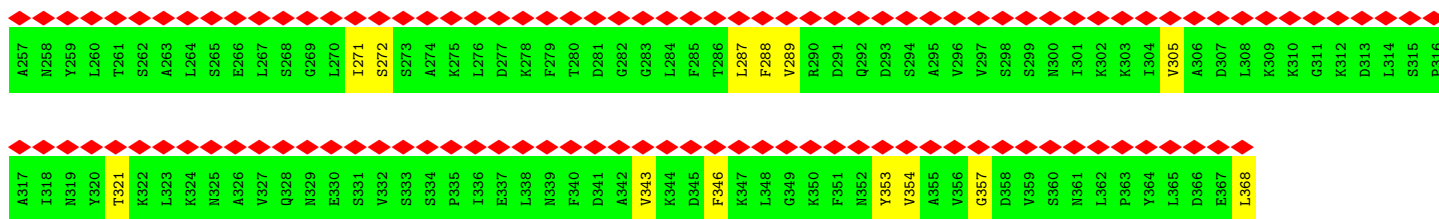
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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; SYNONYM: COMPLEX III SUBUNIT 1, CORE PROTEIN I, UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN 1

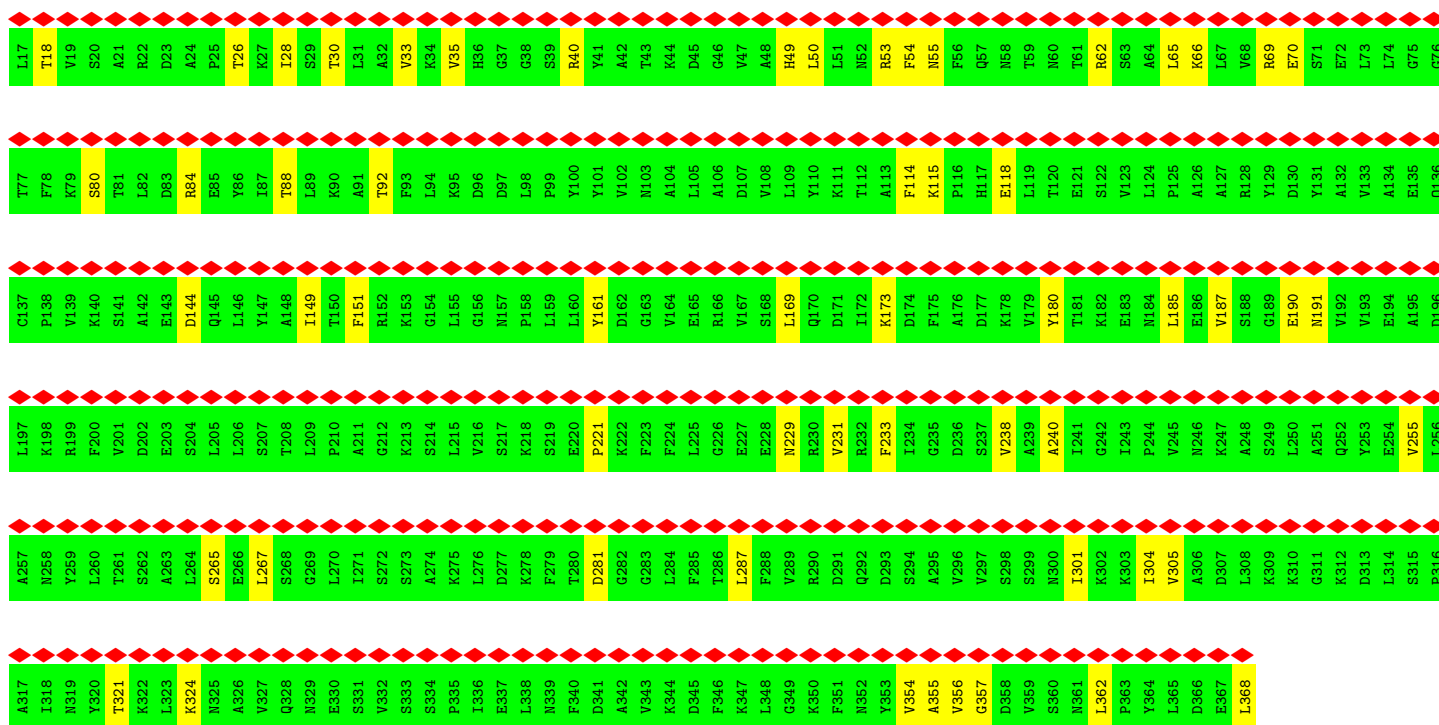
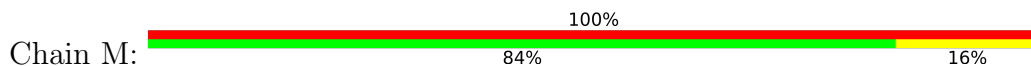


- Molecule 1: CYTOCHROME B-C1 COMPLEX SUBUNIT 1, MITOCHONDRIAL; SYNONYM: COMPLEX III SUBUNIT 1, CORE PROTEIN I, UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN 1

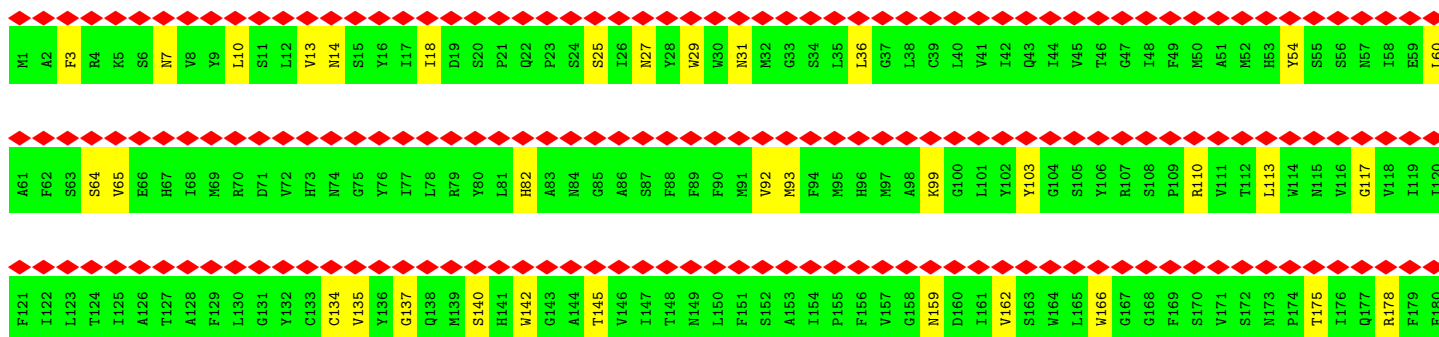
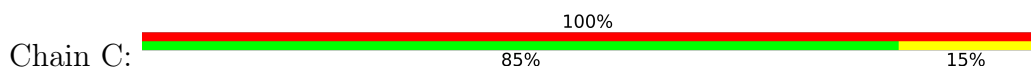


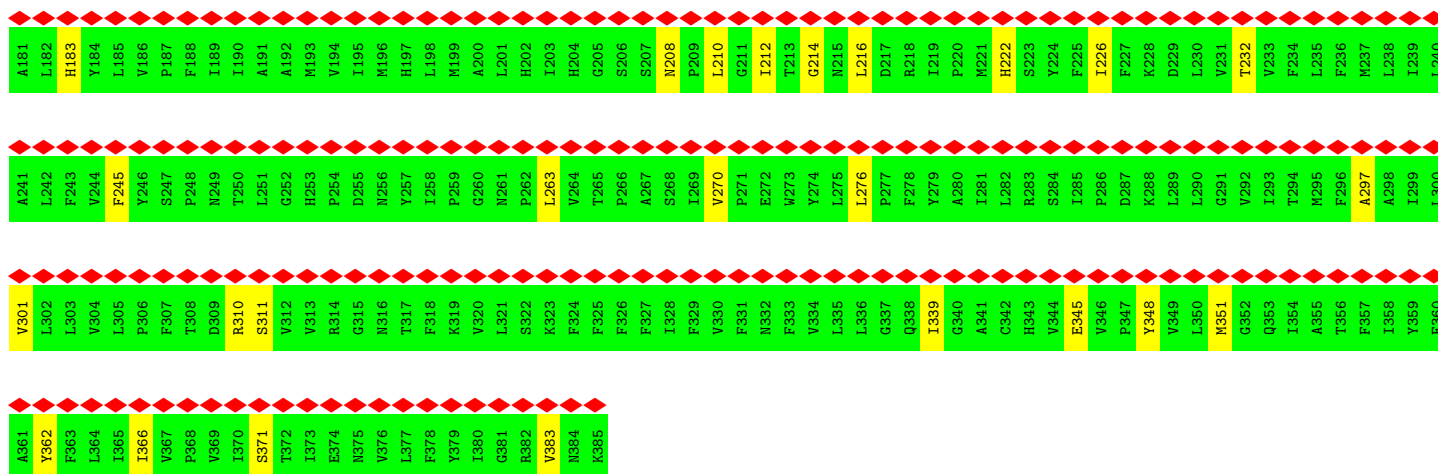


● Molecule 2: CYTOCHROME B-C1 COMPLEX SUBUNIT 2, MITOCHONDRIAL; SYNONYM: COMPLEX III SUBUNIT 2, CORE PROTEIN II, UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN 2

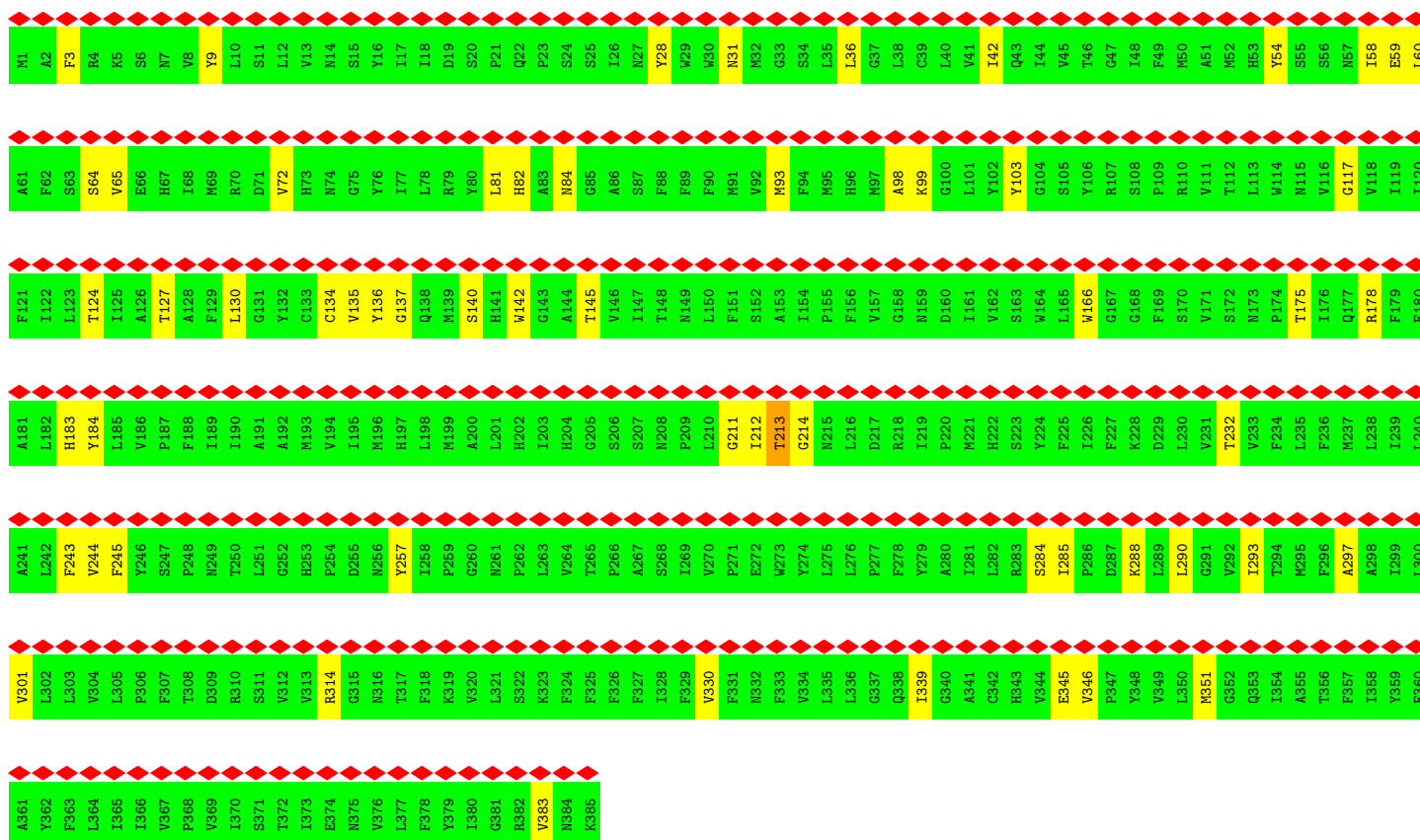
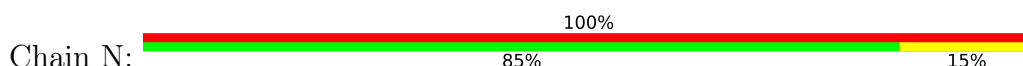


● Molecule 3: CYTOCHROME B-C1 COMPLEX SUBUNIT 2, MITOCHONDRIAL; SYNONYM: COMPLEX III SUBUNIT 2, CORE PROTEIN II, UBIQUINOL-CYTOCHROME-C COMPLEX CORE PROTEIN 2

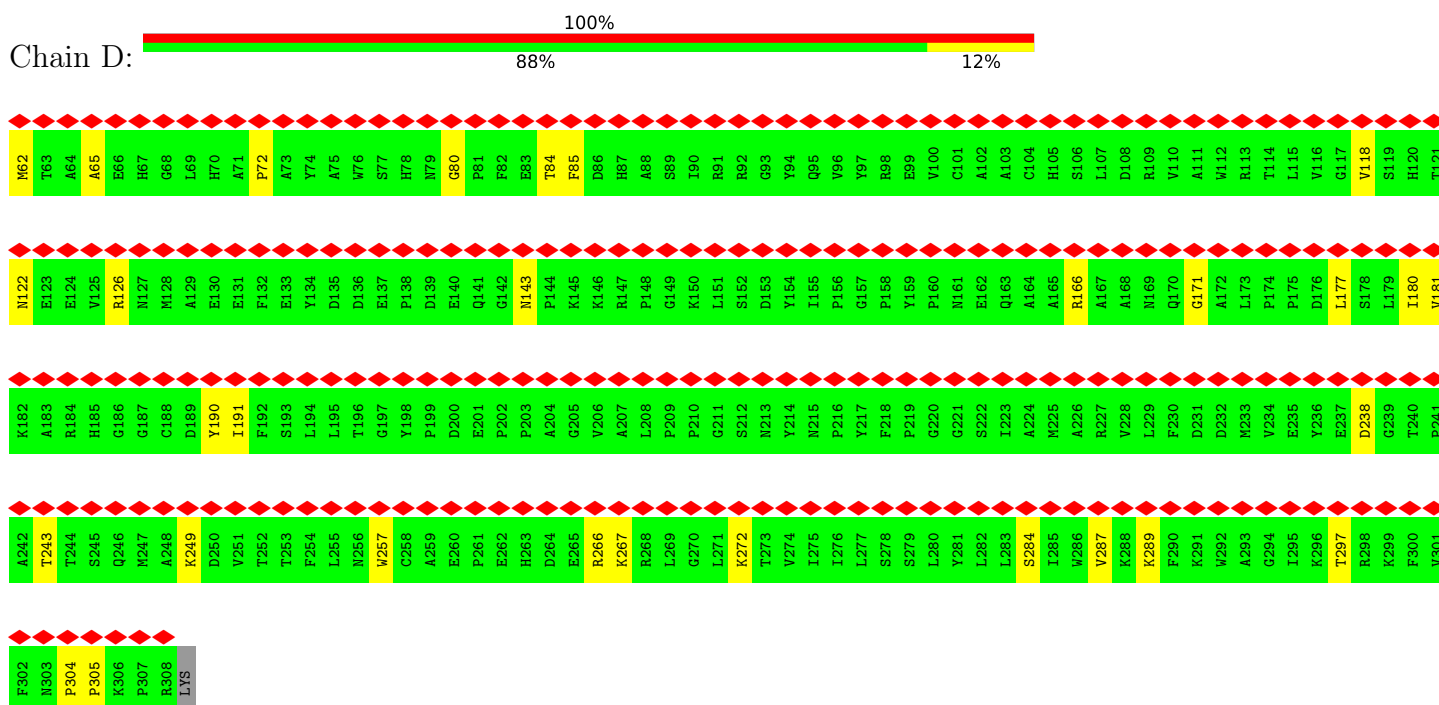




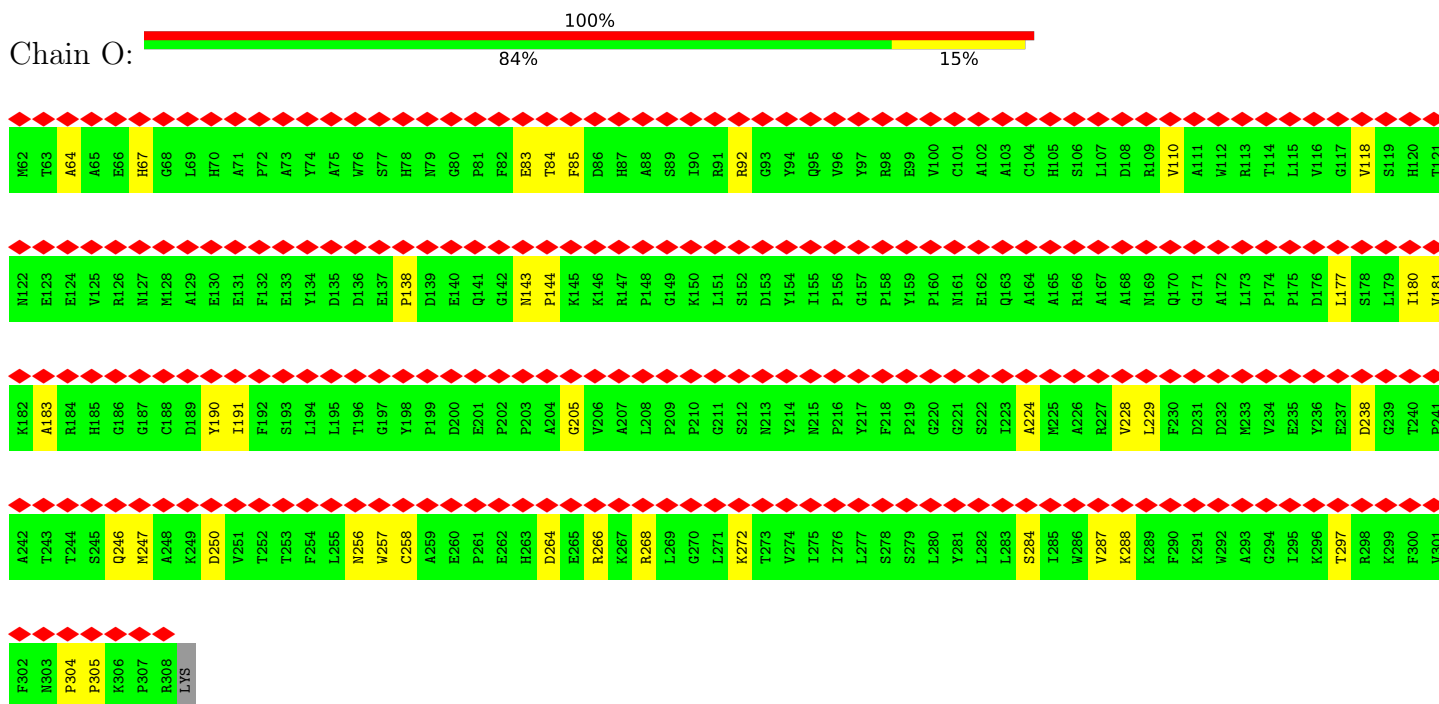
- Molecule 3: CYTOCHROME B-C1 COMPLEX SUBUNIT 2, MITOCHONDRIAL; SYNONYM: COMPLEX III SUBUNIT 2, CORE PROTEIN II, UBIQUINOL-CYTOCHROME-C COMPLEX CORE PROTEIN 2



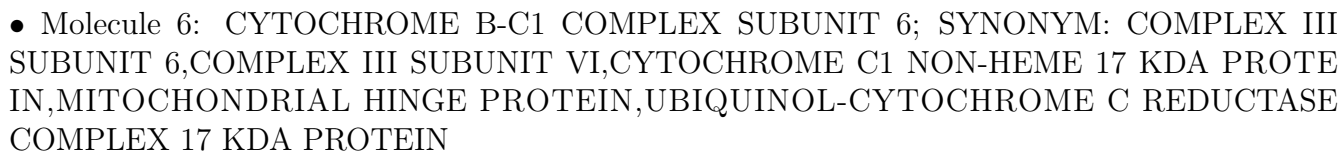
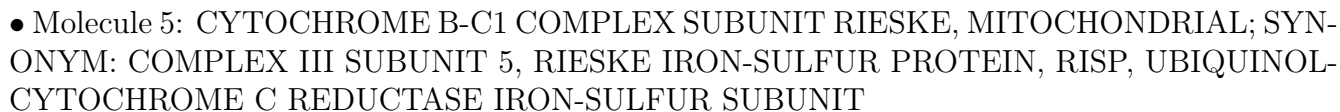
- Molecule 4: CYTOCHROME C1, HEME PROTEIN, MITOCHONDRIAL; SYNONYM: COMPLEX III SUBUNIT 4, COMPLEX III SUBUNIT IV, CYTOCHROME B-C1 COMPLEX SUBUNIT 4, UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CYTOCHROME C1 SUBUNIT, CYTOCHROME C-1

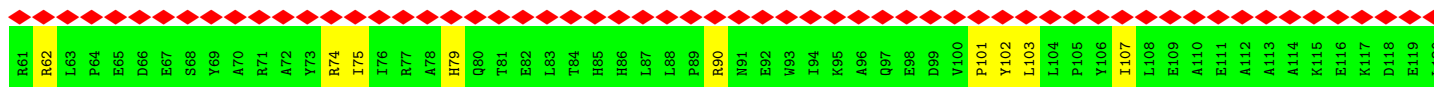


- Molecule 4: CYTOCHROME C1, HEME PROTEIN, MITOCHONDRIAL; SYNONYM: COMPLEX III SUBUNIT 4, COMPLEX III SUBUNIT IV, CYTOCHROME B-C1 COMPLEX SUBUNIT 4, UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CYTOCHROME C1 SUBUNIT, CYTOCHROME C-1



- Molecule 5: CYTOCHROME B-C1 COMPLEX SUBUNIT RIESKE, MITOCHONDRIAL; SYNONYM: COMPLEX III SUBUNIT 5, RIESKE IRON-SULFUR PROTEIN, RISP, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT



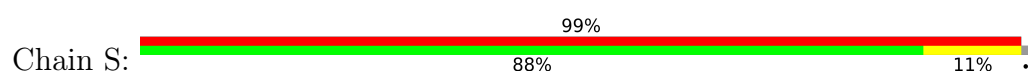




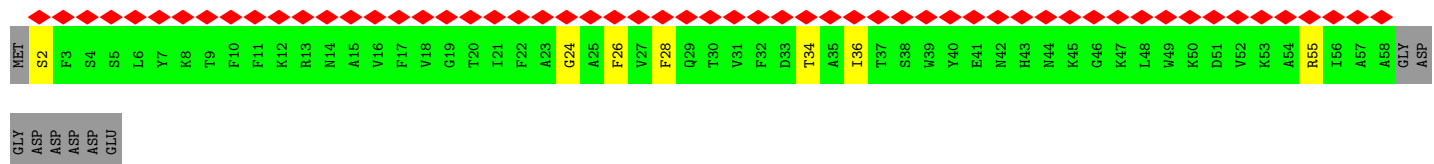
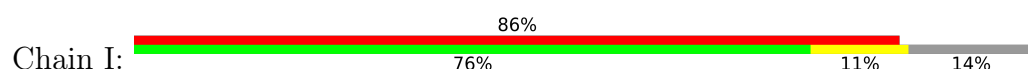
- Molecule 8: CYTOCHROME B-C1 COMPLEX SUBUNIT 8; SYNONYM: COMPLEX III SUBUNIT 8, COMPLEX III SUBUNIT VII, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 11 KDA PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C



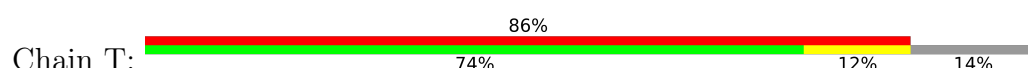
- Molecule 8: CYTOCHROME B-C1 COMPLEX SUBUNIT 8; SYNONYM: COMPLEX III SUBUNIT 8, COMPLEX III SUBUNIT VII, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 11 KDA PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C

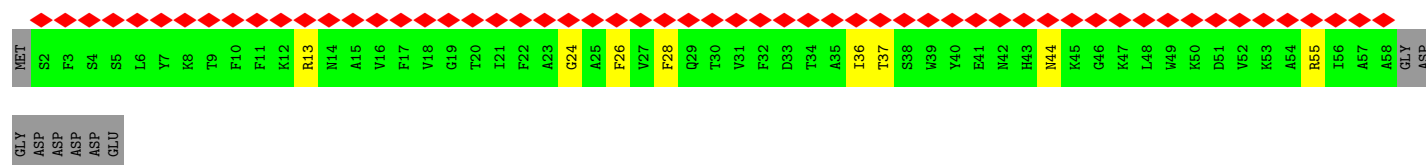


- Molecule 9: CYTOCHROME B-C1 COMPLEX SUBUNIT 9; SYNONYM: COMPLEX III SUBUNIT 9, COMPLEX III SUBUNIT X, CYTOCHROME C1 NON-HEME 7.3 KDA PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.3 KDA PROTEIN

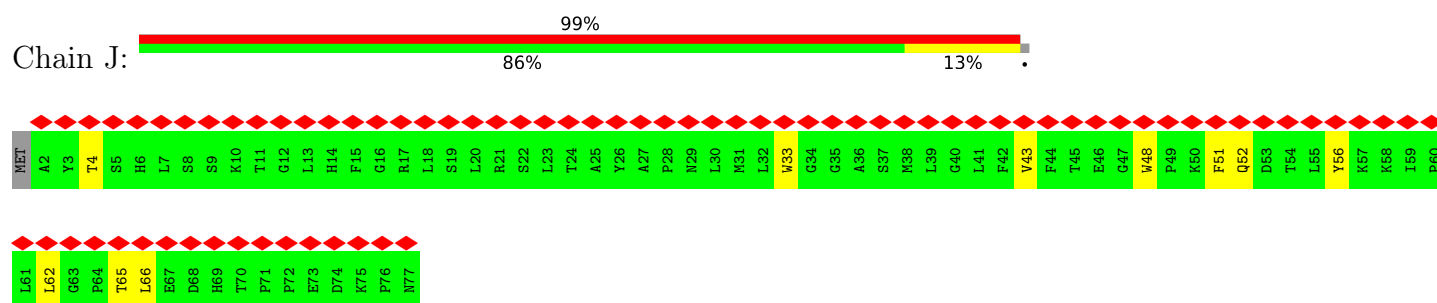


- Molecule 9: CYTOCHROME B-C1 COMPLEX SUBUNIT 9; SYNONYM: COMPLEX III SUBUNIT 9, COMPLEX III SUBUNIT X, CYTOCHROME C1 NON-HEME 7.3 KDA PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.3 KDA PROTEIN

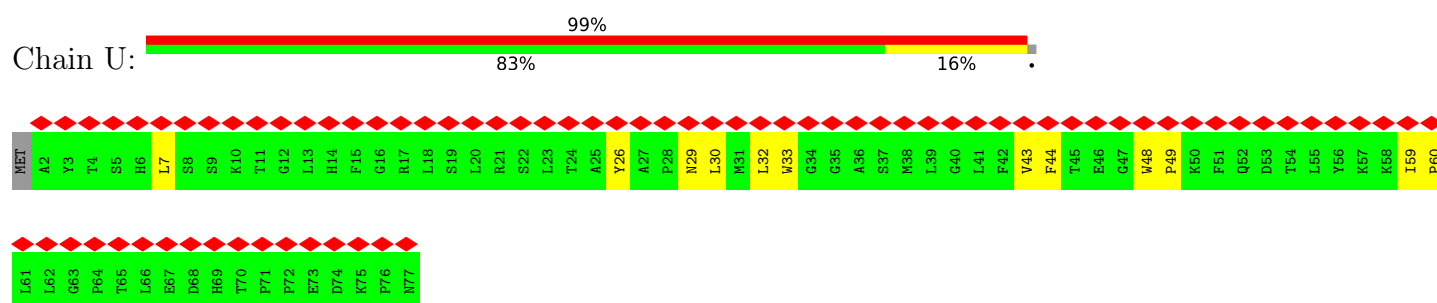




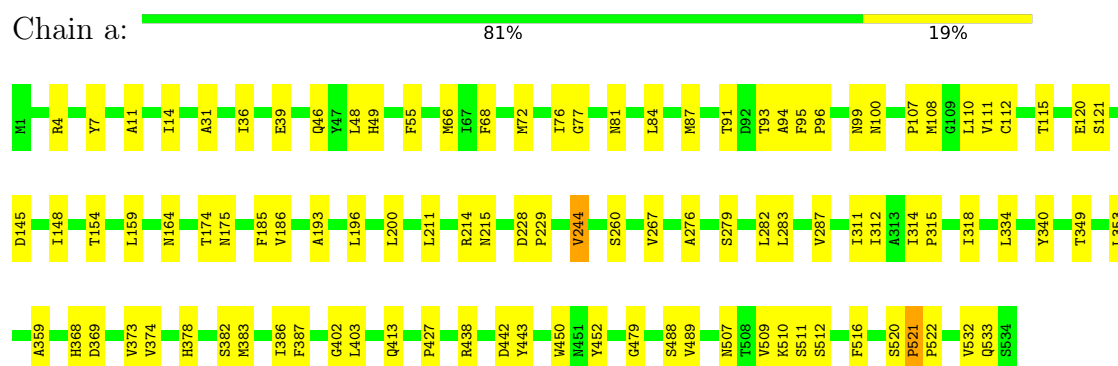
- Molecule 10: CYTOCHROME B-C1 COMPLEX SUBUNIT 10; SYNONYM: COMPLEX III SUBUNIT 10, COMPLEX III SUBUNIT XI, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.5 KDA PROTEIN



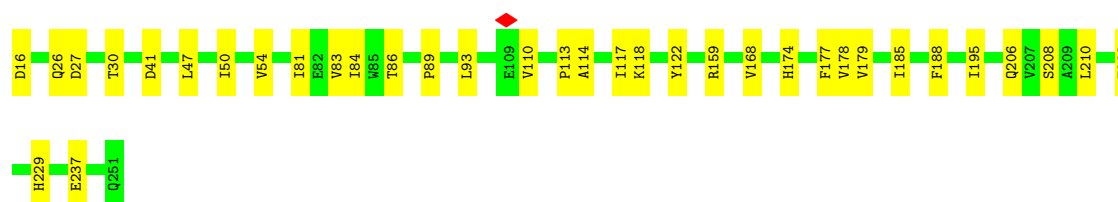
- Molecule 10: CYTOCHROME B-C1 COMPLEX SUBUNIT 10; SYNONYM: COMPLEX III SUBUNIT 10, COMPLEX III SUBUNIT XI, UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.5 KDA PROTEIN



- Molecule 11: CYTOCHROME C OXIDASE SUBUNIT 1; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE I, COX1

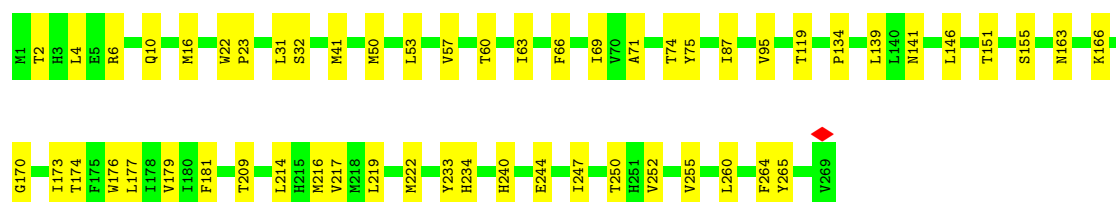


- Molecule 12: CYTOCHROME C OXIDASE SUBUNIT 2; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE II, COX2



- Molecule 13: CYTOCHROME C OXIDASE SUBUNIT 3; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE III, COX3

Chain c: 80% 20%



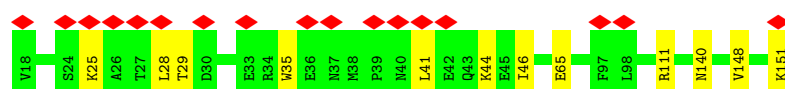
- Molecule 14: CYTOCHROME C OXIDASE SUBUNIT 4, MITOCHONDRIAL; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE IV, COX4

Chain d: 75% 18% 7%



- Molecule 15: CYTOCHROME C OXIDASE POLYPEPTIDE 5B, MITOCHONDRIAL; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE VB, COX5B

Chain e: 13% 91% 9%



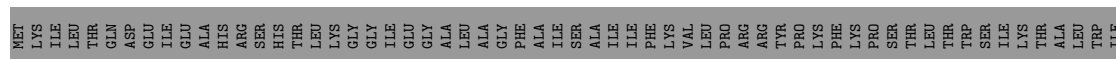
- Molecule 16: CYTOCHROME C OXIDASE SUBUNIT 6, MITOCHONDRIAL; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE VI, COX6

Chain f: 86% 10%



- Molecule 17: CYTOCHROME C OXIDASE SUBUNIT 7; SYNONYM: CYTOCHROME C OXIDASE POLYPEPTIDE VII, COX7

Chain g: 93% 7%



W188	G205	ARG	ARG	THR	GLY	TYR	VAL	SER	ASN	GLU	GLU	ARG	ILE	ASN	SER	LYS	ILE	PHE	LYS	SER
------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	73042	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 ($e^-/\text{\AA}^2$)	56.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.004	Depositor
Minimum map value	-1.391	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.081	Depositor
Recommended contour level	0.424	Depositor
Map size (Å)	402.432, 402.432, 402.432	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.048, 1.048, 1.048	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, PEF, HEM, CU, FES, CUA, MG, HEC, PCF, HEA, ZN

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	0.21	0/3406	0.49	0/4615
1	L	0.22	0/3406	0.53	0/4615
2	B	0.22	0/2781	0.50	0/3764
2	M	0.22	0/2781	0.51	0/3764
3	C	0.26	0/3192	0.59	1/4354 (0.0%)
3	N	0.26	0/3192	0.57	0/4354
4	D	0.20	0/2012	0.44	0/2740
4	O	0.21	0/2012	0.44	0/2740
5	E	0.28	0/1444	0.65	2/1957 (0.1%)
5	P	0.30	0/1444	0.67	0/1957
6	F	0.31	0/647	0.71	2/870 (0.2%)
6	Q	0.28	0/647	0.67	2/870 (0.2%)
7	G	0.24	0/1040	0.54	0/1408
7	R	0.22	0/1040	0.47	0/1408
8	H	0.19	0/804	0.44	0/1088
8	S	0.22	0/804	0.48	0/1088
9	I	0.22	0/479	0.48	0/646
9	T	0.20	0/479	0.47	0/646
10	J	0.21	0/619	0.52	0/841
10	U	0.26	0/619	0.58	0/841
11	a	0.29	0/4290	0.66	1/5857 (0.0%)
12	b	0.26	0/1941	0.66	0/2653
13	c	0.27	0/2218	0.62	0/3036
14	d	0.26	0/932	0.61	0/1269
15	e	0.24	0/1111	0.59	0/1503
16	f	0.28	0/884	0.56	0/1196
17	g	0.30	0/500	0.70	1/681 (0.1%)
18	h	0.25	0/424	0.68	2/569 (0.4%)
19	i	0.25	0/468	0.56	0/626
20	j	0.31	0/664	0.75	1/899 (0.1%)
21	k	0.24	0/1002	0.55	0/1364
22	l	0.25	0/372	0.64	0/502

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
23	m	0.29	0/813	0.64	0/1093
All	All	0.25	0/48467	0.57	12/65814 (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
1	L	0	1
2	B	0	1
3	N	0	1
5	E	0	1
5	P	0	1
11	a	0	4
13	c	0	1
14	d	0	1
21	k	0	1
All	All	0	12

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	j	46	ALA	N-CA-C	10.14	117.34	108.22
11	a	14	ILE	N-CA-C	-6.09	106.86	112.96
18	h	77	ALA	CA-C-N	5.71	131.98	121.70
18	h	77	ALA	C-N-CA	5.71	131.98	121.70
6	F	117	LEU	CA-C-N	5.64	132.30	121.54

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	220	GLU	Peptide
5	E	167	ILE	Peptide
1	L	444	ASP	Peptide
3	N	345	GLU	Peptide
5	P	125	GLU	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	3345	0	3323	29	0
1	L	3345	0	3323	37	0
2	B	2735	0	2774	30	0
2	M	2735	0	2774	35	0
3	C	3090	0	3127	42	0
3	N	3090	0	3129	45	0
4	D	1951	0	1874	22	0
4	O	1951	0	1874	28	0
5	E	1411	0	1386	30	0
5	P	1411	0	1386	29	0
6	F	633	0	587	7	0
6	Q	633	0	587	4	0
7	G	1019	0	1034	11	0
7	R	1019	0	1034	11	0
8	H	773	0	736	14	0
8	S	773	0	735	8	0
9	I	465	0	459	6	0
9	T	465	0	459	7	0
10	J	599	0	594	8	0
10	U	599	0	594	9	0
11	a	4162	0	4189	66	0
12	b	1889	0	1866	26	0
13	c	2146	0	2137	38	0
14	d	913	0	910	20	0
15	e	1083	0	1081	9	0
16	f	866	0	834	6	0
17	g	484	0	517	2	0
18	h	409	0	408	5	0
19	i	456	0	469	4	0
20	j	642	0	586	7	0
21	k	967	0	933	11	0
22	l	361	0	363	4	0
23	m	799	0	819	4	0
24	A	31	0	35	2	0
24	C	83	0	113	3	0
24	E	43	0	62	2	0
24	H	32	0	37	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	J	29	0	31	0	0
24	L	36	0	43	1	0
24	N	83	0	118	3	0
24	P	42	0	60	1	0
24	S	36	0	48	1	0
24	U	47	0	73	0	0
24	a	33	0	39	1	0
24	b	73	0	95	1	0
24	c	77	0	100	2	0
24	e	42	0	60	1	0
25	C	86	0	60	3	0
25	N	86	0	60	5	0
26	C	55	0	52	0	0
26	D	67	0	78	1	0
26	H	53	0	50	3	0
26	L	58	0	60	2	0
26	N	66	0	75	4	0
26	O	71	0	89	2	0
26	S	53	0	50	2	0
27	C	50	0	80	0	0
27	I	39	0	52	0	0
27	N	39	0	55	3	0
27	S	32	0	38	0	0
27	T	50	0	80	1	0
27	e	36	0	44	3	0
28	D	43	0	31	1	0
28	O	43	0	31	3	0
29	E	4	0	0	0	0
29	P	4	0	0	1	0
30	a	1	0	0	0	0
31	a	120	0	105	9	0
32	a	1	0	0	0	0
33	b	2	0	0	0	0
34	d	1	0	0	0	0
All	All	48966	0	48905	533	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 533 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)
19:i:34:TRP:O	19:i:38:MET:HB2	1.84	0.78
11:a:66:MET:HG2	31:a:602:HEA:HBC1	1.65	0.76
2:M:50:LEU:O	2:M:54:PHE:HB2	1.84	0.75
5:E:118:ILE:HA	5:E:153:LEU:O	1.87	0.72
2:B:255:VAL:HG12	2:B:321:THR:HG21	1.74	0.69

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	429/431 (100%)	397 (92%)	32 (8%)	0	100	100
1	L	429/431 (100%)	394 (92%)	35 (8%)	0	100	100
2	B	350/352 (99%)	334 (95%)	16 (5%)	0	100	100
2	M	350/352 (99%)	334 (95%)	16 (5%)	0	100	100
3	C	383/385 (100%)	363 (95%)	20 (5%)	0	100	100
3	N	383/385 (100%)	357 (93%)	26 (7%)	0	100	100
4	D	245/248 (99%)	239 (98%)	6 (2%)	0	100	100
4	O	245/248 (99%)	241 (98%)	4 (2%)	0	100	100
5	E	183/185 (99%)	163 (89%)	20 (11%)	0	100	100
5	P	183/185 (99%)	167 (91%)	16 (9%)	0	100	100
6	F	73/147 (50%)	68 (93%)	5 (7%)	0	100	100
6	Q	73/147 (50%)	70 (96%)	3 (4%)	0	100	100
7	G	124/127 (98%)	121 (98%)	3 (2%)	0	100	100
7	R	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
8	H	91/94 (97%)	83 (91%)	8 (9%)	0	100	100
8	S	91/94 (97%)	85 (93%)	6 (7%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	55/66 (83%)	54 (98%)	1 (2%)	0	100	100
9	T	55/66 (83%)	55 (100%)	0	0	100	100
10	J	74/77 (96%)	70 (95%)	4 (5%)	0	100	100
10	U	74/77 (96%)	72 (97%)	2 (3%)	0	100	100
11	a	532/534 (100%)	490 (92%)	40 (8%)	2 (0%)	30	60
12	b	234/236 (99%)	214 (92%)	20 (8%)	0	100	100
13	c	267/269 (99%)	256 (96%)	10 (4%)	1 (0%)	30	60
14	d	119/130 (92%)	101 (85%)	18 (15%)	0	100	100
15	e	132/134 (98%)	123 (93%)	9 (7%)	0	100	100
16	f	102/108 (94%)	96 (94%)	6 (6%)	0	100	100
17	g	57/59 (97%)	53 (93%)	4 (7%)	0	100	100
18	h	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
19	i	53/55 (96%)	51 (96%)	2 (4%)	0	100	100
20	j	75/82 (92%)	67 (89%)	8 (11%)	0	100	100
21	k	116/131 (88%)	103 (89%)	13 (11%)	0	100	100
22	l	43/66 (65%)	42 (98%)	1 (2%)	0	100	100
23	m	97/224 (43%)	91 (94%)	6 (6%)	0	100	100
All	All	5890/6303 (93%)	5521 (94%)	366 (6%)	3 (0%)	49	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	a	121	SER
11	a	521	PRO
13	c	23	PRO

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	370/370 (100%)	370 (100%)	0	100	100
1	L	370/370 (100%)	370 (100%)	0	100	100
2	B	301/301 (100%)	300 (100%)	1 (0%)	86	86
2	M	301/301 (100%)	300 (100%)	1 (0%)	86	86
3	C	338/338 (100%)	338 (100%)	0	100	100
3	N	338/338 (100%)	337 (100%)	1 (0%)	86	86
4	D	205/206 (100%)	205 (100%)	0	100	100
4	O	205/206 (100%)	205 (100%)	0	100	100
5	E	151/151 (100%)	150 (99%)	1 (1%)	76	80
5	P	151/151 (100%)	149 (99%)	2 (1%)	61	74
6	F	68/131 (52%)	68 (100%)	0	100	100
6	Q	68/131 (52%)	67 (98%)	1 (2%)	57	72
7	G	110/111 (99%)	110 (100%)	0	100	100
7	R	110/111 (99%)	109 (99%)	1 (1%)	70	78
8	H	77/78 (99%)	77 (100%)	0	100	100
8	S	77/78 (99%)	77 (100%)	0	100	100
9	I	47/54 (87%)	47 (100%)	0	100	100
9	T	47/54 (87%)	47 (100%)	0	100	100
10	J	65/66 (98%)	65 (100%)	0	100	100
10	U	65/66 (98%)	65 (100%)	0	100	100
11	a	447/447 (100%)	446 (100%)	1 (0%)	87	88
12	b	209/209 (100%)	209 (100%)	0	100	100
13	c	228/228 (100%)	228 (100%)	0	100	100
14	d	102/111 (92%)	101 (99%)	1 (1%)	68	76
15	e	115/115 (100%)	114 (99%)	1 (1%)	70	78
16	f	92/96 (96%)	91 (99%)	1 (1%)	65	76
17	g	50/50 (100%)	50 (100%)	0	100	100
18	h	41/41 (100%)	41 (100%)	0	100	100
19	i	46/46 (100%)	46 (100%)	0	100	100
20	j	69/73 (94%)	69 (100%)	0	100	100
21	k	104/113 (92%)	104 (100%)	0	100	100
22	l	36/53 (68%)	35 (97%)	1 (3%)	38	62

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	m	84/191 (44%)	84 (100%)	0	100	100
All	All	5087/5385 (94%)	5074 (100%)	13 (0%)	84	86

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	R	125	VAL
11	a	244	VAL
22	l	29	VAL
15	e	148	VAL
16	f	111	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 128 such sidechains are listed below:

Mol	Chain	Res	Type
15	e	115	ASN
16	f	44	HIS
1	L	121	ASN
1	L	102	GLN
17	g	13	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 45 ligands modelled in this entry, 3 are monoatomic - leaving 42 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
24	PEF	C	605	-	42,42,46	1.01	2 (4%)	45,47,51	1.16	3 (6%)
27	PCF	e	202	-	35,35,49	1.14	2 (5%)	41,43,57	1.08	3 (7%)
24	PEF	L	502	-	35,35,46	1.08	2 (5%)	38,40,51	1.15	4 (10%)
28	HEC	O	401	4	46,50,50	2.67	27 (58%)	58,82,82	2.15	20 (34%)
24	PEF	c	302	-	40,40,46	1.02	2 (5%)	43,45,51	1.05	2 (4%)
29	FES	E	301	5	0,4,4	-	-	-	-	-
27	PCF	S	103	-	31,31,49	1.20	2 (6%)	37,39,57	1.11	4 (10%)
25	HEM	N	601	3	50,50,50	1.61	10 (20%)	67,82,82	1.67	13 (19%)
26	CDL	D	402	-	66,66,99	1.12	4 (6%)	72,78,111	1.21	6 (8%)
24	PEF	c	301	-	35,35,46	1.09	2 (5%)	38,40,51	1.16	3 (7%)
24	PEF	N	604	-	43,43,46	0.98	2 (4%)	46,48,51	1.06	3 (6%)
24	PEF	a	605	-	32,32,46	1.16	2 (6%)	35,37,51	1.20	3 (8%)
24	PEF	C	604	27	39,39,46	1.04	2 (5%)	42,44,51	1.11	3 (7%)
31	HEA	a	603	11	67,67,67	2.40	24 (35%)	81,103,103	2.64	34 (41%)
24	PEF	U	101	-	46,46,46	0.96	2 (4%)	49,51,51	1.04	2 (4%)
27	PCF	I	101	24	38,38,49	1.08	2 (5%)	44,46,57	1.10	4 (9%)
26	CDL	C	603	-	54,54,99	1.16	4 (7%)	60,66,111	1.25	6 (10%)
28	HEC	D	401	4	46,50,50	2.66	27 (58%)	58,82,82	2.10	19 (32%)
31	HEA	a	602	11	67,67,67	2.38	25 (37%)	81,103,103	2.53	35 (43%)
24	PEF	e	201	-	41,41,46	1.04	2 (4%)	44,46,51	0.98	2 (4%)
25	HEM	C	602	3	50,50,50	1.63	9 (18%)	67,82,82	1.63	13 (19%)
24	PEF	b	302	-	39,39,46	1.05	2 (5%)	42,44,51	1.06	2 (4%)
24	PEF	S	102	-	35,35,46	1.09	2 (5%)	38,40,51	1.12	3 (7%)
26	CDL	N	603	26	65,65,99	1.13	4 (6%)	71,77,111	1.18	7 (9%)
26	CDL	O	402	26	70,70,99	1.09	4 (5%)	76,82,111	1.22	7 (9%)
26	CDL	H	601	-	52,52,99	1.27	4 (7%)	58,64,111	1.28	6 (10%)
24	PEF	N	605	-	38,38,46	1.08	2 (5%)	41,43,51	1.00	2 (4%)
25	HEM	N	602	3	50,50,50	1.61	9 (18%)	67,82,82	1.62	14 (20%)
26	CDL	S	101	-	52,52,99	1.26	4 (7%)	58,64,111	1.27	7 (12%)
27	PCF	N	606	-	38,38,49	1.11	2 (5%)	44,46,57	1.06	3 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	PEF	E	302	-	42,42,46	1.01	2 (4%)	45,47,51	1.12	3 (6%)
27	PCF	C	606	-	49,49,49	0.97	2 (4%)	55,57,57	1.02	4 (7%)
33	CUA	b	301	12	0,1,1	-	-	-	-	-
29	FES	P	301	5	0,4,4	-	-	-	-	-
24	PEF	A	501	-	30,30,46	1.18	2 (6%)	33,35,51	1.14	3 (9%)
24	PEF	H	602	-	31,31,46	1.16	2 (6%)	34,36,51	1.25	4 (11%)
27	PCF	T	101	-	49,49,49	0.97	2 (4%)	55,57,57	1.03	3 (5%)
24	PEF	J	101	-	28,28,46	1.22	2 (7%)	31,33,51	1.20	3 (9%)
24	PEF	P	302	-	41,41,46	1.01	2 (4%)	44,46,51	1.06	3 (6%)
25	HEM	C	601	3	50,50,50	1.61	10 (20%)	67,82,82	1.69	14 (20%)
26	CDL	L	501	-	57,57,99	1.21	4 (7%)	63,69,111	1.22	6 (9%)
24	PEF	b	303	-	32,32,46	1.13	2 (6%)	35,37,51	1.24	4 (11%)

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
24	PEF	C	605	-	-	13/46/46/50	-
27	PCF	e	202	-	-	8/39/39/53	-
24	PEF	L	502	-	-	14/39/39/50	-
28	HEC	O	401	4	-	3/14/54/54	-
24	PEF	c	302	-	-	11/44/44/50	-
29	FES	E	301	5	-	-	0/1/1/1
27	PCF	S	103	-	-	8/35/35/53	-
25	HEM	N	601	3	-	10/14/54/54	-
26	CDL	D	402	-	-	28/77/77/110	-
24	PEF	c	301	-	-	10/39/39/50	-
24	PEF	N	604	-	-	9/47/47/50	-
24	PEF	a	605	-	-	4/36/36/50	-
24	PEF	C	604	27	-	8/43/43/50	-
31	HEA	a	603	11	-	6/36/76/76	-
24	PEF	U	101	-	-	12/50/50/50	-
27	PCF	I	101	24	-	6/42/42/53	-
26	CDL	C	603	-	-	22/64/64/110	-
28	HEC	D	401	4	-	0/14/54/54	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
31	HEA	a	602	11	-	14/36/76/76	-
24	PEF	e	201	-	-	13/45/45/50	-
25	HEM	C	602	3	-	6/14/54/54	-
24	PEF	b	302	-	-	19/43/43/50	-
24	PEF	S	102	-	-	8/39/39/50	-
26	CDL	N	603	26	-	10/76/76/110	-
26	CDL	O	402	26	-	17/81/81/110	-
26	CDL	H	601	-	-	18/63/63/110	-
24	PEF	N	605	-	-	10/42/42/50	-
25	HEM	N	602	3	-	6/14/54/54	-
26	CDL	S	101	-	-	20/63/63/110	-
27	PCF	N	606	-	-	11/42/42/53	-
24	PEF	E	302	-	-	13/46/46/50	-
27	PCF	C	606	-	-	16/53/53/53	-
29	FES	P	301	5	-	-	0/1/1/1
24	PEF	A	501	-	-	7/34/34/50	-
24	PEF	H	602	-	-	4/35/35/50	-
27	PCF	T	101	-	-	7/53/53/53	-
24	PEF	J	101	-	-	14/32/32/50	-
24	PEF	P	302	-	-	13/45/45/50	-
25	HEM	C	601	3	-	10/14/54/54	-
26	CDL	L	501	-	-	17/68/68/110	-
24	PEF	b	303	-	-	14/36/36/50	-

The worst 5 of 217 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	a	602	HEA	FE-NB	5.53	2.11	1.94
31	a	603	HEA	FE-NB	5.48	2.11	1.94
31	a	603	HEA	FE-ND	5.41	2.11	1.94
31	a	602	HEA	C3B-C2B	5.35	1.46	1.34
28	O	401	HEC	CHC-C4B	5.34	1.48	1.38

The worst 5 of 280 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	a	603	HEA	C3D-C4D-ND	6.67	116.80	110.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	a	603	HEA	C2D-C1D-ND	6.56	117.38	109.84
31	a	602	HEA	C2B-C1B-NB	6.22	117.09	109.90
31	a	603	HEA	C3B-C4B-NB	6.15	116.91	109.84
31	a	602	HEA	C3D-C4D-ND	6.09	116.24	110.35

There are no chirality outliers.

5 of 439 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A	501	PEF	C1-O3P-P-O1P
24	A	501	PEF	C1-O3P-P-O2P
24	A	501	PEF	C1-O3P-P-O4P
24	C	604	PEF	C4-O4P-P-O3P
24	C	605	PEF	C11-C10-O2-C2

There are no ring outliers.

32 monomers are involved in 59 short contacts:

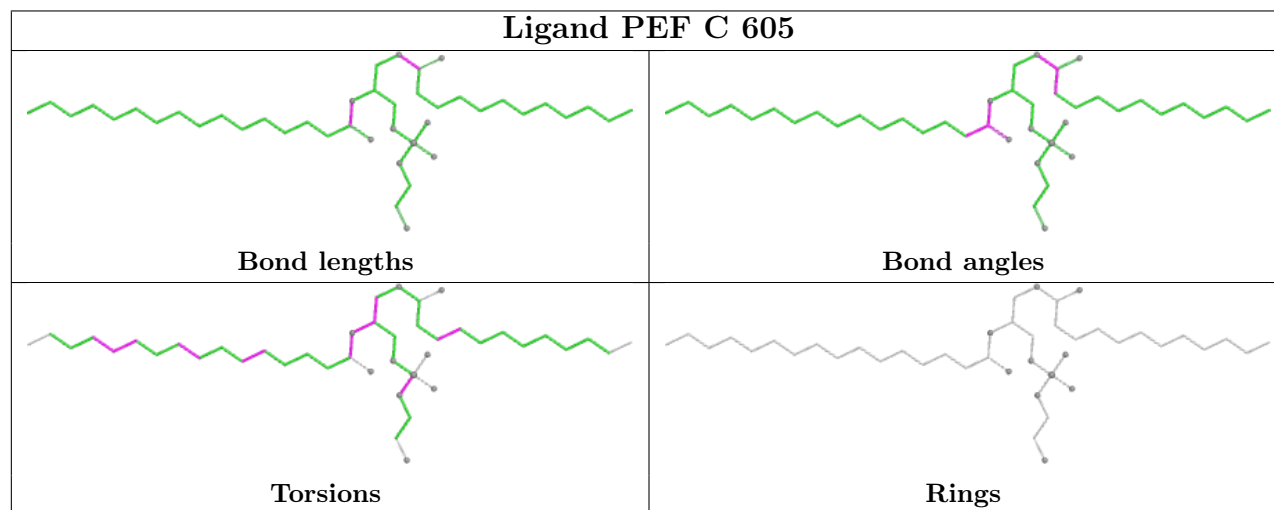
Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	C	605	PEF	1	0
27	e	202	PCF	3	0
24	L	502	PEF	1	0
28	O	401	HEC	3	0
24	c	302	PEF	1	0
25	N	601	HEM	3	0
26	D	402	CDL	1	0
24	c	301	PEF	1	0
24	N	604	PEF	2	0
24	a	605	PEF	1	0
24	C	604	PEF	2	0
31	a	603	HEA	8	0
28	D	401	HEC	1	0
31	a	602	HEA	1	0
24	e	201	PEF	1	0
25	C	602	HEM	1	0
24	b	302	PEF	1	0
24	S	102	PEF	1	0
26	N	603	CDL	4	0
26	O	402	CDL	2	0
26	H	601	CDL	3	0
24	N	605	PEF	1	0

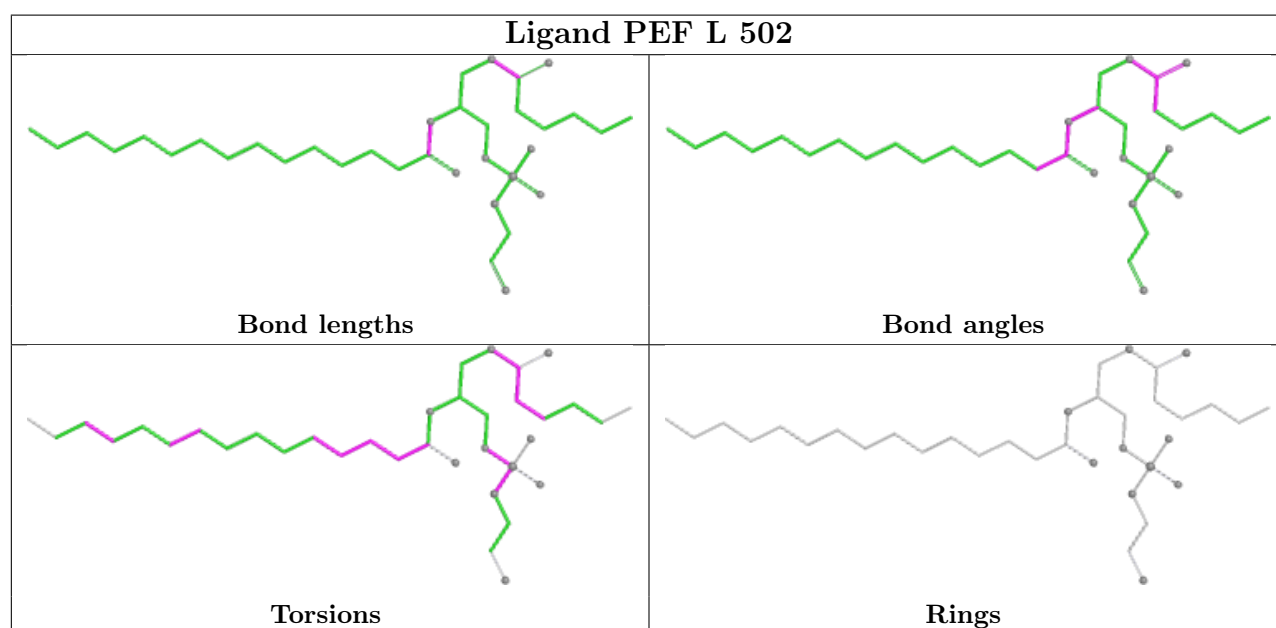
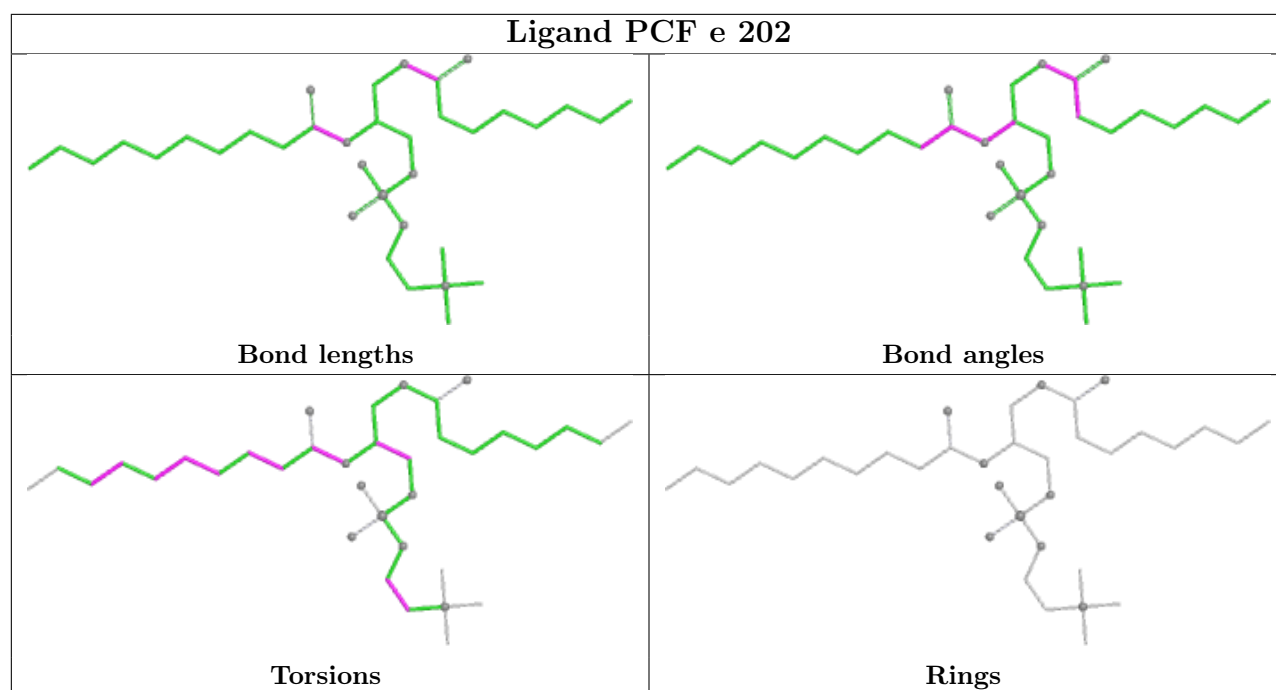
Continued on next page...

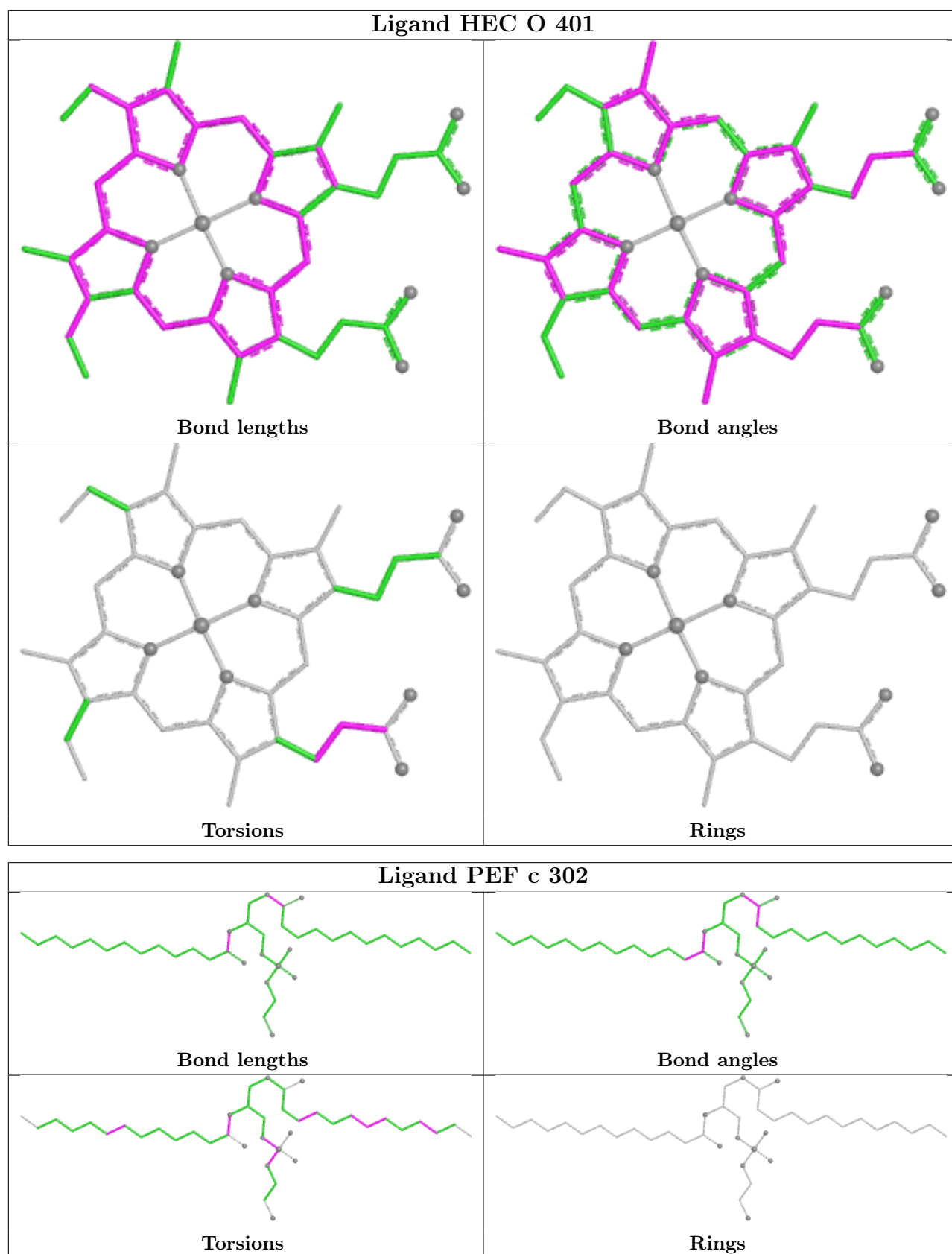
Continued from previous page...

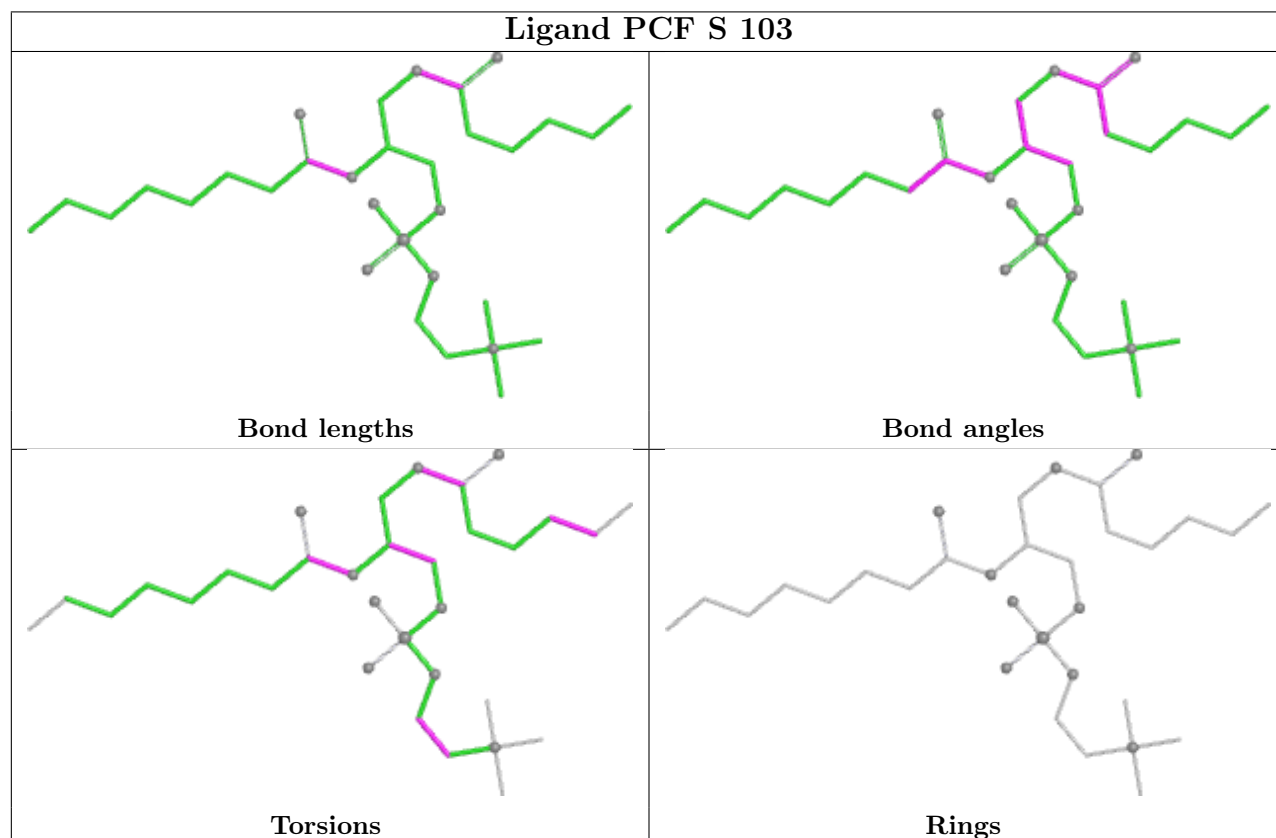
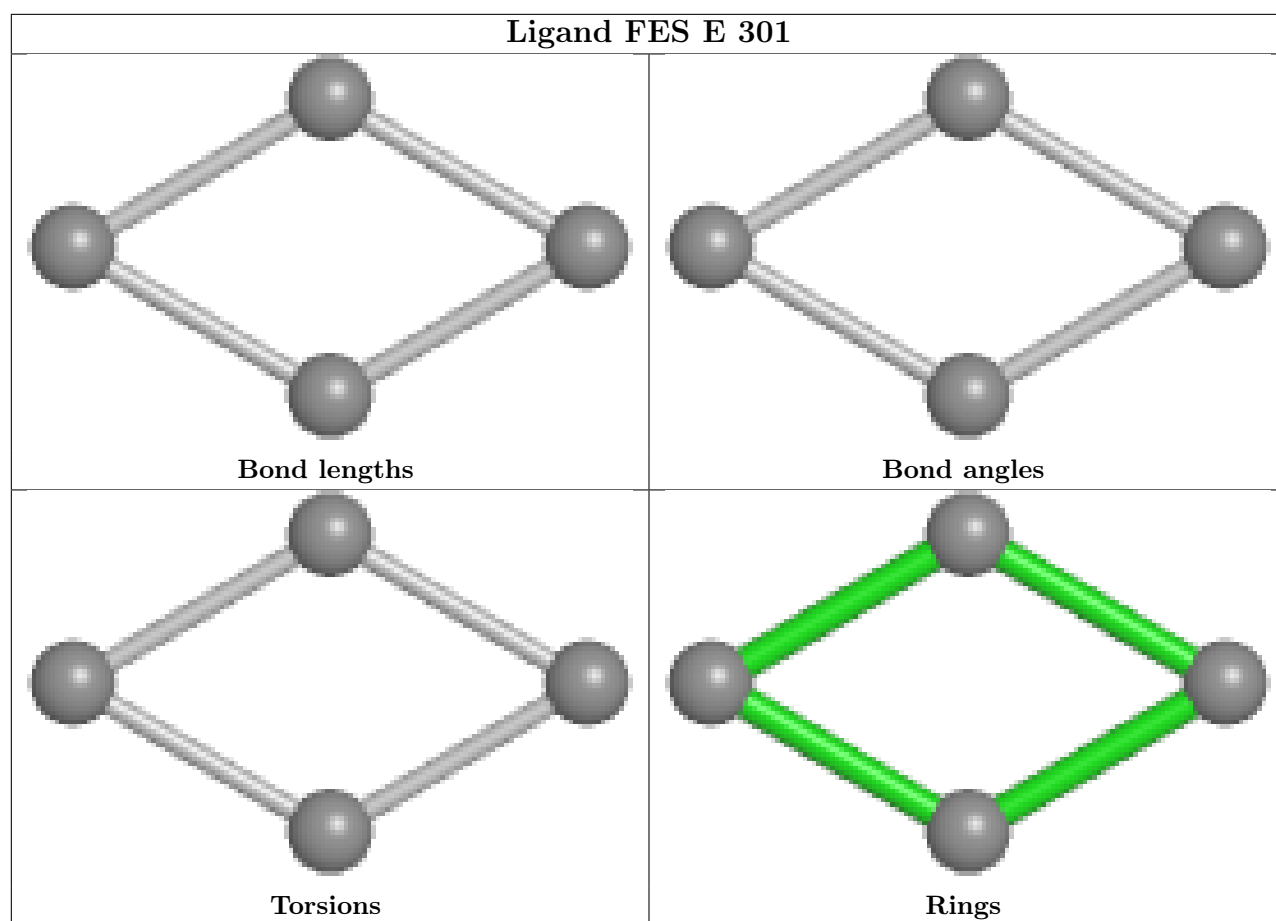
Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	N	602	HEM	2	0
26	S	101	CDL	2	0
27	N	606	PCF	3	0
24	E	302	PEF	2	0
29	P	301	FES	1	0
24	A	501	PEF	2	0
27	T	101	PCF	1	0
24	P	302	PEF	1	0
25	C	601	HEM	2	0
26	L	501	CDL	2	0

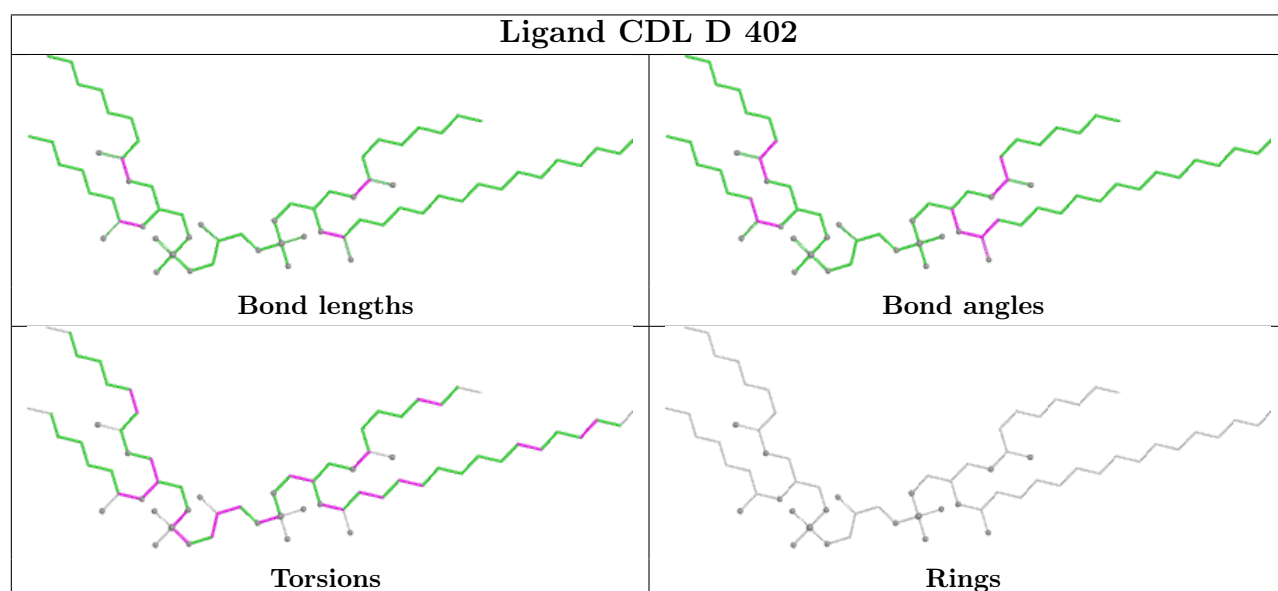
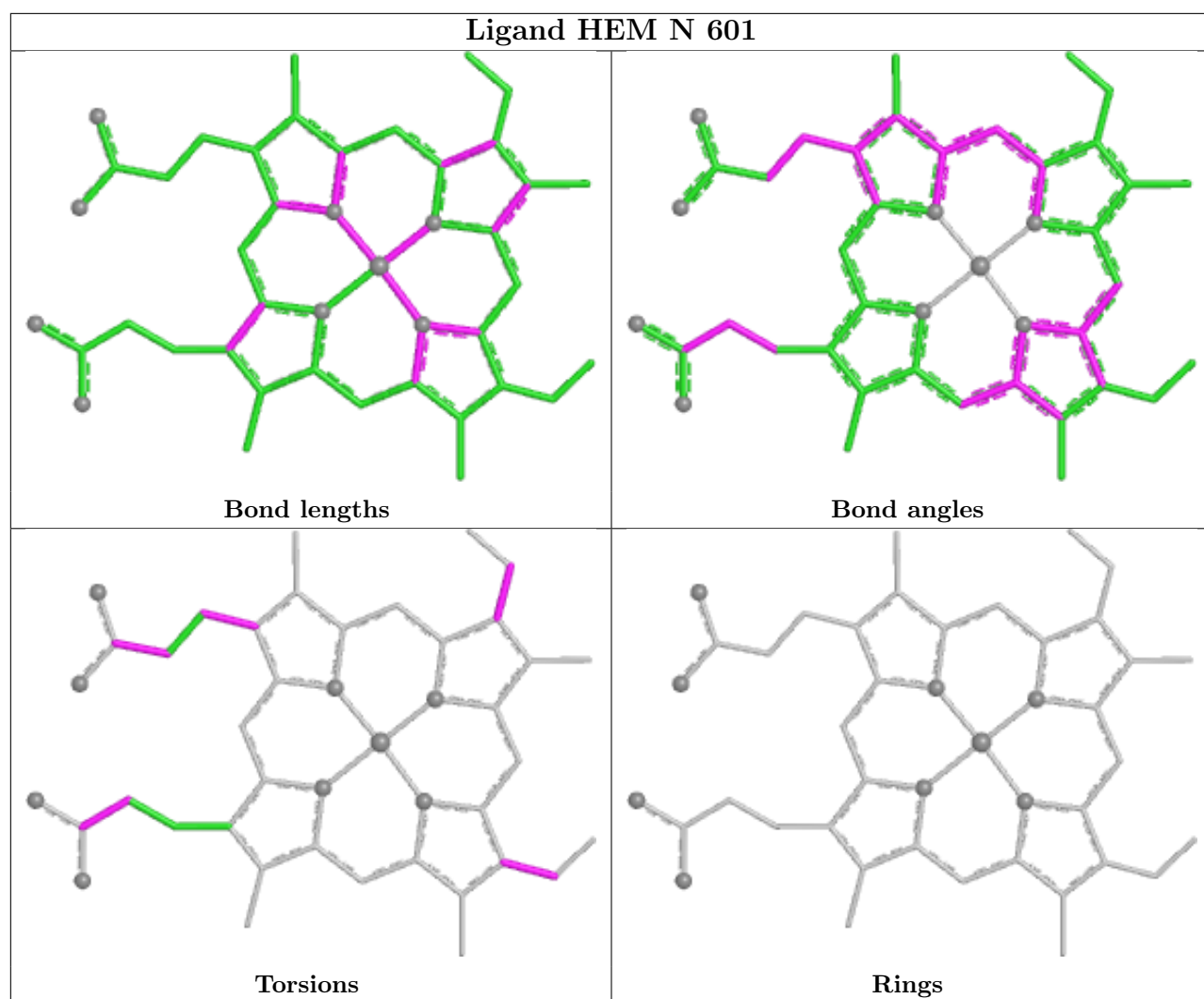
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

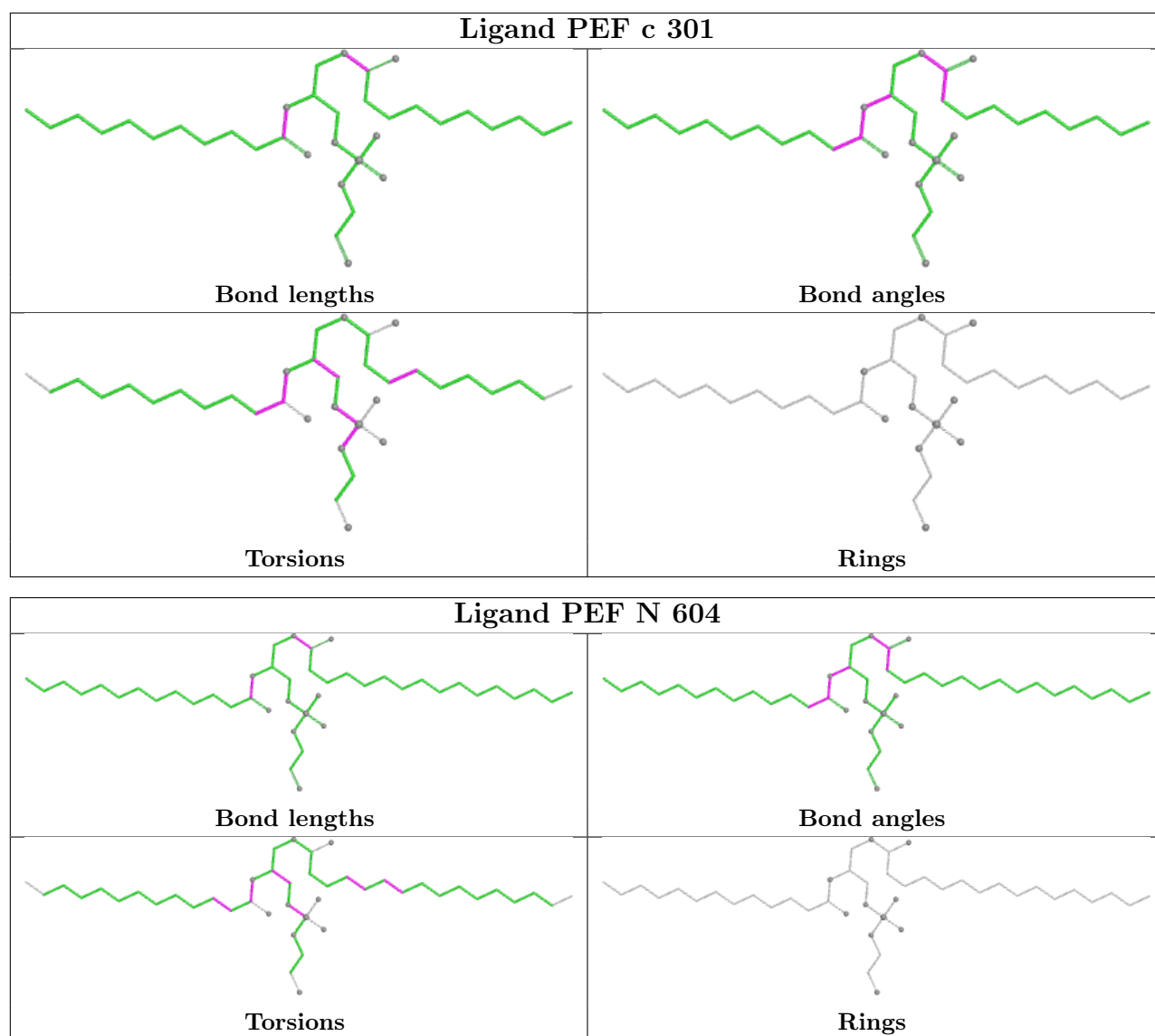


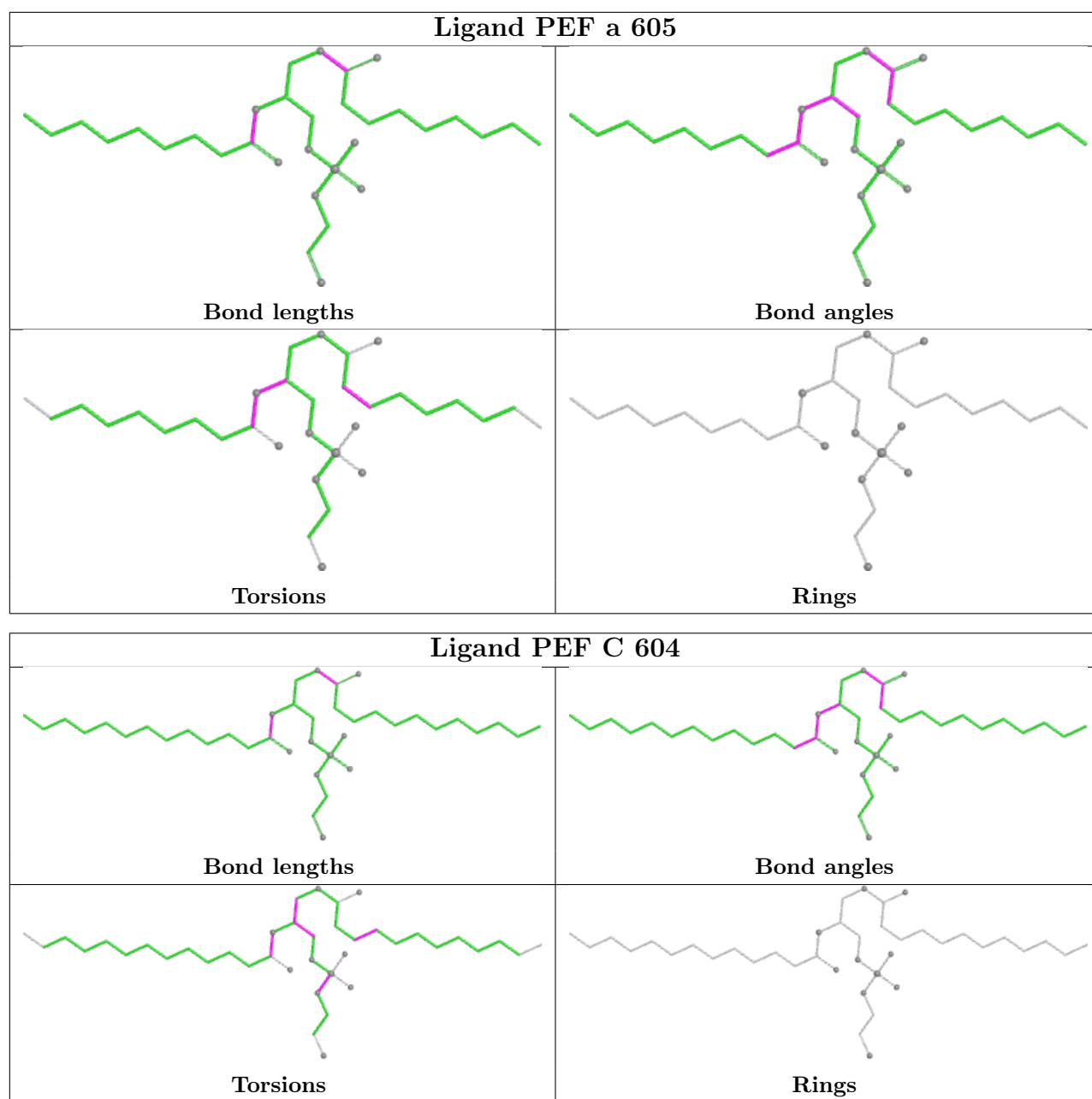


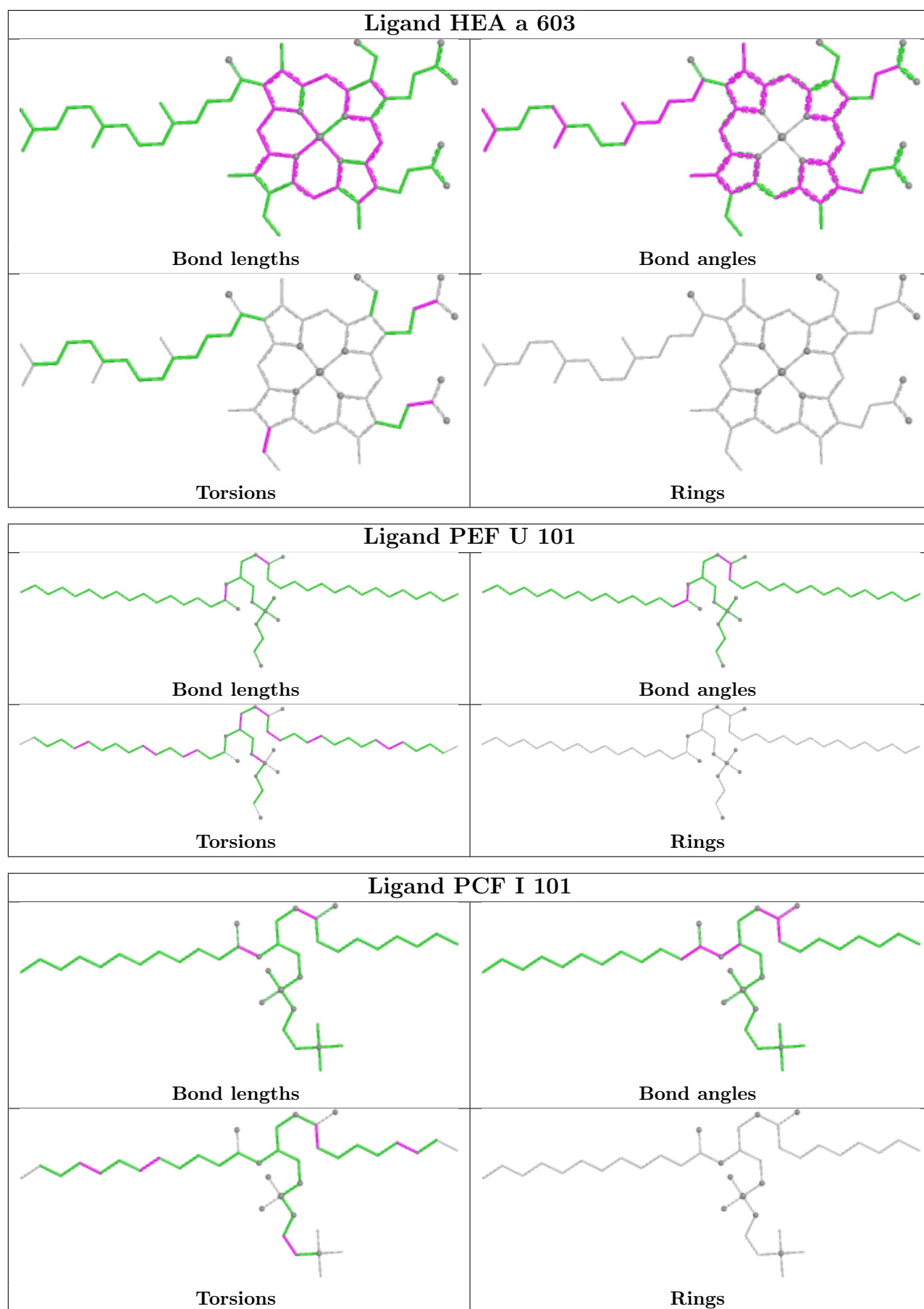


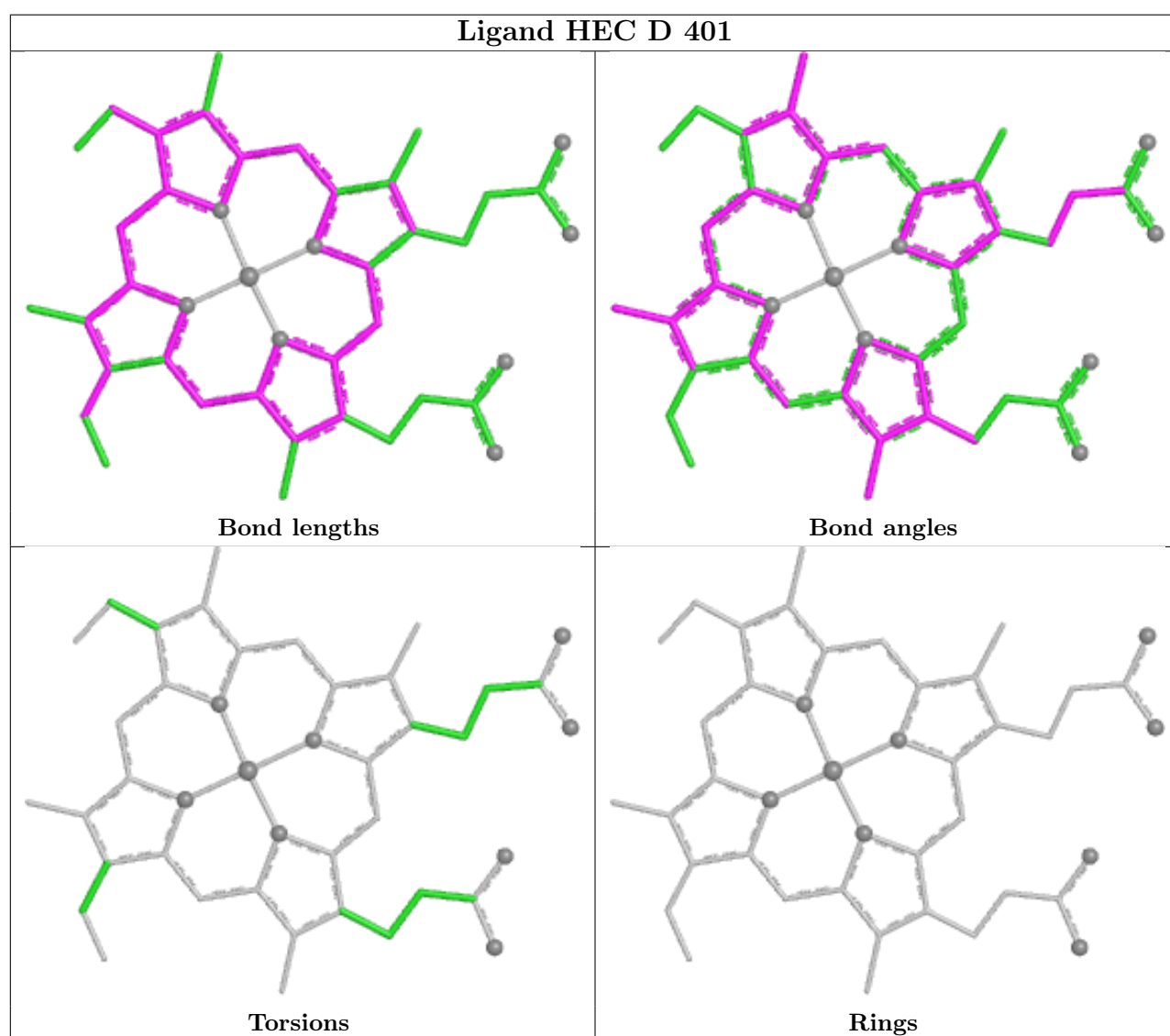
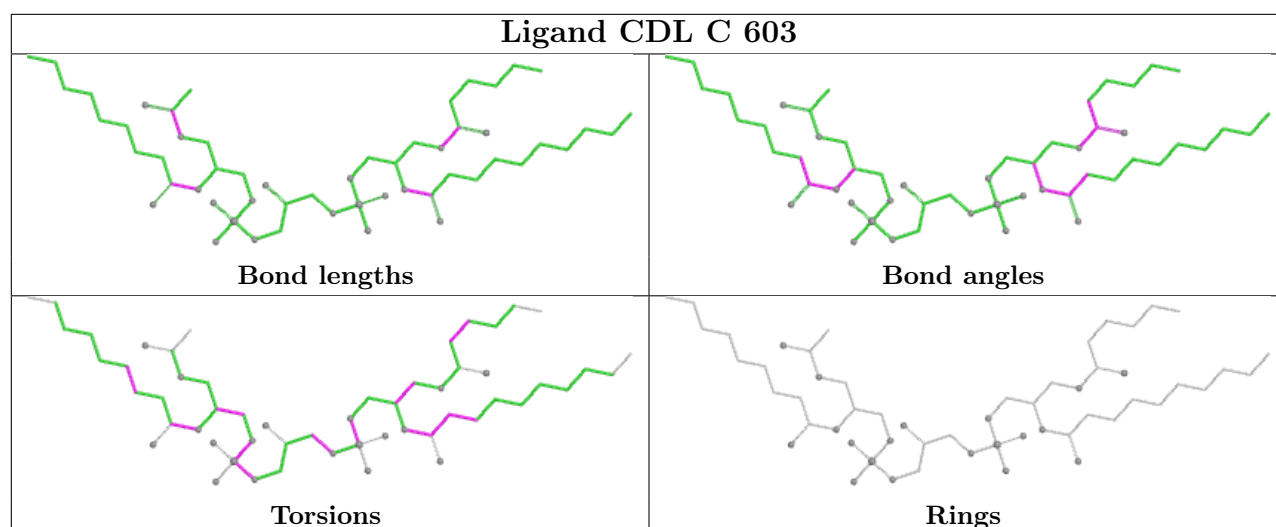


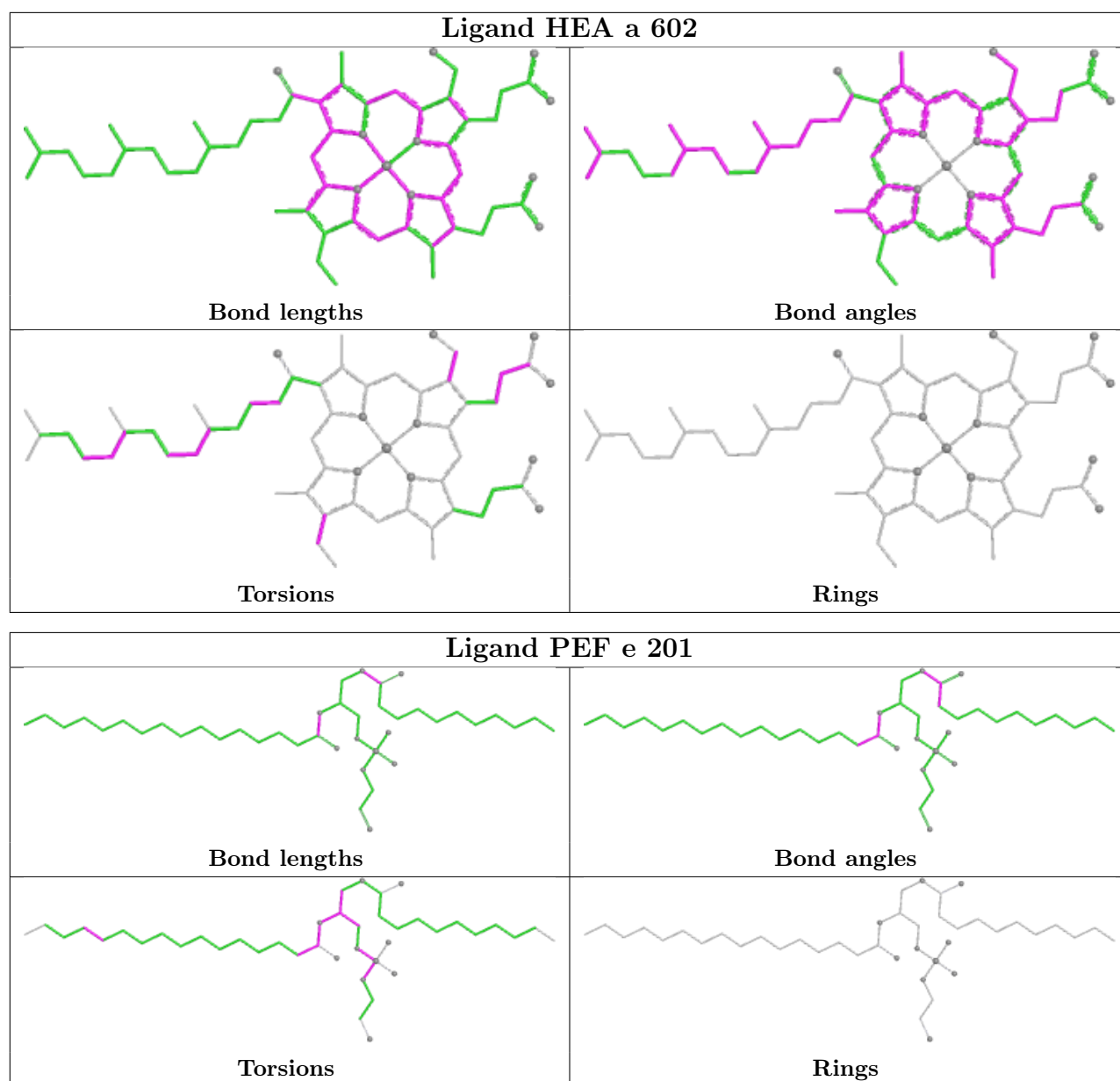


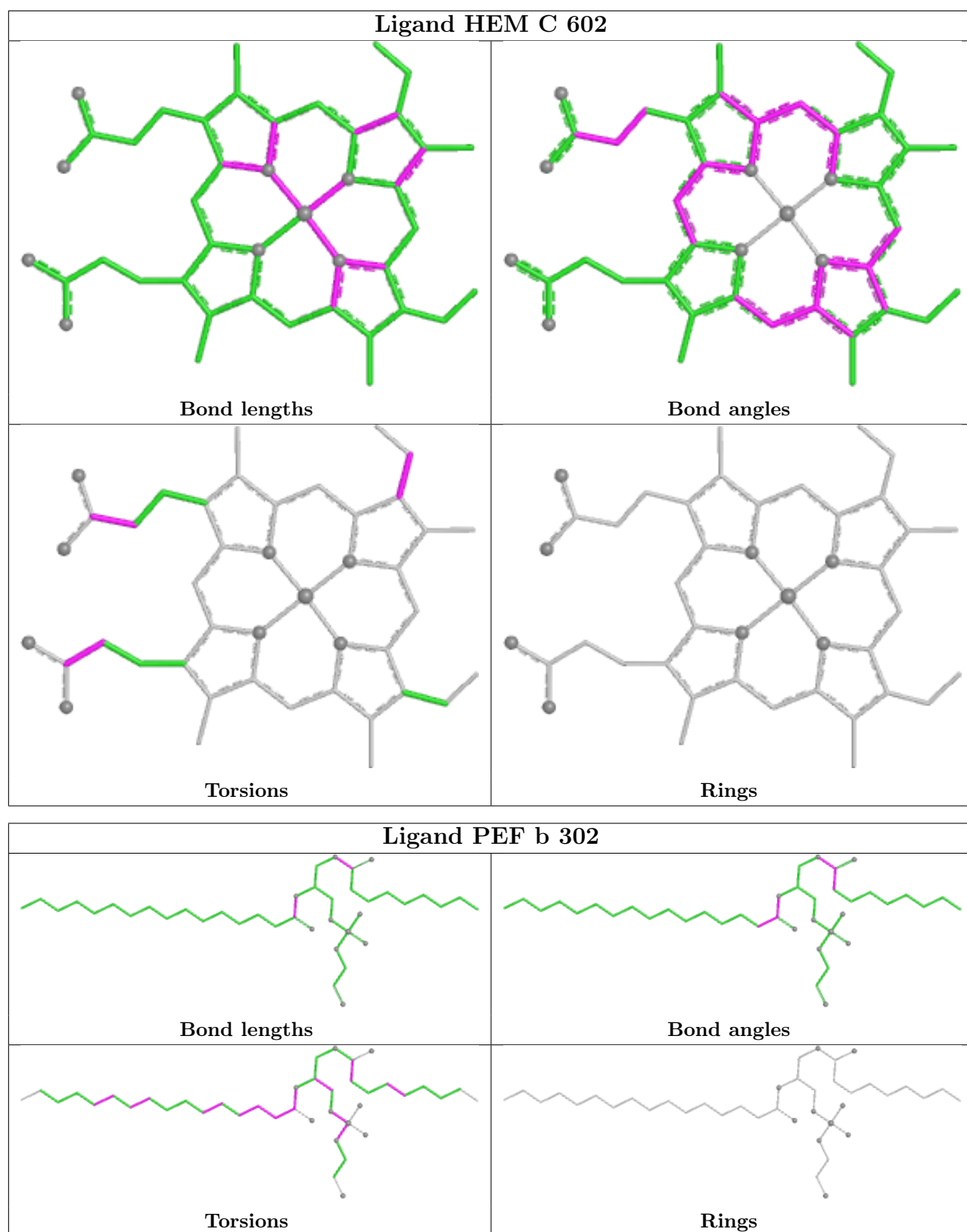


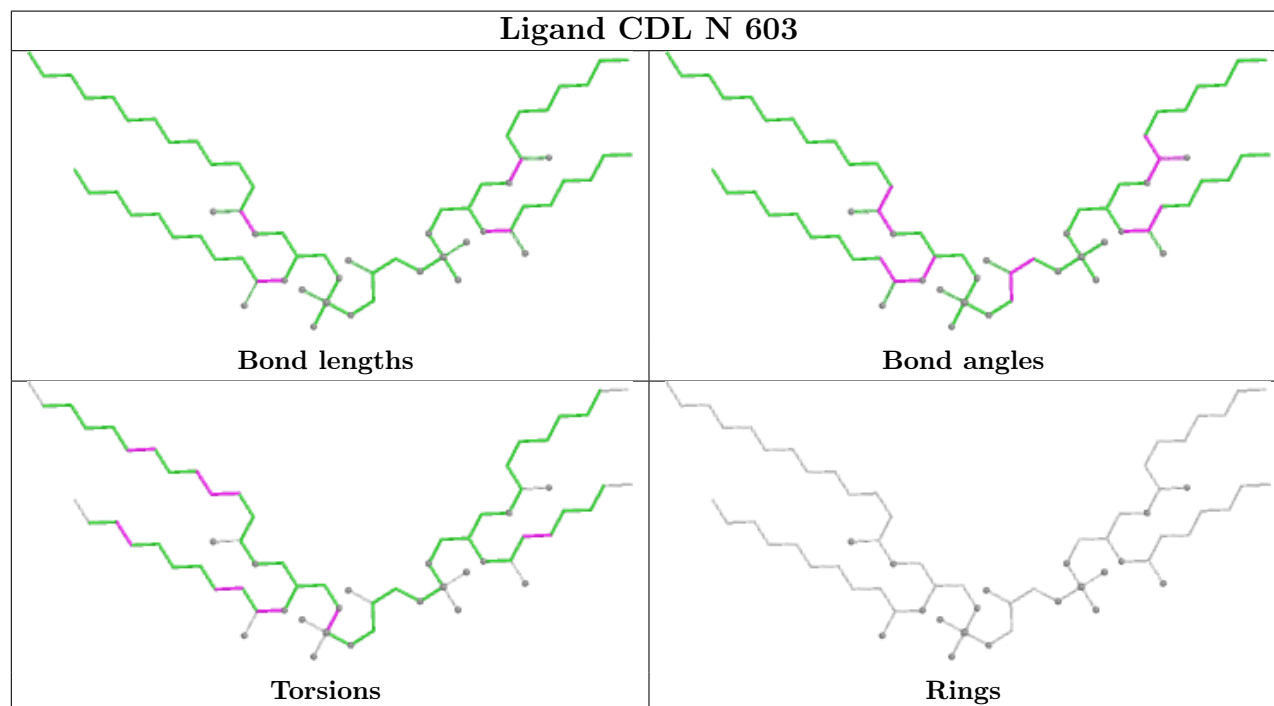
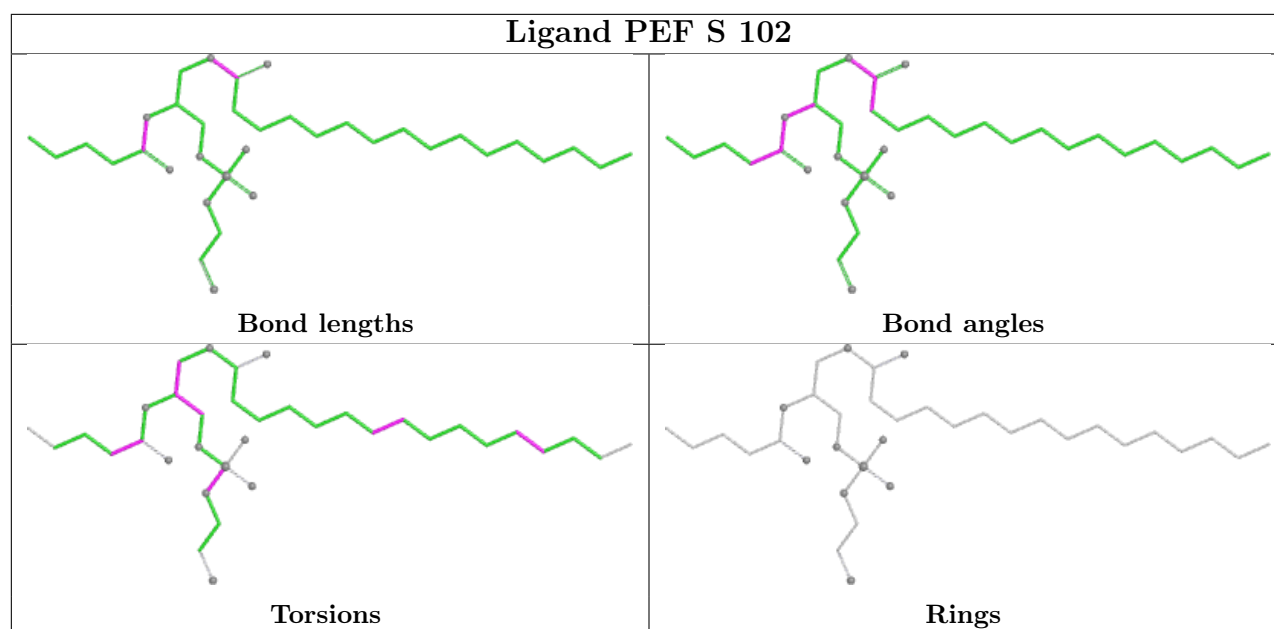


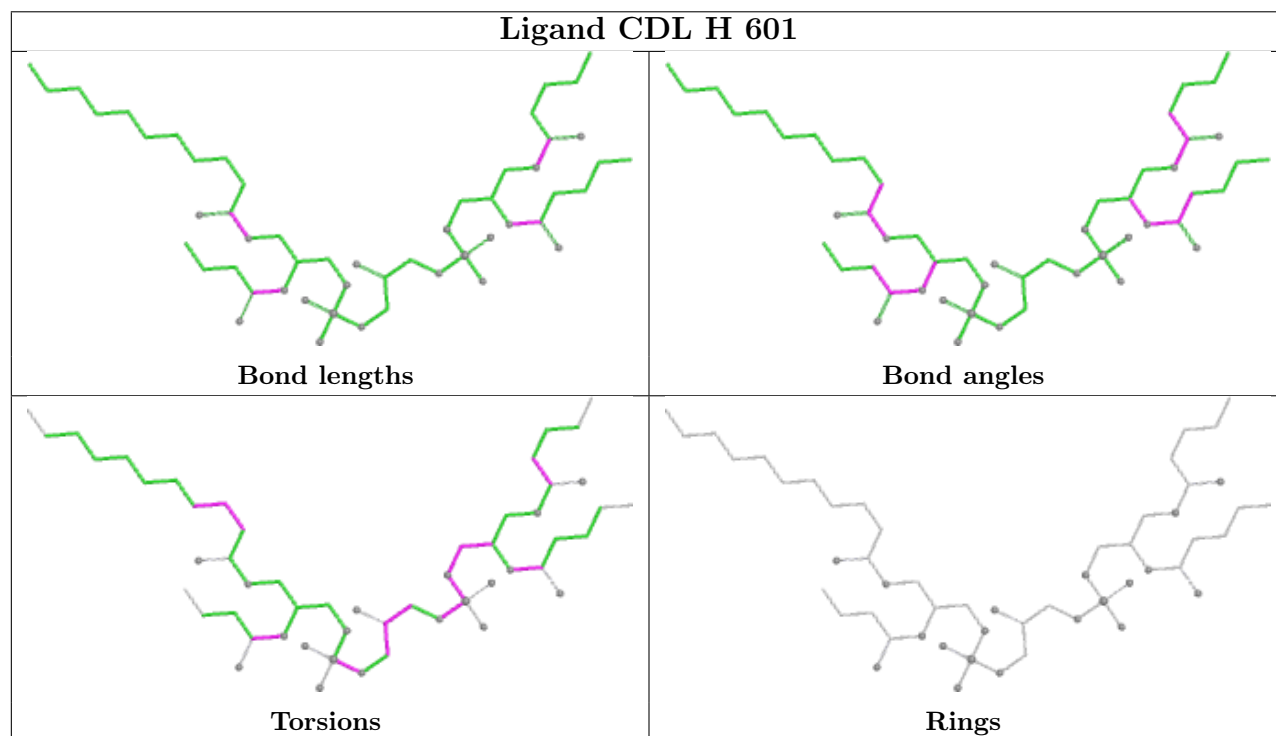
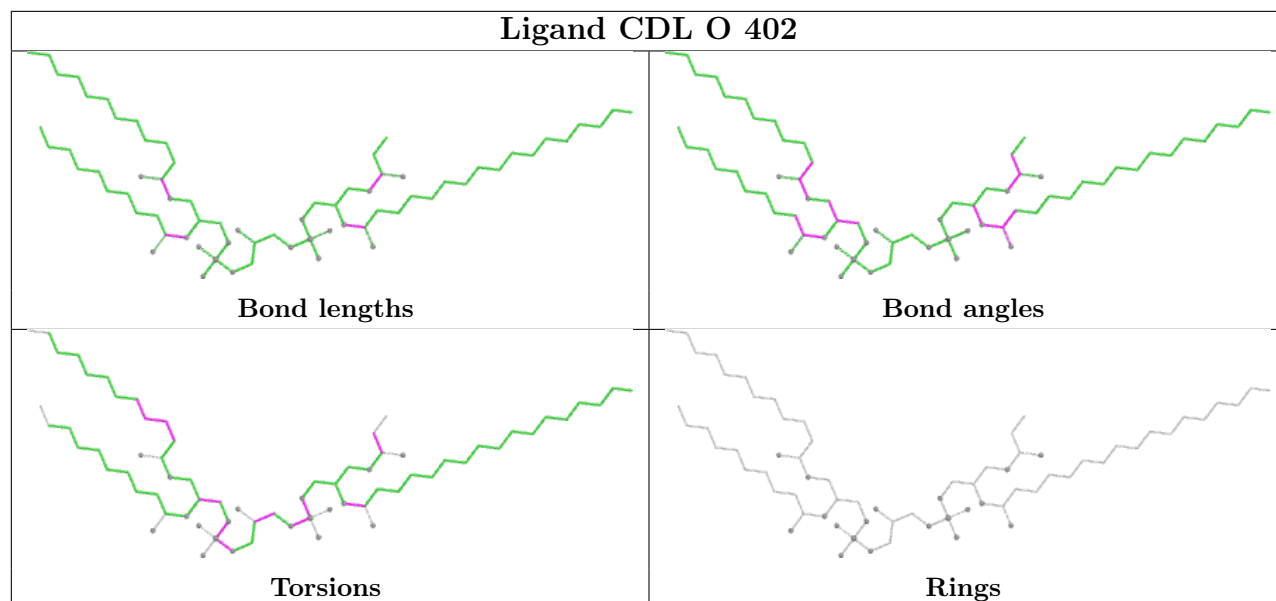


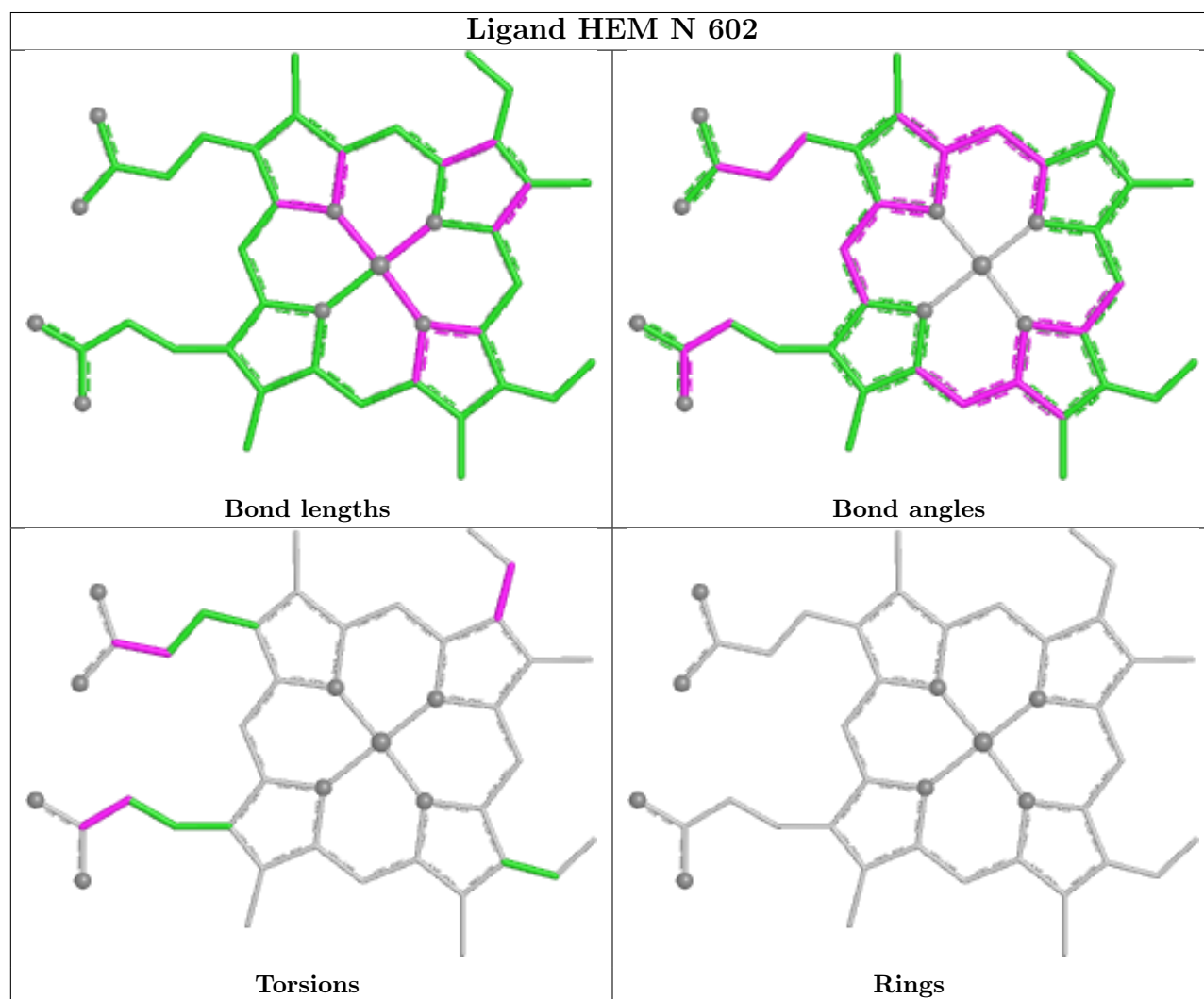
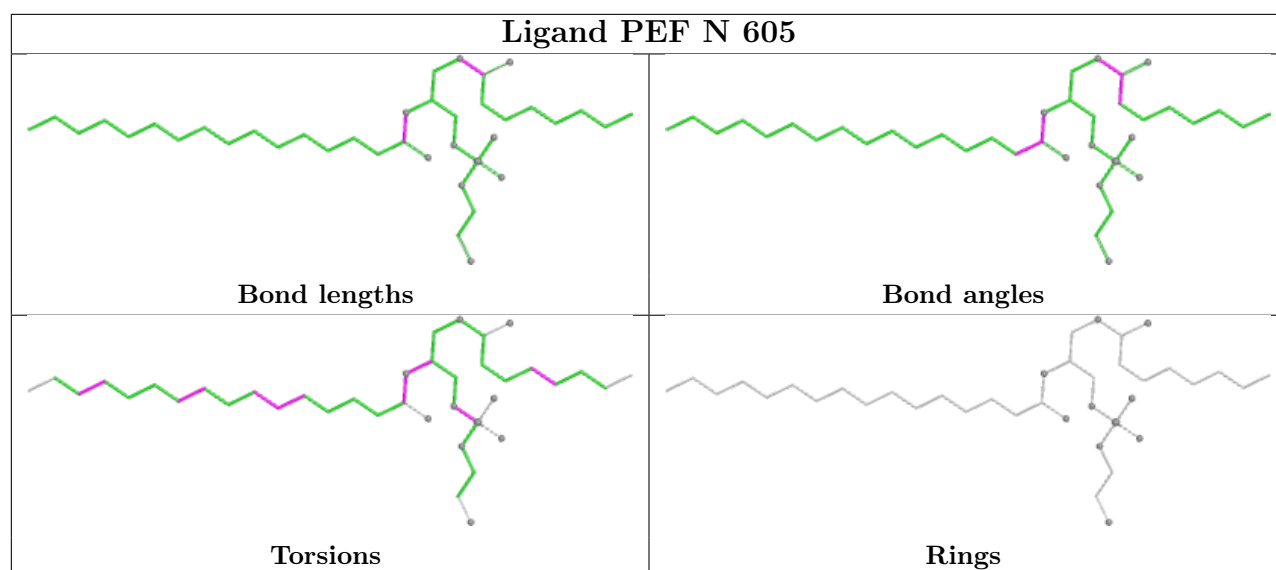


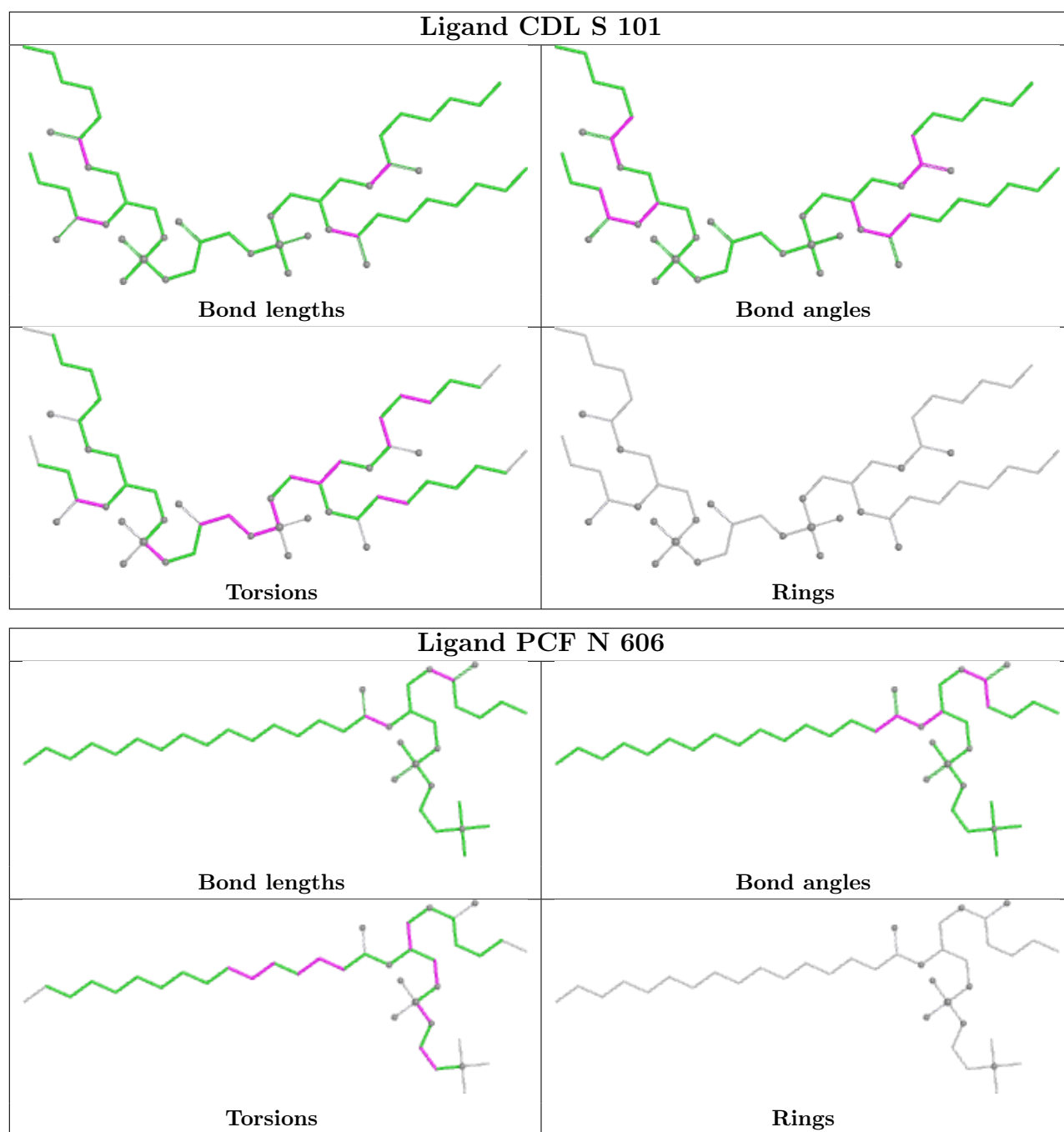


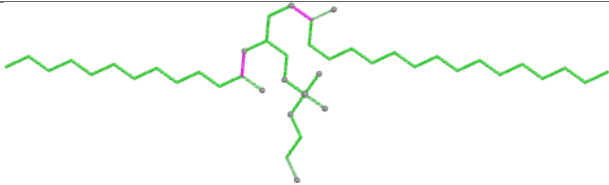
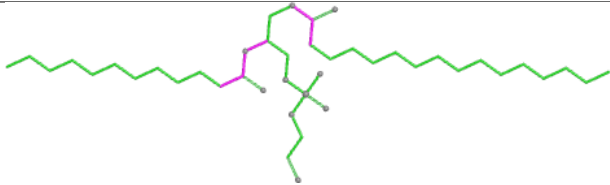
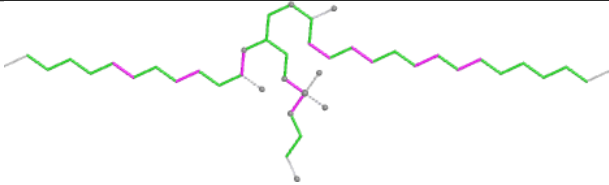
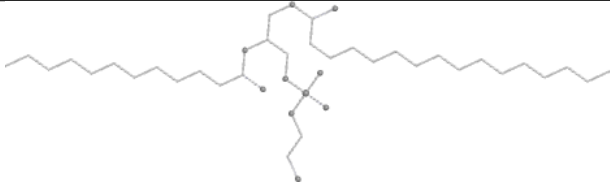


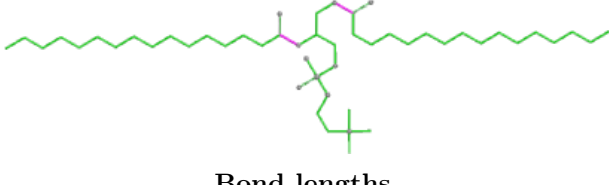
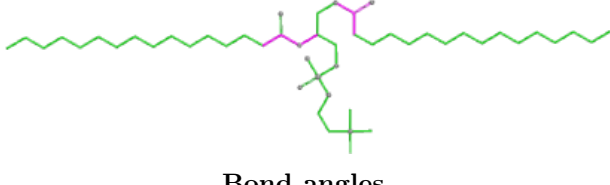
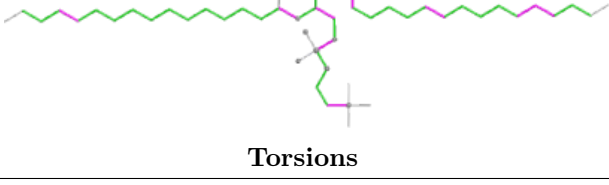
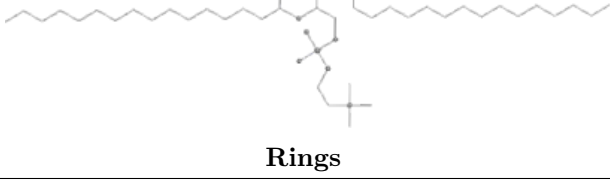




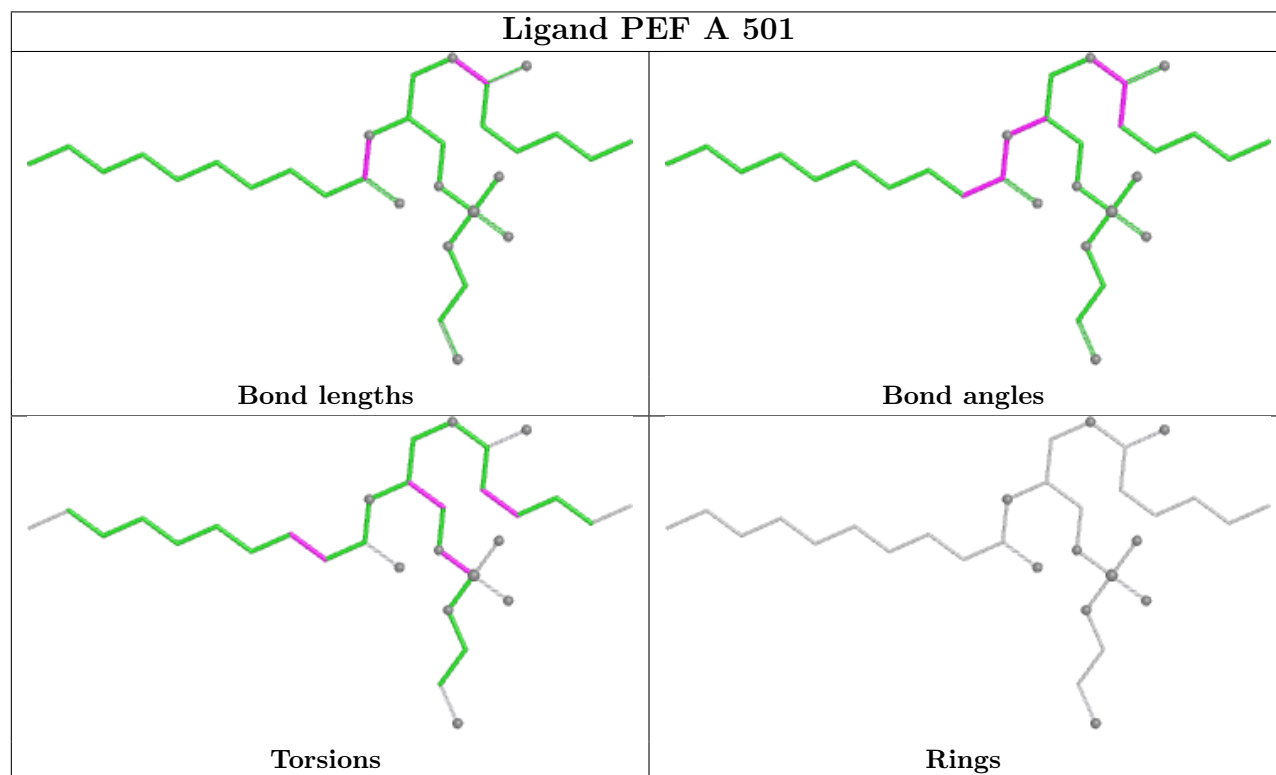
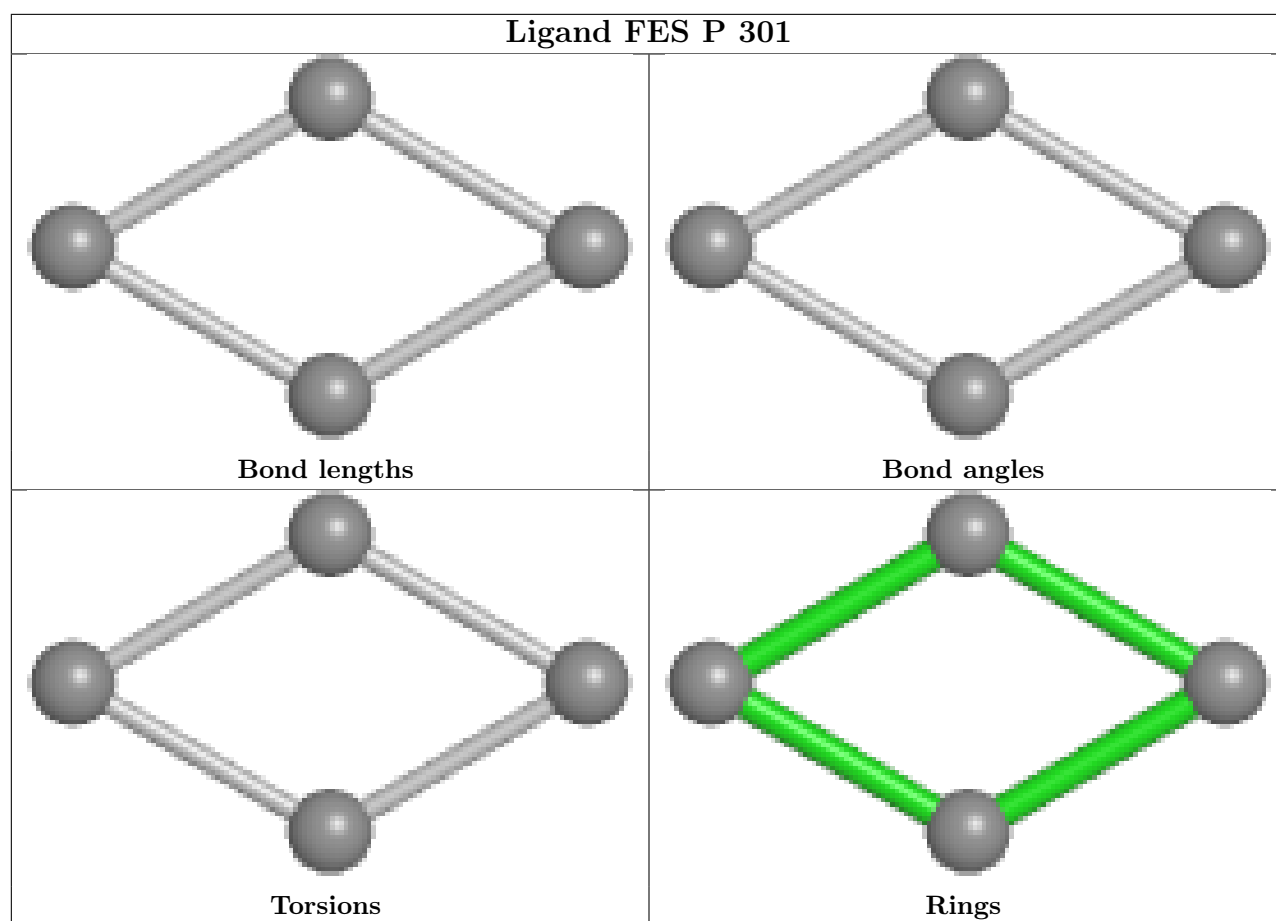


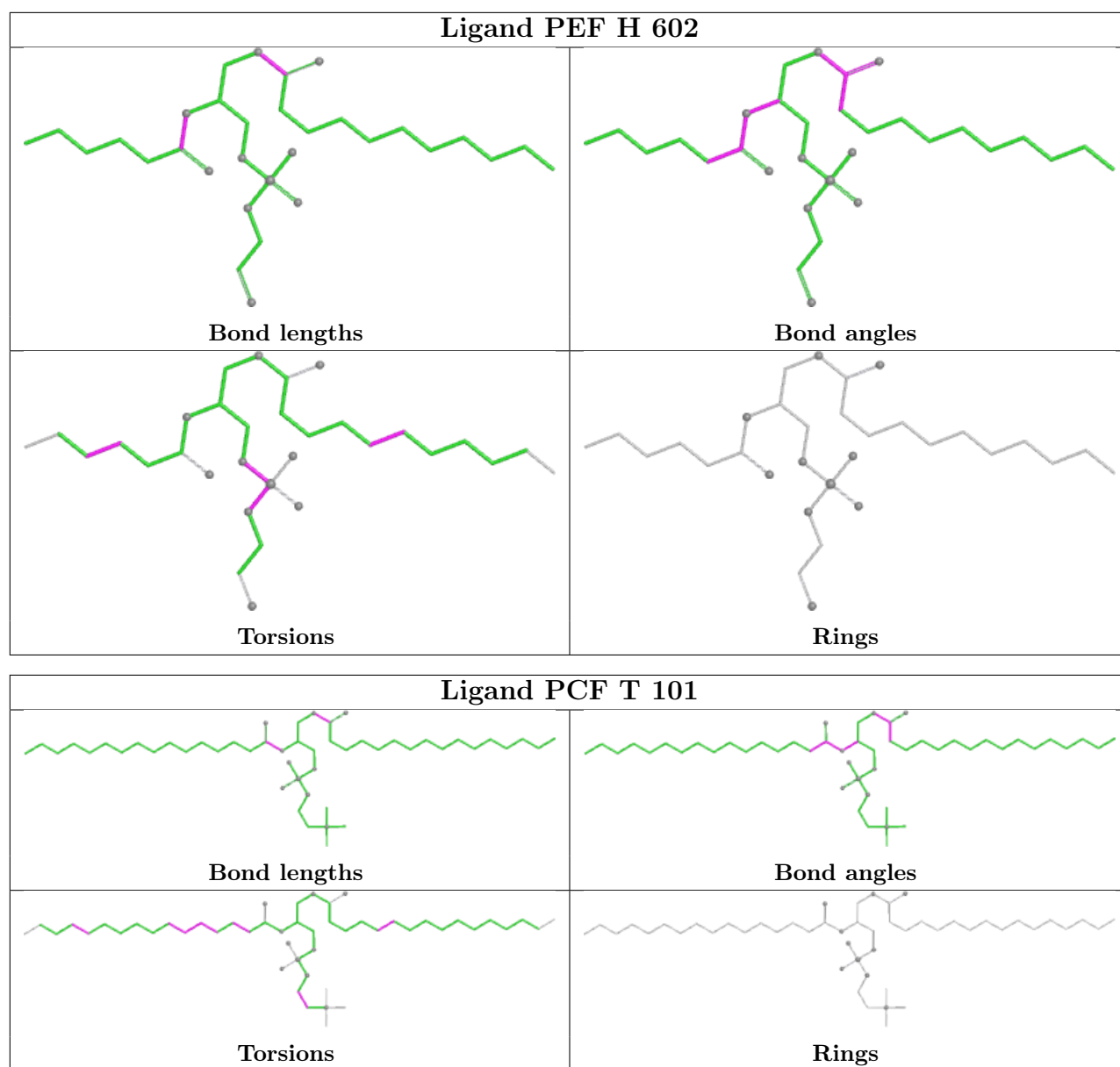


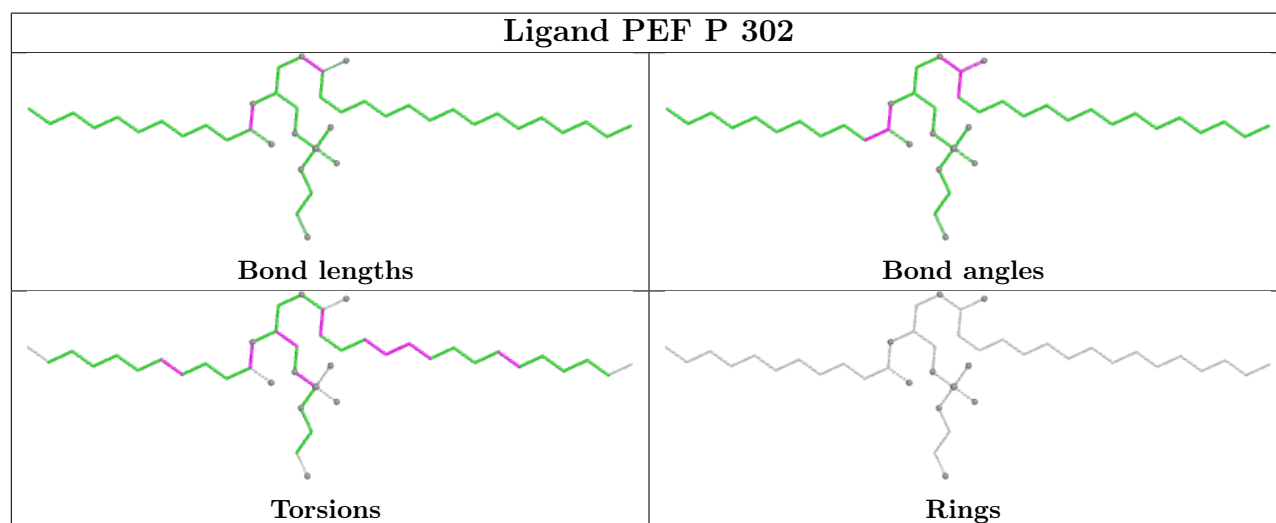
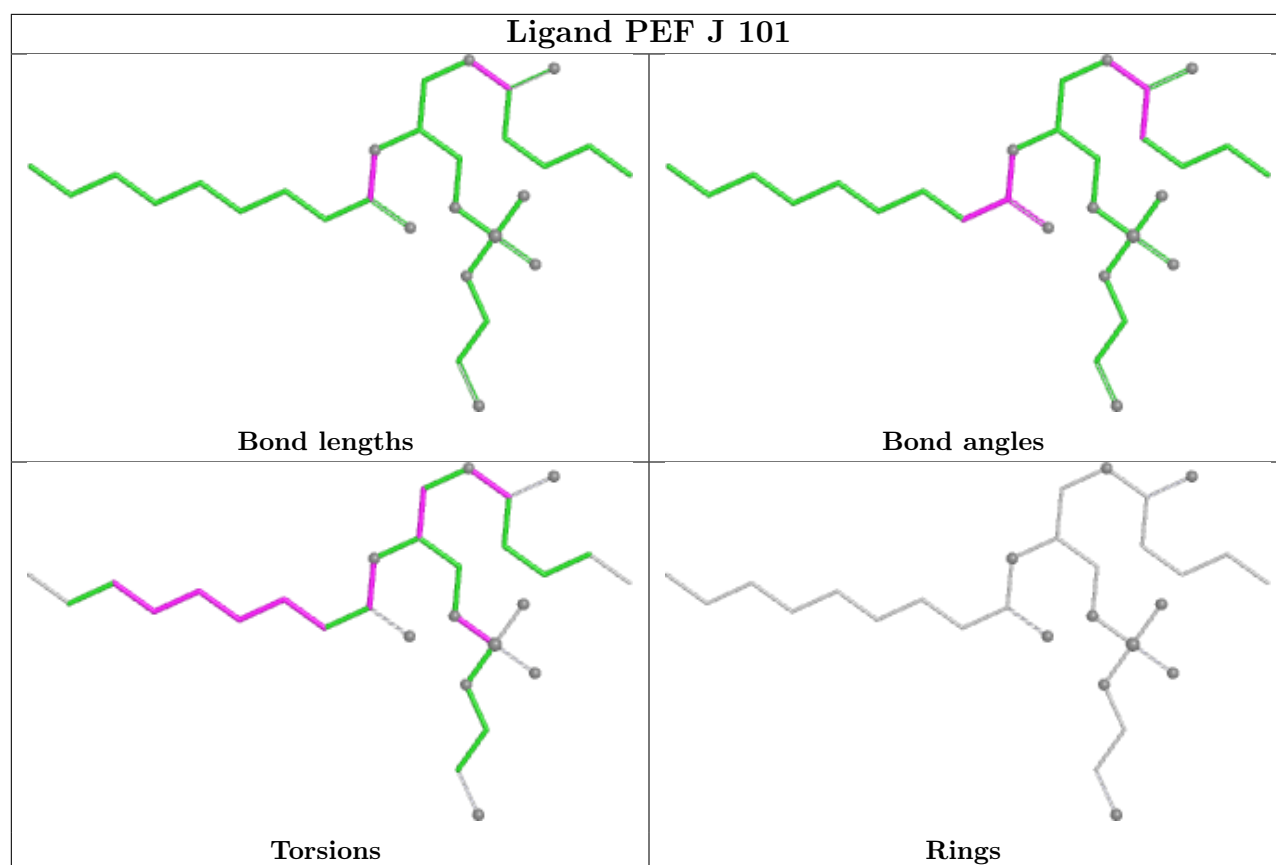
Ligand PEF E 302	
	
Bond lengths	Bond angles
	
Torsions	Rings

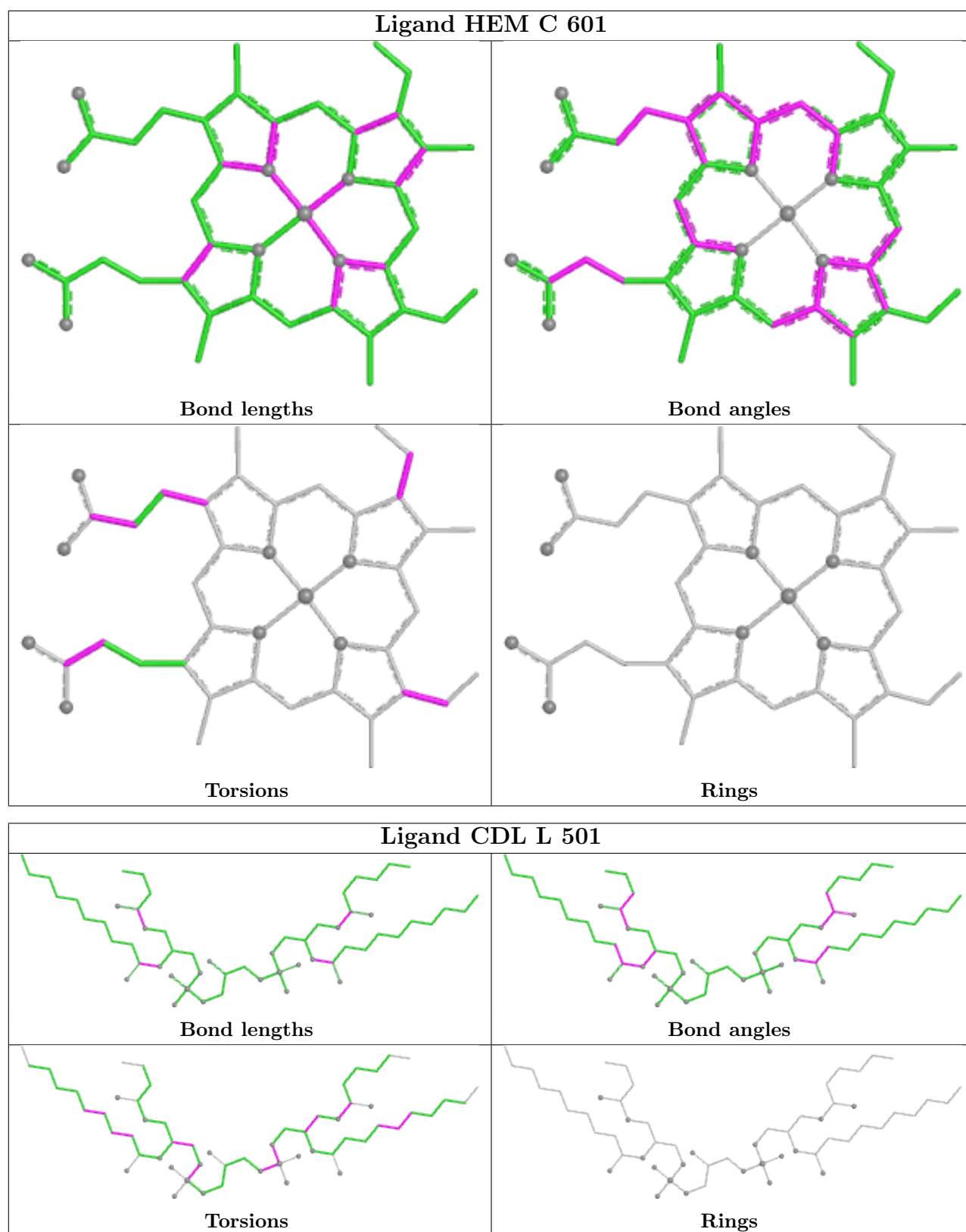
Ligand PCF C 606	
	
Bond lengths	Bond angles
	
Torsions	Rings

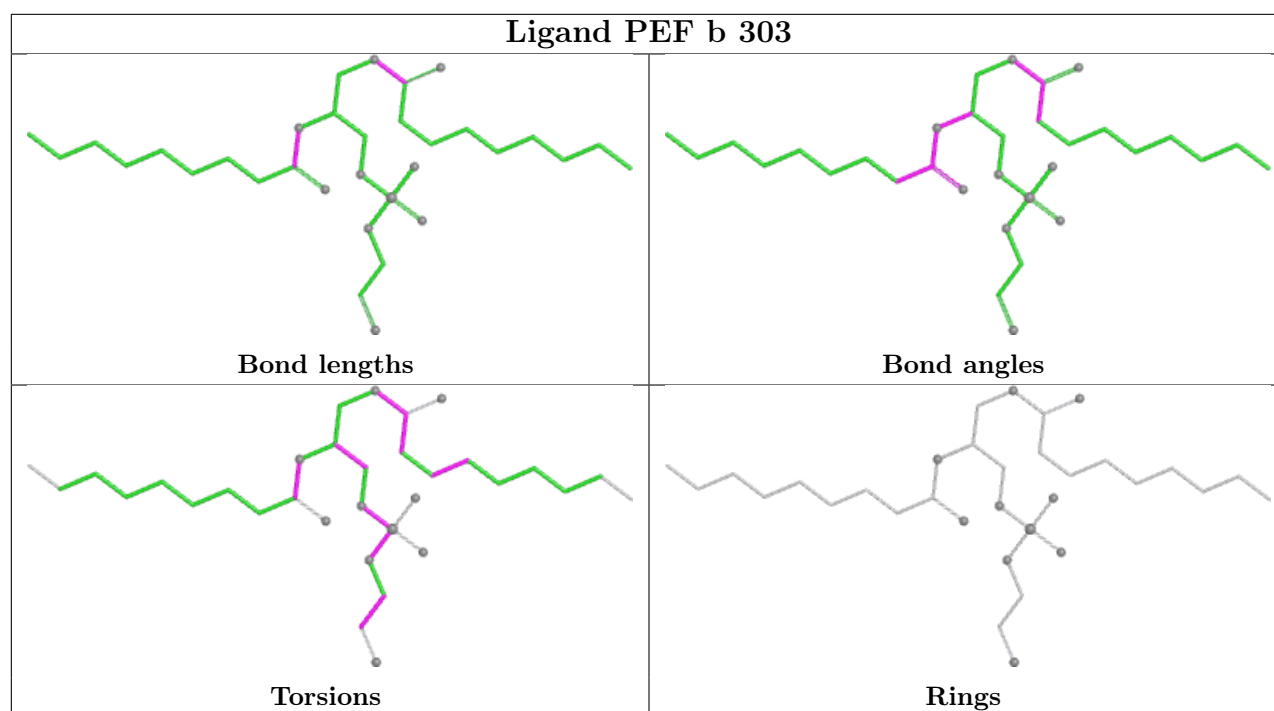
Ligand CUA b 301	
	
Bond lengths	Bond angles
	
Torsions	Rings











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.

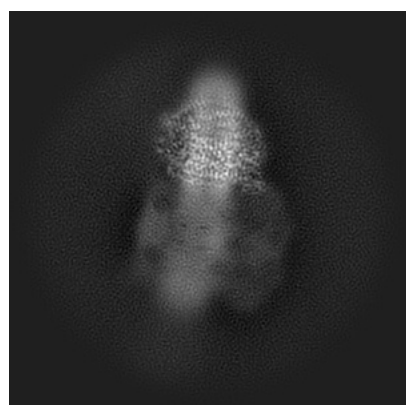
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10318. These allow visual inspection of the internal detail of the map and identification of artifacts.

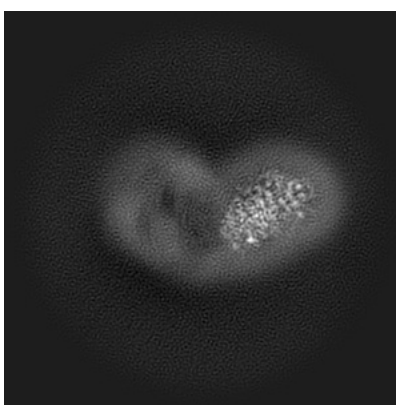
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

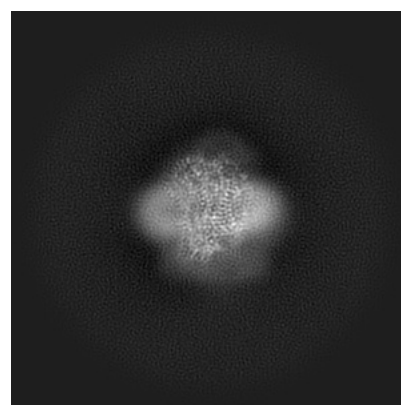
6.1.1 Primary map



X



Y

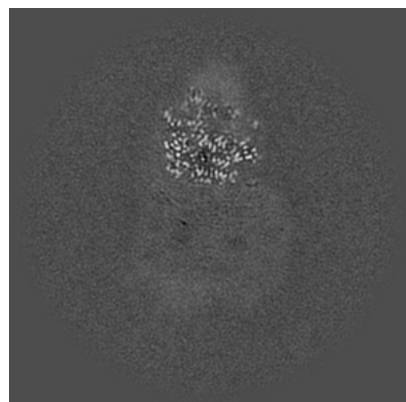


Z

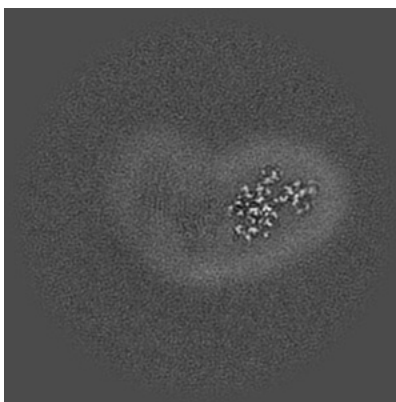
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

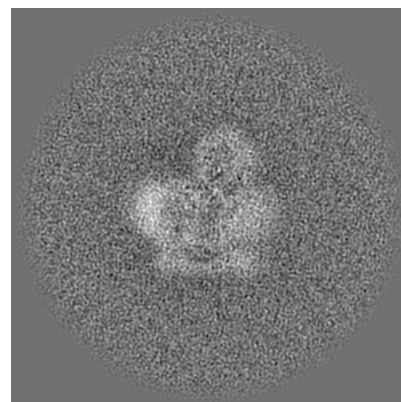
6.2.1 Primary map



X Index: 192



Y Index: 192

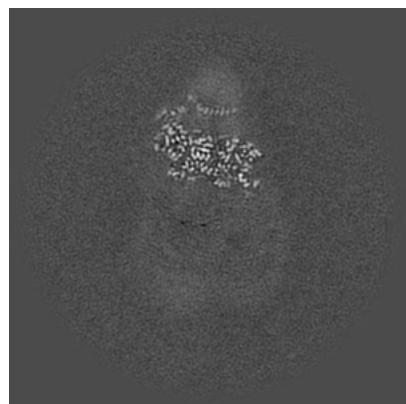


Z Index: 192

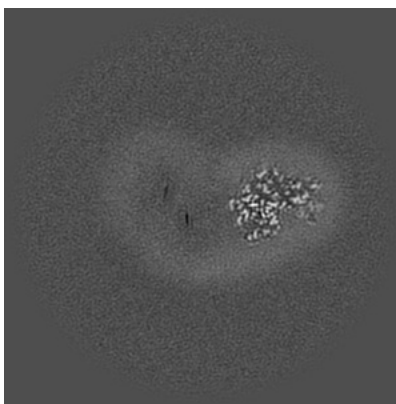
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

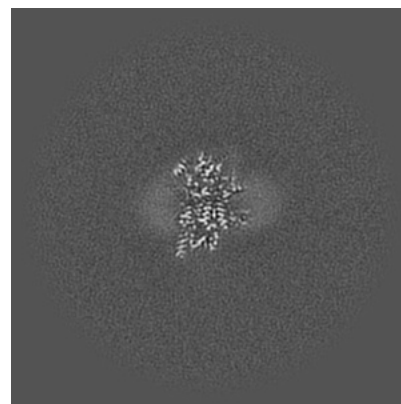
6.3.1 Primary map



X Index: 186



Y Index: 184

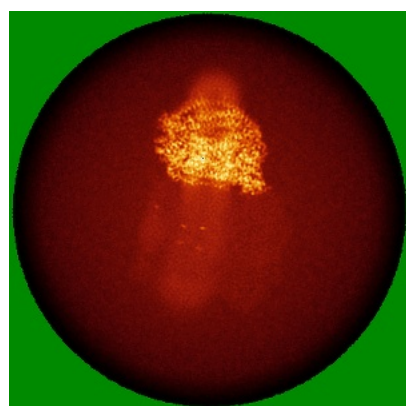


Z Index: 241

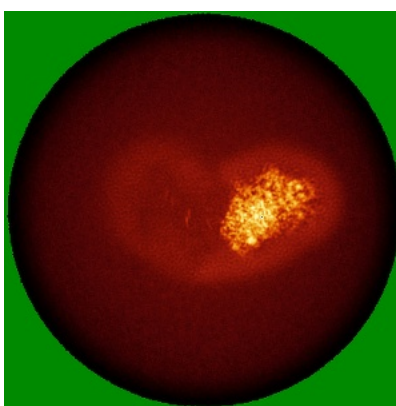
The images above show the largest variance slices of the map in three orthogonal directions.

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

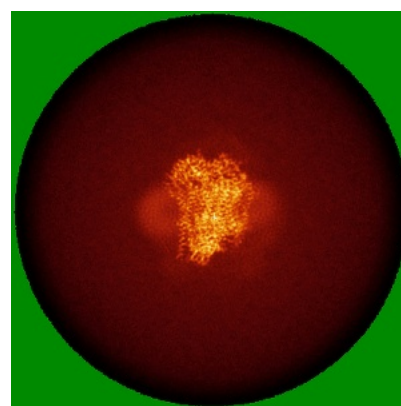
6.4.1 Primary map



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

This section was not generated.

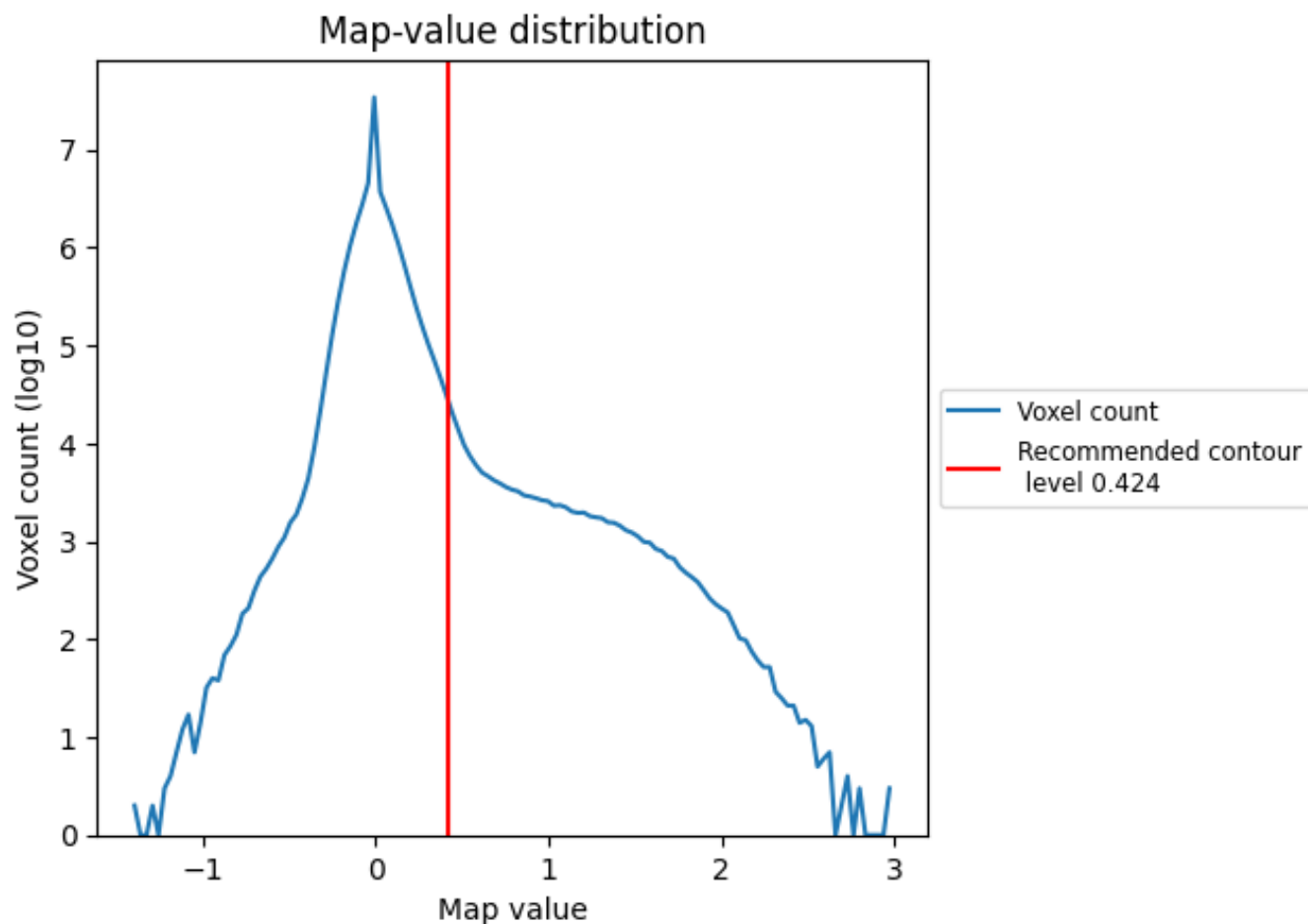
6.6 Mask visualisation

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

7 Map analysis [i](#)

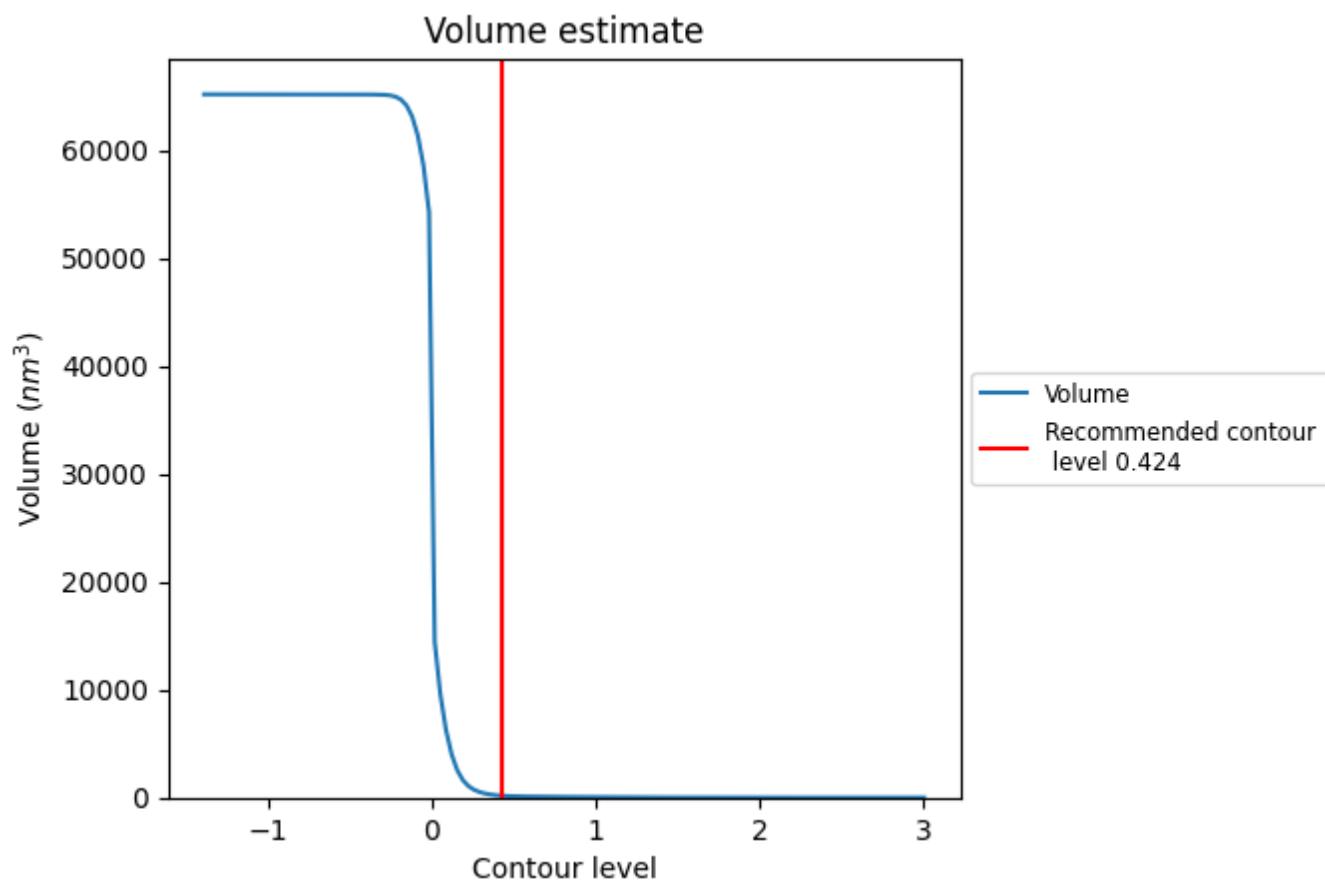
This section contains the results of statistical analysis of the map.

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.

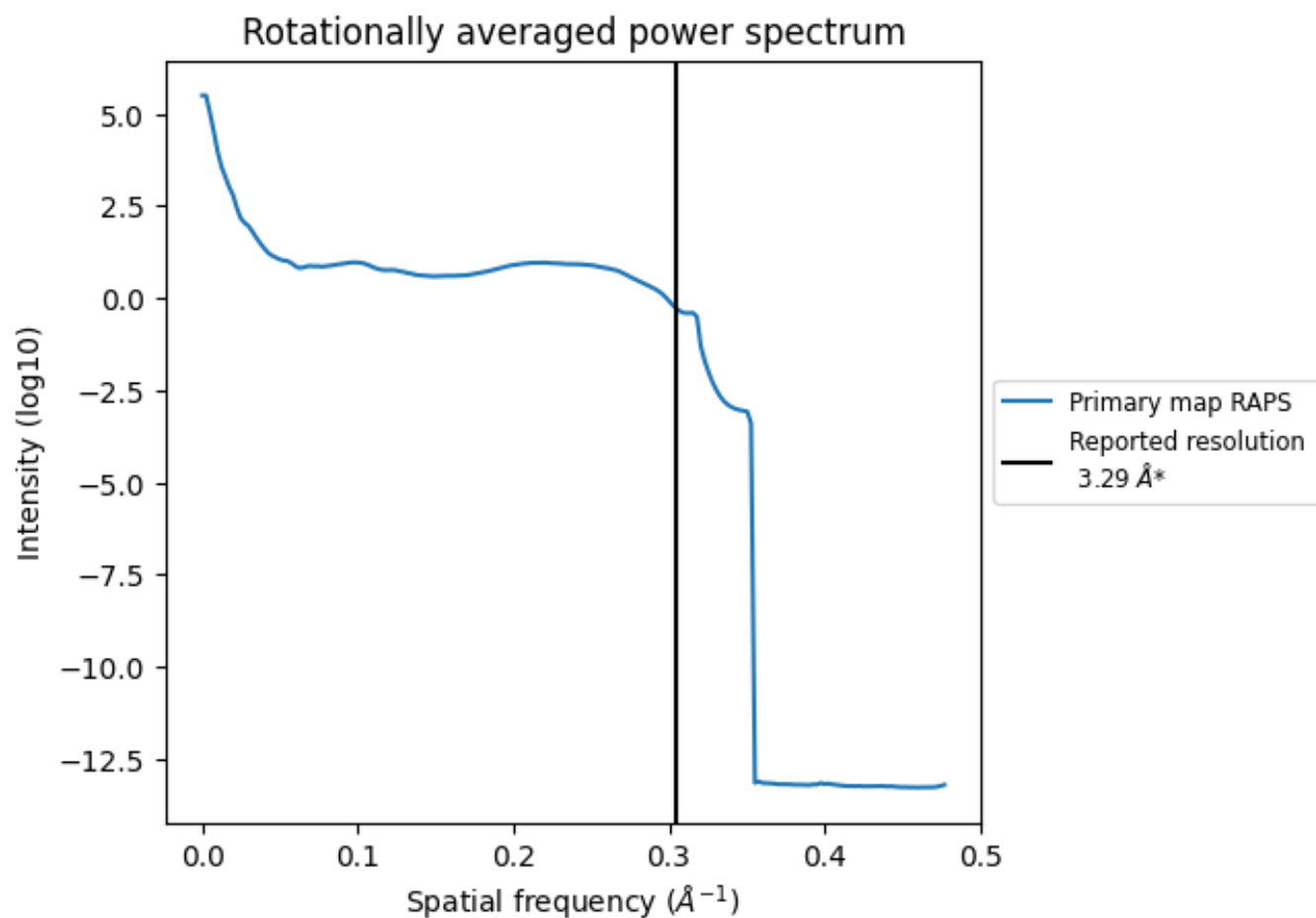
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 174 nm³; this corresponds to an approximate mass of 158 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 ⓘ

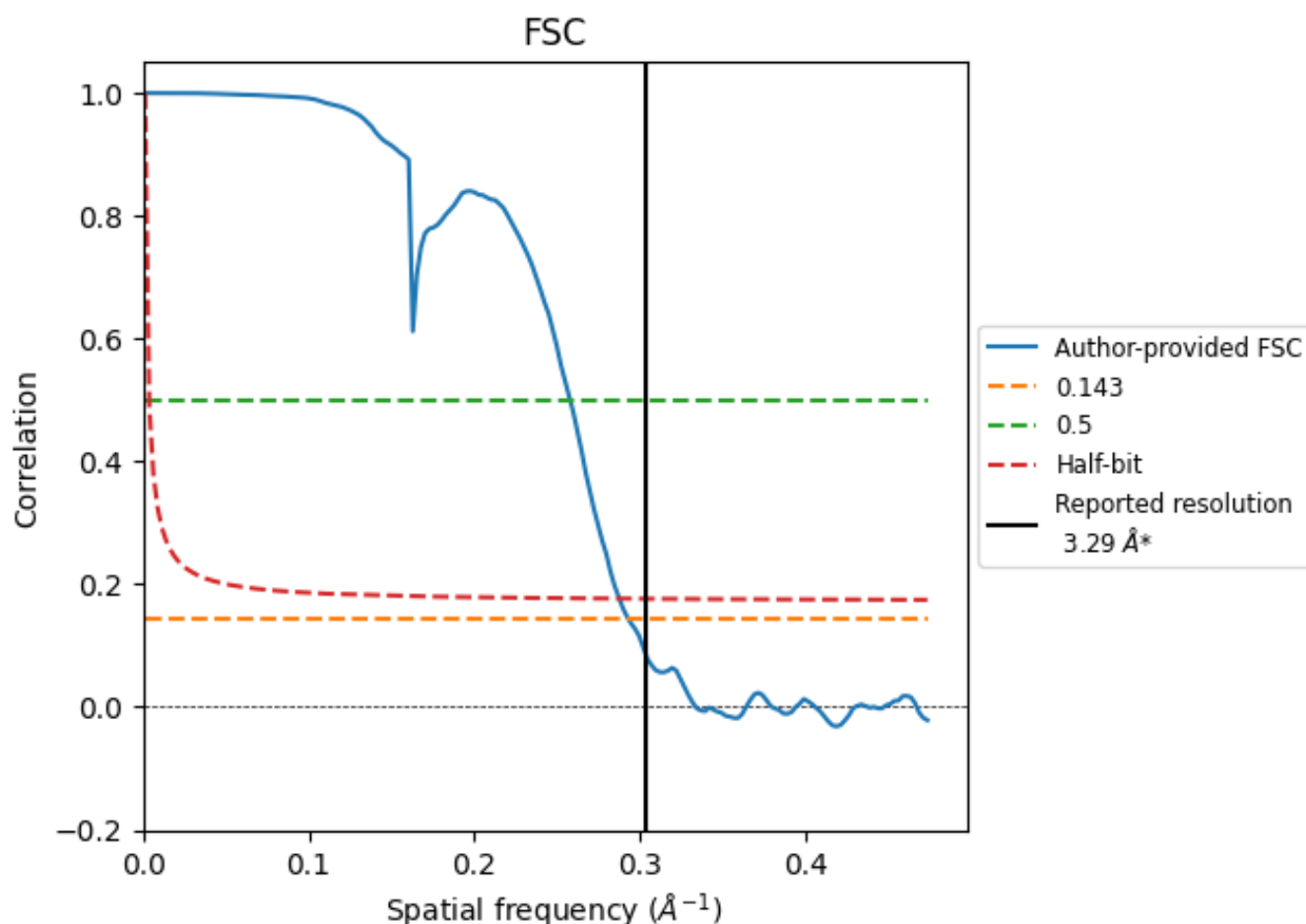


*Reported resolution corresponds to spatial frequency of 0.304 Å⁻¹

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 0.304 Å⁻¹

8.2 Resolution estimates [i](#)

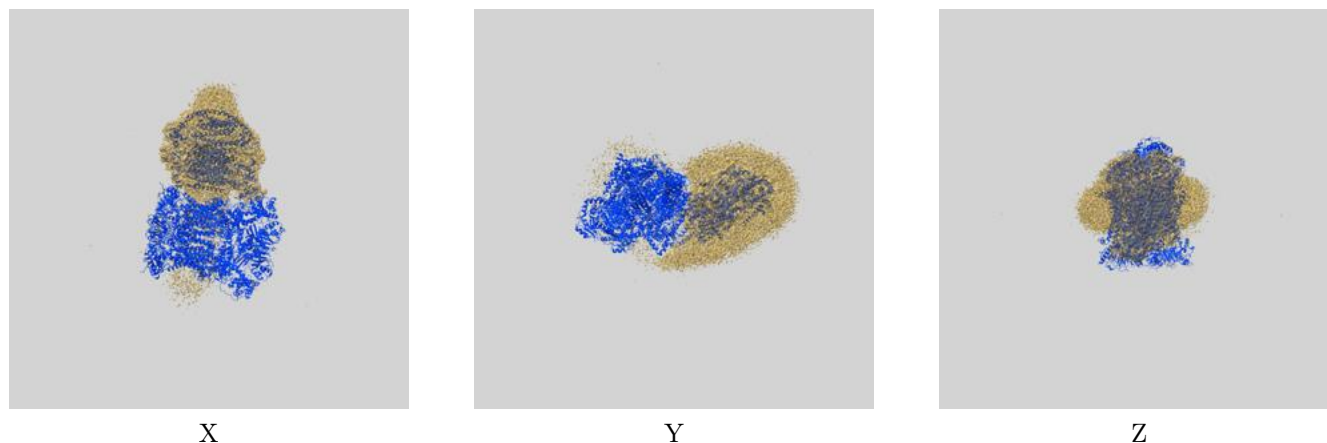
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.29	-	-
Author-provided FSC curve	3.41	3.88	3.48
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

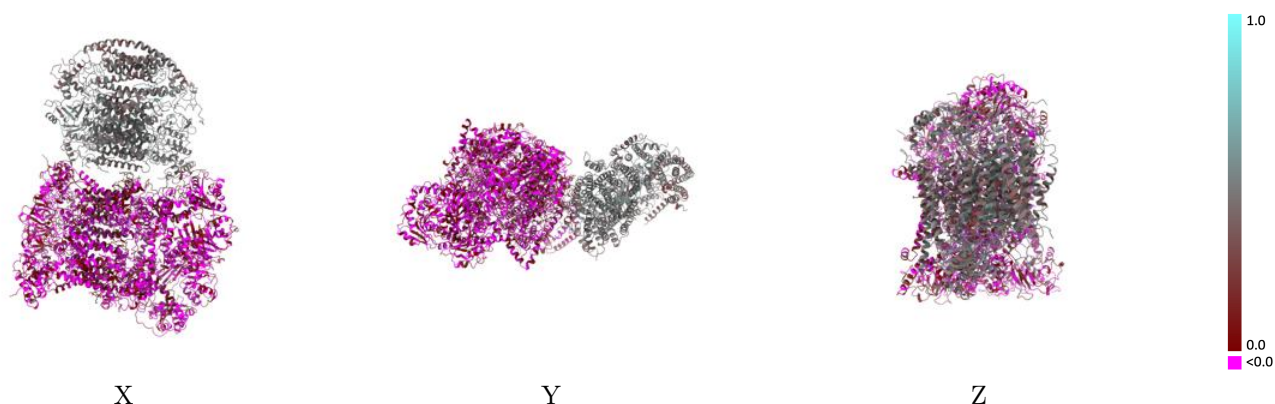
This section contains information regarding the fit between EMDB map EMD-10318 and PDB model 6T15. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.424 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](#)

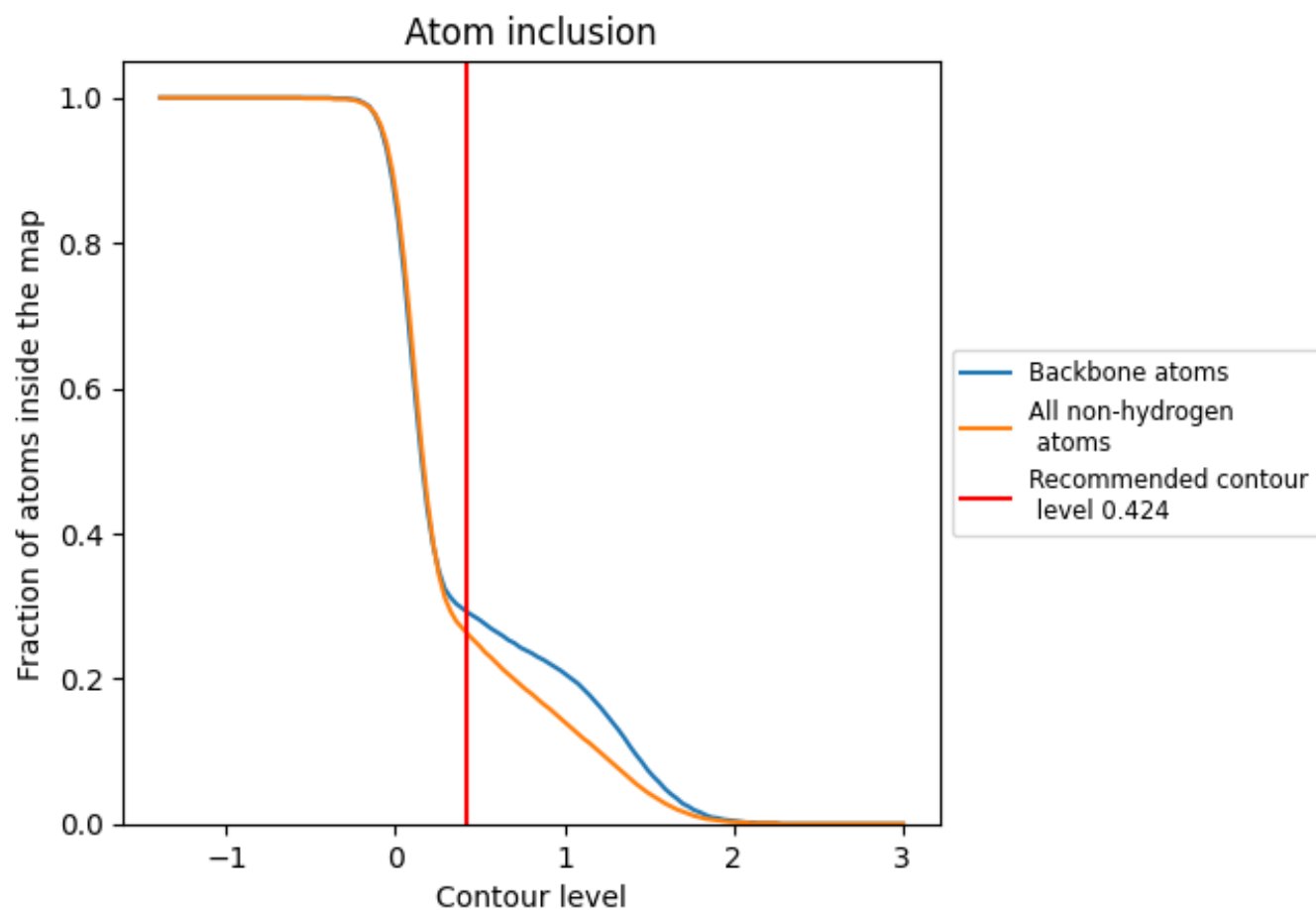


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 29% of all backbone atoms, 26% 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 (0.424) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2620	 0.1510
A	 0.0000	 -0.0120
B	 0.0000	 -0.0220
C	 0.0010	 -0.0200
D	 0.0000	 -0.0080
E	 0.0030	 0.0720
F	 0.0000	 0.0100
G	 0.0000	 -0.0100
H	 0.0000	 0.0110
I	 0.0000	 0.0150
J	 0.0030	 0.0320
L	 0.0020	 0.0170
M	 0.0000	 -0.0140
N	 0.0010	 0.0040
O	 0.0010	 0.0200
P	 0.0040	 0.0560
Q	 0.0000	 0.0360
R	 0.0000	 -0.0030
S	 0.0050	 0.0550
T	 0.0020	 0.0320
U	 0.0080	 0.0530
a	 0.8290	 0.4840
b	 0.8270	 0.4750
c	 0.8200	 0.4630
d	 0.8740	 0.4750
e	 0.7480	 0.4390
f	 0.8390	 0.4470
g	 0.8520	 0.4730
h	 0.8440	 0.4610
i	 0.8260	 0.4400
j	 0.8400	 0.4460
k	 0.8330	 0.4310
l	 0.8220	 0.4540
m	 0.7720	 0.3910

