



Full wwPDB EM Validation Report ⓘ

Mar 13, 2023 – 01:52 pm GMT

PDB ID : 8BQ5
EMDB ID : EMD-16171
Title : Cryo-EM structure of the Arabidopsis thaliana I+III2 supercomplex (Complete conformation 1 composition)
Authors : Klusch, N.; Kuehlbrandt, W.
Deposited on : 2022-11-18
Resolution : 2.73 Å(reported)

This is a Full wwPDB EM Validation 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:

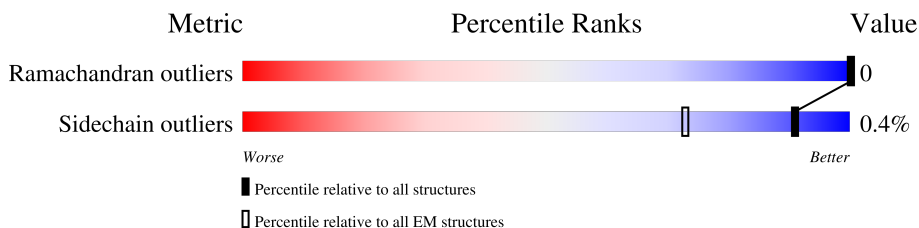
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.32.1

1 Overall quality at a glance

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

The reported resolution of this entry is 2.73 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	78% 21%
2	B	218	71% 28%
3	C	190	94% 5%
4	D	394	98%
5	E	255	21% 75% 25%
6	F	486	12% 89% 11%
7	G	748	10% 92% 8%
8	H	325	99%
9	I	222	74% 26%

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Mol	Chain	Length	Quality of chain
10	J	205	83% 15%
11	K	100	99%
12	L	669	99%
13	M	495	100%
14	N	499	97%
15	O	159	77% 23%
16	P	402	78% 21%
17	Q	154	68% 32%
18	R	110	66% 34%
19	S	97	96%
20	T	122	68% 32%
21	U	126	69% 31%
22	V	169	83% 17%
23	W	133	84% 16%
24	X	106	92% 8%
25	Y	159	79% 21%
26	Z	143	87% 13%
27	a	65	89% 11%
28	b	65	66% 34%
29	c	88	86% 14%
30	d	81	91% 7%
31	e	83	76% 23%
32	f	106	93% 5%
33	g	114	61% 39%
34	i	98	67% 31%

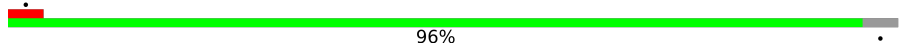
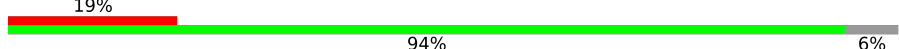
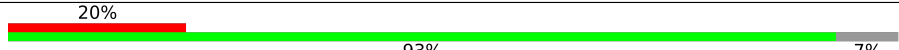
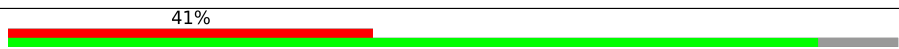
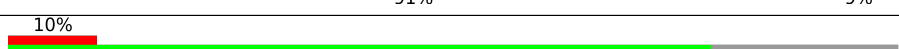
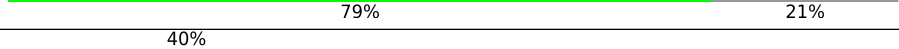

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Mol	Chain	Length	Quality of chain
35	j	69	
36	k	72	
37	l	125	
38	m	71	
39	n	117	
40	o	103	
41	p	106	
42	q	159	
43	u	63	
44	v	113	
45	x	256	
46	y	278	
47	z	275	
48	AA	503	
48	BA	503	
49	AB	531	
49	BB	531	
50	AC	393	
50	BC	393	
51	AD	272	
51	BD	272	
52	AE	307	
52	BE	307	
53	AF	122	
53	BF	122	

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Mol	Chain	Length	Quality of chain
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
66	COO	x	301	X	-	-	-

2 Entry composition

There are 69 unique types of molecules in this entry. The entry contains 96290 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
			Total	C	N	O	S		
1	A	94	802	565	110	123	4	0	0

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

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

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

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

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

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

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
			Total	C	N	O	S		
5	E	192	1500	954	248	287	11	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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
			Total	C	N	O	S		
13	M	494	3946	2664	610	647	25	0	0

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
			Total	C	N	O	S		
14	N	488	3832	2582	578	644	28	1	0

- Molecule 15 is a protein called AT3G07480.1.

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

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

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

- 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
			Total	C	N	O	S		
24	X	98	776	486	134	144	12	0	0

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

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

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

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

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

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

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

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

- Molecule 29 is a protein called Transmembrane protein.

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

- 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	64	Total	C	N	O	S	0	0
			546	338	102	99	7		

- 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	69	Total	C	N	O	S	0	0
			559	362	95	99	3		

- Molecule 34 is a protein called P1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	68	Total	C	N	O	S	0	0
			591	370	110	108	3		

- 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
			Total	C	N	O	S		
37	l	74	562	367	91	103	1	0	0

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

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

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

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

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

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

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

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

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

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

- 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	S	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	418	Total	C	N	O	S	0	0
			3190	2029	528	618	15		

- 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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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		

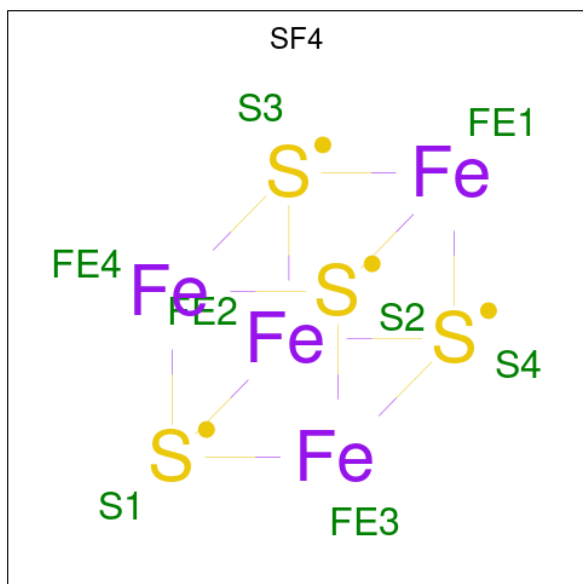
- Molecule 56 is a protein called Cytochrome b-c1 complex subunit 9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
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.

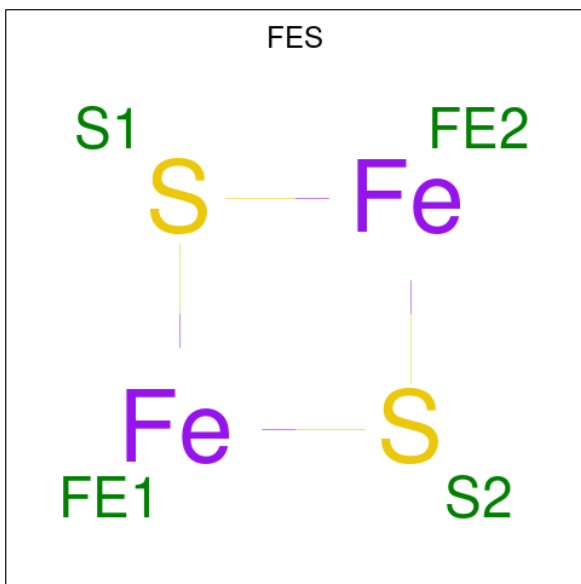
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
57	AJ	28	Total	C	N	O	0	0
			203	137	33	33		
57	BJ	28	Total	C	N	O	0	0
			205	139	34	32		

- Molecule 58 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).



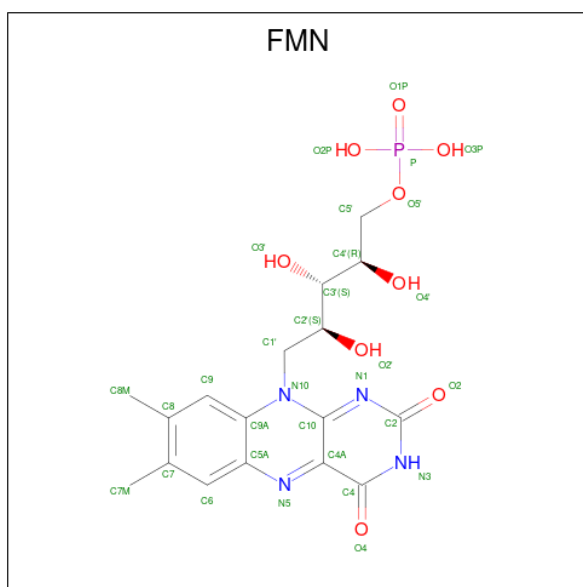
Mol	Chain	Residues	Atoms			AltConf
58	B	1	Total	Fe	S	0
			8	4	4	
58	F	1	Total	Fe	S	0
			8	4	4	
58	G	1	Total	Fe	S	0
			8	4	4	
58	G	1	Total	Fe	S	0
			8	4	4	
58	I	1	Total	Fe	S	0
			8	4	4	
58	I	1	Total	Fe	S	0
			8	4	4	

- Molecule 59 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



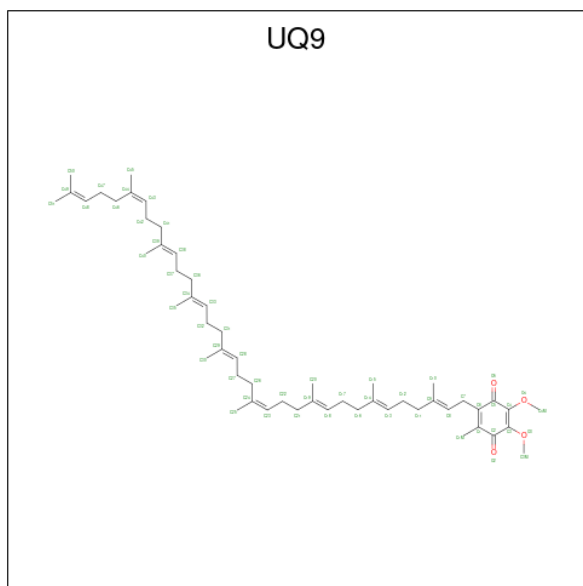
Mol	Chain	Residues	Atoms			AltConf
59	E	1	Total	Fe	S	0
			4	2	2	
59	G	1	Total	Fe	S	0
			4	2	2	
59	AD	1	Total	Fe	S	0
			4	2	2	
59	BD	1	Total	Fe	S	0
			4	2	2	

- Molecule 60 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P) (labeled as "Ligand of Interest" by depositor).



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

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

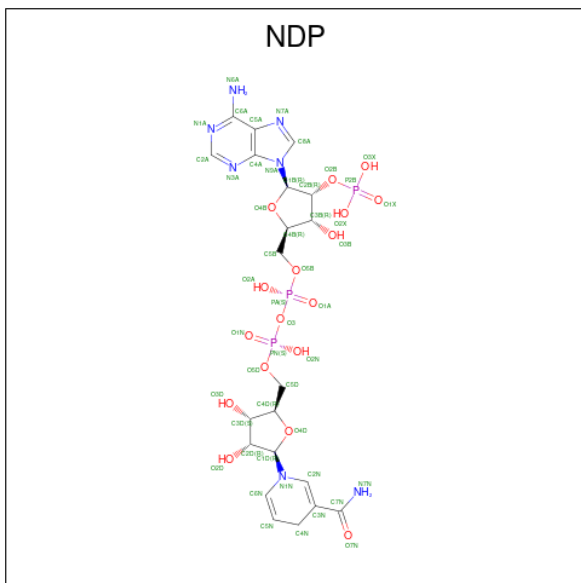


Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
61	H	1	35	31	4	0

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

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

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

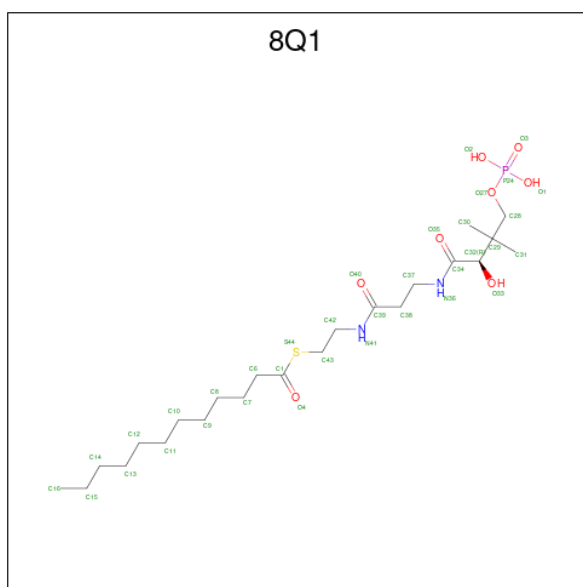


Mol	Chain	Residues	Atoms	AltConf
63	P	1	Total C N O P 48 21 7 17 3	0

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

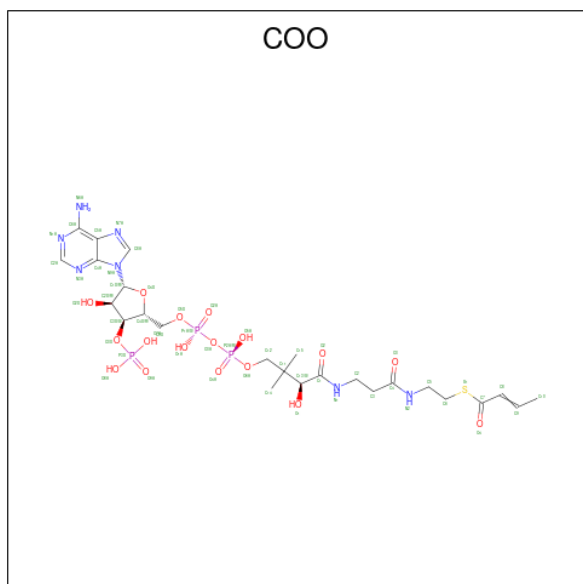
Mol	Chain	Residues	Atoms	AltConf
64	R	1	Total Zn 1 1	0
64	y	1	Total Zn 1 1	0
64	AB	1	Total Zn 1 1	0
64	BB	1	Total Zn 1 1	0

- Molecule 65 is S-[2-({N-[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonoxy)butanoyl]-beta-alanyl}amino)ethyl] dodecanethioate (three-letter code: 8Q1) (formula: $C_{23}H_{45}N_2O_8PS$) (labeled as "Ligand of Interest" by depositor).



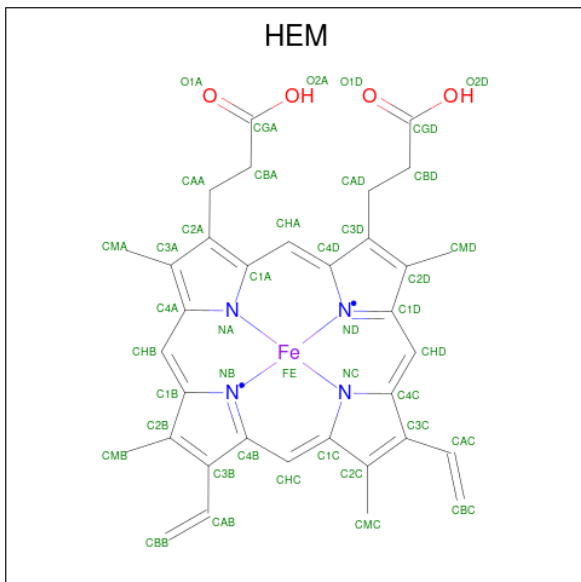
Mol	Chain	Residues	Atoms					AltConf	
			Total	C	N	O	P		S
65	W	1	35	23	2	8	1	1	0
65	n	1	35	23	2	8	1	1	0

- Molecule 66 is CROTONYL COENZYME A (three-letter code: COO) (formula: $C_{25}H_{40}N_7O_{17}P_3S$) (labeled as "Ligand of Interest" by depositor).



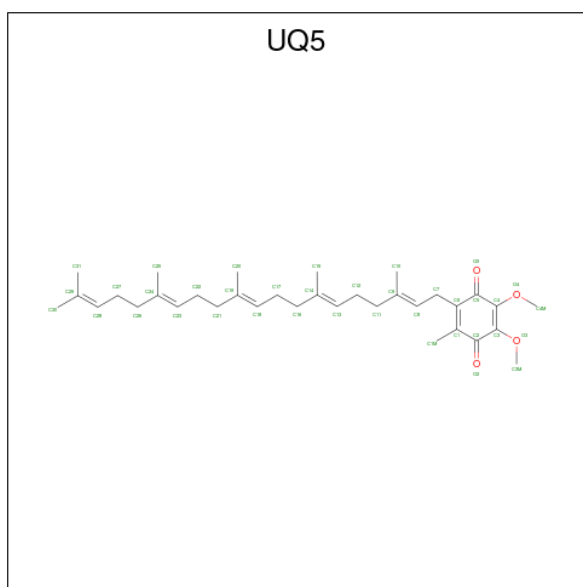
Mol	Chain	Residues	Atoms					AltConf	
			Total	C	N	O	P		S
66	x	1	53	25	7	17	3	1	0

- Molecule 67 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



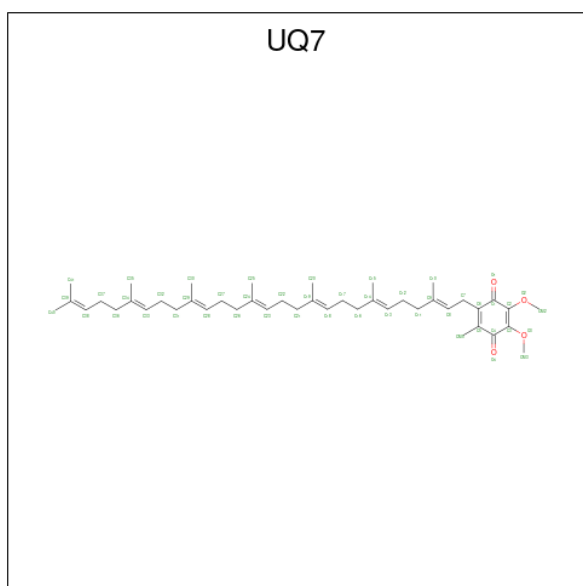
Mol	Chain	Residues	Atoms				AltConf	
			Total	C	Fe	N		O
67	AC	1	Total 43	C 34	Fe 1	N 4	O 4	0
67	AC	1	Total 43	C 34	Fe 1	N 4	O 4	0
67	AE	1	Total 43	C 34	Fe 1	N 4	O 4	0
67	BC	1	Total 43	C 34	Fe 1	N 4	O 4	0
67	BC	1	Total 43	C 34	Fe 1	N 4	O 4	0
67	BE	1	Total 43	C 34	Fe 1	N 4	O 4	0

- Molecule 68 is 2,3-DIMETHOXY-5-METHYL-6-(3,11,15,19-TETRAMETHYL-EICOSA-2,6,10,14,18-PENTAENYL)-[1,4]BENZOQUINONE (three-letter code: UQ5) (formula: $C_{34}H_{50}O_4$) (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 (three-letter code: UQ7) (formula: $C_{44}H_{66}O_4$) (labeled as "Ligand of Interest" by depositor).

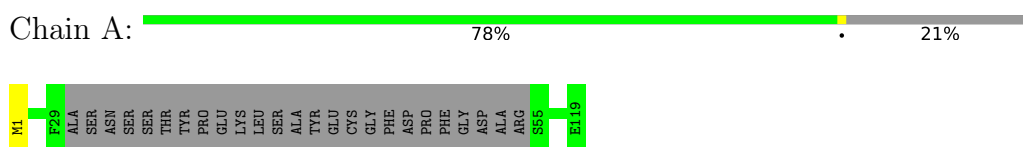


Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
69	BC	1	48	44	4	0

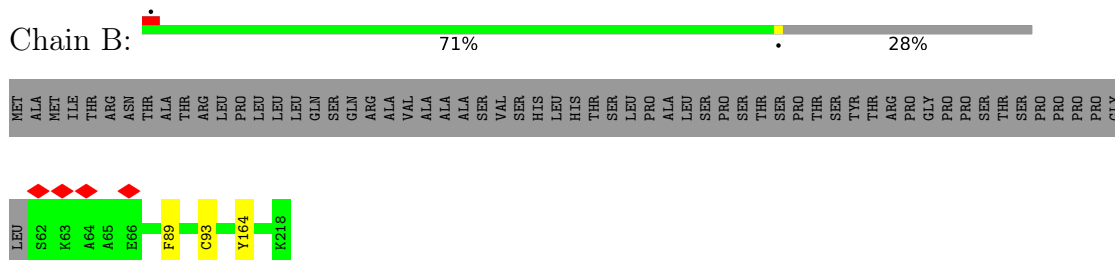
3 Residue-property plots [i](#)

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

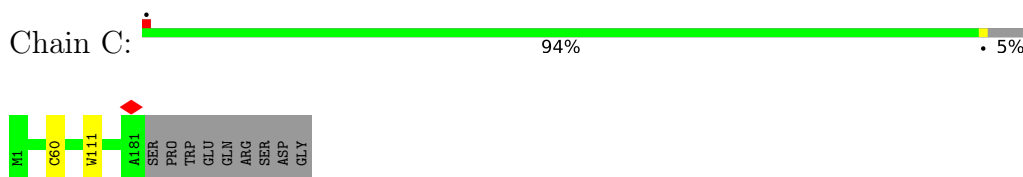
- Molecule 1: NADH-ubiquinone oxidoreductase chain 3



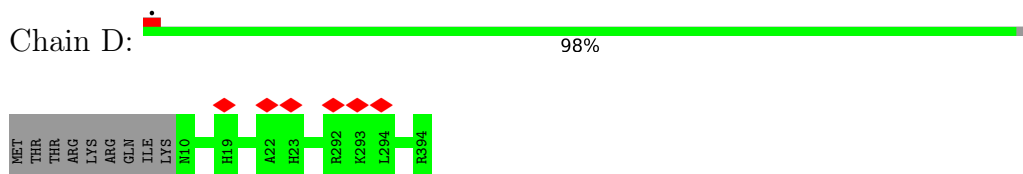
- Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial



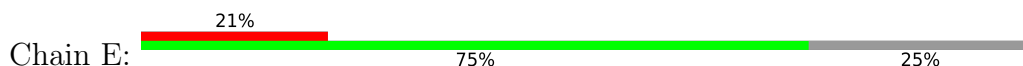
- Molecule 3: NADH dehydrogenase [ubiquinone] iron-sulfur protein 3

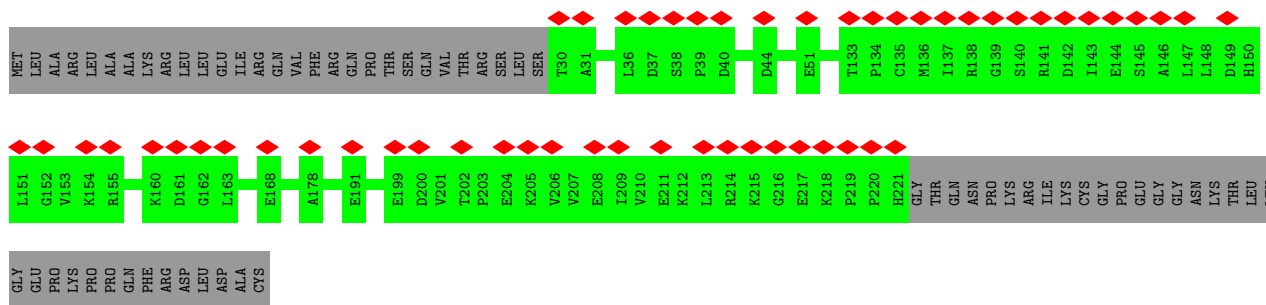


- Molecule 4: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2

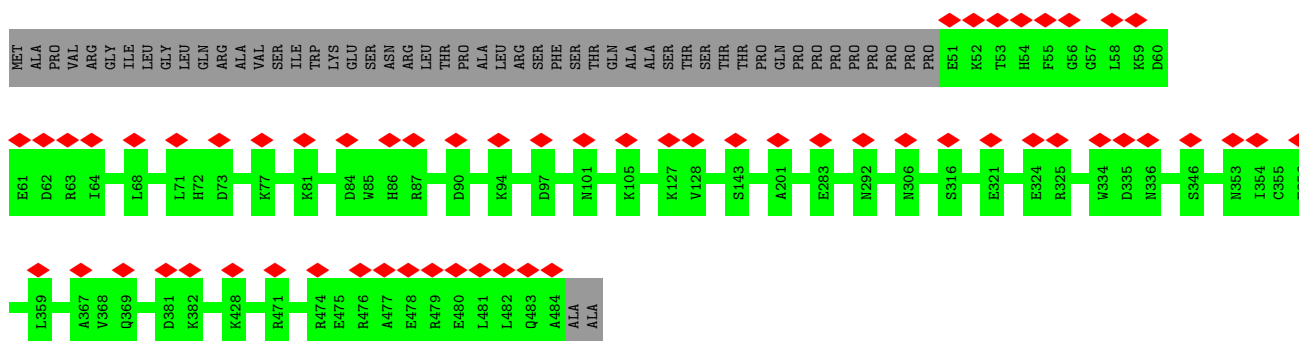
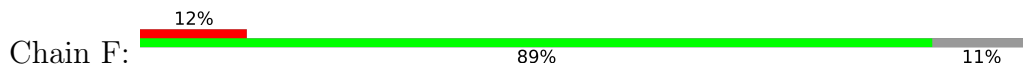


- Molecule 5: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial

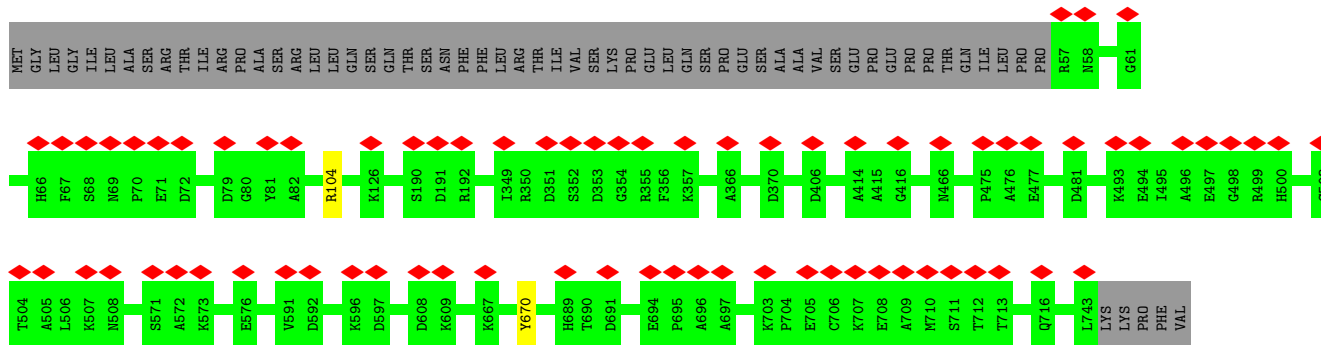
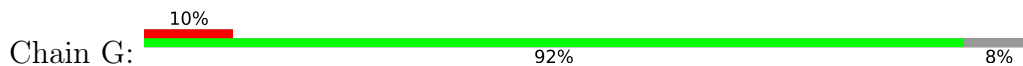




• Molecule 6: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial



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

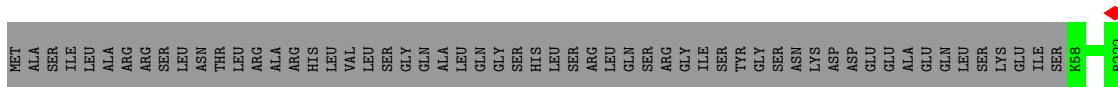


• Molecule 8: NADH-ubiquinone oxidoreductase chain 1

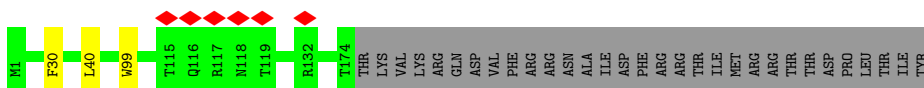
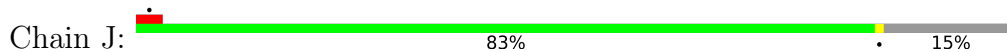


• Molecule 9: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8-A, mitochondrial





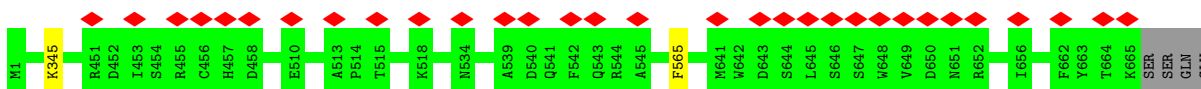
• Molecule 10: NADH-ubiquinone oxidoreductase chain 6



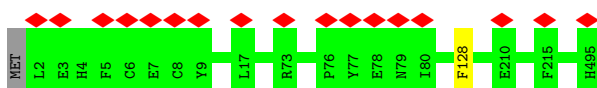
• Molecule 11: NADH dehydrogenase subunit 4L



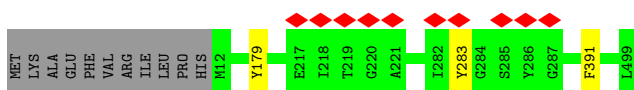
• Molecule 12: NADH-ubiquinone oxidoreductase chain 5



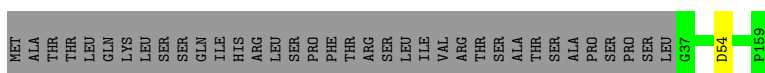
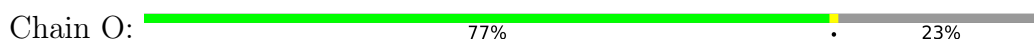
• Molecule 13: NADH-ubiquinone oxidoreductase chain 4



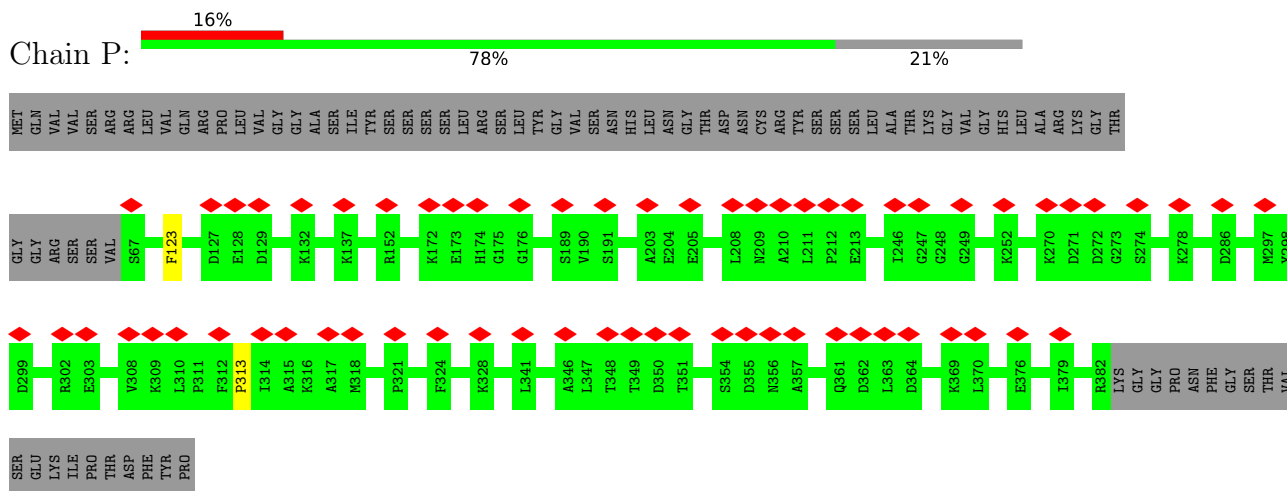
• Molecule 14: NADH-ubiquinone oxidoreductase chain 2



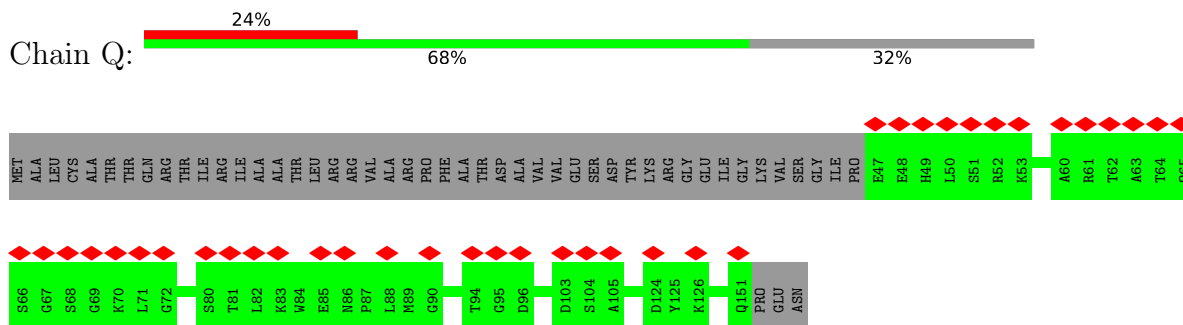
• Molecule 15: AT3G07480.1



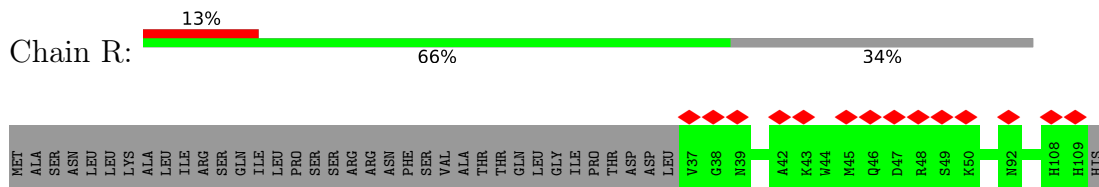
• Molecule 16: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial



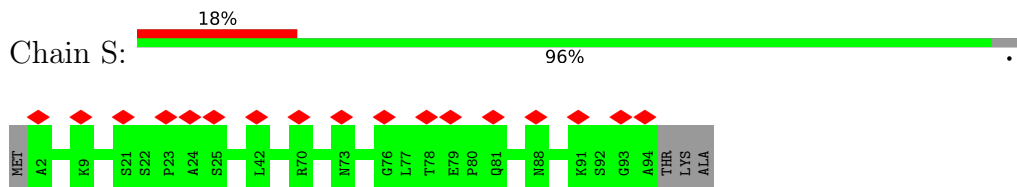
• Molecule 17: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial



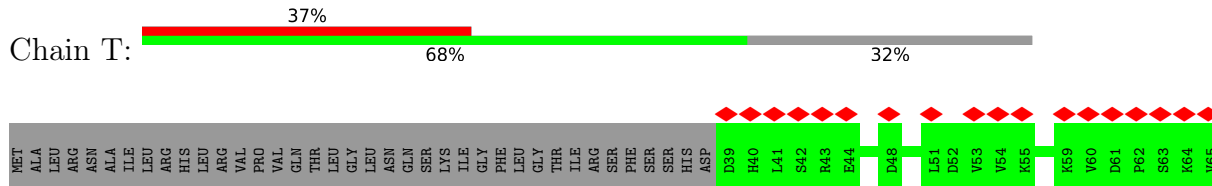
• Molecule 18: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial

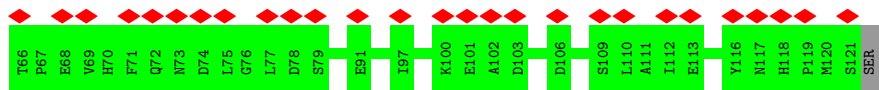


• Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2

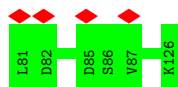
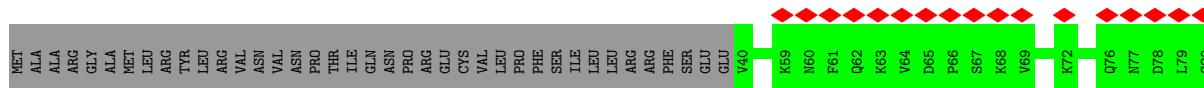


• Molecule 20: Acyl carrier protein 1, mitochondrial

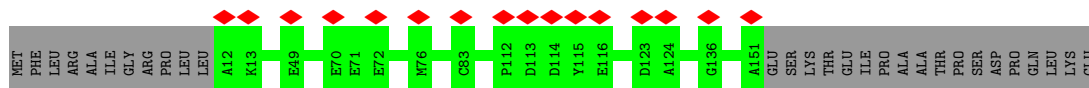
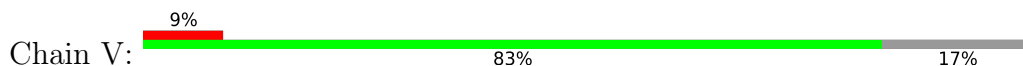




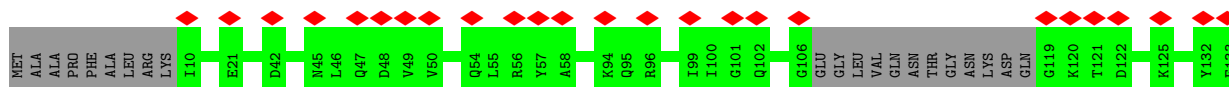
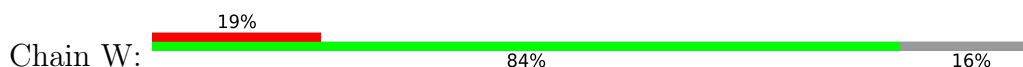
- Molecule 21: Acyl carrier protein 2, mitochondrial



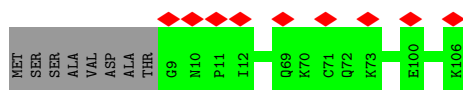
- Molecule 22: Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5, mitochondrial



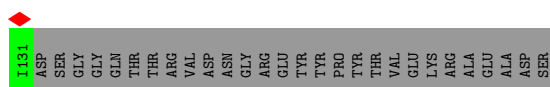
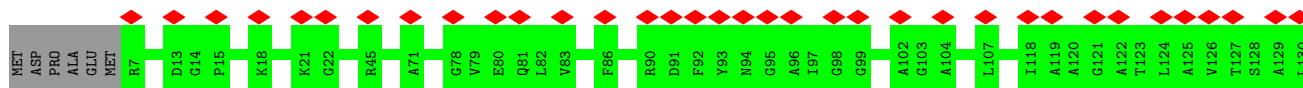
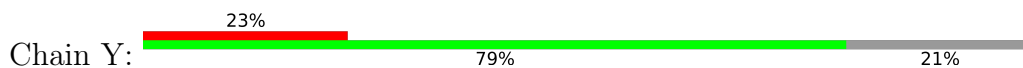
- Molecule 23: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6



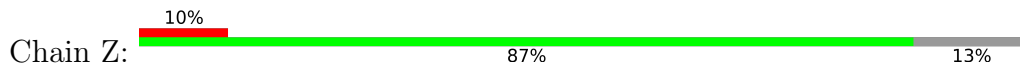
- Molecule 24: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8-B



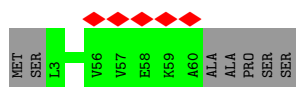
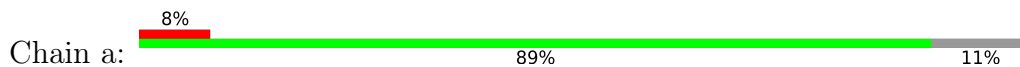
- Molecule 25: Outer envelope pore protein 16-3, chloroplatic/mitochondrial



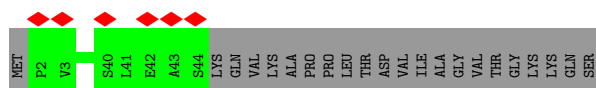
- Molecule 26: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13-A



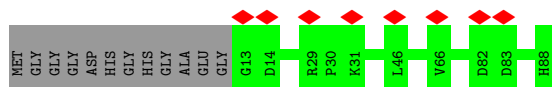
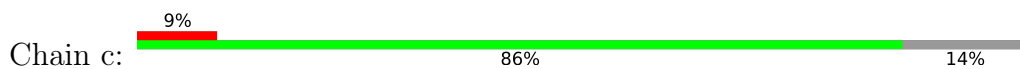
- Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1



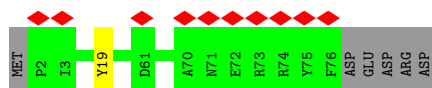
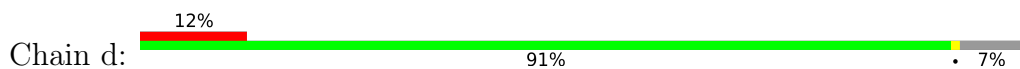
- Molecule 28: At2g46540/F11C10.23



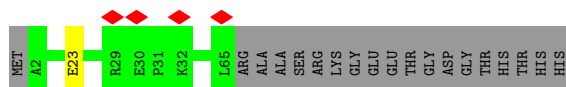
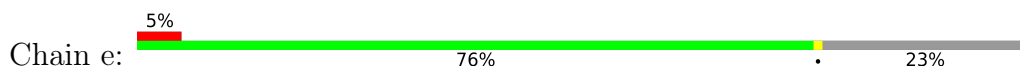
- Molecule 29: Transmembrane protein



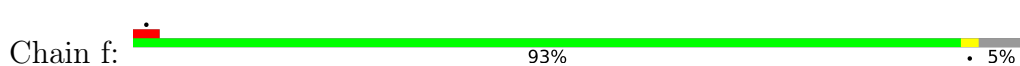
- Molecule 30: Excitatory amino acid transporter

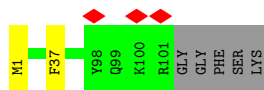


- Molecule 31: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5-B

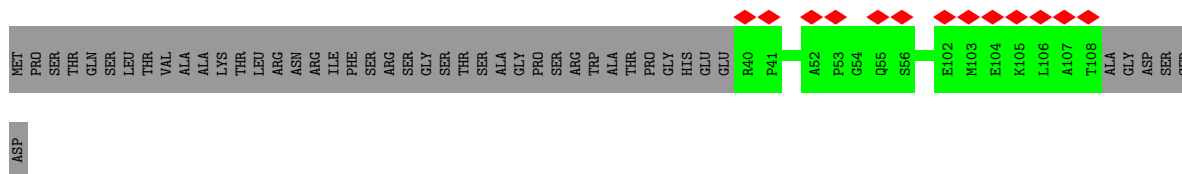


- Molecule 32: At4g16450

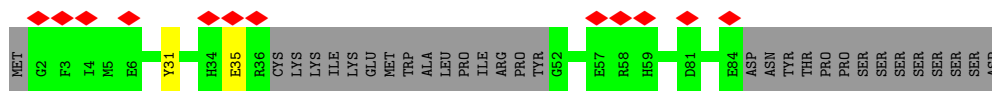




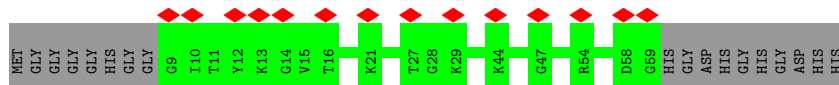
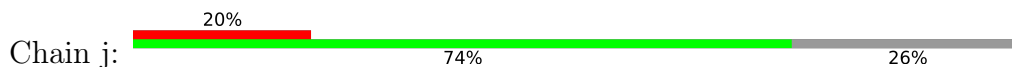
- Molecule 33: ESSS subunit of NADH:ubiquinone oxidoreductase (Complex I) protein



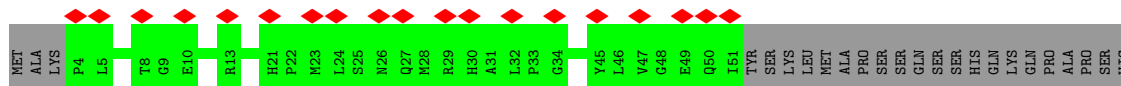
- Molecule 34: P1



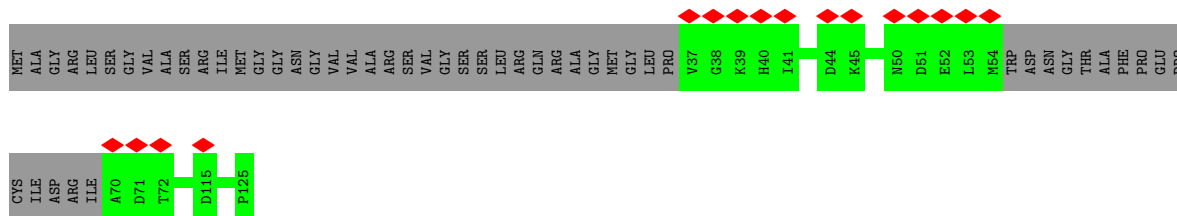
- Molecule 35: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2



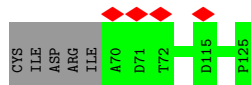
- Molecule 36: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3-A

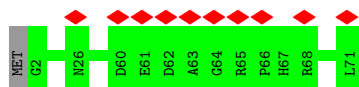


- Molecule 37: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

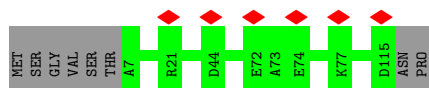
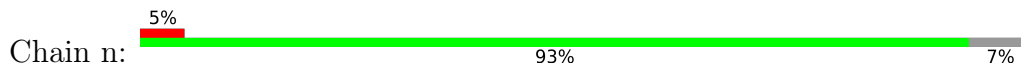


- Molecule 38: B15 – 1 beta subcomplex subunit 4

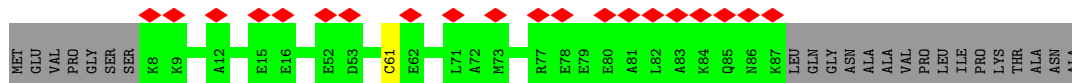




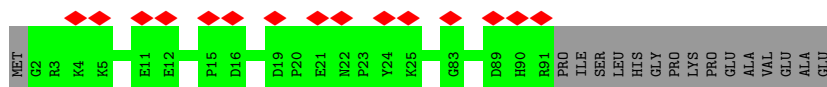
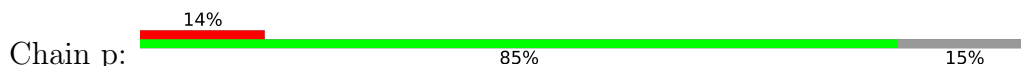
- Molecule 39: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9



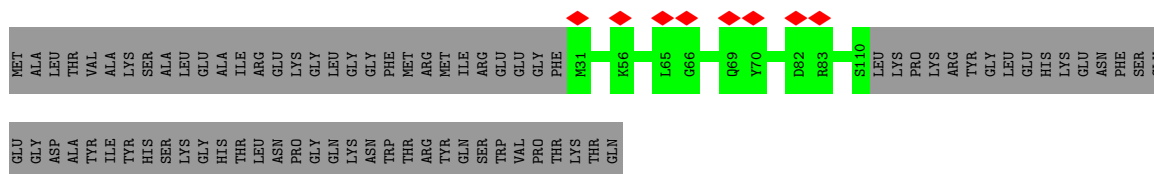
- Molecule 40: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7



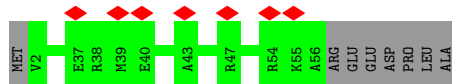
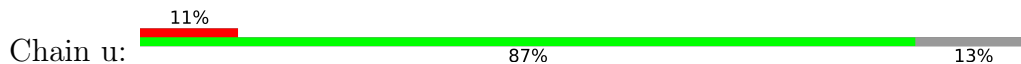
- Molecule 41: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10-B



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

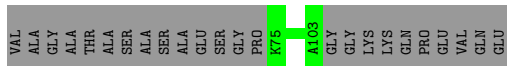
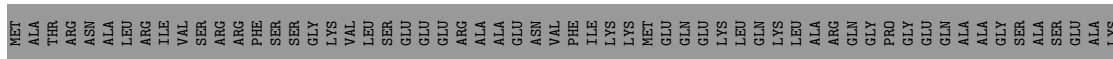


- Molecule 43: Uncharacterized protein At1g67785

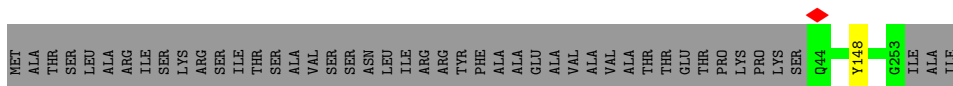
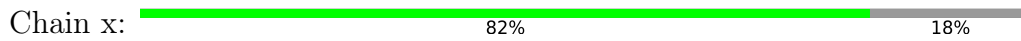


- Molecule 44: Uncharacterized protein At2g27730, mitochondrial

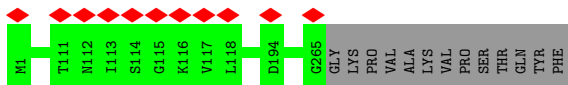




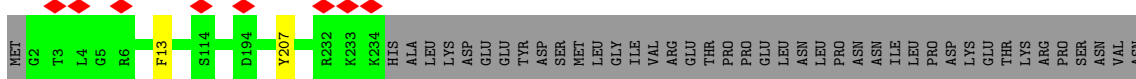
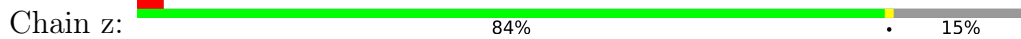
- Molecule 45: Gamma carbonic anhydrase-like 2, mitochondrial



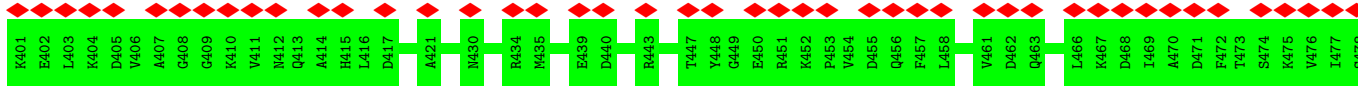
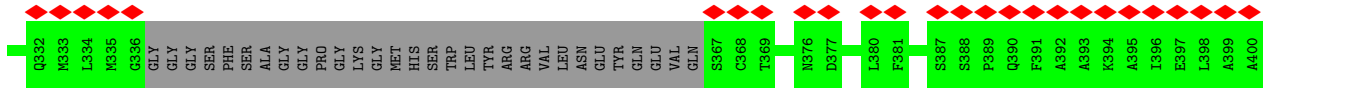
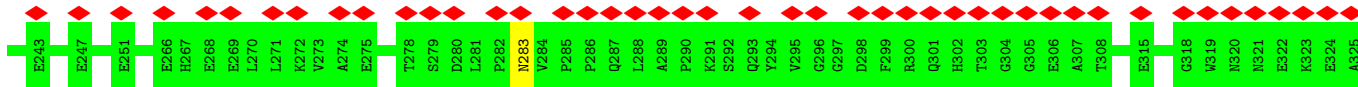
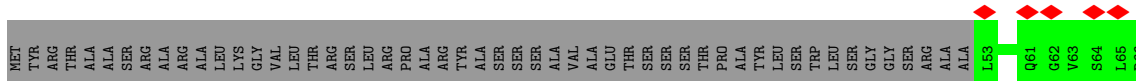
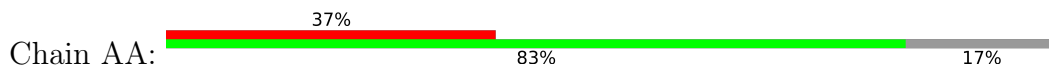
- Molecule 46: Gamma carbonic anhydrase 2, mitochondrial

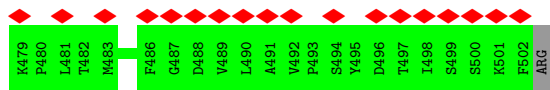


- Molecule 47: Gamma carbonic anhydrase 1, mitochondrial

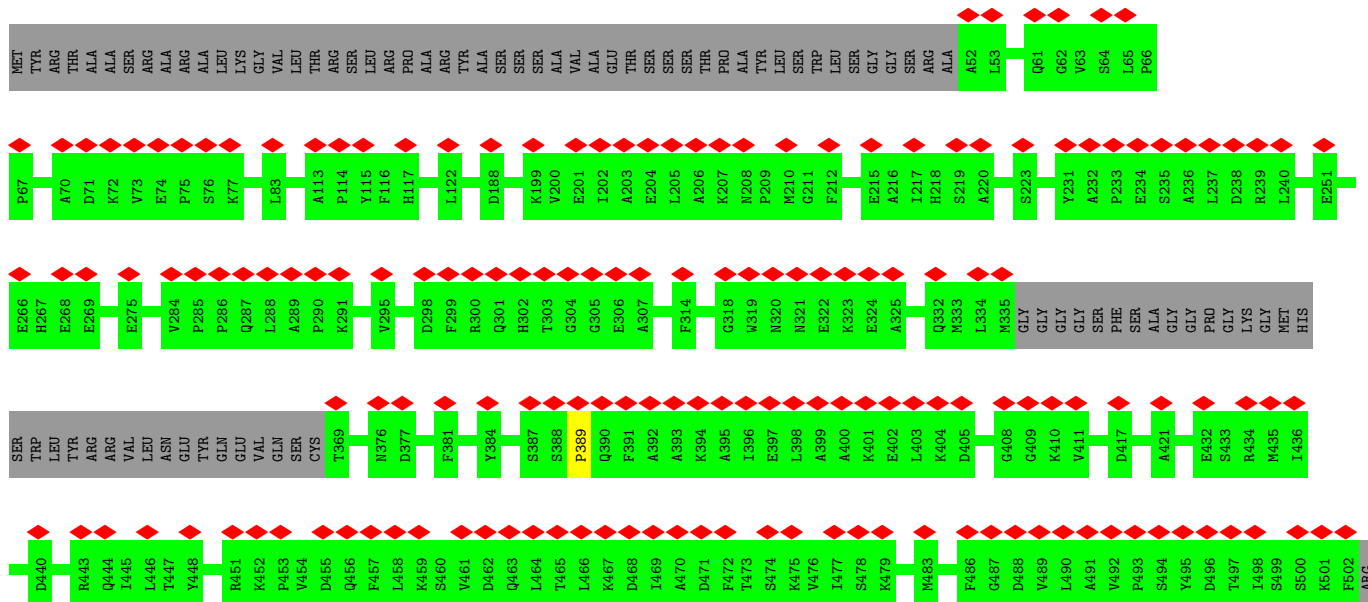
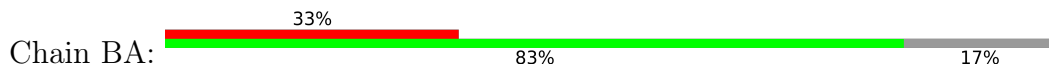


- Molecule 48: Probable mitochondrial-processing peptidase subunit alpha-1, mitochondrial

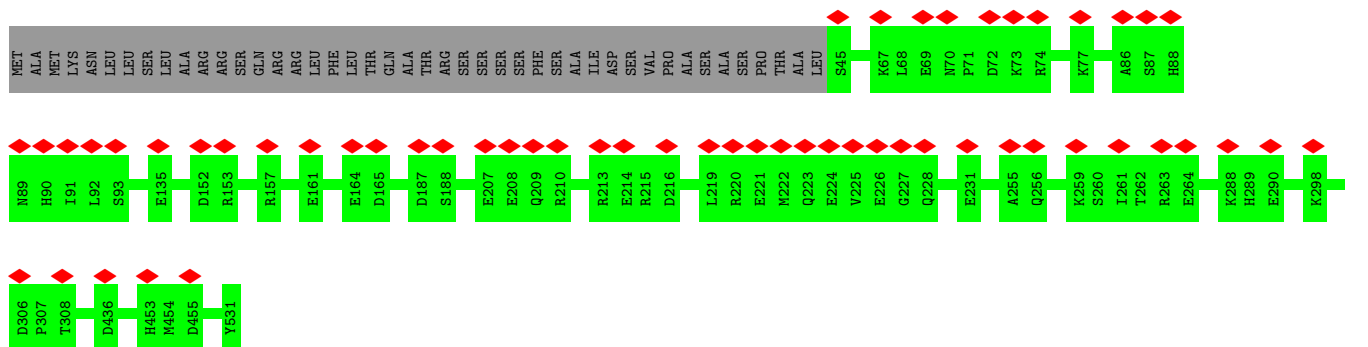




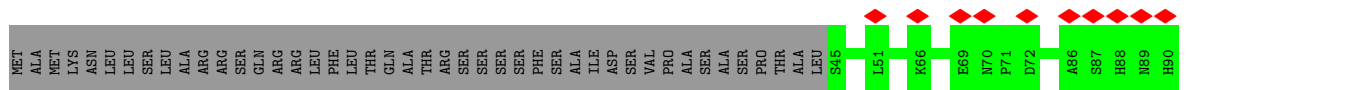
• Molecule 48: Probable mitochondrial-processing peptidase subunit alpha-1, mitochondrial

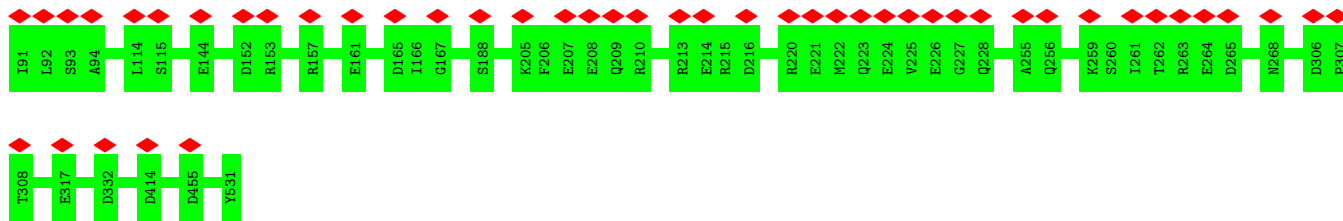


• Molecule 49: Probable mitochondrial-processing peptidase subunit beta, mitochondrial

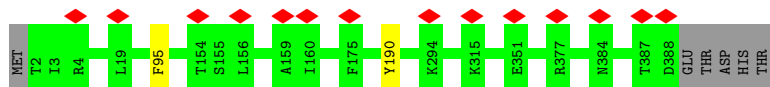


• Molecule 49: Probable mitochondrial-processing peptidase subunit beta, mitochondrial

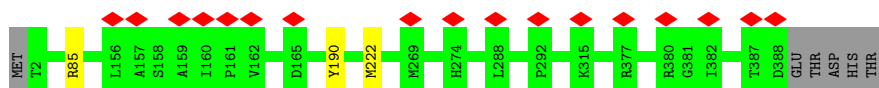




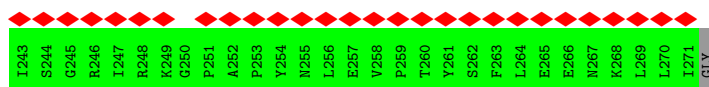
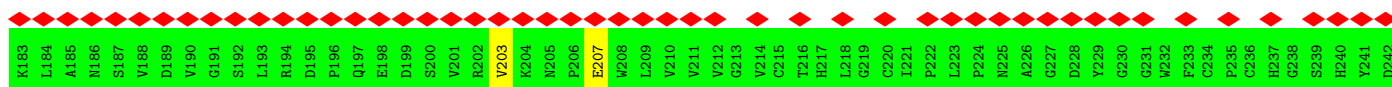
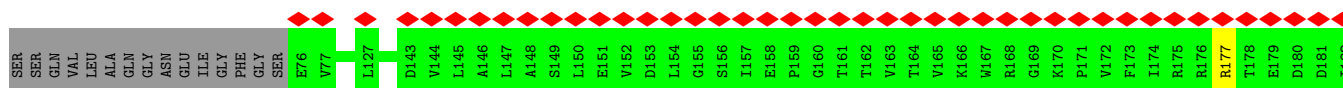
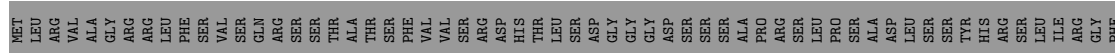
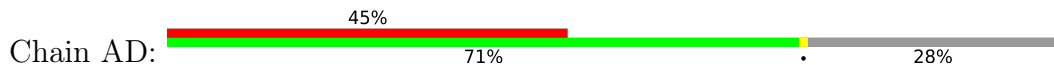
• Molecule 50: Cytochrome b



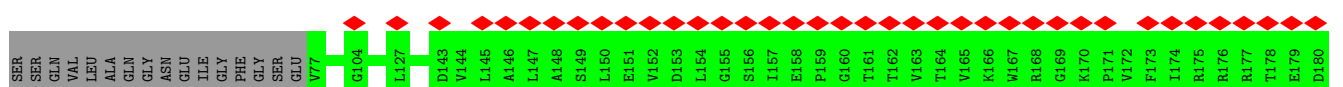
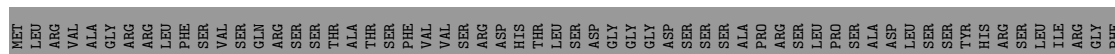
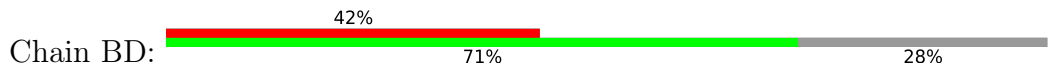
• Molecule 50: Cytochrome b

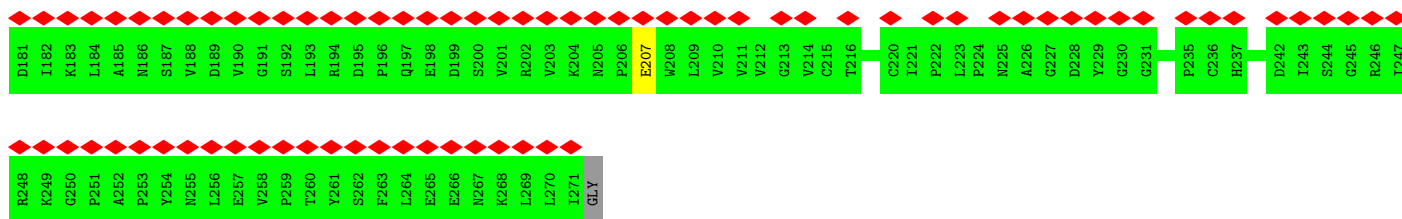


• Molecule 51: Cytochrome b-c1 complex subunit Rieske-1, mitochondrial

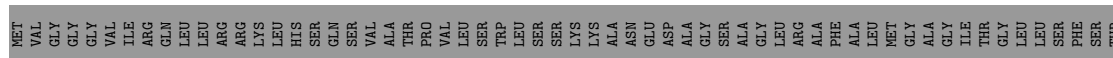
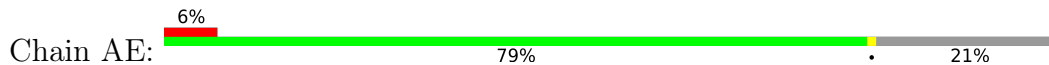


• Molecule 51: Cytochrome b-c1 complex subunit Rieske-1, mitochondrial

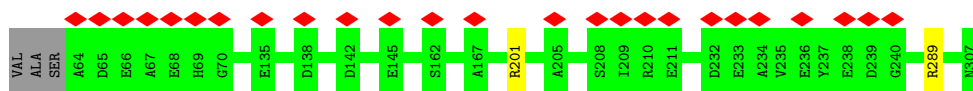
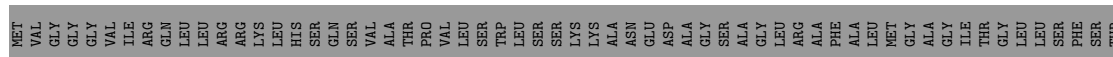
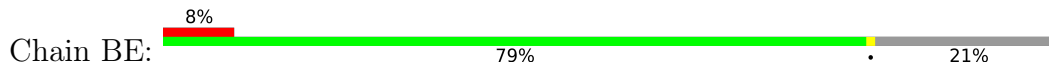




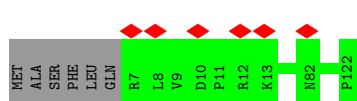
• Molecule 52: Cytochrome c1 2, heme protein, mitochondrial



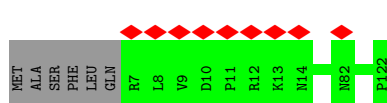
• Molecule 52: Cytochrome c1 2, heme protein, mitochondrial



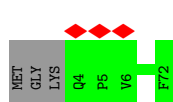
• Molecule 53: Cytochrome b-c1 complex subunit 7-2, mitochondrial



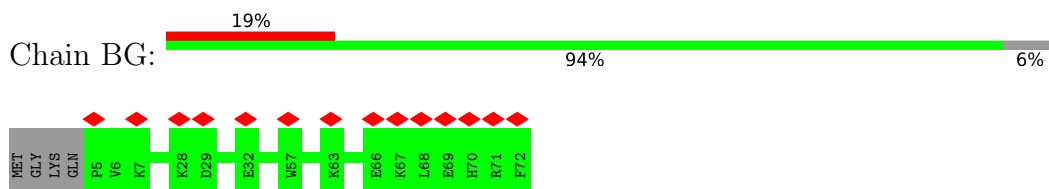
• Molecule 53: Cytochrome b-c1 complex subunit 7-2, mitochondrial



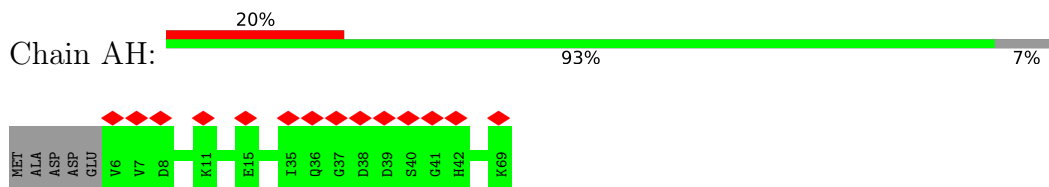
• Molecule 54: Cytochrome b-c1 complex subunit 8-1, mitochondrial



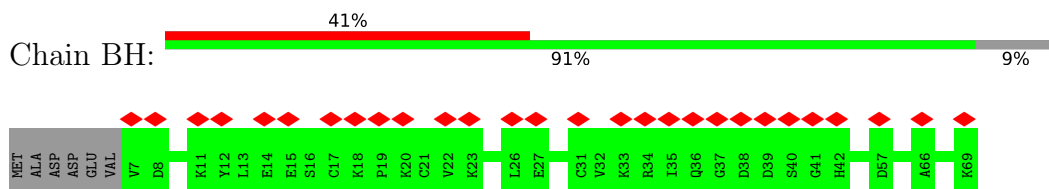
- Molecule 54: Cytochrome b-c1 complex subunit 8-1, mitochondrial



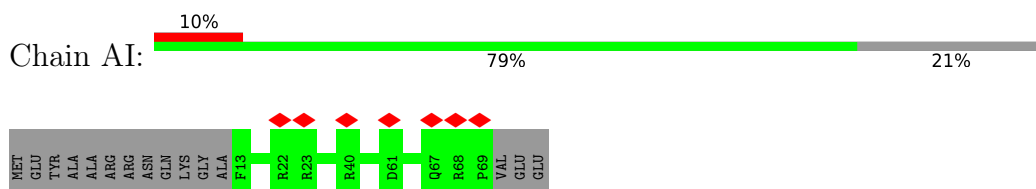
- Molecule 55: Cytochrome b-c1 complex subunit 6-1, mitochondrial



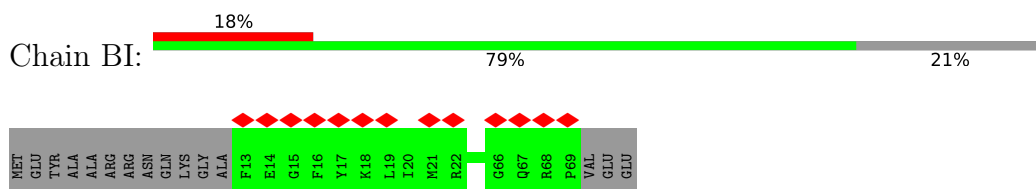
- Molecule 55: Cytochrome b-c1 complex subunit 6-1, mitochondrial



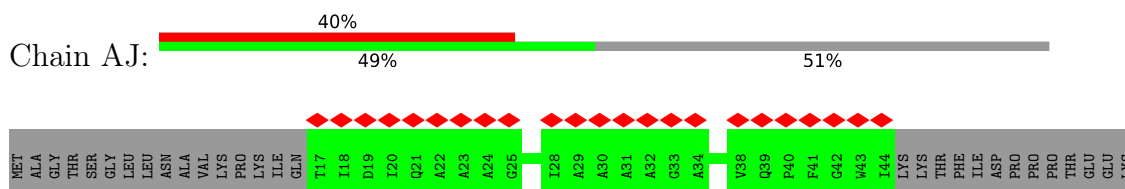
- Molecule 56: Cytochrome b-c1 complex subunit 9, mitochondrial



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

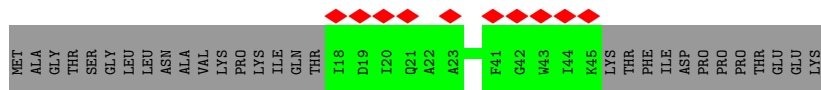


- Molecule 57: Cytochrome b-c1 complex subunit 10, mitochondrial



- 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	61200	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	0.099	Depositor
Minimum map value	-0.040	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 i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SF4, UQ7, UQ5, FME, FMN, NDP, COO, FE, FES, 8Q1, UQ9, HEM

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	0.36	0/820	0.52	0/1113
2	B	0.37	0/1279	0.55	0/1734
3	C	0.31	0/1590	0.55	0/2152
4	D	0.33	0/3149	0.54	0/4259
5	E	0.35	0/1535	0.52	0/2084
6	F	0.31	0/3441	0.51	0/4641
7	G	0.31	0/5338	0.52	0/7231
8	H	0.37	0/2609	0.54	0/3553
9	I	0.31	0/1378	0.55	0/1862
10	J	0.35	0/1435	0.54	1/1957 (0.1%)
11	K	0.39	0/785	0.53	0/1062
12	L	0.36	0/5368	0.51	0/7291
13	M	0.35	0/4057	0.51	0/5513
14	N	0.36	0/3937	0.52	0/5345
15	O	0.36	0/979	0.59	1/1326 (0.1%)
16	P	0.36	0/2509	0.58	1/3401 (0.0%)
17	Q	0.41	0/862	0.54	0/1166
18	R	0.27	0/585	0.44	0/793
19	S	0.30	0/739	0.52	0/996
20	T	0.41	0/671	0.50	0/911
21	U	0.46	0/687	0.57	0/929
22	V	0.33	0/1146	0.49	0/1555
23	W	0.35	0/923	0.50	0/1249
24	X	0.38	0/790	0.52	0/1060
25	Y	0.28	0/944	0.51	0/1277
26	Z	0.36	0/1027	0.55	0/1392
27	a	0.32	0/481	0.49	0/646
28	b	0.26	0/320	0.51	0/434
29	c	0.34	0/637	0.53	0/860
30	d	0.33	0/605	0.52	0/815
31	e	0.43	1/559 (0.2%)	0.55	0/745
32	f	0.43	0/771	0.55	0/1042

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.25	0/575	0.45	0/781
34	i	0.60	1/605 (0.2%)	0.66	1/812 (0.1%)
35	j	0.36	0/433	0.52	0/592
36	k	0.42	0/392	0.56	0/526
37	l	0.34	0/575	0.55	0/781
38	m	0.30	0/592	0.47	0/793
39	n	0.30	0/938	0.52	0/1273
40	o	0.52	1/666 (0.2%)	0.55	1/886 (0.1%)
41	p	0.40	0/777	0.56	0/1043
42	q	0.25	0/690	0.50	0/936
43	u	0.30	0/472	0.48	0/632
44	v	0.26	0/222	0.43	0/300
45	x	0.32	0/1669	0.54	0/2279
46	y	0.32	0/2046	0.53	0/2772
47	z	0.40	0/1804	0.60	0/2441
48	AA	0.39	0/3265	0.53	0/4431
48	BA	0.31	0/3254	0.51	2/4417 (0.0%)
49	AB	0.29	0/3908	0.50	0/5305
49	BB	0.30	0/3908	0.49	0/5305
50	AC	0.33	0/3208	0.48	0/4395
50	BC	0.35	0/3208	0.49	0/4395
51	AD	0.33	0/1567	0.52	0/2135
51	BD	0.33	0/1558	0.55	0/2123
52	AE	0.31	0/1968	0.48	0/2672
52	BE	0.28	0/1968	0.45	0/2672
53	AF	0.31	0/993	0.55	0/1336
53	BF	0.35	0/993	0.57	0/1336
54	AG	0.33	0/600	0.48	0/815
54	BG	0.28	0/591	0.43	0/802
55	AH	0.26	0/531	0.44	0/713
55	BH	0.27	0/524	0.41	0/703
56	AI	0.25	0/488	0.52	0/655
56	BI	0.25	0/488	0.49	0/655
57	AJ	0.23	0/210	0.35	0/290
57	BJ	0.39	0/212	0.50	0/291
All	All	0.34	3/97854 (0.0%)	0.52	7/132687 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	o	61	CYS	CB-SG	-8.88	1.67	1.82
31	e	23	GLU	CD-OE2	-7.33	1.17	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	i	31	TYR	CE2-CZ	-6.11	1.30	1.38

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	P	313	PRO	CA-N-CD	-9.37	98.39	111.50
48	BA	389	PRO	CA-N-CD	-7.93	100.40	111.50
15	O	54	ASP	CB-CG-OD1	6.44	124.10	118.30
48	BA	389	PRO	N-CD-CG	-6.21	93.89	103.20
40	o	61	CYS	CA-CB-SG	5.41	123.73	114.00
10	J	40	LEU	CB-CG-CD1	-5.08	102.37	111.00
34	i	35	GLU	CG-CD-OE1	-5.08	108.15	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	155/218 (71%)	148 (96%)	7 (4%)	0	100	100
3	C	179/190 (94%)	178 (99%)	1 (1%)	0	100	100
4	D	383/394 (97%)	367 (96%)	16 (4%)	0	100	100
5	E	190/255 (74%)	184 (97%)	6 (3%)	0	100	100
6	F	432/486 (89%)	423 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	685/748 (92%)	668 (98%)	17 (2%)	0	100	100
8	H	322/325 (99%)	314 (98%)	8 (2%)	0	100	100
9	I	163/222 (73%)	161 (99%)	2 (1%)	0	100	100
10	J	172/205 (84%)	168 (98%)	4 (2%)	0	100	100
11	K	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
12	L	663/669 (99%)	641 (97%)	22 (3%)	0	100	100
13	M	492/495 (99%)	486 (99%)	6 (1%)	0	100	100
14	N	487/499 (98%)	472 (97%)	15 (3%)	0	100	100
15	O	121/159 (76%)	117 (97%)	4 (3%)	0	100	100
16	P	314/402 (78%)	302 (96%)	12 (4%)	0	100	100
17	Q	103/154 (67%)	98 (95%)	5 (5%)	0	100	100
18	R	71/110 (64%)	70 (99%)	1 (1%)	0	100	100
19	S	91/97 (94%)	89 (98%)	2 (2%)	0	100	100
20	T	81/122 (66%)	77 (95%)	4 (5%)	0	100	100
21	U	85/126 (68%)	82 (96%)	3 (4%)	0	100	100
22	V	138/169 (82%)	137 (99%)	1 (1%)	0	100	100
23	W	108/133 (81%)	105 (97%)	3 (3%)	0	100	100
24	X	96/106 (91%)	94 (98%)	2 (2%)	0	100	100
25	Y	123/159 (77%)	119 (97%)	4 (3%)	0	100	100
26	Z	123/143 (86%)	120 (98%)	3 (2%)	0	100	100
27	a	56/65 (86%)	53 (95%)	3 (5%)	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%)	72 (99%)	1 (1%)	0	100	100
31	e	62/83 (75%)	60 (97%)	2 (3%)	0	100	100
32	f	99/106 (93%)	97 (98%)	2 (2%)	0	100	100
33	g	67/114 (59%)	67 (100%)	0	0	100	100
34	i	64/98 (65%)	64 (100%)	0	0	100	100
35	j	49/69 (71%)	48 (98%)	1 (2%)	0	100	100
36	k	46/72 (64%)	43 (94%)	3 (6%)	0	100	100
37	l	70/125 (56%)	67 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	m	68/71 (96%)	67 (98%)	1 (2%)	0	100	100
39	n	107/117 (92%)	106 (99%)	1 (1%)	0	100	100
40	o	78/103 (76%)	76 (97%)	2 (3%)	0	100	100
41	p	88/106 (83%)	85 (97%)	3 (3%)	0	100	100
42	q	79/159 (50%)	74 (94%)	5 (6%)	0	100	100
43	u	53/63 (84%)	53 (100%)	0	0	100	100
44	v	27/113 (24%)	27 (100%)	0	0	100	100
45	x	208/256 (81%)	204 (98%)	4 (2%)	0	100	100
46	y	263/278 (95%)	258 (98%)	5 (2%)	0	100	100
47	z	231/275 (84%)	226 (98%)	5 (2%)	0	100	100
48	AA	416/503 (83%)	404 (97%)	12 (3%)	0	100	100
48	BA	414/503 (82%)	401 (97%)	13 (3%)	0	100	100
49	AB	485/531 (91%)	476 (98%)	9 (2%)	0	100	100
49	BB	485/531 (91%)	477 (98%)	8 (2%)	0	100	100
50	AC	385/393 (98%)	375 (97%)	10 (3%)	0	100	100
50	BC	385/393 (98%)	379 (98%)	6 (2%)	0	100	100
51	AD	194/272 (71%)	185 (95%)	9 (5%)	0	100	100
51	BD	193/272 (71%)	181 (94%)	12 (6%)	0	100	100
52	AE	242/307 (79%)	239 (99%)	3 (1%)	0	100	100
52	BE	242/307 (79%)	241 (100%)	1 (0%)	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%)	65 (98%)	1 (2%)	0	100	100
55	AH	62/69 (90%)	62 (100%)	0	0	100	100
55	BH	61/69 (88%)	60 (98%)	1 (2%)	0	100	100
56	AI	55/72 (76%)	54 (98%)	1 (2%)	0	100	100
56	BI	55/72 (76%)	55 (100%)	0	0	100	100
57	AJ	26/57 (46%)	24 (92%)	2 (8%)	0	100	100
57	BJ	26/57 (46%)	24 (92%)	2 (8%)	0	100	100
All	All	11955/14108 (85%)	11657 (98%)	298 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	85/105 (81%)	85 (100%)	0	100	100
2	B	132/184 (72%)	129 (98%)	3 (2%)	50	70
3	C	171/179 (96%)	169 (99%)	2 (1%)	71	83
4	D	331/340 (97%)	331 (100%)	0	100	100
5	E	166/220 (76%)	166 (100%)	0	100	100
6	F	353/396 (89%)	353 (100%)	0	100	100
7	G	570/625 (91%)	568 (100%)	2 (0%)	91	94
8	H	271/272 (100%)	269 (99%)	2 (1%)	84	90
9	I	147/195 (75%)	147 (100%)	0	100	100
10	J	156/186 (84%)	154 (99%)	2 (1%)	69	82
11	K	85/85 (100%)	85 (100%)	0	100	100
12	L	564/568 (99%)	562 (100%)	2 (0%)	91	94
13	M	433/434 (100%)	432 (100%)	1 (0%)	93	96
14	N	407/416 (98%)	404 (99%)	3 (1%)	84	90
15	O	108/141 (77%)	108 (100%)	0	100	100
16	P	263/334 (79%)	262 (100%)	1 (0%)	91	94
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%)	82 (100%)	0	100	100
20	T	78/112 (70%)	78 (100%)	0	100	100
21	U	78/113 (69%)	78 (100%)	0	100	100
22	V	123/148 (83%)	123 (100%)	0	100	100
23	W	98/114 (86%)	98 (100%)	0	100	100
24	X	88/94 (94%)	88 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	Y	92/120 (77%)	92 (100%)	0	100	100
26	Z	100/115 (87%)	100 (100%)	0	100	100
27	a	48/53 (91%)	48 (100%)	0	100	100
28	b	35/53 (66%)	35 (100%)	0	100	100
29	c	66/71 (93%)	66 (100%)	0	100	100
30	d	60/66 (91%)	59 (98%)	1 (2%)	60	76
31	e	59/73 (81%)	59 (100%)	0	100	100
32	f	80/83 (96%)	79 (99%)	1 (1%)	69	82
33	g	60/96 (62%)	60 (100%)	0	100	100
34	i	61/90 (68%)	61 (100%)	0	100	100
35	j	42/51 (82%)	42 (100%)	0	100	100
36	k	39/60 (65%)	39 (100%)	0	100	100
37	l	60/97 (62%)	60 (100%)	0	100	100
38	m	58/59 (98%)	58 (100%)	0	100	100
39	n	92/99 (93%)	92 (100%)	0	100	100
40	o	70/87 (80%)	70 (100%)	0	100	100
41	p	80/93 (86%)	80 (100%)	0	100	100
42	q	69/133 (52%)	69 (100%)	0	100	100
43	u	47/54 (87%)	47 (100%)	0	100	100
44	v	22/84 (26%)	22 (100%)	0	100	100
45	x	179/216 (83%)	178 (99%)	1 (1%)	86	91
46	y	221/232 (95%)	221 (100%)	0	100	100
47	z	188/228 (82%)	186 (99%)	2 (1%)	73	84
48	AA	347/408 (85%)	346 (100%)	1 (0%)	92	95
48	BA	345/408 (85%)	345 (100%)	0	100	100
49	AB	415/452 (92%)	415 (100%)	0	100	100
49	BB	415/452 (92%)	415 (100%)	0	100	100
50	AC	330/336 (98%)	328 (99%)	2 (1%)	86	91
50	BC	330/336 (98%)	327 (99%)	3 (1%)	78	87
51	AD	170/232 (73%)	167 (98%)	3 (2%)	59	75
51	BD	169/232 (73%)	168 (99%)	1 (1%)	86	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	AE	200/247 (81%)	198 (99%)	2 (1%)	76	85
52	BE	200/247 (81%)	198 (99%)	2 (1%)	76	85
53	AF	105/110 (96%)	105 (100%)	0	100	100
53	BF	105/110 (96%)	105 (100%)	0	100	100
54	AG	63/65 (97%)	63 (100%)	0	100	100
54	BG	62/65 (95%)	62 (100%)	0	100	100
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%)	48 (100%)	0	100	100
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	10269/11908 (86%)	10232 (100%)	37 (0%)	91	94

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	89	PHE
2	B	93	CYS
2	B	164	TYR
3	C	60	CYS
3	C	111	TRP
7	G	104	ARG
7	G	670	TYR
8	H	71	PHE
8	H	126	ARG
10	J	30	PHE
10	J	99	TRP
12	L	345	LYS
12	L	565	PHE
13	M	128	PHE
14	N	179	TYR
14	N	283	TYR
14	N	391	PHE
16	P	123	PHE
30	d	19	TYR
32	f	37	PHE
45	x	148	TYR

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Mol	Chain	Res	Type
47	z	13	PHE
47	z	207	TYR
48	AA	283	ASN
50	AC	95	PHE
50	AC	190	TYR
51	AD	177	ARG
51	AD	203	VAL
51	AD	207	GLU
52	AE	289	ARG
52	AE	292	LYS
50	BC	85	ARG
50	BC	190	TYR
50	BC	222	MET
51	BD	207	GLU
52	BE	201	ARG
52	BE	289	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	121	GLN
2	B	145	GLN
2	B	207	ASN
3	C	76	ASN
4	D	311	HIS
5	E	150	HIS
7	G	184	GLN
7	G	302	ASN
7	G	446	GLN
8	H	129	ASN
12	L	305	ASN
13	M	341	HIS
13	M	411	ASN
13	M	434	ASN
13	M	487	ASN
16	P	143	ASN
16	P	182	GLN
21	U	60	ASN
25	Y	84	GLN
31	e	10	ASN
34	i	34	HIS
38	m	8	ASN

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Mol	Chain	Res	Type
40	o	56	HIS
42	q	45	HIS
48	AA	136	HIS
48	AA	390	GLN
48	AA	413	GLN
49	AB	90	HIS
50	AC	183	ASN
52	AE	80	HIS
48	BA	136	HIS
49	BB	453	HIS
50	BC	5	ASN
50	BC	183	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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	0.69	0	7,9,11	1.61	1 (14%)
11	FME	K	1	11	8,9,10	0.94	0	7,9,11	1.17	1 (14%)
1	FME	A	1	1	8,9,10	1.72	1 (12%)	7,9,11	1.49	1 (14%)

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	-	2/7/9/11	-
11	FME	K	1	11	-	5/7/9/11	-
1	FME	A	1	1	-	1/7/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	FME	O-C	4.16	1.36	1.19

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	FME	O-C-CA	-3.47	115.69	124.78
32	f	1	FME	O-C-CA	-3.41	115.85	124.78
11	K	1	FME	C-CA-N	2.32	113.93	109.73

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1	FME	O-C-CA-CB
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	C-CA-CB-CG
11	K	1	FME	CA-CB-CG-SD
11	K	1	FME	C-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides 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	BE	400	52	41,50,50	1.43	3 (7%)	45,82,82	1.39	7 (15%)
58	SF4	B	500	2	0,12,12	-	-	-		
58	SF4	F	501	6	0,12,12	-	-	-		
58	SF4	G	802	7	0,12,12	-	-	-		
59	FES	E	500	5	0,4,4	-	-	-		
59	FES	BD	301	51	0,4,4	-	-	-		
58	SF4	G	803	7	0,12,12	-	-	-		
67	HEM	AC	501	50	41,50,50	1.35	4 (9%)	45,82,82	1.79	10 (22%)
65	8Q1	W	200	-	31,34,34	0.35	0	40,43,43	0.48	0
58	SF4	I	501	9	0,12,12	-	-	-		
61	UQ9	H	500	-	35,35,58	2.51	13 (37%)	42,45,73	2.08	12 (28%)
67	HEM	BC	501	50	41,50,50	1.35	5 (12%)	45,82,82	1.82	9 (20%)
68	UQ5	AC	503	-	38,38,38	0.50	0	46,49,49	0.83	1 (2%)
67	HEM	AE	400	-	41,50,50	1.65	4 (9%)	45,82,82	1.76	11 (24%)
59	FES	G	801	7	0,4,4	-	-	-		
68	UQ5	BC	502	-	38,38,38	0.45	0	46,49,49	0.57	0
69	UQ7	BC	503	-	48,48,48	0.43	0	58,61,61	0.53	1 (1%)
63	NDP	P	500	-	45,52,52	0.62	0	53,80,80	0.60	1 (1%)
60	FMN	F	500	-	33,33,33	1.07	2 (6%)	48,50,50	1.19	6 (12%)
65	8Q1	n	200	-	31,34,34	1.74	6 (19%)	40,43,43	1.82	8 (20%)
68	UQ5	AC	502	-	38,38,38	0.49	0	46,49,49	0.64	1 (2%)
58	SF4	I	500	9	0,12,12	-	-	-		
67	HEM	BC	500	50	41,50,50	1.45	4 (9%)	45,82,82	1.37	6 (13%)
59	FES	AD	301	51	0,4,4	-	-	-		
66	COO	x	301	-	45,55,55	3.96	16 (35%)	55,81,81	2.54	11 (20%)
67	HEM	AC	500	50	41,50,50	1.35	4 (9%)	45,82,82	1.76	9 (20%)

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	BE	400	52	-	1/12/54/54	-
58	SF4	B	500	2	-	-	0/6/5/5
58	SF4	F	501	6	-	-	0/6/5/5
58	SF4	G	802	7	-	-	0/6/5/5
59	FES	E	500	5	-	-	0/1/1/1
59	FES	BD	301	51	-	-	0/1/1/1
67	HEM	AC	501	50	-	5/12/54/54	-
58	SF4	G	803	7	-	-	0/6/5/5
65	8Q1	W	200	-	-	18/41/41/41	-
58	SF4	I	501	9	-	-	0/6/5/5
61	UQ9	H	500	-	-	7/30/54/81	0/1/1/1
67	HEM	BC	501	50	-	7/12/54/54	-
68	UQ5	AC	503	-	-	11/33/57/57	0/1/1/1
67	HEM	AE	400	-	-	2/12/54/54	-
59	FES	G	801	7	-	-	0/1/1/1
68	UQ5	BC	502	-	-	8/33/57/57	0/1/1/1
69	UQ7	BC	503	-	-	8/45/69/69	0/1/1/1
63	NDP	P	500	-	-	7/30/77/77	0/5/5/5
60	FMN	F	500	-	-	2/18/18/18	0/3/3/3
65	8Q1	n	200	-	-	22/41/41/41	-
68	UQ5	AC	502	-	-	11/33/57/57	0/1/1/1
58	SF4	I	500	9	-	-	0/6/5/5
67	HEM	BC	500	50	-	2/12/54/54	-
59	FES	AD	301	51	-	-	0/1/1/1
66	COO	x	301	-	1/1/12/16	11/50/70/70	0/3/3/3
67	HEM	AC	500	50	-	6/12/54/54	-

All (61) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	x	301	COO	C2A-N1A	-15.86	1.04	1.33
61	H	500	UQ9	C6-C1	9.65	1.52	1.35
66	x	301	COO	C2A-N3A	-9.06	1.17	1.32
66	x	301	COO	C5A-C4A	8.11	1.62	1.40
66	x	301	COO	C1-N1	7.45	1.49	1.33
66	x	301	COO	C4-N2	6.55	1.48	1.33
67	AE	400	HEM	FE-NB	6.19	2.27	1.96
66	x	301	COO	O4X-C1X	6.13	1.49	1.41
65	n	200	8Q1	C34-N36	5.96	1.46	1.33
66	x	301	COO	C6A-N1A	-5.58	1.12	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	x	301	COO	C4A-N3A	5.53	1.43	1.35
65	n	200	8Q1	C39-N41	5.33	1.45	1.33
61	H	500	UQ9	C4-C3	4.69	1.55	1.36
61	H	500	UQ9	C7-C8	4.33	1.56	1.50
66	x	301	COO	C5A-N7A	-4.13	1.24	1.39
67	AE	400	HEM	C3C-C2C	-4.01	1.34	1.40
67	BE	400	HEM	C3C-C2C	-3.97	1.34	1.40
67	BC	500	HEM	C3C-C2C	-3.85	1.35	1.40
67	BC	500	HEM	C3C-CAC	3.83	1.55	1.47
67	BE	400	HEM	C3C-CAC	3.73	1.55	1.47
67	AE	400	HEM	C3C-CAC	3.68	1.55	1.47
60	F	500	FMN	C4A-N5	3.65	1.37	1.30
67	BC	501	HEM	C1B-NB	-3.63	1.34	1.40
67	AC	501	HEM	C1B-NB	-3.58	1.34	1.40
66	x	301	COO	C2X-C1X	-3.57	1.48	1.53
67	AC	500	HEM	C1B-NB	-3.47	1.34	1.40
66	x	301	COO	P3X-O3X	3.45	1.65	1.59
67	AC	500	HEM	C4D-ND	-3.41	1.34	1.40
67	BC	501	HEM	C4D-ND	-3.36	1.34	1.40
67	AC	501	HEM	C4D-ND	-3.28	1.34	1.40
66	x	301	COO	C6A-N6A	3.01	1.45	1.34
67	AC	501	HEM	FE-NB	3.00	2.11	1.96
67	BC	501	HEM	FE-NB	2.96	2.11	1.96
67	AC	500	HEM	FE-NB	2.95	2.11	1.96
67	BC	500	HEM	CAB-C3B	2.91	1.55	1.47
67	BE	400	HEM	CAB-C3B	2.85	1.55	1.47
61	H	500	UQ9	O4-C4M	-2.79	1.38	1.45
61	H	500	UQ9	C7-C6	2.75	1.55	1.51
61	H	500	UQ9	C11-C9	2.72	1.56	1.51
66	x	301	COO	C3-C4	2.65	1.56	1.51
67	AE	400	HEM	CAB-C3B	2.54	1.54	1.47
60	F	500	FMN	C10-N1	2.47	1.38	1.33
61	H	500	UQ9	C16-C14	2.46	1.56	1.51
66	x	301	COO	C2X-C3X	-2.39	1.47	1.52
65	n	200	8Q1	C1-S44	2.33	1.81	1.76
65	n	200	8Q1	O35-C34	-2.31	1.18	1.23
65	n	200	8Q1	O40-C39	-2.24	1.18	1.23
66	x	301	COO	P1A-O5X	2.22	1.68	1.59
61	H	500	UQ9	C26-C24	2.19	1.55	1.51
66	x	301	COO	O3-C4	-2.18	1.18	1.23
65	n	200	8Q1	C6-C1	2.16	1.53	1.50
61	H	500	UQ9	C21-C19	2.15	1.55	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	H	500	UQ9	O5-C5	-2.12	1.18	1.23
67	AC	500	HEM	C1D-ND	-2.10	1.34	1.38
67	AC	501	HEM	C1D-ND	-2.07	1.34	1.38
67	BC	501	HEM	C4B-NB	-2.05	1.34	1.38
67	BC	501	HEM	C1D-ND	-2.05	1.34	1.38
61	H	500	UQ9	O2-C2	-2.04	1.18	1.23
61	H	500	UQ9	O3-C3M	-2.03	1.40	1.45
61	H	500	UQ9	O3-C3	2.02	1.41	1.36
67	BC	500	HEM	CMB-C2B	2.01	1.55	1.50

All (93) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
66	x	301	COO	C4A-C5A-N7A	-13.77	95.05	109.40
65	n	200	8Q1	C6-C1-S44	6.04	120.49	113.46
66	x	301	COO	C6-S1-C7	5.93	107.25	99.80
61	H	500	UQ9	C7-C8-C9	-5.76	117.20	126.79
66	x	301	COO	C1X-N9A-C4A	-5.36	117.23	126.64
61	H	500	UQ9	C7-C6-C5	5.13	124.65	118.48
67	AE	400	HEM	C1B-NB-C4B	4.83	110.06	105.07
67	BC	501	HEM	CHC-C4B-NB	4.62	129.45	124.43
67	AC	500	HEM	CHC-C4B-NB	4.49	129.31	124.43
67	AC	501	HEM	CHC-C4B-NB	4.41	129.22	124.43
67	BC	501	HEM	CHD-C1D-ND	4.38	129.19	124.43
67	AC	501	HEM	CHD-C1D-ND	4.31	129.11	124.43
67	AC	500	HEM	CHD-C1D-ND	4.21	129.01	124.43
61	H	500	UQ9	C12-C13-C14	-4.21	117.52	127.66
66	x	301	COO	C2A-N1A-C6A	4.18	125.91	118.75
65	n	200	8Q1	C32-C34-N36	4.18	124.90	116.58
68	AC	503	UQ5	C7-C6-C5	-4.06	113.60	118.48
67	BC	501	HEM	CHA-C4D-ND	3.93	129.24	124.38
67	BC	501	HEM	C1B-NB-C4B	3.92	109.12	105.07
67	AC	501	HEM	CHA-C4D-ND	3.89	129.19	124.38
67	AC	501	HEM	C1B-NB-C4B	3.72	108.91	105.07
67	AC	500	HEM	C1B-NB-C4B	3.69	108.89	105.07
67	AC	500	HEM	CHB-C1B-NB	3.64	128.88	124.38
67	BC	501	HEM	CHB-C1B-NB	3.62	128.85	124.38
61	H	500	UQ9	C1M-C1-C6	-3.49	118.70	124.40
67	AC	501	HEM	CHB-C1B-NB	3.47	128.66	124.38
66	x	301	COO	C5A-C6A-N1A	3.46	128.21	120.35
67	AC	500	HEM	CHA-C4D-ND	3.44	128.63	124.38
61	H	500	UQ9	C27-C26-C24	-3.42	109.03	114.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	H	500	UQ9	C6-C1-C2	3.36	121.84	119.18
65	n	200	8Q1	O4-C1-C6	-3.29	120.11	123.99
66	x	301	COO	C5A-C6A-N6A	-3.24	115.43	120.35
60	F	500	FMN	C4-N3-C2	-3.23	119.68	125.64
67	AE	400	HEM	C4D-ND-C1D	3.11	108.28	105.07
67	AE	400	HEM	C2B-C1B-NB	-3.09	106.17	109.84
61	H	500	UQ9	C17-C18-C19	-3.02	120.38	127.66
67	AE	400	HEM	C4B-CHC-C1C	2.93	126.42	122.56
65	n	200	8Q1	C37-C38-C39	-2.91	107.52	112.36
67	AE	400	HEM	C3B-C2B-C1B	2.86	108.61	106.49
67	BC	500	HEM	C4D-ND-C1D	2.80	107.96	105.07
60	F	500	FMN	C4A-C4-N3	2.79	120.27	113.19
61	H	500	UQ9	C8-C7-C6	2.78	119.55	112.05
67	AC	501	HEM	C4D-ND-C1D	2.78	107.94	105.07
61	H	500	UQ9	C20-C19-C21	2.75	119.90	115.27
67	AC	500	HEM	CBD-CAD-C3D	-2.75	104.99	112.63
69	BC	503	UQ7	C7-C6-C1	-2.74	115.18	118.48
67	AE	400	HEM	CAA-CBA-CGA	-2.70	106.18	113.76
61	H	500	UQ9	C25-C24-C26	2.69	119.80	115.27
67	BC	500	HEM	C1B-NB-C4B	2.69	107.85	105.07
67	BE	400	HEM	CMC-C2C-C3C	2.68	129.68	124.68
60	F	500	FMN	O4-C4-C4A	-2.66	119.53	126.60
65	n	200	8Q1	C38-C39-N41	2.66	120.90	116.42
67	BE	400	HEM	C4D-ND-C1D	2.66	107.82	105.07
66	x	301	COO	C3X-C2X-C1X	2.66	105.78	99.89
67	BC	501	HEM	C4D-ND-C1D	2.62	107.78	105.07
68	AC	502	UQ5	C7-C8-C9	2.59	131.11	126.79
61	H	500	UQ9	C15-C14-C16	2.59	119.62	115.27
67	AE	400	HEM	CMC-C2C-C3C	2.56	129.47	124.68
67	AE	400	HEM	C4A-C3A-C2A	2.56	108.77	107.00
65	n	200	8Q1	O35-C34-N36	-2.53	117.56	122.99
65	n	200	8Q1	C42-N41-C39	-2.53	118.15	122.84
67	AC	500	HEM	C4D-ND-C1D	2.53	107.68	105.07
67	BE	400	HEM	C1B-NB-C4B	2.50	107.65	105.07
67	BC	501	HEM	CHD-C1D-C2D	-2.49	121.10	124.98
65	n	200	8Q1	O4-C1-S44	-2.47	119.40	122.61
67	BE	400	HEM	C4B-CHC-C1C	2.45	125.79	122.56
67	BC	500	HEM	C4B-CHC-C1C	2.45	125.79	122.56
60	F	500	FMN	C4A-C10-N10	2.45	120.06	116.48
67	AC	500	HEM	CHD-C1D-C2D	-2.44	121.17	124.98
67	AE	400	HEM	C4C-CHD-C1D	2.42	125.75	122.56
67	BE	400	HEM	CAA-CBA-CGA	-2.41	106.99	113.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
66	x	301	COO	P1A-O3A-P2A	-2.41	124.56	132.83
67	AC	501	HEM	CHD-C1D-C2D	-2.39	121.25	124.98
67	BC	500	HEM	C4C-CHD-C1D	2.37	125.69	122.56
66	x	301	COO	C10-C9-C8	-2.30	120.80	125.34
67	BC	501	HEM	CHA-C4D-C3D	-2.29	121.03	125.33
67	AE	400	HEM	C3D-C4D-ND	-2.28	107.63	110.17
67	BC	500	HEM	CMC-C2C-C3C	2.25	128.88	124.68
67	AE	400	HEM	CMA-C3A-C4A	-2.24	125.02	128.46
60	F	500	FMN	C4A-C10-N1	-2.23	119.55	124.73
67	AC	500	HEM	CHB-C1B-C2B	-2.18	120.69	126.72
67	AC	501	HEM	CHA-C4D-C3D	-2.17	121.25	125.33
61	H	500	UQ9	C22-C23-C24	-2.17	122.44	127.66
63	P	500	NDP	C5A-C6A-N6A	2.15	123.63	120.35
67	BC	500	HEM	C3D-C4D-ND	-2.15	107.78	110.17
67	AC	501	HEM	CHB-C1B-C2B	-2.13	120.82	126.72
67	BC	501	HEM	CHB-C1B-C2B	-2.12	120.87	126.72
67	BE	400	HEM	CMA-C3A-C4A	-2.11	125.22	128.46
67	BE	400	HEM	C3B-C2B-C1B	2.09	108.04	106.49
67	AC	501	HEM	CBD-CAD-C3D	-2.06	106.91	112.63
66	x	301	COO	C2-N1-C1	-2.05	118.93	122.59
60	F	500	FMN	C10-C4A-N5	-2.05	120.51	124.86
66	x	301	COO	C14-C11-C13	2.04	112.36	108.82

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
66	x	301	COO	C13

All (128) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
61	H	500	UQ9	C1-C6-C7-C8
61	H	500	UQ9	C5-C6-C7-C8
65	W	200	8Q1	O27-C28-C29-C31
65	W	200	8Q1	O27-C28-C29-C32
65	W	200	8Q1	C28-C29-C32-C34
65	W	200	8Q1	C28-C29-C32-O33
65	W	200	8Q1	C30-C29-C32-C34
65	W	200	8Q1	C30-C29-C32-O33
65	W	200	8Q1	C31-C29-C32-C34
65	W	200	8Q1	C31-C29-C32-O33
65	W	200	8Q1	C28-O27-P24-O2

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Mol	Chain	Res	Type	Atoms
65	W	200	8Q1	C28-O27-P24-O1
65	n	200	8Q1	C1-C6-C7-C8
65	n	200	8Q1	O4-C1-S44-C43
65	n	200	8Q1	C6-C1-S44-C43
65	n	200	8Q1	C28-C29-C32-C34
65	n	200	8Q1	C28-C29-C32-O33
65	n	200	8Q1	C30-C29-C32-C34
65	n	200	8Q1	C30-C29-C32-O33
65	n	200	8Q1	C31-C29-C32-C34
65	n	200	8Q1	C31-C29-C32-O33
65	n	200	8Q1	O33-C32-C34-N36
65	n	200	8Q1	O33-C32-C34-O35
65	n	200	8Q1	C32-C34-N36-C37
65	n	200	8Q1	C28-O27-P24-O3
65	n	200	8Q1	C28-O27-P24-O2
65	n	200	8Q1	C28-O27-P24-O1
66	x	301	COO	C5X-O5X-P1A-O2A
66	x	301	COO	C5X-O5X-P1A-O1A
66	x	301	COO	C5-C6-S1-C7
66	x	301	COO	O4-C7-S1-C6
66	x	301	COO	C8-C7-S1-C6
66	x	301	COO	S1-C7-C8-C9
68	AC	503	UQ5	C13-C14-C16-C17
68	AC	503	UQ5	C15-C14-C16-C17
68	AC	503	UQ5	C19-C21-C22-C23
68	BC	502	UQ5	C9-C11-C12-C13
68	BC	502	UQ5	C19-C21-C22-C23
68	BC	502	UQ5	C24-C26-C27-C28
69	BC	503	UQ7	C23-C24-C26-C27
69	BC	503	UQ7	C25-C24-C26-C27
68	BC	502	UQ5	C12-C11-C9-C10
65	n	200	8Q1	O35-C34-N36-C37
61	H	500	UQ9	C12-C11-C9-C10
68	AC	502	UQ5	C12-C11-C9-C10
68	BC	502	UQ5	C25-C24-C26-C27
61	H	500	UQ9	C12-C11-C9-C8
68	AC	502	UQ5	C12-C11-C9-C8
68	BC	502	UQ5	C23-C24-C26-C27
68	AC	503	UQ5	C14-C16-C17-C18
69	BC	503	UQ7	C14-C16-C17-C18
66	x	301	COO	O4-C7-C8-C9
61	H	500	UQ9	C24-C26-C27-C28

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Mol	Chain	Res	Type	Atoms
68	BC	502	UQ5	C12-C11-C9-C8
68	AC	502	UQ5	C9-C11-C12-C13
68	AC	503	UQ5	C24-C26-C27-C28
69	BC	503	UQ7	C9-C11-C12-C13
69	BC	503	UQ7	C19-C21-C22-C23
69	BC	503	UQ7	C29-C31-C32-C33
63	P	500	NDP	C2D-C1D-N1N-C6N
65	W	200	8Q1	O27-C28-C29-C30
65	n	200	8Q1	C12-C13-C14-C15
65	W	200	8Q1	C7-C8-C9-C10
63	P	500	NDP	C2D-C1D-N1N-C2N
67	AC	501	HEM	C2A-CAA-CBA-CGA
67	BC	501	HEM	C2A-CAA-CBA-CGA
66	x	301	COO	O4X-C4X-C5X-O5X
66	x	301	COO	C3X-C4X-C5X-O5X
65	W	200	8Q1	C10-C11-C12-C13
65	n	200	8Q1	N36-C37-C38-C39
65	n	200	8Q1	C11-C12-C13-C14
68	AC	502	UQ5	C6-C7-C8-C9
65	n	200	8Q1	C11-C10-C9-C8
68	AC	503	UQ5	C20-C19-C21-C22
69	BC	503	UQ7	C30-C29-C31-C32
68	AC	503	UQ5	C18-C19-C21-C22
69	BC	503	UQ7	C28-C29-C31-C32
65	W	200	8Q1	C11-C12-C13-C14
68	AC	503	UQ5	C12-C11-C9-C10
68	AC	503	UQ5	C12-C11-C9-C8
65	W	200	8Q1	C1-C6-C7-C8
63	P	500	NDP	O4D-C1D-N1N-C6N
67	AC	500	HEM	C2B-C3B-CAB-CBB
67	BC	501	HEM	C2B-C3B-CAB-CBB
63	P	500	NDP	O4D-C1D-N1N-C2N
65	W	200	8Q1	C13-C14-C15-C16
65	n	200	8Q1	C13-C14-C15-C16
65	W	200	8Q1	C29-C28-O27-P24
60	F	500	FMN	N10-C1'-C2'-O2'
68	AC	502	UQ5	C2-C3-O3-C3M
68	AC	502	UQ5	C5-C4-O4-C4M
68	AC	503	UQ5	C2-C3-O3-C3M
67	AC	501	HEM	C2B-C3B-CAB-CBB
68	AC	502	UQ5	C19-C21-C22-C23
67	BC	501	HEM	C4B-C3B-CAB-CBB

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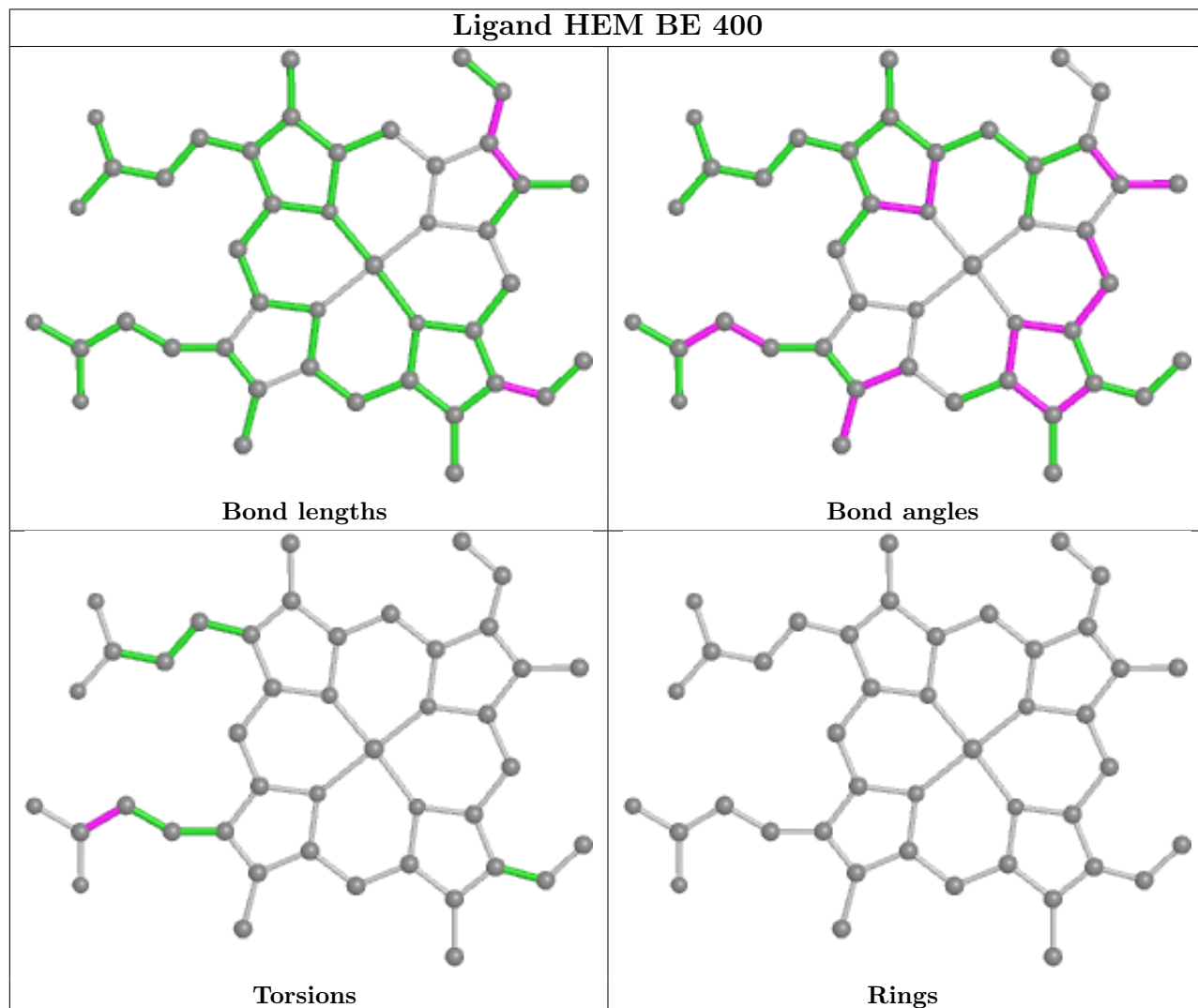
Mol	Chain	Res	Type	Atoms
65	W	200	8Q1	O40-C39-N41-C42
67	AC	500	HEM	CAD-CBD-CGD-O1D
67	BC	501	HEM	CAD-CBD-CGD-O2D
67	AC	501	HEM	CAD-CBD-CGD-O2D
67	BC	501	HEM	CAD-CBD-CGD-O1D
63	P	500	NDP	PN-O3-PA-O1A
67	BC	500	HEM	CAA-CBA-CGA-O2A
67	AC	500	HEM	CAA-CBA-CGA-O2A
67	AC	501	HEM	CAD-CBD-CGD-O1D
68	BC	502	UQ5	C14-C16-C17-C18
67	AC	500	HEM	CAD-CBD-CGD-O2D
67	AE	400	HEM	CAA-CBA-CGA-O1A
66	x	301	COO	N2-C5-C6-S1
67	AC	500	HEM	CAA-CBA-CGA-O1A
61	H	500	UQ9	C15-C14-C16-C17
68	AC	502	UQ5	C15-C14-C16-C17
67	AE	400	HEM	CAA-CBA-CGA-O2A
61	H	500	UQ9	C5-C4-O4-C4M
67	BC	500	HEM	CAA-CBA-CGA-O1A
67	AC	500	HEM	C4B-C3B-CAB-CBB
67	AC	501	HEM	C4B-C3B-CAB-CBB
68	AC	502	UQ5	C13-C14-C16-C17
65	n	200	8Q1	C9-C10-C11-C12
66	x	301	COO	C5X-O5X-P1A-O3A
68	AC	502	UQ5	C3-C4-O4-C4M
68	AC	503	UQ5	C4-C3-O3-C3M
63	P	500	NDP	O4B-C4B-C5B-O5B
63	P	500	NDP	PN-O3-PA-O2A
67	BC	501	HEM	CAA-CBA-CGA-O2A
67	BE	400	HEM	CAA-CBA-CGA-O1A
60	F	500	FMN	N10-C1'-C2'-C3'
67	BC	501	HEM	CAA-CBA-CGA-O1A
68	AC	502	UQ5	C4-C3-O3-C3M

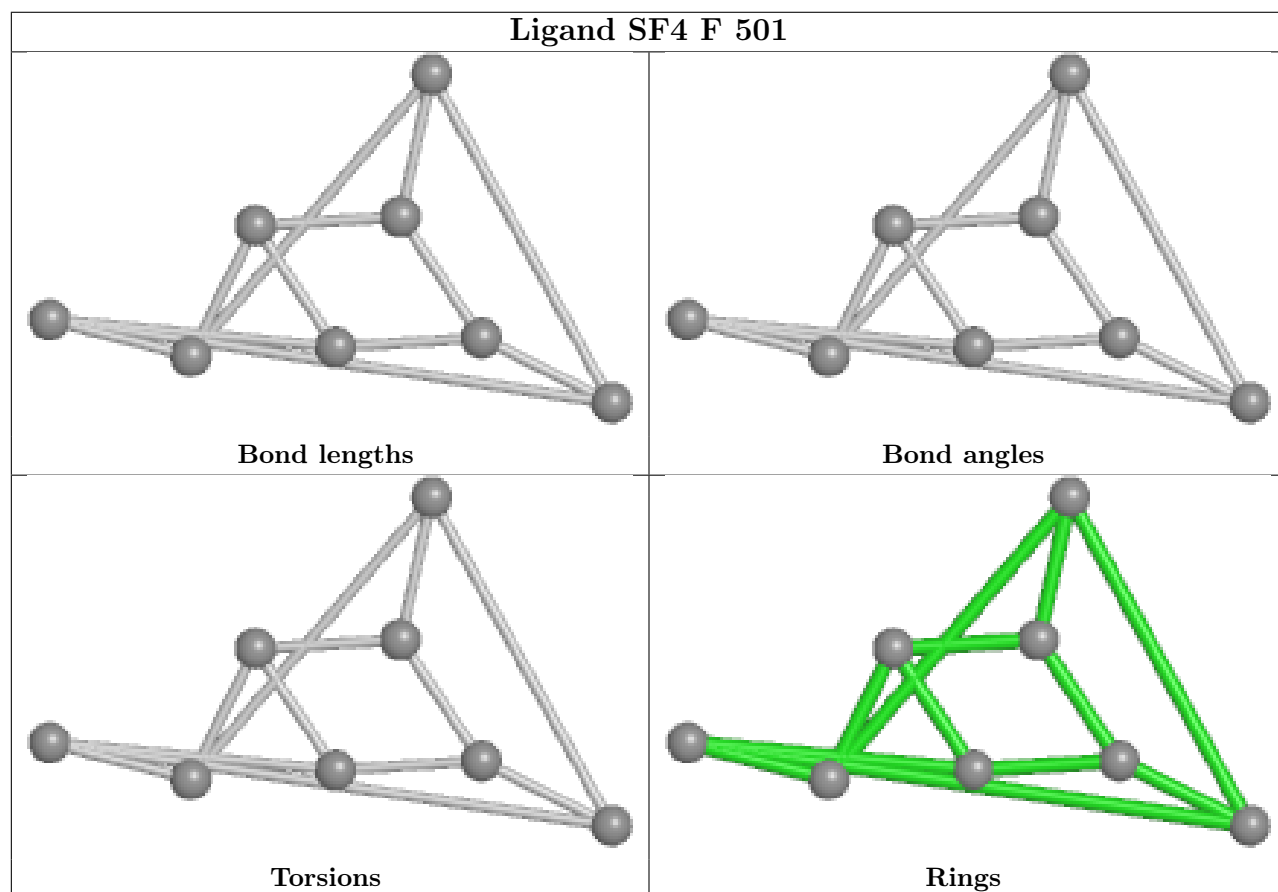
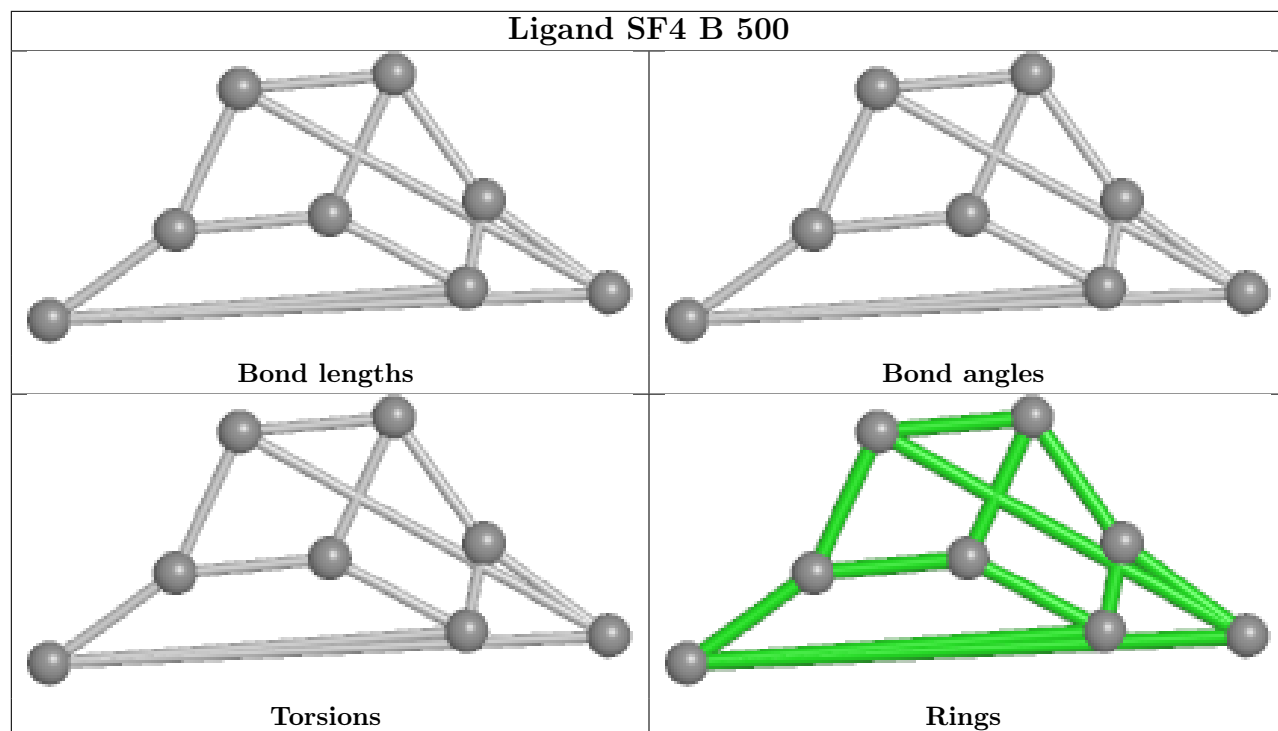
There are no ring outliers.

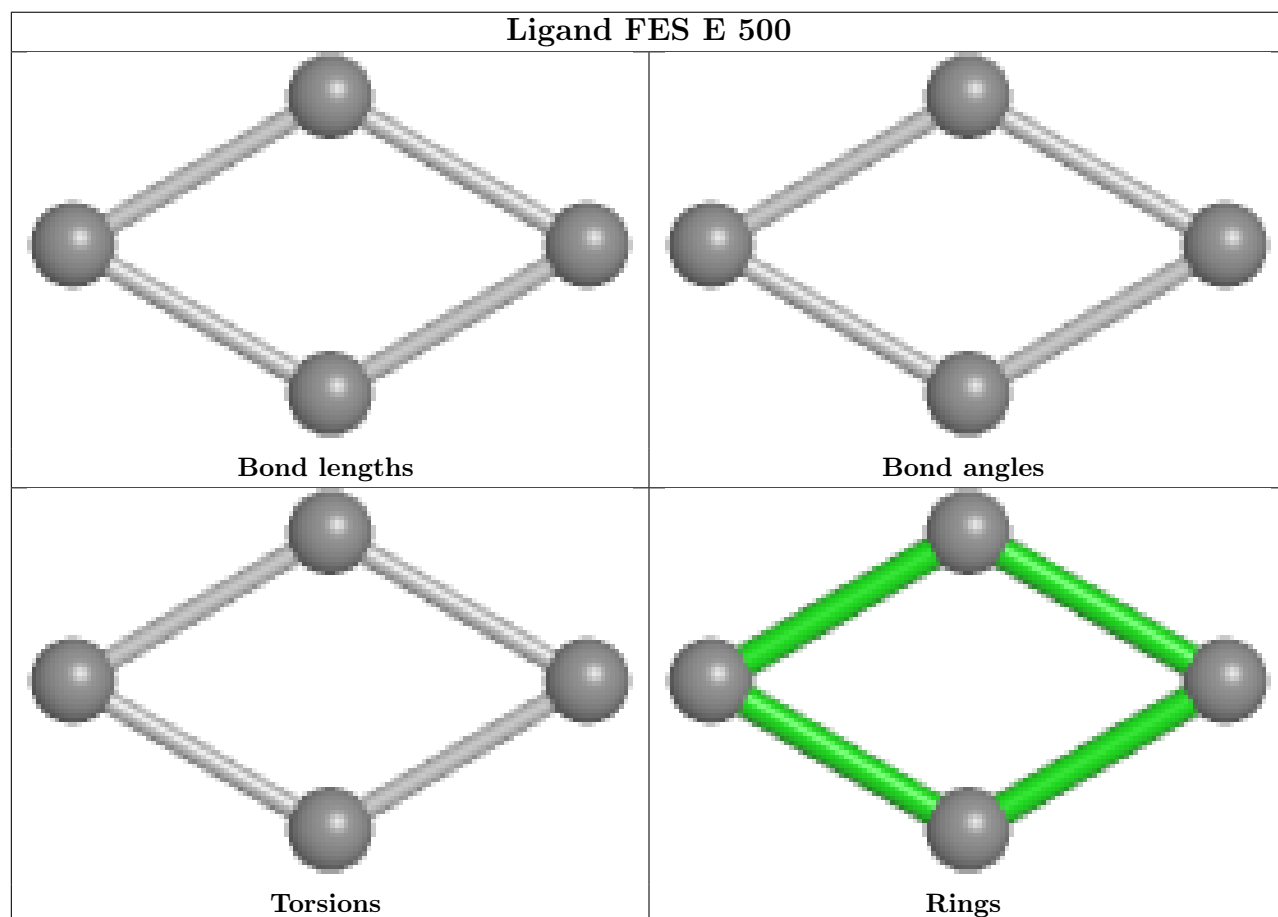
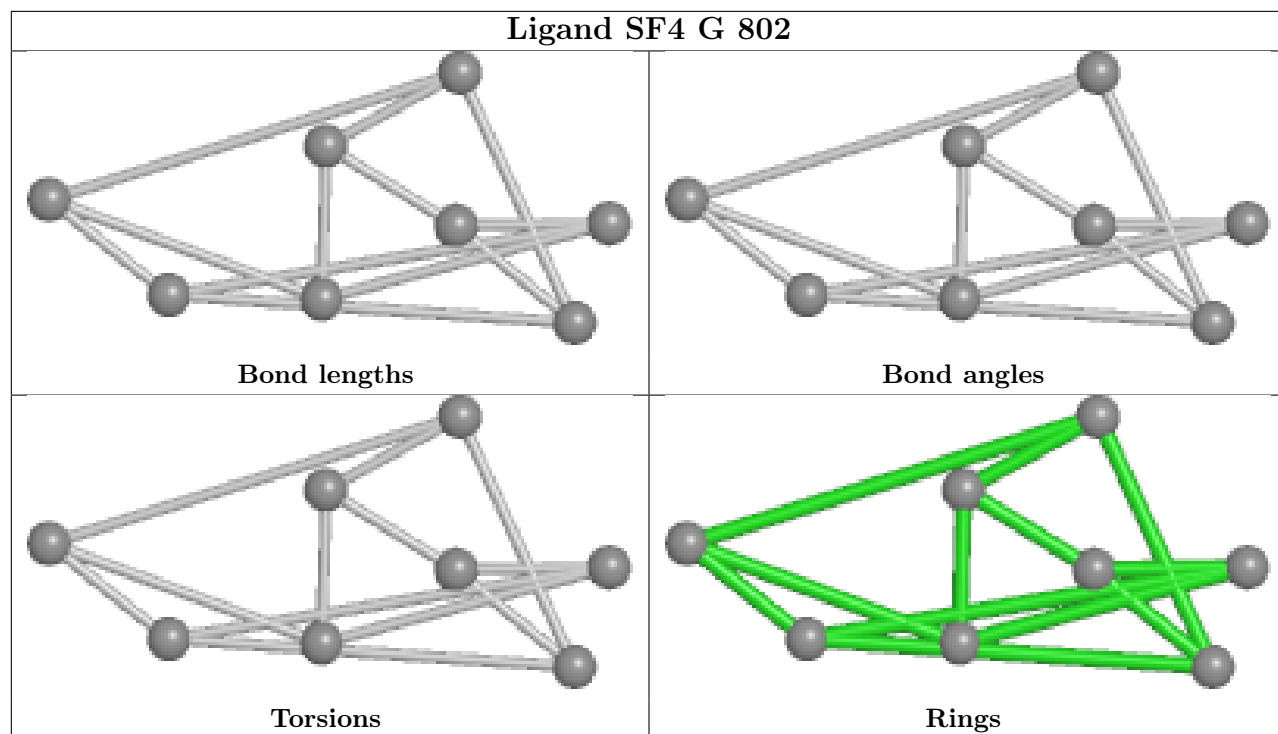
No monomer is involved in short contacts.

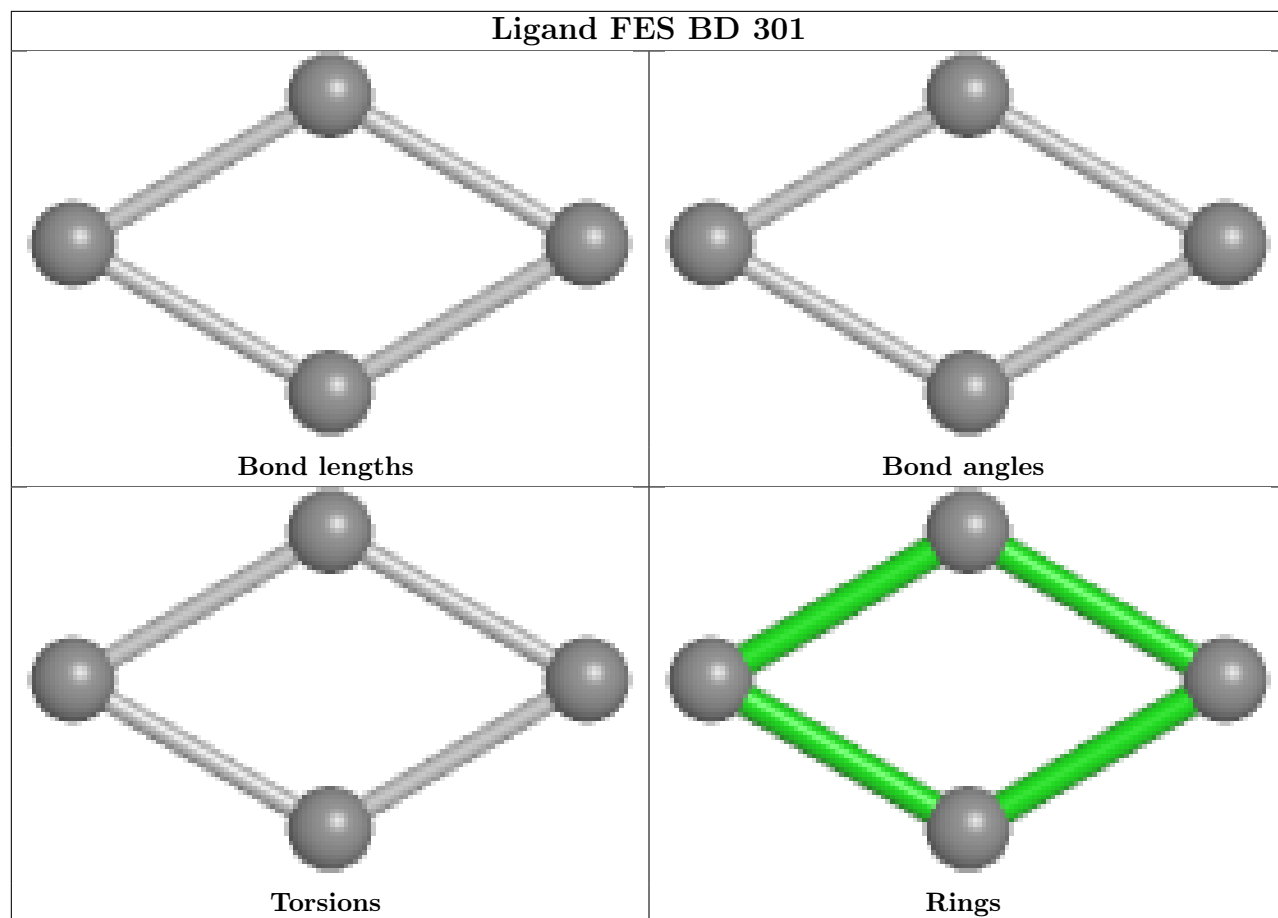
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

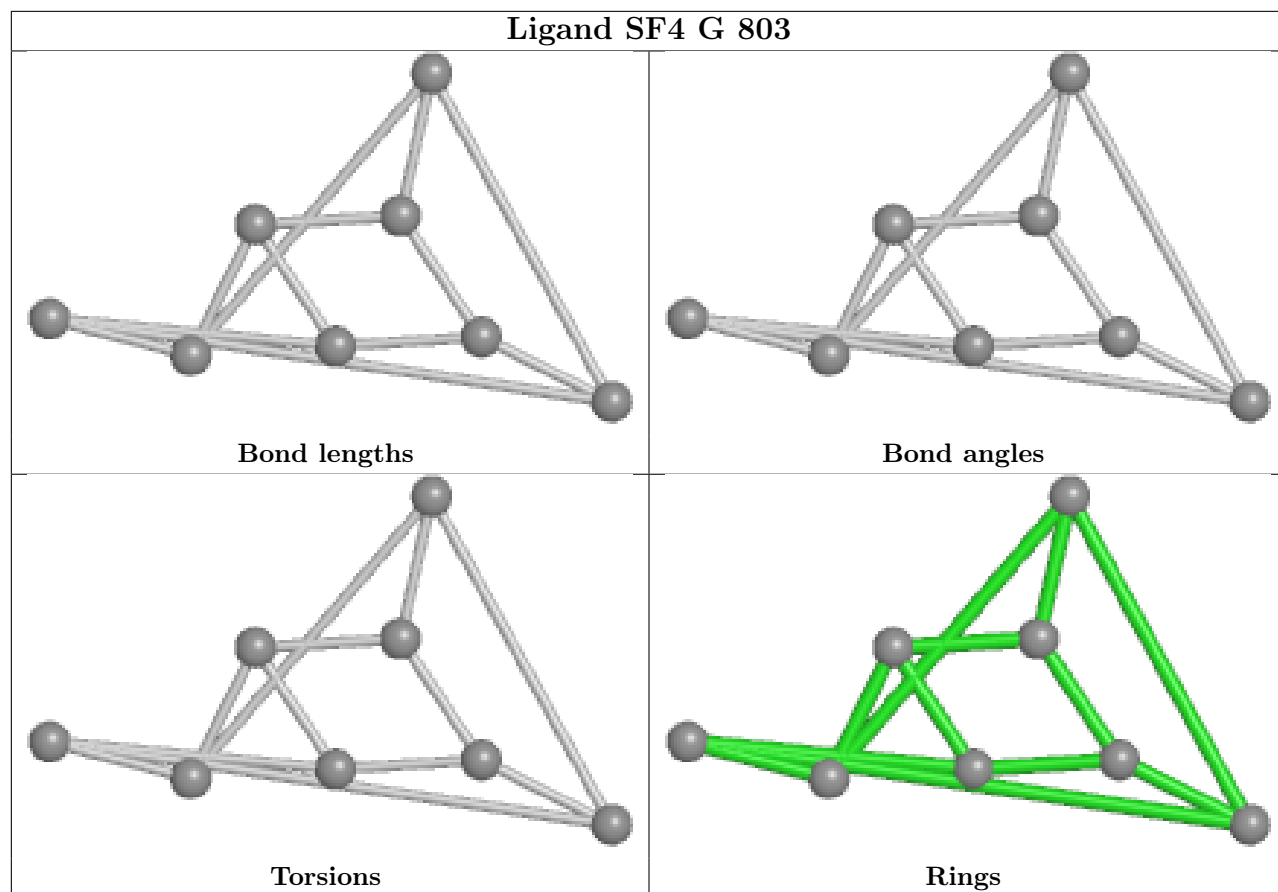
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

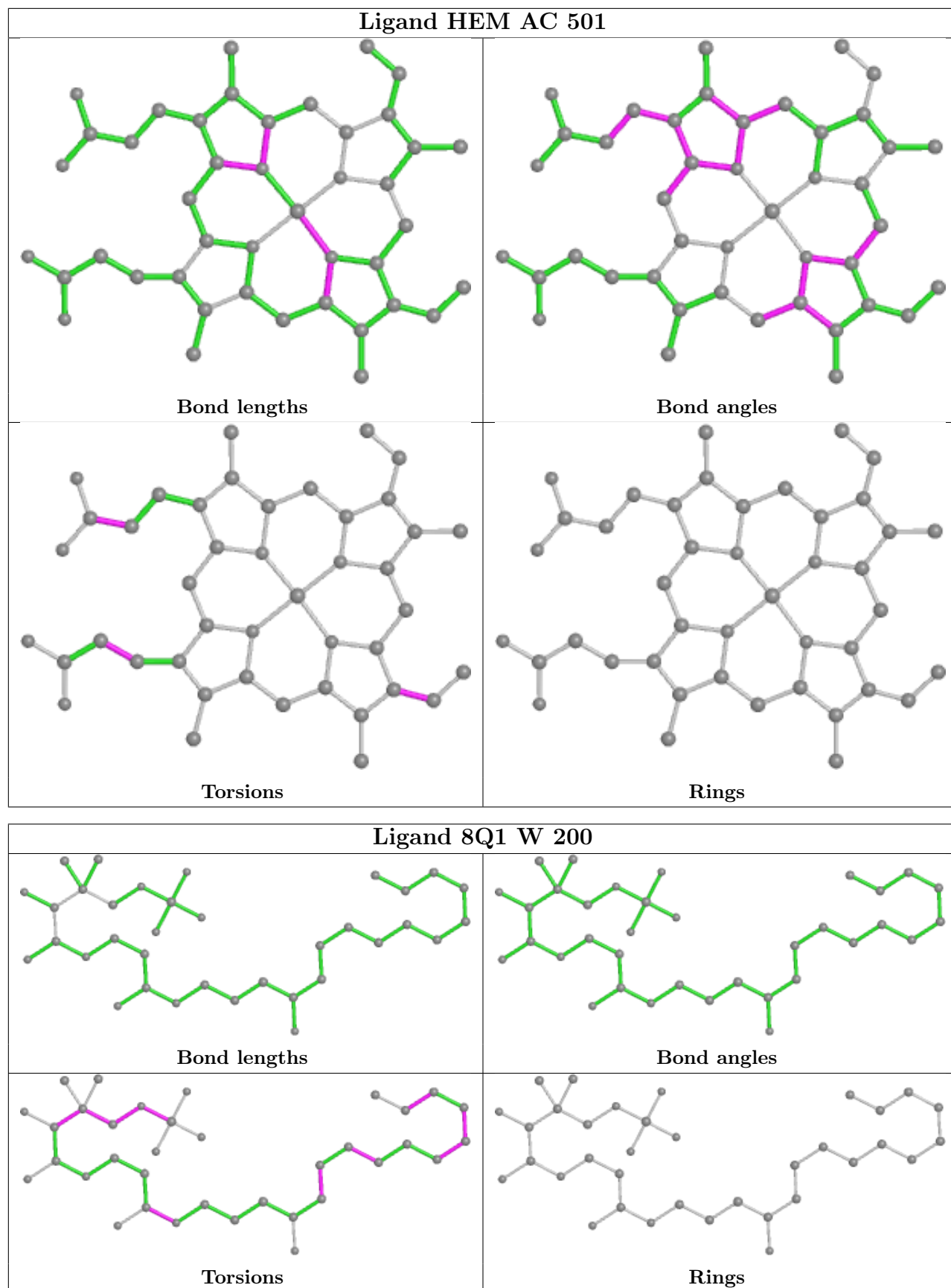


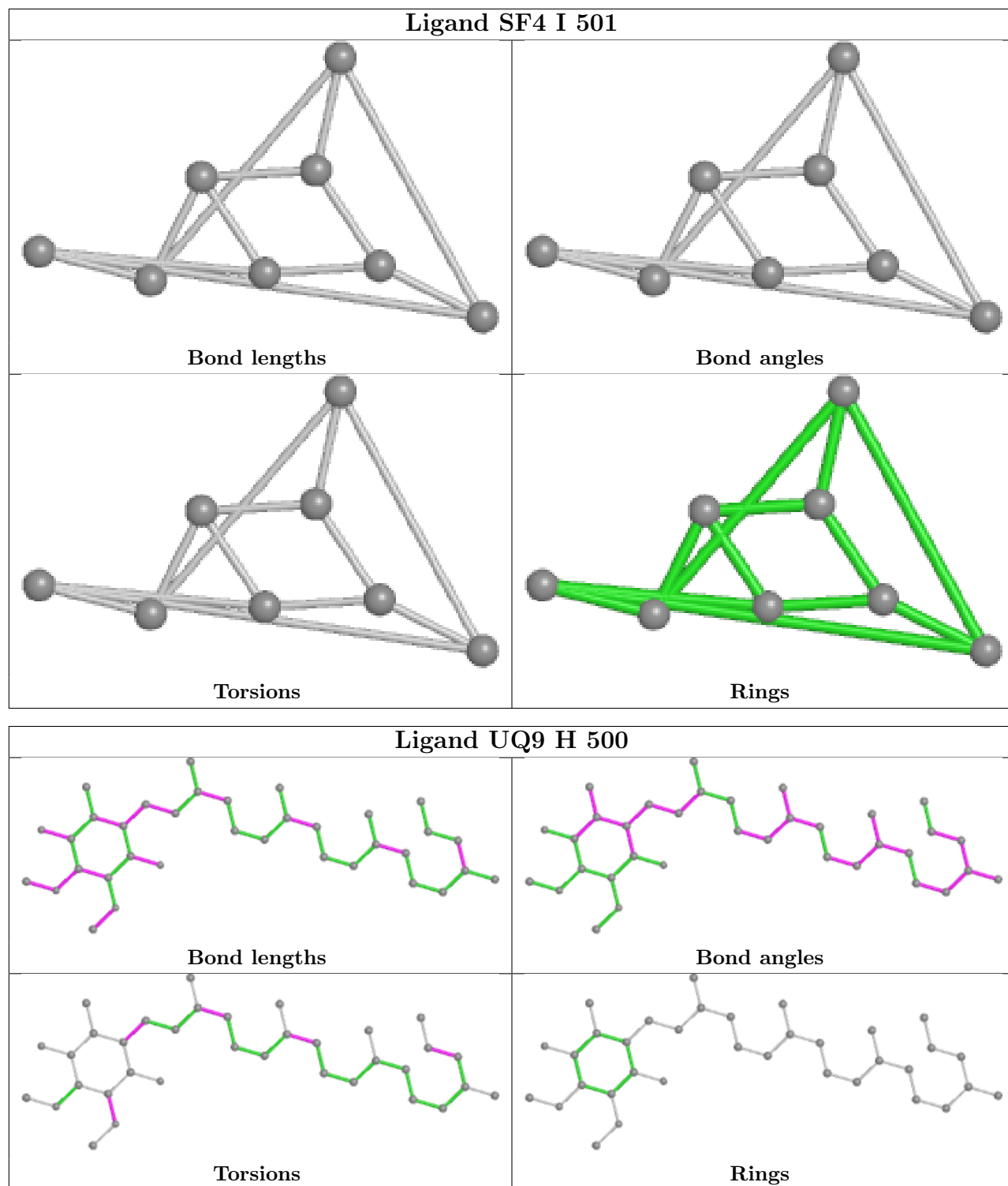


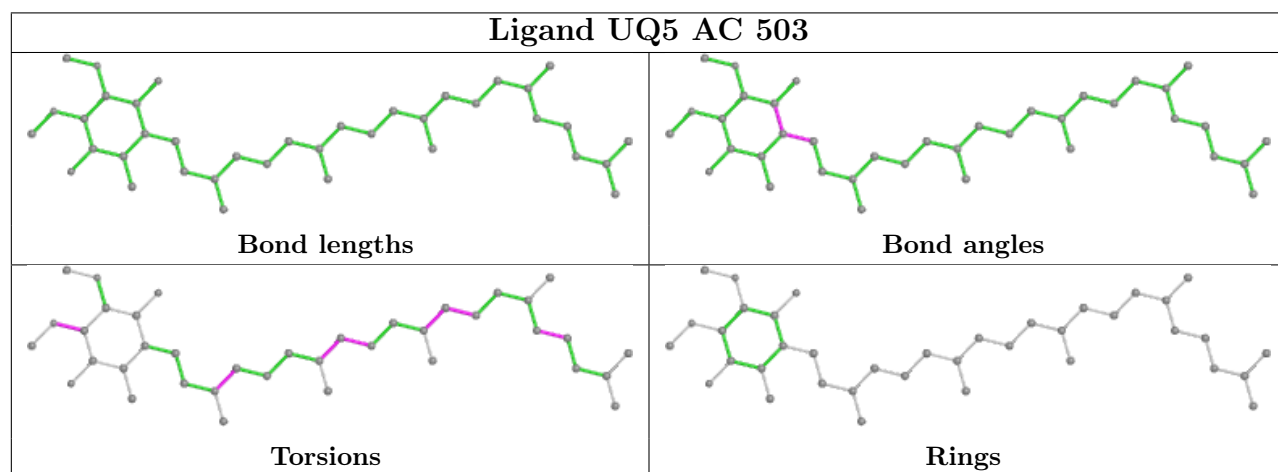
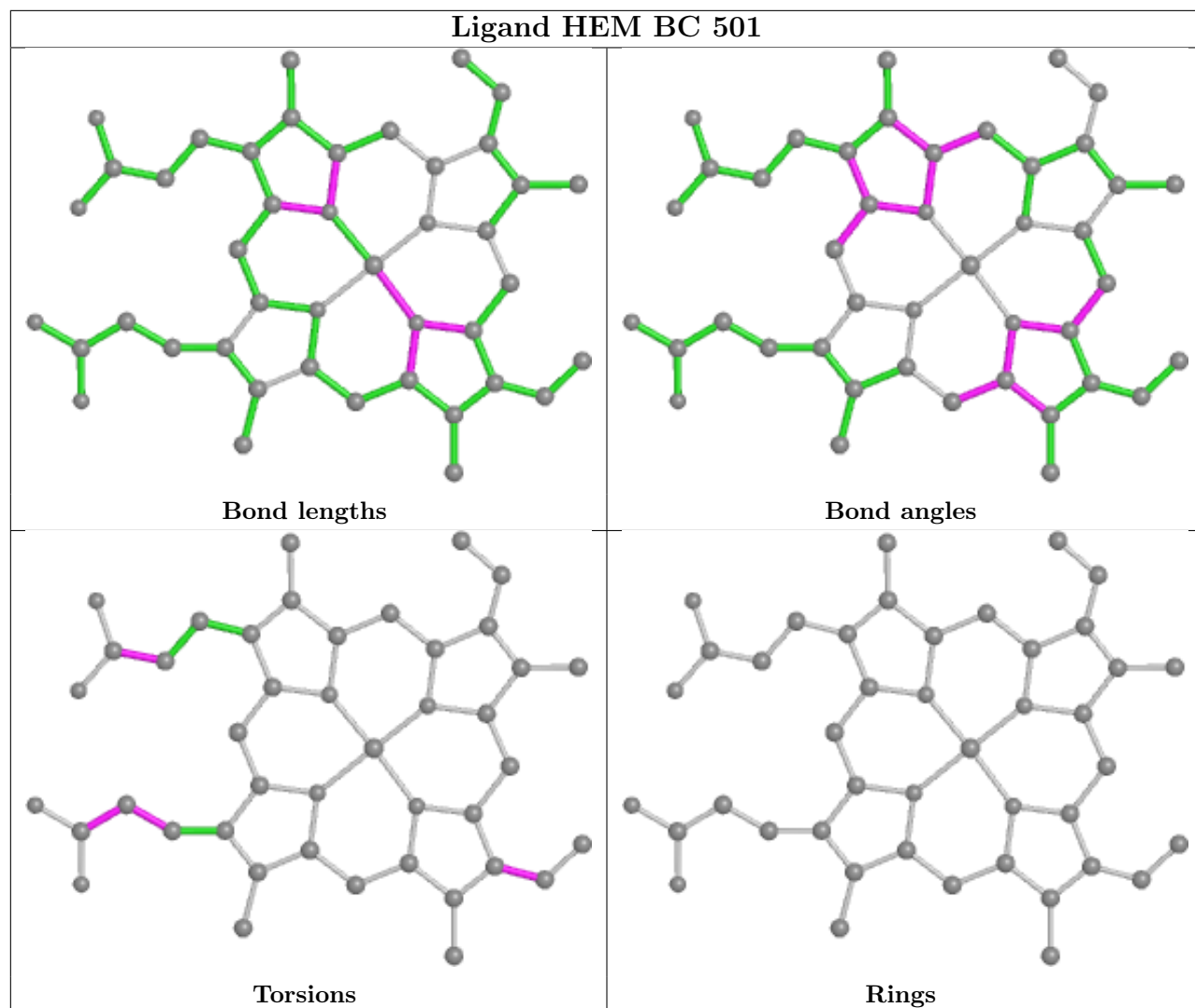


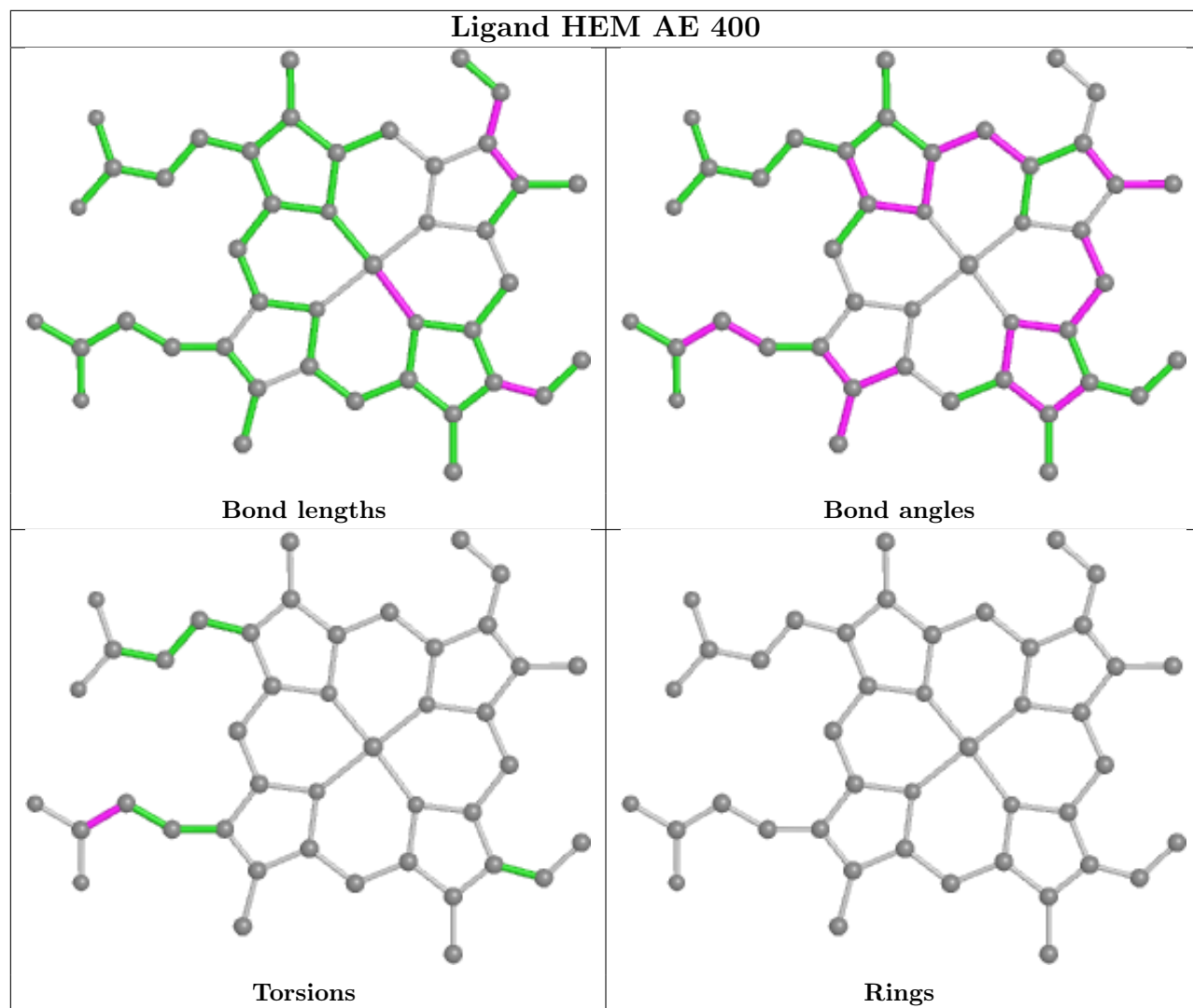


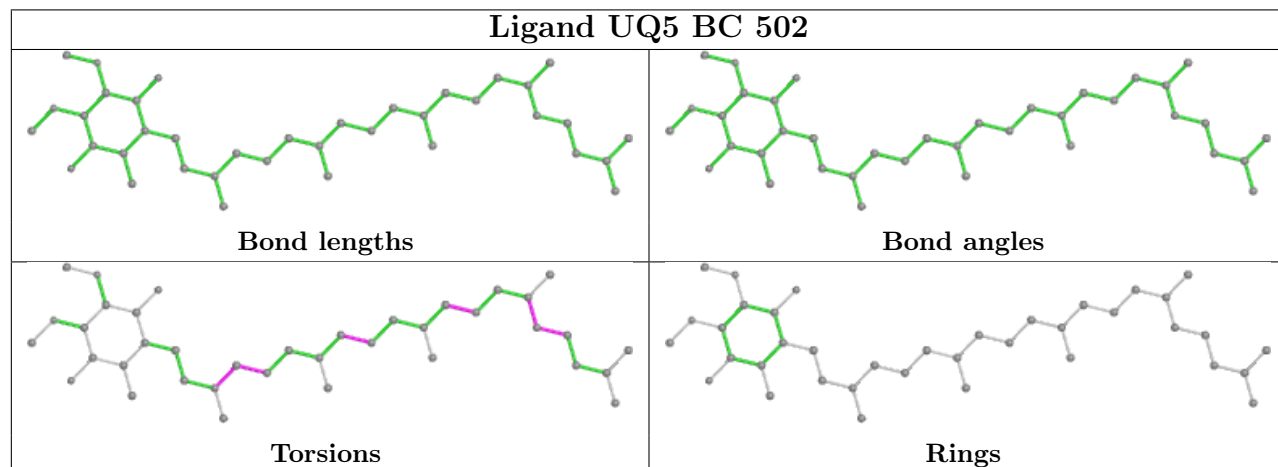
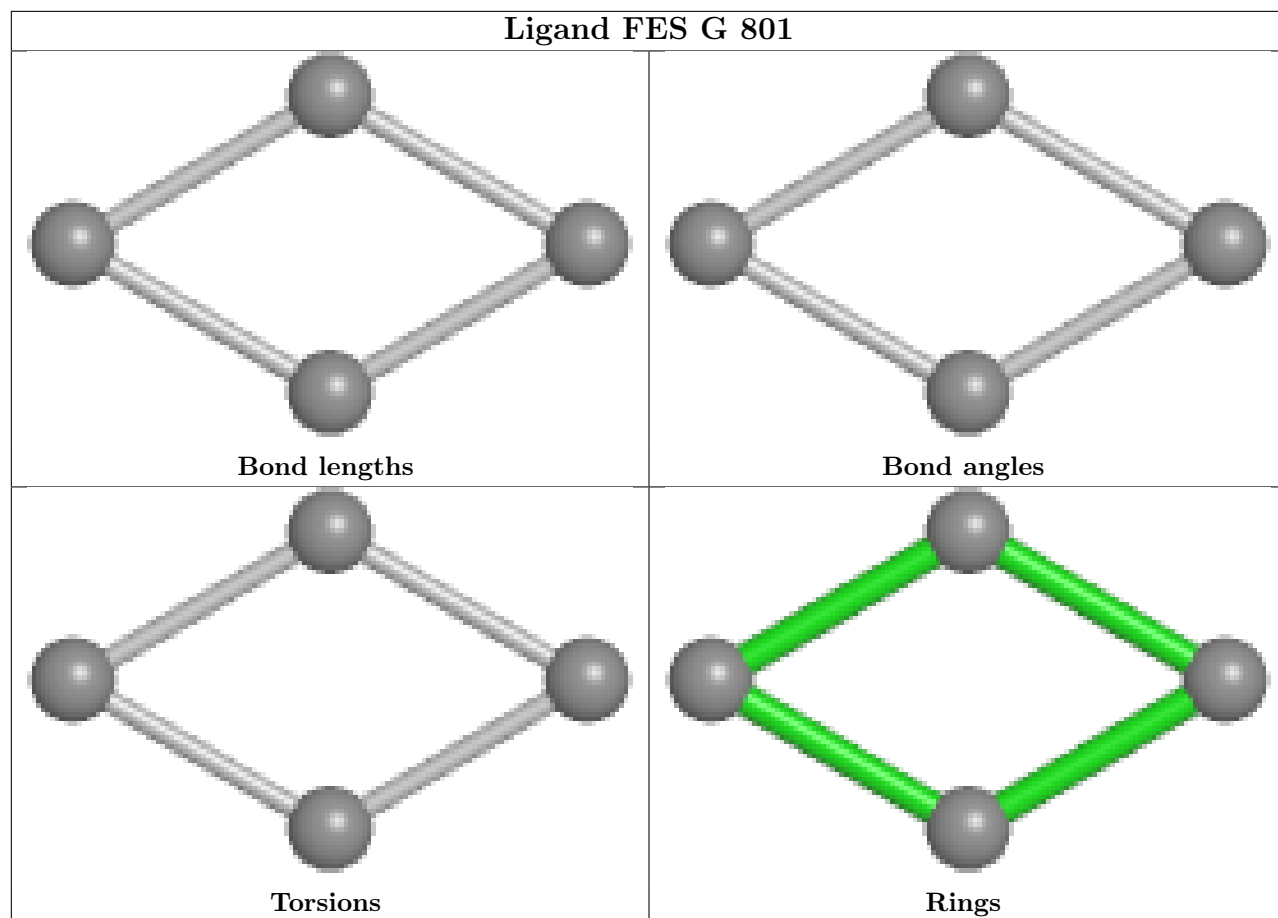


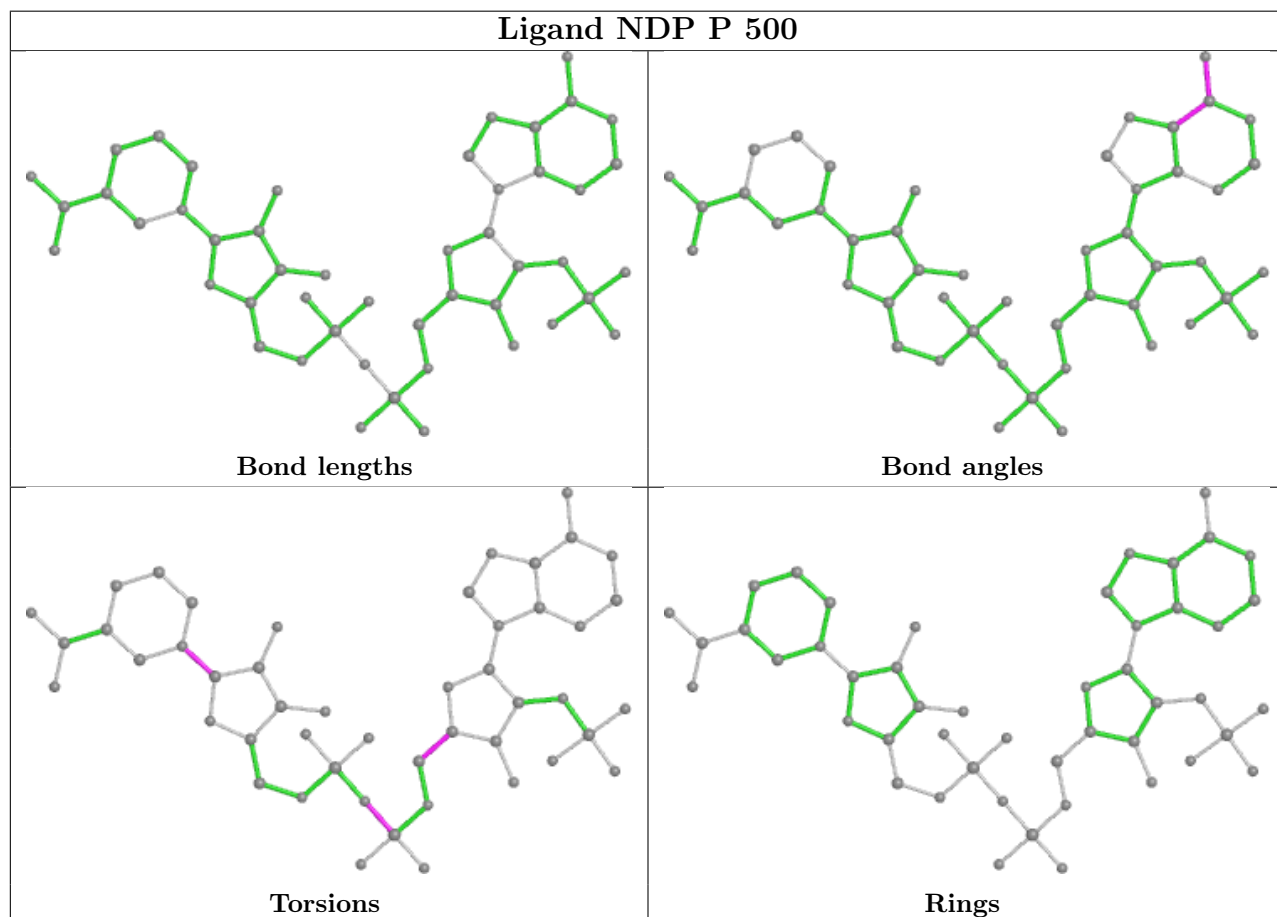
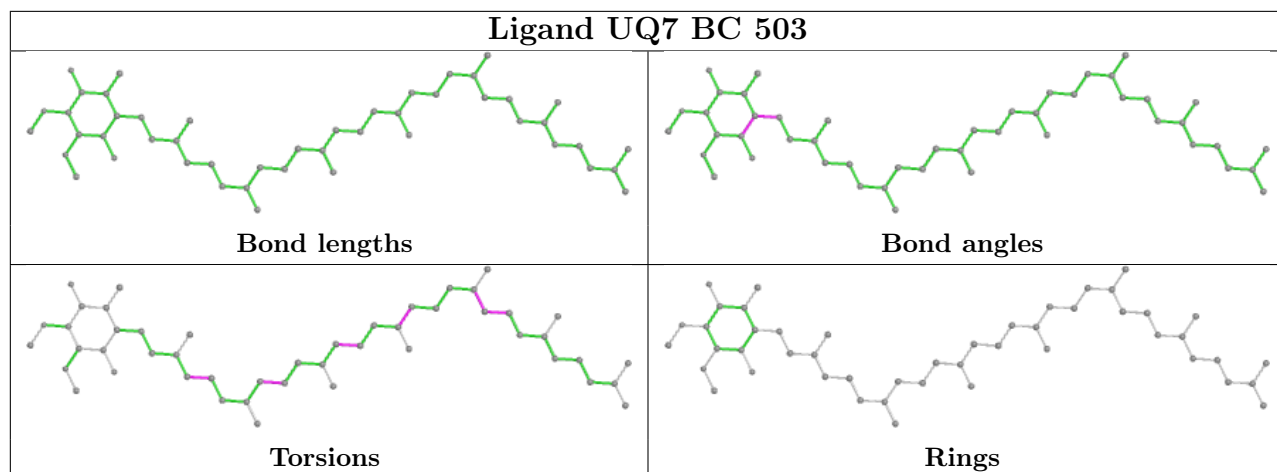


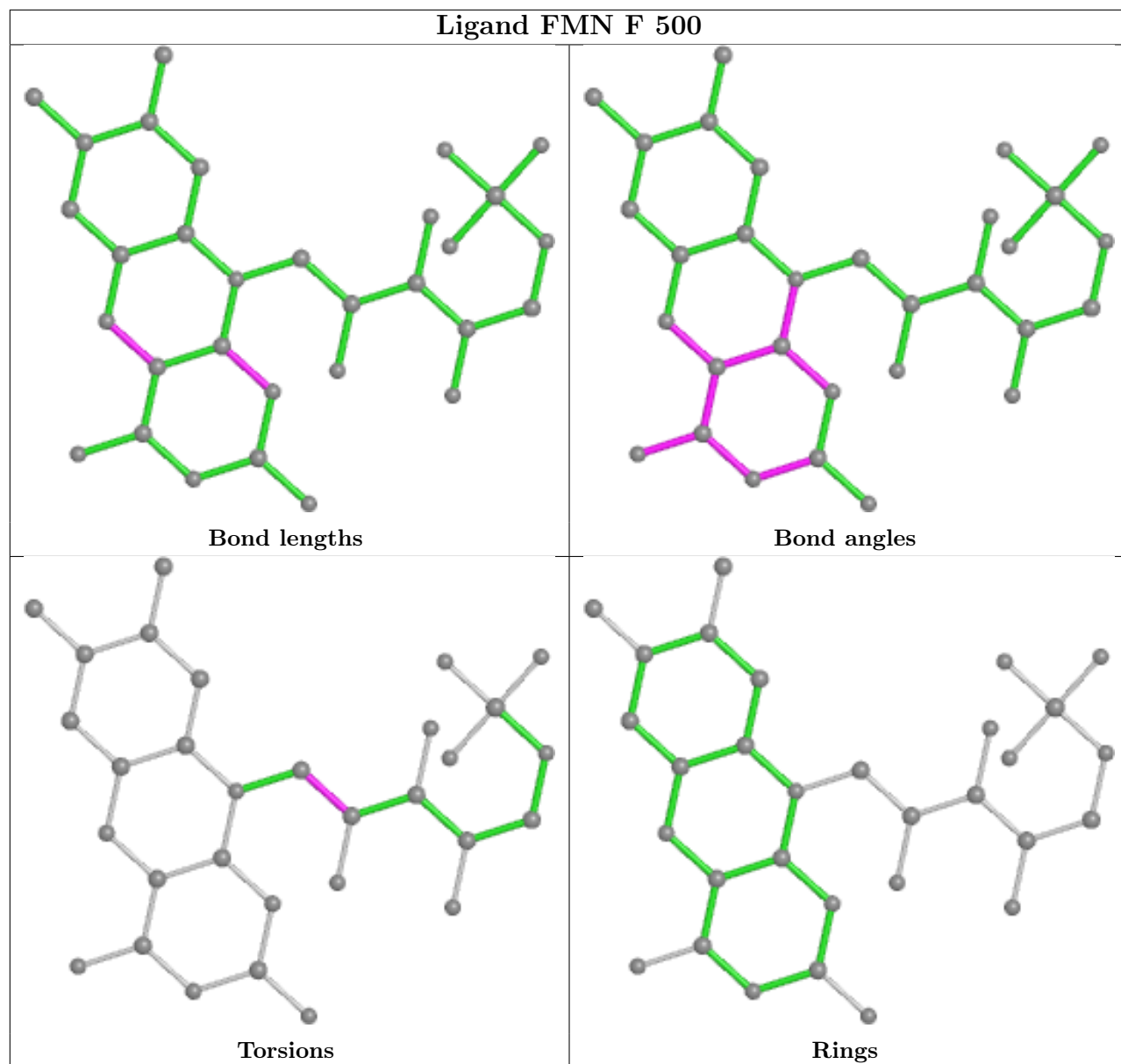


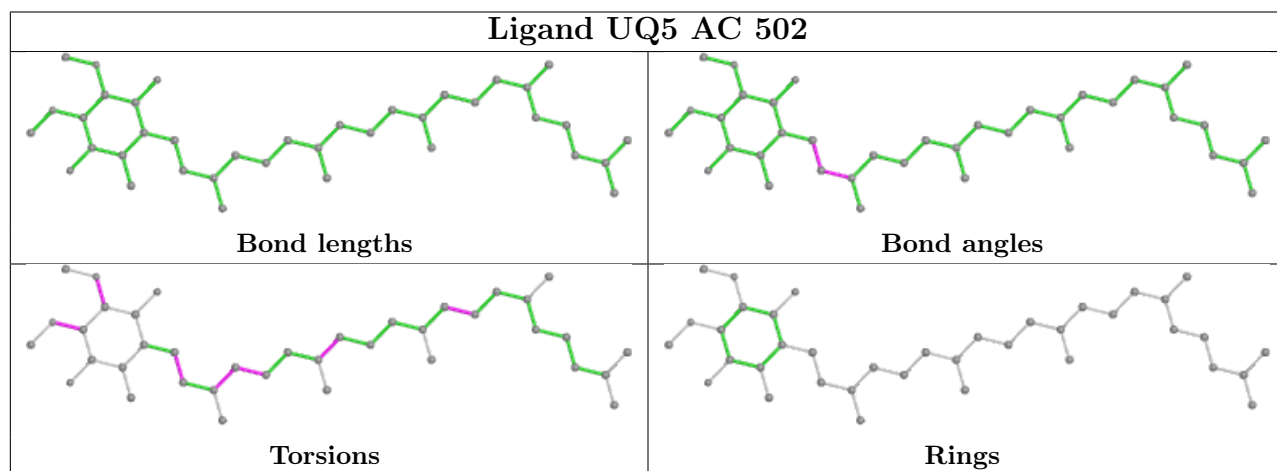
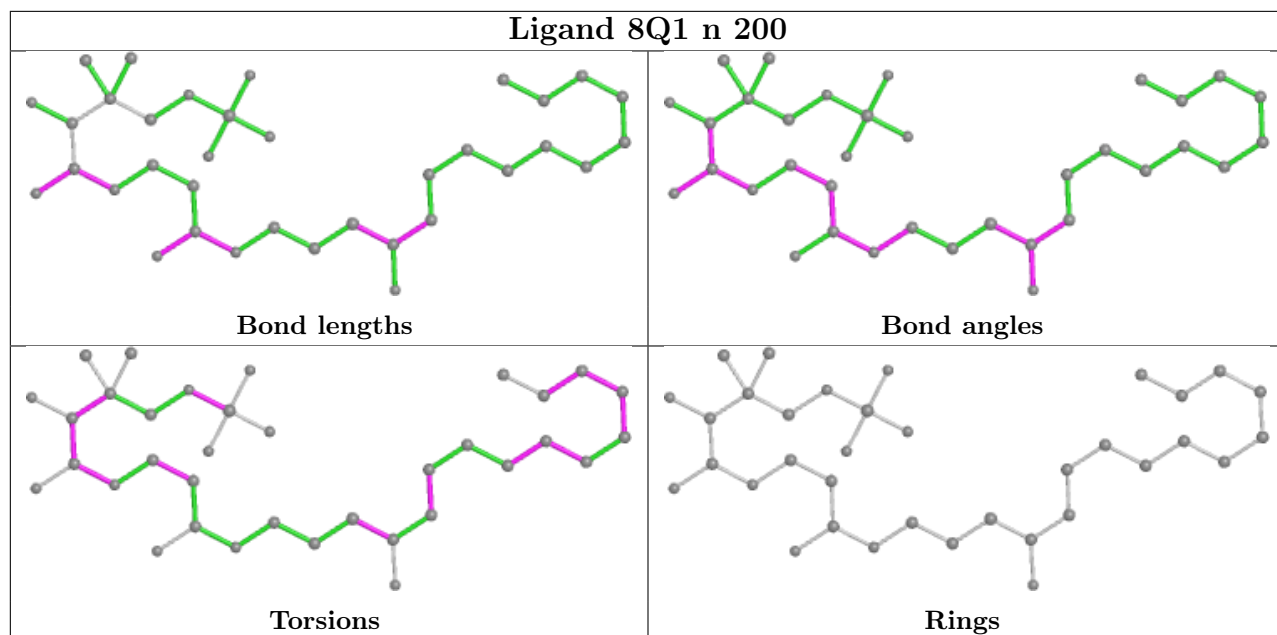


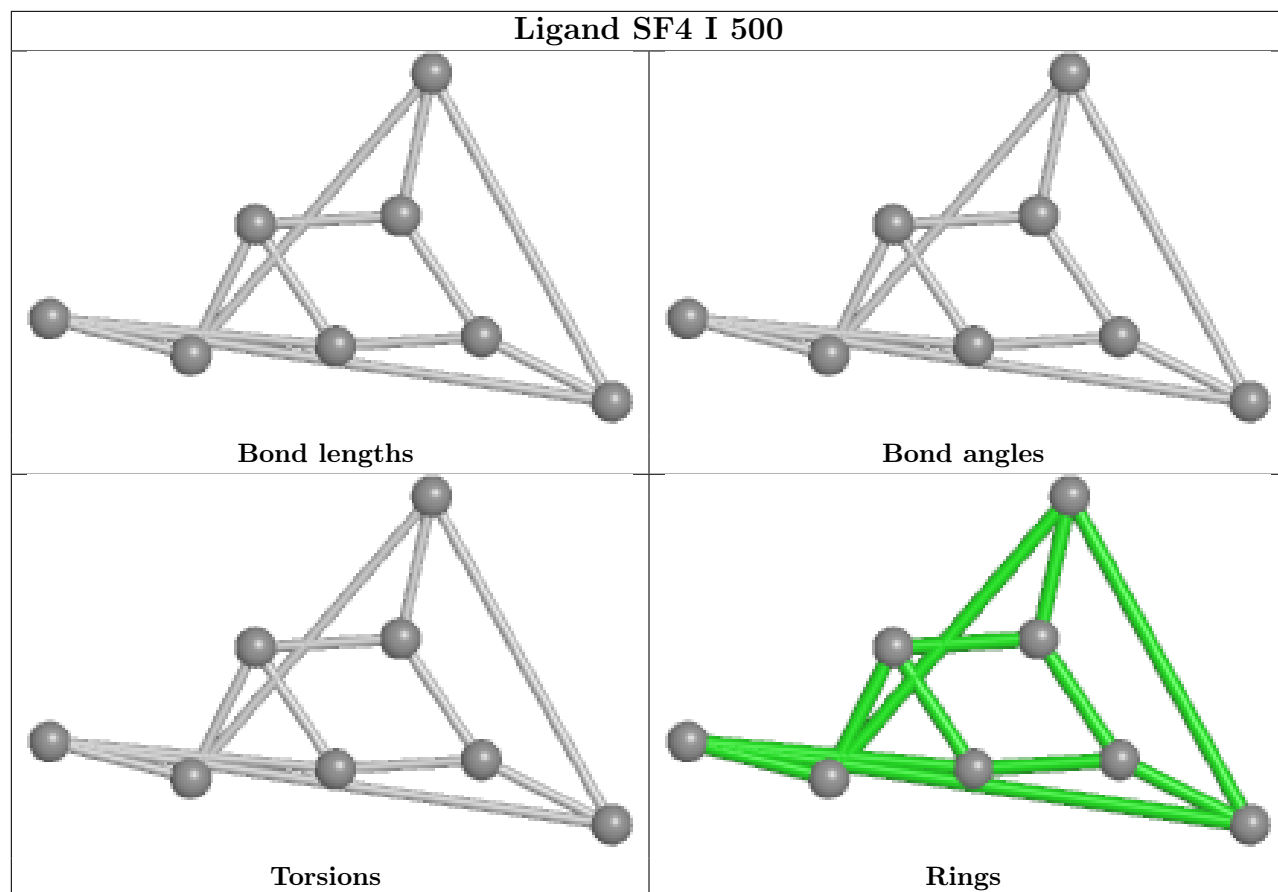


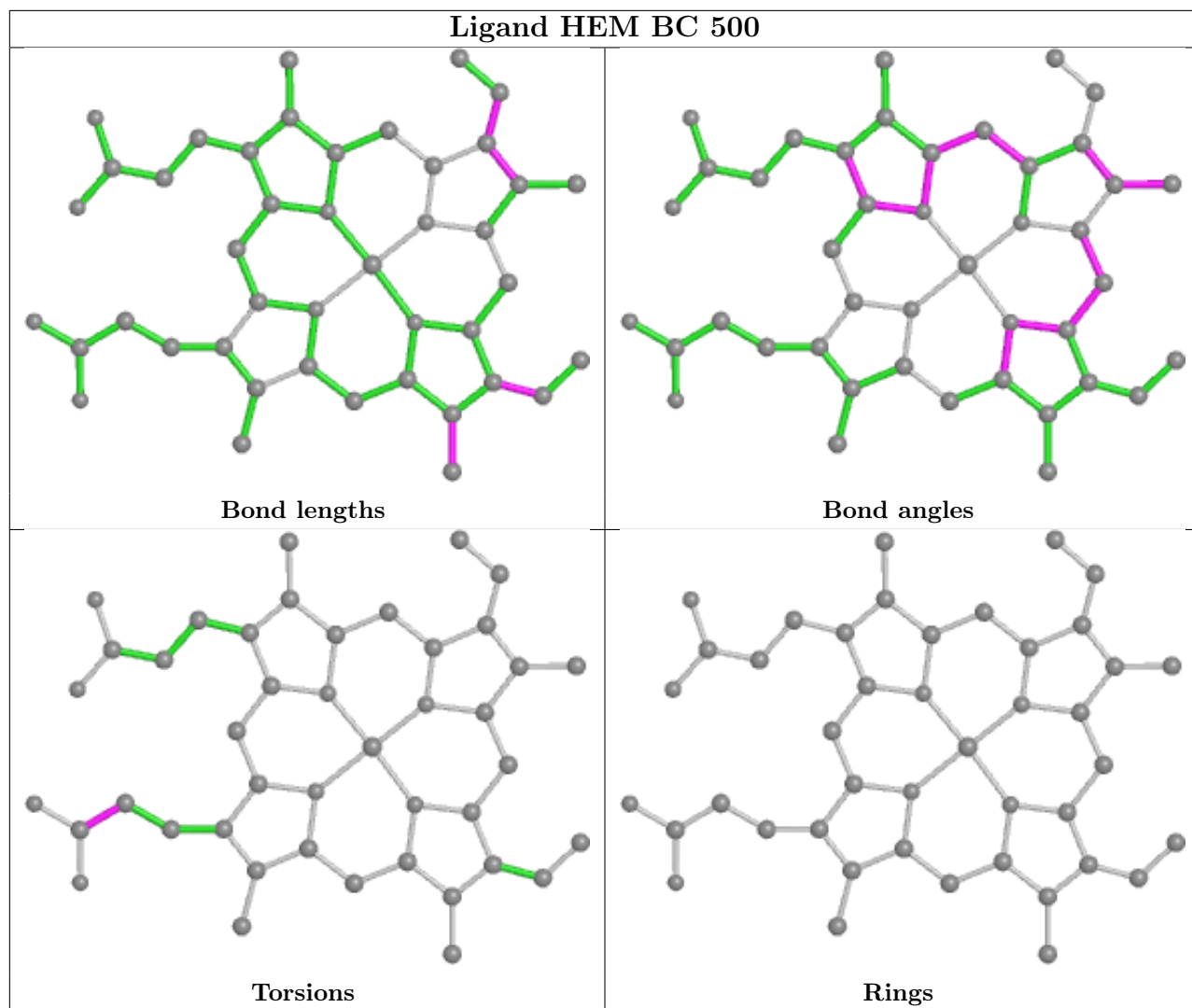


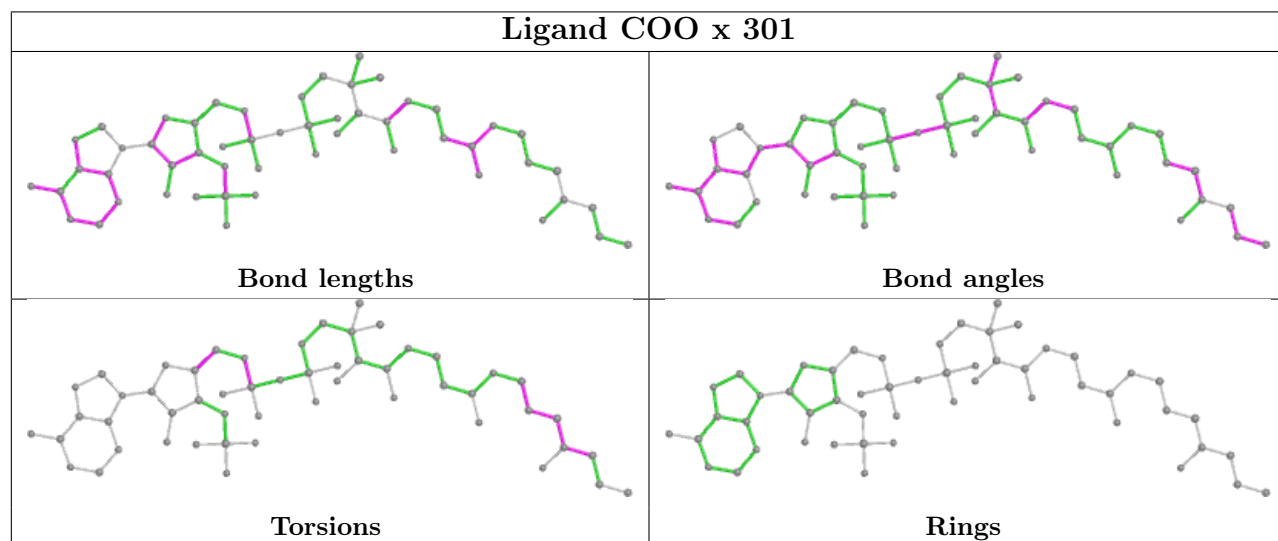
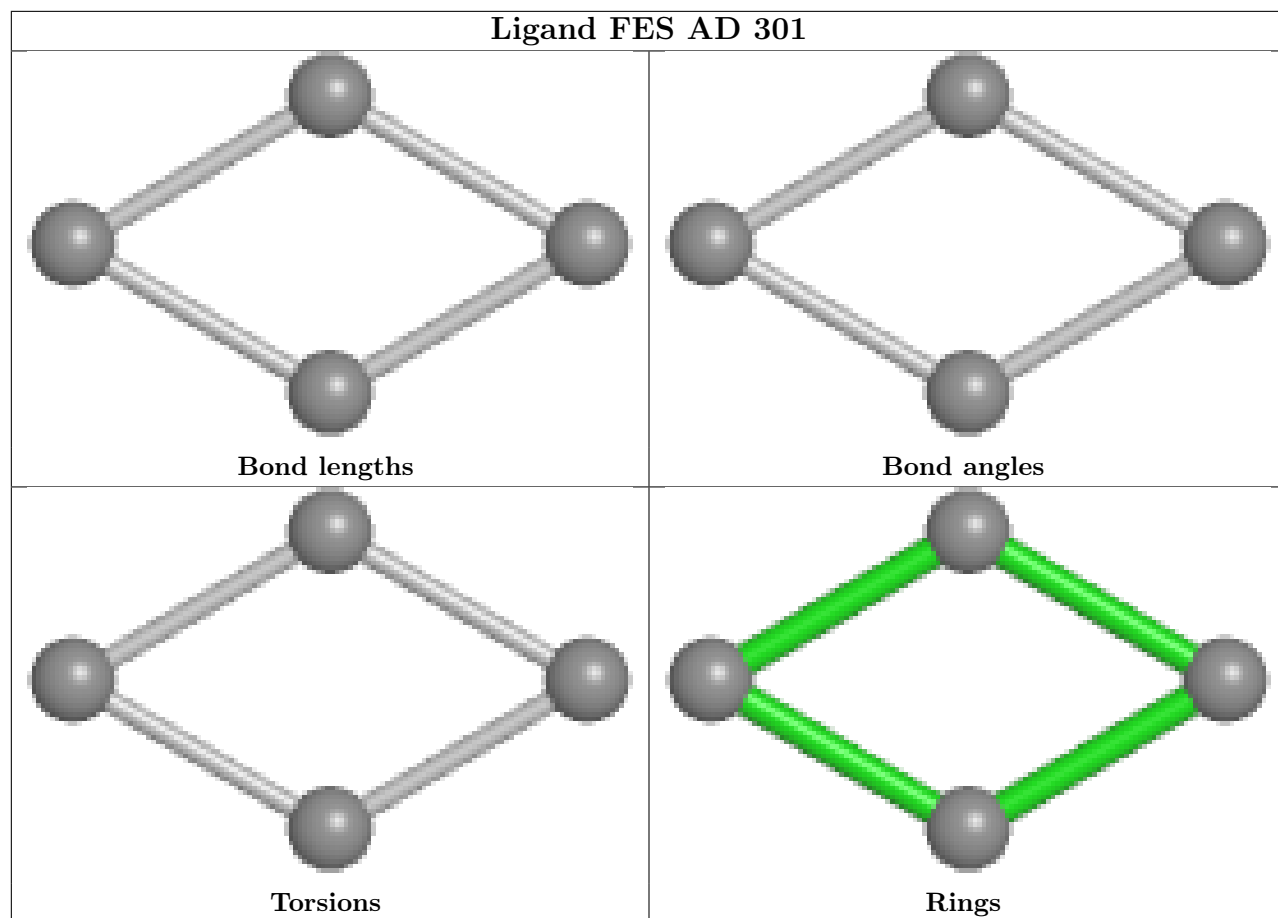


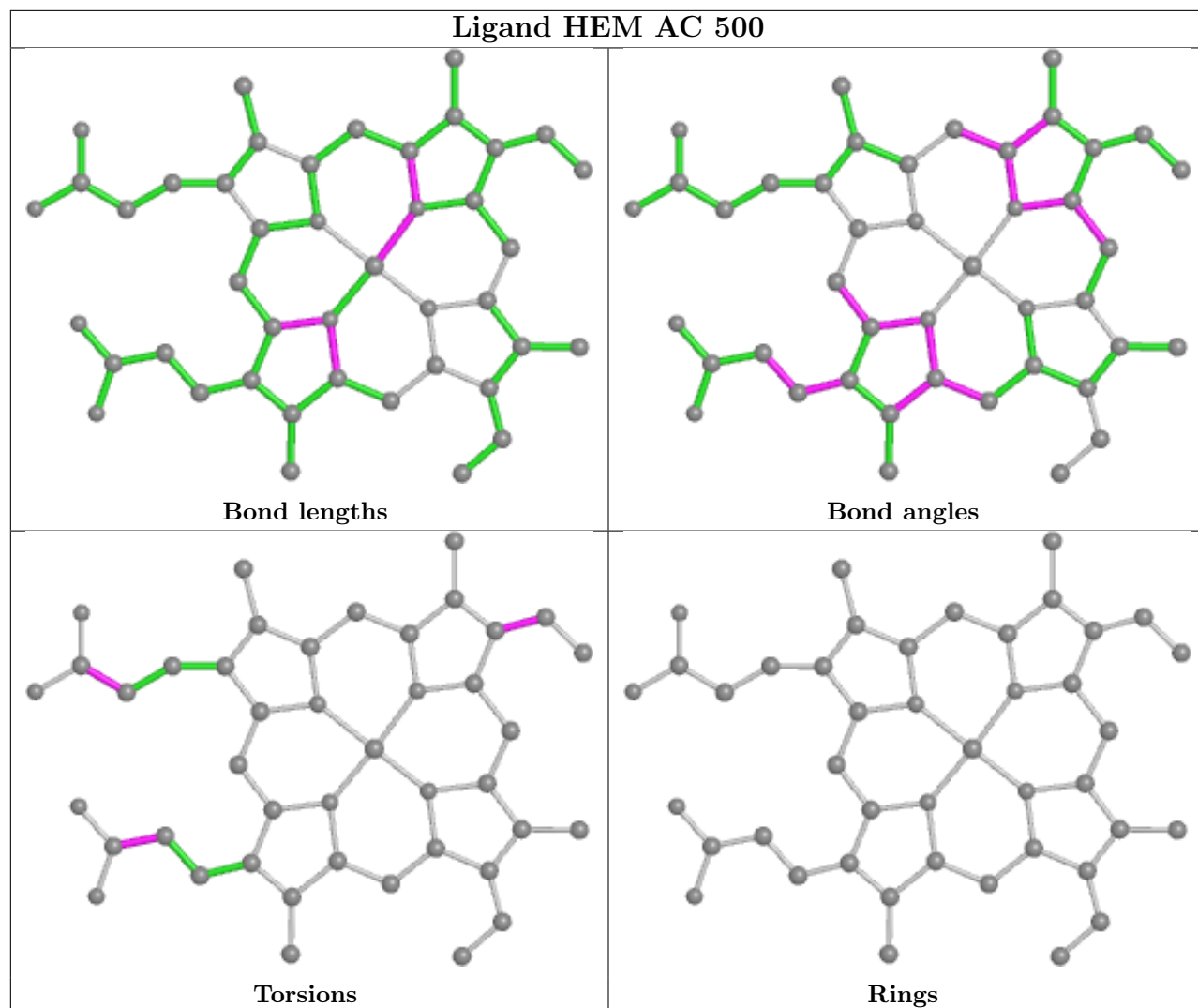












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

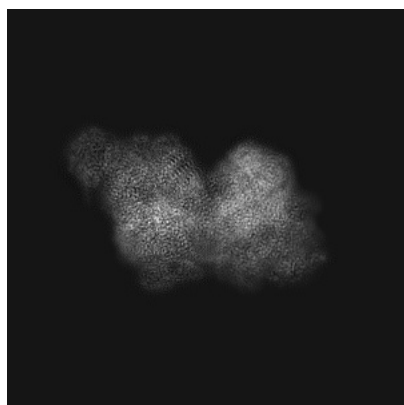
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16171. These allow visual inspection of the internal detail of the map and identification of artifacts.

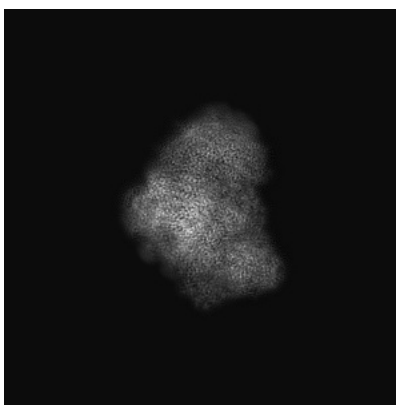
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

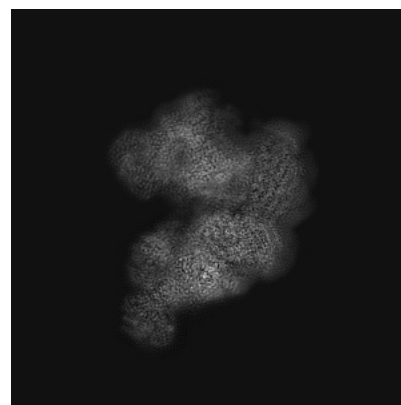
6.1.1 Primary map



X



Y

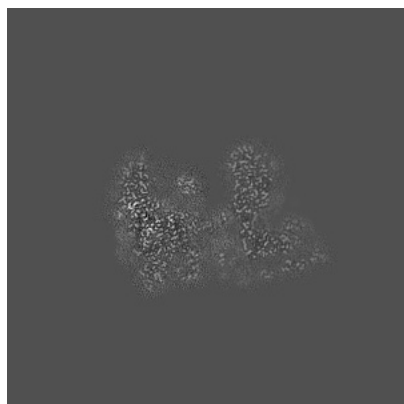


Z

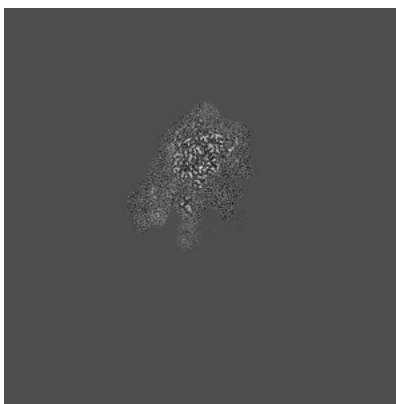
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

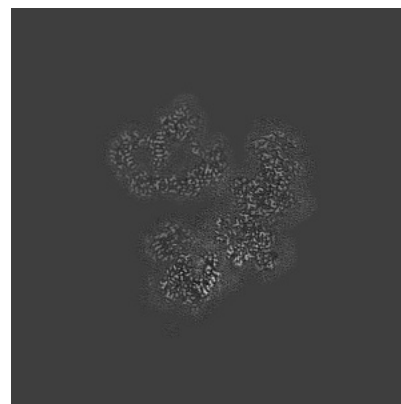
6.2.1 Primary map



X Index: 375



Y Index: 375

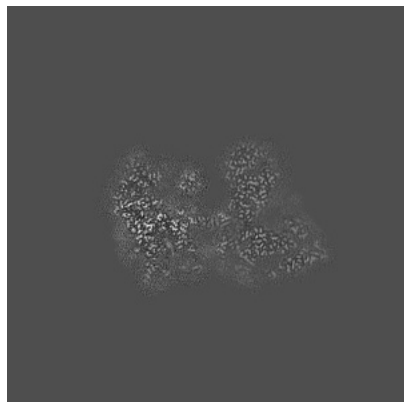


Z Index: 375

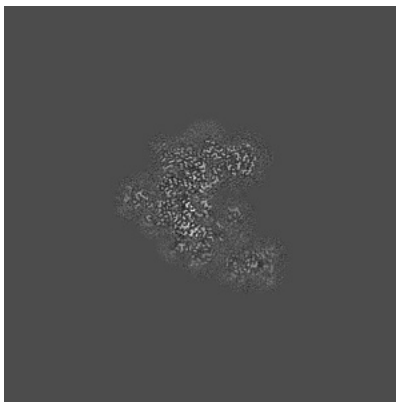
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

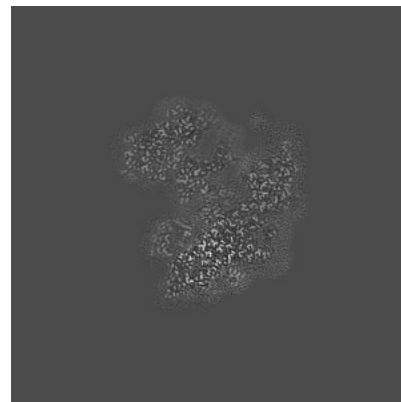
6.3.1 Primary map



X Index: 367



Y Index: 284

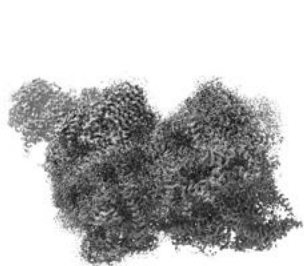


Z Index: 350

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.013. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

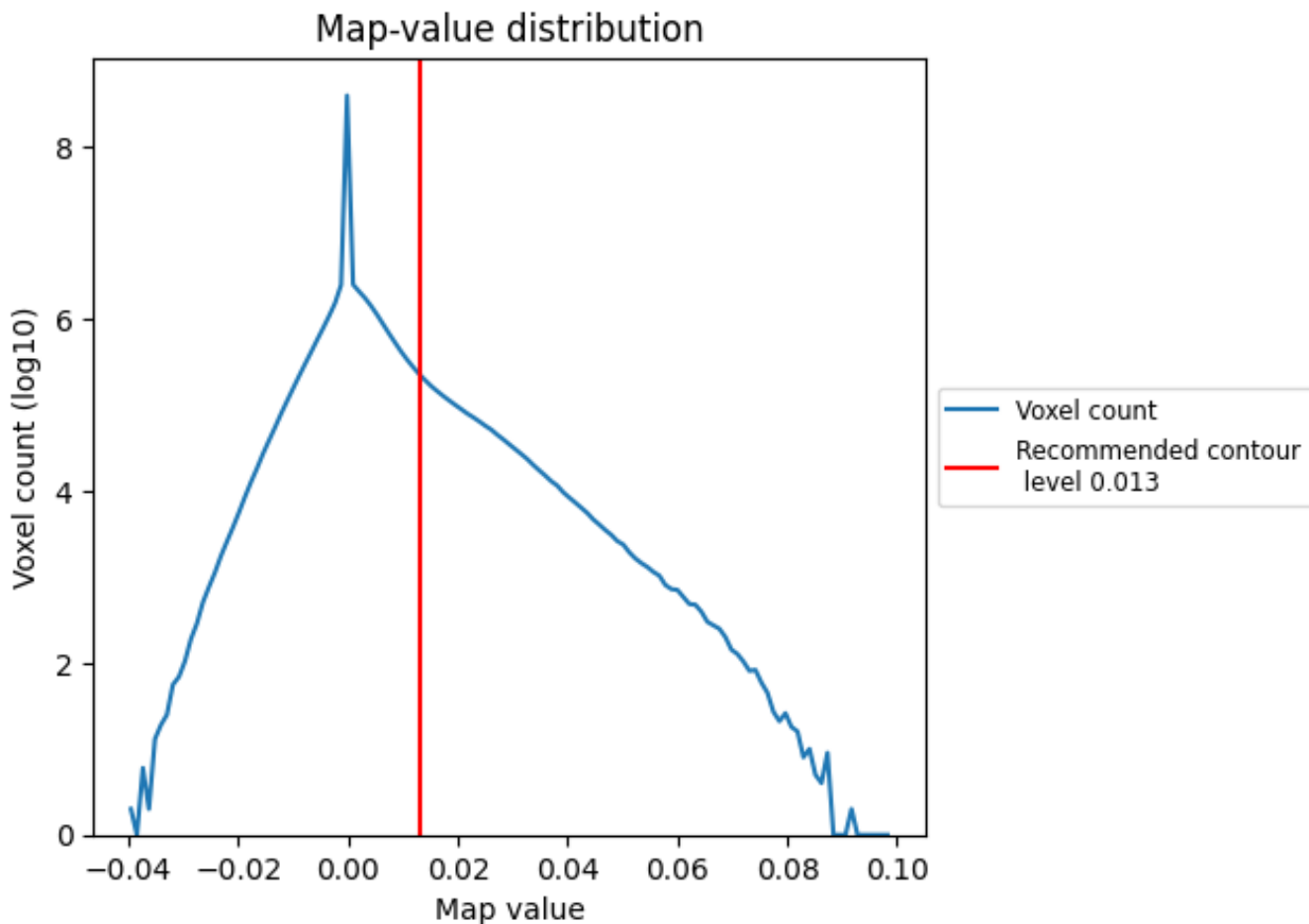
6.5 Mask visualisation

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

7 Map analysis [i](#)

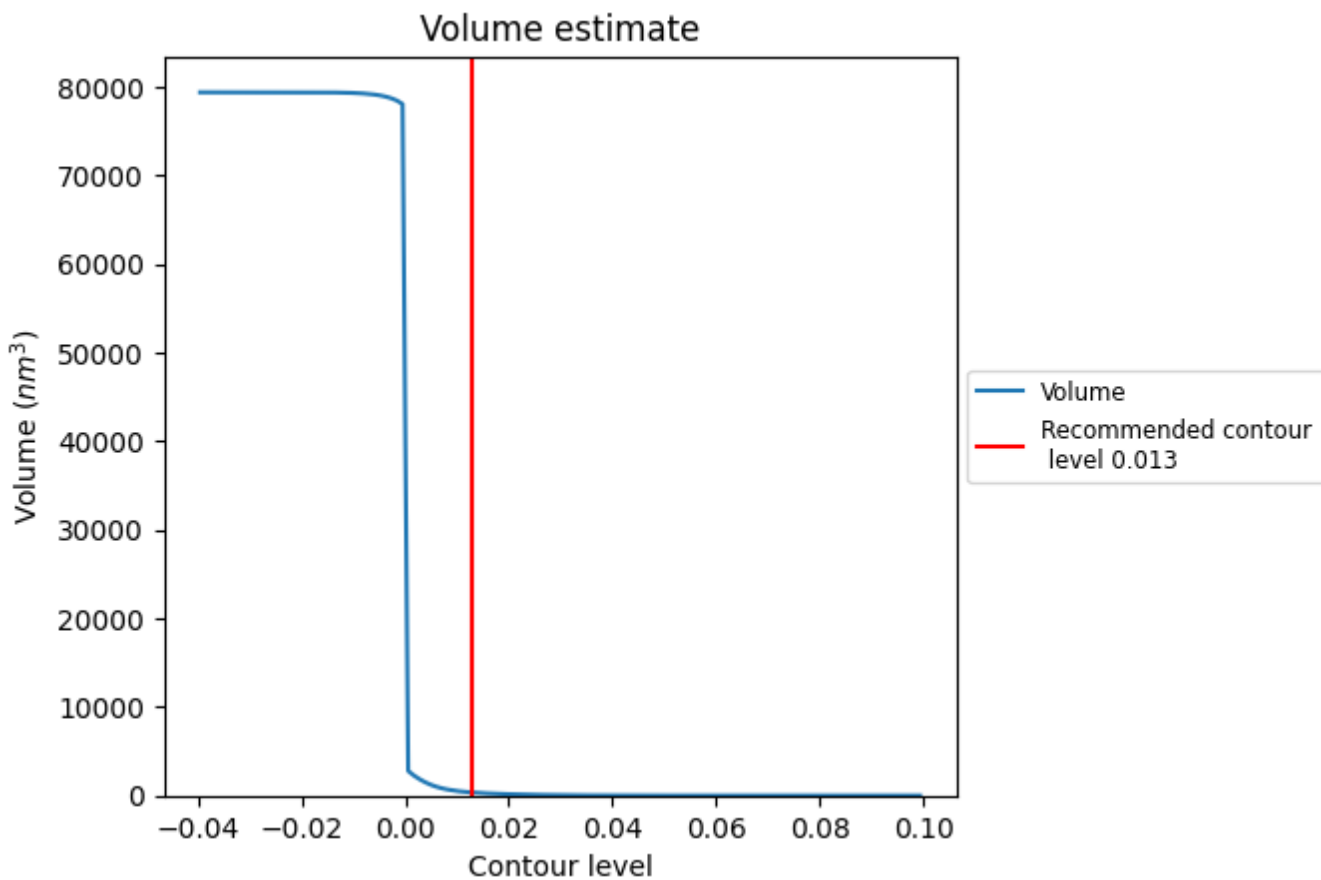
This section contains the results of statistical analysis of the map.

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.

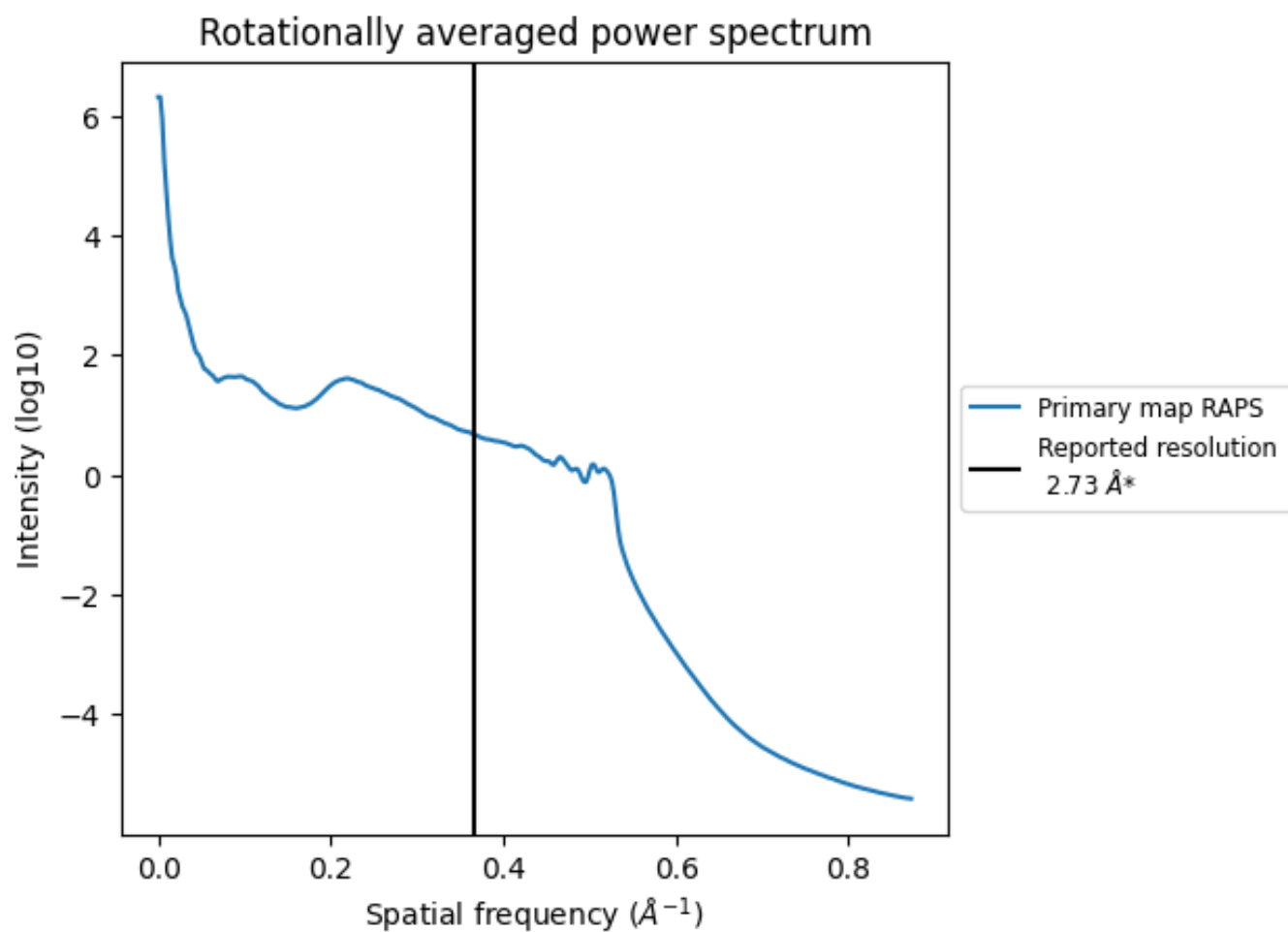
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 345 nm^3 ; this corresponds to an approximate mass of 312 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

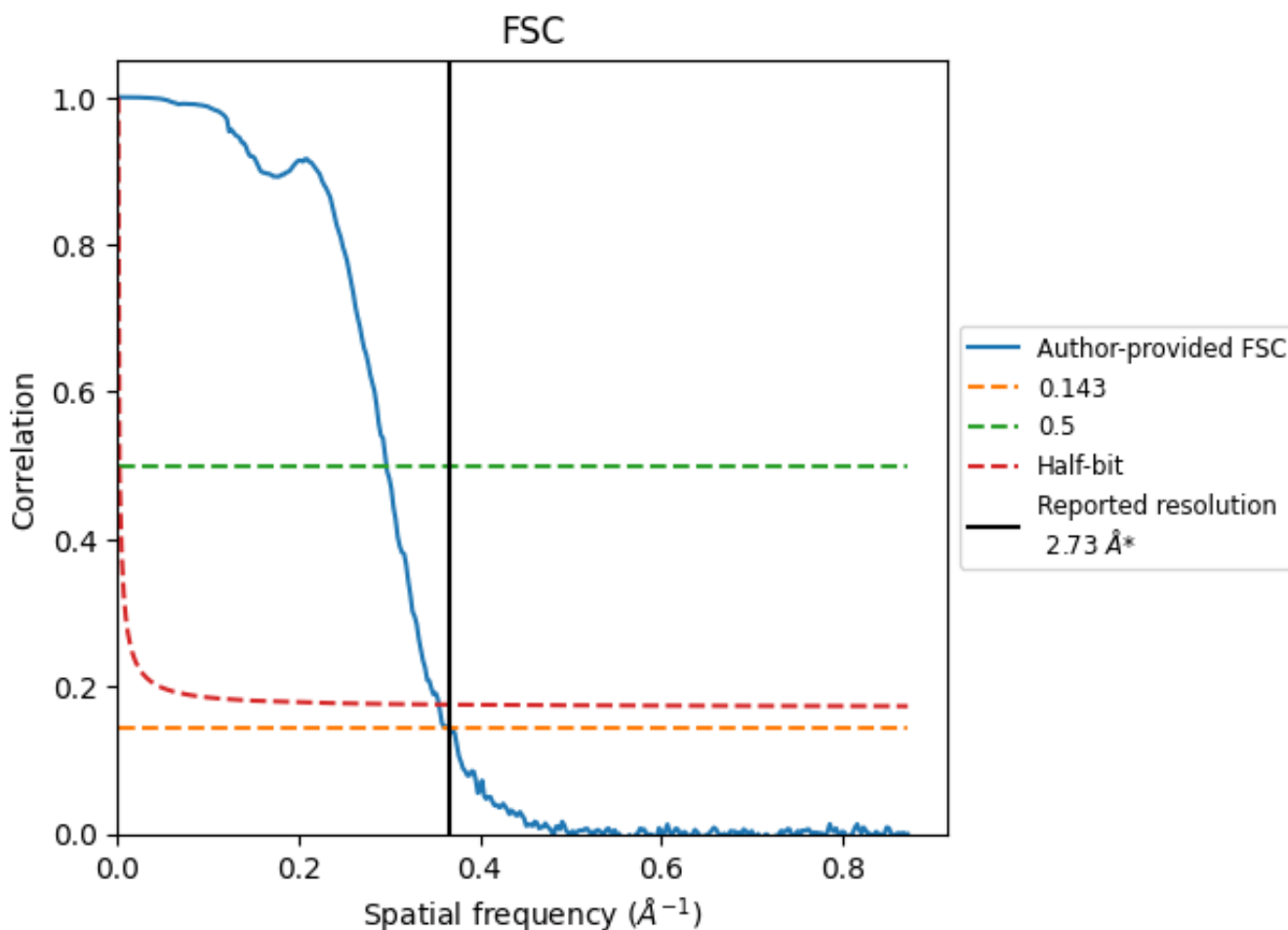


*Reported resolution corresponds to spatial frequency of 0.366\AA^{-1}

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 0.366 Å⁻¹

8.2 Resolution estimates [i](#)

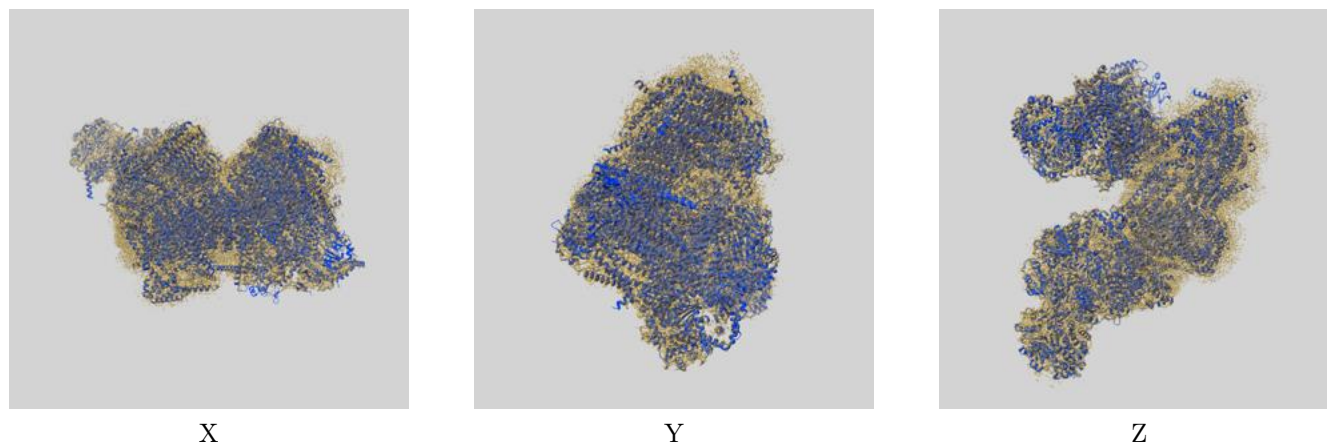
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.73	-	-
Author-provided FSC curve	2.73	3.37	2.82
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

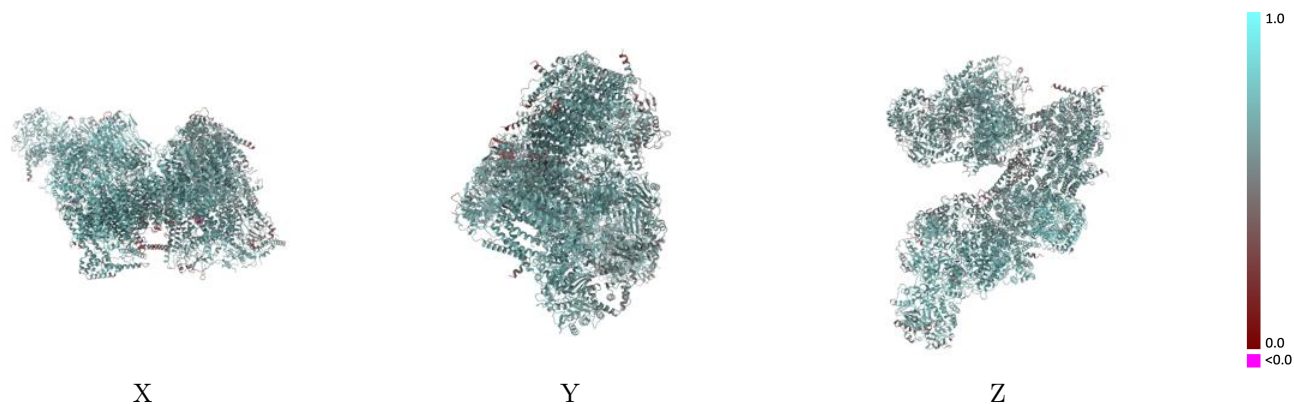
This section contains information regarding the fit between EMDB map EMD-16171 and PDB model 8BQ5. Per-residue inclusion information can be found in section 3 on page 23.

9.1 Map-model overlay [i](#)



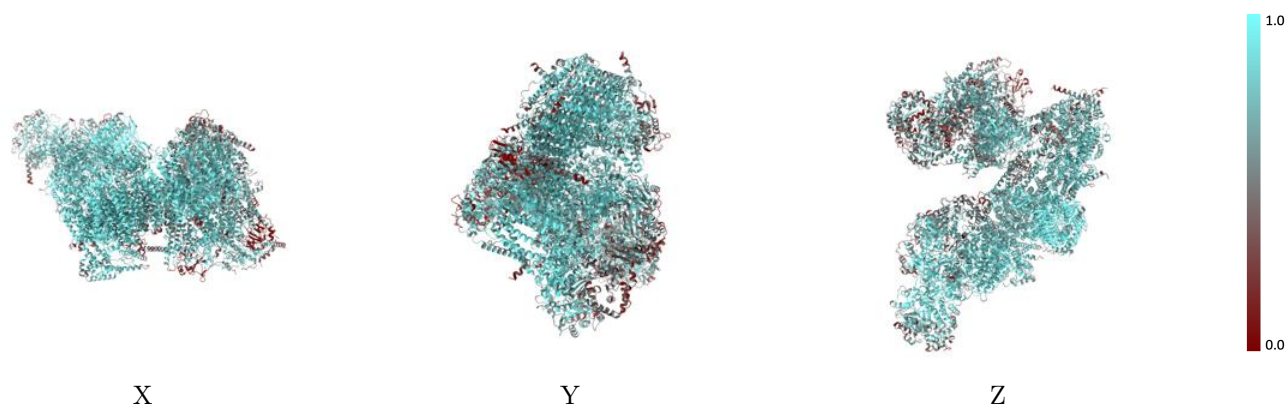
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



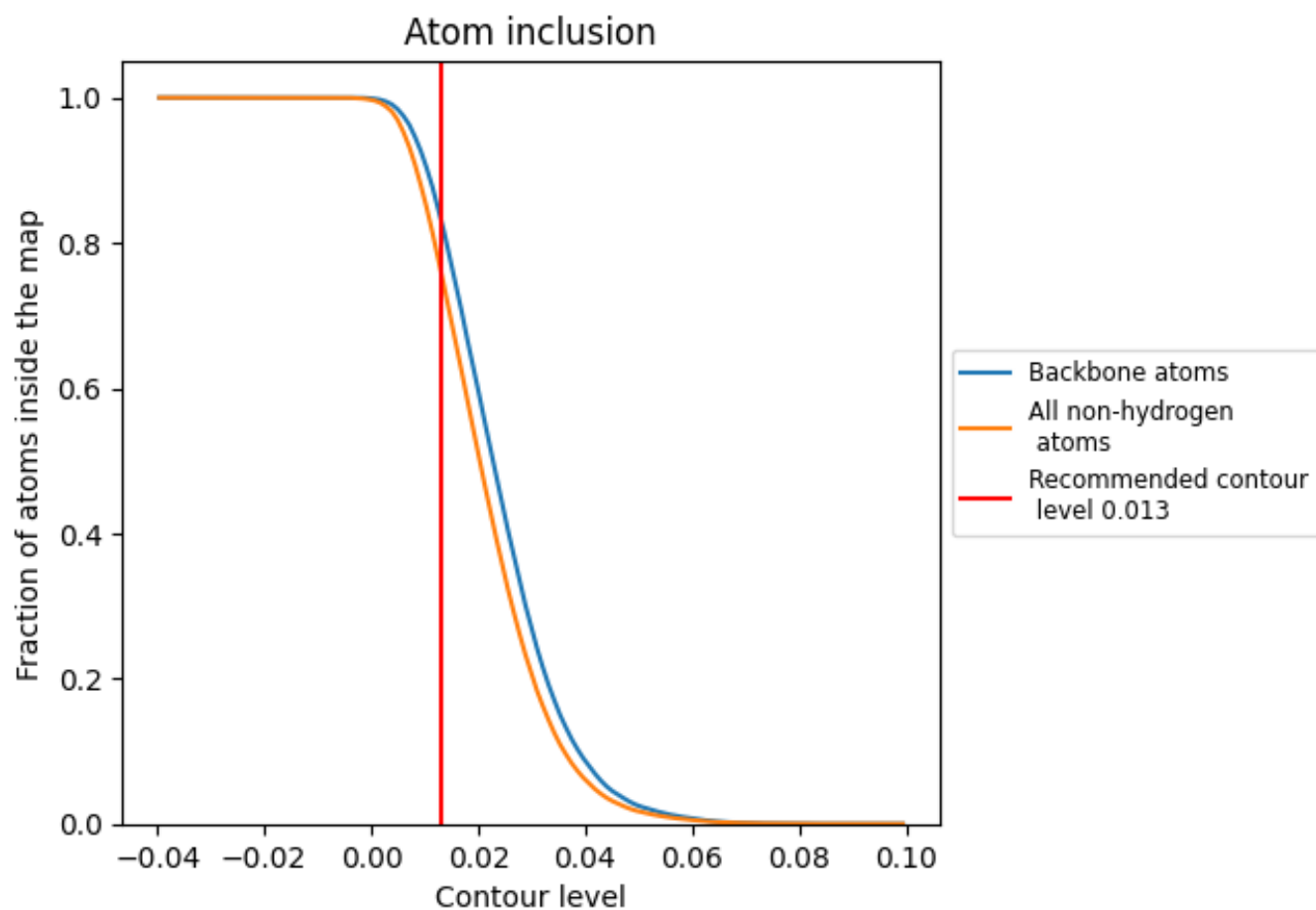
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.7618	 0.6420
A	 0.9442	 0.7030
AA	 0.4633	 0.5720
AB	 0.7395	 0.6440
AC	 0.8504	 0.6750
AD	 0.3440	 0.5320
AE	 0.8264	 0.6630
AF	 0.8321	 0.6700
AG	 0.8199	 0.6390
AH	 0.6849	 0.5870
AI	 0.6972	 0.6380
AJ	 0.2300	 0.5310
B	 0.9548	 0.7280
BA	 0.4843	 0.5810
BB	 0.7440	 0.6430
BC	 0.8165	 0.6610
BD	 0.3730	 0.5390
BE	 0.7704	 0.6500
BF	 0.7679	 0.6440
BG	 0.6394	 0.6190
BH	 0.4603	 0.5750
BI	 0.5991	 0.5890
BJ	 0.4851	 0.5590
C	 0.8951	 0.7170
D	 0.9457	 0.7240
E	 0.6464	 0.5950
F	 0.7233	 0.6360
G	 0.7816	 0.6650
H	 0.9395	 0.6990
I	 0.9518	 0.7250
J	 0.9004	 0.6860
K	 0.9561	 0.7090
L	 0.8426	 0.6460
M	 0.8947	 0.6710
N	 0.9288	 0.7030



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Chain	Atom inclusion	Q-score
O	 0.9396	 0.6760
P	 0.6507	 0.6050
Q	 0.5292	 0.6230
R	 0.7531	 0.6760
S	 0.6371	 0.5910
T	 0.3905	 0.4860
U	 0.6345	 0.5230
V	 0.7196	 0.6410
W	 0.6220	 0.6120
X	 0.7526	 0.6160
Y	 0.5828	 0.4920
Z	 0.7867	 0.6240
a	 0.8668	 0.6600
b	 0.7781	 0.5950
c	 0.7038	 0.5920
d	 0.7747	 0.6170
e	 0.8406	 0.6450
f	 0.9081	 0.6930
g	 0.7106	 0.5760
i	 0.6661	 0.5550
j	 0.5297	 0.5110
k	 0.4486	 0.4800
l	 0.6047	 0.5550
m	 0.7776	 0.6320
n	 0.7697	 0.5780
o	 0.5739	 0.5280
p	 0.7302	 0.5910
q	 0.8232	 0.6780
u	 0.7578	 0.5500
v	 0.8645	 0.6560
x	 0.9416	 0.7140
y	 0.8949	 0.6870
z	 0.8791	 0.6770