



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 01:07 PM UTC

PDB ID : 8BQ6 / pdb_00008bq6
EMDB ID : EMD-16172
Title : Cryo-EM structure of the Arabidopsis thaliana I+III2 supercomplex (Complete conformation 2 composition)
Authors : Klusch, N.; Kuehlbrandt, W.
Deposited on : 2022-11-18
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

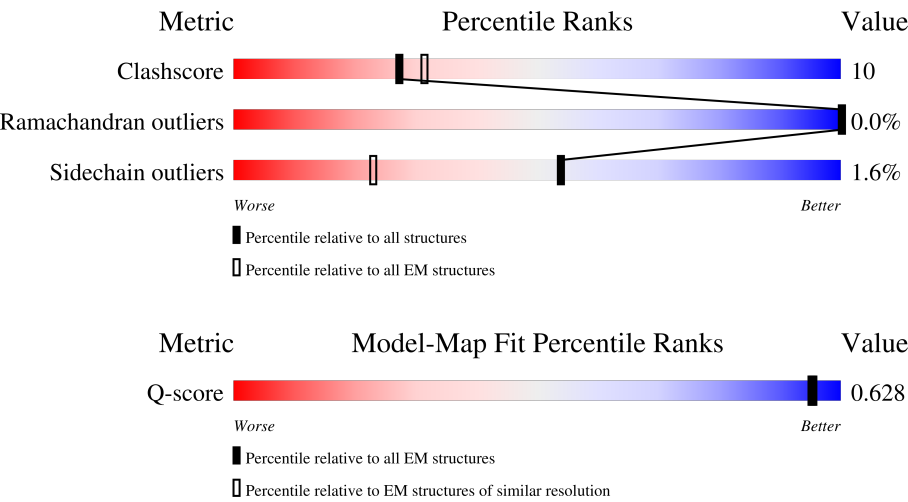
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.80 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	119	
2	B	218	
3	C	190	
4	D	394	

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Mol	Chain	Length	Quality of chain
5	E	255	
6	F	486	
7	G	748	
8	H	325	
9	I	222	
10	J	205	
11	K	100	
12	L	669	
13	M	495	
14	N	499	
15	O	159	
16	P	402	
17	Q	154	
18	R	110	
19	S	97	
20	T	122	
21	U	126	
22	V	169	
23	W	133	
24	X	106	
25	Y	159	
26	Z	143	
27	a	65	
28	b	65	
29	c	88	

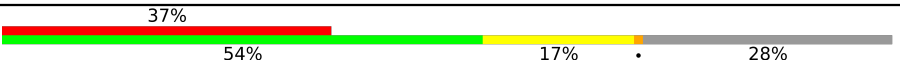
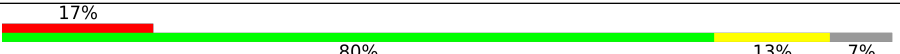
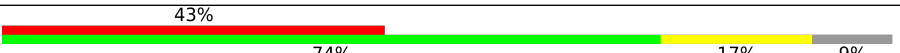
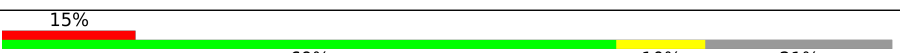
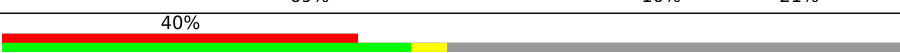
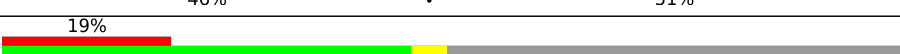
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Mol	Chain	Length	Quality of chain
30	d	81	
31	e	83	
32	f	106	
33	g	114	
34	i	98	
35	j	69	
36	k	72	
37	l	125	
38	m	71	
39	n	117	
40	o	103	
41	p	106	
42	q	159	
43	u	63	
44	v	113	
45	x	256	
46	y	278	
47	z	275	
48	AA	503	
48	BA	503	
49	AB	531	
49	BB	531	
50	AC	393	
50	BC	393	
51	AD	272	

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Mol	Chain	Length	Quality of chain
51	BD	272	
52	AE	307	
52	BE	307	
53	AF	122	
53	BF	122	
54	AG	72	
54	BG	72	
55	AH	69	
55	BH	69	
56	AI	72	
56	BI	72	
57	AJ	57	
57	BJ	57	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
58	SF4	F	501	-	-	X	-
58	SF4	I	500	-	-	X	-
59	FES	BD	301	-	-	X	-
66	COO	y	301	X	-	-	-

2 Entry composition

There are 69 unique types of molecules in this entry. The entry contains 96522 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 NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	94	Total	C	N	O	S	0	0
			802	565	110	123	4		

- Molecule 2 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	157	Total	C	N	O	S	0	0
			1244	797	218	215	14		

- Molecule 3 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	181	Total	C	N	O	S	0	0
			1545	997	266	276	6		

- Molecule 4 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	385	Total	C	N	O	S	0	0
			3079	1957	542	556	24		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	70	LEU	SER	conflict	UNP P93306
D	227	SER	PRO	conflict	UNP P93306
D	309	LEU	SER	conflict	UNP P93306

- Molecule 5 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	192	Total	C	N	O	S	0	0
			1500	954	248	287	11		

- Molecule 6 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	434	Total	C	N	O	S	0	0
			3368	2125	600	618	25		

- Molecule 7 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	687	Total	C	N	O	S	0	0
			5243	3285	919	1000	39		

- Molecule 8 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	324	Total	C	N	O	S	0	0
			2536	1719	386	416	15		

- Molecule 9 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 8-A, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	165	Total	C	N	O	S	0	0
			1349	849	229	261	10		

- Molecule 10 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	174	Total	C	N	O	S	0	0
			1399	949	213	228	9		

- Molecule 11 is a protein called NADH dehydrogenase subunit 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	100	Total	C	N	O	S	0	0
			784	525	121	131	7		

- Molecule 12 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	665	Total	C	N	O	S	0	0
			5222	3474	808	901	39		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	91	PHE	SER	conflict	UNP B5TM94

- Molecule 13 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	494	Total	C	N	O	S	0	0
			3946	2664	610	647	25		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	326	LEU	PRO	conflict	UNP B5TM93

- Molecule 14 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	488	Total	C	N	O	S	1	0
			3832	2582	578	644	28		

- Molecule 15 is a protein called AT3G07480.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	123	Total	C	N	O	S	0	0
			963	603	170	186	4		

- Molecule 16 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	316	Total	C	N	O	S	0	0
			2453	1580	414	444	15		

- Molecule 17 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	105	Total	C	N	O	S	0	0
			837	536	144	156	1		

- Molecule 18 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	73	Total	C	N	O	S	0	0
			571	359	101	105	6		

- Molecule 19 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	93	Total	C	N	O	S	0	0
			727	459	129	133	6		

- Molecule 20 is a protein called Acyl carrier protein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	83	Total	C	N	O	S	0	0
			659	417	104	135	3		

- Molecule 21 is a protein called Acyl carrier protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	87	Total	C	N	O	S	0	0
			677	427	110	139	1		

- Molecule 22 is a protein called Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	140	Total	C	N	O	S	0	0
			1123	712	187	219	5		

- Molecule 23 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	112	Total	C	N	O	S	0	0
			904	578	161	162	3		

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	98	Total	C	N	O	S	0	0
			776	486	134	144	12		

- Molecule 25 is a protein called Outer envelope pore protein 16-3, chloroplastic/mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	125	Total	C	N	O	S	0	0
			928	596	162	167	3		

- Molecule 26 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	125	Total	C	N	O	S	0	0
			997	640	175	177	5		

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	58	Total	C	N	O	S	0	0
			469	302	84	78	5		

- Molecule 28 is a protein called At2g46540/F11C10.23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	43	Total	C	N	O	S	0	0
			315	206	51	55	3		

- Molecule 29 is a protein called Transmembrane protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	76	Total	C	N	O	S	0	0
			617	396	115	100	6		

- Molecule 30 is a protein called Excitatory amino acid transporter.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	75	Total	C	N	O	S	0	0
			592	382	106	99	5		

- Molecule 31 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	65	Total	C	N	O	S	0	0
			554	343	103	100	8		

- Molecule 32 is a protein called At4g16450.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	101	Total	C	N	O	S	0	0
			765	491	126	143	5		

- Molecule 33 is a protein called ESSS subunit of NADH:ubiquinone oxidoreductase (Complex I) protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	79	Total	C	N	O	S	0	0
			641	412	111	115	3		

- Molecule 34 is a protein called P1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	83	Total	C	N	O	S	0	0
			721	458	132	126	5		

- Molecule 35 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	51	Total	C	N	O	S	0	0
			415	275	73	64	3		

- Molecule 36 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	48	Total	C	N	O	S	0	0
			382	244	72	63	3		

- Molecule 37 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit

8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	74	Total	C	N	O	S	0	0
			562	367	91	103	1		

- Molecule 38 is a protein called B15 – 1 beta subcomplex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	70	Total	C	N	O	S	0	0
			577	370	107	98	2		

- Molecule 39 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	109	Total	C	N	O	S	0	0
			911	580	170	160	1		

- Molecule 40 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	80	Total	C	N	O	S	0	0
			657	413	115	119	10		

- Molecule 41 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	90	Total	C	N	O	S	0	0
			757	479	141	133	4		

- Molecule 42 is a protein called Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	80	Total	C	N	O	S	1	0
			669	427	120	120	2		

- Molecule 43 is a protein called Uncharacterized protein At1g67785.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	u	55	Total	C	N	O	S	0	0
			463	298	84	78	3		

- Molecule 44 is a protein called Uncharacterized protein At2g27730, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	v	29	Total	C	N	O		0	0
			219	142	38	39			

- Molecule 45 is a protein called Gamma carbonic anhydrase-like 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	x	210	Total	C	N	O	S	0	0
			1629	1043	280	301	5		

- Molecule 46 is a protein called Gamma carbonic anhydrase 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	y	265	Total	C	N	O	S	0	0
			2013	1258	359	388	8		

- Molecule 47 is a protein called Gamma carbonic anhydrase 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	z	233	Total	C	N	O	S	0	0
			1772	1111	325	330	6		

- Molecule 48 is a protein called Probable mitochondrial-processing peptidase subunit alpha-1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AA	420	Total	C	N	O	S	0	0
			3201	2034	530	621	16		
48	BA	420	Total	C	N	O	S	0	0
			3202	2035	530	621	16		

- Molecule 49 is a protein called Probable mitochondrial-processing peptidase subunit beta, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	AB	487	Total	C	N	O	S	0	0
			3834	2407	672	743	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
49	BB	487	Total	C	N	O	S	0	0
			3834	2407	672	743	12		

- Molecule 50 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AC	387	Total	C	N	O	S	0	0
			3093	2083	487	508	15		
50	BC	387	Total	C	N	O	S	0	0
			3093	2083	487	508	15		

- Molecule 51 is a protein called Cytochrome b-c1 complex subunit Rieske-1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AD	196	Total	C	N	O	S	0	0
			1528	978	264	281	5		
51	BD	195	Total	C	N	O	S	0	0
			1519	973	263	278	5		

- Molecule 52 is a protein called Cytochrome c1 2, heme protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AE	244	Total	C	N	O	S	0	0
			1917	1216	326	364	11		
52	BE	244	Total	C	N	O	S	0	0
			1917	1216	326	364	11		

- Molecule 53 is a protein called Cytochrome b-c1 complex subunit 7-2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AF	116	Total	C	N	O	S	0	0
			976	613	186	171	6		
53	BF	116	Total	C	N	O	S	0	0
			976	613	186	171	6		

- Molecule 54 is a protein called Cytochrome b-c1 complex subunit 8-1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AG	69	Total	C	N	O	S	0	0
			581	387	95	98	1		
54	BG	68	Total	C	N	O	S	0	0
			572	382	93	96	1		

- Molecule 55 is a protein called Cytochrome b-c1 complex subunit 6-1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AH	64	Total	C	N	O	S	0	0
			518	334	87	91	6		
55	BH	63	Total	C	N	O	S	0	0
			511	329	86	90	6		

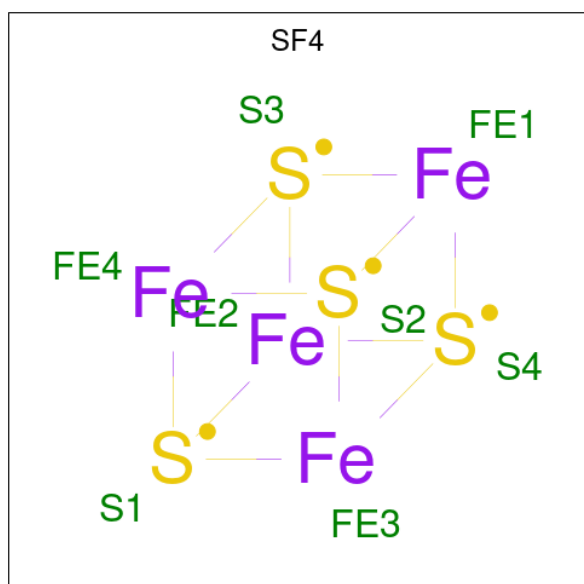
- Molecule 56 is a protein called Cytochrome b-c1 complex subunit 9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AI	57	Total	C	N	O	S	0	0
			476	310	85	80	1		
56	BI	57	Total	C	N	O	S	0	0
			476	310	85	80	1		

- Molecule 57 is a protein called Cytochrome b-c1 complex subunit 10, mitochondrial.

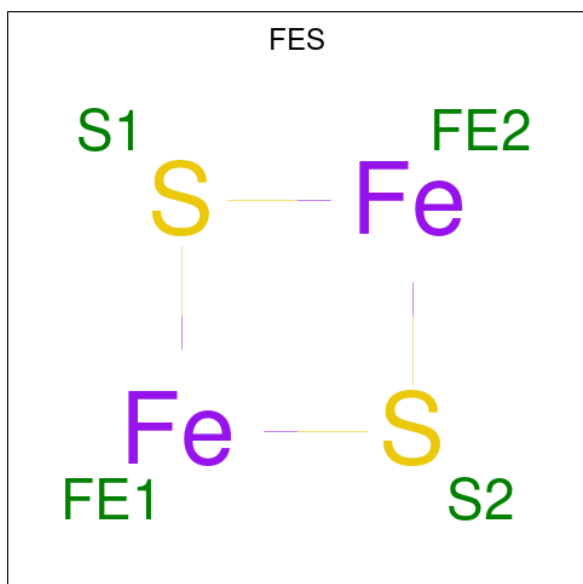
Mol	Chain	Residues	Atoms				AltConf	Trace
57	AJ	28	Total	C	N	O	0	0
			203	137	33	33		
57	BJ	28	Total	C	N	O	0	0
			205	139	34	32		

- Molecule 58 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).



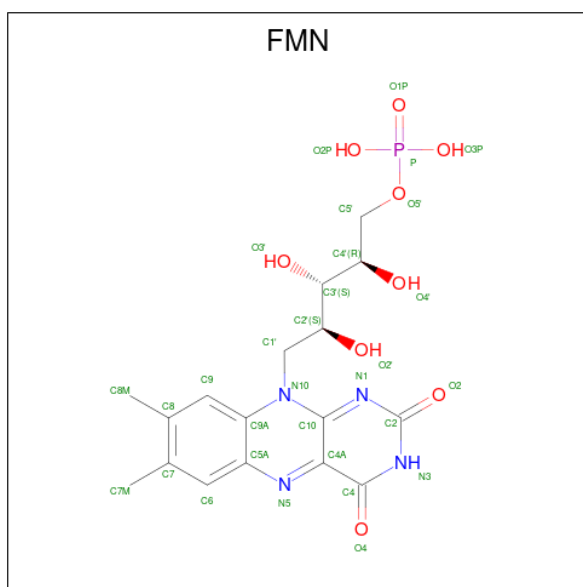
Mol	Chain	Residues	Atoms			AltConf
58	B	1	Total	Fe	S	0
			8	4	4	
58	F	1	Total	Fe	S	0
			8	4	4	
58	G	1	Total	Fe	S	0
			8	4	4	
58	G	1	Total	Fe	S	0
			8	4	4	
58	I	1	Total	Fe	S	0
			8	4	4	
58	I	1	Total	Fe	S	0
			8	4	4	

- Molecule 59 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2) (labeled as "Ligand of Interest" by depositor).



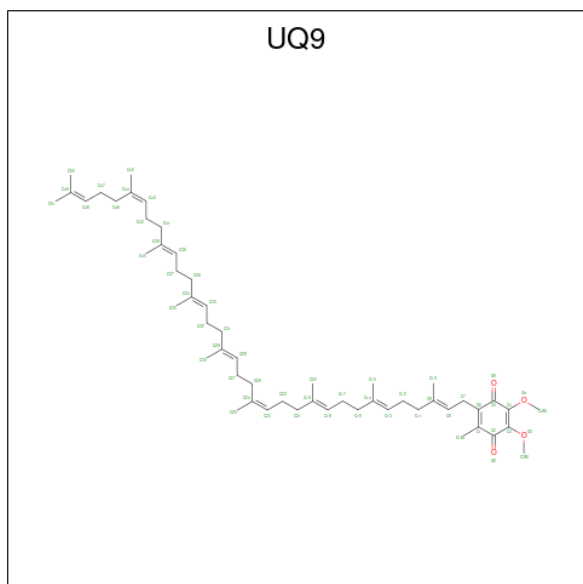
Mol	Chain	Residues	Atoms			AltConf
59	E	1	Total	Fe	S	0
			4	2	2	
59	G	1	Total	Fe	S	0
			4	2	2	
59	AD	1	Total	Fe	S	0
			4	2	2	
59	BD	1	Total	Fe	S	0
			4	2	2	

- Molecule 60 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $\text{C}_{17}\text{H}_{21}\text{N}_4\text{O}_9\text{P}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
60	F	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 61 is Ubiquinone-9 (CCD ID: UQ9) (formula: $C_{54}H_{82}O_4$) (labeled as "Ligand of Interest" by depositor).

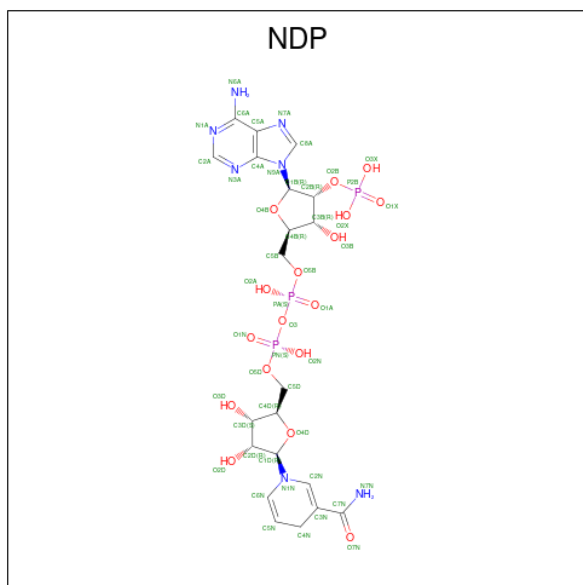


Mol	Chain	Residues	Atoms			AltConf
61	H	1	Total	C	O	0
			35	31	4	

- Molecule 62 is FE (III) ION (CCD ID: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
62	O	1	Total	Fe	0
			1	1	

- Molecule 63 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$) (labeled as "Ligand of Interest" by depositor).

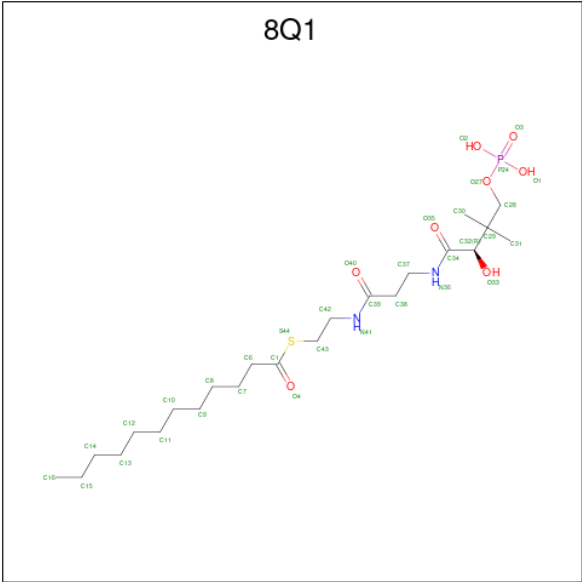


Mol	Chain	Residues	Atoms					AltConf
63	P	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 64 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

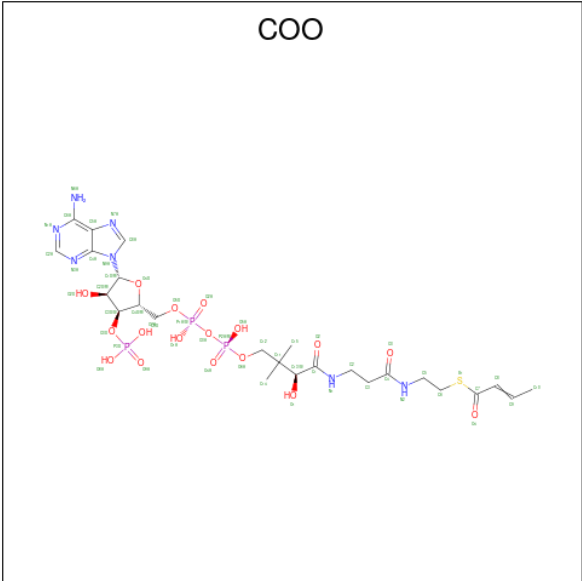
Mol	Chain	Residues	Atoms		AltConf
64	R	1	Total	Zn	0
			1	1	
64	y	1	Total	Zn	0
			1	1	
64	AB	1	Total	Zn	0
			1	1	
64	BB	1	Total	Zn	0
			1	1	

- Molecule 65 is S-[2-($\{N-[(2R)-2\text{-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-\beta\text{-alaninyl}\}$ amino)ethyl] dodecanethioate (CCD ID: 8Q1) (formula: $C_{23}H_{45}N_2O_8PS$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
65	W	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	
65	n	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	

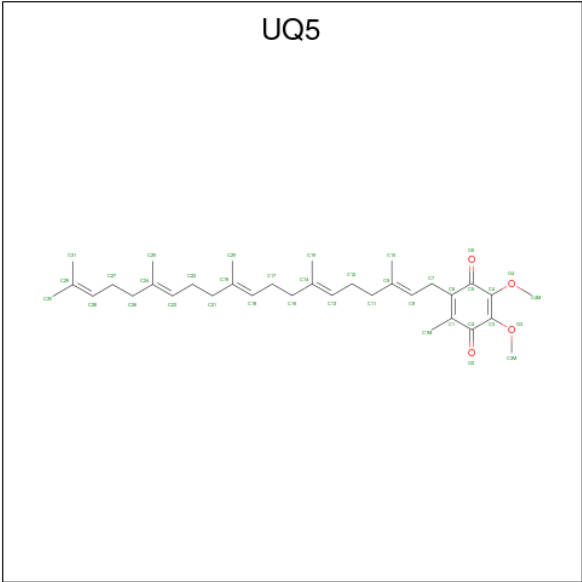
- Molecule 66 is CROTONYL COENZYME A (CCD ID: COO) (formula: C₂₅H₄₀N₇O₁₇P₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
66	y	1	Total	C	N	O	P	S	0
			53	25	7	17	3	1	

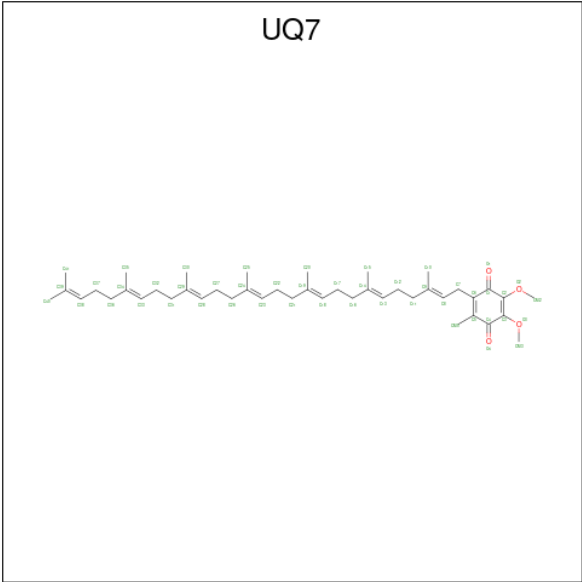
-
- Chemical structure of HEM (heme) showing a central iron atom coordinated by four nitrogen atoms in a porphyrin-like ring, with various side chains and a central heme label.

- Molecule 68 is 2,3-DIMETHOXY-5-METHYL-6-(3,11,15,19-TETRAMETHYL-EICOSA-2,6,10,14,18-PENTAENYL)-[1,4]BENZOQUINONE (CCD ID: UQ5) (formula: C₃₄H₅₀O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
68	AC	1	Total	C	O	0
			38	34	4	
68	AC	1	Total	C	O	0
			38	34	4	
68	BC	1	Total	C	O	0
			38	34	4	

- Molecule 69 is UBIQUINONE-7 (CCD ID: UQ7) (formula: C₄₄H₆₆O₄) (labeled as "Ligand of Interest" by depositor).



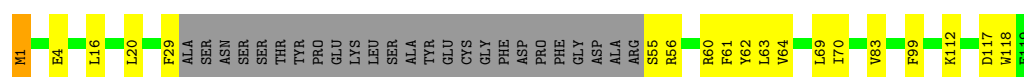
Mol	Chain	Residues	Atoms			AltConf
69	BC	1	Total	C	O	0
			48	44	4	

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

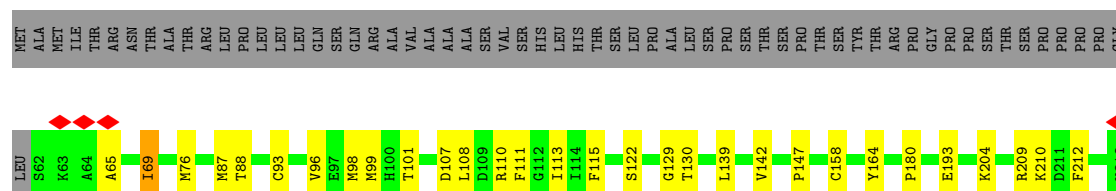
- Molecule 1: NADH-ubiquinone oxidoreductase chain 3

Chain A: 



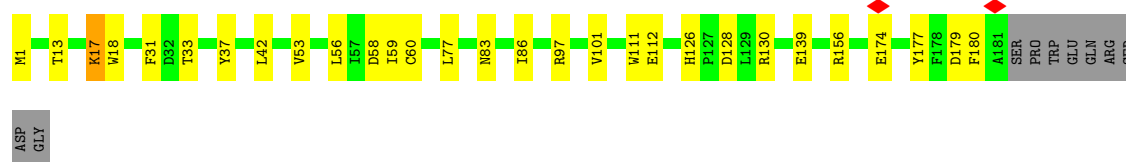
- Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial

Chain B: 



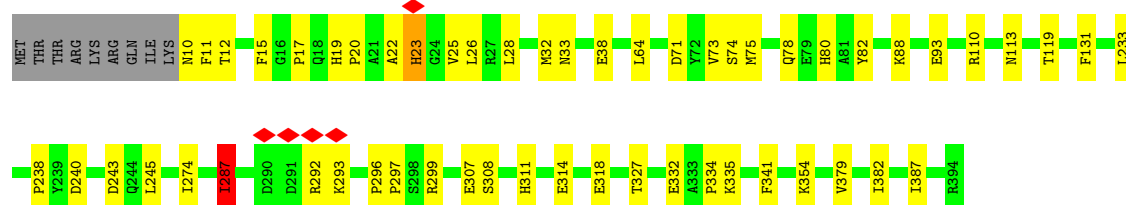
- Molecule 3: NADH dehydrogenase [ubiquinone] iron-sulfur protein 3

Chain C: 

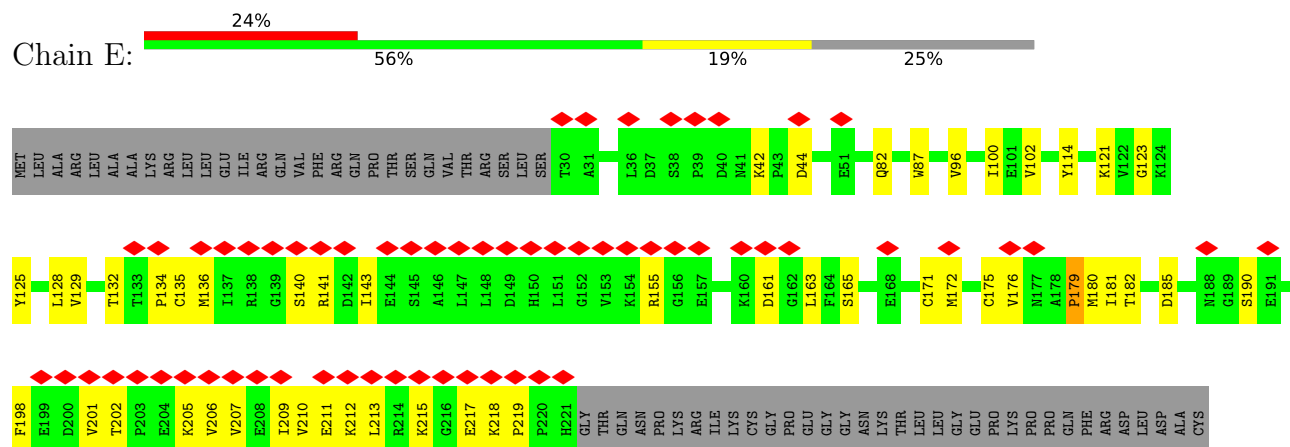


- Molecule 4: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2

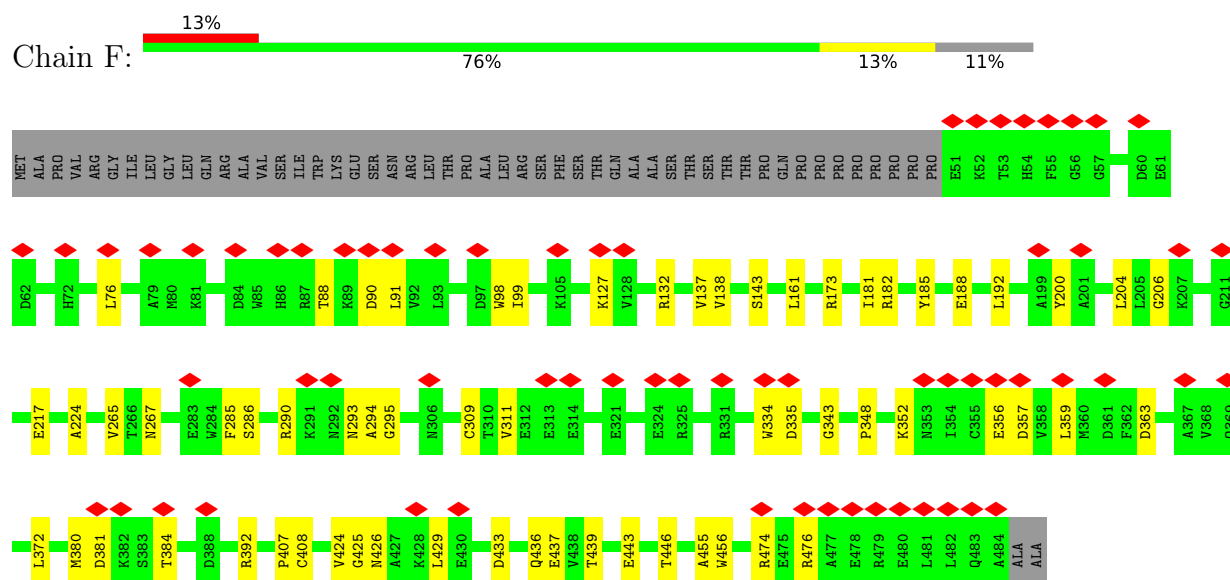
Chain D: 



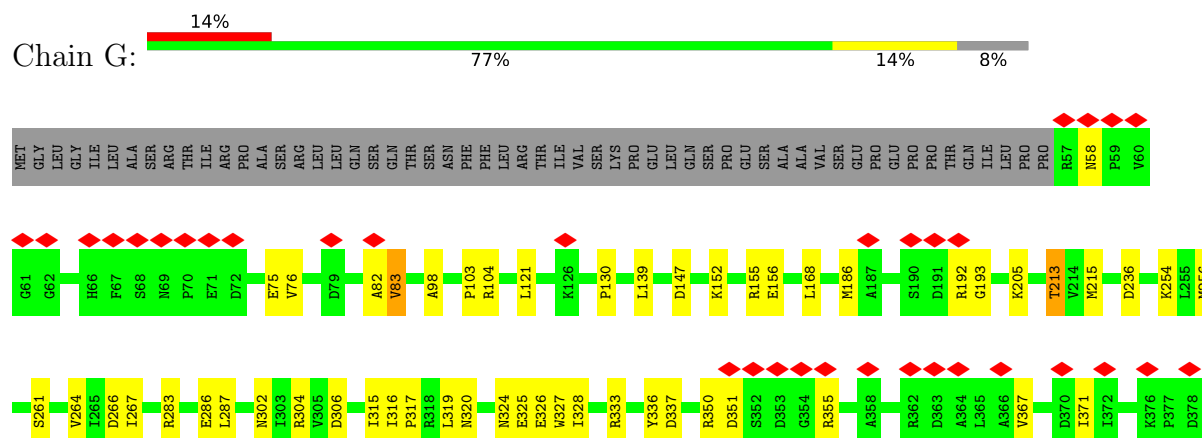
• Molecule 5: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial

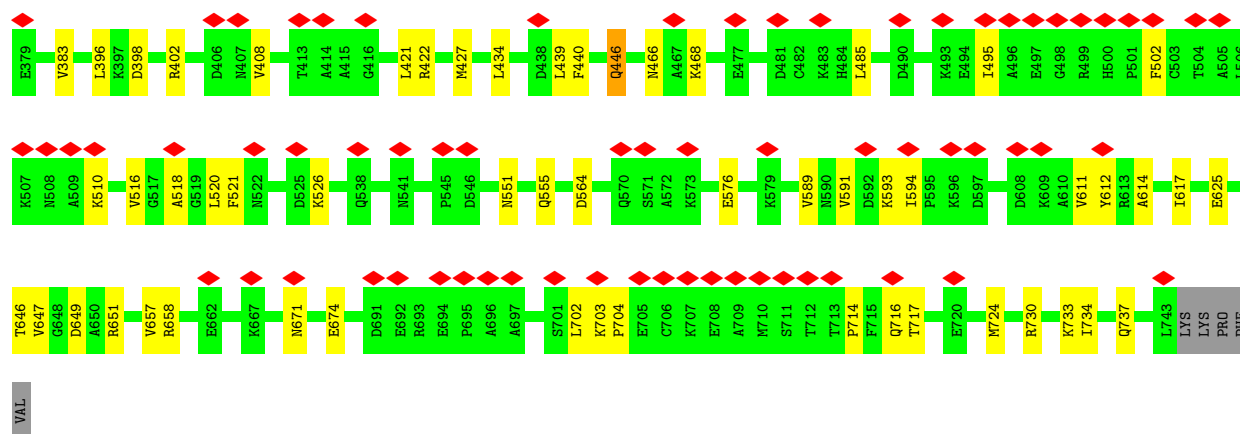


• Molecule 6: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial



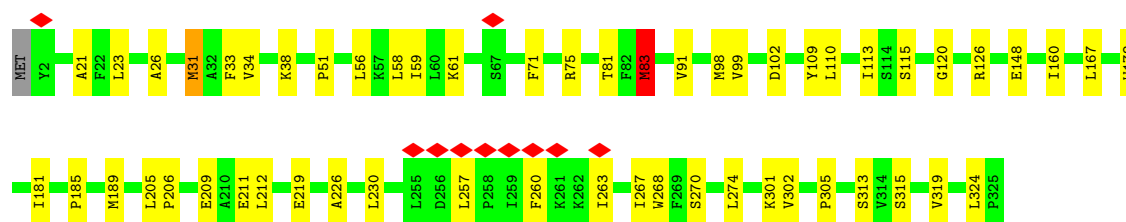
• Molecule 7: NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial





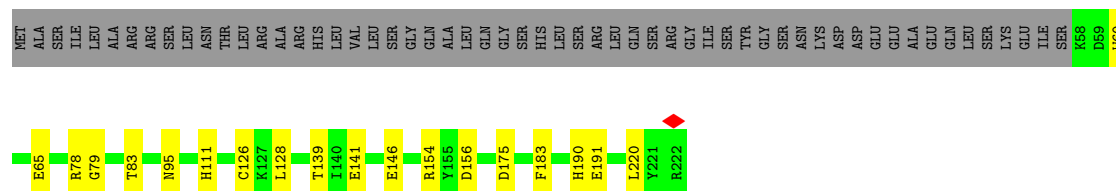
- Molecule 8: NADH-ubiquinone oxidoreductase chain 1

Chain H: 83% 16%



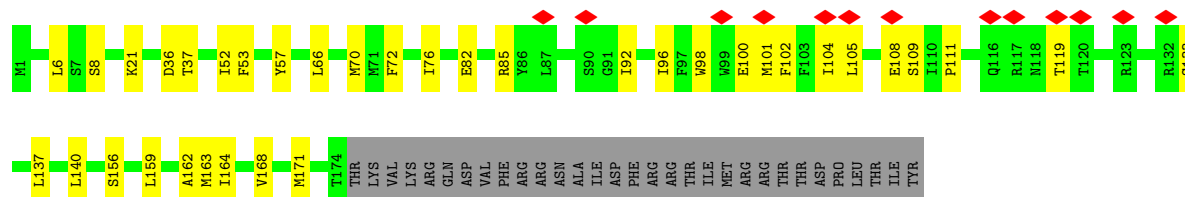
- Molecule 9: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8-A, mitochondrial

Chain I: 66% 9% 26%



- Molecule 10: NADH-ubiquinone oxidoreductase chain 6

Chain J: 6% 67% 18% 15%

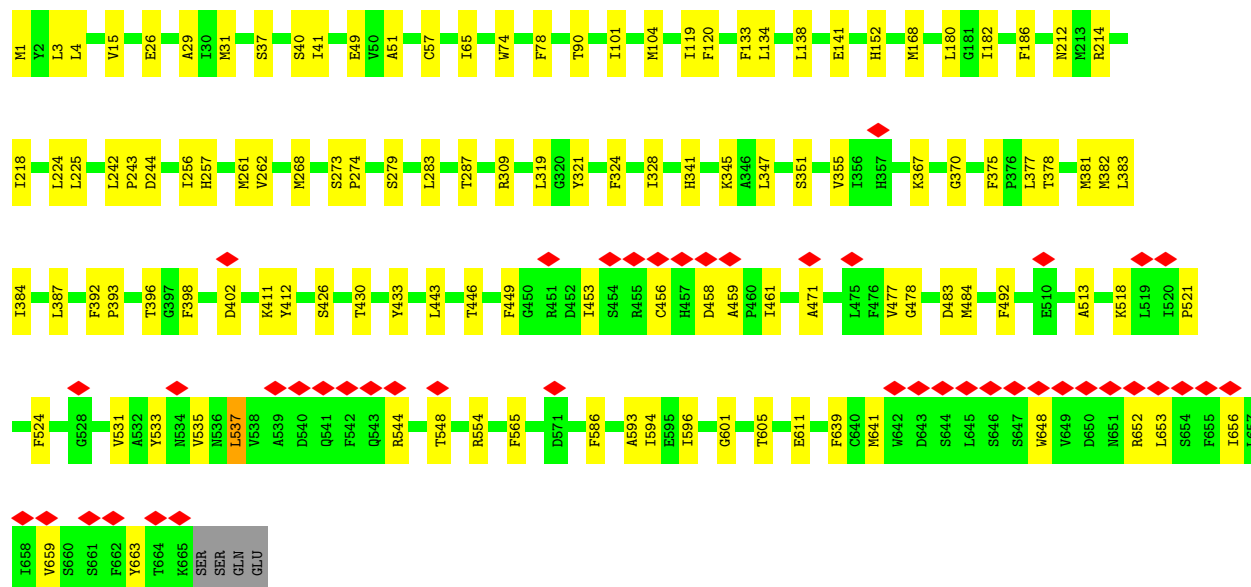
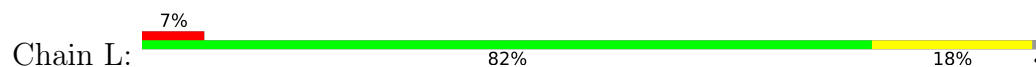


- Molecule 11: NADH dehydrogenase subunit 4L

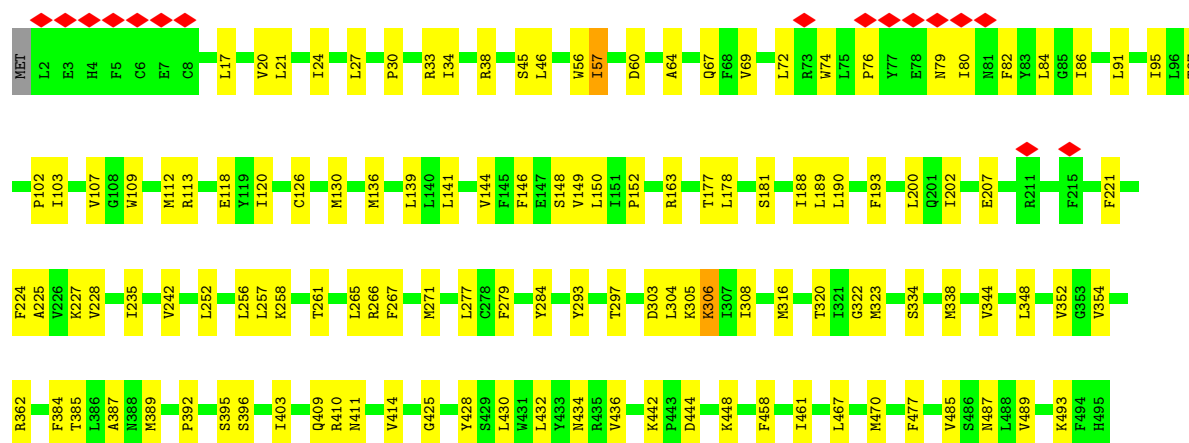
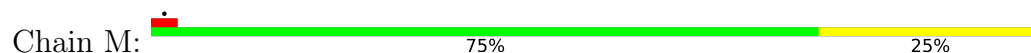
Chain K: 76% 23%



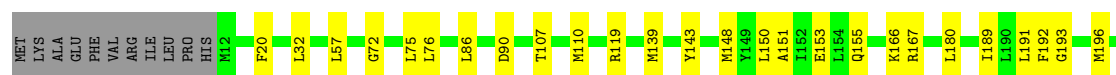
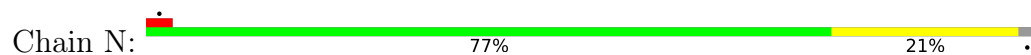
• Molecule 12: NADH-ubiquinone oxidoreductase chain 5

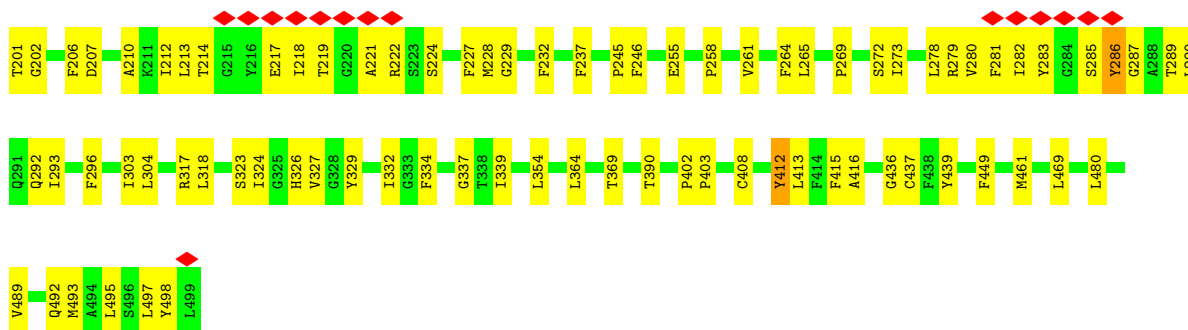


• Molecule 13: NADH-ubiquinone oxidoreductase chain 4

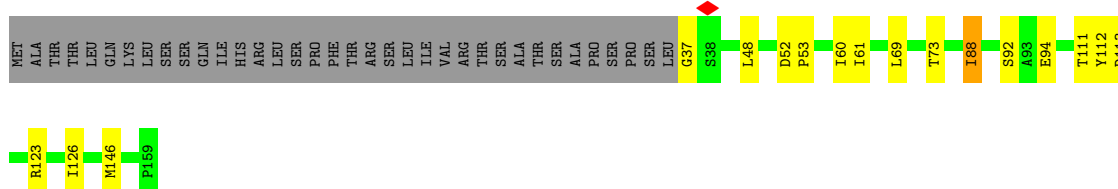


• Molecule 14: NADH-ubiquinone oxidoreductase chain 2

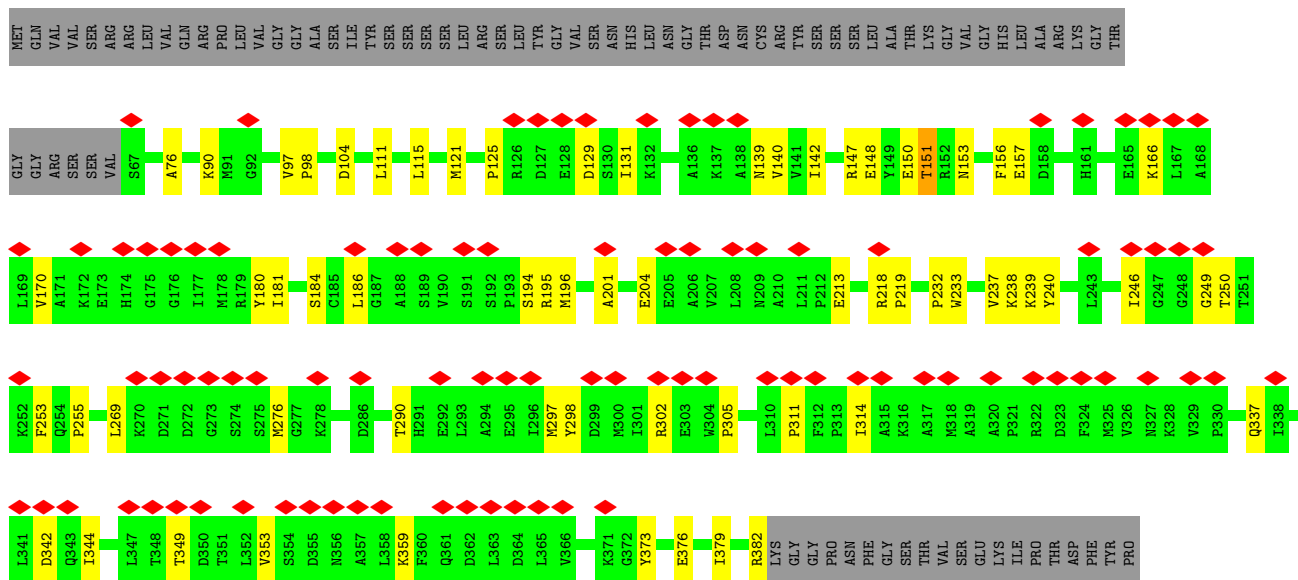




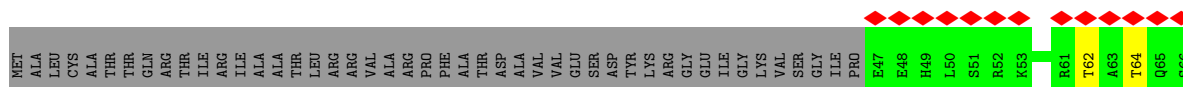
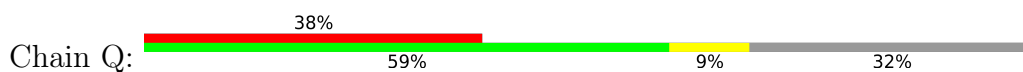
• Molecule 15: AT3G07480.1

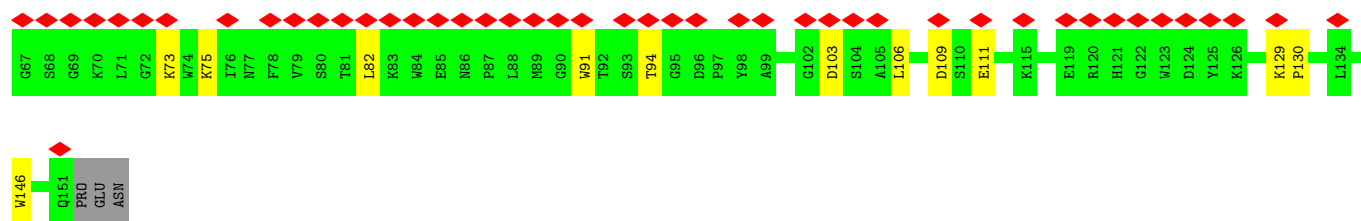


• Molecule 16: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial

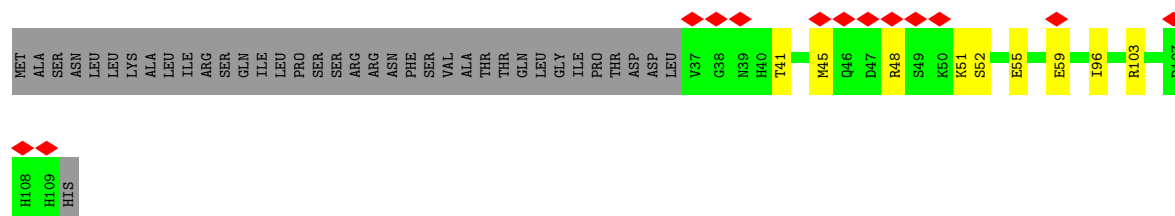


• Molecule 17: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

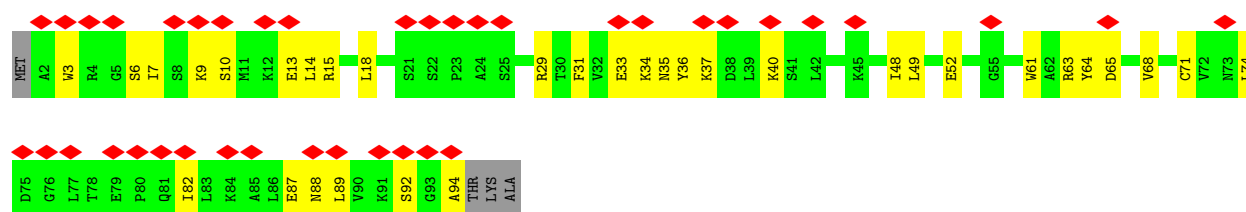




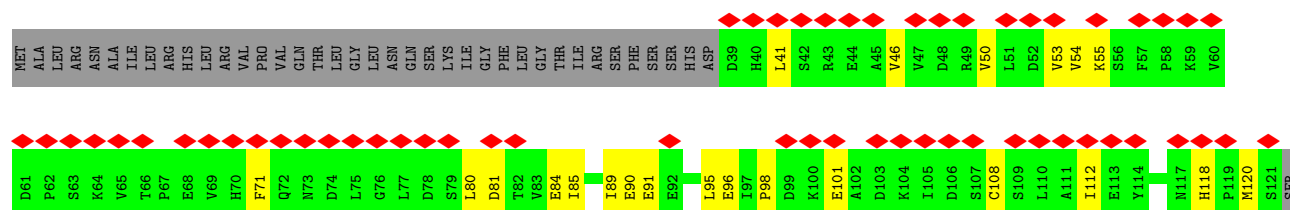
- Molecule 18: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial



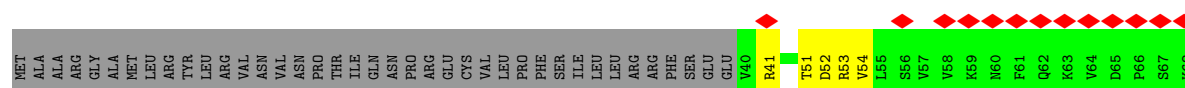
- Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2

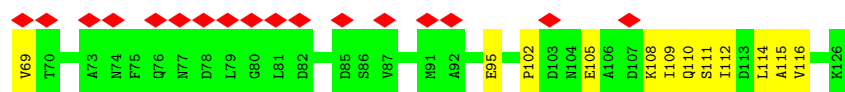


- Molecule 20: Acyl carrier protein 1, mitochondrial

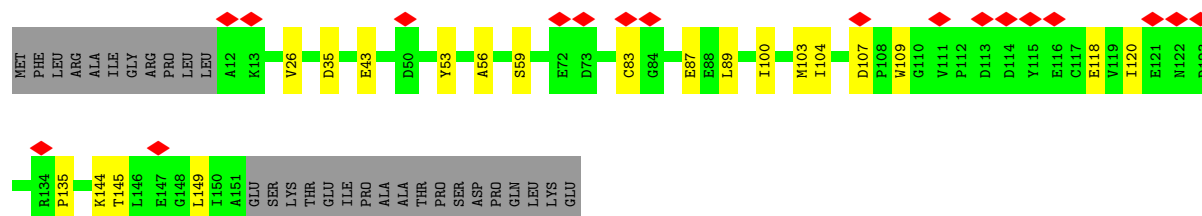


- Molecule 21: Acyl carrier protein 2, mitochondrial

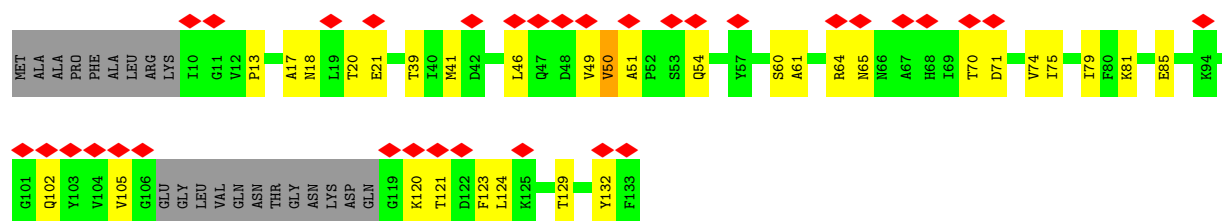




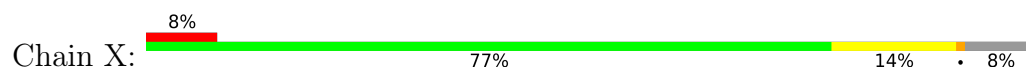
- Molecule 22: Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5, mitochondrial



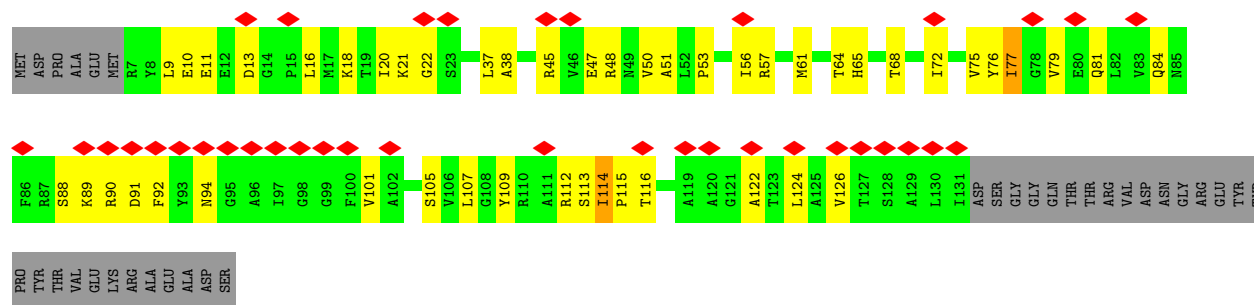
- Molecule 23: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6



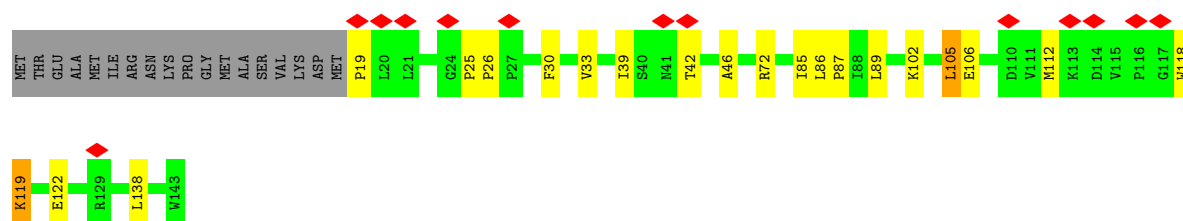
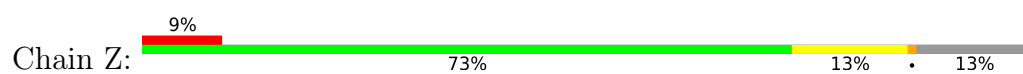
- Molecule 24: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8-B



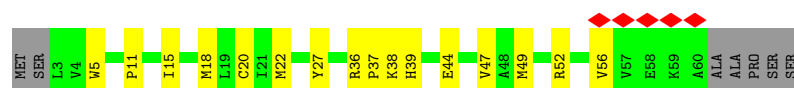
- Molecule 25: Outer envelope pore protein 16-3, chloroplastic/mitochondrial



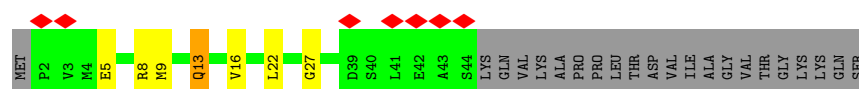
- Molecule 26: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-A



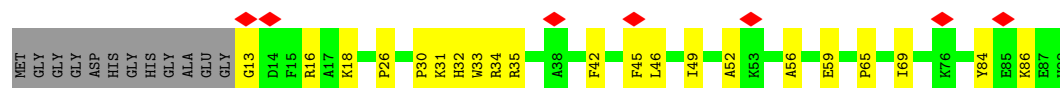
- Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1



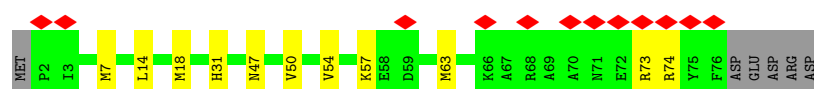
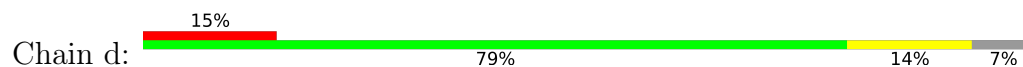
- Molecule 28: At2g46540/F11C10.23



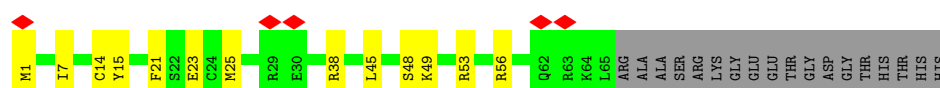
- Molecule 29: Transmembrane protein



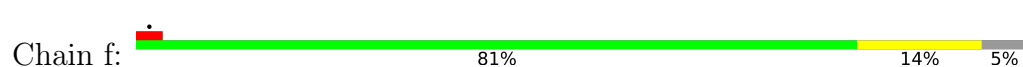
- Molecule 30: Excitatory amino acid transporter

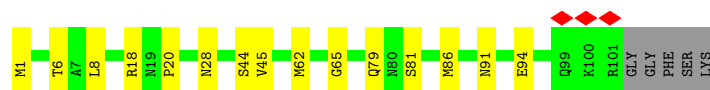


- Molecule 31: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5-B

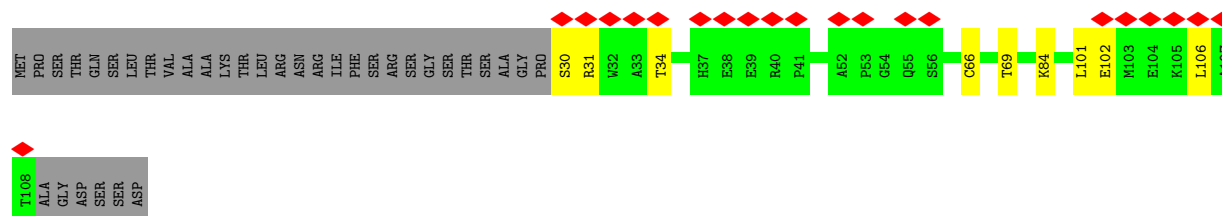


- Molecule 32: At4g16450

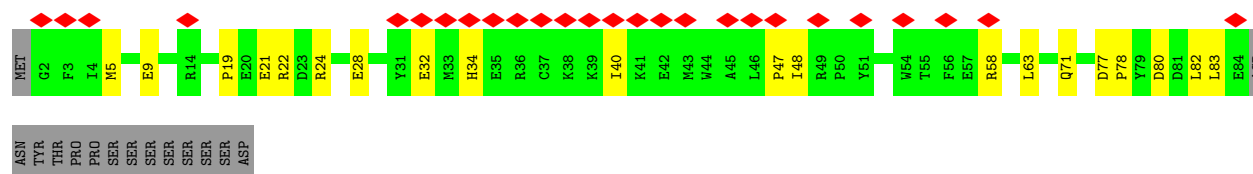




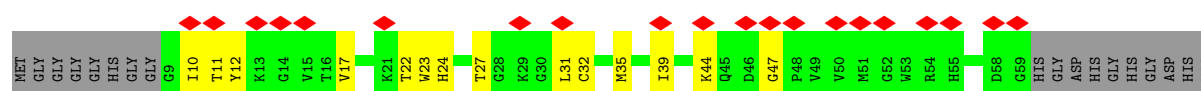
- Molecule 33: ESSS subunit of NADH:ubiquinone oxidoreductase (Complex I) protein



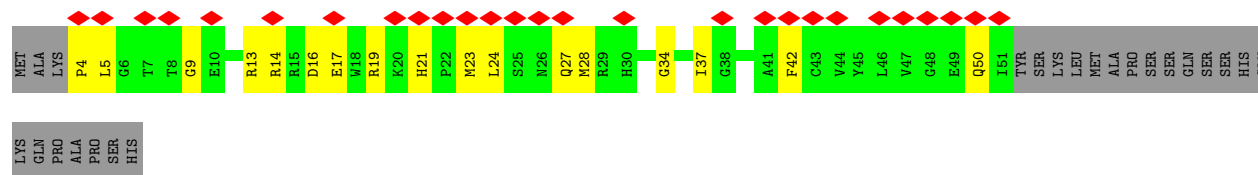
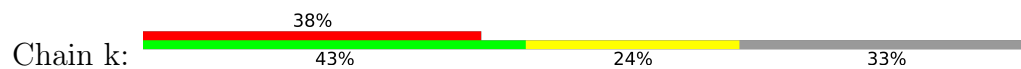
- Molecule 34: P1



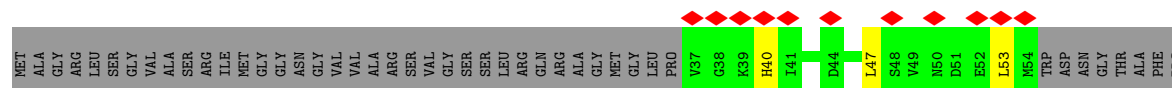
- Molecule 35: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2

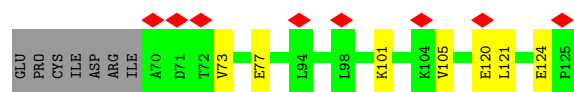


- Molecule 36: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3-A

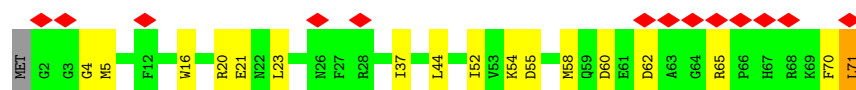
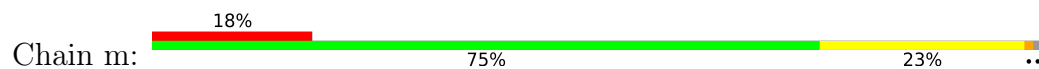


- Molecule 37: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

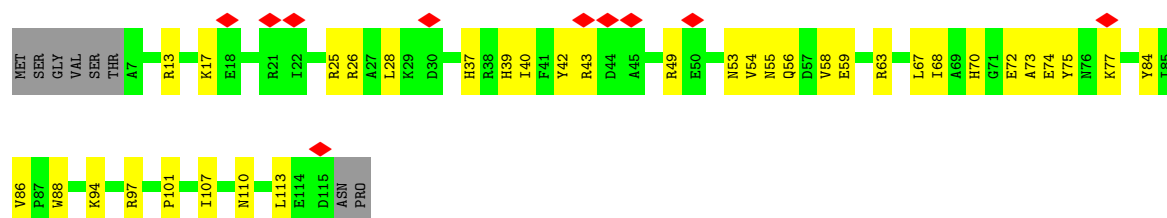




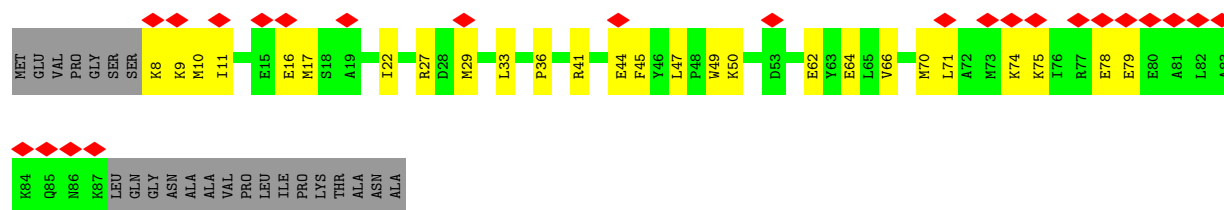
- Molecule 38: B15 – 1 beta subcomplex subunit 4



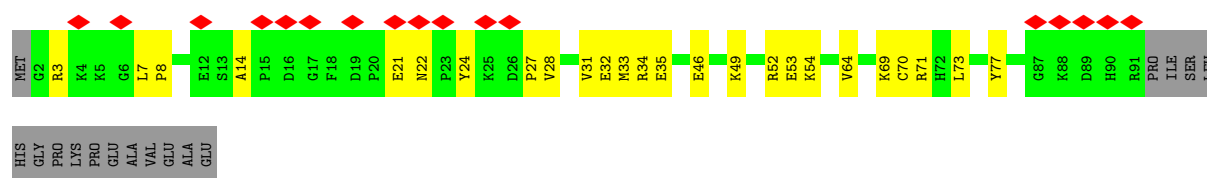
- Molecule 39: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9



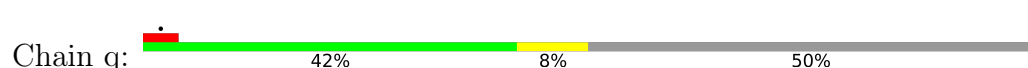
- Molecule 40: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7

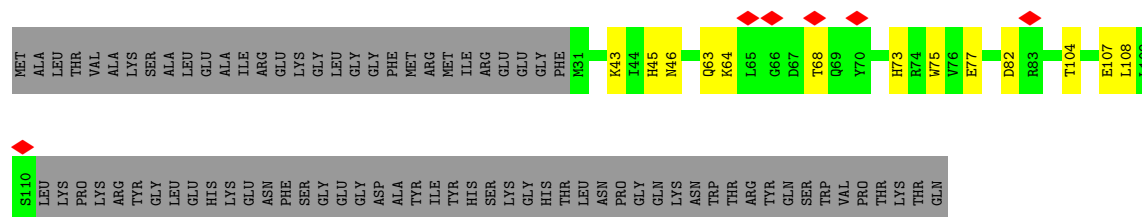


- Molecule 41: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10-B

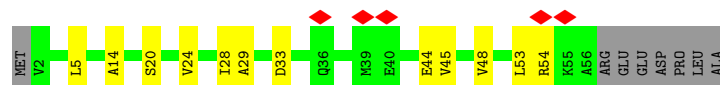


- Molecule 42: Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12





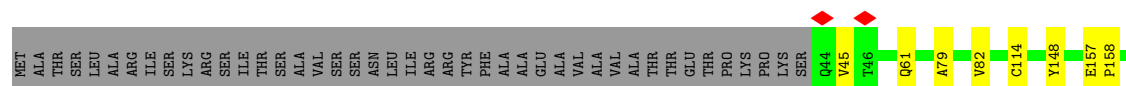
- Molecule 43: Uncharacterized protein At1g67785



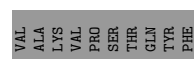
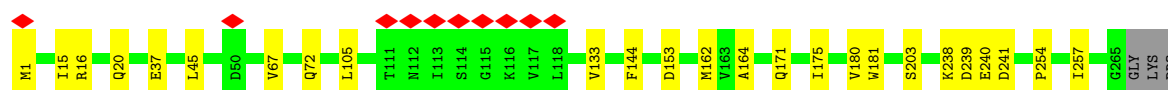
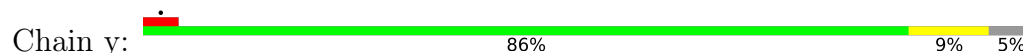
- Molecule 44: Uncharacterized protein At2g27730, mitochondrial



- Molecule 45: Gamma carbonic anhydrase-like 2, mitochondrial

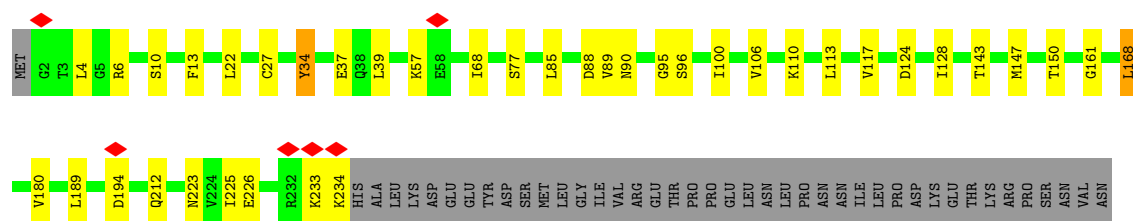


- Molecule 46: Gamma carbonic anhydrase 2, mitochondrial



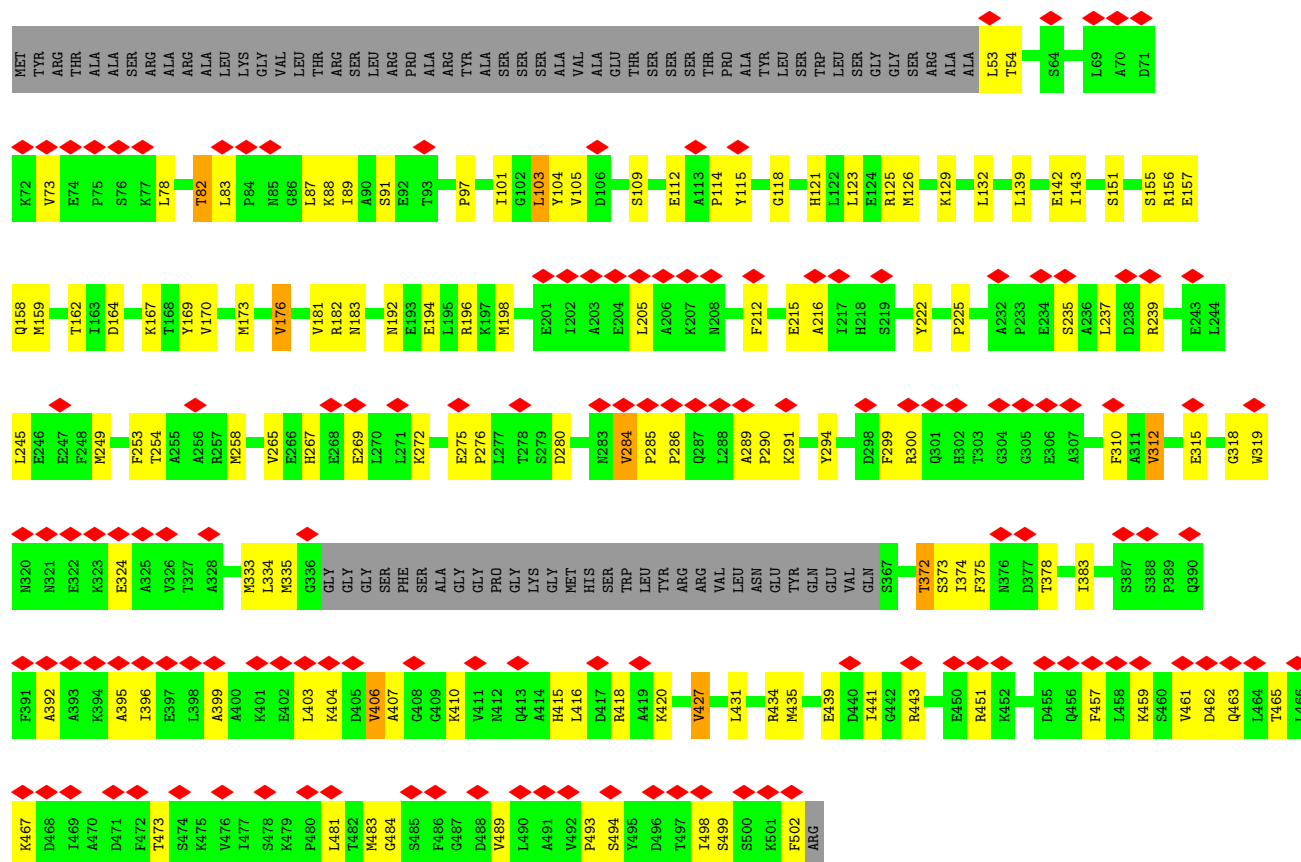
- Molecule 47: Gamma carbonic anhydrase 1, mitochondrial





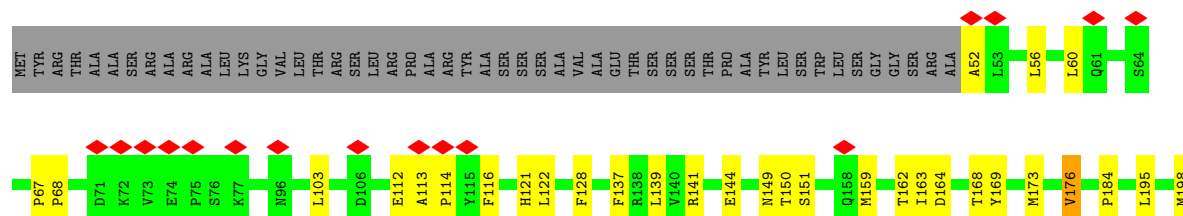
- Molecule 48: Probable mitochondrial-processing peptidase subunit alpha-1, mitochondrial

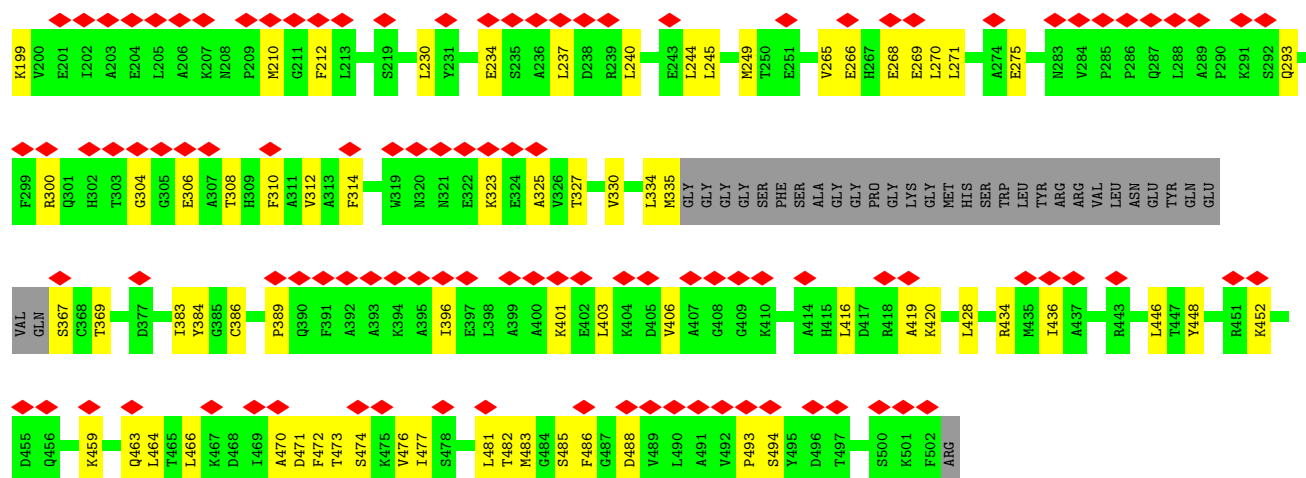
Chain AA: 26% 57% 25% 17%



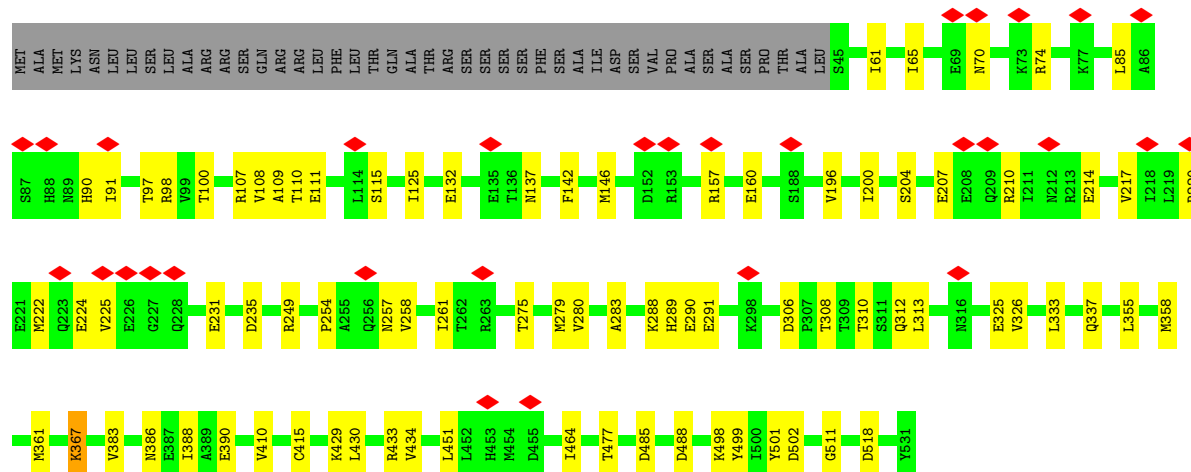
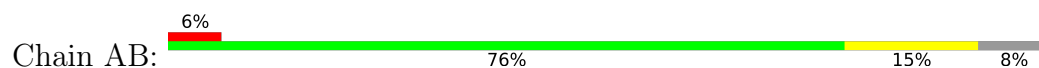
- Molecule 48: Probable mitochondrial-processing peptidase subunit alpha-1, mitochondrial

Chain BA: 24% 64% 20% 17%

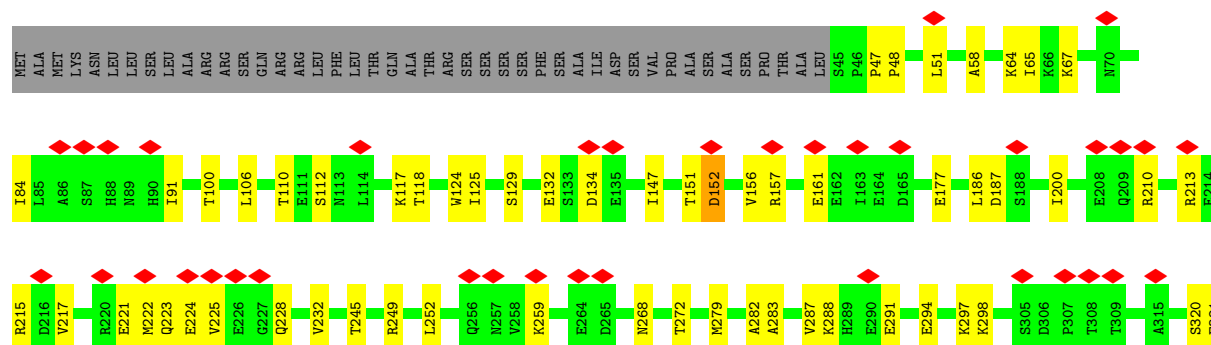
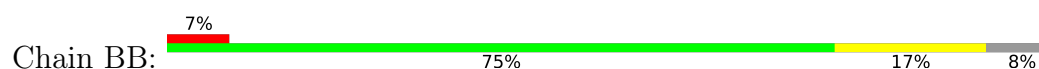


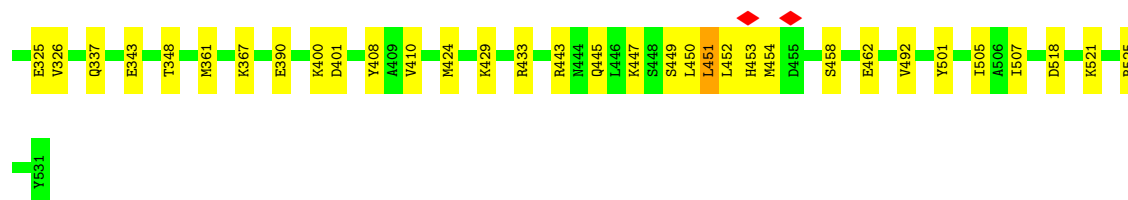


- Molecule 49: Probable mitochondrial-processing peptidase subunit beta, mitochondrial

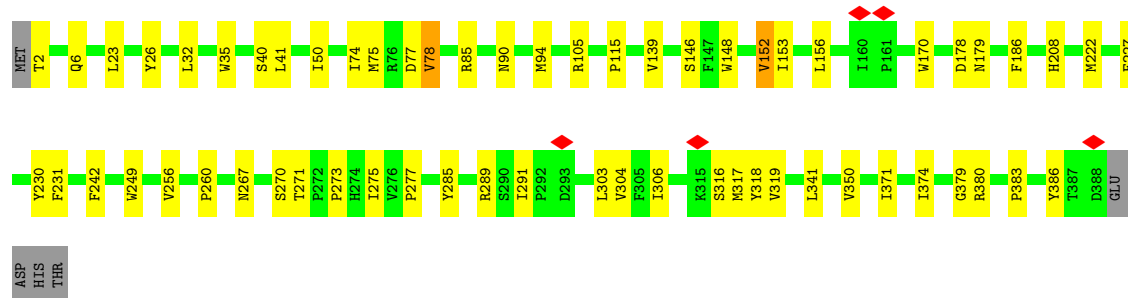
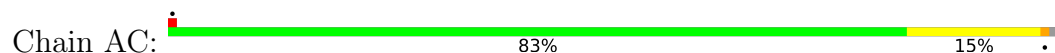


- Molecule 49: Probable mitochondrial-processing peptidase subunit beta, mitochondrial

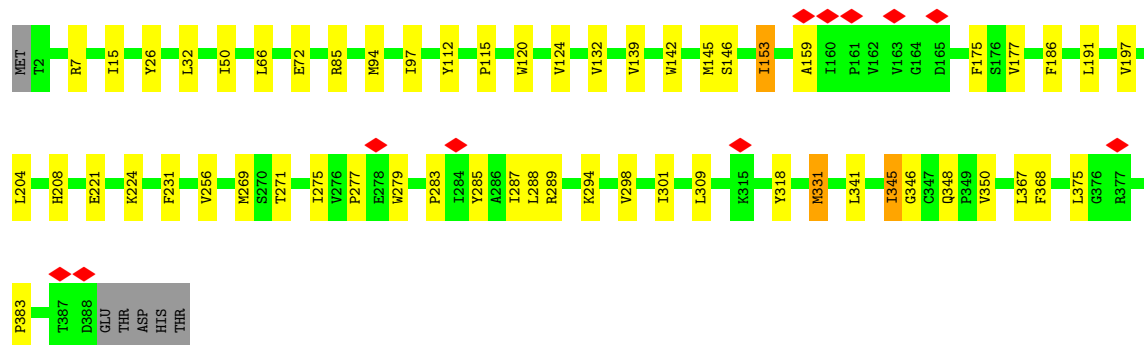
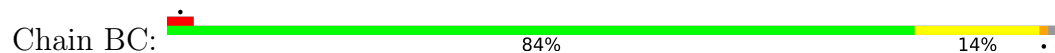




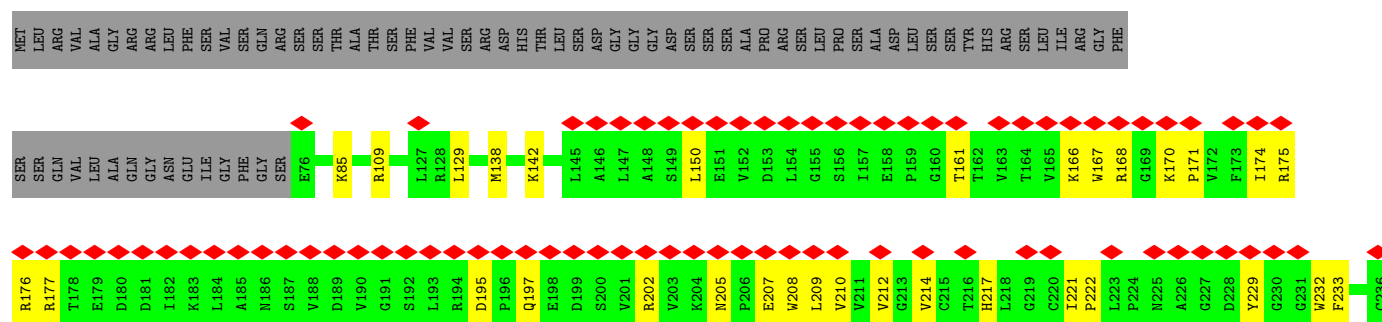
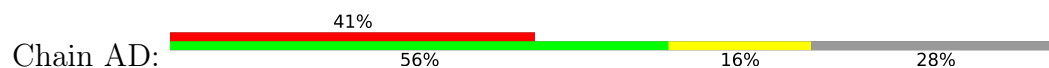
• Molecule 50: Cytochrome b

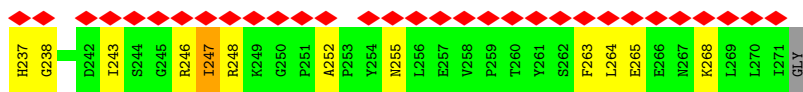


• Molecule 50: Cytochrome b

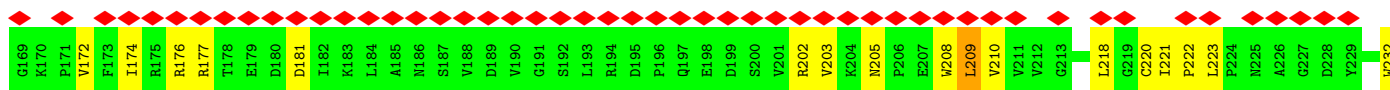
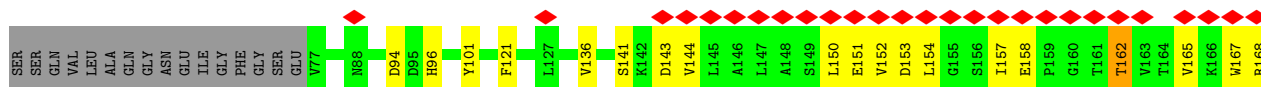
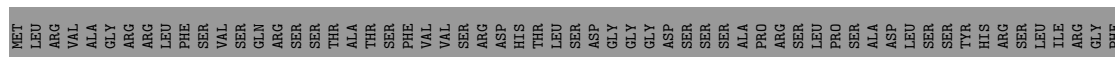
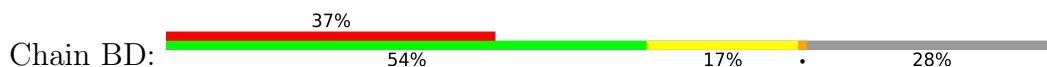


• Molecule 51: Cytochrome b-c1 complex subunit Rieske-1, mitochondrial

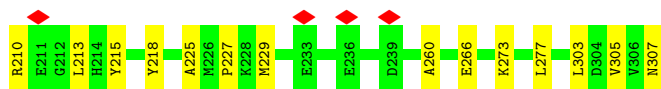
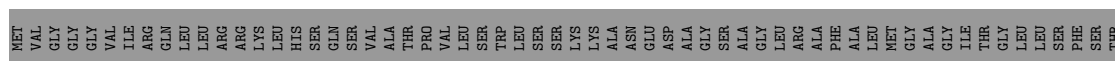




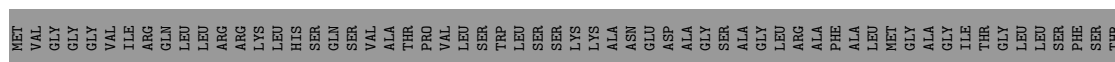
- Molecule 51: Cytochrome b-c1 complex subunit Rieske-1, mitochondrial



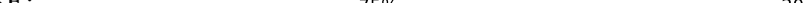
- Molecule 52: Cytochrome c1 2, heme protein, mitochondrial



- Molecule 52: Cytochrome c1 2, heme protein, mitochondrial



- Molecule 53: Cytochrome b-c1 complex subunit 7-2, mitochondrial

- Chain BF: 

MET ALA SER PHE LEU GLN R7 L8 Y9 D10 P11 M12 K13 M14 F15 L28 Y36 D36 D37 L38 L45 D46 L47 K48 P55 R56 E57 F58 R65 F66 M67 D71 K75 H76 E77 P80 L83 Y93 M97 L98 A99 L100 F101 K102 P115 R119

- Chain AG: 81% 15% .

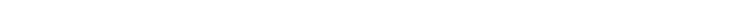
MET
GLY
LYS
Q4
P5
V6
K7
L8
A14
H36
E40
Y61
Q65
E69
F72

- Chain BG: 

Category	Count
MET	1
GLY	1
LYS	1
GLN	1
P5	1
V6	1
K7	1
K21	1
I22	1
M23	1
T24	1
W27	1
L30	1
E40	1
E64	1
Q65	1
E66	1
K67	1
L68	1
E69	1
H70	1
R71	1
F72	1

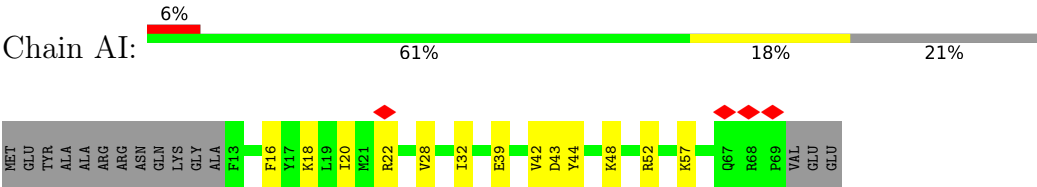
- Chain AH: 

[illegible]

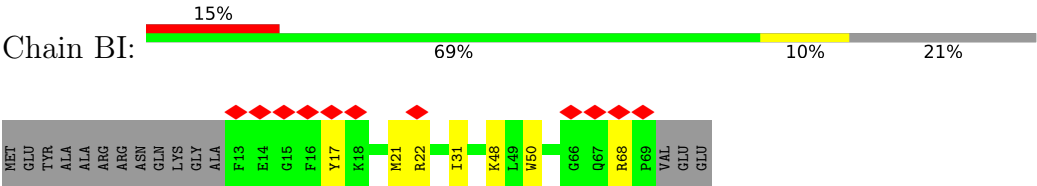
- Chain BH: 

[illegible]

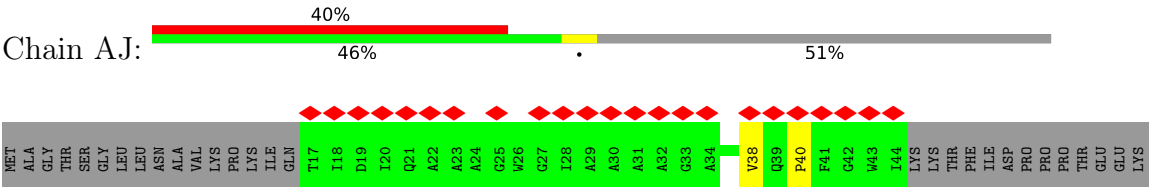
- 



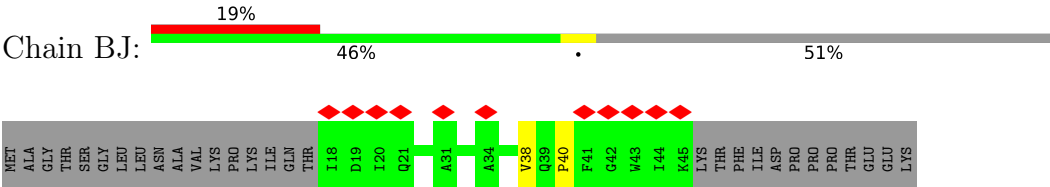
• Molecule 56: Cytochrome b-c1 complex subunit 9, mitochondrial



• Molecule 57: Cytochrome b-c1 complex subunit 10, mitochondrial



• Molecule 57: Cytochrome b-c1 complex subunit 10, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	50886	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	215000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.088	Depositor
Minimum map value	-0.037	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.013	Depositor
Map size (Å)	429.75, 429.75, 429.75	wwPDB
Map dimensions	750, 750, 750	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.573, 0.573, 0.573	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FE, NDP, UQ5, SF4, FME, FES, 8Q1, HEM, COO, UQ7, UQ9, FMN, 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	0.48	0/820	0.68	0/1113
2	B	0.38	0/1279	0.56	0/1734
3	C	0.39	0/1590	0.53	0/2152
4	D	0.48	0/3149	0.71	3/4259 (0.1%)
5	E	0.29	0/1535	0.53	1/2084 (0.0%)
6	F	0.25	0/3441	0.41	0/4641
7	G	0.41	0/5338	0.57	0/7231
8	H	0.49	1/2609 (0.0%)	0.70	0/3553
9	I	0.28	0/1378	0.43	0/1862
10	J	0.36	0/1435	0.56	0/1957
11	K	0.47	0/785	0.69	0/1062
12	L	0.38	0/5368	0.58	0/7291
13	M	0.42	0/4057	0.62	0/5513
14	N	0.43	0/3937	0.69	2/5345 (0.0%)
15	O	0.31	0/979	0.46	0/1326
16	P	0.48	0/2509	0.65	0/3401
17	Q	0.18	0/862	0.35	0/1166
18	R	0.21	0/585	0.37	0/793
19	S	0.29	0/739	0.41	0/996
20	T	0.70	0/671	0.92	0/911
21	U	0.94	0/687	1.20	2/929 (0.2%)
22	V	0.21	0/1146	0.38	0/1555
23	W	0.55	0/923	0.74	0/1249
24	X	0.49	0/790	0.72	0/1060
25	Y	0.28	0/944	0.60	1/1277 (0.1%)
26	Z	0.31	0/1027	0.51	2/1392 (0.1%)
27	a	0.22	0/481	0.38	0/646
28	b	0.31	0/320	0.48	0/434
29	c	0.42	0/637	0.58	0/860
30	d	0.58	0/605	0.83	2/815 (0.2%)
31	e	0.35	0/567	0.50	0/755
32	f	0.24	0/771	0.38	0/1042

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.24	0/661	0.44	0/899
34	i	0.37	0/741	0.59	0/997
35	j	0.50	0/433	0.69	1/592 (0.2%)
36	k	0.30	0/392	0.47	0/526
37	l	0.45	0/575	0.64	0/781
38	m	0.43	0/592	0.60	0/793
39	n	0.45	0/938	0.60	0/1273
40	o	0.38	1/666 (0.2%)	0.58	0/886
41	p	0.45	0/777	0.68	0/1043
42	q	0.20	0/690	0.38	0/936
43	u	0.50	0/472	0.75	0/632
44	v	0.27	0/222	0.42	0/300
45	x	0.24	0/1669	0.44	0/2279
46	y	0.28	0/2046	0.44	0/2772
47	z	0.39	0/1804	0.62	0/2441
48	AA	0.36	1/3265 (0.0%)	0.56	0/4431
48	BA	0.31	0/3266	0.54	0/4433
49	AB	0.25	0/3908	0.45	0/5305
49	BB	0.23	0/3908	0.41	0/5305
50	AC	0.30	0/3208	0.47	0/4395
50	BC	0.27	0/3208	0.45	0/4395
51	AD	0.31	0/1567	0.48	0/2135
51	BD	0.29	0/1558	0.46	0/2123
52	AE	0.35	0/1968	0.51	1/2672 (0.0%)
52	BE	0.24	0/1968	0.38	0/2672
53	AF	0.25	0/993	0.46	1/1336 (0.1%)
53	BF	0.27	0/993	0.38	0/1336
54	AG	0.18	0/600	0.39	0/815
54	BG	0.17	0/591	0.37	0/802
55	AH	0.53	0/531	0.71	0/713
55	BH	0.17	0/524	0.35	0/703
56	AI	0.49	0/488	0.73	0/655
56	BI	0.36	0/488	0.52	0/655
57	AJ	0.19	0/210	0.37	0/290
57	BJ	0.18	0/212	0.35	0/291
All	All	0.37	3/98096 (0.0%)	0.56	16/133016 (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
14	N	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	83	MET	SD-CE	-7.41	1.61	1.79
40	o	75	LYS	C-O	-5.11	1.18	1.24
48	AA	284	VAL	N-CA	5.03	1.49	1.45

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	179	PRO	N-CA-C	-10.29	93.65	110.74
14	N	287	GLY	N-CA-C	6.97	120.02	111.45
4	D	73	VAL	N-CA-C	-6.60	105.70	113.42
4	D	25	VAL	N-CA-C	-5.86	106.61	112.17
53	AF	40	ASP	CA-CB-CG	5.86	118.46	112.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	N	412[B]	TYR	Mainchain

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	802	0	817	32	0
2	B	1244	0	1231	32	0
3	C	1545	0	1501	31	0
4	D	3079	0	3049	70	0
5	E	1500	0	1473	39	0
6	F	3368	0	3354	48	0
7	G	5243	0	5228	99	0
8	H	2536	0	2641	56	0
9	I	1349	0	1293	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	1399	0	1472	46	0
11	K	784	0	843	31	0
12	L	5222	0	5253	101	0
13	M	3946	0	4086	139	0
14	N	3832	0	3934	107	0
15	O	963	0	975	14	0
16	P	2453	0	2493	45	0
17	Q	837	0	818	18	0
18	R	571	0	559	6	0
19	S	727	0	759	26	0
20	T	659	0	644	26	0
21	U	677	0	665	11	0
22	V	1123	0	1112	13	0
23	W	904	0	901	23	0
24	X	776	0	777	16	0
25	Y	928	0	960	43	0
26	Z	997	0	979	15	0
27	a	469	0	472	18	0
28	b	315	0	338	11	0
29	c	617	0	619	23	0
30	d	592	0	610	18	0
31	e	554	0	522	14	0
32	f	765	0	766	8	0
33	g	641	0	632	10	0
34	i	721	0	695	18	0
35	j	415	0	406	25	0
36	k	382	0	380	18	0
37	l	562	0	567	10	0
38	m	577	0	564	36	0
39	n	911	0	879	32	0
40	o	657	0	669	23	0
41	p	757	0	743	18	0
42	q	669	0	630	9	0
43	u	463	0	471	21	0
44	v	219	0	227	3	0
45	x	1629	0	1636	18	0
46	y	2013	0	2024	33	0
47	z	1772	0	1771	37	0
48	AA	3201	0	3201	125	0
48	BA	3202	0	3203	92	0
49	AB	3834	0	3797	65	0
49	BB	3834	0	3797	70	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	AC	3093	0	3074	67	0
50	BC	3093	0	3074	51	0
51	AD	1528	0	1529	63	0
51	BD	1519	0	1524	42	0
52	AE	1917	0	1844	34	0
52	BE	1917	0	1844	34	0
53	AF	976	0	1001	30	0
53	BF	976	0	1001	18	0
54	AG	581	0	589	25	0
54	BG	572	0	582	7	0
55	AH	518	0	518	9	0
55	BH	511	0	511	9	0
56	AI	476	0	469	12	0
56	BI	476	0	469	8	0
57	AJ	203	0	197	1	0
57	BJ	205	0	203	1	0
58	B	8	0	0	1	0
58	F	8	0	0	2	0
58	G	16	0	0	0	0
58	I	16	0	0	2	0
59	AD	4	0	0	1	0
59	BD	4	0	0	2	0
59	E	4	0	0	1	0
59	G	4	0	0	0	0
60	F	31	0	19	1	0
61	H	35	0	43	6	0
62	O	1	0	0	0	0
63	P	48	0	26	2	0
64	AB	1	0	0	0	0
64	BB	1	0	0	0	0
64	R	1	0	0	0	0
64	y	1	0	0	0	0
65	W	35	0	0	0	0
65	n	35	0	0	0	0
66	y	53	0	35	14	0
67	AC	86	0	60	4	0
67	AE	43	0	30	4	0
67	BC	86	0	60	3	0
67	BE	43	0	30	10	0
68	AC	76	0	100	13	0
68	BC	38	0	50	6	0
69	BC	48	0	66	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	96522	0	96384	1896	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 10.

The worst 5 of 1896 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)
50:AC:222:MET:SD	54:AG:6:VAL:HG11	1.43	1.55
13:M:279:PHE:CE1	38:m:71:LEU:CD2	1.96	1.49
20:T:95:LEU:CD2	20:T:118:HIS:CD2	2.05	1.40
13:M:279:PHE:CE1	38:m:71:LEU:HD22	1.57	1.39
50:AC:222:MET:SD	54:AG:6:VAL:CG1	2.07	1.39

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	90/119 (76%)	88 (98%)	2 (2%)	0	100	100
2	B	24/218 (11%)	24 (100%)	0	0	100	100
3	C	5/190 (3%)	5 (100%)	0	0	100	100
4	D	378/394 (96%)	362 (96%)	15 (4%)	1 (0%)	36	66
5	E	190/255 (74%)	181 (95%)	9 (5%)	0	100	100
6	F	432/486 (89%)	420 (97%)	12 (3%)	0	100	100
7	G	685/748 (92%)	665 (97%)	20 (3%)	0	100	100
8	H	322/325 (99%)	316 (98%)	6 (2%)	0	100	100
9	I	163/222 (73%)	162 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	J	172/205 (84%)	170 (99%)	2 (1%)	0	100	100
11	K	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
12	L	405/669 (60%)	393 (97%)	12 (3%)	0	100	100
18	R	15/110 (14%)	14 (93%)	1 (7%)	0	100	100
19	S	91/97 (94%)	90 (99%)	1 (1%)	0	100	100
20	T	54/122 (44%)	51 (94%)	3 (6%)	0	100	100
21	U	19/126 (15%)	19 (100%)	0	0	100	100
22	V	1/169 (1%)	1 (100%)	0	0	100	100
23	W	93/133 (70%)	88 (95%)	5 (5%)	0	100	100
24	X	96/106 (91%)	94 (98%)	2 (2%)	0	100	100
25	Y	108/159 (68%)	104 (96%)	4 (4%)	0	100	100
26	Z	84/143 (59%)	80 (95%)	4 (5%)	0	100	100
27	a	56/65 (86%)	56 (100%)	0	0	100	100
28	b	41/65 (63%)	39 (95%)	2 (5%)	0	100	100
29	c	74/88 (84%)	71 (96%)	3 (4%)	0	100	100
30	d	73/81 (90%)	71 (97%)	2 (3%)	0	100	100
31	e	63/83 (76%)	62 (98%)	1 (2%)	0	100	100
32	f	99/106 (93%)	97 (98%)	2 (2%)	0	100	100
33	g	77/114 (68%)	76 (99%)	1 (1%)	0	100	100
34	i	81/98 (83%)	79 (98%)	2 (2%)	0	100	100
35	j	49/69 (71%)	48 (98%)	1 (2%)	0	100	100
36	k	46/72 (64%)	45 (98%)	1 (2%)	0	100	100
37	l	70/125 (56%)	68 (97%)	2 (3%)	0	100	100
38	m	68/71 (96%)	65 (96%)	3 (4%)	0	100	100
39	n	107/117 (92%)	105 (98%)	2 (2%)	0	100	100
40	o	78/103 (76%)	75 (96%)	3 (4%)	0	100	100
41	p	88/106 (83%)	86 (98%)	2 (2%)	0	100	100
42	q	79/159 (50%)	75 (95%)	4 (5%)	0	100	100
43	u	53/63 (84%)	50 (94%)	3 (6%)	0	100	100
44	v	27/113 (24%)	26 (96%)	1 (4%)	0	100	100
45	x	208/256 (81%)	206 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	y	263/278 (95%)	261 (99%)	2 (1%)	0	100	100
47	z	231/275 (84%)	228 (99%)	3 (1%)	0	100	100
48	AA	296/503 (59%)	287 (97%)	9 (3%)	0	100	100
48	BA	416/503 (83%)	402 (97%)	14 (3%)	0	100	100
49	AB	485/531 (91%)	473 (98%)	12 (2%)	0	100	100
49	BB	485/531 (91%)	478 (99%)	7 (1%)	0	100	100
50	AC	385/393 (98%)	378 (98%)	7 (2%)	0	100	100
50	BC	385/393 (98%)	377 (98%)	8 (2%)	0	100	100
51	AD	194/272 (71%)	181 (93%)	13 (7%)	0	100	100
51	BD	193/272 (71%)	182 (94%)	11 (6%)	0	100	100
52	AE	242/307 (79%)	239 (99%)	3 (1%)	0	100	100
52	BE	242/307 (79%)	240 (99%)	2 (1%)	0	100	100
53	AF	114/122 (93%)	113 (99%)	1 (1%)	0	100	100
53	BF	114/122 (93%)	113 (99%)	1 (1%)	0	100	100
54	AG	67/72 (93%)	67 (100%)	0	0	100	100
54	BG	66/72 (92%)	66 (100%)	0	0	100	100
55	AH	62/69 (90%)	60 (97%)	2 (3%)	0	100	100
55	BH	61/69 (88%)	59 (97%)	2 (3%)	0	100	100
56	AI	55/72 (76%)	53 (96%)	2 (4%)	0	100	100
56	BI	55/72 (76%)	53 (96%)	2 (4%)	0	100	100
57	AJ	26/57 (46%)	26 (100%)	0	0	100	100
57	BJ	26/57 (46%)	24 (92%)	2 (8%)	0	100	100
All	All	9425/12399 (76%)	9184 (97%)	240 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	23	HIS

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	85/105 (81%)	85 (100%)	0	100	100
2	B	132/184 (72%)	128 (97%)	4 (3%)	36	72
3	C	171/179 (96%)	170 (99%)	1 (1%)	78	92
4	D	331/340 (97%)	327 (99%)	4 (1%)	63	87
5	E	166/220 (76%)	165 (99%)	1 (1%)	78	92
6	F	353/396 (89%)	353 (100%)	0	100	100
7	G	570/625 (91%)	561 (98%)	9 (2%)	55	83
8	H	271/272 (100%)	268 (99%)	3 (1%)	65	87
9	I	147/195 (75%)	146 (99%)	1 (1%)	76	91
10	J	156/186 (84%)	153 (98%)	3 (2%)	50	81
11	K	85/85 (100%)	83 (98%)	2 (2%)	43	77
12	L	564/568 (99%)	555 (98%)	9 (2%)	55	83
13	M	433/434 (100%)	427 (99%)	6 (1%)	59	85
14	N	407/416 (98%)	402 (99%)	5 (1%)	63	87
15	O	108/141 (77%)	106 (98%)	2 (2%)	50	81
16	P	263/334 (79%)	258 (98%)	5 (2%)	50	81
17	Q	89/128 (70%)	89 (100%)	0	100	100
18	R	64/97 (66%)	64 (100%)	0	100	100
19	S	82/85 (96%)	80 (98%)	2 (2%)	43	77
20	T	78/112 (70%)	77 (99%)	1 (1%)	61	86
21	U	78/113 (69%)	75 (96%)	3 (4%)	29	64
22	V	123/148 (83%)	123 (100%)	0	100	100
23	W	98/114 (86%)	93 (95%)	5 (5%)	21	54
24	X	88/94 (94%)	87 (99%)	1 (1%)	65	87
25	Y	92/120 (77%)	88 (96%)	4 (4%)	26	60
26	Z	100/115 (87%)	96 (96%)	4 (4%)	28	63
27	a	48/53 (91%)	48 (100%)	0	100	100
28	b	35/53 (66%)	33 (94%)	2 (6%)	18	49
29	c	66/71 (93%)	65 (98%)	1 (2%)	57	84
30	d	60/66 (91%)	59 (98%)	1 (2%)	53	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	e	60/73 (82%)	60 (100%)	0	100	100
32	f	80/83 (96%)	80 (100%)	0	100	100
33	g	68/96 (71%)	67 (98%)	1 (2%)	57	84
34	i	75/90 (83%)	74 (99%)	1 (1%)	61	86
35	j	42/51 (82%)	40 (95%)	2 (5%)	23	56
36	k	39/60 (65%)	37 (95%)	2 (5%)	21	54
37	l	60/97 (62%)	59 (98%)	1 (2%)	53	83
38	m	58/59 (98%)	57 (98%)	1 (2%)	53	83
39	n	92/99 (93%)	90 (98%)	2 (2%)	45	78
40	o	70/87 (80%)	69 (99%)	1 (1%)	59	85
41	p	80/93 (86%)	77 (96%)	3 (4%)	29	64
42	q	69/133 (52%)	68 (99%)	1 (1%)	59	85
43	u	47/54 (87%)	45 (96%)	2 (4%)	26	60
44	v	22/84 (26%)	22 (100%)	0	100	100
45	x	179/216 (83%)	178 (99%)	1 (1%)	78	92
46	y	221/232 (95%)	220 (100%)	1 (0%)	81	93
47	z	188/228 (82%)	185 (98%)	3 (2%)	55	83
48	AA	347/408 (85%)	334 (96%)	13 (4%)	30	65
48	BA	347/408 (85%)	341 (98%)	6 (2%)	53	83
49	AB	415/452 (92%)	410 (99%)	5 (1%)	63	87
49	BB	415/452 (92%)	410 (99%)	5 (1%)	63	87
50	AC	330/336 (98%)	325 (98%)	5 (2%)	57	84
50	BC	330/336 (98%)	322 (98%)	8 (2%)	43	77
51	AD	170/232 (73%)	168 (99%)	2 (1%)	63	87
51	BD	169/232 (73%)	166 (98%)	3 (2%)	51	82
52	AE	200/247 (81%)	197 (98%)	3 (2%)	57	84
52	BE	200/247 (81%)	197 (98%)	3 (2%)	57	84
53	AF	105/110 (96%)	103 (98%)	2 (2%)	50	81
53	BF	105/110 (96%)	102 (97%)	3 (3%)	37	73
54	AG	63/65 (97%)	63 (100%)	0	100	100
54	BG	62/65 (95%)	62 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	AH	58/62 (94%)	58 (100%)	0	100	100
55	BH	57/62 (92%)	57 (100%)	0	100	100
56	AI	48/59 (81%)	47 (98%)	1 (2%)	47	79
56	BI	48/59 (81%)	48 (100%)	0	100	100
57	AJ	16/41 (39%)	16 (100%)	0	100	100
57	BJ	16/41 (39%)	16 (100%)	0	100	100
All	All	10294/11908 (86%)	10134 (98%)	160 (2%)	54	83

5 of 160 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	AB	196	VAL
50	BC	66	LEU
50	AC	78	VAL
53	AF	105	ARG
50	BC	345	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
47	z	107	HIS
52	AE	101	GLN
48	AA	320	ASN
50	AC	6	GLN
48	BA	320	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
32	FME	f	1	32	8,9,10	0.80	1 (12%)	8,9,11	1.71	1 (12%)
11	FME	K	1	11	8,9,10	0.99	0	8,9,11	1.10	0
1	FME	A	1	1	8,9,10	1.78	1 (12%)	8,9,11	1.98	3 (37%)

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
32	FME	f	1	32	-	5/7/9/11	-
11	FME	K	1	11	-	6/7/9/11	-
1	FME	A	1	1	-	0/7/9/11	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	FME	O-C	4.34	1.36	1.20
32	f	1	FME	O-C	2.13	1.28	1.20

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	f	1	FME	O-C-CA	-4.35	113.59	124.77
1	A	1	FME	O-C-CA	-4.16	114.07	124.77
1	A	1	FME	C-CA-N	2.62	114.56	109.50
1	A	1	FME	CA-N-CN	2.23	126.25	122.82

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	K	1	FME	O1-CN-N-CA
11	K	1	FME	N-CA-CB-CG
11	K	1	FME	O-C-CA-CB
32	f	1	FME	O1-CN-N-CA
32	f	1	FME	CB-CA-N-CN

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1	FME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 31 ligands modelled in this entry, 5 are monoatomic - leaving 26 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
67	HEM	AE	400	52	50,50,50	1.34	7 (14%)	67,82,82	1.16	5 (7%)
60	FMN	F	500	-	33,33,33	1.04	2 (6%)	48,50,50	1.24	6 (12%)
59	FES	BD	301	51	0,4,4	-	-	-	-	-
67	HEM	BC	501	50	50,50,50	1.66	10 (20%)	67,82,82	1.60	14 (20%)
68	UQ5	BC	502	-	38,38,38	0.46	0	48,49,49	0.69	1 (2%)
68	UQ5	AC	503	-	38,38,38	0.47	0	48,49,49	0.93	1 (2%)
58	SF4	G	802	7	0,12,12	-	-	-	-	-
65	8Q1	W	200	-	32,34,34	0.33	0	39,43,43	0.50	0
58	SF4	I	501	9	0,12,12	-	-	-	-	-
67	HEM	AC	501	50	50,50,50	1.67	8 (16%)	67,82,82	1.57	12 (17%)
67	HEM	AC	500	50	50,50,50	1.36	6 (12%)	67,82,82	1.07	3 (4%)
59	FES	G	801	7	0,4,4	-	-	-	-	-
69	UQ7	BC	503	-	48,48,48	0.45	0	60,61,61	0.59	0
63	NDP	P	500	-	51,52,52	0.52	0	71,80,80	0.67	1 (1%)
59	FES	E	500	5	0,4,4	-	-	-	-	-
66	COO	y	301	-	51,55,55	4.39	19 (37%)	73,81,81	4.16	21 (28%)
58	SF4	F	501	6	0,12,12	-	-	-	-	-
65	8Q1	n	200	-	32,34,34	0.30	0	39,43,43	0.64	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
58	SF4	G	803	7	0,12,12	-	-	-		
58	SF4	B	500	2	0,12,12	-	-	-		
58	SF4	I	500	9	0,12,12	-	-	-		
59	FES	AD	301	51	0,4,4	-	-	-		
68	UQ5	AC	502	-	38,38,38	0.52	0	48,49,49	0.74	0
67	HEM	BC	500	50	50,50,50	1.32	7 (14%)	67,82,82	1.08	6 (8%)
67	HEM	BE	400	52	50,50,50	1.29	6 (12%)	67,82,82	1.13	5 (7%)
61	UQ9	H	500	-	35,35,58	0.79	2 (5%)	43,45,73	1.01	6 (13%)

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
67	HEM	AE	400	52	-	2/14/54/54	-
60	FMN	F	500	-	-	5/18/18/18	0/3/3/3
59	FES	BD	301	51	-	-	0/1/1/1
67	HEM	BC	501	50	-	9/14/54/54	-
68	UQ5	BC	502	-	-	8/33/57/57	0/1/1/1
68	UQ5	AC	503	-	-	12/33/57/57	0/1/1/1
58	SF4	G	802	7	-	-	0/6/5/5
65	8Q1	W	200	-	-	22/41/41/41	-
58	SF4	I	501	9	-	-	0/6/5/5
67	HEM	AC	501	50	-	9/14/54/54	-
67	HEM	AC	500	50	-	4/14/54/54	-
59	FES	G	801	7	-	-	0/1/1/1
69	UQ7	BC	503	-	-	8/45/69/69	0/1/1/1
63	NDP	P	500	-	-	6/34/77/77	0/5/5/5
59	FES	E	500	5	-	-	0/1/1/1
66	COO	y	301	-	1/1/12/16	23/54/70/70	0/3/3/3
65	8Q1	n	200	-	-	21/41/41/41	-
61	UQ9	H	500	-	-	19/30/54/81	0/1/1/1
58	SF4	G	803	7	-	-	0/6/5/5
58	SF4	B	500	2	-	-	0/6/5/5
58	SF4	I	500	9	-	-	0/6/5/5
59	FES	AD	301	51	-	-	0/1/1/1
68	UQ5	AC	502	-	-	7/33/57/57	0/1/1/1
67	HEM	BC	500	50	-	2/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
67	HEM	BE	400	52	-	2/14/54/54	-
58	SF4	F	501	6	-	-	0/6/5/5

The worst 5 of 67 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	y	301	COO	C2A-N1A	-16.62	1.04	1.33
66	y	301	COO	C5A-C4A	12.91	1.62	1.39
66	y	301	COO	C2A-N3A	-9.20	1.17	1.33
66	y	301	COO	C6A-N1A	-8.32	1.12	1.35
66	y	301	COO	C5A-N7A	-7.65	1.25	1.39

The worst 5 of 82 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
66	y	301	COO	C5A-C4A-N3A	-14.87	106.24	126.72
66	y	301	COO	C6A-C5A-N7A	14.18	159.43	132.09
66	y	301	COO	C4A-C5A-N7A	-13.83	94.77	110.58
66	y	301	COO	C4A-N9A-C8A	-11.92	93.22	105.74
66	y	301	COO	C5A-C4A-N9A	8.93	115.54	105.81

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
66	y	301	COO	C13

5 of 159 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	F	500	FMN	N10-C1'-C2'-O2'
60	F	500	FMN	N10-C1'-C2'-C3'
60	F	500	FMN	C5'-O5'-P-O2P
60	F	500	FMN	C5'-O5'-P-O3P
61	H	500	UQ9	C17-C18-C19-C21

There are no ring outliers.

20 monomers are involved in 78 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
67	AE	400	HEM	4	0
60	F	500	FMN	1	0

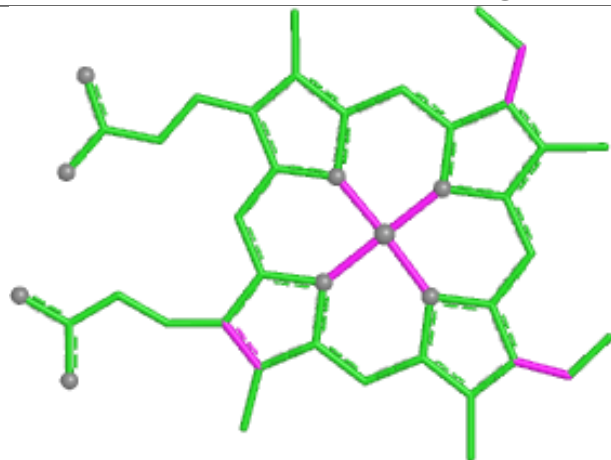
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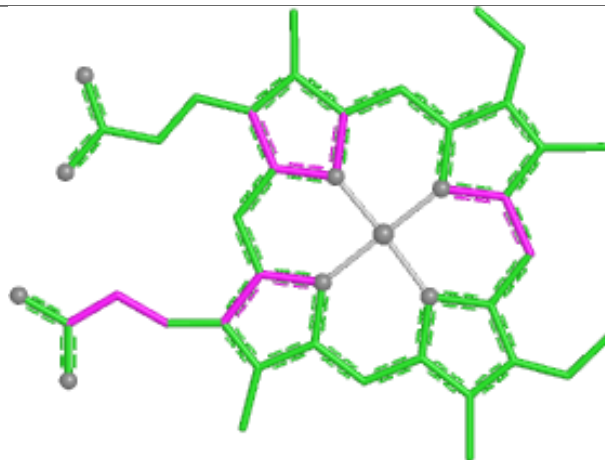
Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	BD	301	FES	2	0
67	BC	501	HEM	1	0
68	BC	502	UQ5	6	0
68	AC	503	UQ5	6	0
67	AC	501	HEM	1	0
67	AC	500	HEM	3	0
69	BC	503	UQ7	7	0
63	P	500	NDP	2	0
59	E	500	FES	1	0
66	y	301	COO	14	0
58	F	501	SF4	2	0
58	B	500	SF4	1	0
58	I	500	SF4	2	0
59	AD	301	FES	1	0
68	AC	502	UQ5	7	0
67	BC	500	HEM	2	0
67	BE	400	HEM	10	0
61	H	500	UQ9	6	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.

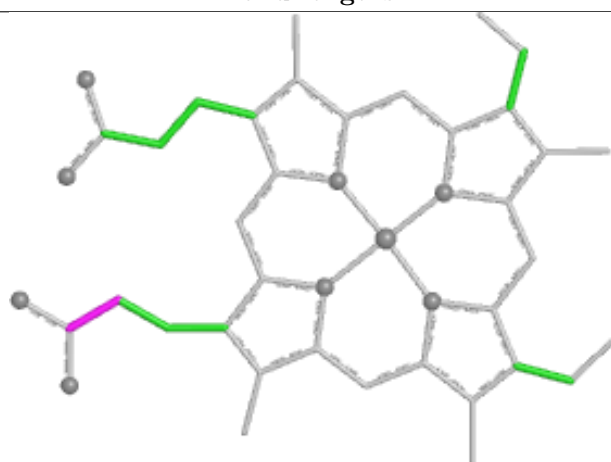
Ligand HEM AE 400



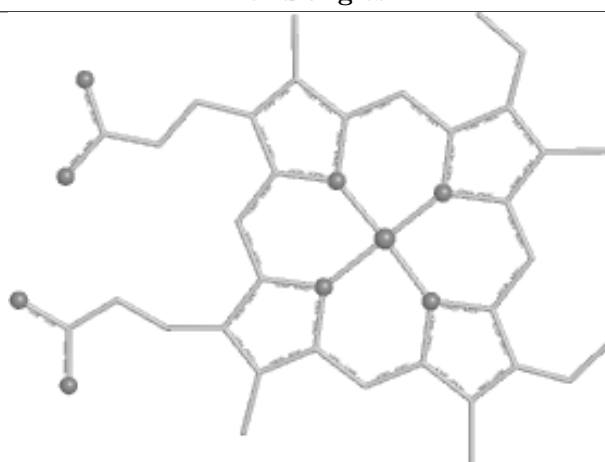
Bond lengths



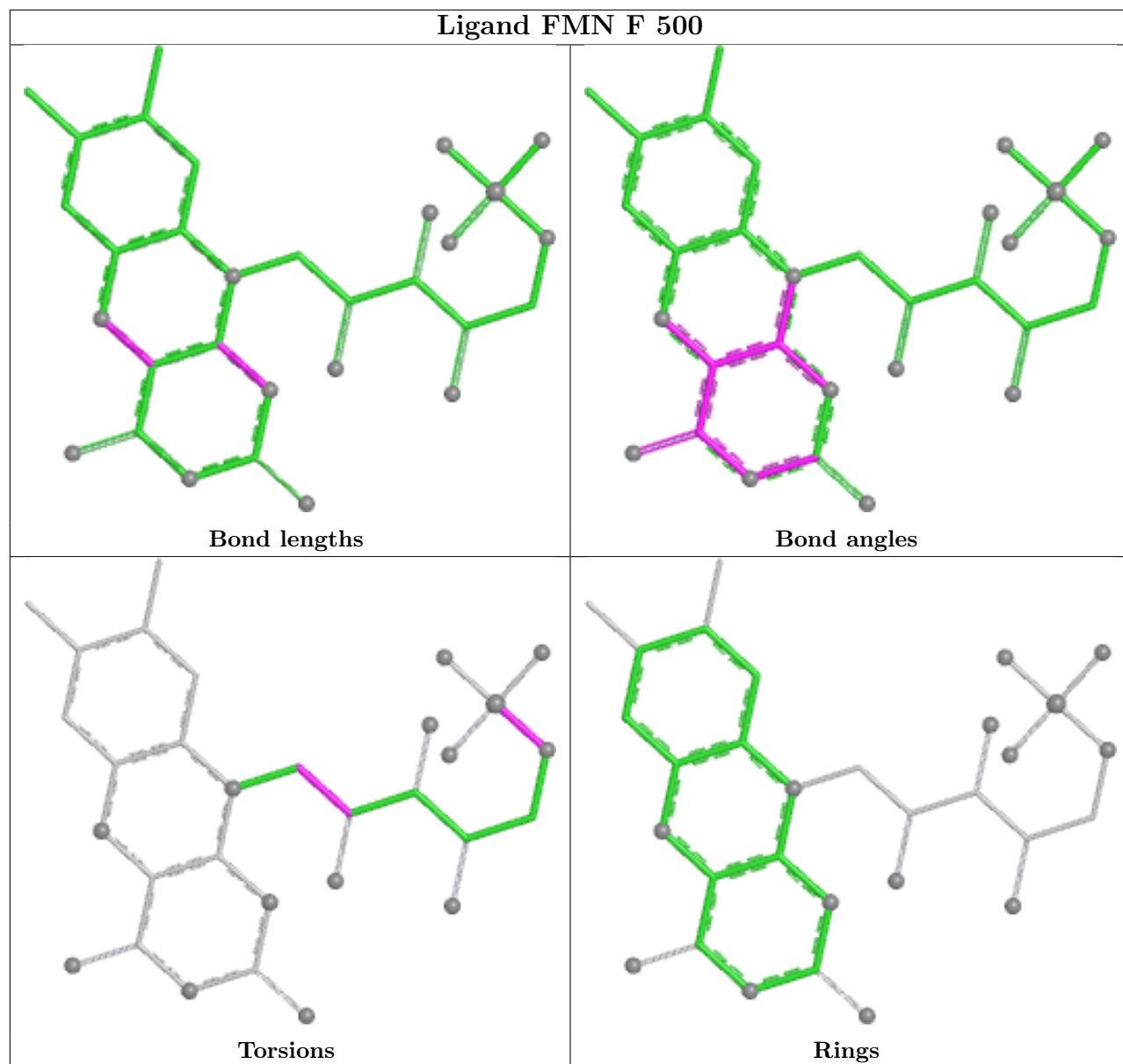
Bond angles

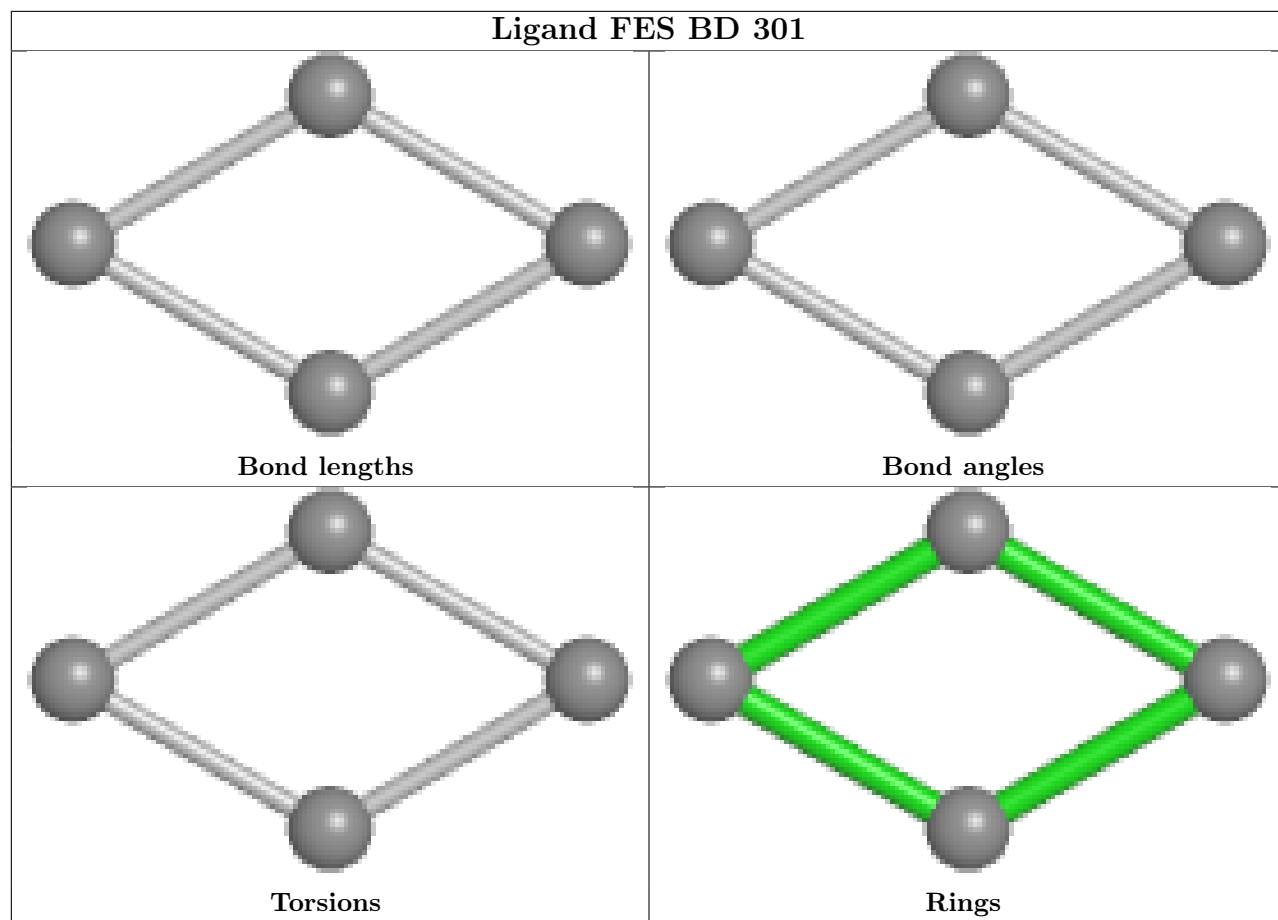


Torsions

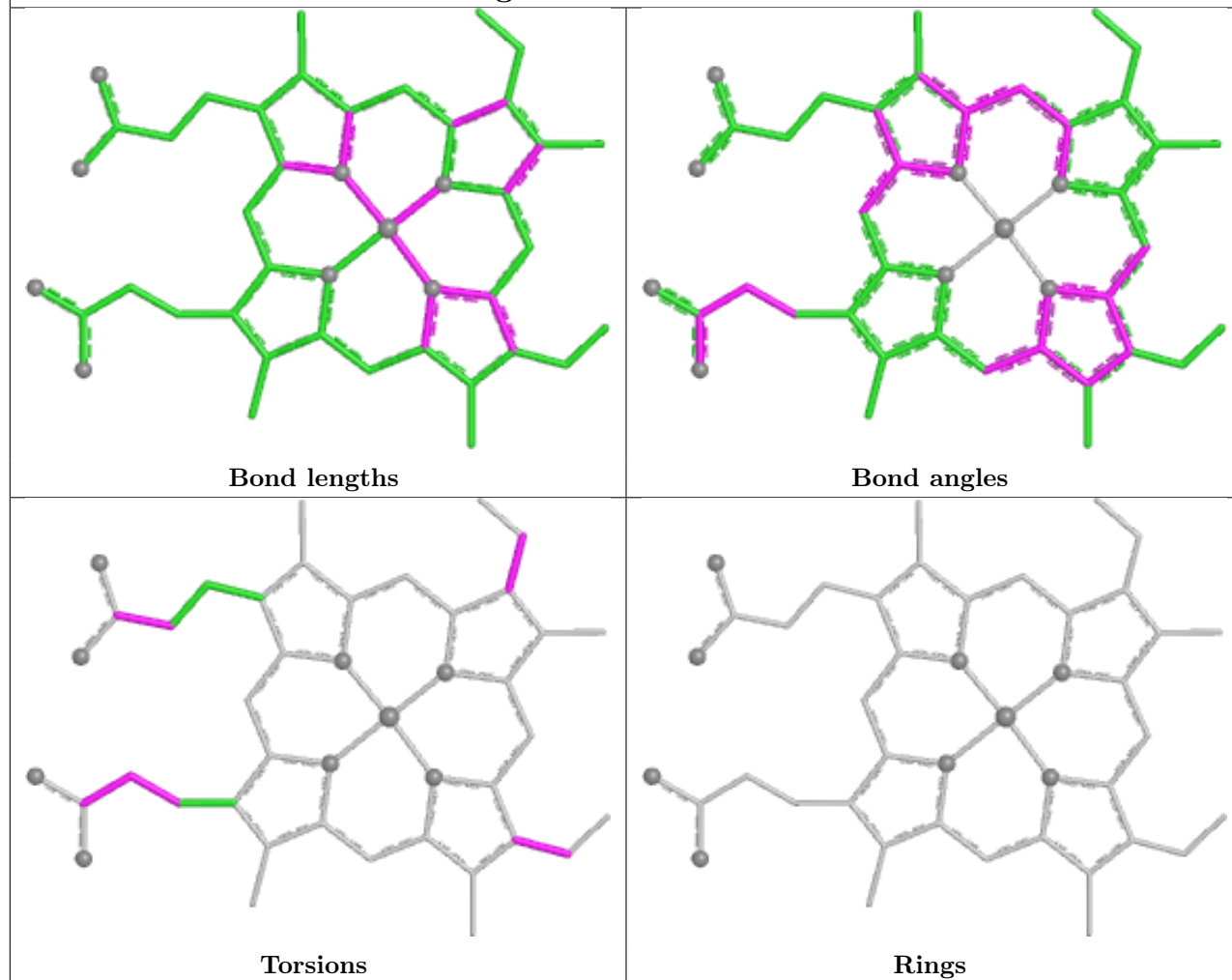


Rings

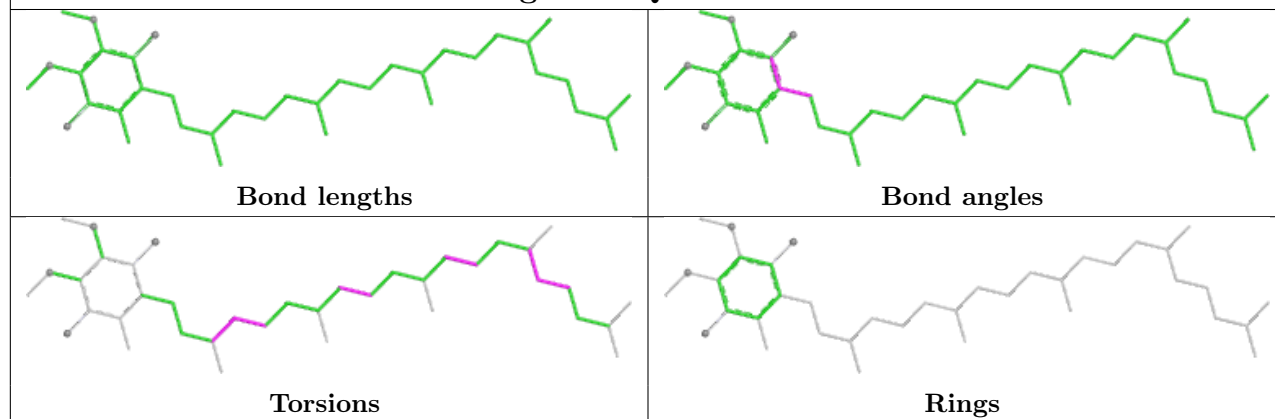


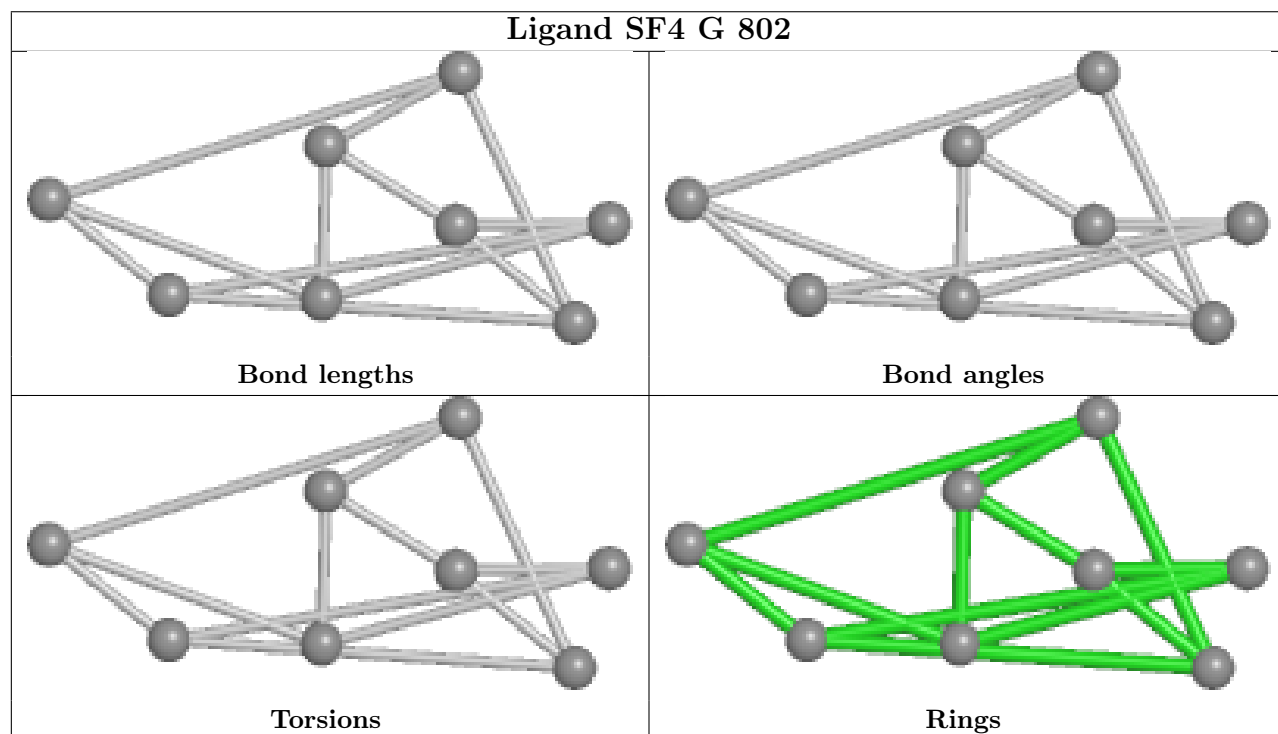
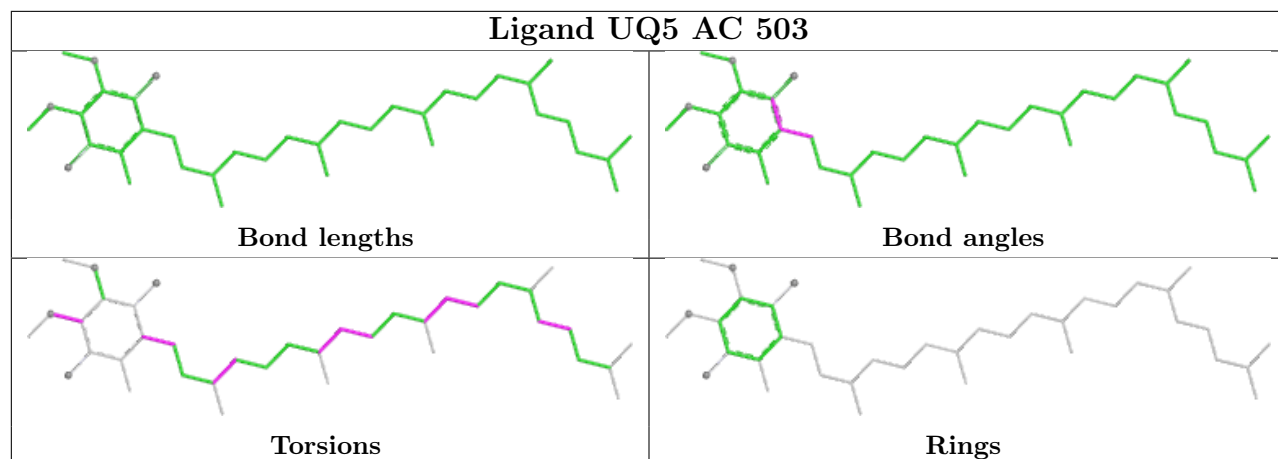


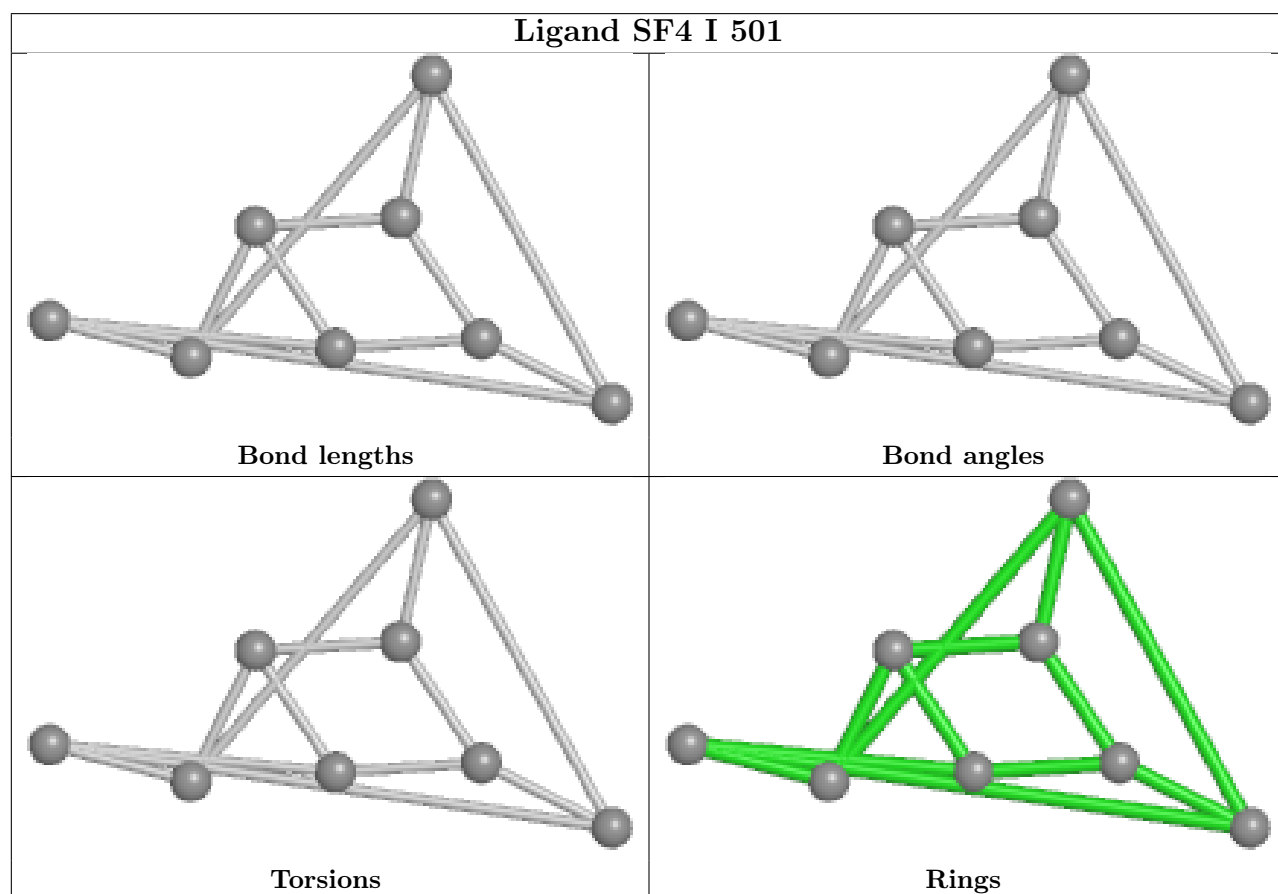
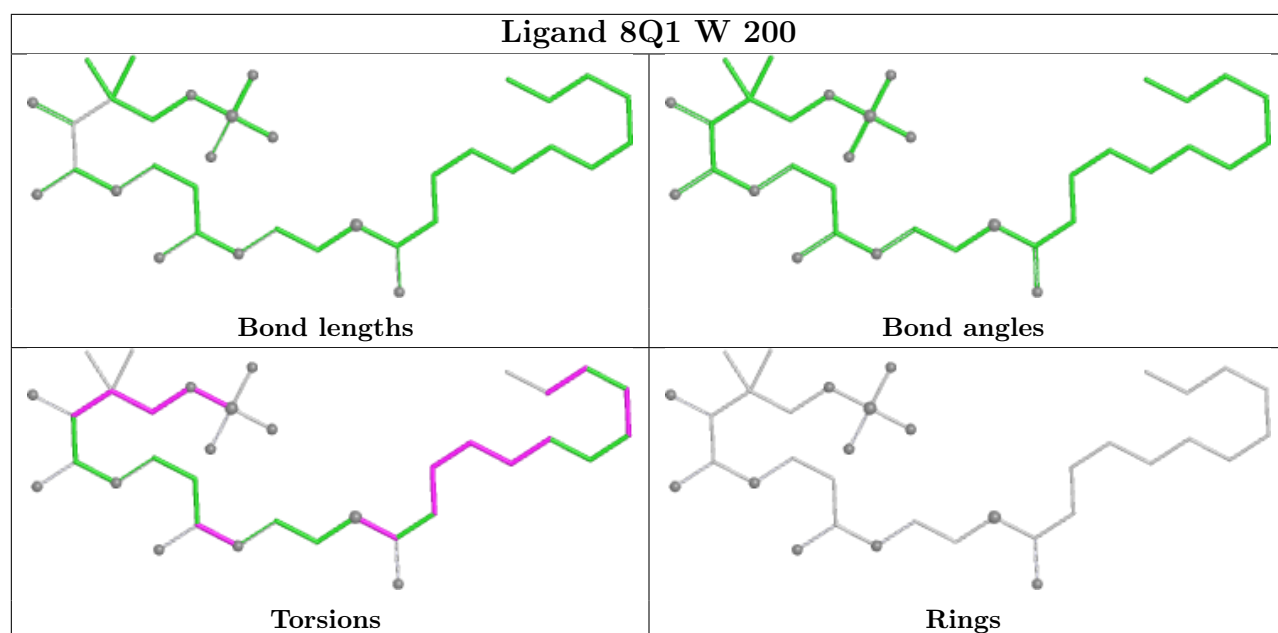
Ligand HEM BC 501



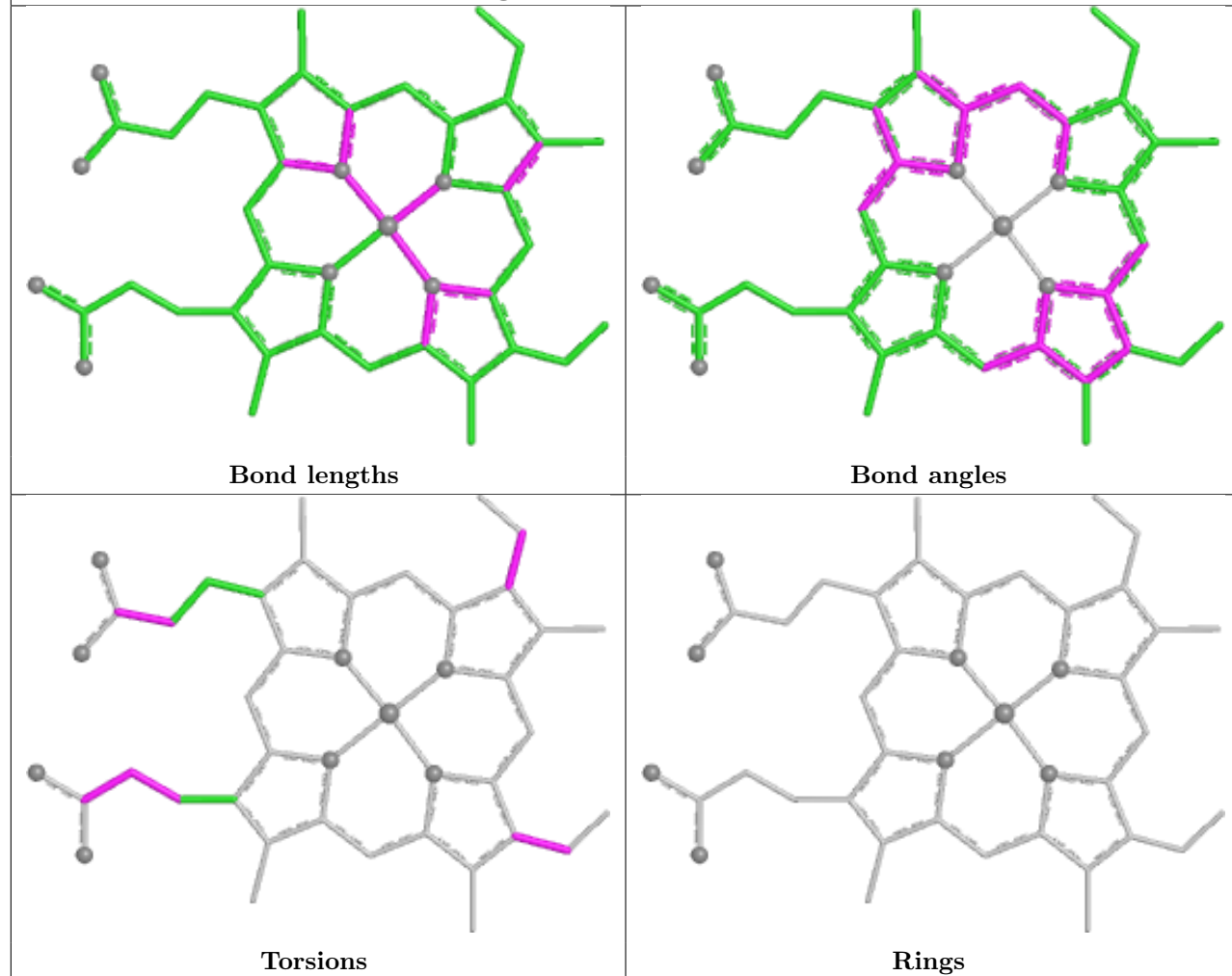
Ligand UQ5 BC 502



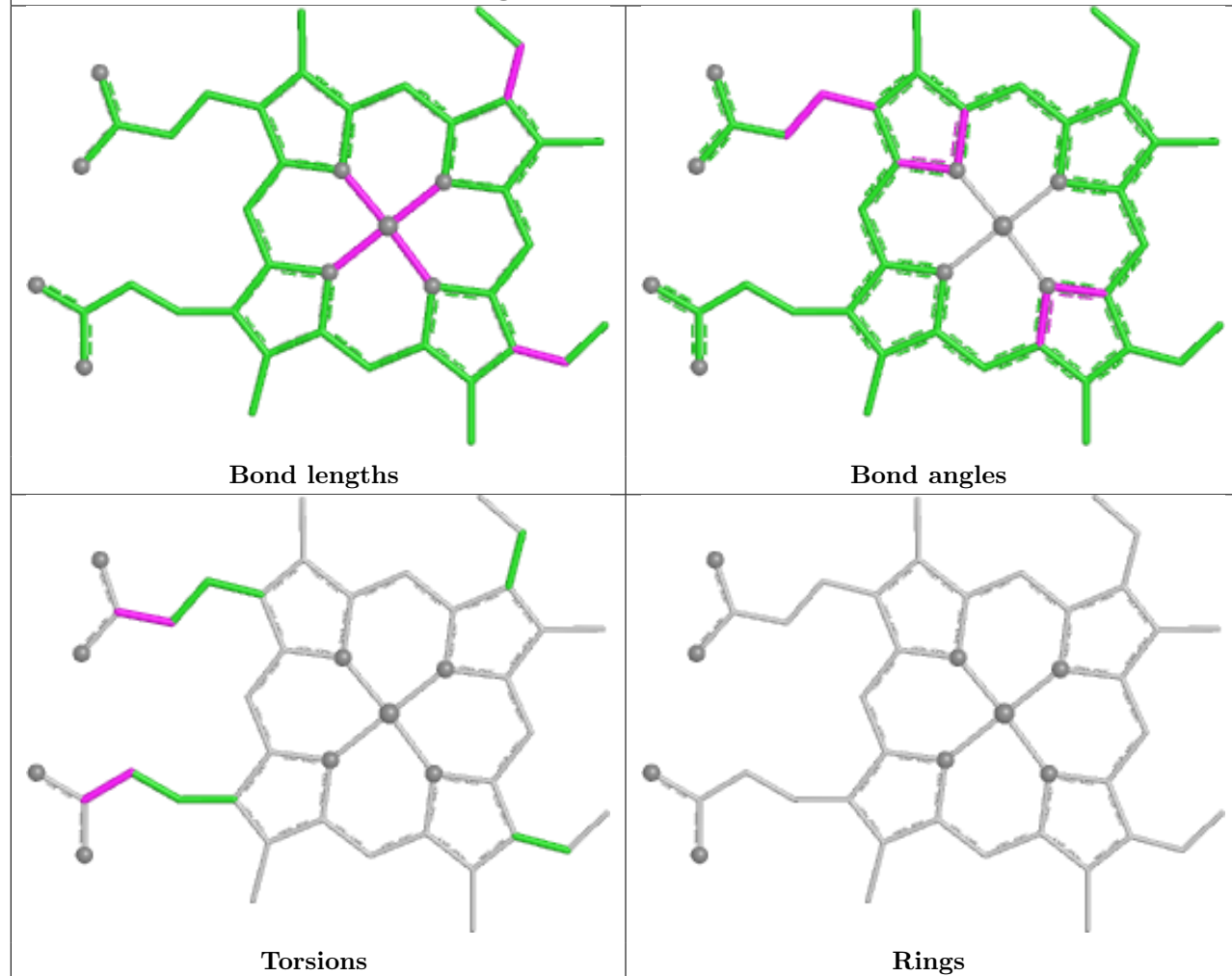


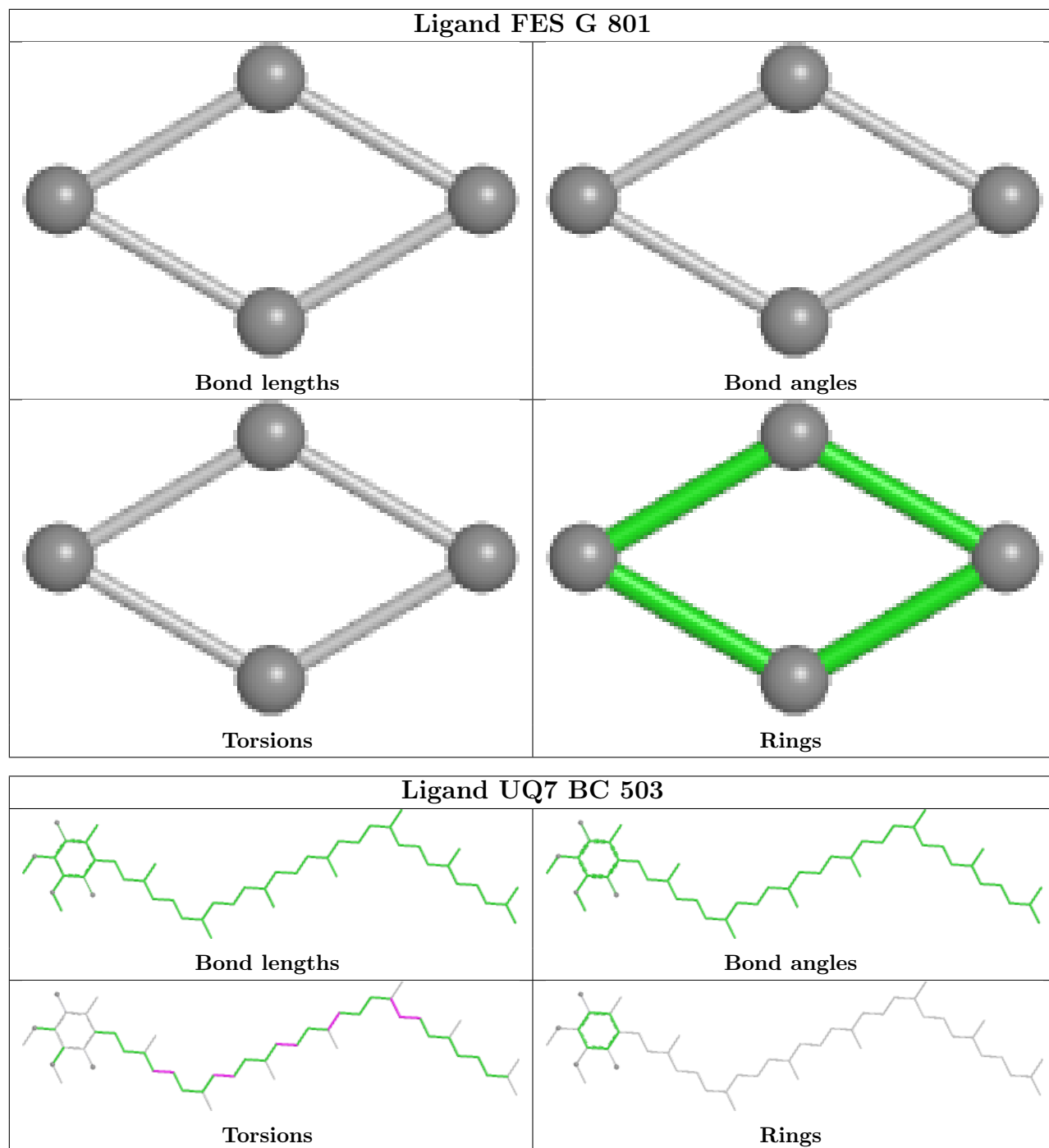


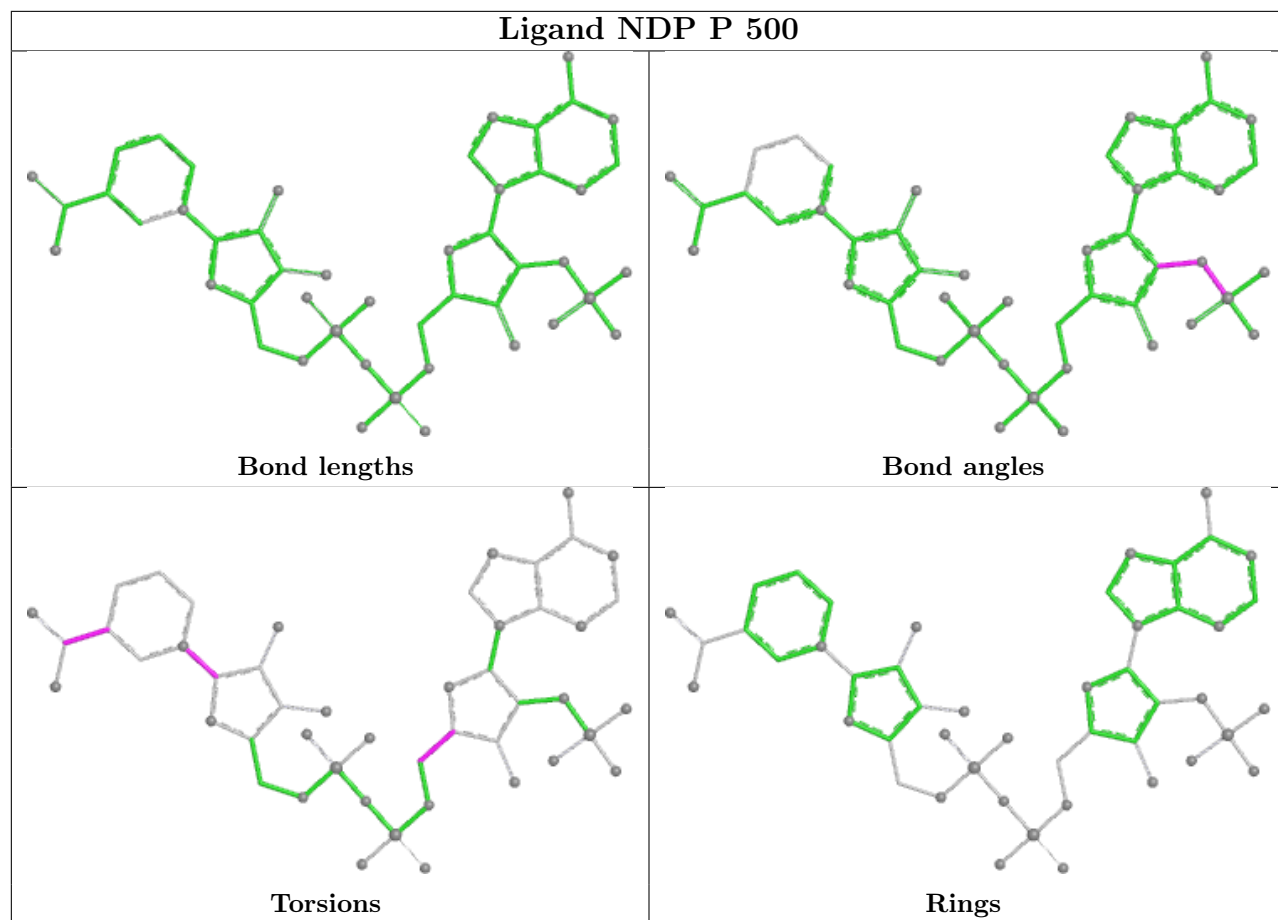
Ligand HEM AC 501

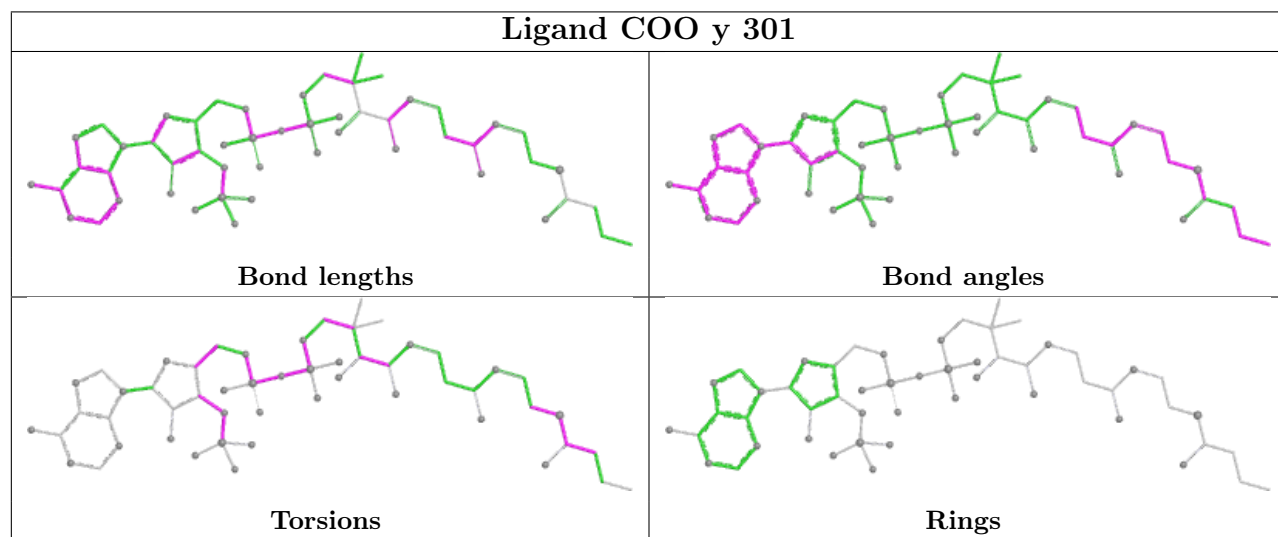
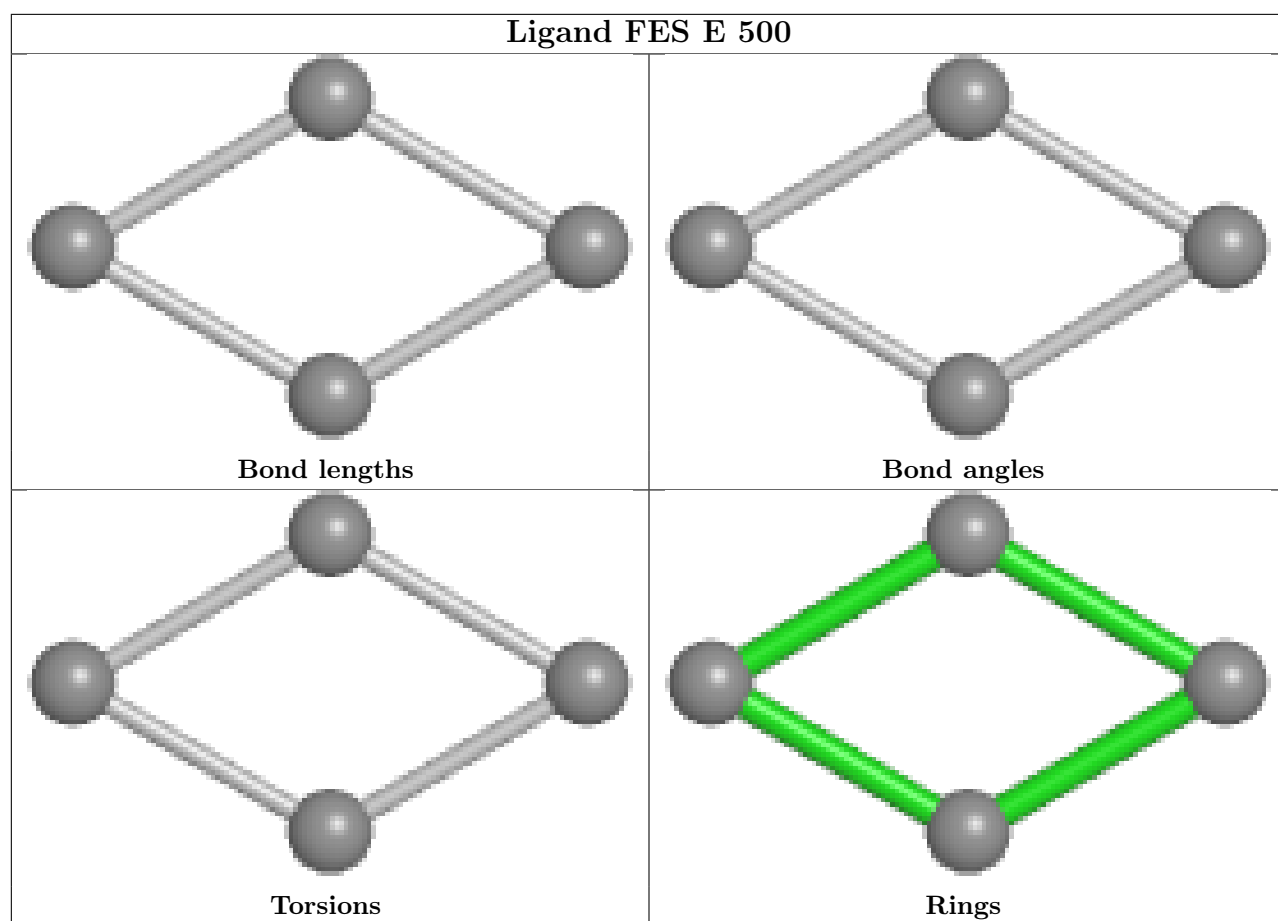


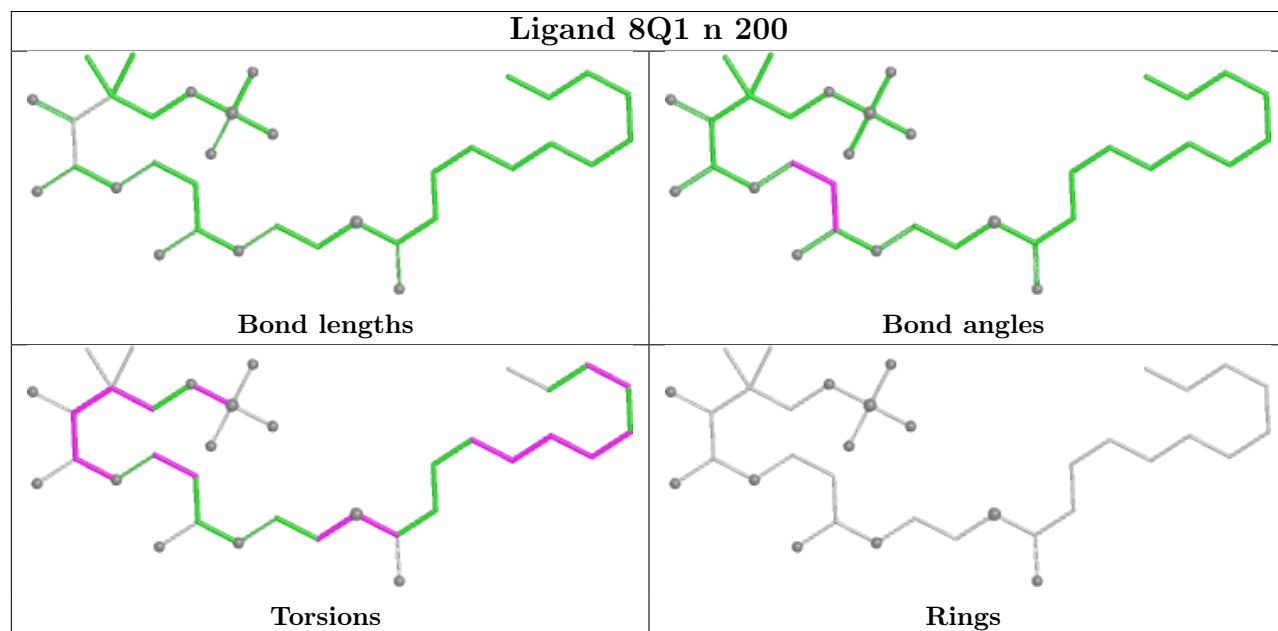
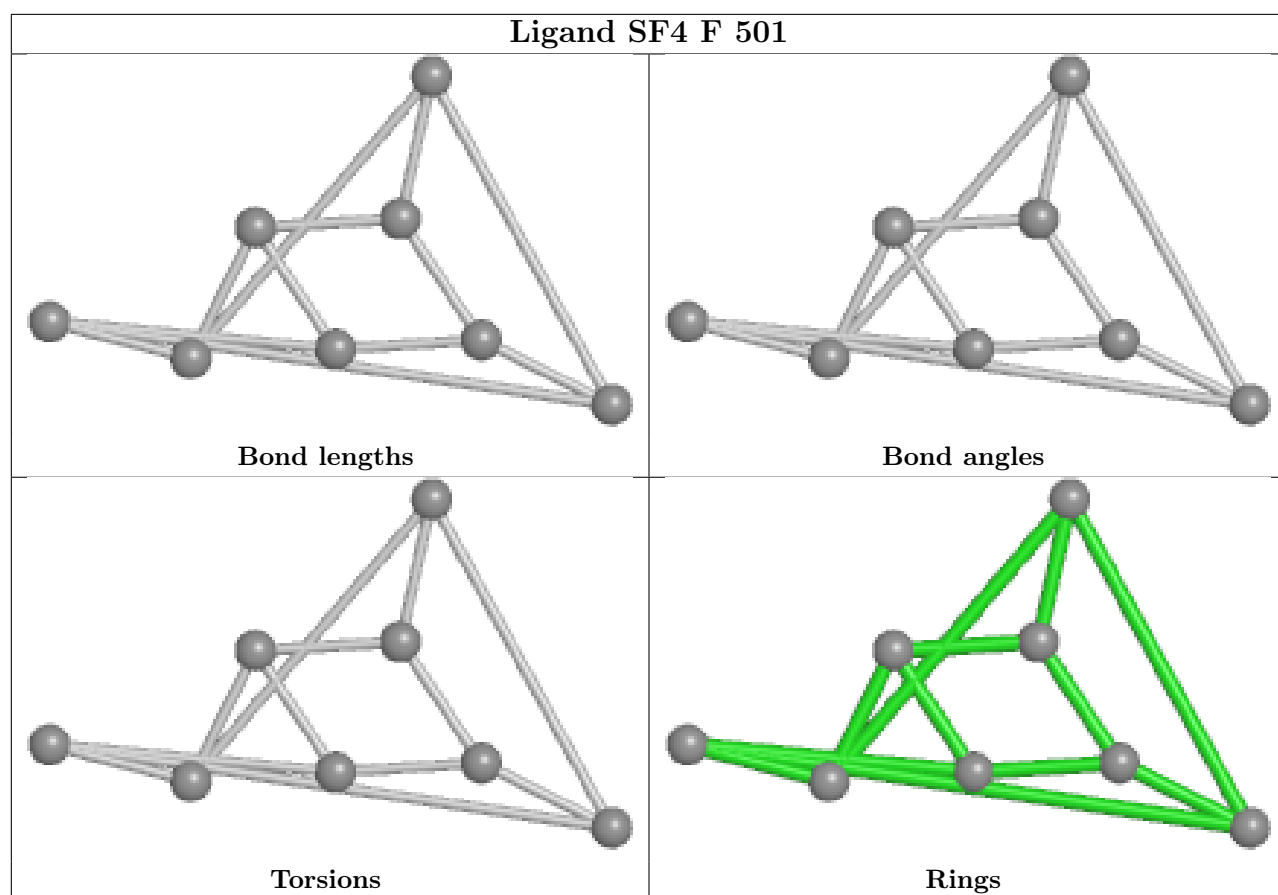
Ligand HEM AC 500



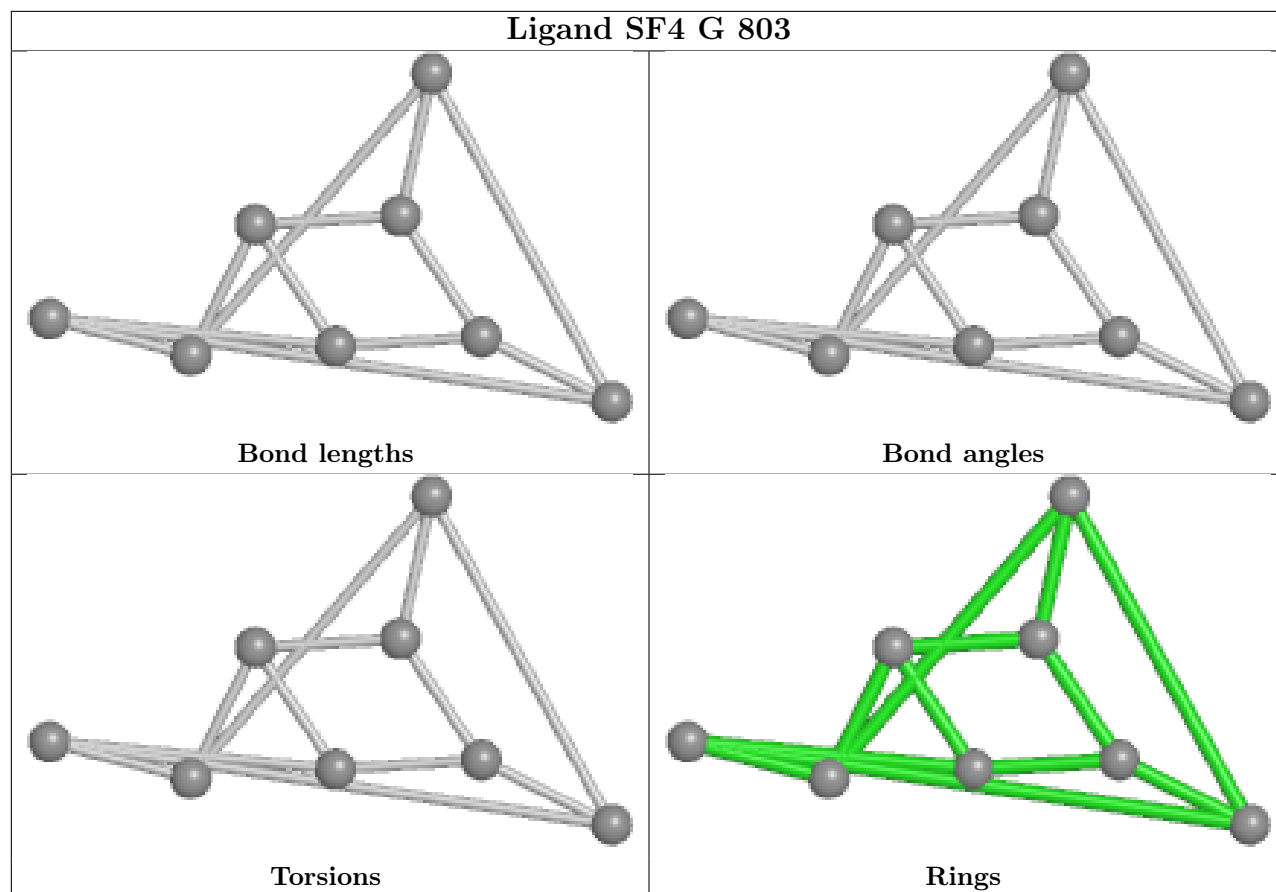




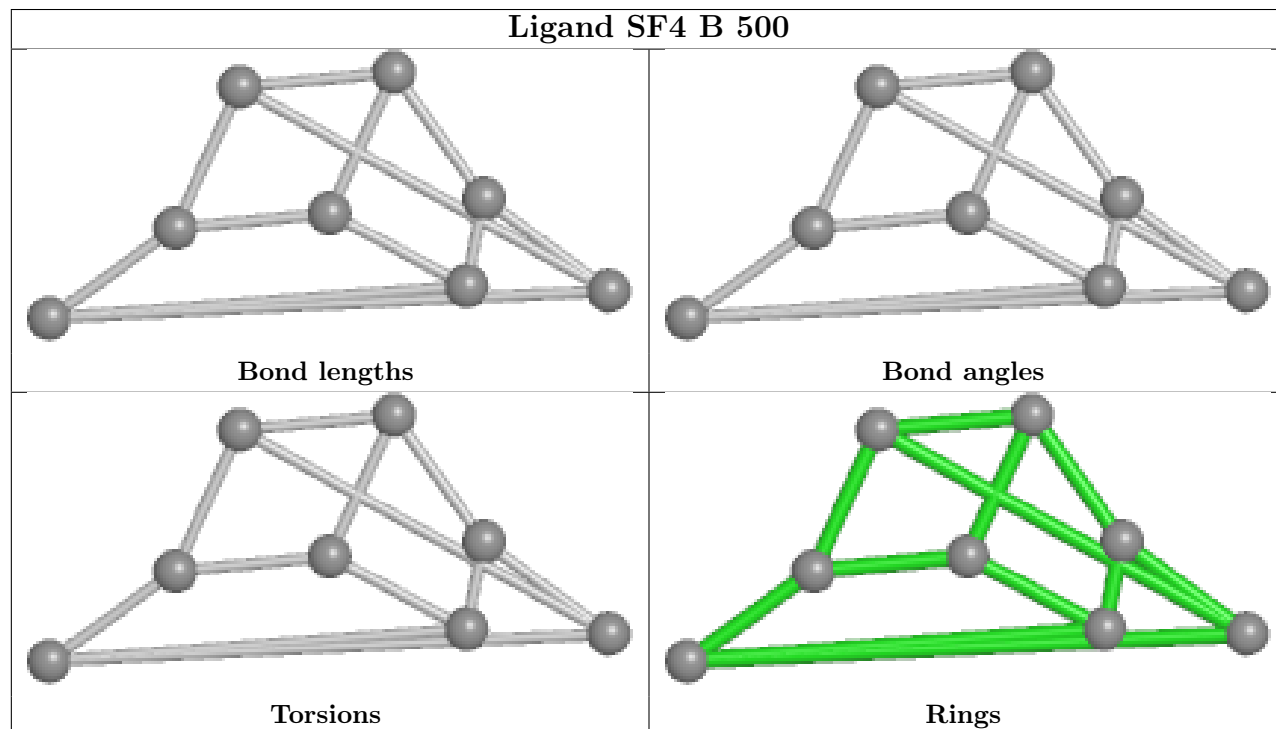


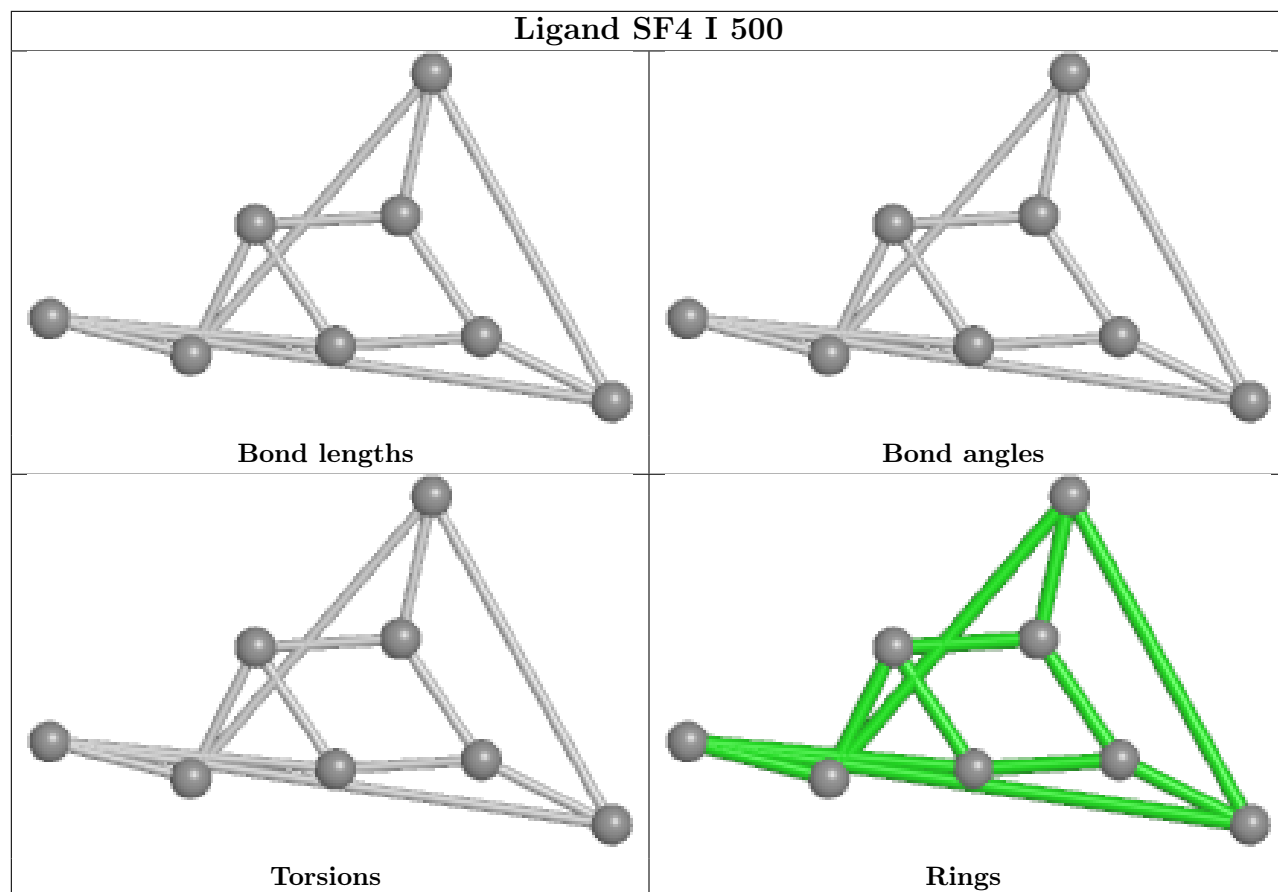


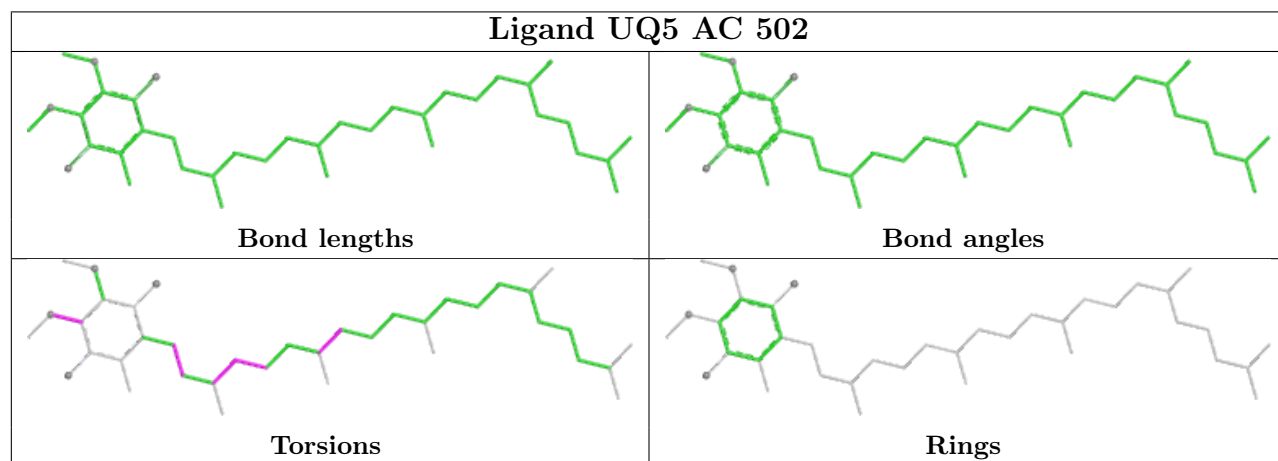
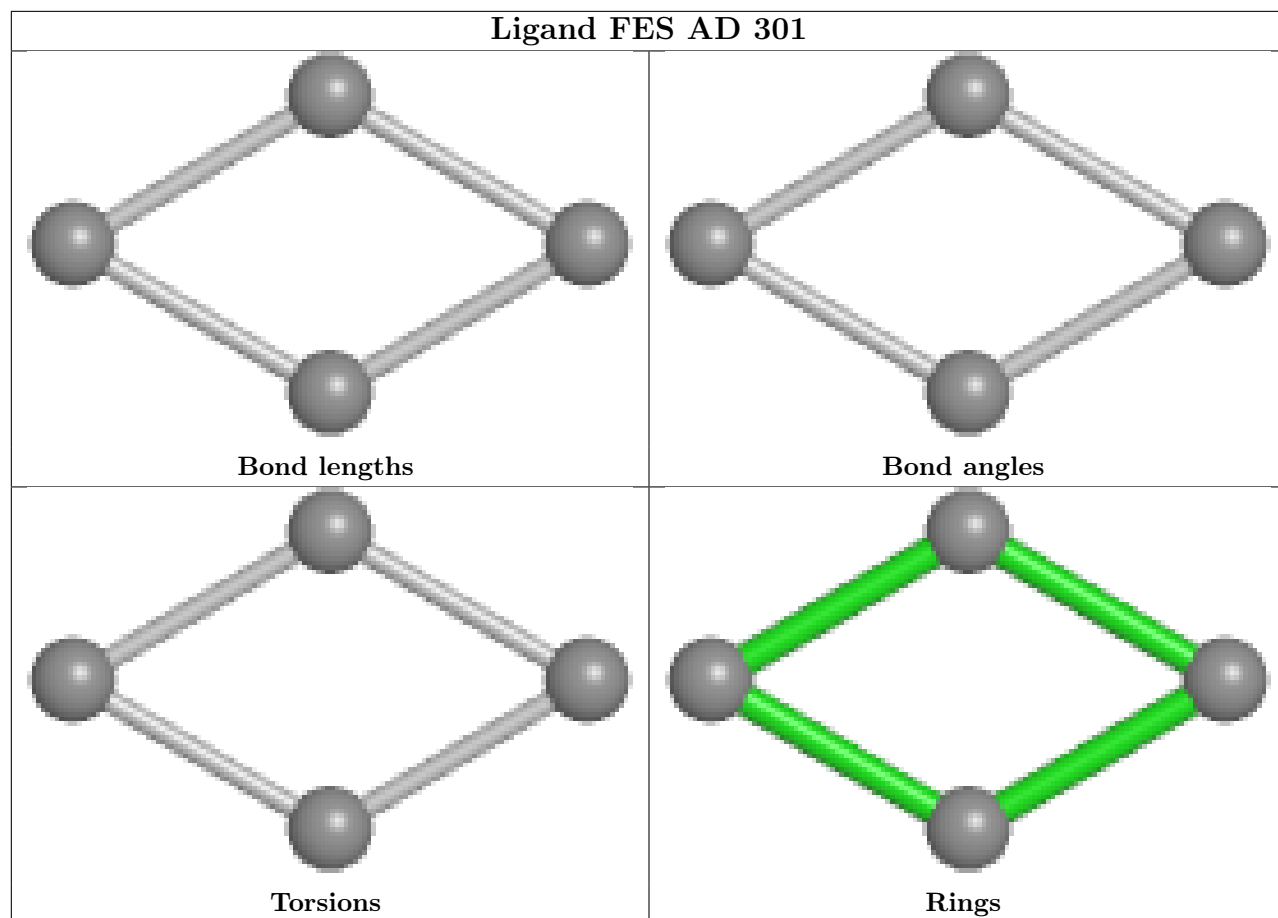
Ligand SF4 G 803



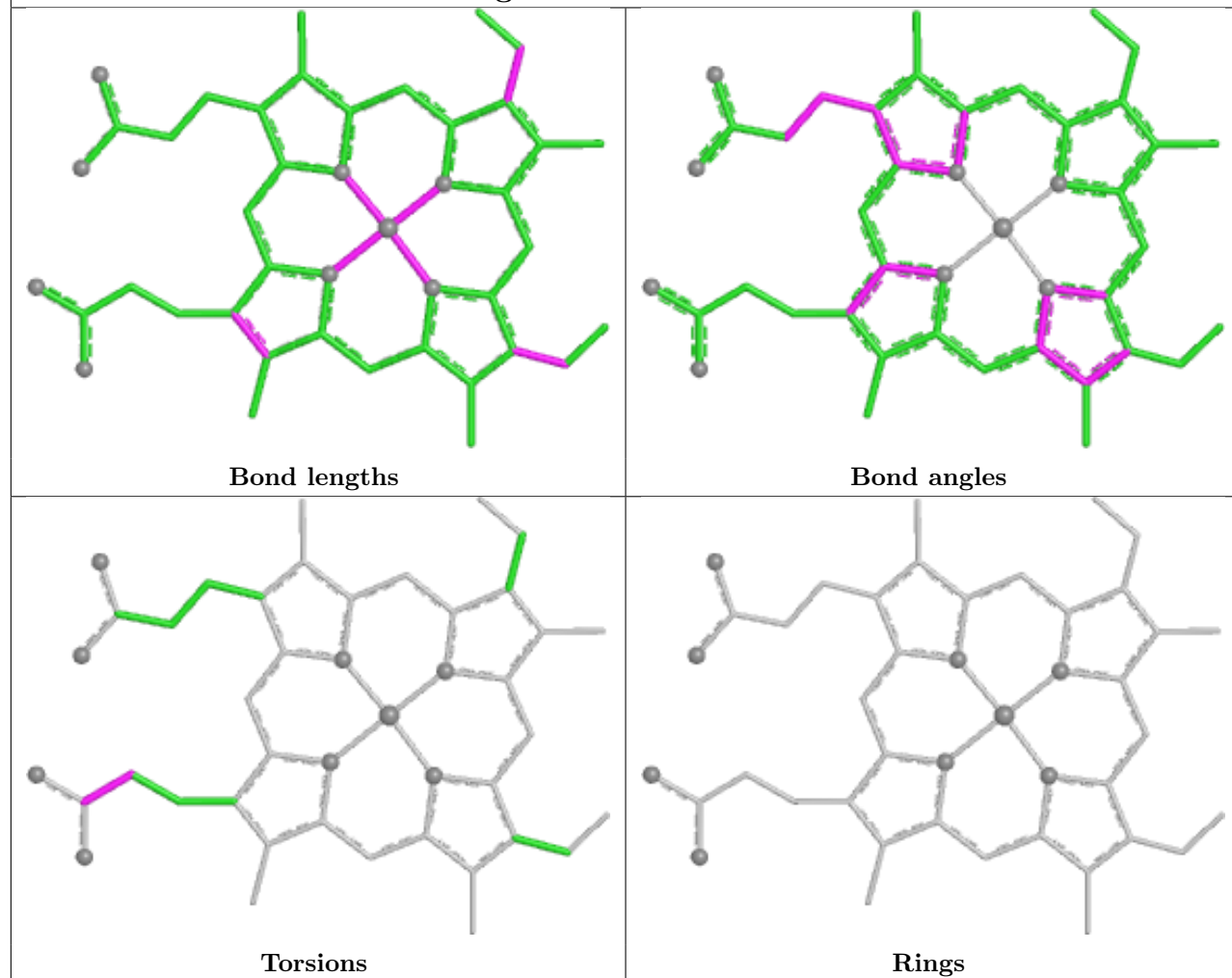
Ligand SF4 B 500



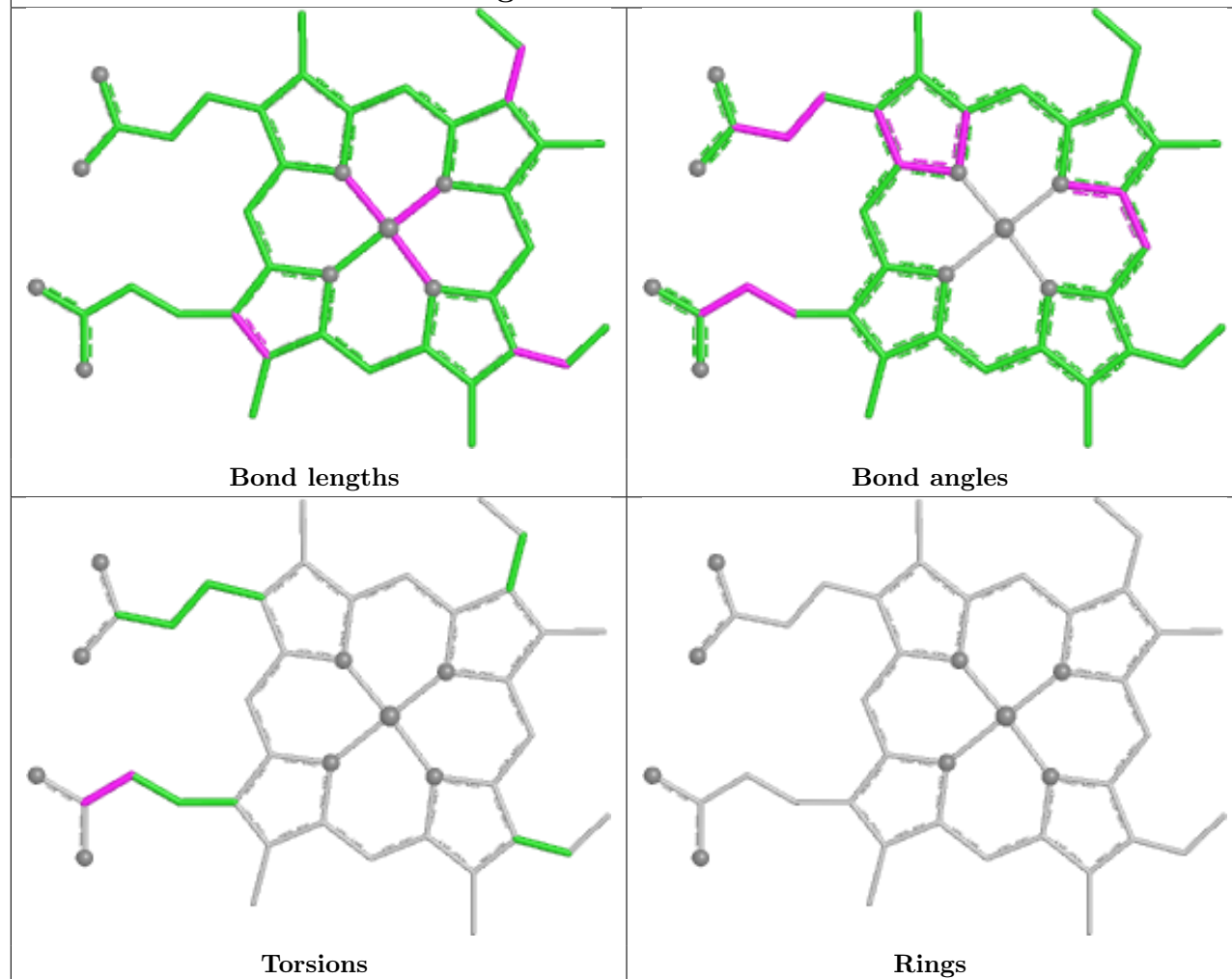




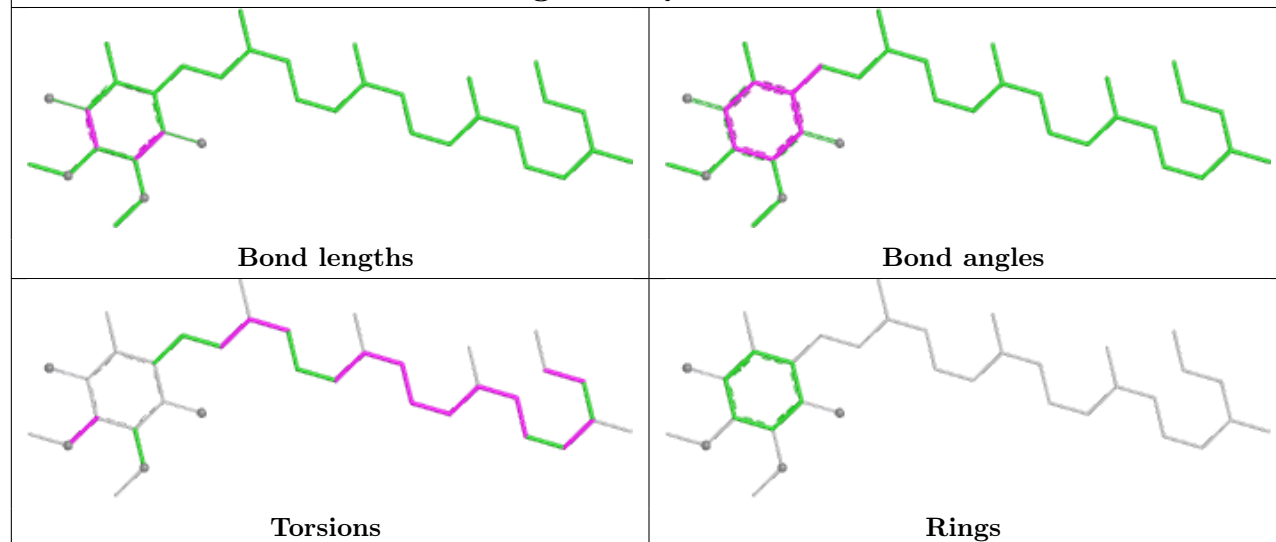
Ligand HEM BC 500



Ligand HEM BE 400



Ligand UQ9 H 500



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.

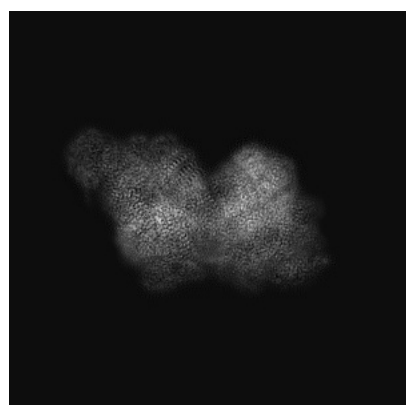
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16172. These allow visual inspection of the internal detail of the map and identification of artifacts.

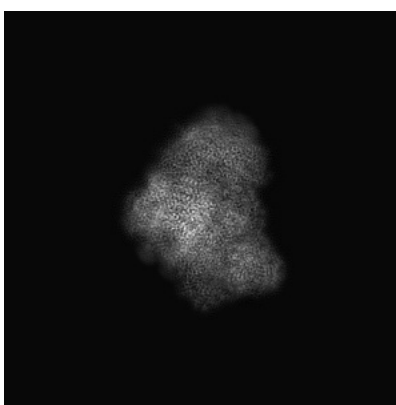
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

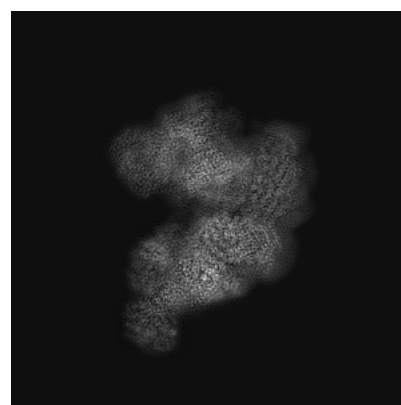
6.1.1 Primary map



X



Y

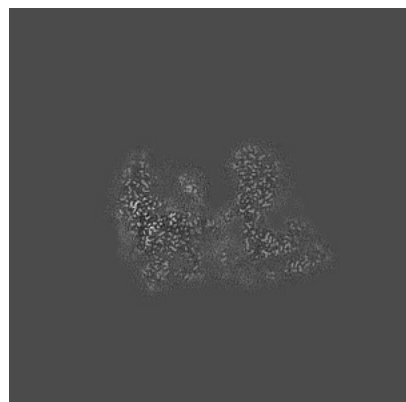


Z

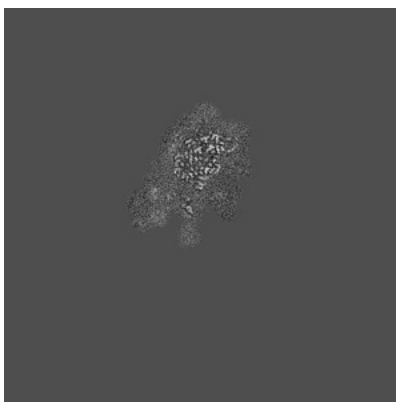
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

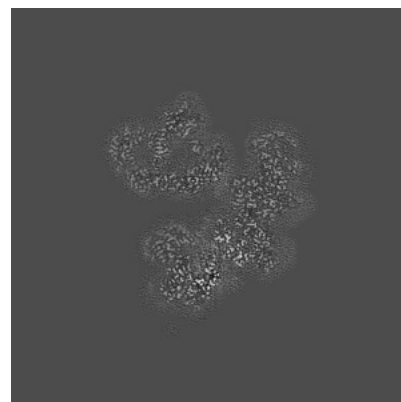
6.2.1 Primary map



X Index: 375



Y Index: 375

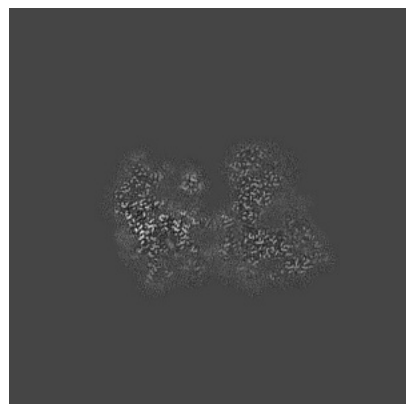


Z Index: 375

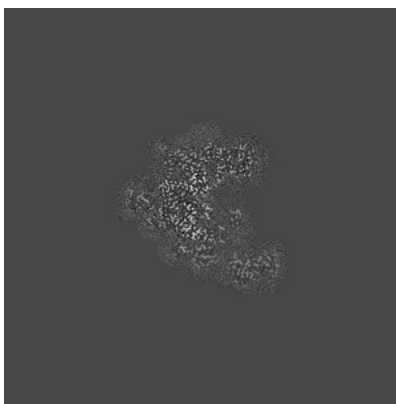
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

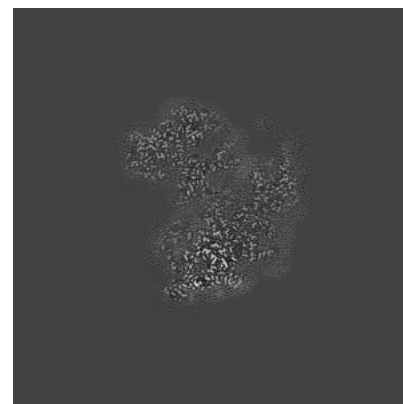
6.3.1 Primary map



X Index: 366



Y Index: 283

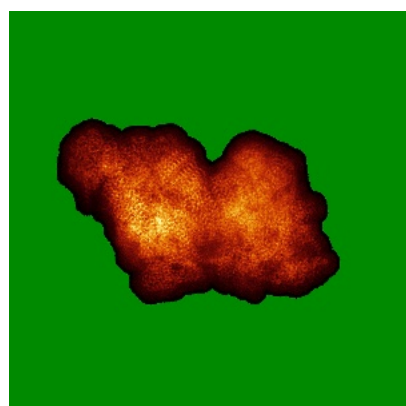


Z Index: 345

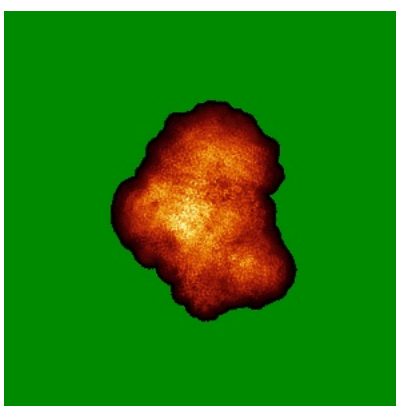
The images above show the largest variance slices of the map in three orthogonal directions.

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

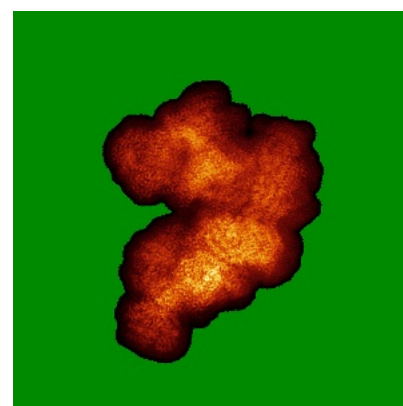
6.4.1 Primary map



X



Y

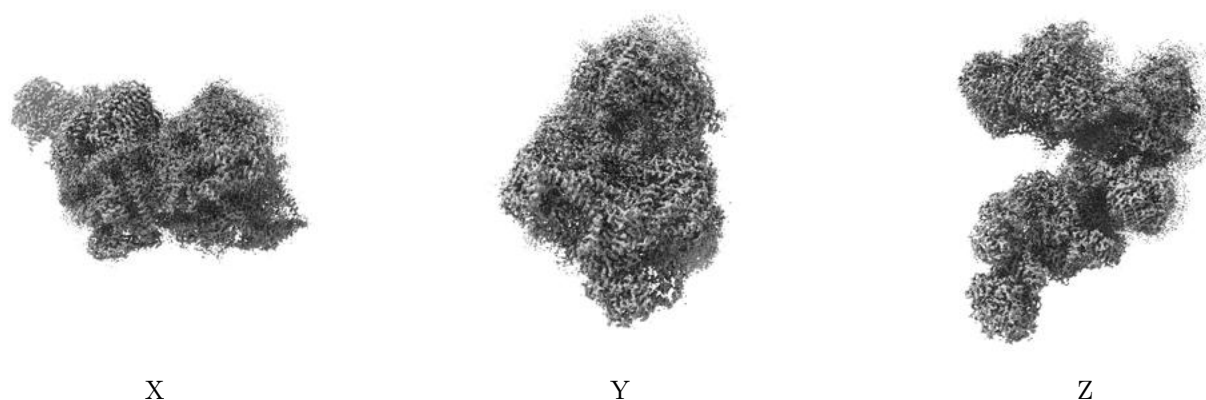


Z

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

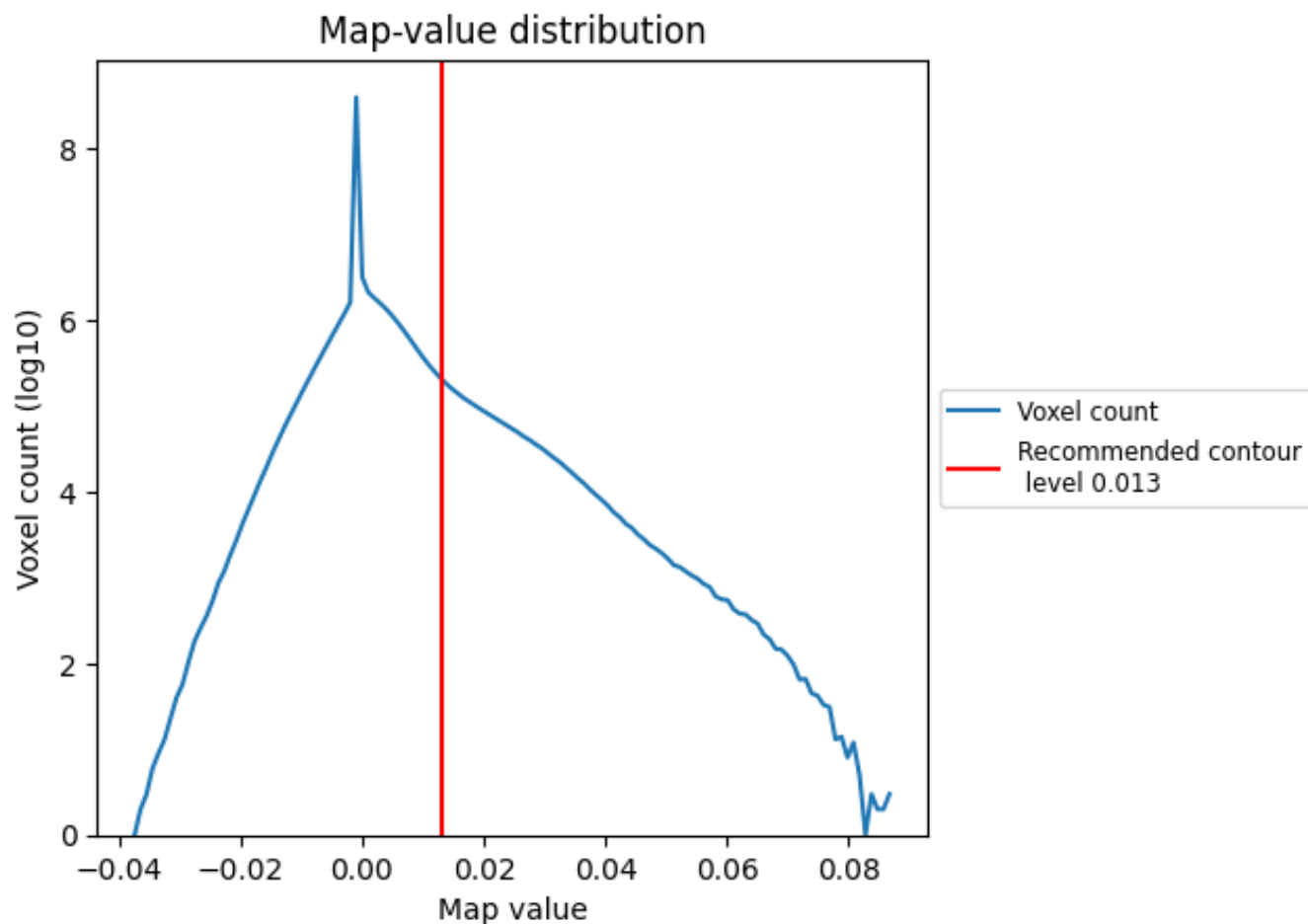
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

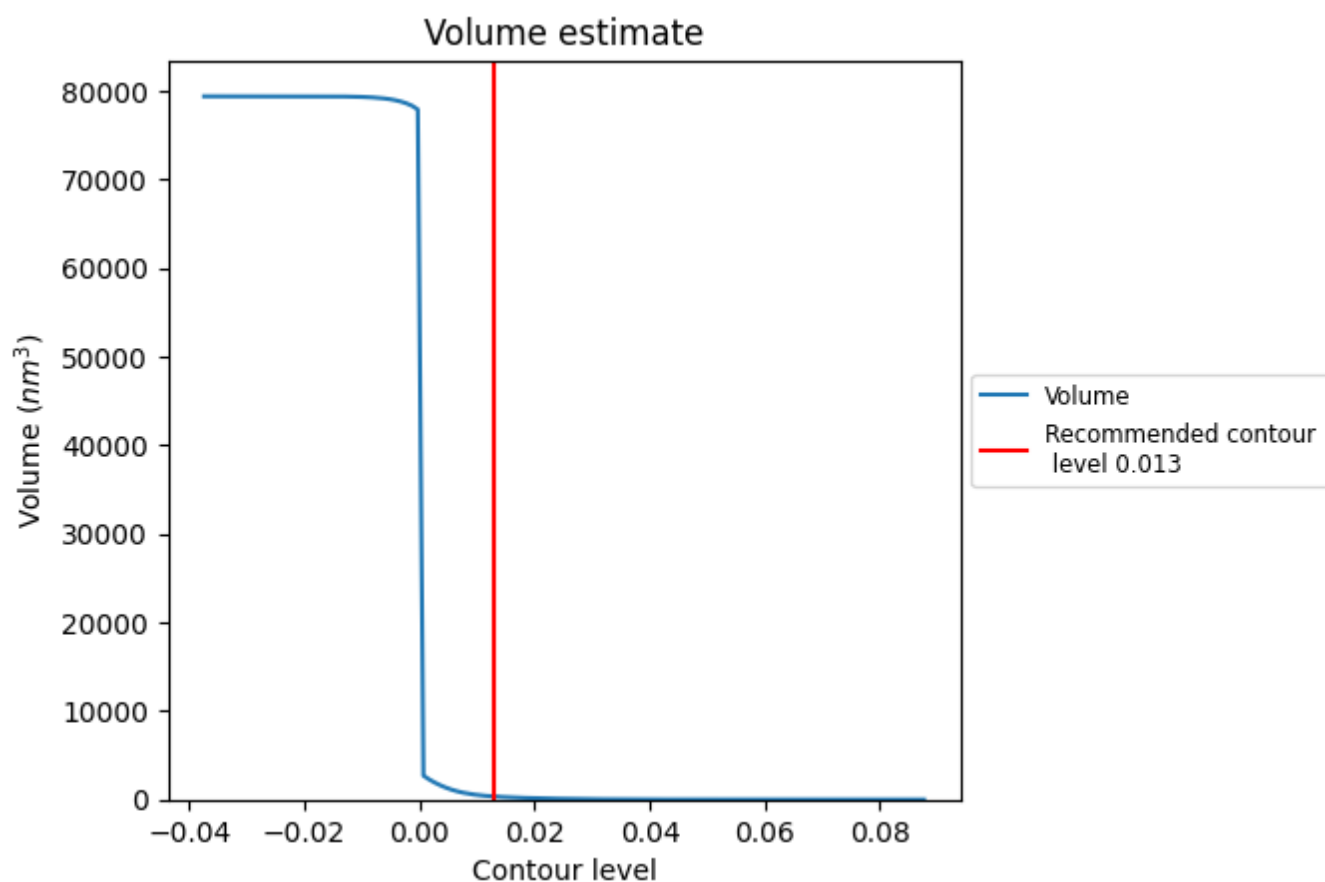
This section contains the results of statistical analysis of the map.

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.

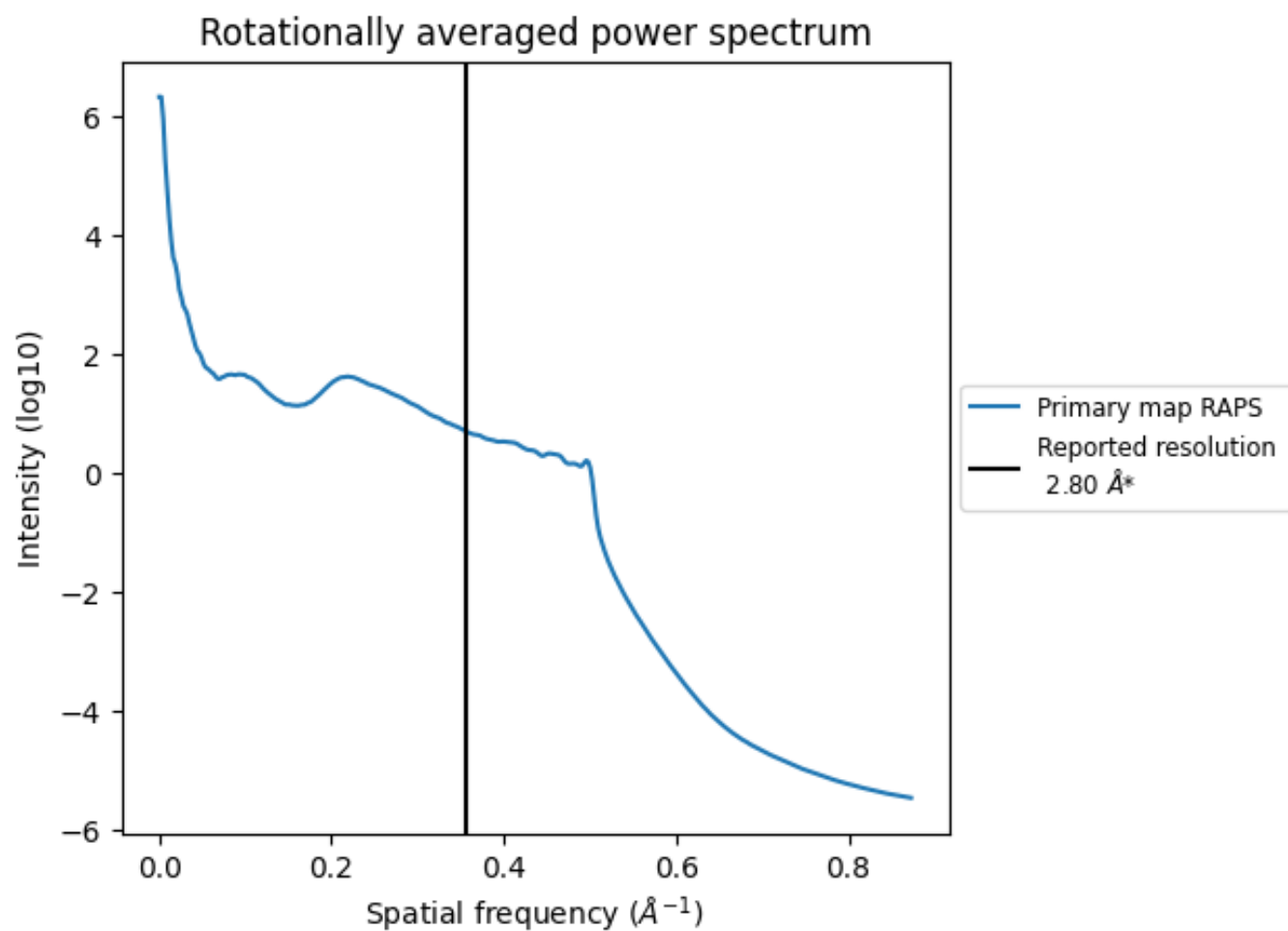
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 348 nm^3 ; this corresponds to an approximate mass of 314 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

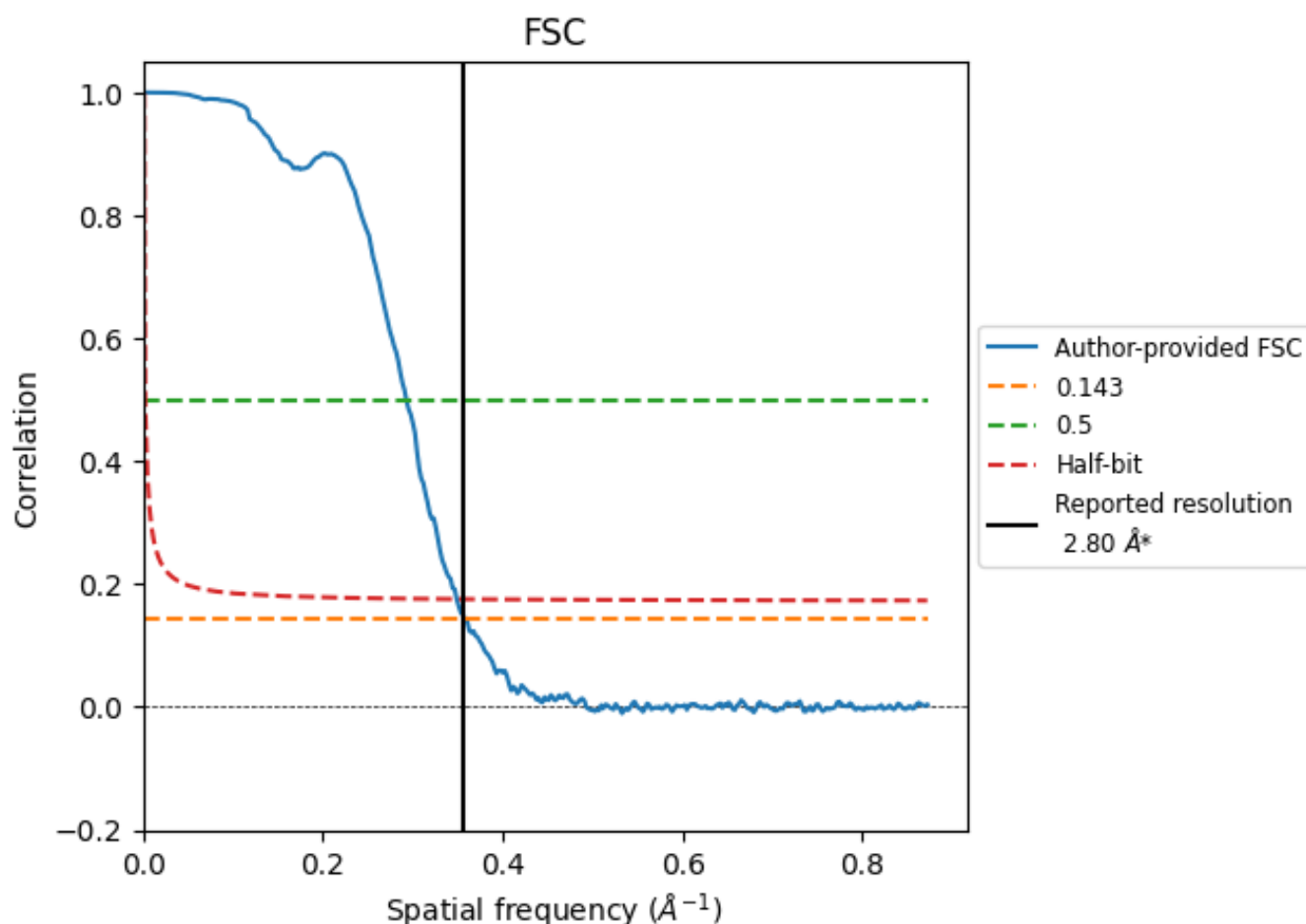


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

8 Fourier-Shell correlation [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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

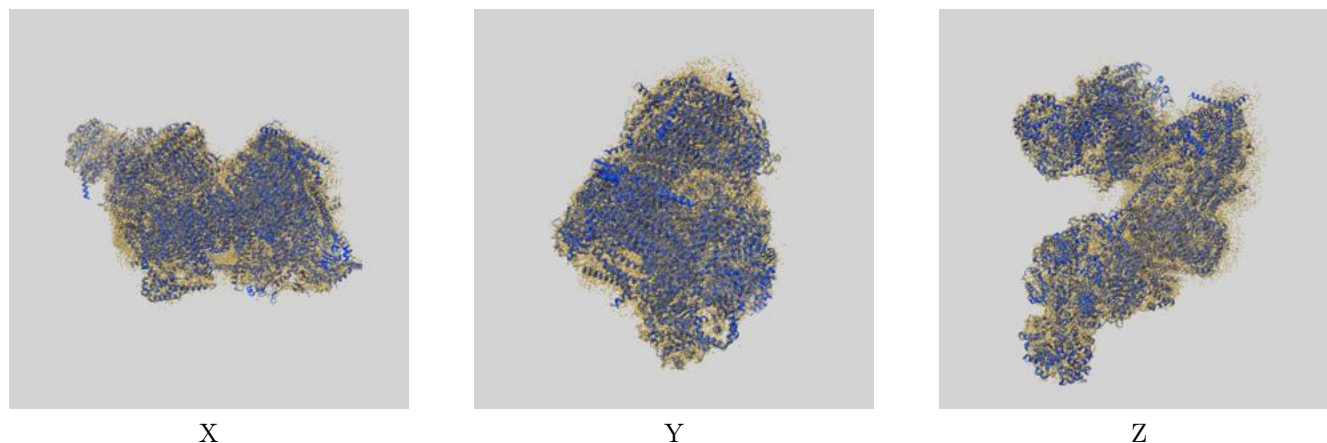
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.79	3.42	2.87
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

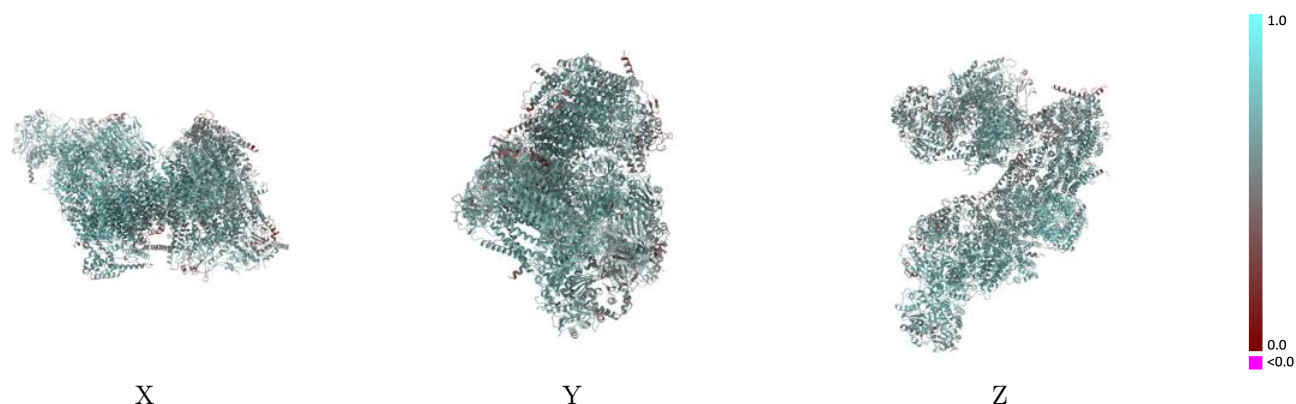
This section contains information regarding the fit between EMDB map EMD-16172 and PDB model 8BQ6. Per-residue inclusion information can be found in section [3](#) on page [23](#).

9.1 Map-model overlay [i](#)



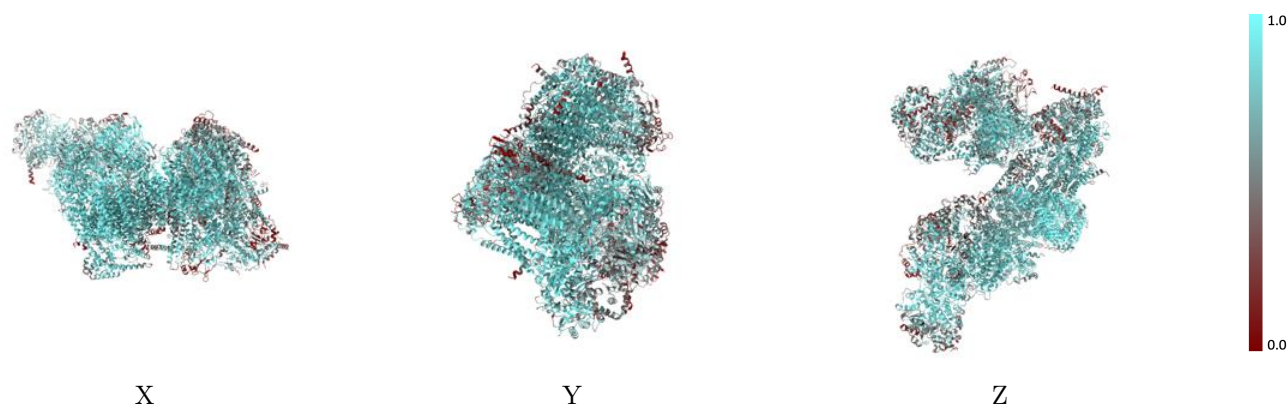
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



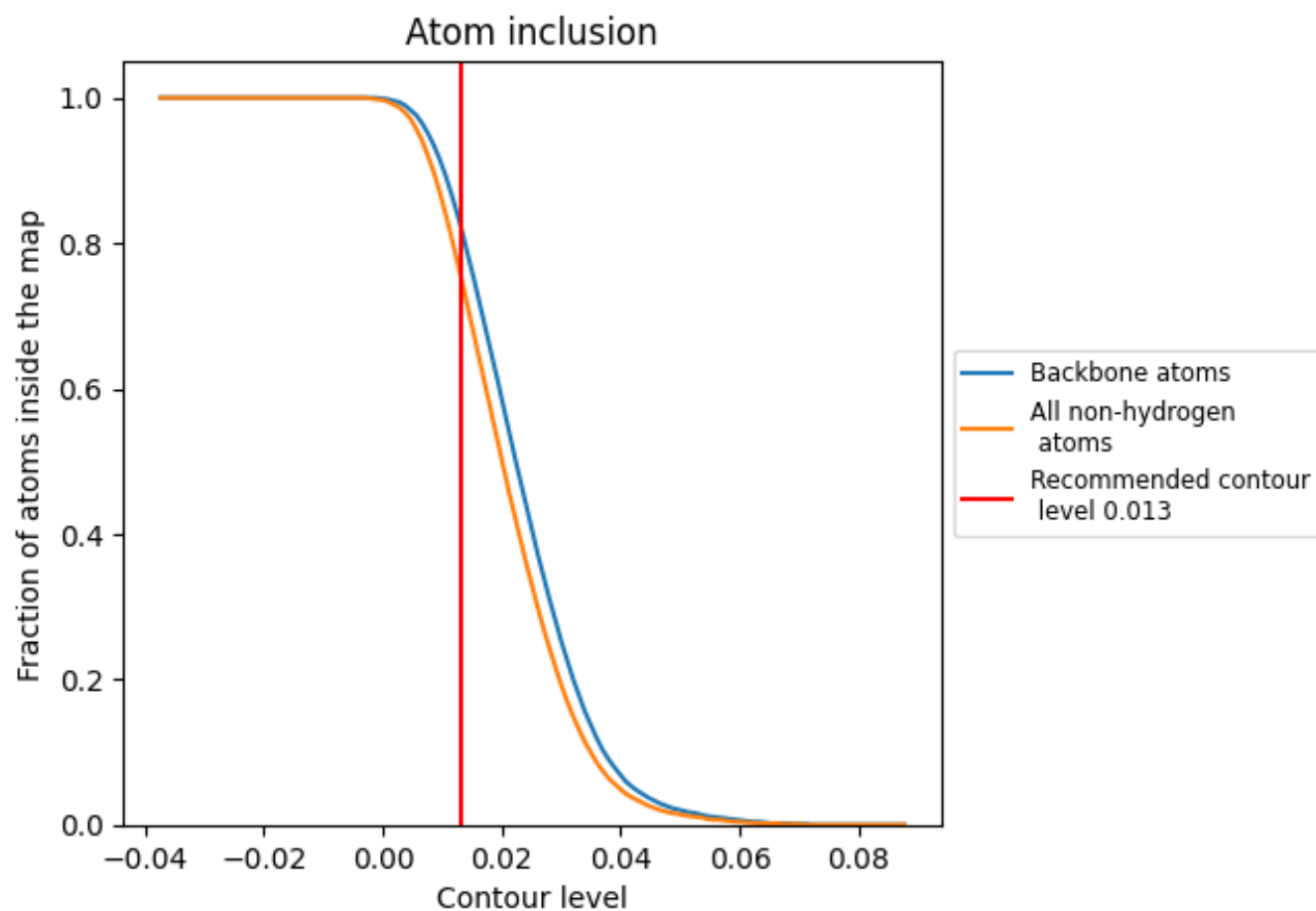
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.013).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 76% 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 (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7580	 0.6280
A	 0.9520	 0.6900
AA	 0.5340	 0.5470
AB	 0.7810	 0.6360
AC	 0.8840	 0.6700
AD	 0.4040	 0.5070
AE	 0.8620	 0.6630
AF	 0.8600	 0.6720
AG	 0.8150	 0.6300
AH	 0.7460	 0.5890
AI	 0.7580	 0.6320
AJ	 0.3000	 0.4920
B	 0.9500	 0.7180
BA	 0.5760	 0.5650
BB	 0.7830	 0.6290
BC	 0.8420	 0.6490
BD	 0.4270	 0.5060
BE	 0.7980	 0.6330
BF	 0.8160	 0.6390
BG	 0.6800	 0.6010
BH	 0.4760	 0.5230
BI	 0.6510	 0.5710
BJ	 0.5450	 0.5330
C	 0.8700	 0.7030
D	 0.9430	 0.7160
E	 0.6000	 0.5770
F	 0.6970	 0.6260
G	 0.7340	 0.6390
H	 0.9370	 0.6930
I	 0.9470	 0.7170
J	 0.8790	 0.6680
K	 0.9390	 0.7030
L	 0.8040	 0.6340
M	 0.8840	 0.6630
N	 0.9120	 0.6930



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Chain	Atom inclusion	Q-score
O	 0.9420	 0.6630
P	 0.5970	 0.5790
Q	 0.4090	 0.5980
R	 0.7530	 0.6680
S	 0.4770	 0.5330
T	 0.3030	 0.4250
U	 0.5600	 0.4830
V	 0.6930	 0.6390
W	 0.5540	 0.5930
X	 0.7130	 0.5920
Y	 0.5750	 0.4950
Z	 0.7760	 0.6180
a	 0.8520	 0.6460
b	 0.7680	 0.5950
c	 0.6990	 0.5860
d	 0.7310	 0.5990
e	 0.8340	 0.6500
f	 0.8870	 0.6750
g	 0.6300	 0.5600
i	 0.5660	 0.5190
j	 0.4430	 0.4690
k	 0.3950	 0.4610
l	 0.5870	 0.5510
m	 0.7310	 0.6100
n	 0.7370	 0.5620
o	 0.5320	 0.5230
p	 0.6880	 0.5690
q	 0.8280	 0.6690
u	 0.7270	 0.5670
v	 0.8550	 0.6630
x	 0.9380	 0.7090
y	 0.8800	 0.6720
z	 0.8710	 0.6690