



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 08:52 PM UTC

PDB ID : 7O71 / pdb_00007o71
EMDB ID : EMD-12742
Title : Cryo-EM structure of a respiratory complex I
Authors : Parey, K.; Vonck, J.
Deposited on : 2021-04-12
Resolution : 2.40 Å(reported)
Based on initial model : 6RFR

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

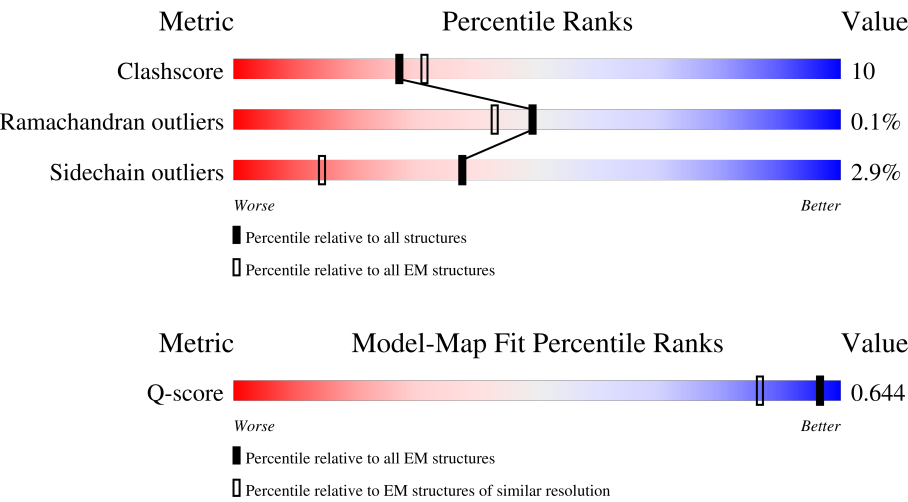
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5628 (1.90 - 2.90)

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	728	<div><div>25%</div><div>74%</div><div>20%</div><div>• 5%</div></div>
2	B	488	<div><div>66%</div><div>59%</div><div>33%</div><div>• 7%</div></div>
3	C	466	<div><div>11%</div><div>73%</div><div>19%</div><div>• 6%</div></div>
4	G	281	<div><div>7%</div><div>70%</div><div>15%</div><div>15%</div></div>

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Mol	Chain	Length	Quality of chain
5	H	243	
6	I	229	
7	K	210	
8	L	89	
9	S	249	
10	j	93	
11	1	341	
12	2	469	
13	3	128	
14	4	486	
15	5	655	
16	6	185	
17	g	78	
18	D	87	
19	E	375	
20	F	144	
21	J	198	
22	M	136	
23	O	109	
24	P	124	
25	Q	132	
26	R	109	
27	U	172	
28	W	123	
29	X	169	

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Mol	Chain	Length	Quality of chain
30	Y	161	
31	Z	182	
32	a	149	
33	b	74	
34	c	60	
35	d	92	
36	e	67	
37	f	87	
38	h	138	
39	i	90	
40	n	120	
41	8	99	
42	9	89	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 67428 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 78 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	693	Total	C	N	O	S	0	0
			5269	3272	927	1041	29		

- Molecule 2 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	455	Total	C	N	O	S	0	0
			3517	2223	617	653	24		

- Molecule 3 is a protein called NUCM protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	437	Total	C	N	O	S	1	0
			3470	2205	595	648	22		

- Molecule 4 is a protein called Subunit NUGM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	239	Total	C	N	O	S	0	0
			1978	1272	336	366	4		

- Molecule 5 is a protein called Subunit NUHM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	216	Total	C	N	O	S	0	0
			1688	1060	284	326	18		

- Molecule 6 is a protein called Subunit NUIM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	190	Total	C	N	O	S	0	0
			1519	966	254	289	10		

- Molecule 7 is a protein called Subunit NUKM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	177	Total	C	N	O	S	0	0
			1395	885	246	249	15		

- Molecule 8 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	89	Total	C	N	O	S	0	0
			693	465	109	116	3		

- Molecule 9 is a protein called Subunit NESM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	S	182	Total	C	N	O	S	0	0
			1492	961	255	274	2		

- Molecule 10 is a protein called Subunit NB5M of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	90	Total	C	N	O	S	0	0
			724	465	132	127			

- Molecule 11 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	1	340	Total	C	N	O	S	0	0
			2716	1850	393	466	7		

- Molecule 12 is a protein called NADH dehydrogenase subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	2	469	Total	C	N	O	S	0	0
			3776	2558	550	656	12		

- Molecule 13 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	3	128	Total	C	N	O	S	0	0
			1027	701	151	172	3		

- Molecule 14 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	4	481	Total	C	N	O	S	0	0
			3815	2573	581	647	14		

- Molecule 15 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	5	654	Total	C	N	O	S	0	0
			5197	3479	785	905	28		

- Molecule 16 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	6	184	Total	C	N	O	S	0	0
			1453	985	208	251	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	1	FME	-	insertion	UNP S5U3X7

- Molecule 17 is a protein called subunit NI9M of protein NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms				AltConf	Trace
17	g	76	Total	C	N	O	0	0
			622	408	113	101		

- Molecule 18 is a protein called Subunit NIMM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
18	D	86	Total	C	N	O	S	0	0
			681	432	127	119	3		

- Molecule 19 is a protein called NADH-ubiquinone oxidoreductase 40 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	E	350	Total	C	N	O	S	0	0
			2806	1782	490	524	10		

- Molecule 20 is a protein called Subunit NUFM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
20	F	120	Total	C	N	O	S	0	0
			981	624	164	191	2		

- Molecule 21 is a protein called Subunit NUJM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
21	J	178	Total	C	N	O	S	0	0
			1319	838	238	238	5		

- Molecule 22 is a protein called Subunit NUMM of protein NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
22	M	117	Total	C	N	O	S	0	0
			912	568	163	176	5		

- Molecule 23 is a protein called Acyl carrier protein ACPM1 of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms				AltConf	Trace
23	O	71	Total	C	N	O	0	0
			543	344	83	116		

- Molecule 24 is a protein called Subunit NB4M of protein NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	123	Total	C	N	O	S	0	0
			1036	667	182	185	2		

- Molecule 25 is a protein called Acyl carrier protein ACPM2 of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	85	Total	C	N	O	S	0	0
			648	405	103	138	2		

- Molecule 26 is a protein called Subunit NI2M of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	106	Total	C	N	O	S	0	0
			884	562	168	151	3		

- Molecule 27 is a protein called Subunit NUPM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	171	Total	C	N	O	S	0	0
			1345	847	236	252	10		

- Molecule 28 is a protein called Subunit NB6M of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	121	Total	C	N	O	S	0	0
			974	623	178	168	5		

- Molecule 29 is a protein called Subunit NUXM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	164	Total	C	N	O	S	0	0
			1275	828	217	226	4		

- Molecule 30 is a protein called Subunit NUYM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	123	Total	C	N	O	S	0	0
			1021	651	187	181	2		

- Molecule 31 is a protein called Subunit NUZM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	181	Total	C	N	O	S	0	0
			1389	893	240	255	1		

- Molecule 32 is a protein called Subunit NIAM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	124	Total	C	N	O	S	0	0
			1030	669	165	194	2		

- Molecule 33 is a protein called Subunit NEBM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms				AltConf	Trace
33	b	64	Total	C	N	O	0	0
			490	326	83	81		

- Molecule 34 is a protein called Subunit NB2M of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms				AltConf	Trace
34	c	44	Total	C	N	O	0	0
			353	229	67	57		

- Molecule 35 is a protein called Subunit NIDM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	89	Total	C	N	O	S	0	0
			751	467	136	145	3		

- Molecule 36 is a protein called Subunit NUVM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	52	Total	C	N	O	S	0	0
			436	293	75	65	3		

- Molecule 37 is a protein called Subunit NI8M of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	82	Total	C	N	O	S	0	0
			642	403	121	117	1		

- Molecule 38 is a protein called Subunit N7BM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	136	Total	C	N	O	S	0	0
			1130	727	193	208	2		

- Molecule 39 is a protein called Subunit NUUM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	83	Total	C	N	O	S	0	0
			646	413	117	115	1		

- Molecule 40 is a protein called Subunit NUNM of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	114	Total	C	N	O	S	0	0
			913	587	154	171	1		

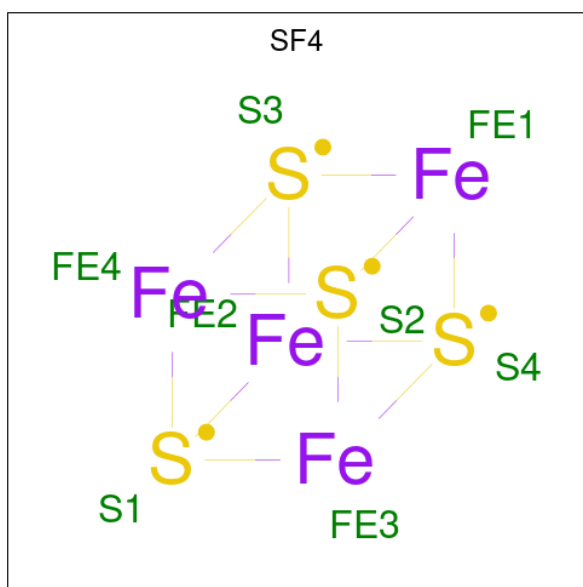
- Molecule 41 is a protein called Subunit NB8M of NADH:Ubiquinone Oxidoreductase (Complex I).

Mol	Chain	Residues	Atoms					AltConf	Trace
41	8	71	Total	C	N	O	S	0	0
			594	375	109	102	8		

- Molecule 42 is a protein called Subunit NIPM of NADH:Ubiquinone Oxidoreductase (Complex I).

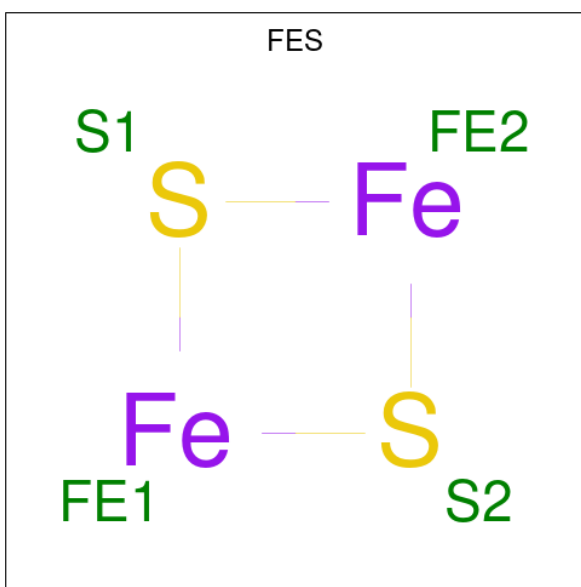
Mol	Chain	Residues	Atoms					AltConf	Trace
42	9	86	Total	C	N	O	S	0	0
			672	422	122	122	6		

- Molecule 43 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



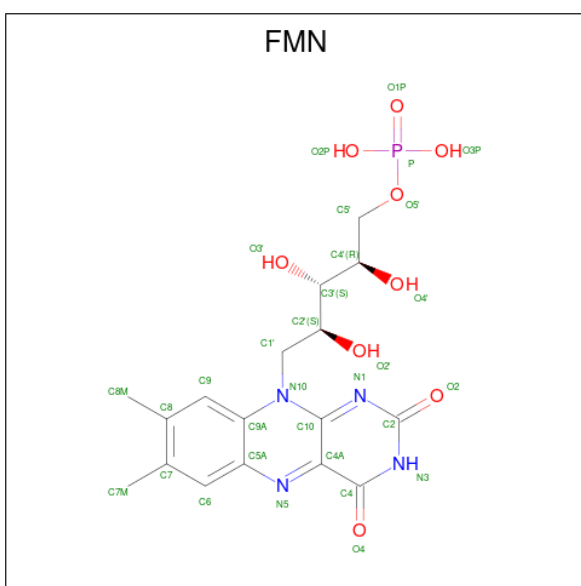
Mol	Chain	Residues	Atoms			AltConf
43	A	1	Total	Fe	S	0
			8	4	4	
43	A	1	Total	Fe	S	0
			8	4	4	
43	B	1	Total	Fe	S	0
			8	4	4	
43	I	1	Total	Fe	S	0
			8	4	4	
43	I	1	Total	Fe	S	0
			8	4	4	
43	K	1	Total	Fe	S	0
			8	4	4	

- Molecule 44 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



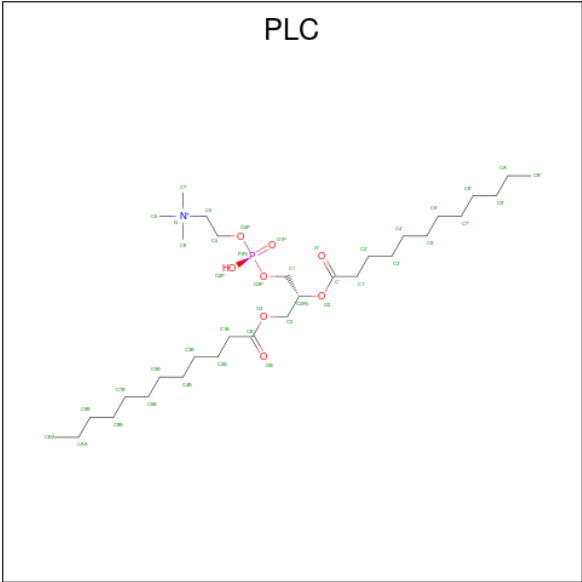
Mol	Chain	Residues	Atoms			AltConf
44	A	1	Total 4	Fe 2	S 2	0
44	H	1	Total 4	Fe 2	S 2	0

- Molecule 45 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



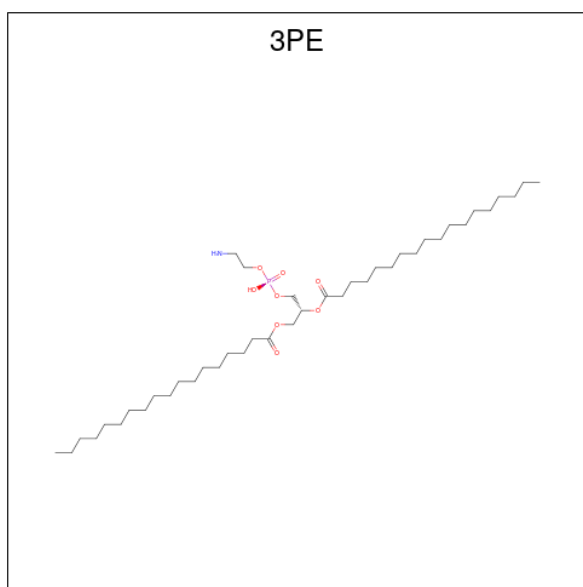
Mol	Chain	Residues	Atoms					AltConf
45	B	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 46 is DIUNDECYL PHOSPHATIDYL CHOLINE (CCD ID: PLC) (formula: $C_{32}H_{65}NO_8P$).



Mol	Chain	Residues	Atoms					AltConf
46	K	1	Total	C	N	O	P	0
			39	29	1	8	1	
46	1	1	Total	C	N	O	P	0
			35	25	1	8	1	
46	1	1	Total	C	N	O	P	0
			42	32	1	8	1	
46	4	1	Total	C	N	O	P	0
			35	25	1	8	1	
46	5	1	Total	C	N	O	P	0
			42	32	1	8	1	
46	W	1	Total	C	N	O	P	0
			41	31	1	8	1	

- Molecule 47 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: C₄₁H₈₂NO₈P).



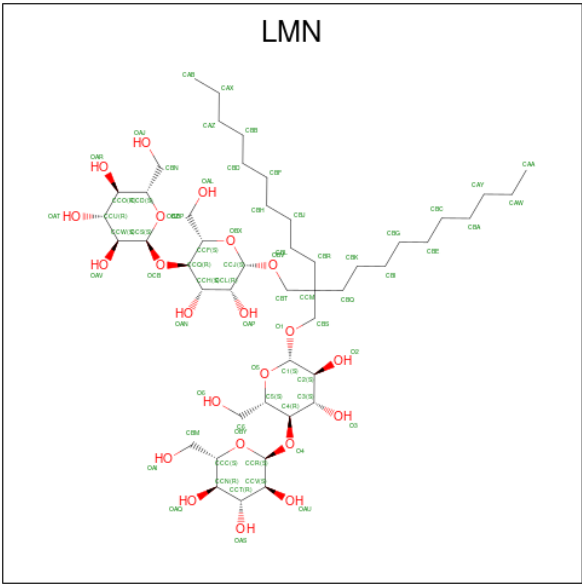
Mol	Chain	Residues	Atoms					AltConf
47	S	1	Total	C	N	O	P	0
			42	32	1	8	1	
47	1	1	Total	C	N	O	P	0
			51	41	1	8	1	
47	1	1	Total	C	N	O	P	0
			36	26	1	8	1	
47	1	1	Total	C	N	O	P	0
			41	31	1	8	1	
47	4	1	Total	C	N	O	P	0
			43	33	1	8	1	
47	4	1	Total	C	N	O	P	0
			42	32	1	8	1	
47	4	1	Total	C	N	O	P	0
			51	41	1	8	1	
47	5	1	Total	C	N	O	P	0
			42	32	1	8	1	
47	5	1	Total	C	N	O	P	0
			41	31	1	8	1	
47	5	1	Total	C	N	O	P	0
			43	33	1	8	1	
47	6	1	Total	C	N	O	P	0
			36	26	1	8	1	
47	6	1	Total	C	N	O	P	0
			48	38	1	8	1	
47	g	1	Total	C	N	O	P	0
			43	33	1	8	1	
47	E	1	Total	C	N	O	P	0
			36	26	1	8	1	

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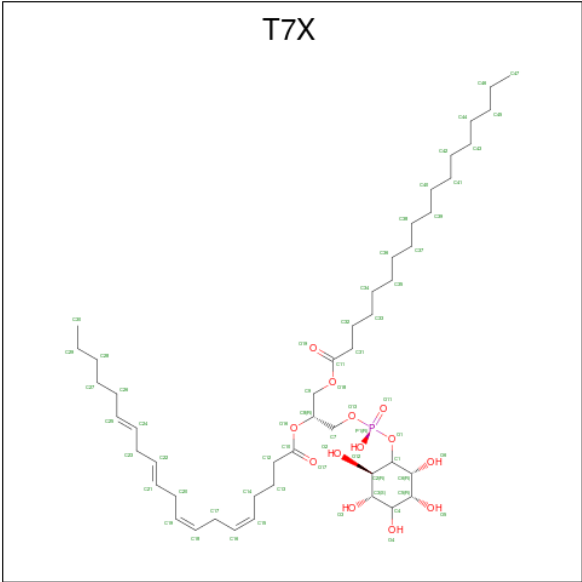
Mol	Chain	Residues	Atoms					AltConf
47	J	1	Total	C	N	O	P	0
			41	31	1	8	1	
47	J	1	Total	C	N	O	P	0
			44	34	1	8	1	
47	J	1	Total	C	N	O	P	0
			34	24	1	8	1	
47	b	1	Total	C	N	O	P	0
			42	32	1	8	1	

- Molecule 48 is Lauryl Maltose Neopentyl Glycol (CCD ID: LMN) (formula: C₄₇H₈₈O₂₂).



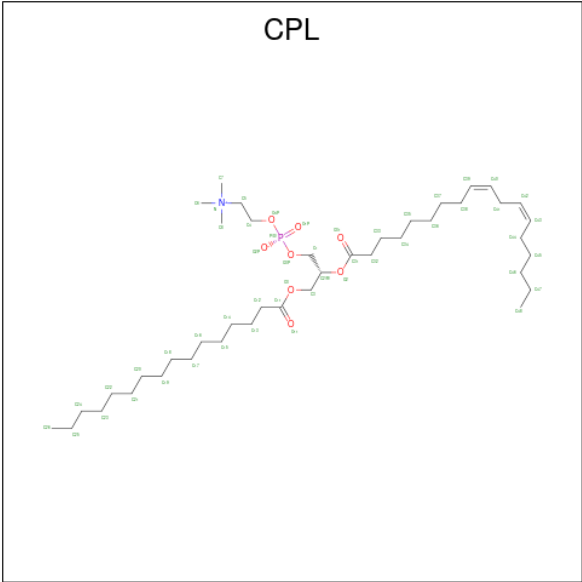
Mol	Chain	Residues	Atoms			AltConf
48	j	1	Total	C	O	0
			65	43	22	
48	J	1	Total	C	O	0
			69	47	22	

- Molecule 49 is Phosphatidylinositol (CCD ID: T7X) (formula: C₄₇H₈₃O₁₃P).



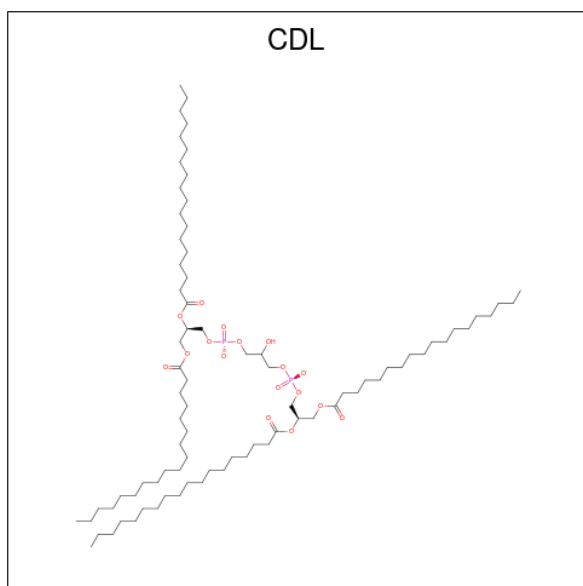
Mol	Chain	Residues	Atoms				AltConf
49	2	1	Total	C	O	P	0
			48	34	13	1	
49	2	1	Total	C	O	P	0
			52	38	13	1	
49	3	1	Total	C	O	P	0
			49	35	13	1	

- Molecule 50 is 1-PALMITOYL-2-LINOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: CPL) (formula: C₄₂H₈₀NO₈P).



Mol	Chain	Residues	Atoms					AltConf
50	2	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 51 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



Mol	Chain	Residues	Atoms					AltConf
51	g	1	Total	C	O	P		0
			83	64	17	2		
51	E	1	Total	C	O	P		0
			72	53	17	2		
51	W	1	Total	C	O	P		0
			54	35	17	2		
51	X	1	Total	C	O	P		0
			86	67	17	2		
51	Z	1	Total	C	O	P		0
			76	57	17	2		
51	n	1	Total	C	O	P		0
			92	73	17	2		

- Molecule 52 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



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

- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
53	M	1	Total Zn 1 1	0

- Molecule 54 is S-[2-($\{N-[(2S)-2\text{-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-\beta\text{-alanine}\}$ amino)ethyl] tetradecanethioate (CCD ID: ZMP) (formula: $C_{25}H_{49}N_2O_8PS$).



Mol	Chain	Residues	Atoms						AltConf
54	O	1	Total	C	N	O	P	S	0
			33	22	2	7	1	1	
54	Q	1	Total	C	N	O	P	S	0
			33	22	2	7	1	1	

- Molecule 55 is water.

Mol	Chain	Residues	Atoms		AltConf
55	A	135	Total	O	0
			135	135	
55	B	11	Total	O	0
			11	11	
55	C	168	Total	O	0
			168	168	
55	G	114	Total	O	0
			114	114	
55	H	2	Total	O	0
			2	2	
55	I	95	Total	O	0
			95	95	
55	K	78	Total	O	0
			78	78	
55	L	18	Total	O	0
			18	18	
55	S	4	Total	O	0
			4	4	
55	j	15	Total	O	0
			15	15	
55	1	67	Total	O	0
			67	67	
55	2	158	Total	O	0
			158	158	
55	3	10	Total	O	0
			10	10	
55	4	139	Total	O	0
			139	139	
55	5	57	Total	O	0
			57	57	
55	6	24	Total	O	0
			24	24	
55	g	2	Total	O	0
			2	2	
55	D	17	Total	O	0
			17	17	

Continued on next page...

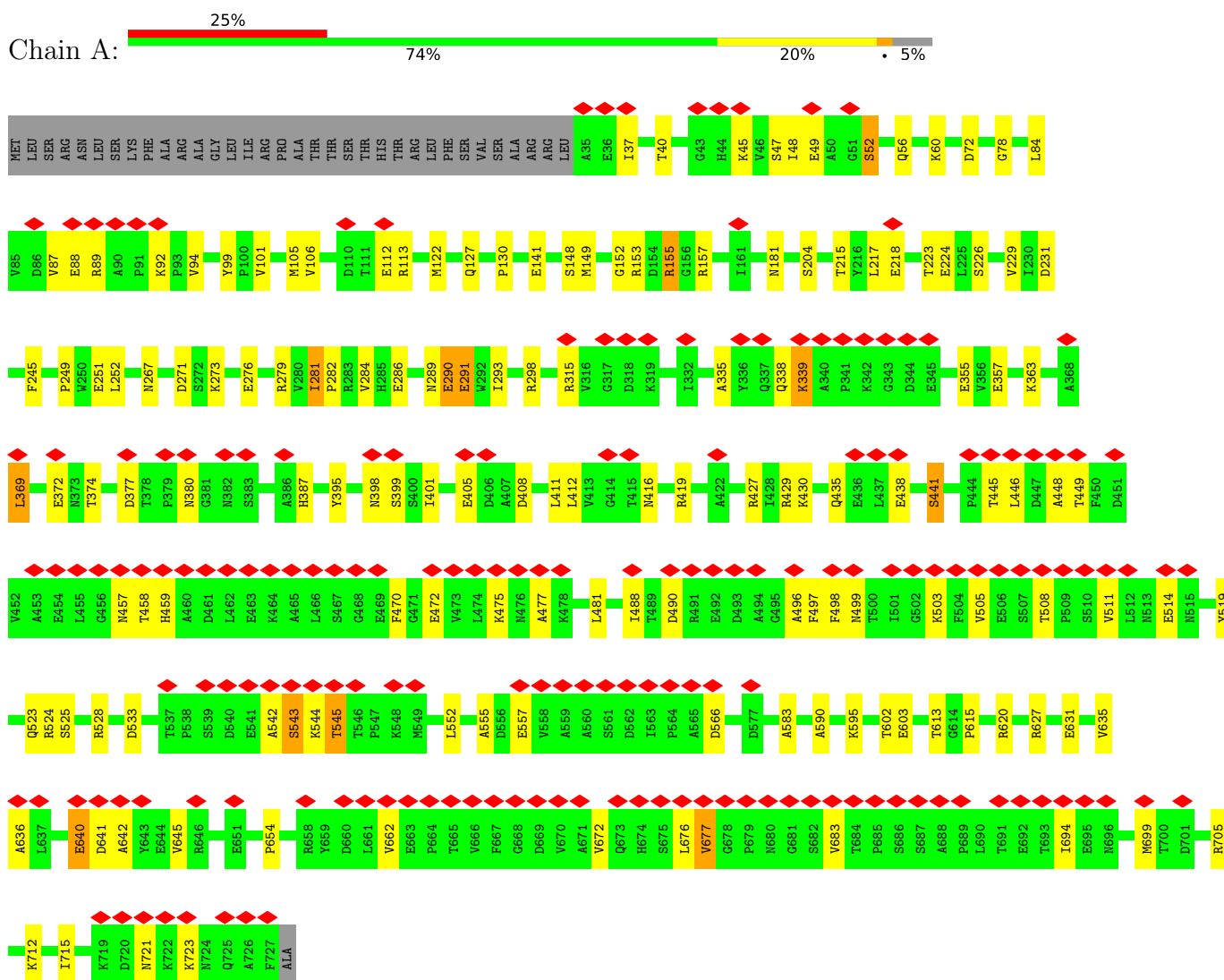
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
55	E	79	Total 79	O 79	0
55	F	15	Total 15	O 15	0
55	J	14	Total 14	O 14	0
55	M	45	Total 45	O 45	0
55	P	15	Total 15	O 15	0
55	R	11	Total 11	O 11	0
55	U	39	Total 39	O 39	0
55	W	23	Total 23	O 23	0
55	X	39	Total 39	O 39	0
55	Y	53	Total 53	O 53	0
55	Z	52	Total 52	O 52	0
55	a	11	Total 11	O 11	0
55	b	6	Total 6	O 6	0
55	d	8	Total 8	O 8	0
55	h	61	Total 61	O 61	0
55	i	3	Total 3	O 3	0
55	n	12	Total 12	O 12	0
55	9	16	Total 16	O 16	0

3 Residue-property plots

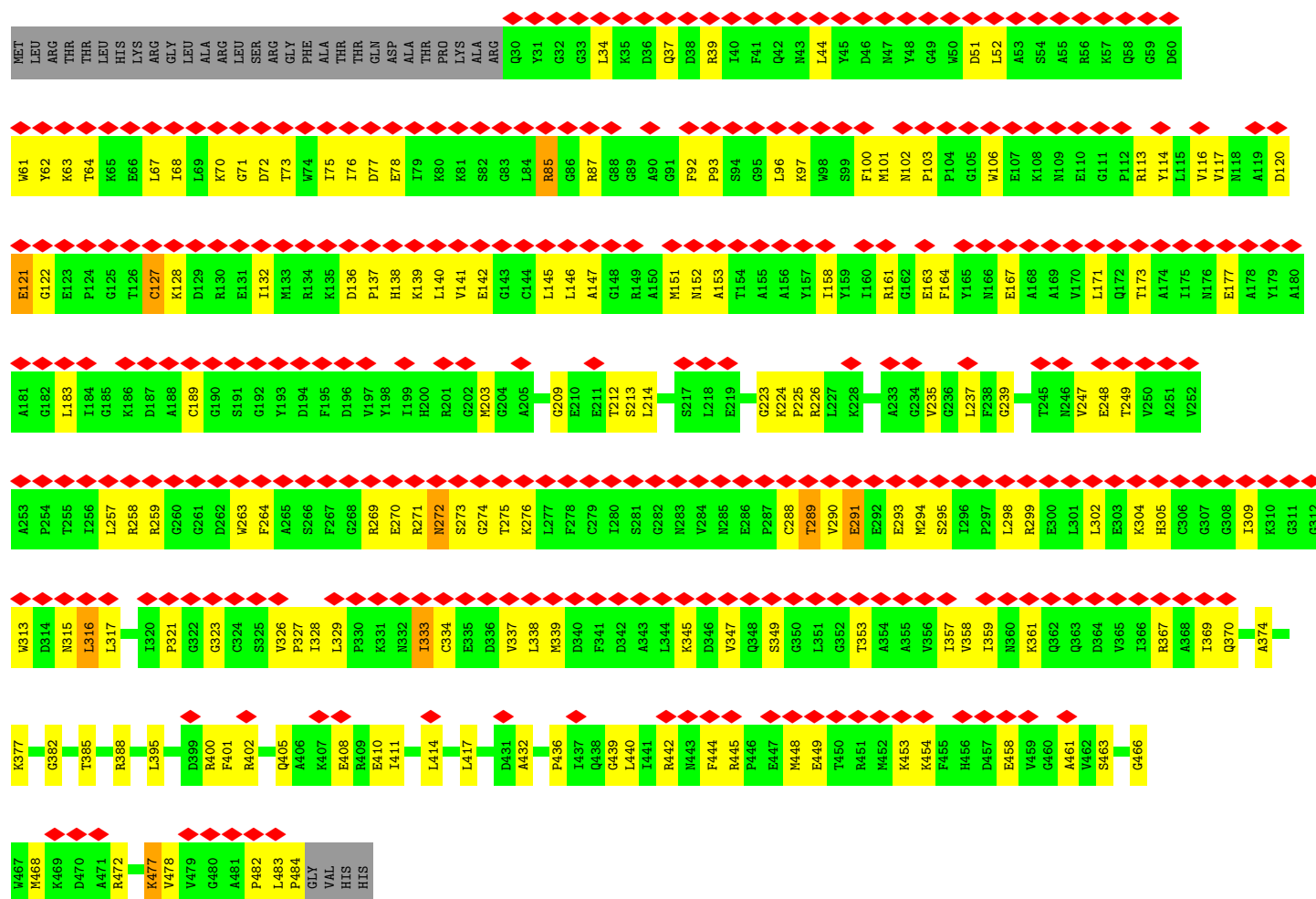
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: NADH-ubiquinone oxidoreductase 78 kDa subunit

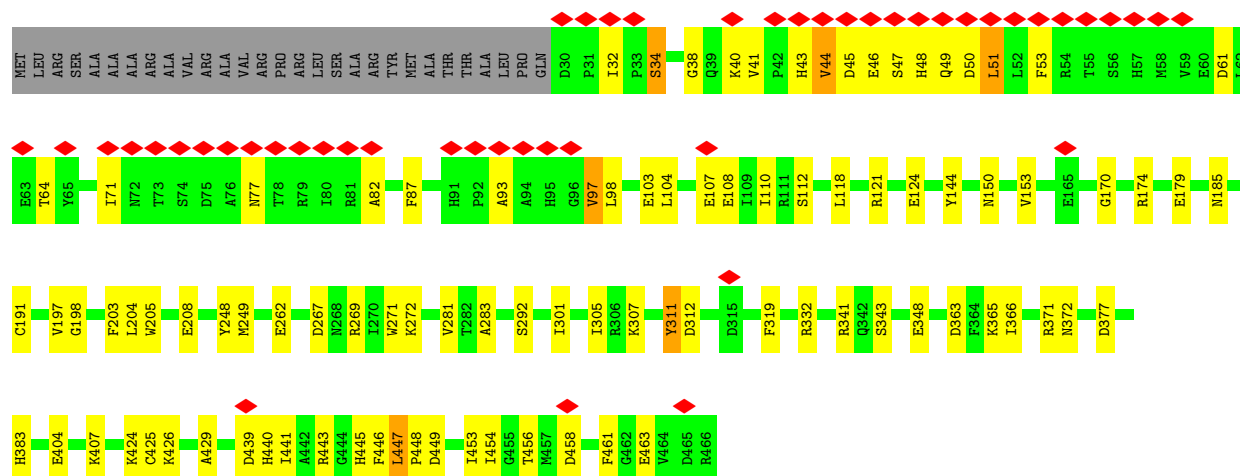
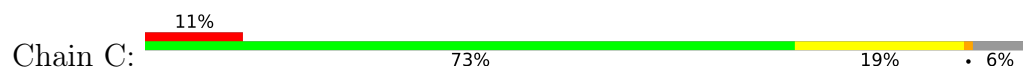


• Molecule 2: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial



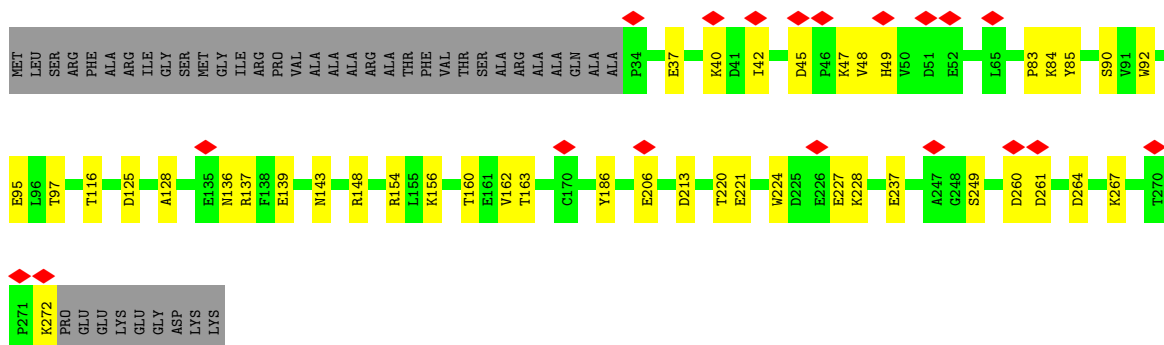


• Molecule 3: NUCM protein

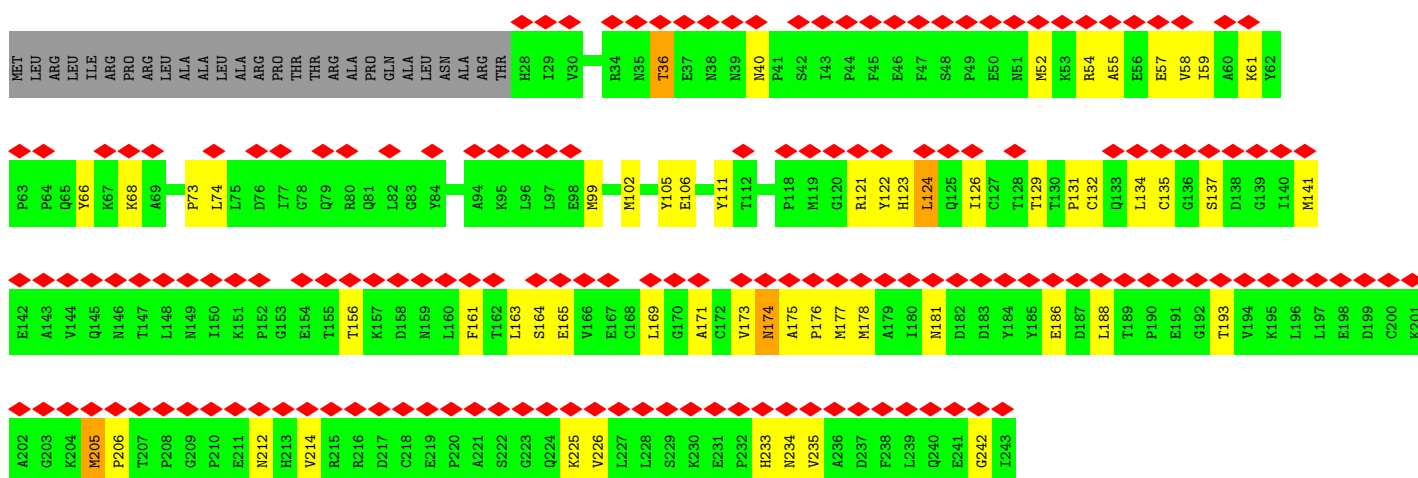


• Molecule 4: Subunit NUGM of NADH:Ubiquinone Oxidoreductase (Complex I)

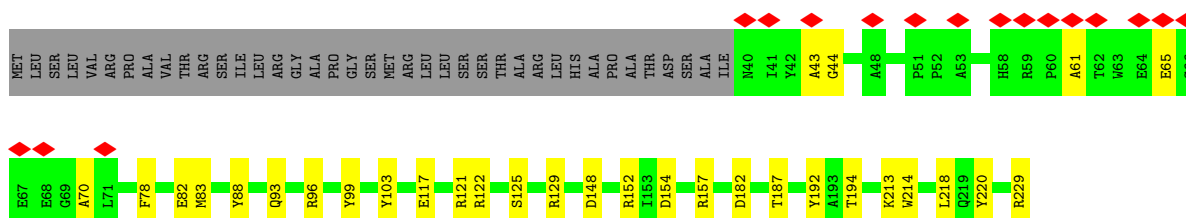




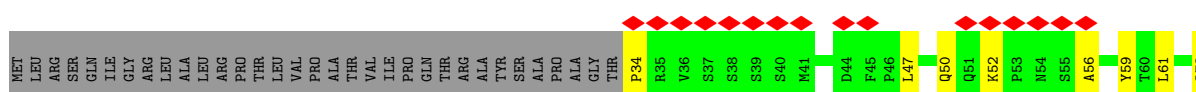
• Molecule 5: Subunit NUHM of NADH:Ubiquinone Oxidoreductase (Complex I)

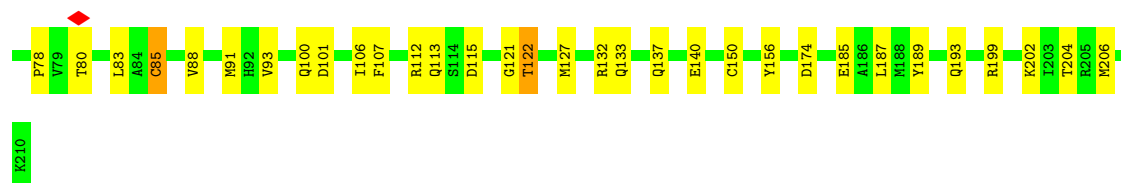


• Molecule 6: Subunit NUIM of NADH:Ubiquinone Oxidoreductase (Complex I)



• Molecule 7: Subunit NUKM of NADH:Ubiquinone Oxidoreductase (Complex I)

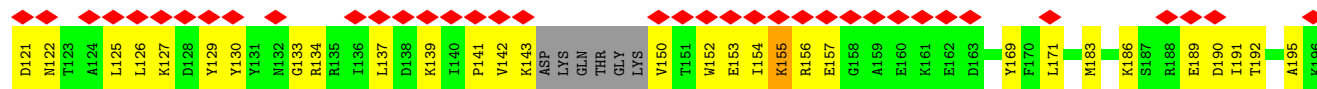
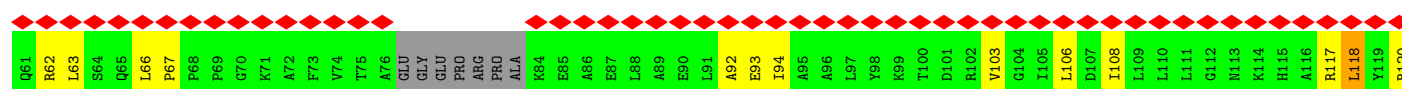
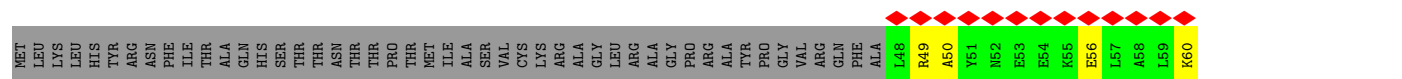




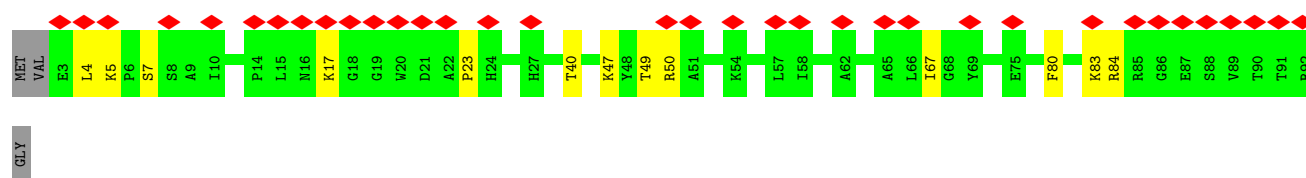
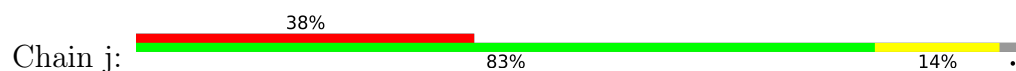
- Molecule 8: NADH-ubiquinone oxidoreductase chain 4L



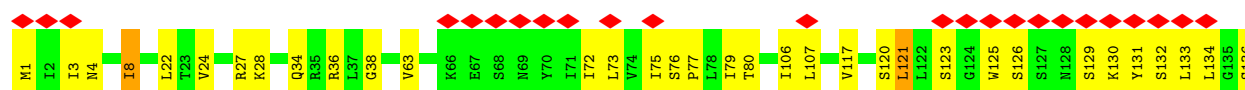
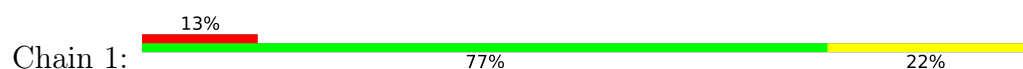
- Molecule 9: Subunit NESM of NADH:Ubiquinone Oxidoreductase (Complex I)

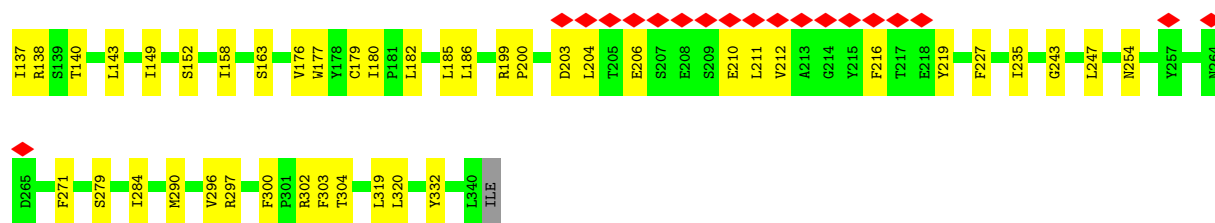


- Molecule 10: Subunit NB5M of NADH:Ubiquinone Oxidoreductase (Complex I)

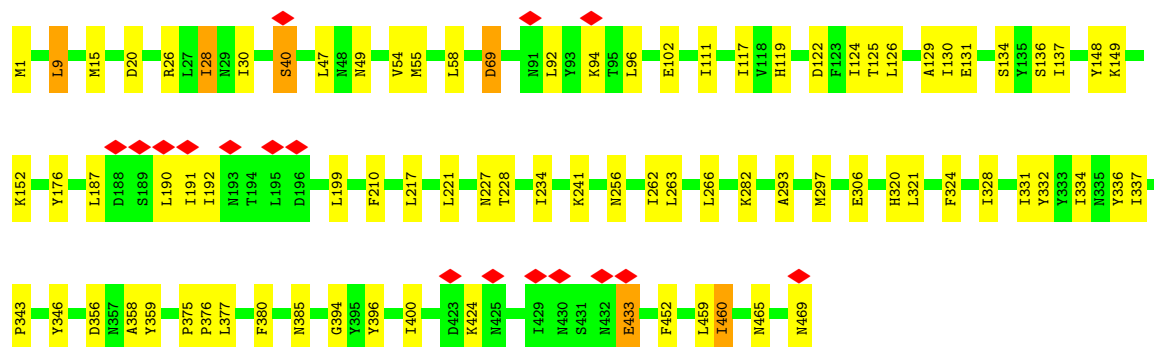
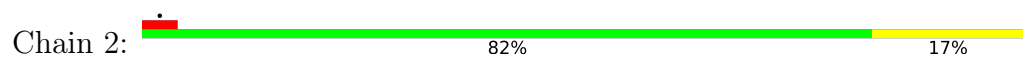


- Molecule 11: NADH-ubiquinone oxidoreductase chain 1

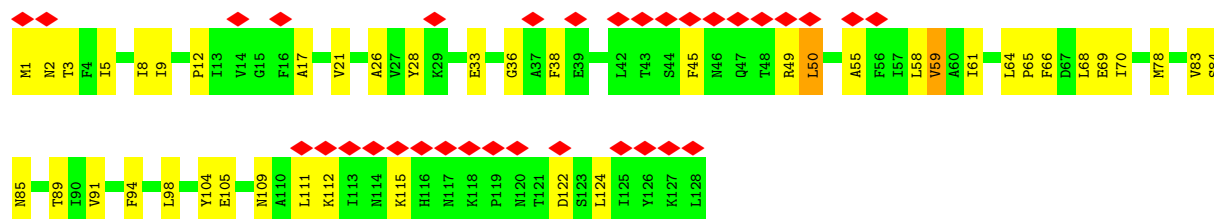




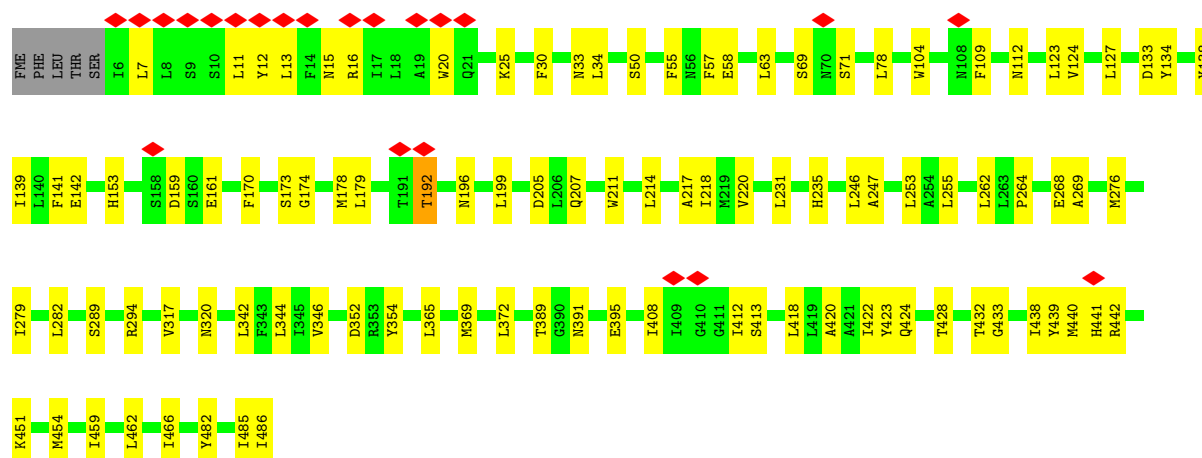
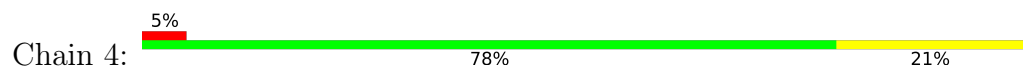
• Molecule 12: NADH dehydrogenase subunit 2



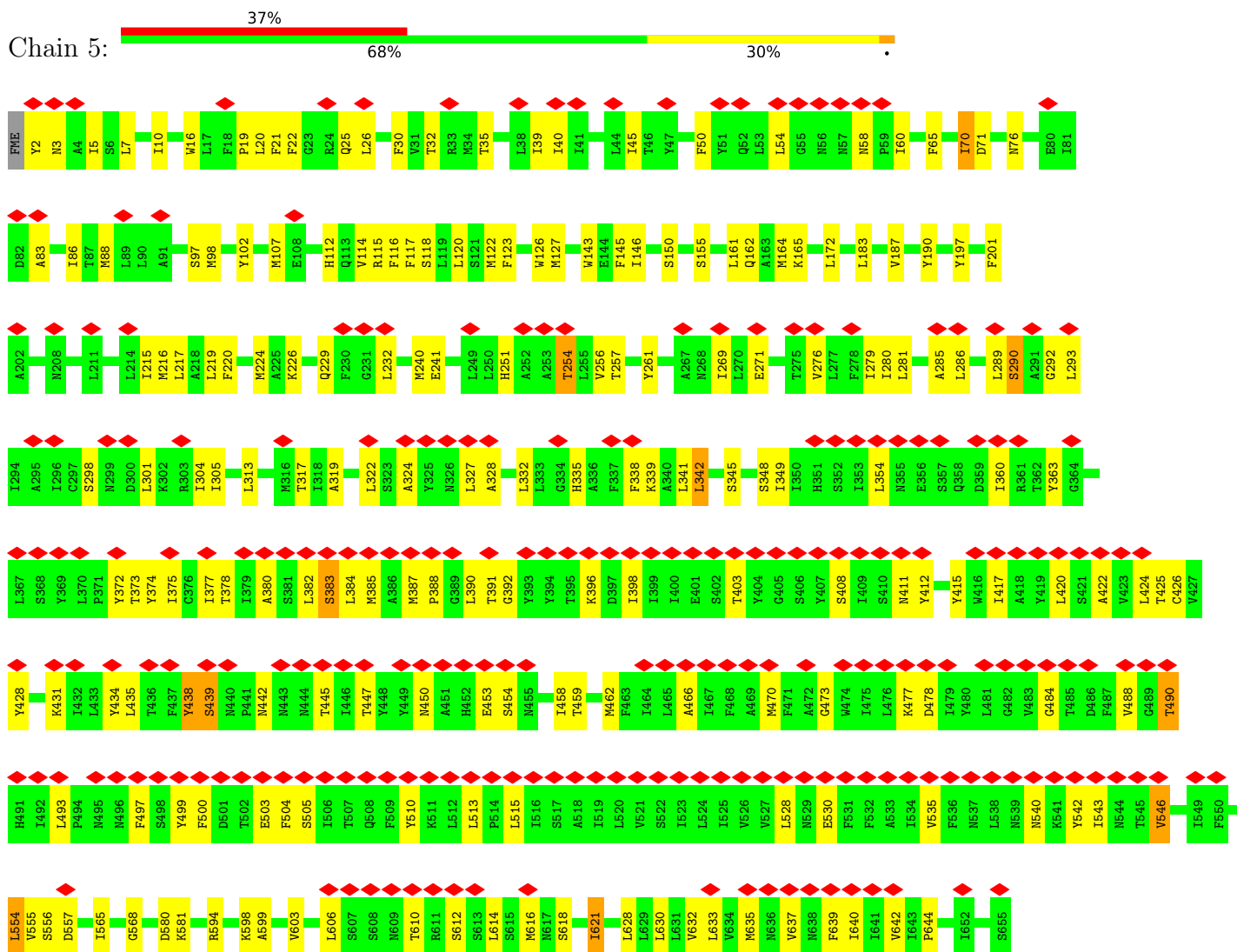
• Molecule 13: NADH-ubiquinone oxidoreductase chain 3



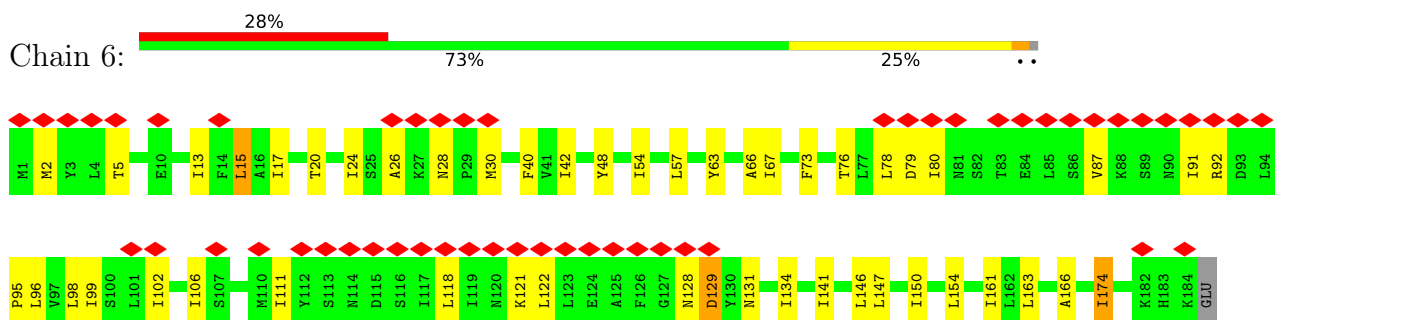
• Molecule 14: NADH-ubiquinone oxidoreductase chain 4



- Molecule 15: NADH-ubiquinone oxidoreductase chain 5



- Molecule 16: NADH-ubiquinone oxidoreductase chain 6

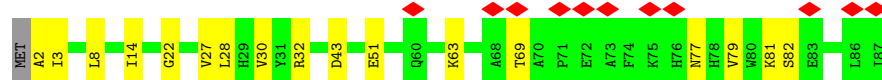
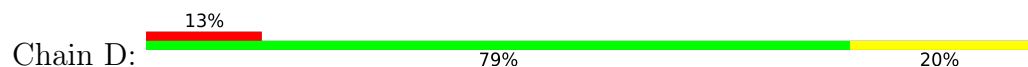


- Molecule 17: subunit NI9M of protein NADH:Ubiquinone Oxidoreductase (Complex I)

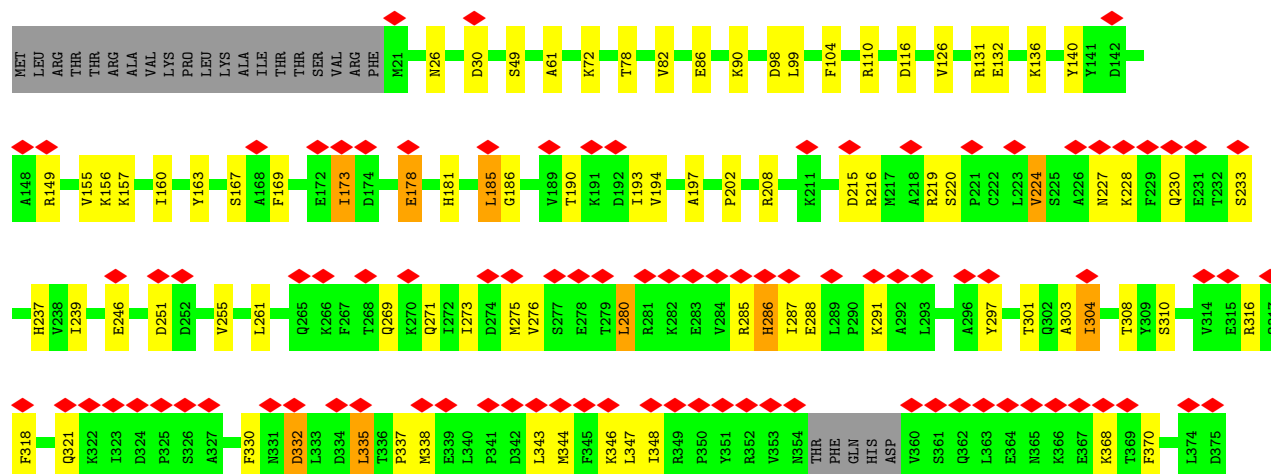




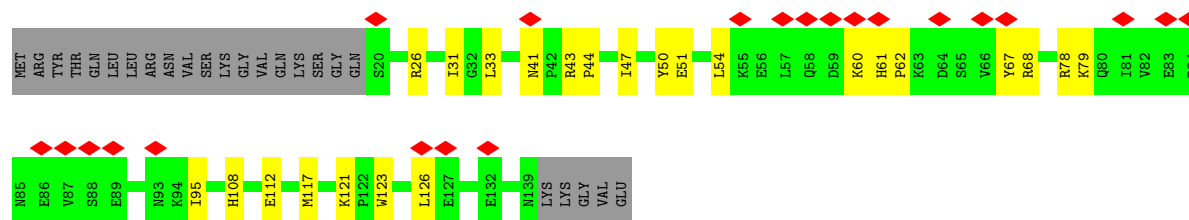
- Molecule 18: Subunit NIMM of NADH:Ubiquinone Oxidoreductase (Complex I)



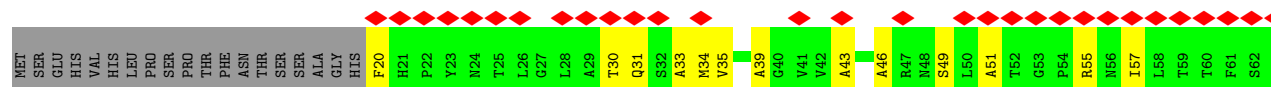
- Molecule 19: NADH-ubiquinone oxidoreductase 40 kDa subunit

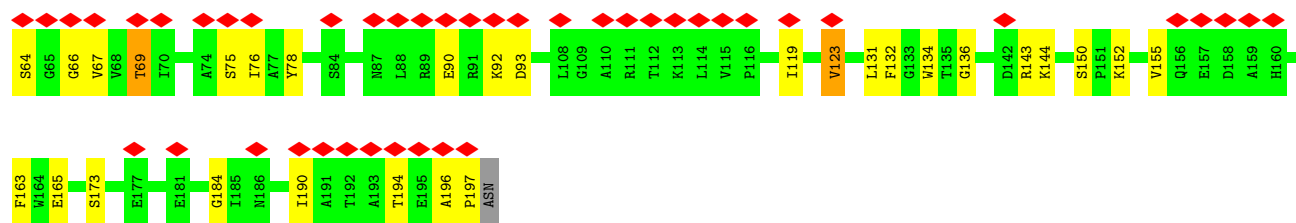


- Molecule 20: Subunit NUFM of NADH:Ubiquinone Oxidoreductase (Complex I)

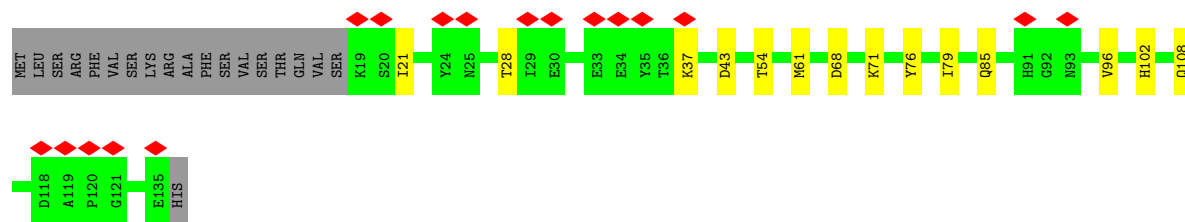
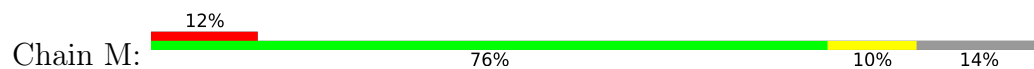


- Molecule 21: Subunit NUJM of NADH:Ubiquinone Oxidoreductase (Complex I)

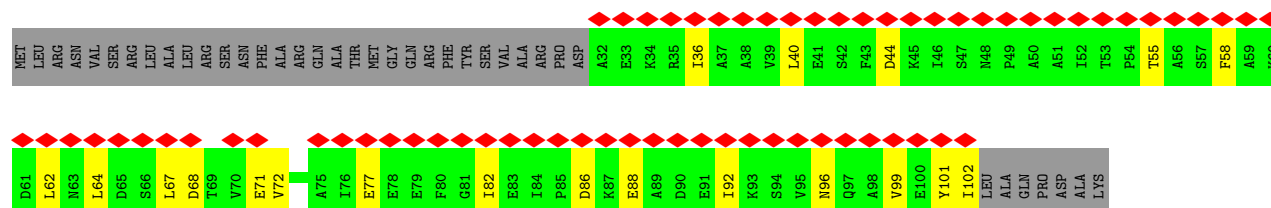




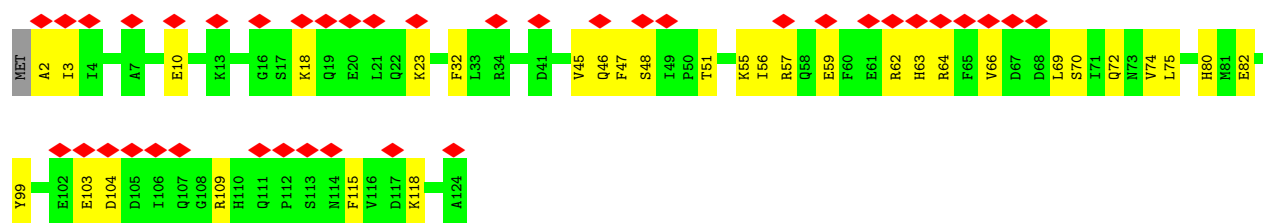
- Molecule 22: Subunit NUMM of protein NADH:Ubiquinone Oxidoreductase (Complex I)



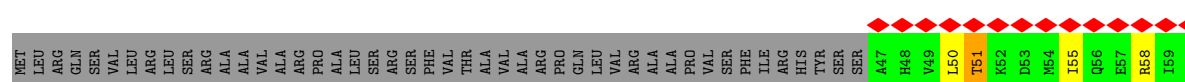
- Molecule 23: Acyl carrier protein ACPM1 of NADH:Ubiquinone Oxidoreductase (Complex I)

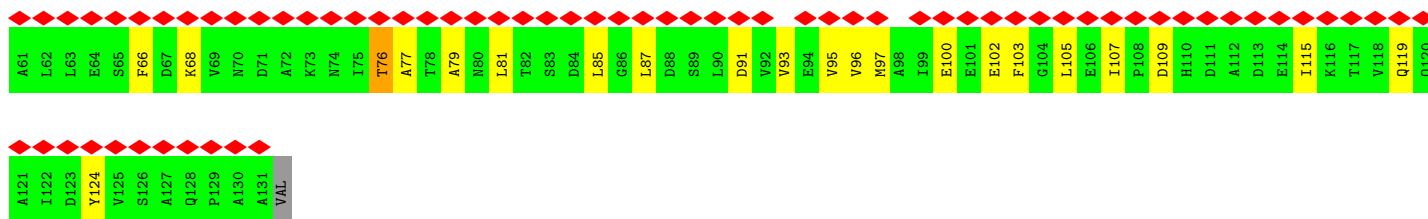


- Molecule 24: Subunit NB4M of protein NADH:Ubiquinone Oxidoreductase (Complex I)

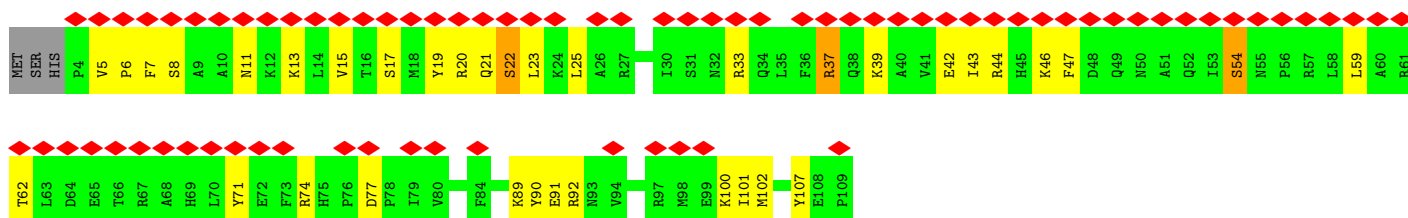


- Molecule 25: Acyl carrier protein ACPM2 of NADH:Ubiquinone Oxidoreductase (Complex I)

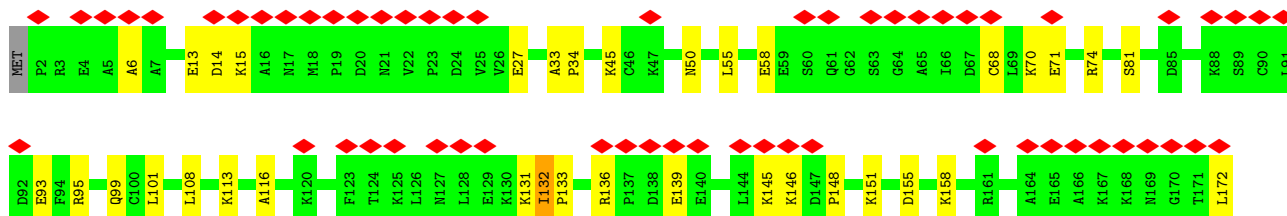
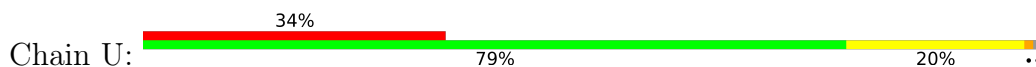




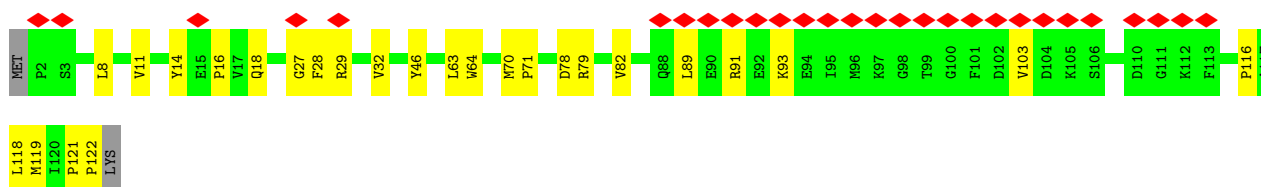
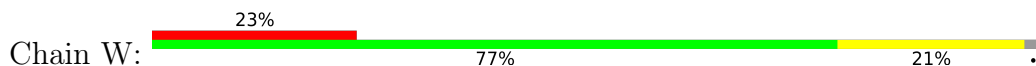
- Molecule 26: Subunit NI2M of NADH:Ubiquinone Oxidoreductase (Complex I)



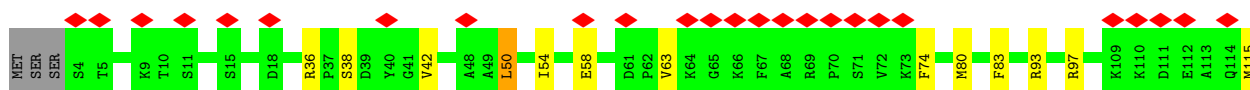
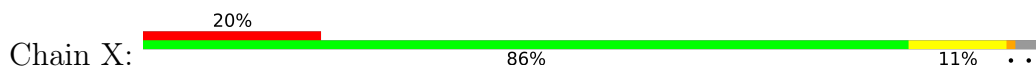
- Molecule 27: Subunit NUPM of NADH:Ubiquinone Oxidoreductase (Complex I)

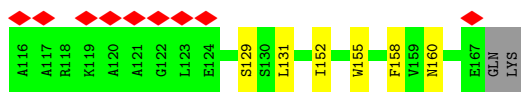


- Molecule 28: Subunit NB6M of NADH:Ubiquinone Oxidoreductase (Complex I)

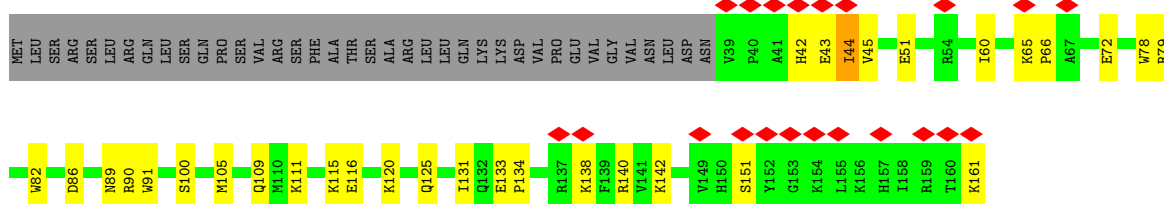


- Molecule 29: Subunit NUXM of NADH:Ubiquinone Oxidoreductase (Complex I)

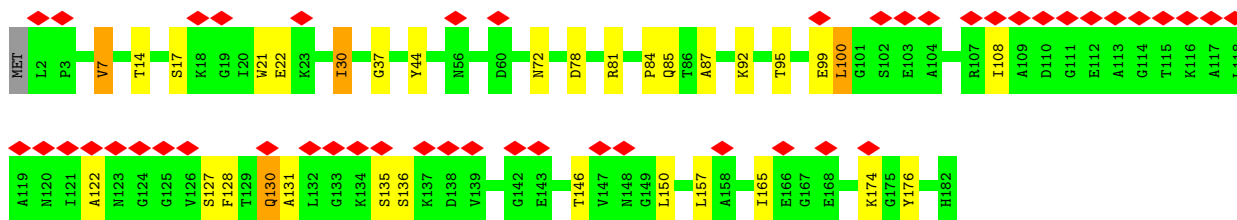
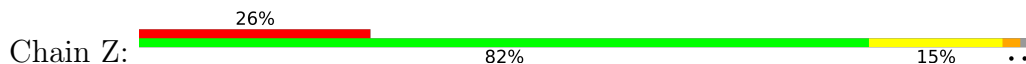




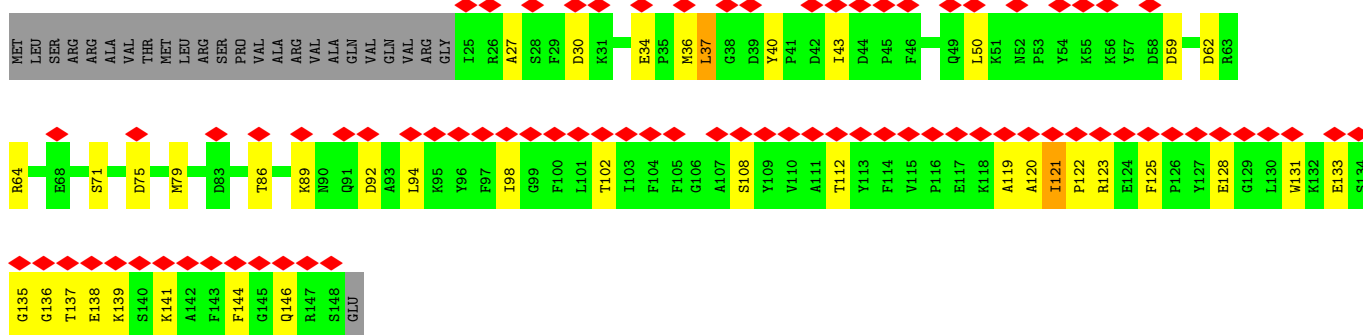
- Molecule 30: Subunit NUYM of NADH:Ubiquinone Oxidoreductase (Complex I)



- Molecule 31: Subunit NUZM of NADH:Ubiquinone Oxidoreductase (Complex I)



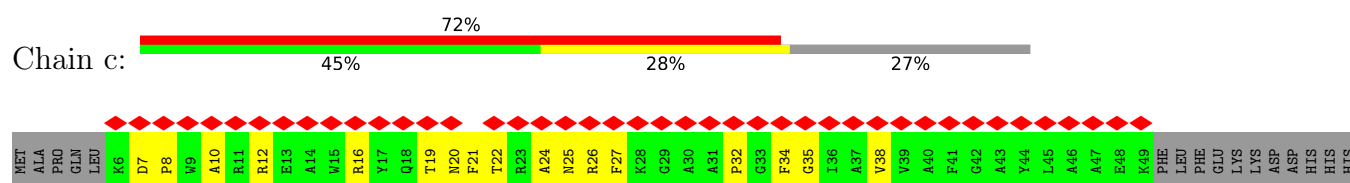
- Molecule 32: Subunit NIAM of NADH:Ubiquinone Oxidoreductase (Complex I)



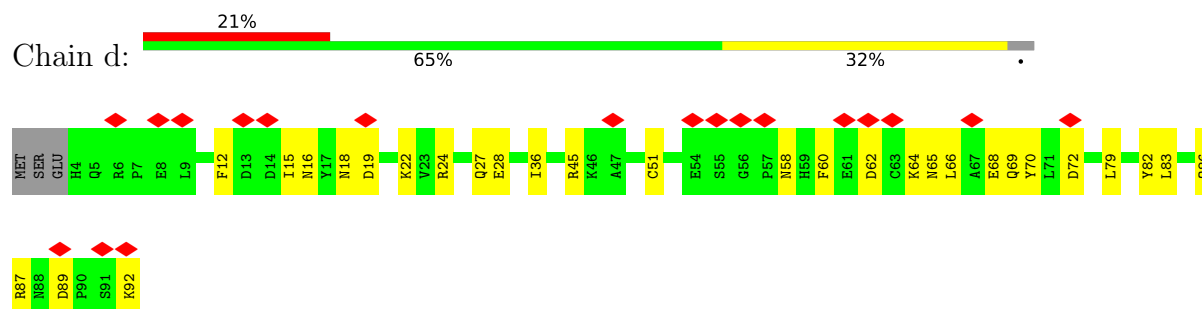
- Molecule 33: Subunit NEBM of NADH:Ubiquinone Oxidoreductase (Complex I)



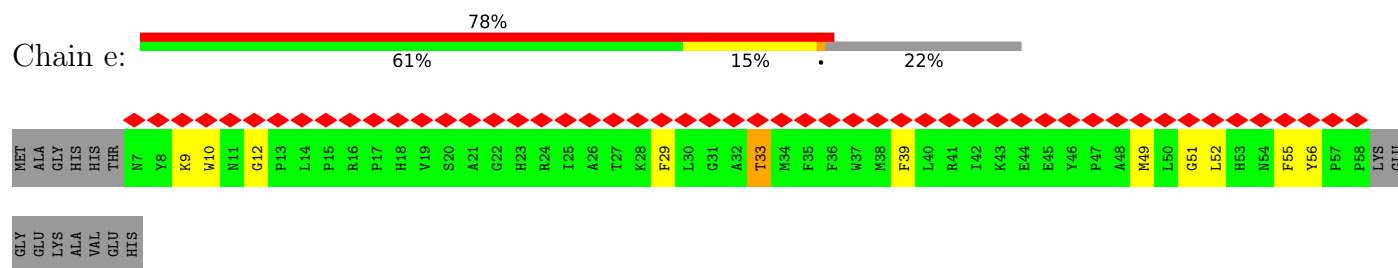
- Molecule 34: Subunit NB2M of NADH:Ubiquinone Oxidoreductase (Complex I)



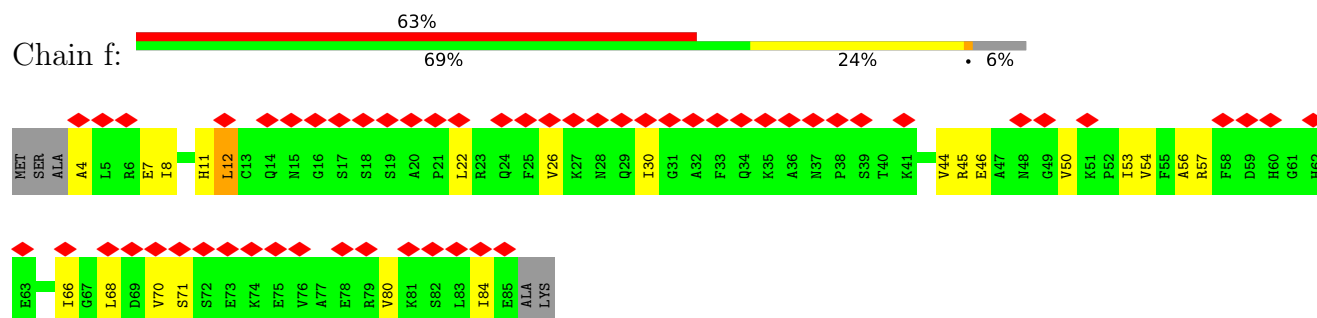
- Molecule 35: Subunit NIDM of NADH:Ubiquinone Oxidoreductase (Complex I)



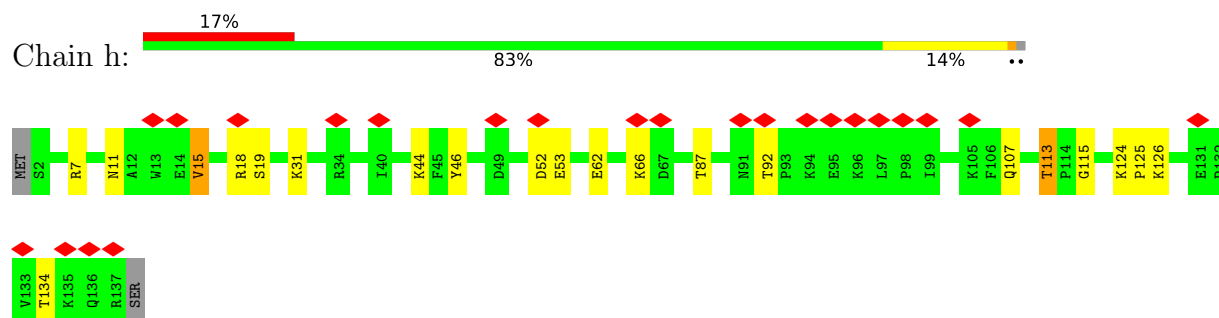
- Molecule 36: Subunit NUVM of NADH:Ubiquinone Oxidoreductase (Complex I)



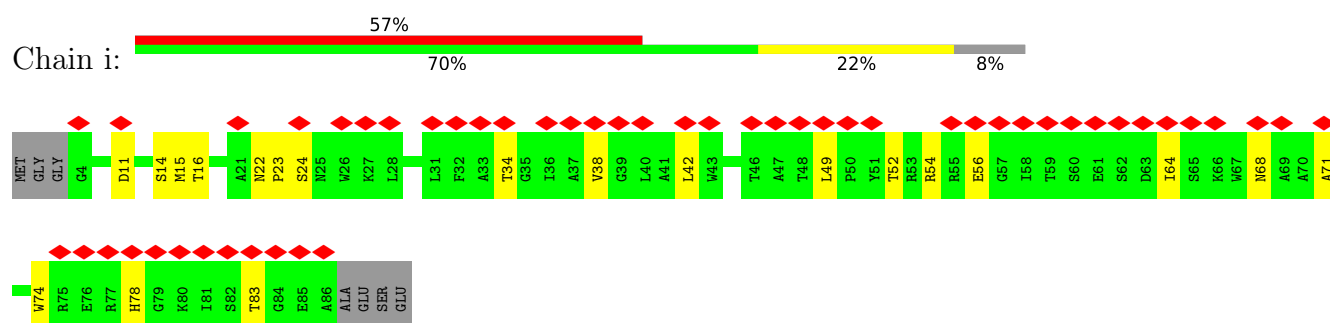
- Molecule 37: Subunit NI8M of NADH:Ubiquinone Oxidoreductase (Complex I)



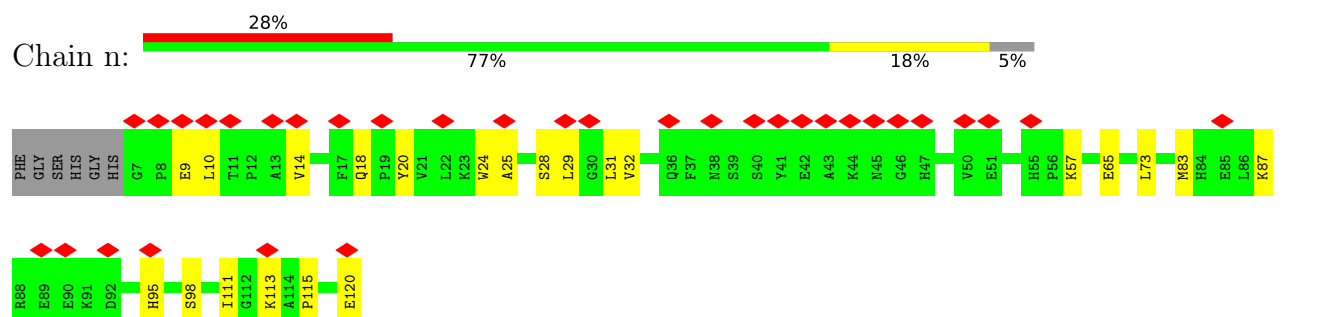
- Molecule 38: Subunit N7BM of NADH:Ubiquinone Oxidoreductase (Complex I)



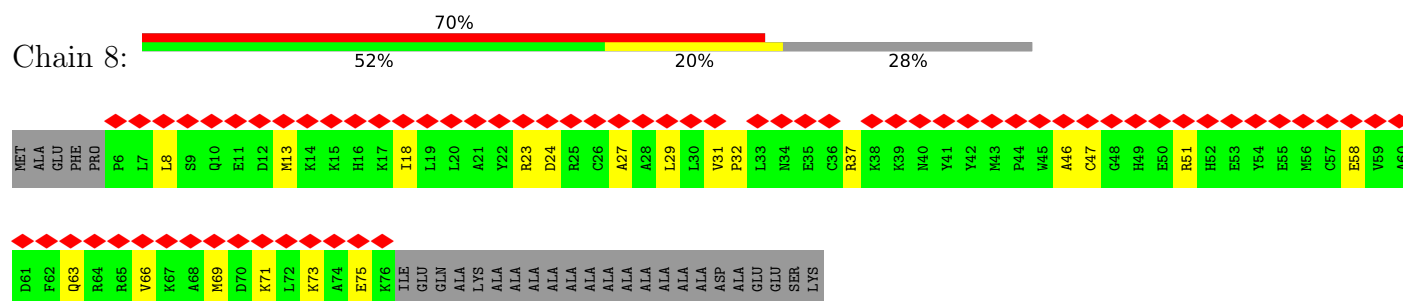
- Molecule 39: Subunit NUUM of NADH:Ubiquinone Oxidoreductase (Complex I)



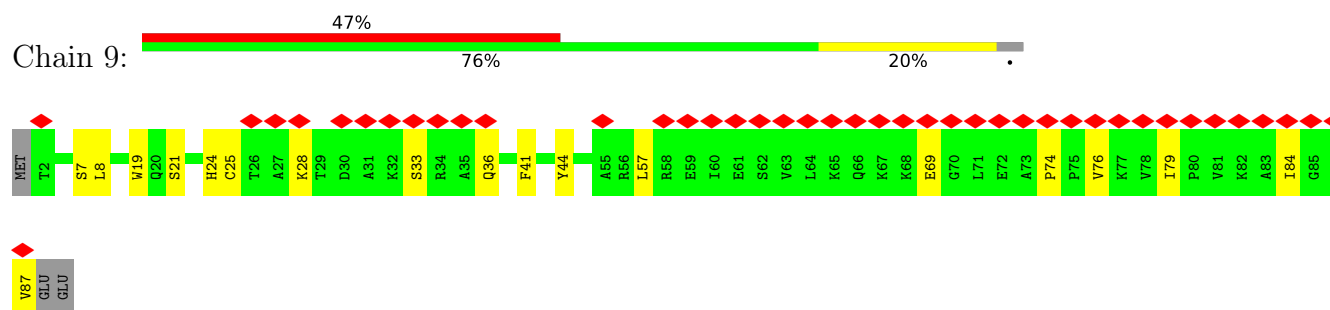
- Molecule 40: Subunit NUNM of NADH:Ubiquinone Oxidoreductase (Complex I)



- Molecule 41: Subunit NB8M of NADH:Ubiquinone Oxidoreductase (Complex I)



- Molecule 42: Subunit NIPM of NADH:Ubiquinone Oxidoreductase (Complex I)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	178960	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 ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	-800	Depositor
Maximum defocus (nm)	-2200	Depositor
Magnification	96899	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.104	Depositor
Minimum map value	-0.045	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	309.59998, 309.59998, 309.59998	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.516, 0.516, 0.516	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, NDP, T7X, PLC, 3PE, FME, LMN, CDL, 2MR, FMN, ZMP, ZN, CPL, FES

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	0.25	0/5363	0.49	2/7278 (0.0%)
2	B	0.25	0/3594	0.48	0/4851
3	C	0.28	0/3541	0.51	0/4799
4	G	0.26	0/2040	0.52	2/2781 (0.1%)
5	H	0.24	0/1725	0.57	1/2343 (0.0%)
6	I	0.27	0/1557	0.44	0/2110
7	K	0.27	0/1434	0.47	0/1950
8	L	0.29	0/692	0.46	0/937
9	S	0.21	0/1517	0.48	0/2046
10	j	0.21	0/745	0.41	0/1006
11	1	0.27	0/2781	0.47	0/3798
12	2	0.26	0/3846	0.43	0/5242
13	3	0.25	0/1041	0.49	0/1420
14	4	0.25	0/3908	0.44	0/5337
15	5	0.25	0/5327	0.49	0/7273
16	6	0.25	0/1468	0.44	0/2003
17	g	0.33	0/648	0.50	0/887
18	D	0.23	0/697	0.41	0/940
19	E	0.27	0/2866	0.50	0/3881
20	F	0.24	0/1002	0.47	0/1359
21	J	0.21	0/1351	0.43	0/1840
22	M	0.24	0/935	0.42	0/1268
23	O	0.19	0/549	0.39	0/746
24	P	0.23	0/1061	0.41	0/1427
25	Q	0.18	0/654	0.38	0/890
26	R	0.23	0/909	0.46	0/1229
27	U	0.25	0/1374	0.48	0/1856
28	W	0.24	0/998	0.45	0/1346
29	X	0.24	0/1314	0.40	0/1783
30	Y	0.26	0/1051	0.44	0/1420
31	Z	0.25	0/1430	0.48	0/1955
32	a	0.23	0/1064	0.42	0/1439

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.20	0/503	0.31	0/679
34	c	0.20	0/364	0.48	0/491
35	d	0.25	0/767	0.41	0/1031
36	e	0.17	0/456	0.38	0/619
37	f	0.23	0/652	0.53	0/874
38	h	0.24	0/1168	0.47	0/1589
39	i	0.21	0/666	0.39	0/907
40	n	0.28	0/941	0.41	0/1276
41	8	0.20	0/606	0.42	0/808
42	9	0.22	0/684	0.39	0/918
All	All	0.25	0/65289	0.47	5/88632 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
3	C	0	1
5	H	0	1
7	K	0	1
13	3	0	1
15	5	0	3
27	U	0	1
28	W	0	1
All	All	0	10

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	92	TRP	CA-C-N	5.80	132.62	121.54
4	G	92	TRP	C-N-CA	5.80	132.62	121.54
1	A	289	ASN	CA-C-N	5.74	132.50	121.54
1	A	289	ASN	C-N-CA	5.74	132.50	121.54
5	H	205	MET	CB-CG-SD	5.51	129.22	112.70

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	3	83	VAL	Peptide
1	A	290	GLU	Peptide
3	C	311	TYR	Peptide
5	H	174	ASN	Peptide
7	K	34	PRO	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5269	0	5168	95	0
2	B	3517	0	3476	117	0
3	C	3470	0	3403	76	0
4	G	1978	0	1908	32	0
5	H	1688	0	1660	38	0
6	I	1519	0	1460	28	0
7	K	1395	0	1375	30	0
8	L	693	0	753	27	0
9	S	1492	0	1536	42	0
10	j	724	0	706	13	0
11	1	2716	0	2812	65	0
12	2	3776	0	4004	69	0
13	3	1027	0	1091	33	0
14	4	3815	0	4010	73	0
15	5	5197	0	5353	149	0
16	6	1453	0	1576	53	0
17	g	622	0	602	13	0
18	D	681	0	671	14	0
19	E	2806	0	2792	65	0
20	F	981	0	969	22	0
21	J	1319	0	1304	33	0
22	M	912	0	869	8	0
23	O	543	0	537	14	0
24	P	1036	0	1018	27	0
25	Q	648	0	636	26	0
26	R	884	0	891	27	0
27	U	1345	0	1327	26	0
28	W	974	0	987	25	0
29	X	1275	0	1250	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	Y	1021	0	984	25	0
31	Z	1389	0	1395	21	0
32	a	1030	0	967	28	0
33	b	490	0	509	8	0
34	c	353	0	343	17	0
35	d	751	0	715	23	0
36	e	436	0	426	9	0
37	f	642	0	656	19	0
38	h	1130	0	1084	17	0
39	i	646	0	630	22	0
40	n	913	0	879	19	0
41	8	594	0	599	16	0
42	9	672	0	683	12	0
43	A	16	0	0	0	0
43	B	8	0	0	0	0
43	I	16	0	0	0	0
43	K	8	0	0	1	0
44	A	4	0	0	1	0
44	H	4	0	0	0	0
45	B	31	0	19	2	0
46	1	77	0	108	4	0
46	4	35	0	44	1	0
46	5	42	0	64	1	0
46	K	39	0	55	3	0
46	W	41	0	59	1	0
47	1	128	0	184	14	0
47	4	136	0	203	14	0
47	5	126	0	177	15	0
47	6	84	0	117	6	0
47	E	36	0	46	0	0
47	J	119	0	160	12	0
47	S	42	0	61	2	0
47	b	42	0	58	7	0
47	g	43	0	63	4	0
48	J	69	0	88	9	0
48	j	65	0	77	5	0
49	2	100	0	0	1	0
49	3	49	0	0	1	0
50	2	52	0	80	3	0
51	E	72	0	88	9	0
51	W	54	0	52	3	0
51	X	86	0	119	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	Z	76	0	96	5	0
51	g	83	0	116	7	0
51	n	92	0	137	13	0
52	E	48	0	26	1	0
53	M	1	0	0	0	0
54	O	33	0	38	3	0
54	Q	33	0	38	3	0
55	1	67	0	0	1	0
55	2	158	0	0	5	0
55	3	10	0	0	0	0
55	4	139	0	0	5	0
55	5	57	0	0	1	0
55	6	24	0	0	1	0
55	9	16	0	0	0	0
55	A	135	0	0	2	0
55	B	11	0	0	0	0
55	C	168	0	0	7	0
55	D	17	0	0	1	0
55	E	79	0	0	1	0
55	F	15	0	0	0	0
55	G	114	0	0	3	0
55	H	2	0	0	0	0
55	I	95	0	0	1	0
55	J	14	0	0	0	0
55	K	78	0	0	2	0
55	L	18	0	0	1	0
55	M	45	0	0	0	0
55	P	15	0	0	1	0
55	R	11	0	0	0	0
55	S	4	0	0	0	0
55	U	39	0	0	1	0
55	W	23	0	0	0	0
55	X	39	0	0	1	0
55	Y	53	0	0	0	0
55	Z	52	0	0	3	0
55	a	11	0	0	0	0
55	b	6	0	0	0	0
55	d	8	0	0	5	0
55	g	2	0	0	0	0
55	h	61	0	0	4	0
55	i	3	0	0	0	0
55	j	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	n	12	0	0	0	0
All	All	67428	0	66387	1299	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 1299 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:E:173:ILE:O	19:E:181:HIS:ND1	2.06	0.88
1:A:47:SER:O	1:A:60:LYS:NZ	2.07	0.86
15:5:354:LEU:HD21	15:5:450:ASN:HB2	1.59	0.83
9:S:56:GLU:HB3	9:S:118:LEU:HD21	1.61	0.83
2:B:64:THR:HA	2:B:67:LEU:HD12	1.60	0.82

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	691/728 (95%)	666 (96%)	24 (4%)	1 (0%)	48	64
2	B	453/488 (93%)	426 (94%)	26 (6%)	1 (0%)	43	58
3	C	435/466 (93%)	416 (96%)	19 (4%)	0	100	100
4	G	237/281 (84%)	230 (97%)	7 (3%)	0	100	100
5	H	214/243 (88%)	194 (91%)	20 (9%)	0	100	100
6	I	188/229 (82%)	184 (98%)	4 (2%)	0	100	100
7	K	175/210 (83%)	168 (96%)	7 (4%)	0	100	100
8	L	87/89 (98%)	85 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	S	176/249 (71%)	173 (98%)	3 (2%)	0	100	100
10	j	88/93 (95%)	85 (97%)	3 (3%)	0	100	100
11	1	338/341 (99%)	328 (97%)	10 (3%)	0	100	100
12	2	467/469 (100%)	462 (99%)	5 (1%)	0	100	100
13	3	126/128 (98%)	124 (98%)	1 (1%)	1 (1%)	16	25
14	4	479/486 (99%)	466 (97%)	13 (3%)	0	100	100
15	5	652/655 (100%)	624 (96%)	26 (4%)	2 (0%)	36	50
16	6	182/185 (98%)	179 (98%)	3 (2%)	0	100	100
17	g	74/78 (95%)	68 (92%)	6 (8%)	0	100	100
18	D	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
19	E	346/375 (92%)	336 (97%)	10 (3%)	0	100	100
20	F	118/144 (82%)	114 (97%)	4 (3%)	0	100	100
21	J	176/198 (89%)	170 (97%)	6 (3%)	0	100	100
22	M	115/136 (85%)	115 (100%)	0	0	100	100
23	O	69/109 (63%)	69 (100%)	0	0	100	100
24	P	121/124 (98%)	121 (100%)	0	0	100	100
25	Q	83/132 (63%)	80 (96%)	3 (4%)	0	100	100
26	R	104/109 (95%)	102 (98%)	2 (2%)	0	100	100
27	U	169/172 (98%)	166 (98%)	3 (2%)	0	100	100
28	W	119/123 (97%)	118 (99%)	1 (1%)	0	100	100
29	X	162/169 (96%)	160 (99%)	2 (1%)	0	100	100
30	Y	121/161 (75%)	119 (98%)	2 (2%)	0	100	100
31	Z	179/182 (98%)	174 (97%)	5 (3%)	0	100	100
32	a	122/149 (82%)	117 (96%)	5 (4%)	0	100	100
33	b	62/74 (84%)	62 (100%)	0	0	100	100
34	c	42/60 (70%)	40 (95%)	2 (5%)	0	100	100
35	d	87/92 (95%)	85 (98%)	2 (2%)	0	100	100
36	e	50/67 (75%)	46 (92%)	4 (8%)	0	100	100
37	f	80/87 (92%)	77 (96%)	3 (4%)	0	100	100
38	h	134/138 (97%)	130 (97%)	4 (3%)	0	100	100
39	i	81/90 (90%)	79 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	n	112/120 (93%)	108 (96%)	4 (4%)	0	100	100
41	8	69/99 (70%)	69 (100%)	0	0	100	100
42	9	84/89 (94%)	84 (100%)	0	0	100	100
All	All	7951/8704 (91%)	7702 (97%)	244 (3%)	5 (0%)	49	64

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	5	555	VAL
13	3	84	SER
1	A	291	GLU
2	B	121	GLU
15	5	439	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	566/595 (95%)	542 (96%)	24 (4%)	26	45
2	B	363/389 (93%)	341 (94%)	22 (6%)	17	30
3	C	373/393 (95%)	366 (98%)	7 (2%)	50	71
4	G	216/245 (88%)	213 (99%)	3 (1%)	59	79
5	H	191/212 (90%)	186 (97%)	5 (3%)	40	63
6	I	156/187 (83%)	154 (99%)	2 (1%)	61	80
7	K	154/180 (86%)	148 (96%)	6 (4%)	28	48
8	L	76/76 (100%)	74 (97%)	2 (3%)	40	63
9	S	157/211 (74%)	152 (97%)	5 (3%)	34	56
10	j	71/73 (97%)	70 (99%)	1 (1%)	59	79
11	1	300/301 (100%)	297 (99%)	3 (1%)	68	84
12	2	432/432 (100%)	422 (98%)	10 (2%)	44	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	3	113/113 (100%)	107 (95%)	6 (5%)	20	36
14	4	429/433 (99%)	419 (98%)	10 (2%)	44	66
15	5	579/579 (100%)	561 (97%)	18 (3%)	35	57
16	6	165/166 (99%)	160 (97%)	5 (3%)	36	58
17	g	63/65 (97%)	61 (97%)	2 (3%)	34	56
18	D	68/69 (99%)	65 (96%)	3 (4%)	25	43
19	E	306/329 (93%)	291 (95%)	15 (5%)	22	39
20	F	108/129 (84%)	107 (99%)	1 (1%)	70	85
21	J	129/147 (88%)	124 (96%)	5 (4%)	28	48
22	M	97/115 (84%)	94 (97%)	3 (3%)	35	57
23	O	60/91 (66%)	59 (98%)	1 (2%)	53	74
24	P	109/110 (99%)	108 (99%)	1 (1%)	70	85
25	Q	72/111 (65%)	70 (97%)	2 (3%)	38	60
26	R	97/100 (97%)	93 (96%)	4 (4%)	27	46
27	U	147/148 (99%)	145 (99%)	2 (1%)	59	79
28	W	100/102 (98%)	100 (100%)	0	100	100
29	X	128/133 (96%)	126 (98%)	2 (2%)	55	76
30	Y	105/140 (75%)	102 (97%)	3 (3%)	37	60
31	Z	147/148 (99%)	140 (95%)	7 (5%)	23	40
32	a	108/129 (84%)	102 (94%)	6 (6%)	19	33
33	b	50/59 (85%)	48 (96%)	2 (4%)	28	47
34	c	30/45 (67%)	30 (100%)	0	100	100
35	d	82/85 (96%)	82 (100%)	0	100	100
36	e	44/55 (80%)	43 (98%)	1 (2%)	44	66
37	f	70/73 (96%)	69 (99%)	1 (1%)	59	79
38	h	121/123 (98%)	117 (97%)	4 (3%)	33	55
39	i	64/68 (94%)	63 (98%)	1 (2%)	55	76
40	n	98/102 (96%)	96 (98%)	2 (2%)	48	70
41	8	63/76 (83%)	63 (100%)	0	100	100
42	9	73/76 (96%)	69 (94%)	4 (6%)	19	34
All	All	6880/7413 (93%)	6679 (97%)	201 (3%)	38	60

5 of 201 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	5	445	THR
19	E	286	HIS
42	9	76	VAL
15	5	557	ASP
17	g	73	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
30	Y	62	GLN
31	Z	79	HIS
38	h	55	HIS
14	4	15	ASN
12	2	392	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 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	$\# Z > 2$
8	FME	L	1	8	8,9,10	0.48	0	8,9,11	1.32	1 (12%)
16	FME	6	1	16	8,9,10	1.00	0	8,9,11	1.00	0
11	FME	1	1	11	8,9,10	0.99	0	8,9,11	1.04	1 (12%)
12	FME	2	1	12	8,9,10	0.96	0	8,9,11	0.98	1 (12%)
3	2MR	C	121	3	10,12,13	1.78	1 (10%)	5,13,15	2.52	2 (40%)
13	FME	3	1	13	8,9,10	0.88	0	8,9,11	1.26	1 (12%)

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
8	FME	L	1	8	-	2/7/9/11	-
16	FME	6	1	16	-	4/7/9/11	-
11	FME	1	1	11	-	0/7/9/11	-
12	FME	2	1	12	-	4/7/9/11	-
3	2MR	C	121	3	-	4/10/13/15	-
13	FME	3	1	13	-	3/7/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	121	2MR	CZ-NE	4.86	1.44	1.34

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	121	2MR	NE-CZ-NH2	4.81	123.89	119.48
3	C	121	2MR	CD-NE-CZ	2.75	128.53	123.36
13	3	1	FME	C-CA-N	2.63	114.58	109.50
8	L	1	FME	C-CA-N	2.53	114.38	109.50
12	2	1	FME	C-CA-N	2.31	113.95	109.50

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	121	2MR	C-CA-CB-CG
8	L	1	FME	N-CA-CB-CG
12	2	1	FME	C-CA-CB-CG
16	6	1	FME	O1-CN-N-CA
16	6	1	FME	N-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	L	1	FME	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 49 ligands modelled in this entry, 1 is monoatomic - leaving 48 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	$\# Z > 2$
54	ZMP	Q	201	25	27,32,36	1.72	5 (18%)	31,39,45	1.71	7 (22%)
44	FES	A	803	1	0,4,4	-	-	-	-	-
51	CDL	g	201	-	82,82,99	0.98	7 (8%)	88,94,111	1.18	6 (6%)
43	SF4	A	801	1	0,12,12	-	-	-	-	-
47	3PE	5	702	-	40,40,50	0.98	3 (7%)	43,45,55	1.22	3 (6%)
47	3PE	J	201	-	40,40,50	0.98	4 (10%)	43,45,55	1.15	2 (4%)
46	PLC	K	302	-	38,38,41	1.39	5 (13%)	44,46,49	1.06	2 (4%)
47	3PE	4	503	-	50,50,50	0.86	3 (6%)	53,55,55	1.22	3 (5%)
54	ZMP	O	201	23	27,32,36	1.71	5 (18%)	31,39,45	1.97	8 (25%)
47	3PE	J	204	-	33,33,50	1.08	3 (9%)	36,38,55	1.17	2 (5%)
49	T7X	2	503	-	52,52,61	0.93	5 (9%)	61,64,73	1.35	6 (9%)
50	CPL	2	502	-	51,51,51	0.99	4 (7%)	57,59,59	1.08	2 (3%)
51	CDL	E	402	-	71,71,99	1.04	7 (9%)	77,83,111	1.16	5 (6%)
43	SF4	A	802	1	0,12,12	-	-	-	-	-
43	SF4	K	301	7	0,12,12	-	-	-	-	-
49	T7X	3	201	-	49,49,61	0.95	3 (6%)	58,61,73	1.17	5 (8%)
47	3PE	4	501	-	42,42,50	0.96	4 (9%)	45,47,55	1.17	2 (4%)
43	SF4	I	302	6	0,12,12	-	-	-	-	-
49	T7X	2	501	-	48,48,61	0.93	5 (10%)	57,60,73	1.25	6 (10%)
46	PLC	1	505	-	41,41,41	1.33	5 (12%)	47,49,49	1.12	2 (4%)
47	3PE	b	201	-	41,41,50	0.97	4 (9%)	44,46,55	1.08	2 (4%)
44	FES	H	301	5	0,4,4	-	-	-	-	-
48	LMN	J	202	-	72,72,72	1.52	9 (12%)	92,98,98	1.53	12 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
47	3PE	6	201	-	35,35,50	1.04	4 (11%)	38,40,55	1.25	2 (5%)
47	3PE	g	202	-	42,42,50	0.97	4 (9%)	45,47,55	1.07	2 (4%)
48	LMN	j	101	-	68,68,72	1.59	10 (14%)	88,94,98	1.24	5 (5%)
47	3PE	1	504	-	40,40,50	0.93	3 (7%)	43,45,55	1.06	1 (2%)
51	CDL	Z	201	-	75,75,99	1.04	7 (9%)	81,87,111	1.17	6 (7%)
46	PLC	W	401	-	40,40,41	1.36	5 (12%)	46,48,49	1.20	3 (6%)
46	PLC	5	704	-	41,41,41	1.32	5 (12%)	47,49,49	1.09	2 (4%)
43	SF4	B	501	2	0,12,12	-	-	-	-	-
43	SF4	I	301	6	0,12,12	-	-	-	-	-
46	PLC	1	502	-	34,34,41	1.43	5 (14%)	40,42,49	1.11	3 (7%)
45	FMN	B	502	-	33,33,33	3.00	14 (42%)	48,50,50	1.50	11 (22%)
47	3PE	1	501	-	50,50,50	0.88	3 (6%)	53,55,55	1.13	4 (7%)
51	CDL	X	201	-	85,85,99	0.95	8 (9%)	91,97,111	1.17	4 (4%)
47	3PE	5	703	-	42,42,50	1.02	3 (7%)	45,47,55	1.08	2 (4%)
47	3PE	4	502	-	41,41,50	0.97	4 (9%)	44,46,55	1.12	2 (4%)
51	CDL	n	200	-	91,91,99	0.92	8 (8%)	97,103,111	1.19	4 (4%)
46	PLC	4	504	-	34,34,41	1.44	6 (17%)	40,42,49	1.25	2 (5%)
51	CDL	W	402	-	53,53,99	1.20	8 (15%)	59,65,111	1.22	4 (6%)
47	3PE	6	202	-	46,46,50	0.92	4 (8%)	49,51,55	1.08	2 (4%)
47	3PE	1	503	-	35,35,50	1.02	4 (11%)	38,40,55	1.14	2 (5%)
47	3PE	E	401	-	35,35,50	1.03	4 (11%)	38,40,55	1.19	2 (5%)
47	3PE	5	701	-	41,41,50	0.98	4 (9%)	44,46,55	1.19	3 (6%)
52	NDP	E	400	-	51,52,52	3.56	21 (41%)	71,80,80	2.06	14 (19%)
47	3PE	S	501	-	41,41,50	0.96	4 (9%)	44,46,55	1.12	2 (4%)
47	3PE	J	203	-	43,43,50	0.94	4 (9%)	46,48,55	1.20	3 (6%)

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
54	ZMP	Q	201	25	-	9/37/39/43	-
44	FES	A	803	1	-	-	0/1/1/1
51	CDL	g	201	-	-	35/93/93/110	-
43	SF4	A	801	1	-	-	0/6/5/5
47	3PE	5	702	-	-	20/44/44/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
47	3PE	J	201	-	-	17/44/44/54	-
46	PLC	K	302	-	-	18/42/42/45	-
47	3PE	4	503	-	-	22/54/54/54	-
54	ZMP	O	201	23	-	17/37/39/43	-
47	3PE	J	204	-	-	16/37/37/54	-
49	T7X	2	503	-	-	25/47/71/80	0/1/1/1
50	CPL	2	502	-	-	20/55/55/55	-
51	CDL	E	402	-	-	30/82/82/110	-
43	SF4	A	802	1	-	-	0/6/5/5
43	SF4	K	301	7	-	-	0/6/5/5
49	T7X	3	201	-	-	15/44/68/80	0/1/1/1
47	3PE	4	501	-	-	19/46/46/54	-
43	SF4	I	302	6	-	-	0/6/5/5
49	T7X	2	501	-	-	13/43/67/80	0/1/1/1
46	PLC	1	505	-	-	26/45/45/45	-
47	3PE	b	201	-	-	21/45/45/54	-
44	FES	H	301	5	-	-	0/1/1/1
48	LMN	J	202	-	-	34/50/130/130	0/4/4/4
47	3PE	6	201	-	-	22/39/39/54	-
47	3PE	g	202	-	-	23/46/46/54	-
48	LMN	j	101	-	-	21/46/126/130	0/4/4/4
47	3PE	1	504	-	-	14/44/44/54	-
51	CDL	Z	201	-	-	40/86/86/110	-
46	PLC	W	401	-	-	20/44/44/45	-
46	PLC	5	704	-	-	17/45/45/45	-
43	SF4	B	501	2	-	-	0/6/5/5
43	SF4	I	301	6	-	-	0/6/5/5
46	PLC	1	502	-	-	16/38/38/45	-
45	FMN	B	502	-	-	8/18/18/18	0/3/3/3
47	3PE	1	501	-	-	29/54/54/54	-
51	CDL	X	201	-	-	35/96/96/110	-
47	3PE	5	703	-	-	24/46/46/54	-
47	3PE	4	502	-	-	22/45/45/54	-
51	CDL	n	200	-	-	43/102/102/110	-
46	PLC	4	504	-	-	20/38/38/45	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
51	CDL	W	402	-	-	30/64/64/110	-
47	3PE	6	202	-	-	23/50/50/54	-
47	3PE	1	503	-	-	19/39/39/54	-
47	3PE	E	401	-	-	14/39/39/54	-
47	3PE	5	701	-	-	14/45/45/54	-
52	NDP	E	400	-	-	4/34/77/77	0/5/5/5
47	3PE	S	501	-	-	17/45/45/54	-
47	3PE	J	203	-	-	24/47/47/54	-

The worst 5 of 223 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	E	400	NDP	C2B-C1B	-7.93	1.33	1.53
52	E	400	NDP	O4D-C1D	7.71	1.59	1.42
52	E	400	NDP	O4B-C1B	7.59	1.59	1.42
52	E	400	NDP	C2D-C1D	-7.33	1.30	1.53
52	E	400	NDP	C6N-C5N	7.20	1.55	1.33

The worst 5 of 160 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	J	202	LMN	CBR-CBL-CBJ	6.36	132.13	113.19
52	E	400	NDP	C4A-N9A-C1B	-6.14	112.28	126.63
52	E	400	NDP	N6A-C6A-N1A	-6.06	104.88	118.38
54	O	201	ZMP	C9-C10-S1	5.89	120.42	113.40
48	j	101	LMN	CBR-CBL-CBJ	5.82	130.53	113.19

There are no chirality outliers.

5 of 856 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
45	B	502	FMN	C3'-C4'-C5'-O5'
45	B	502	FMN	O4'-C4'-C5'-O5'
45	B	502	FMN	C4'-C5'-O5'-P
45	B	502	FMN	C5'-O5'-P-O1P
45	B	502	FMN	C5'-O5'-P-O2P

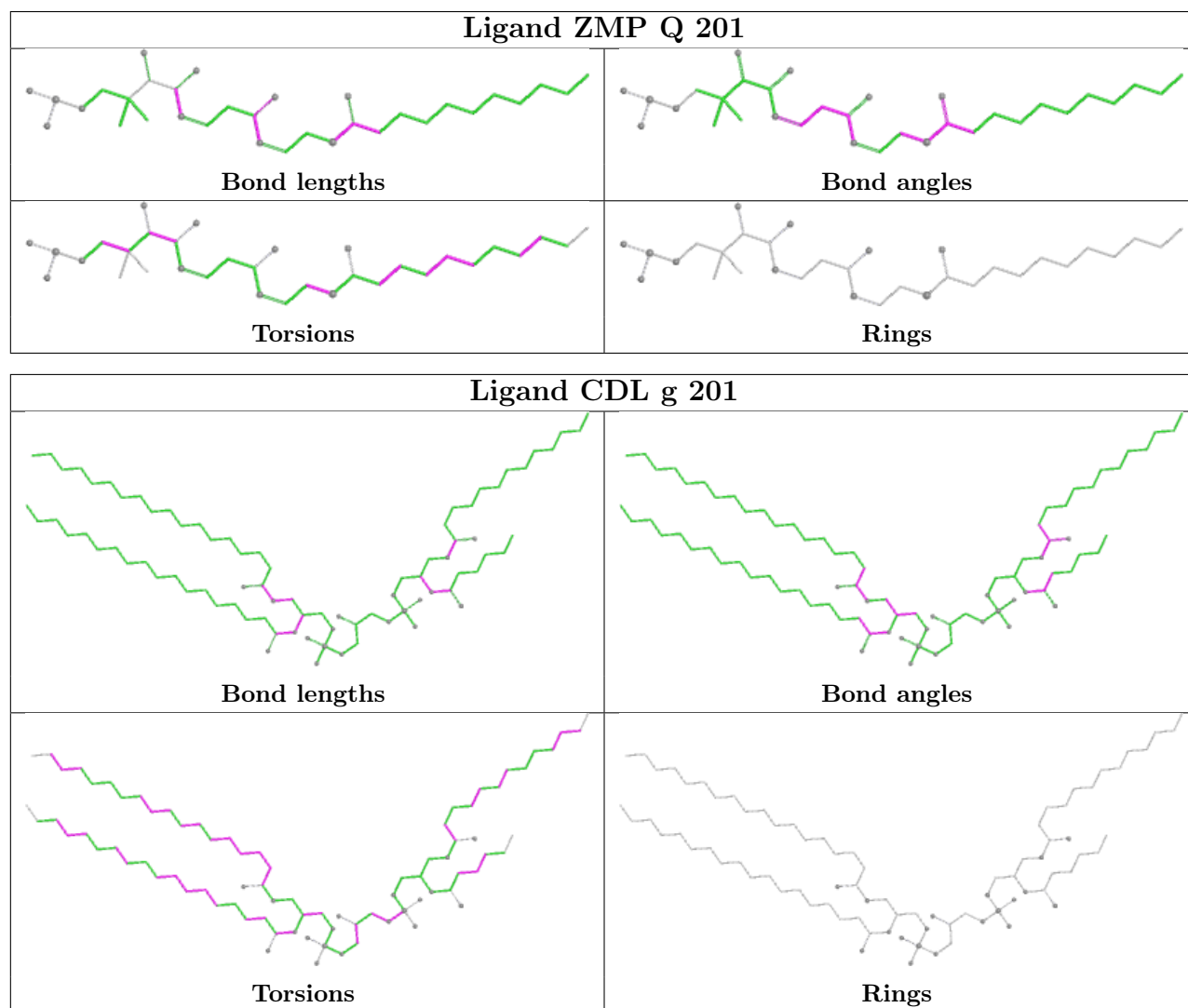
There are no ring outliers.

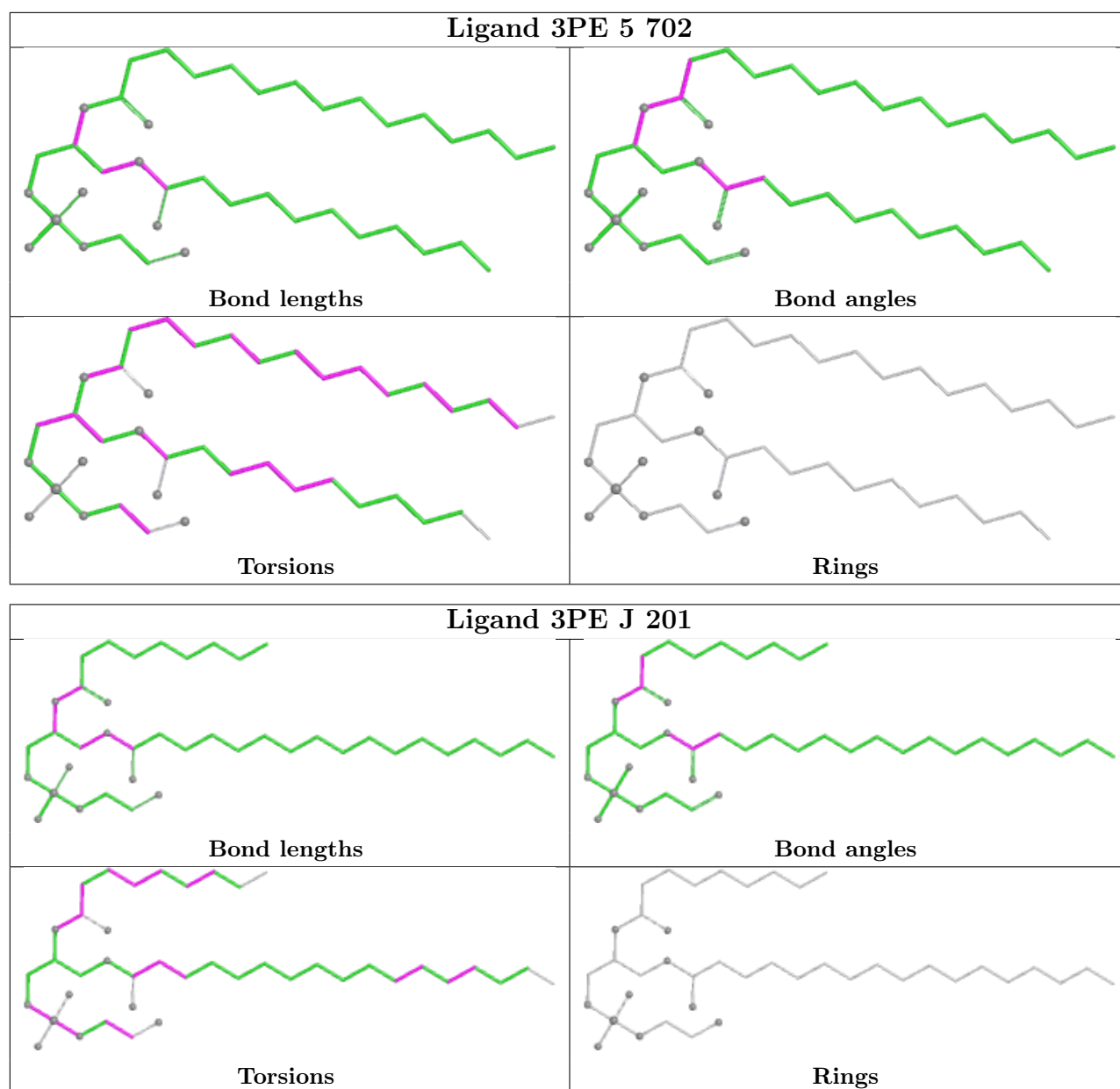
40 monomers are involved in 151 short contacts:

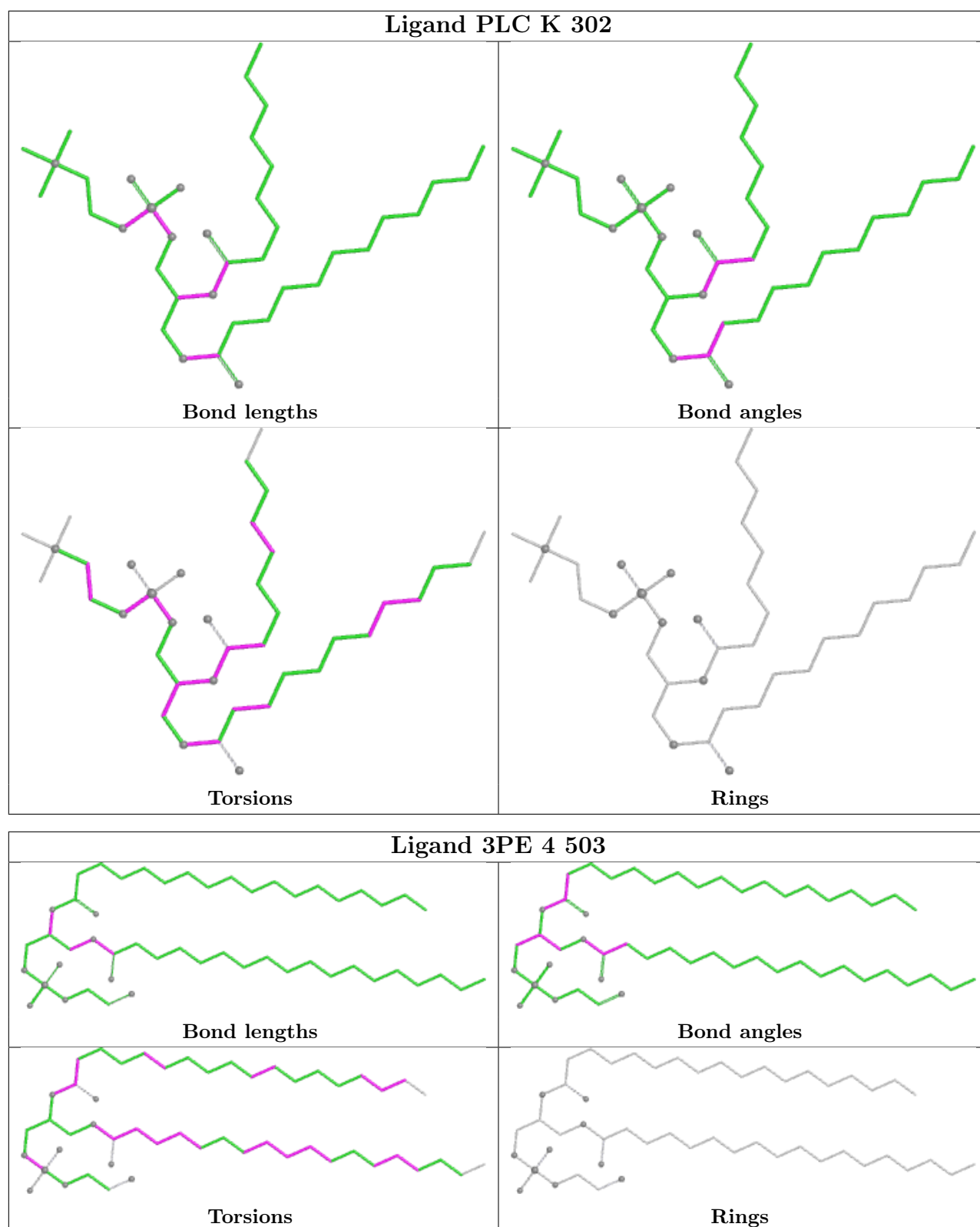
Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	Q	201	ZMP	3	0
44	A	803	FES	1	0
51	g	201	CDL	7	0
47	5	702	3PE	3	0
47	J	201	3PE	3	0
46	K	302	PLC	3	0
47	4	503	3PE	7	0
54	O	201	ZMP	3	0
47	J	204	3PE	4	0
49	2	503	T7X	1	0
50	2	502	CPL	3	0
51	E	402	CDL	9	0
43	K	301	SF4	1	0
49	3	201	T7X	1	0
47	4	501	3PE	6	0
46	1	505	PLC	3	0
47	b	201	3PE	7	0
48	J	202	LMN	9	0
47	6	201	3PE	2	0
47	g	202	3PE	4	0
48	j	101	LMN	5	0
47	1	504	3PE	8	0
51	Z	201	CDL	5	0
46	W	401	PLC	1	0
46	5	704	PLC	1	0
46	1	502	PLC	1	0
45	B	502	FMN	2	0
47	1	501	3PE	4	0
51	X	201	CDL	10	0
47	5	703	3PE	7	0
47	4	502	3PE	1	0
51	n	200	CDL	13	0
46	4	504	PLC	1	0
51	W	402	CDL	3	0
47	6	202	3PE	4	0
47	1	503	3PE	2	0
47	5	701	3PE	5	0
52	E	400	NDP	1	0
47	S	501	3PE	2	0
47	J	203	3PE	5	0

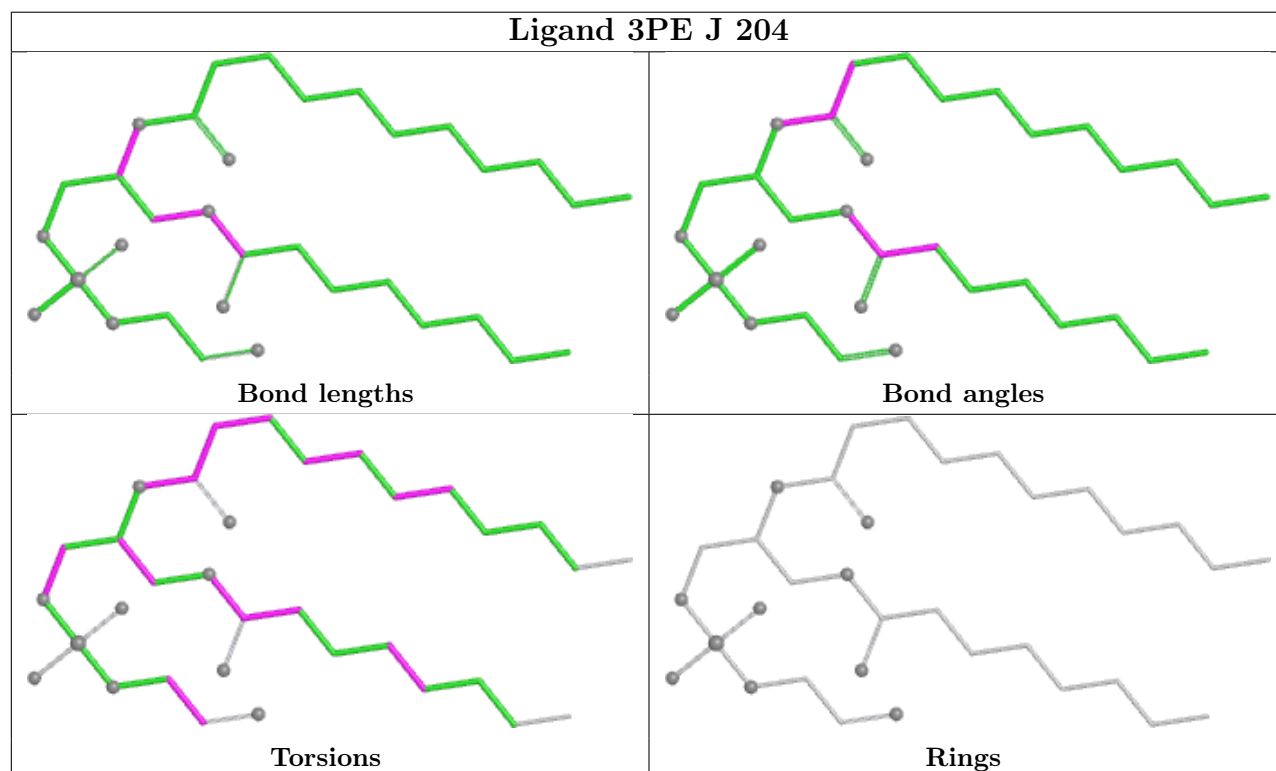
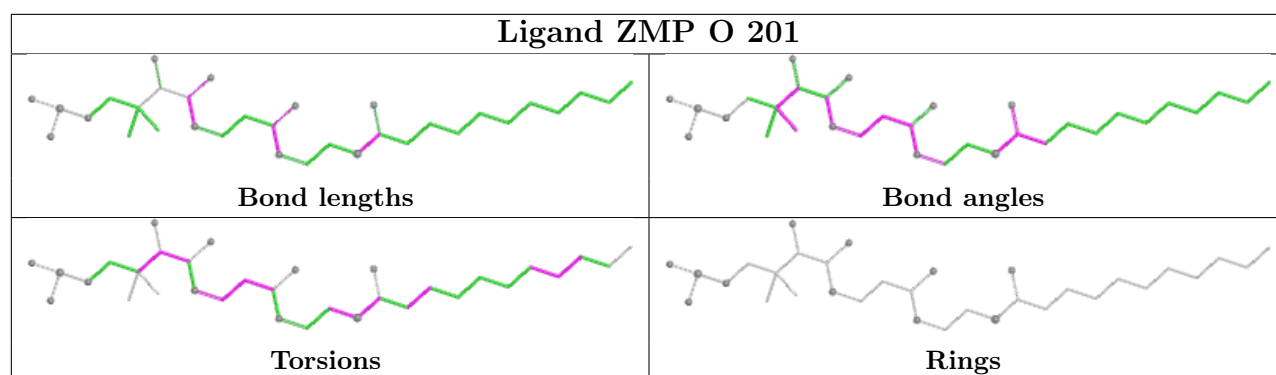
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

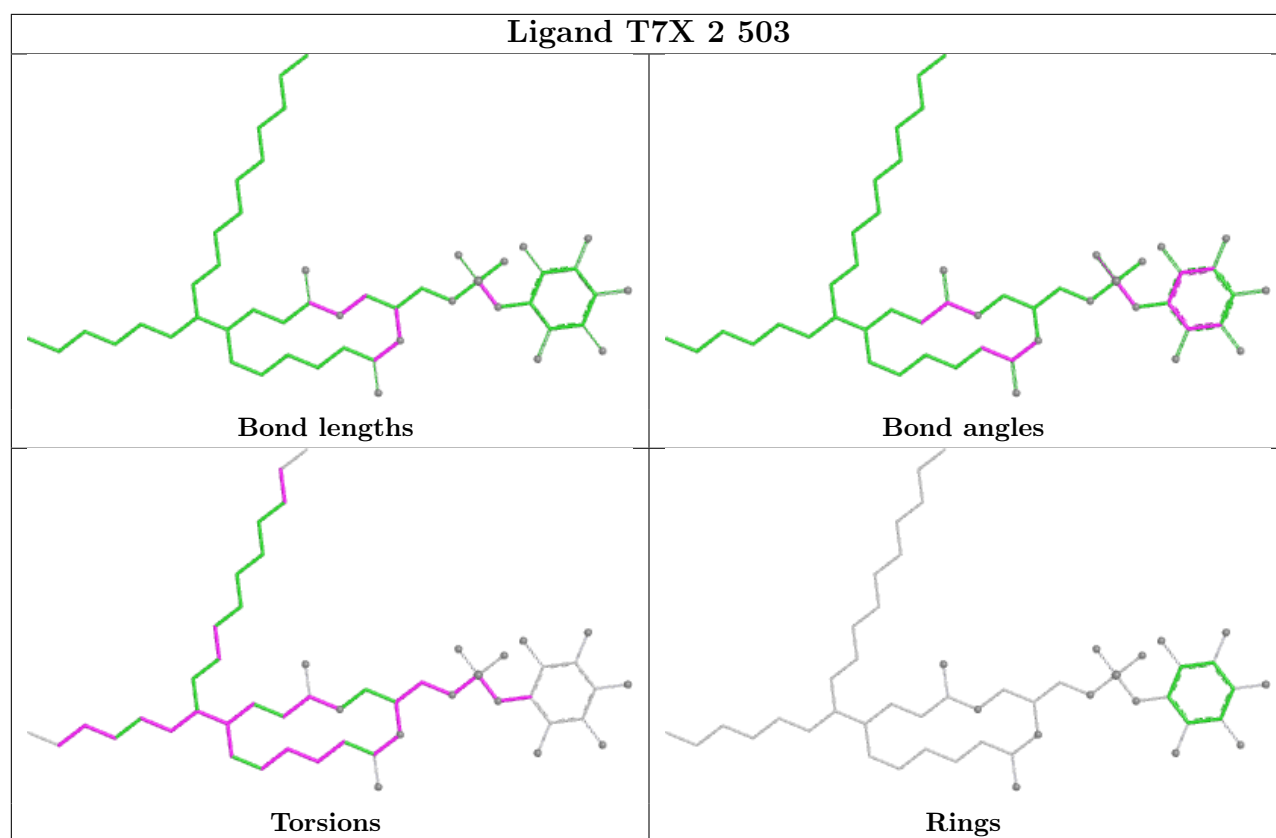
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

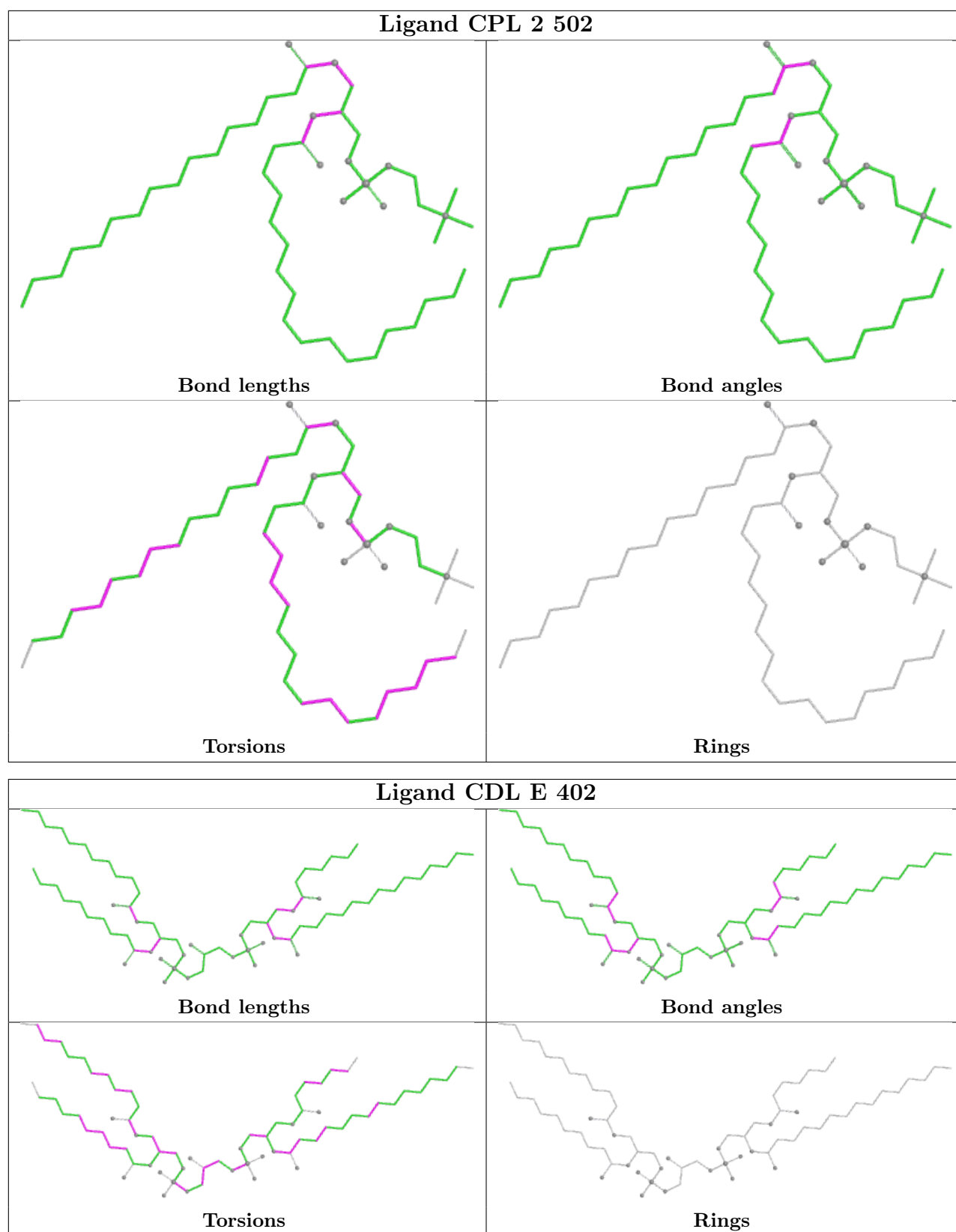


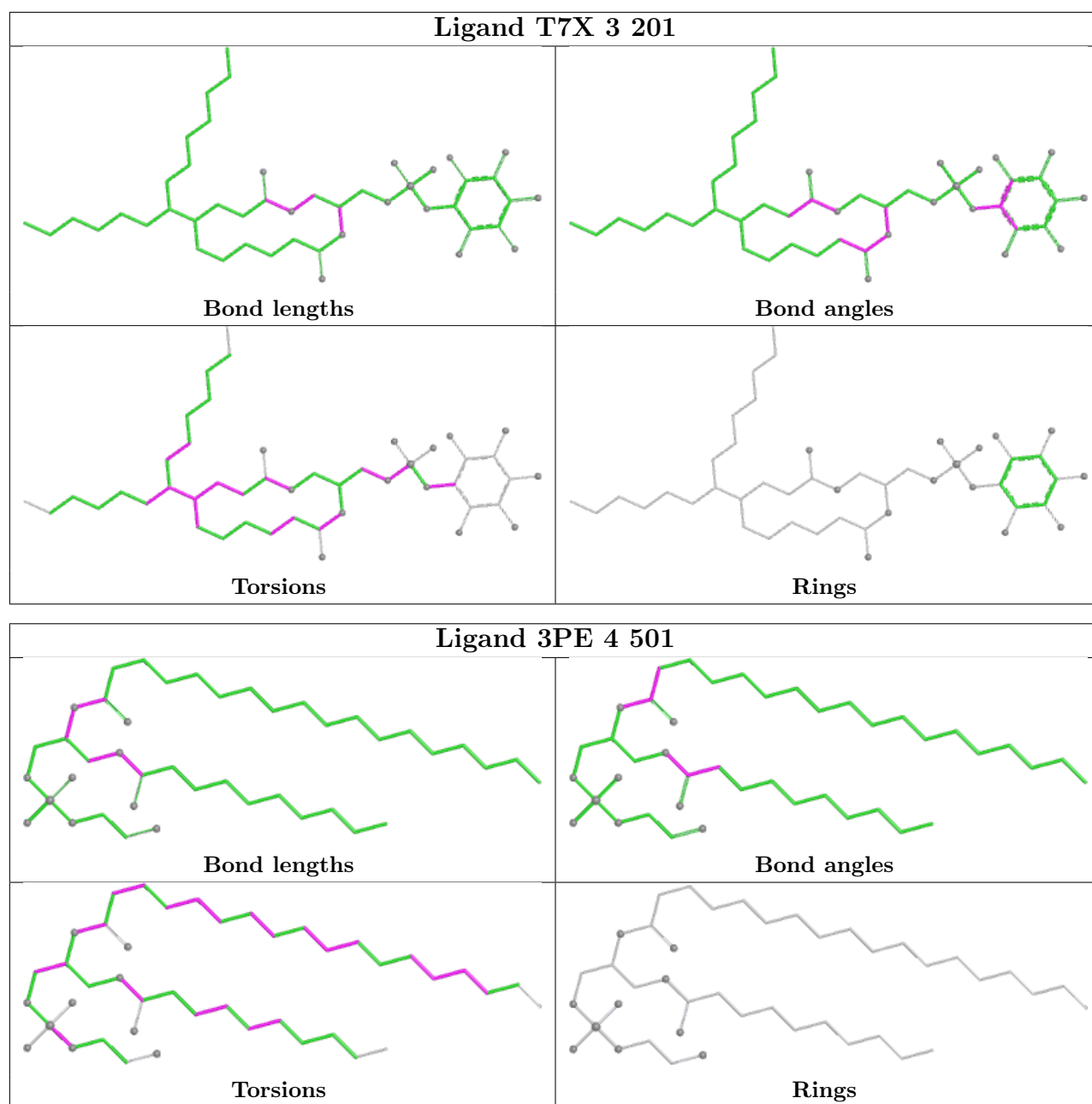


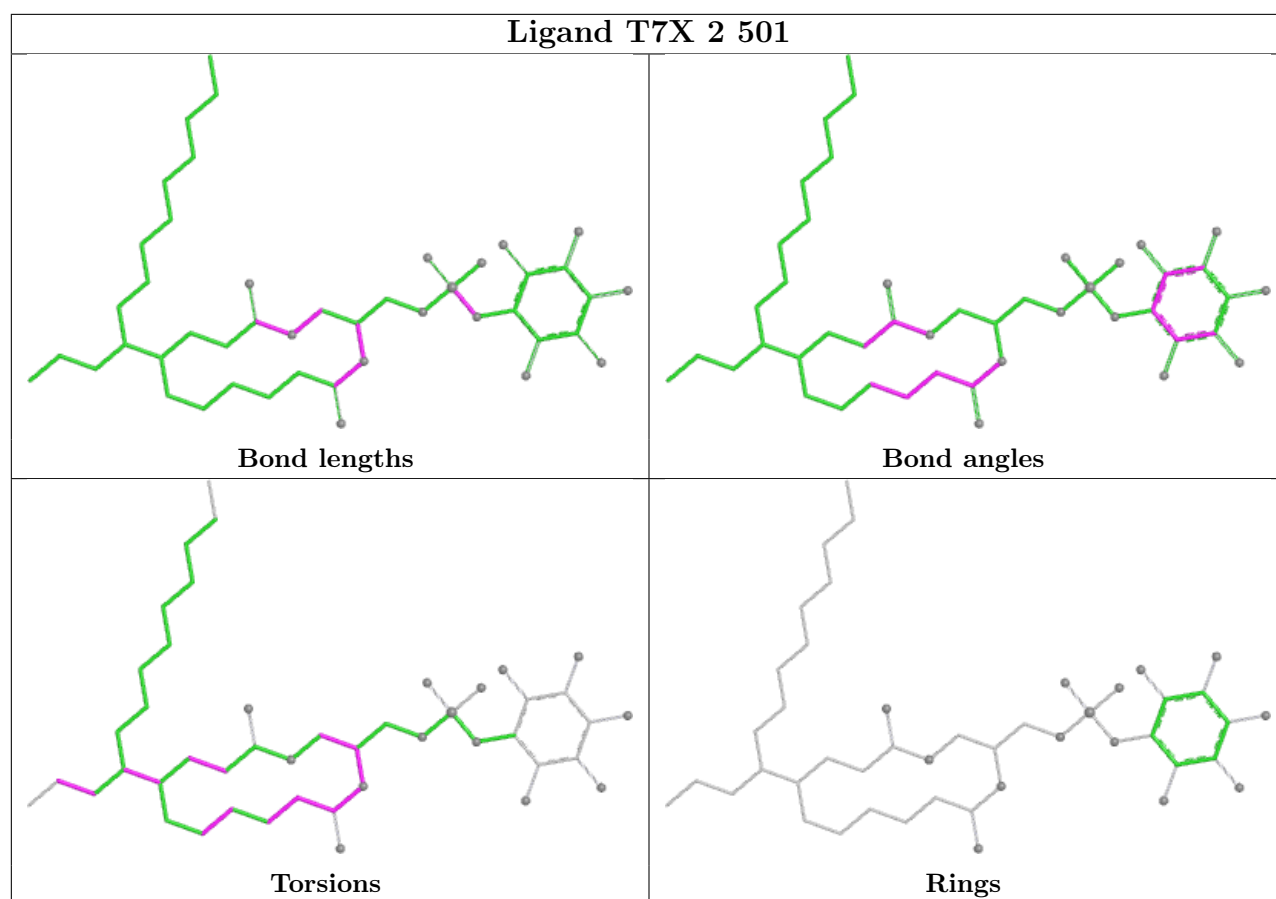


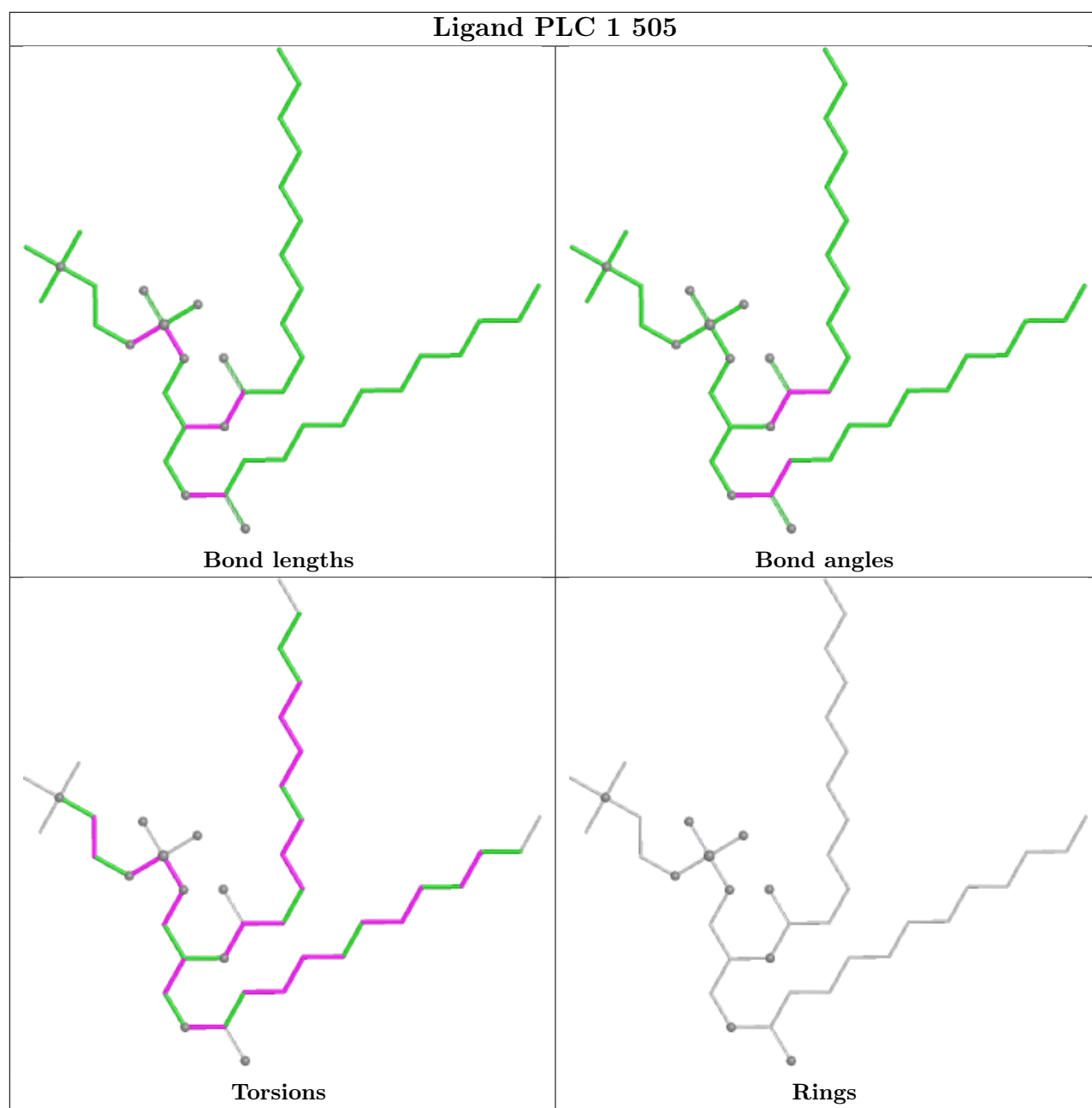


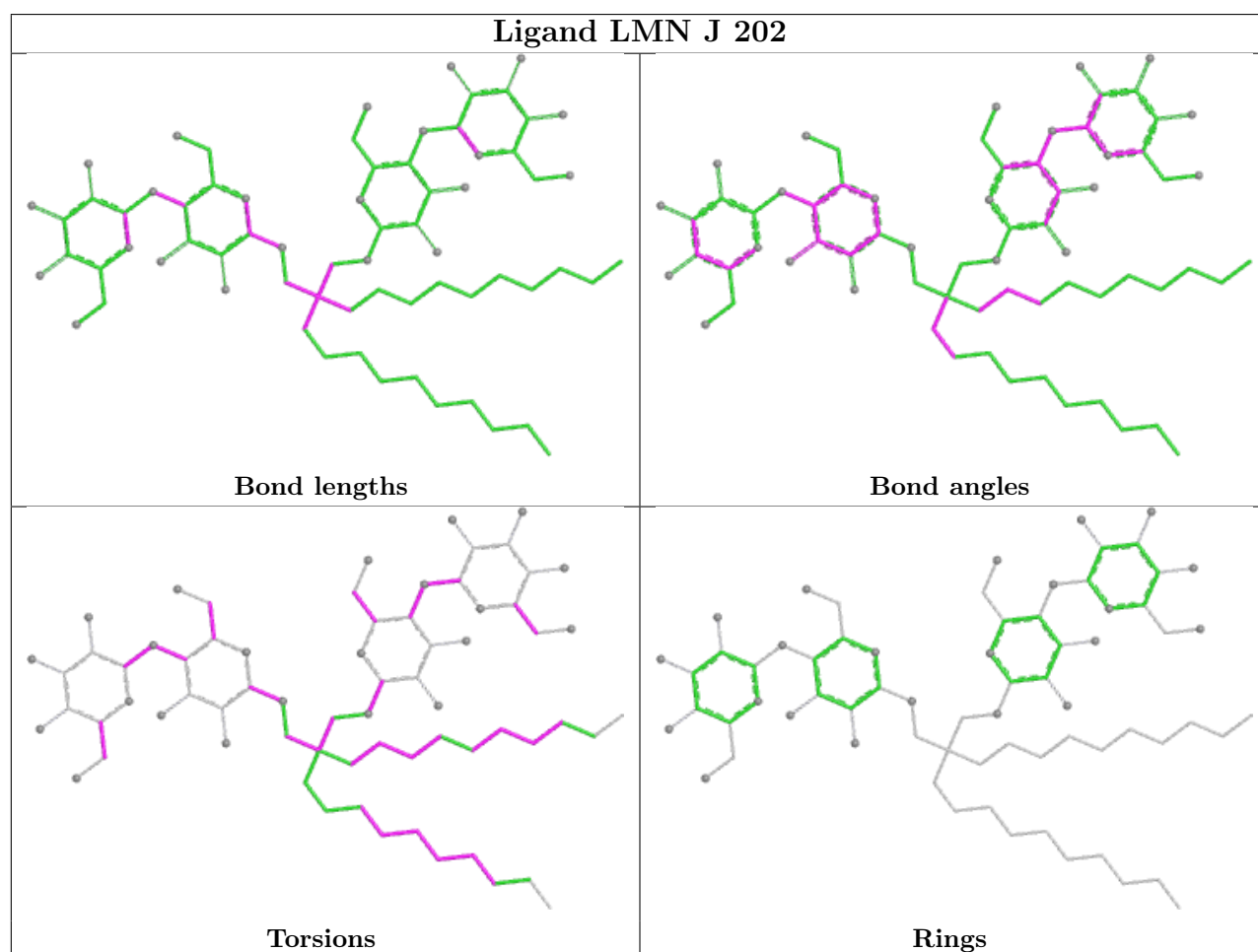
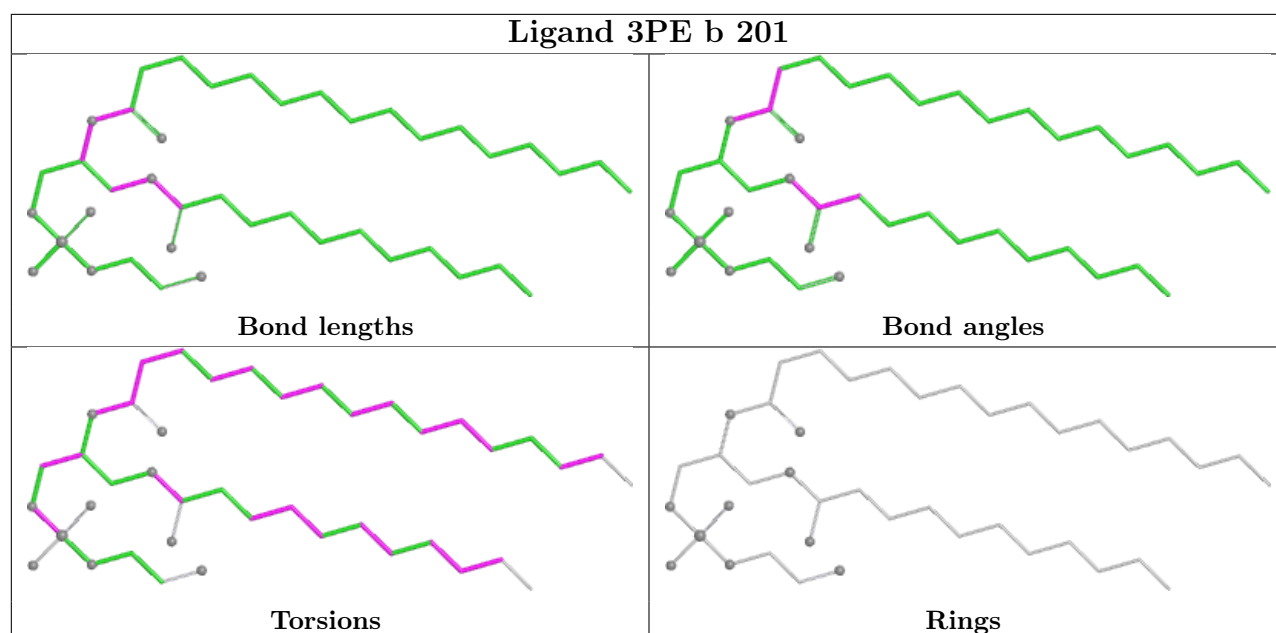


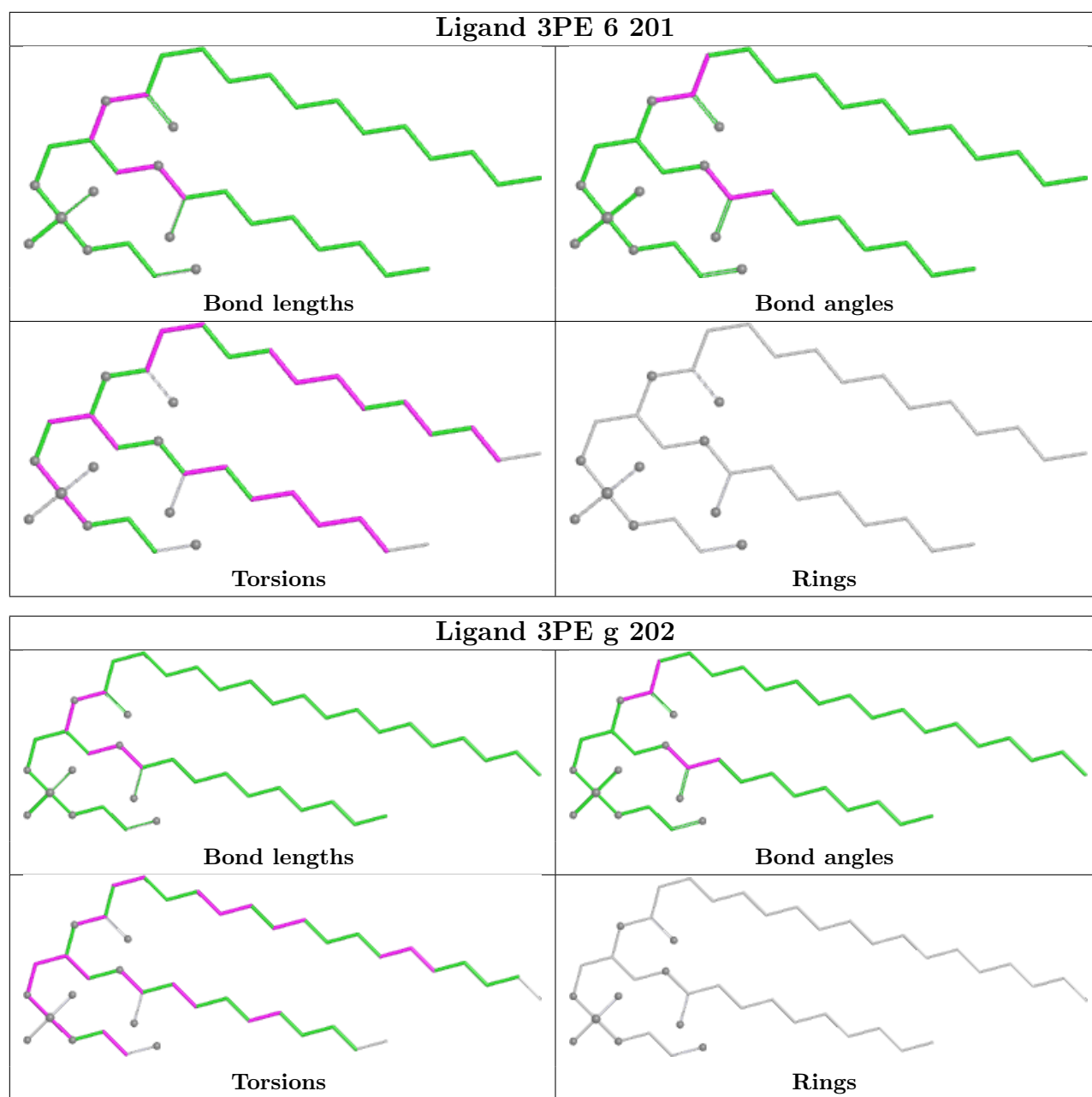


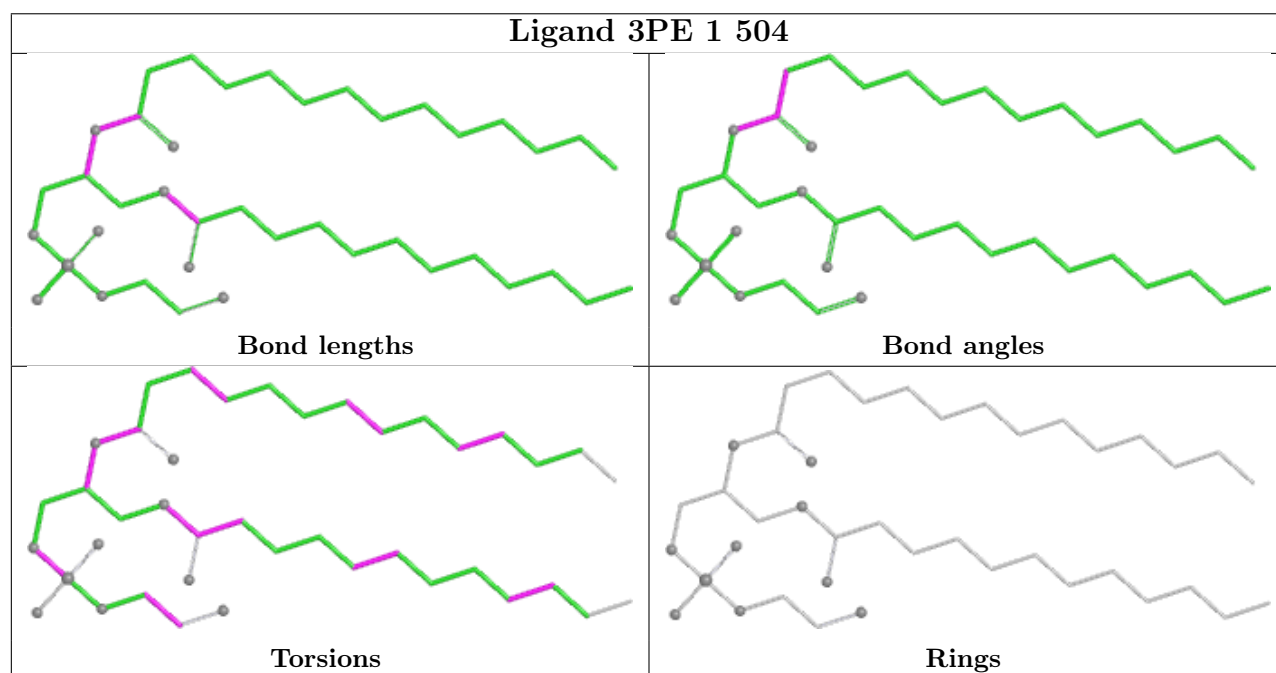
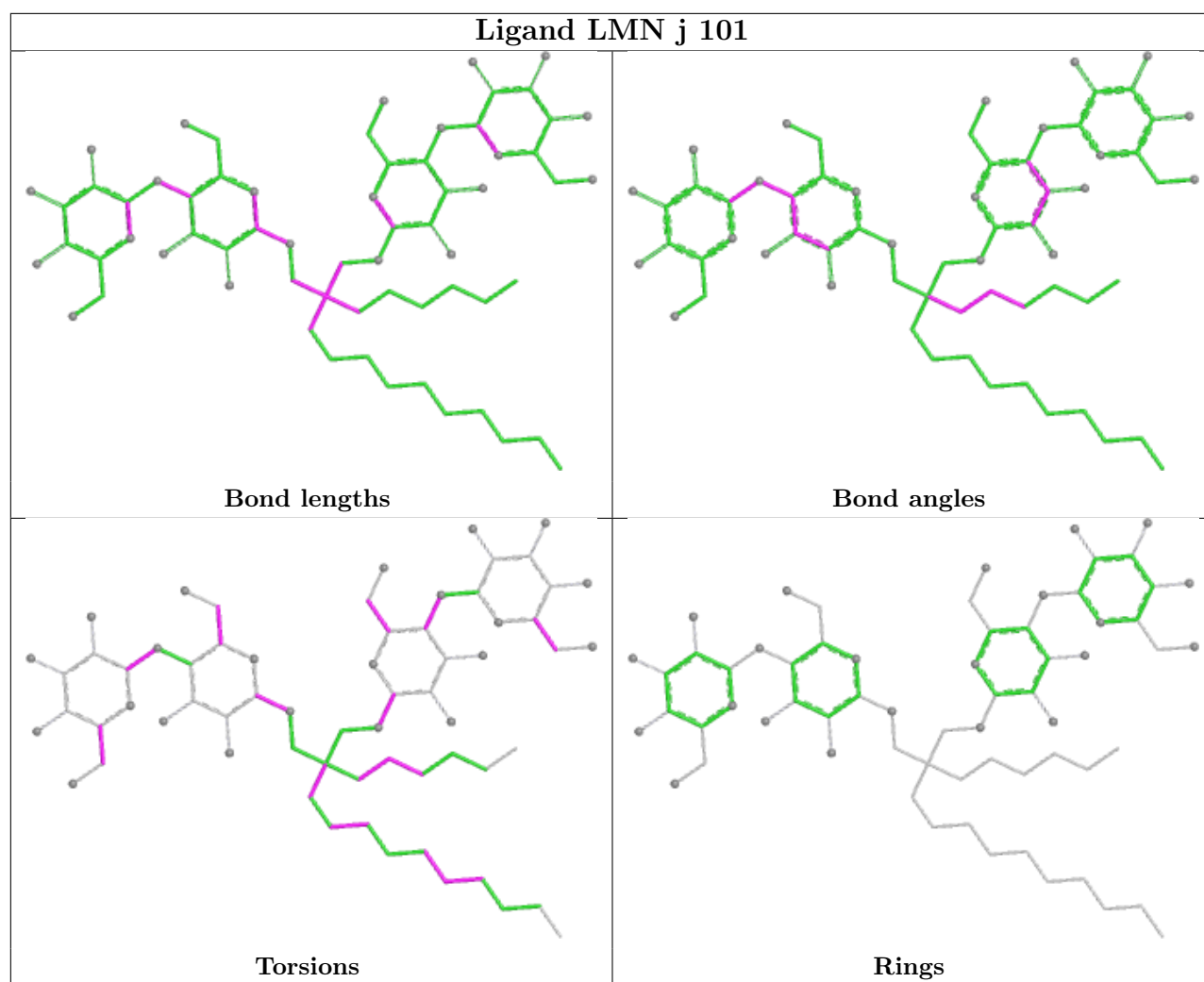


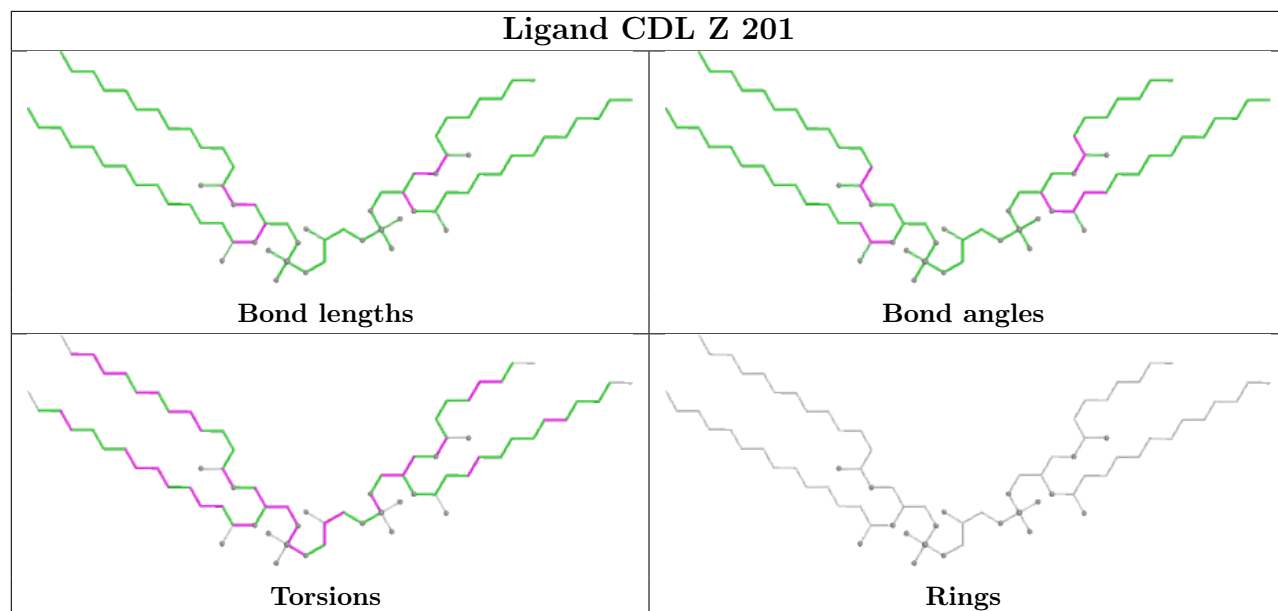


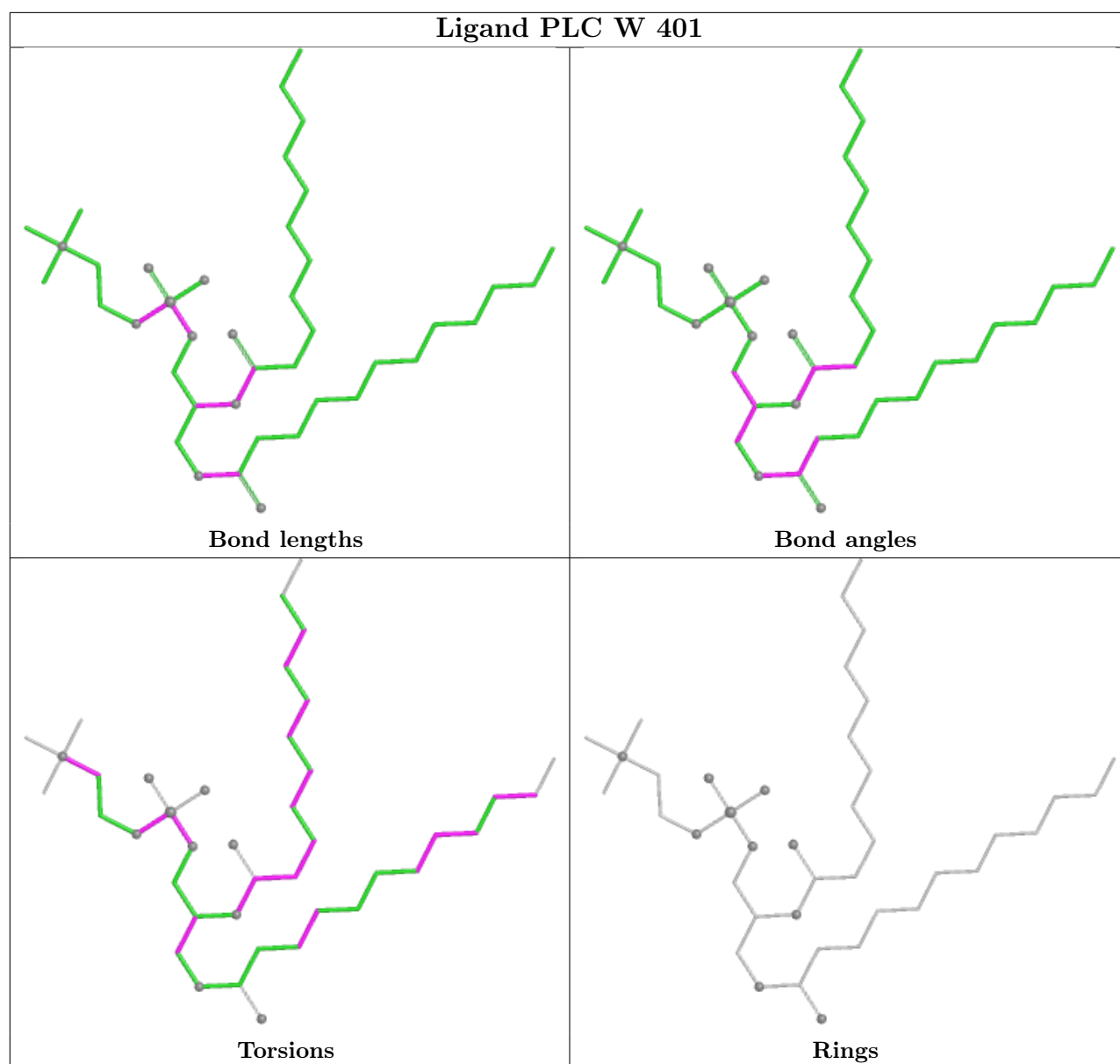


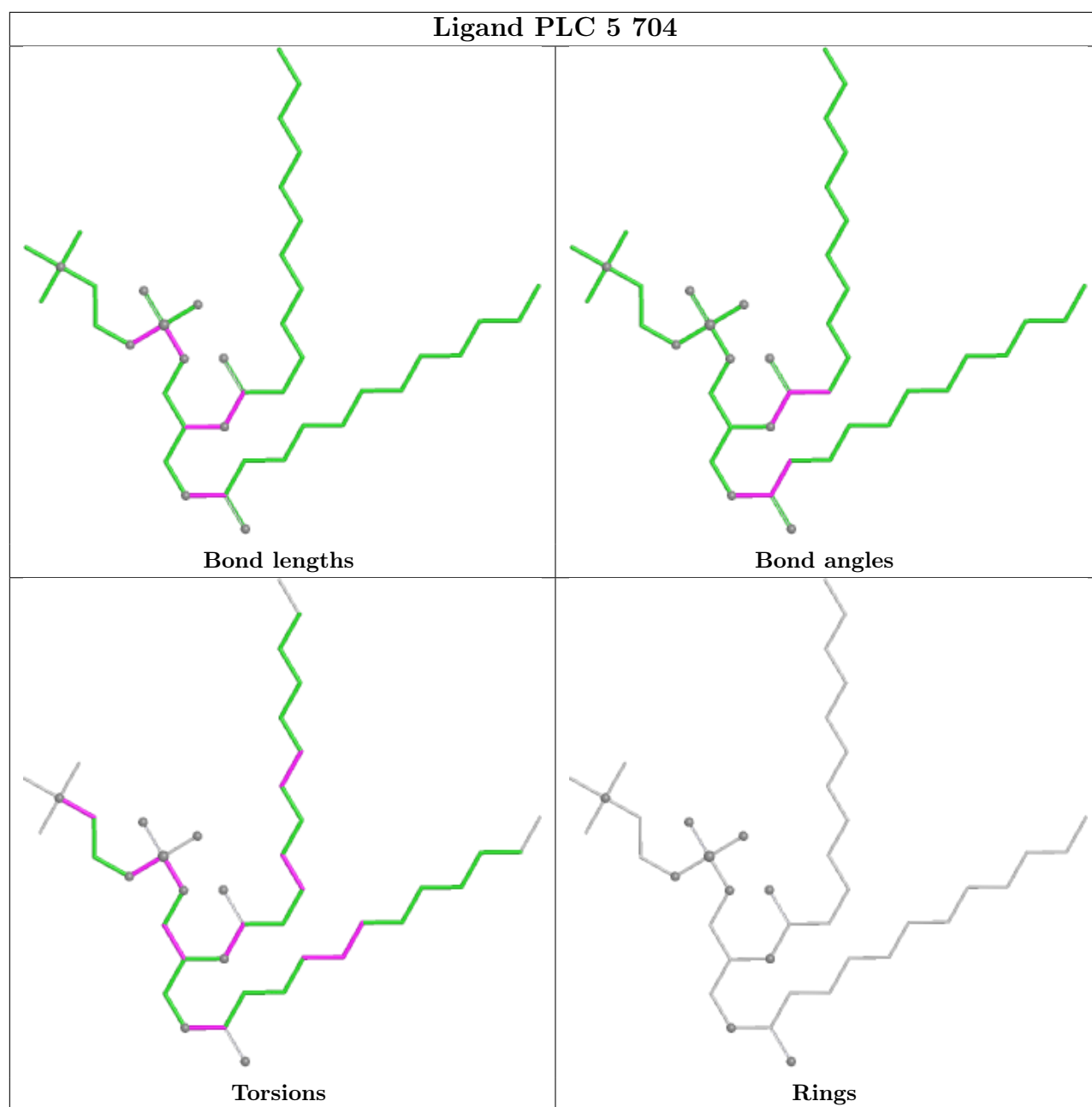


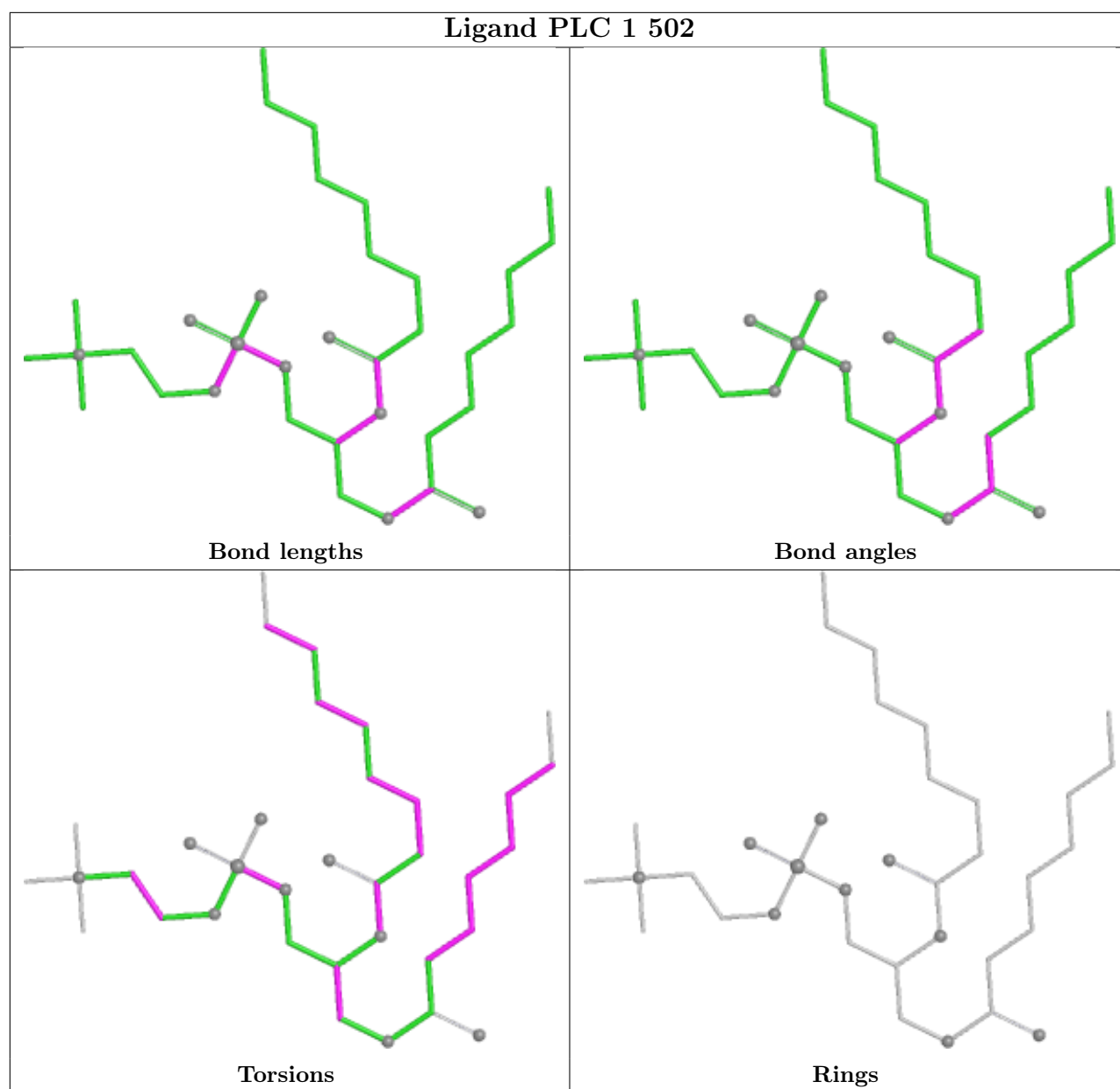


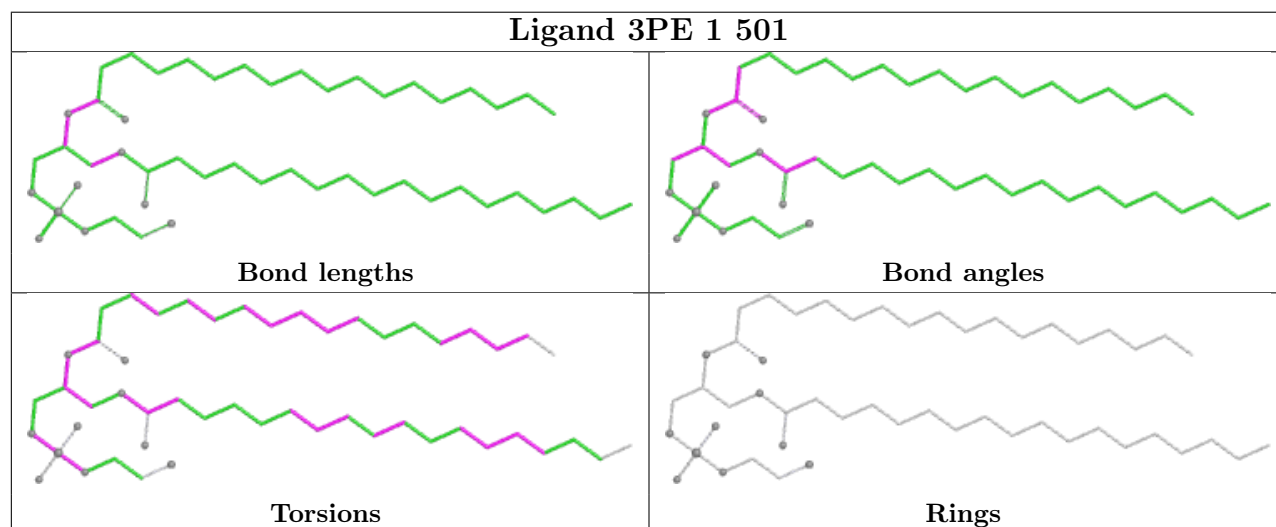
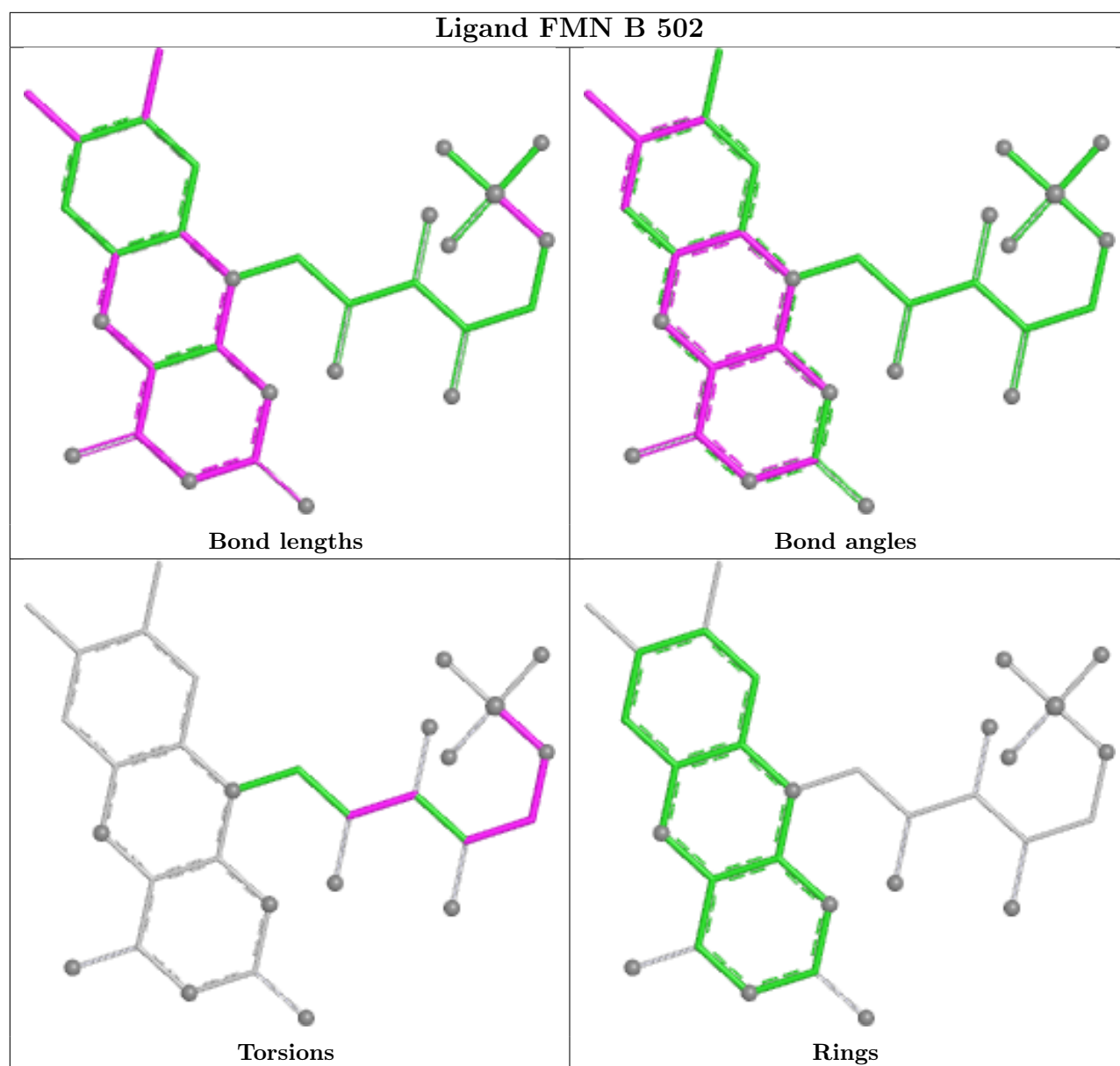


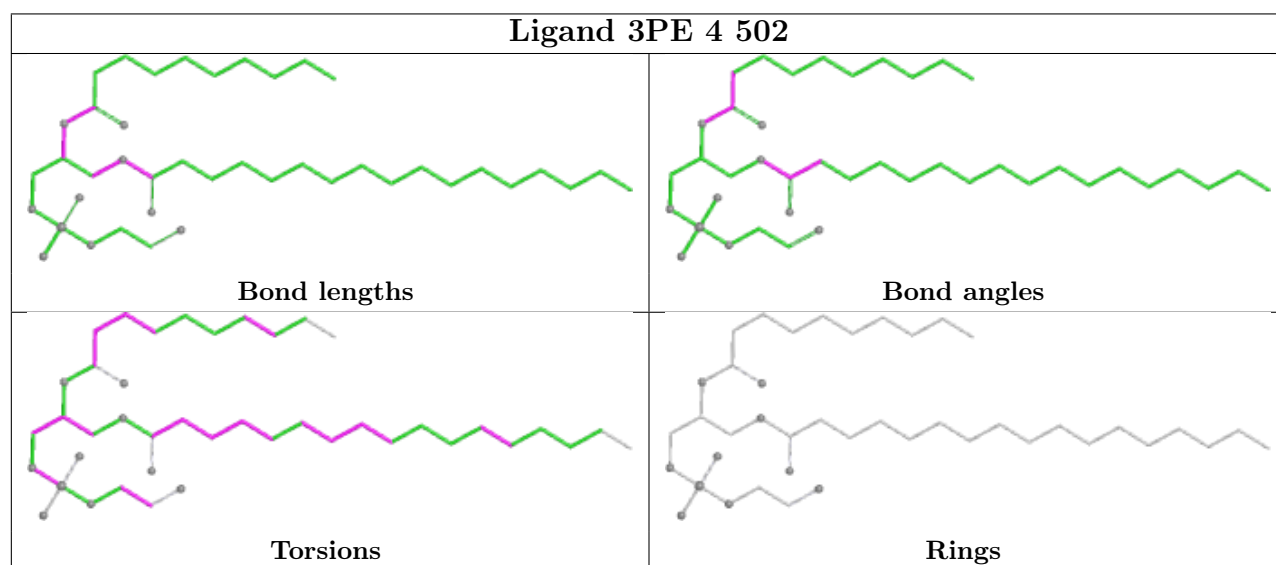
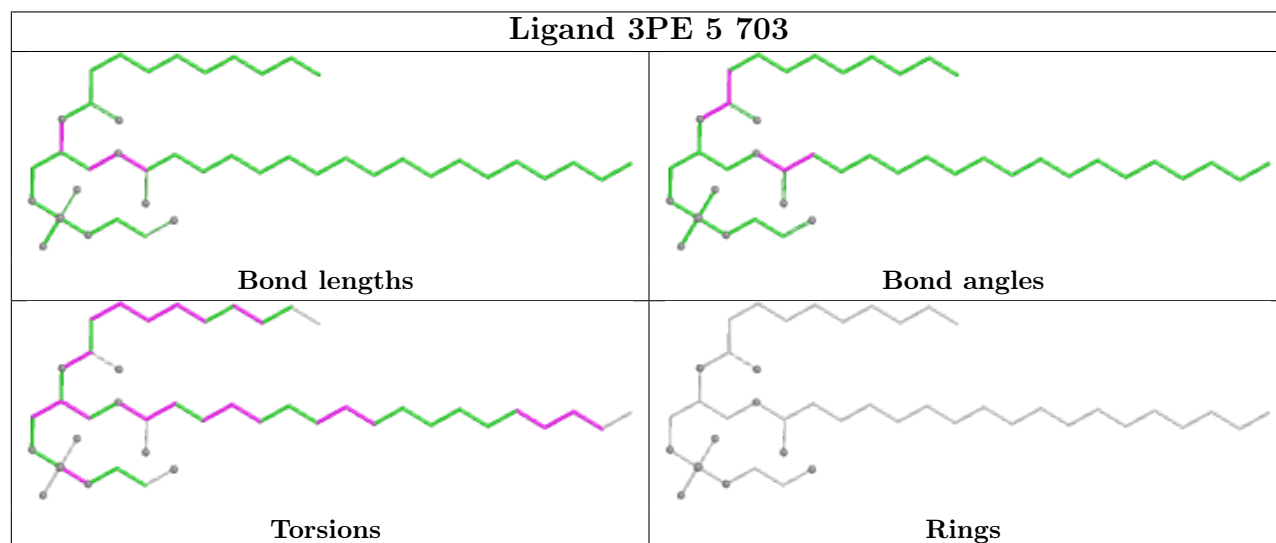
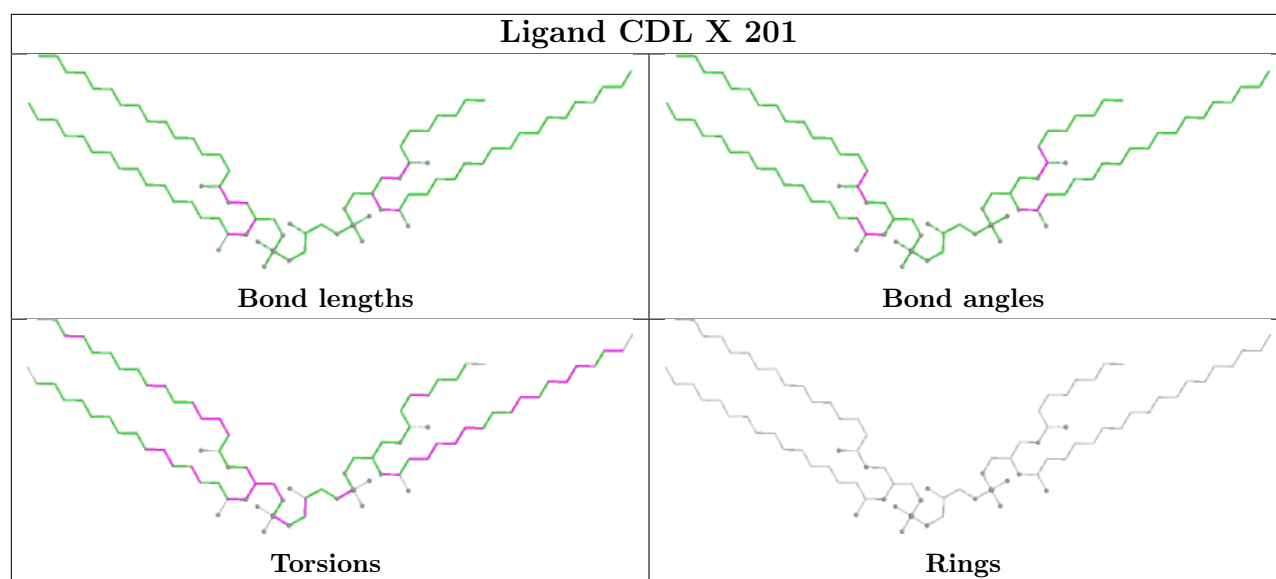


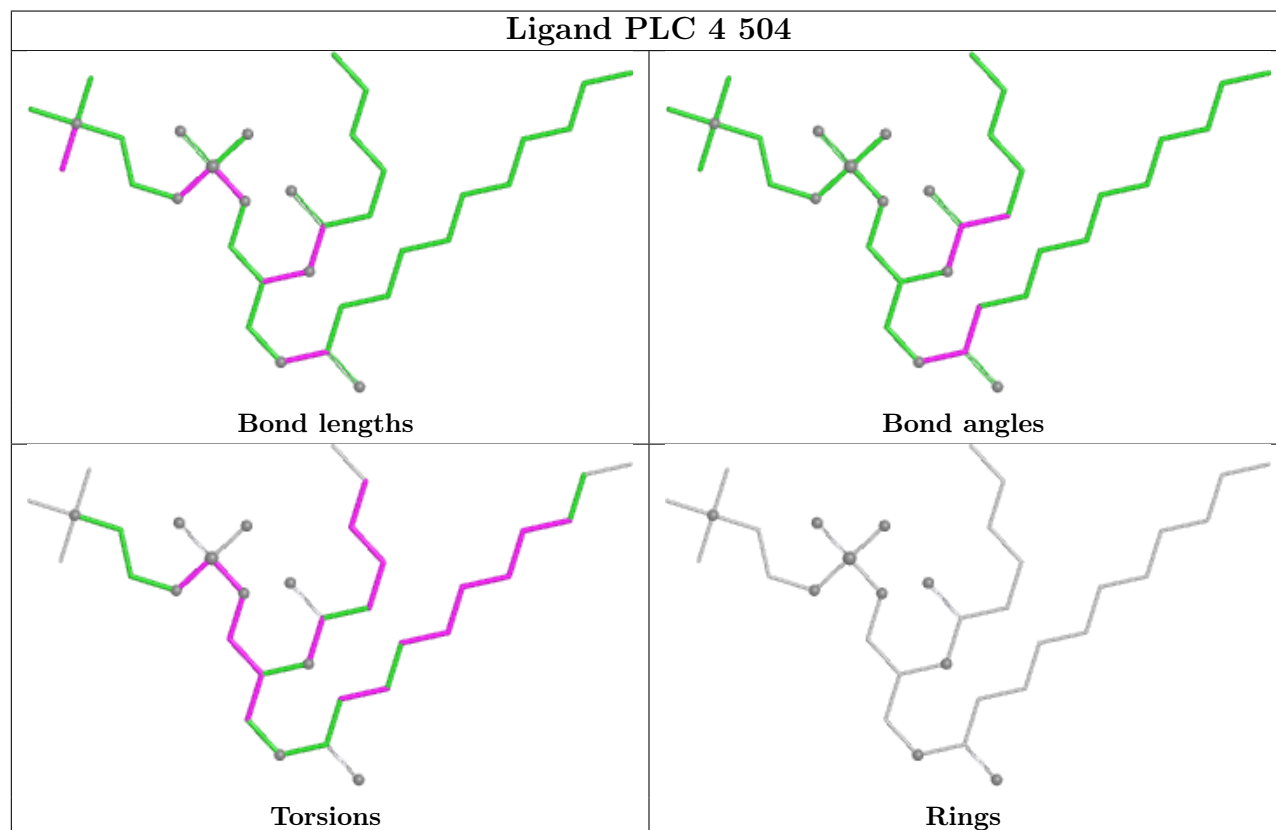
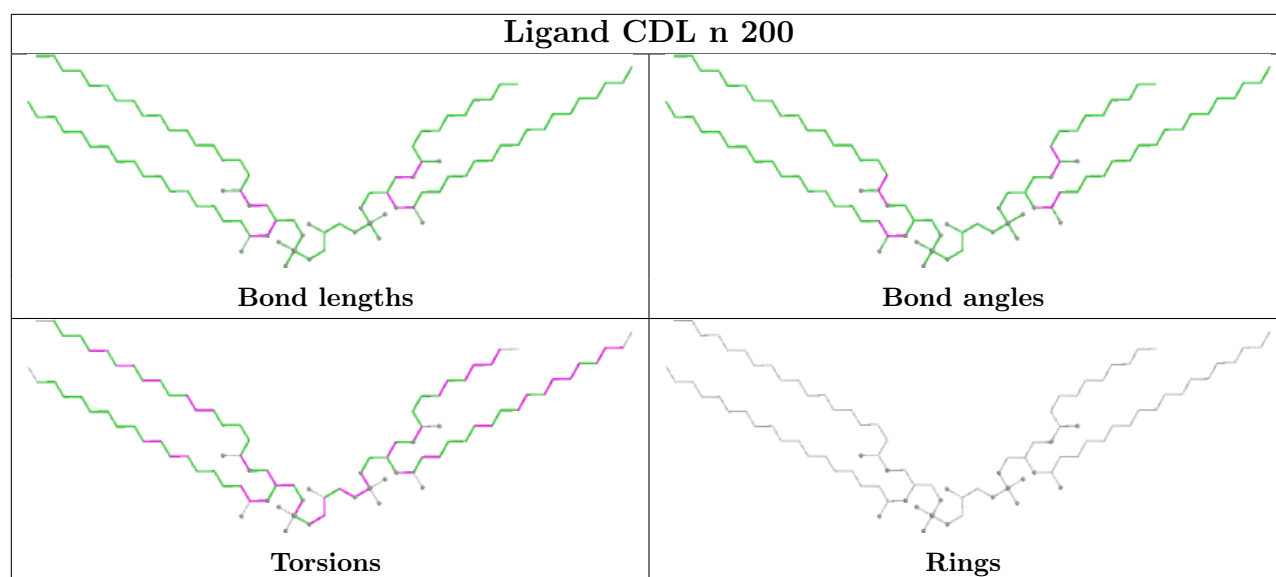


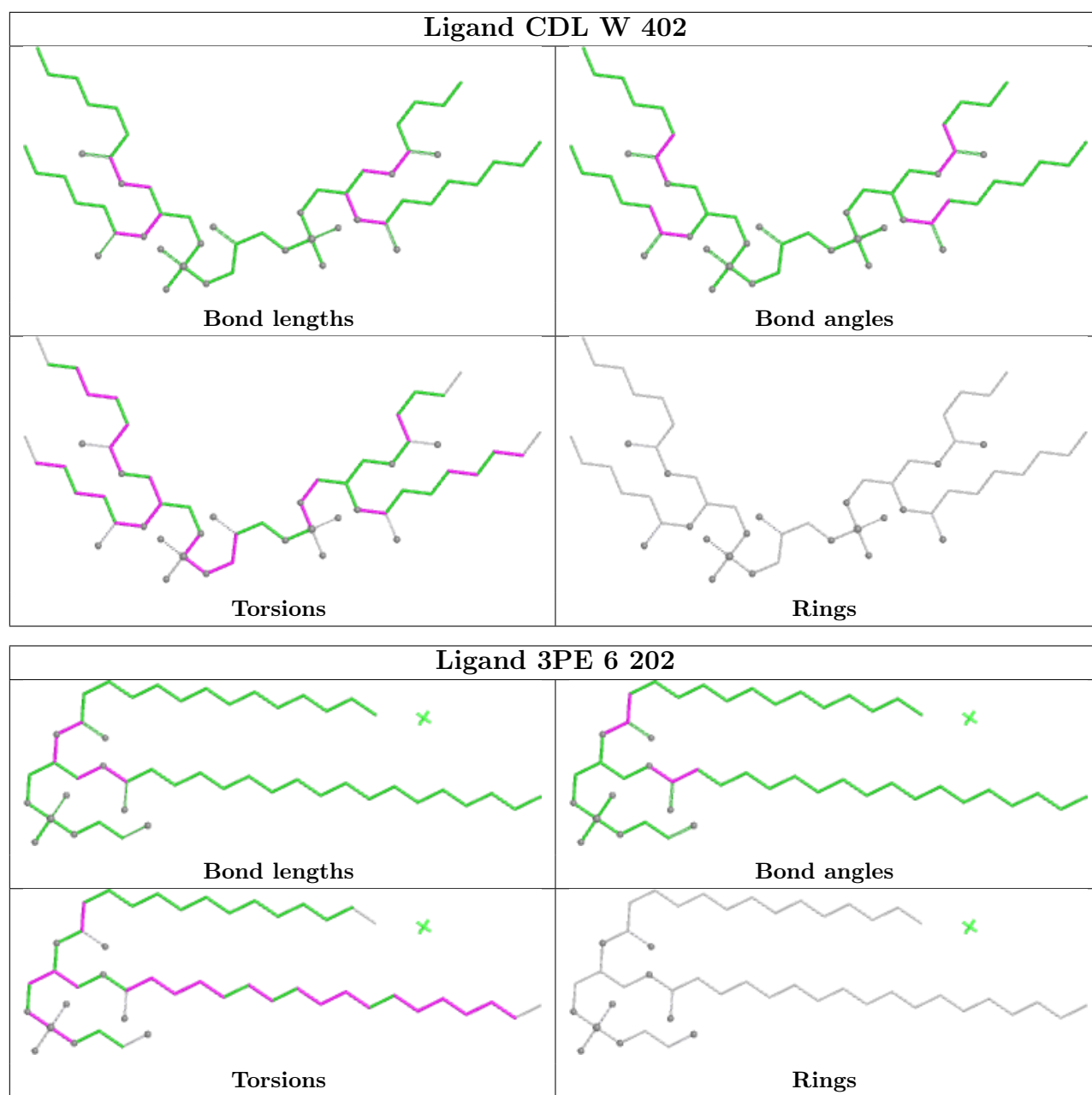


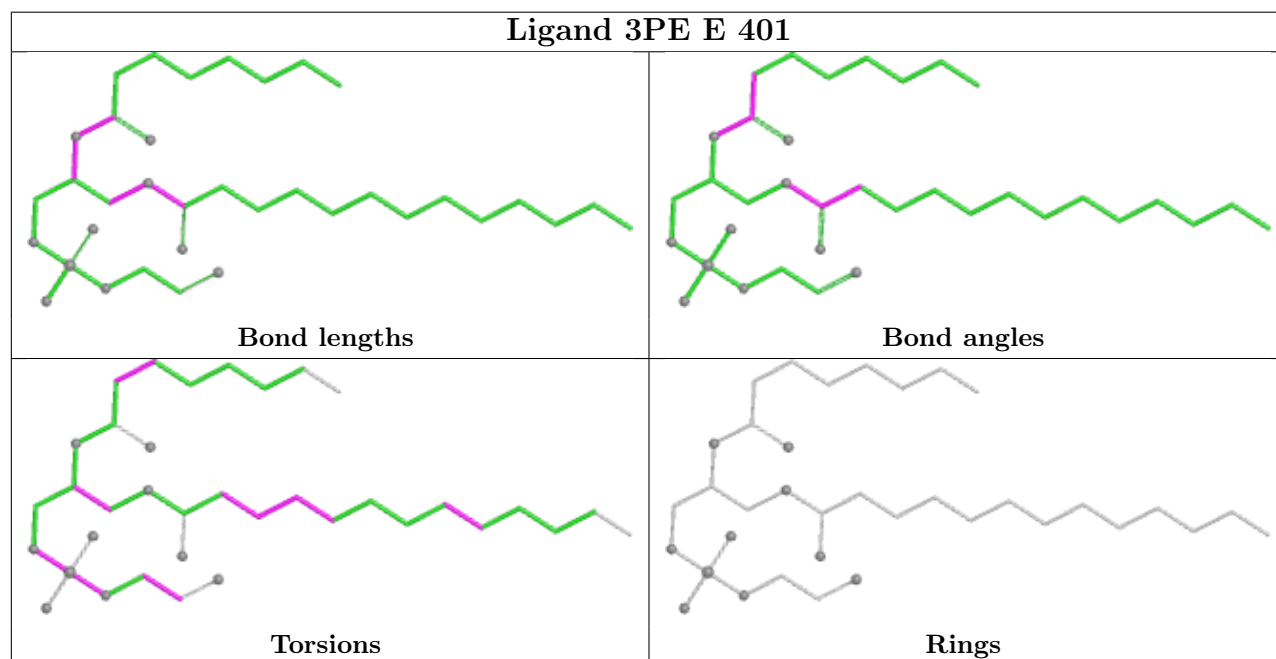
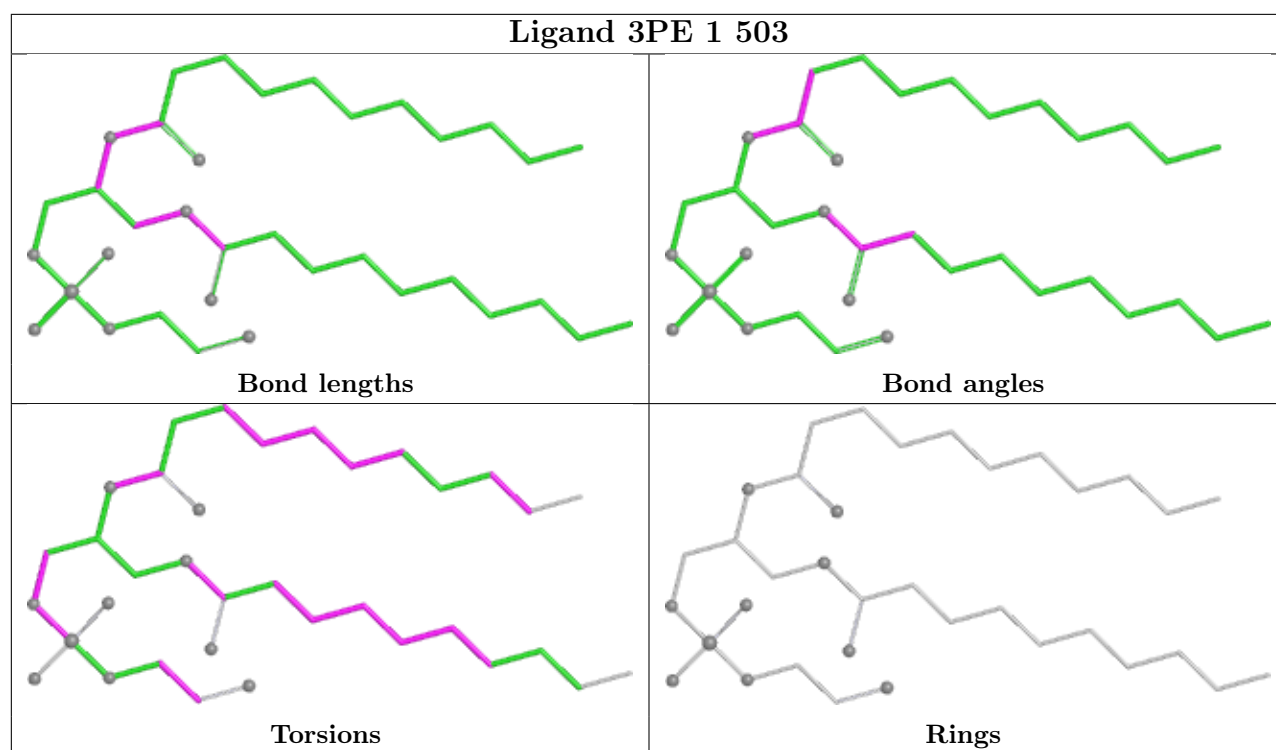


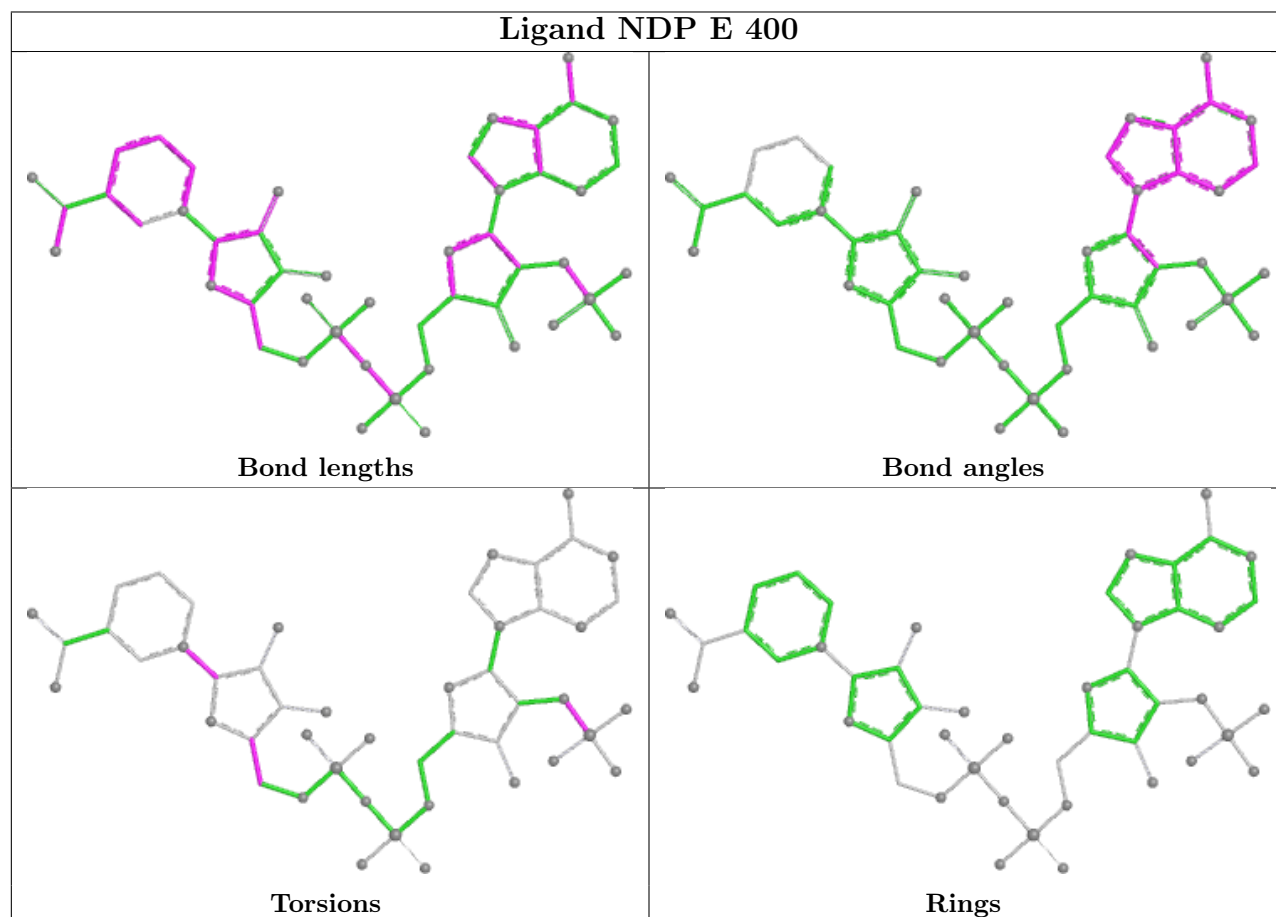
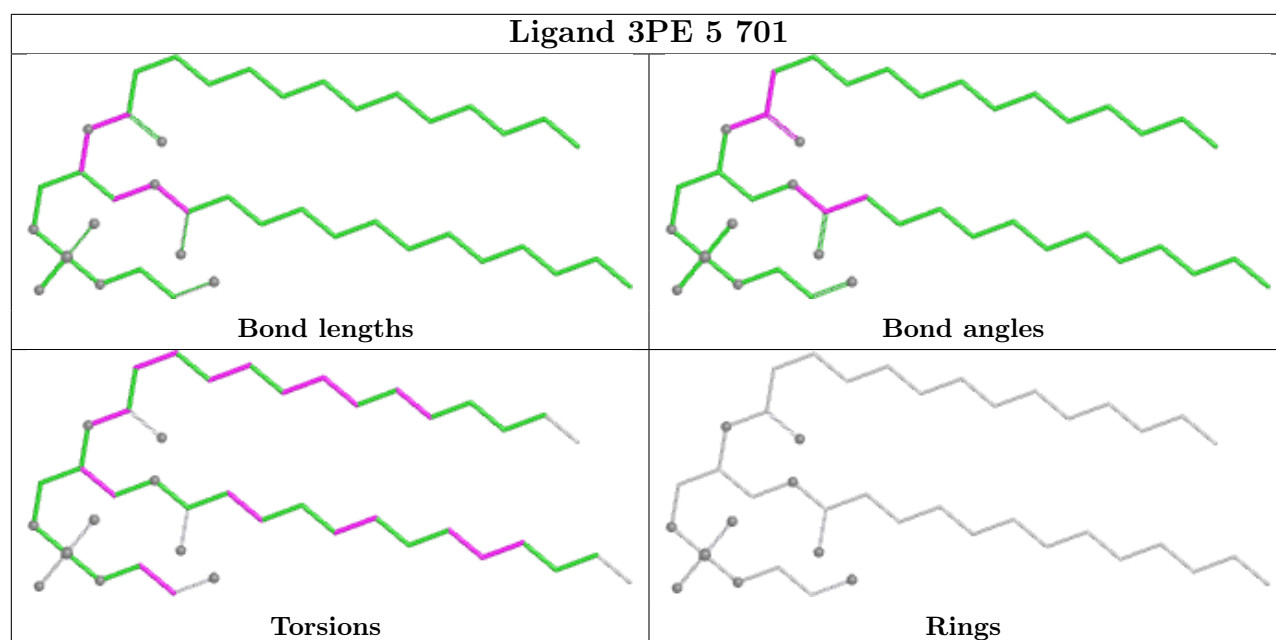


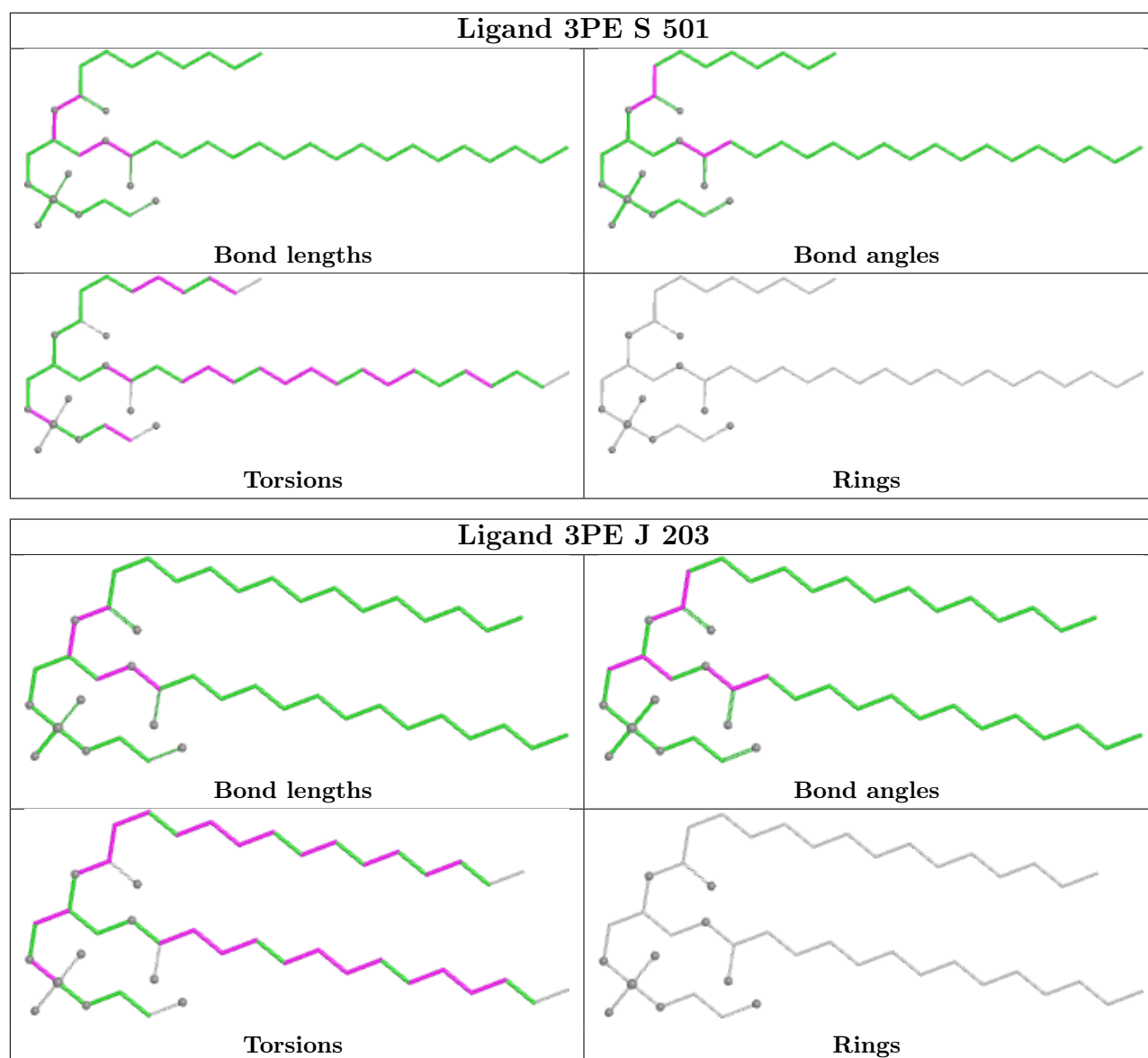












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

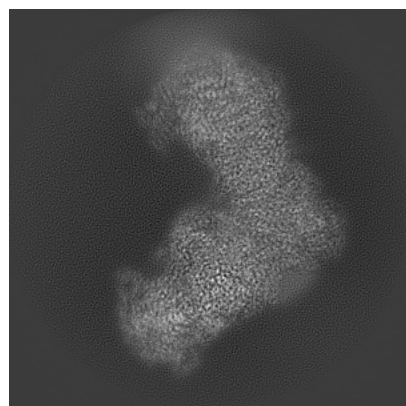
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12742. These allow visual inspection of the internal detail of the map and identification of artifacts.

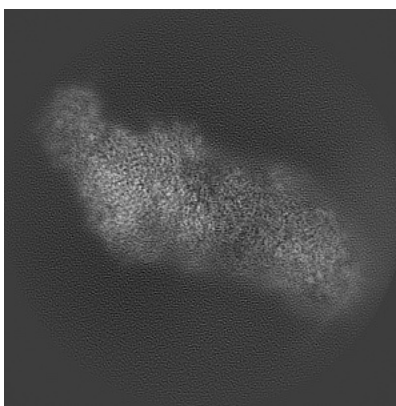
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

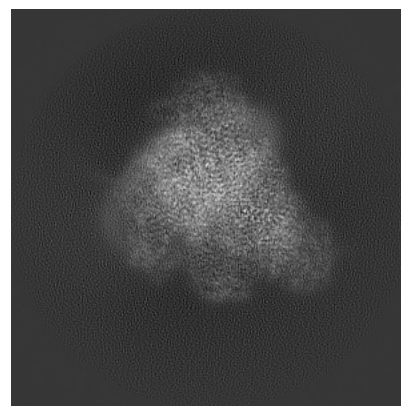
6.1.1 Primary map



X

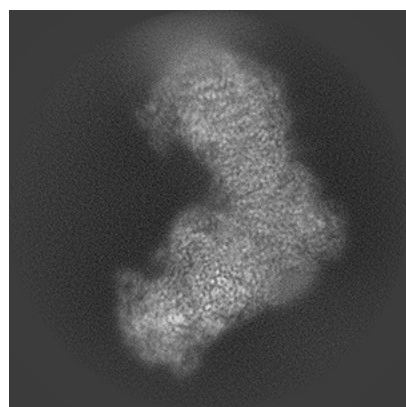


Y

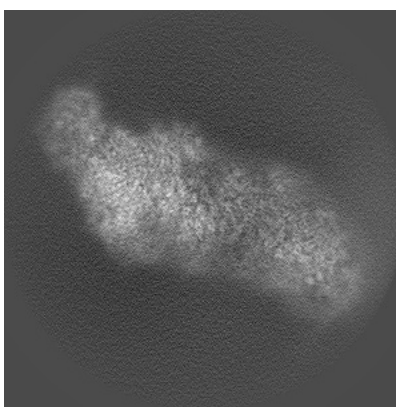


Z

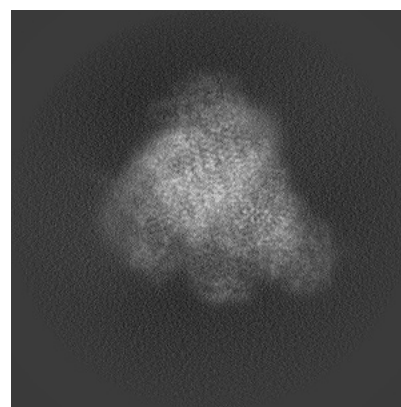
6.1.2 Raw map



X



Y

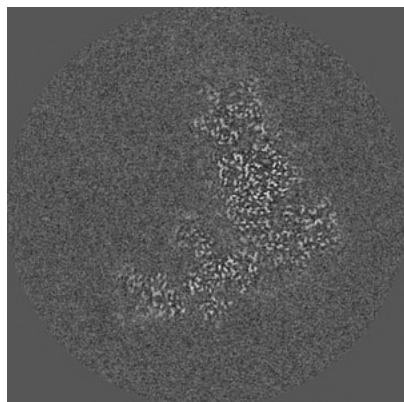


Z

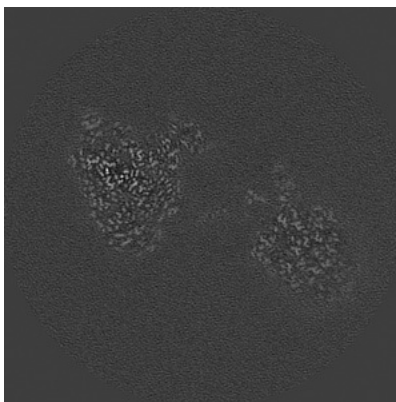
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

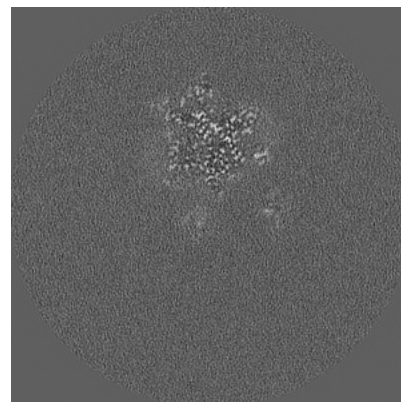
6.2.1 Primary map



X Index: 300

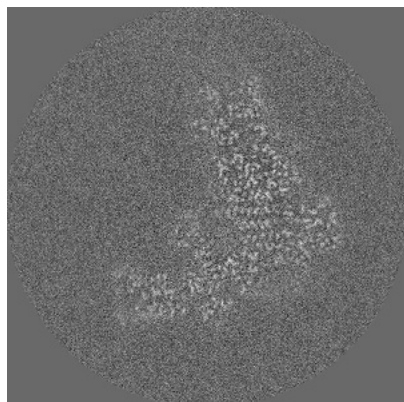


Y Index: 300

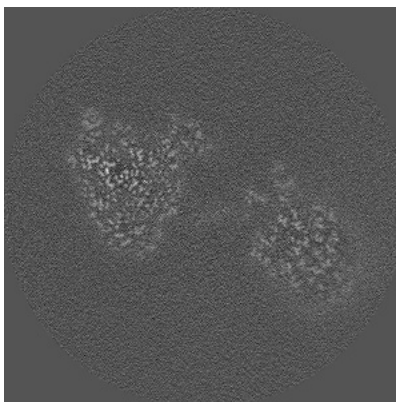


Z Index: 300

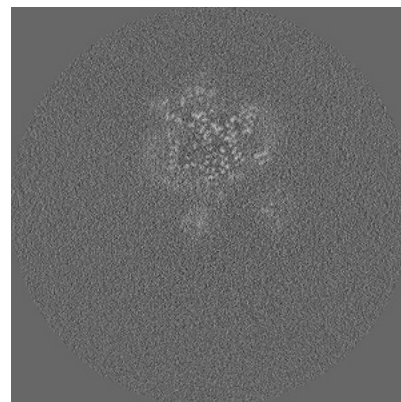
6.2.2 Raw map



X Index: 300



Y Index: 300

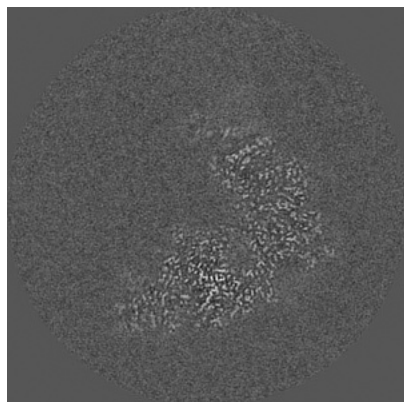


Z Index: 300

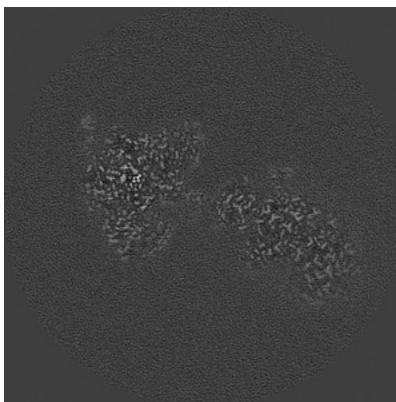
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

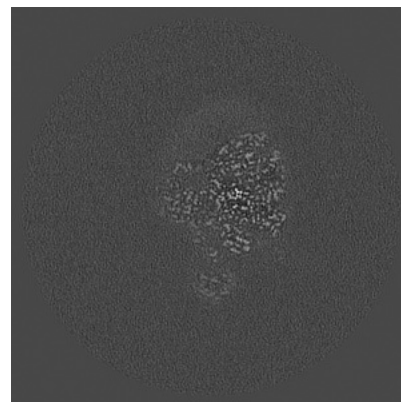
6.3.1 Primary map



X Index: 332

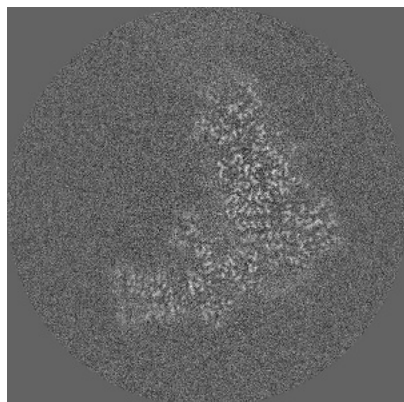


Y Index: 319

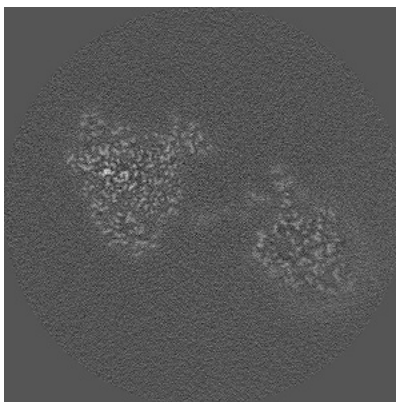


Z Index: 197

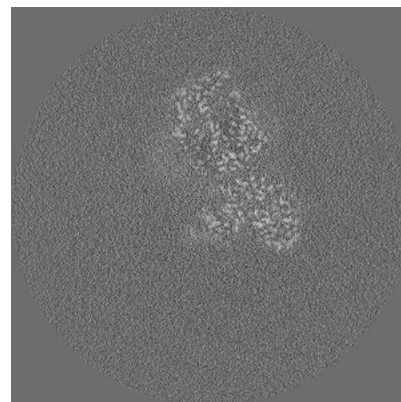
6.3.2 Raw map



X Index: 301



Y Index: 298

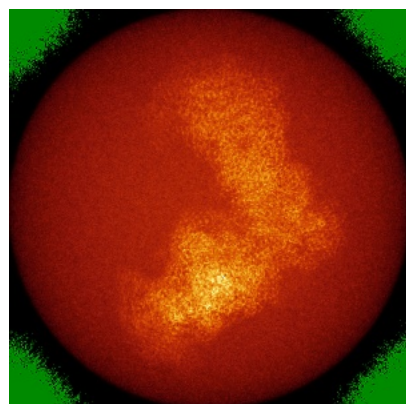


Z Index: 261

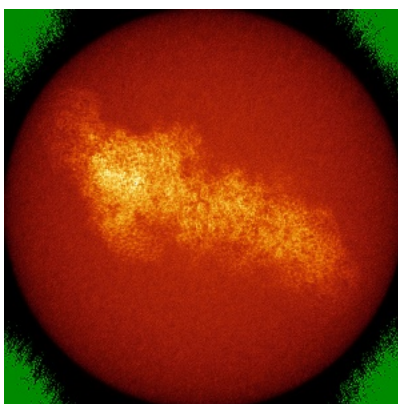
The images above show the largest variance slices of the map in three orthogonal directions.

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

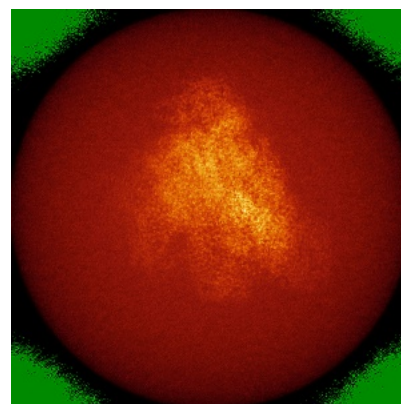
6.4.1 Primary map



X

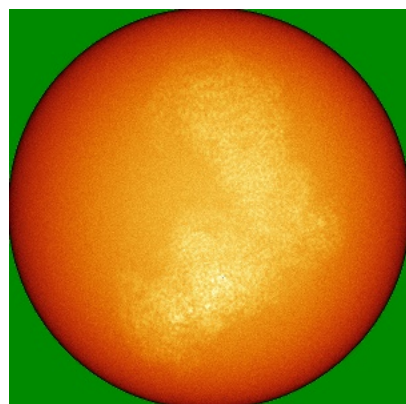


Y

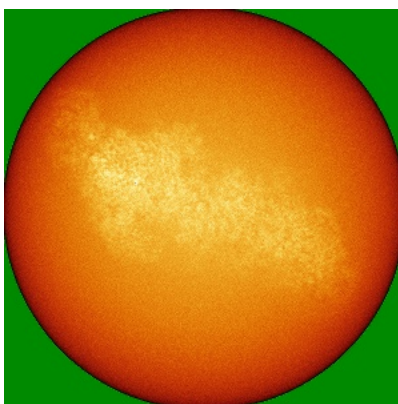


Z

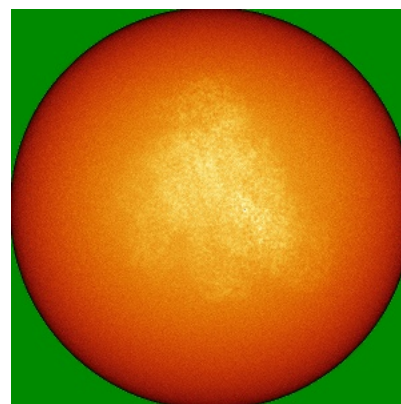
6.4.2 Raw map



X



Y

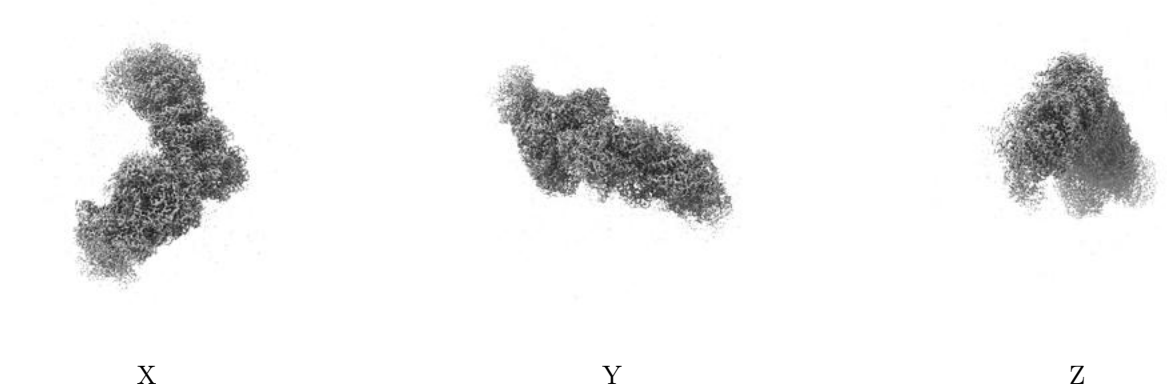


Z

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

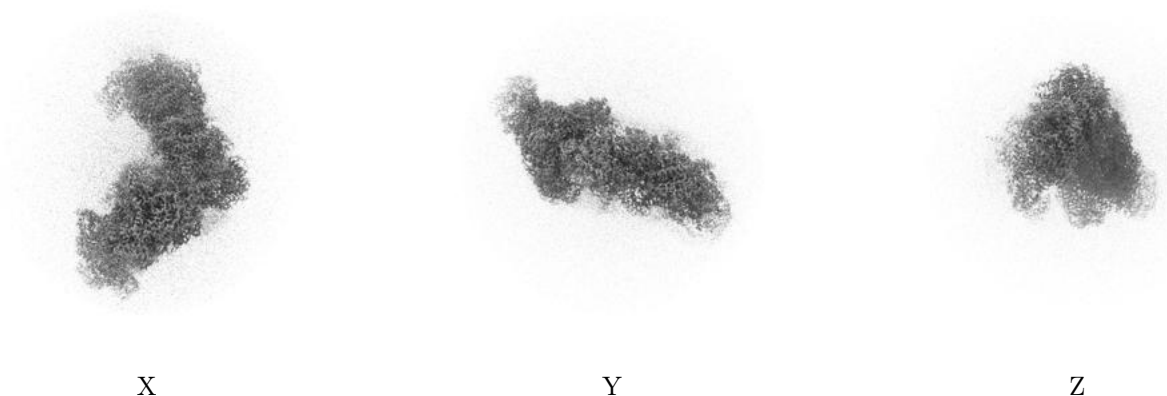
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.016. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

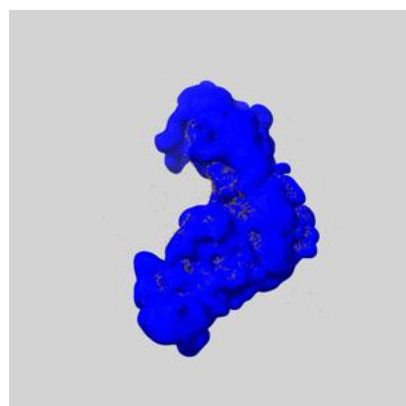
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

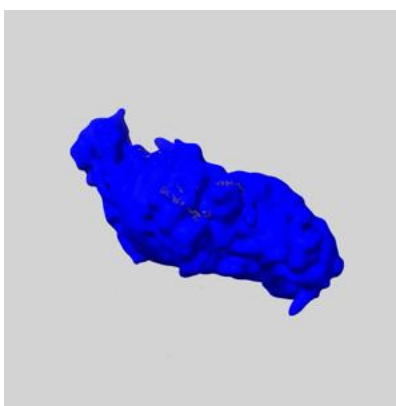
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

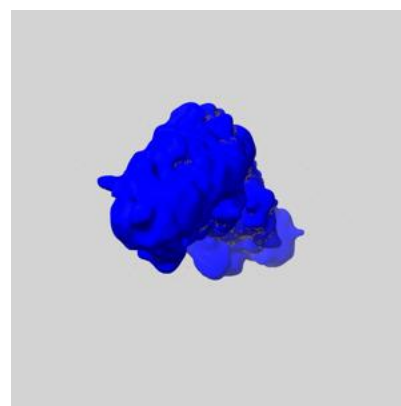
6.6.1 emd_12742_msk_1.map [i](#)



X



Y

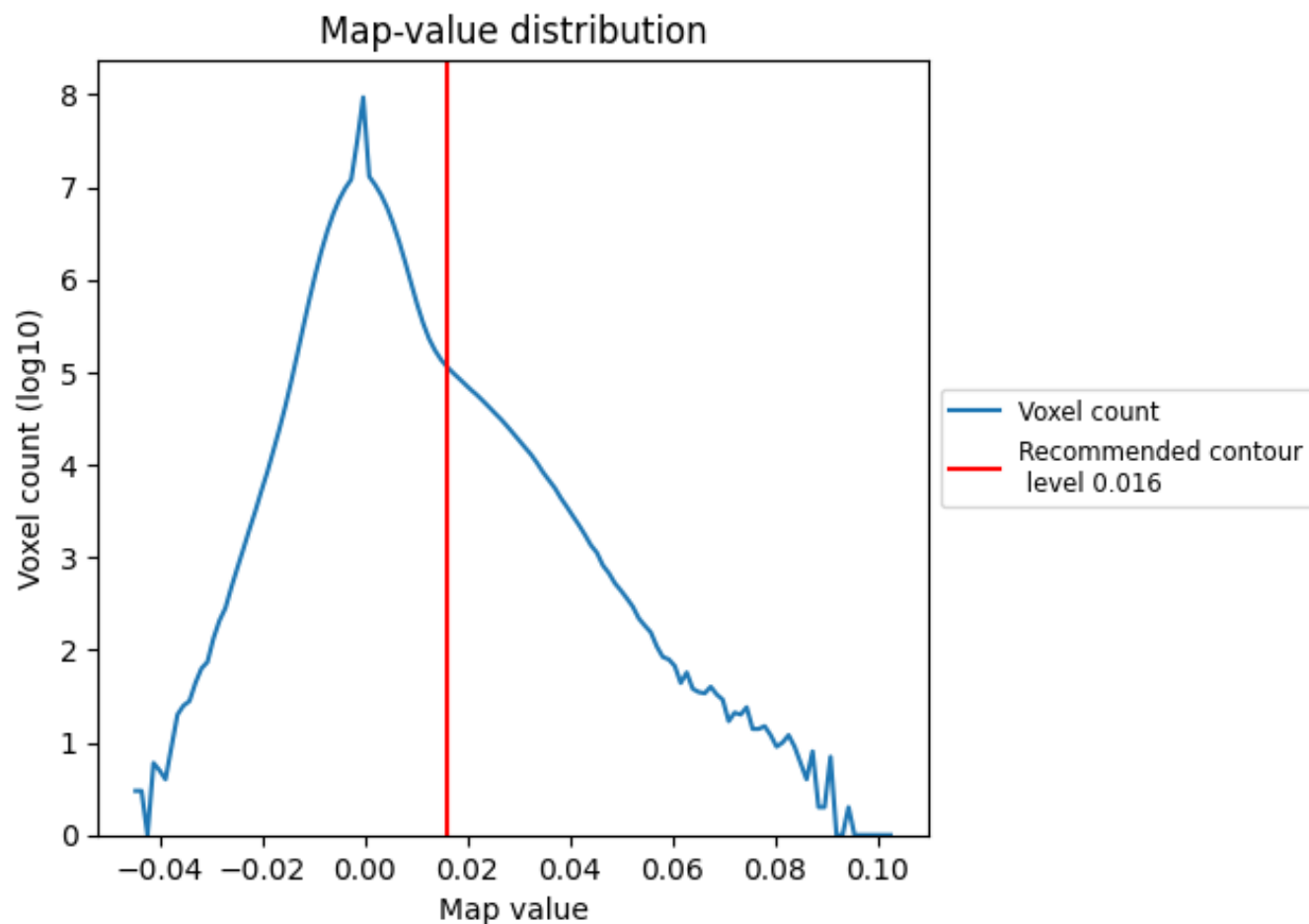


Z

7 Map analysis [i](#)

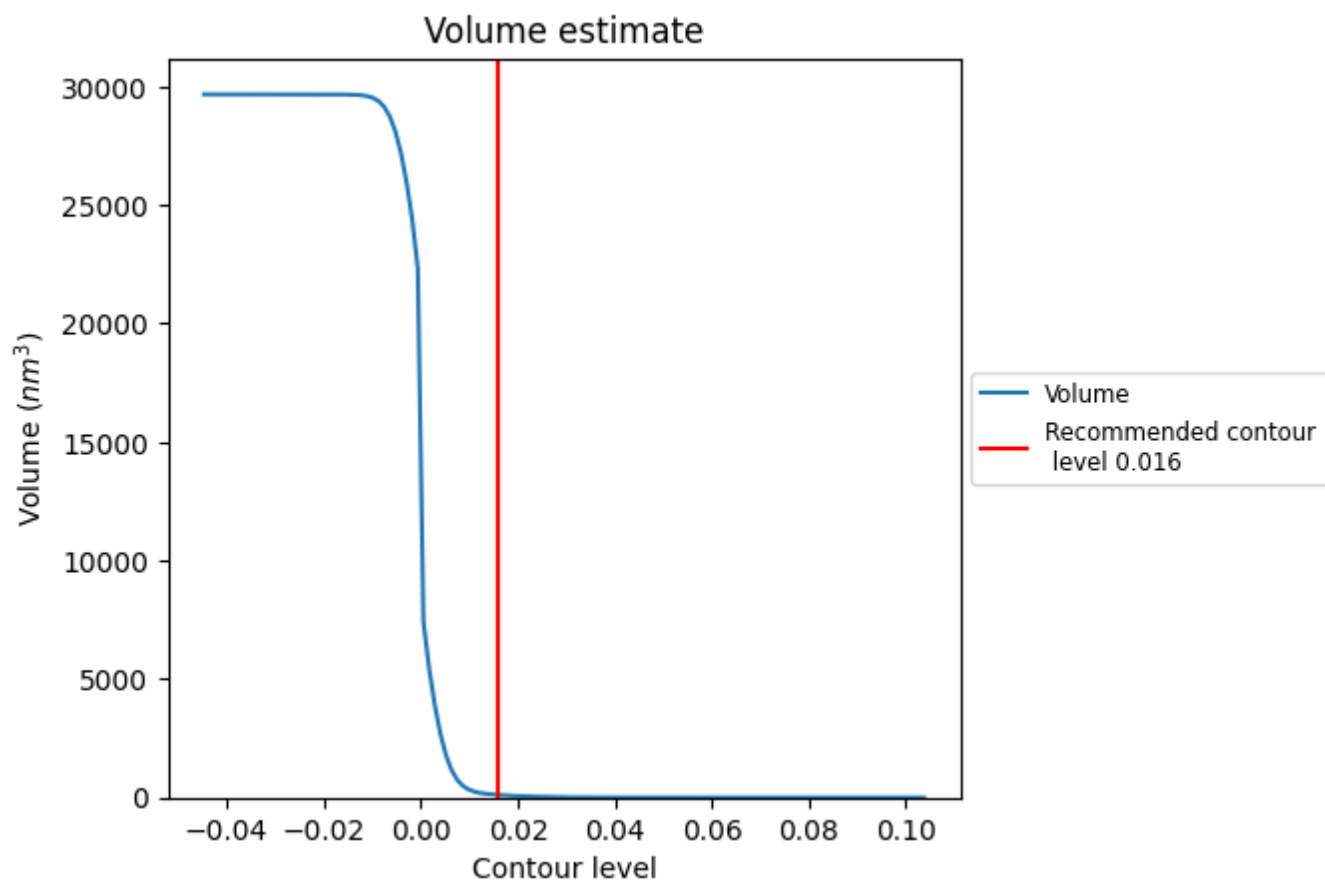
This section contains the results of statistical analysis of the map.

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.

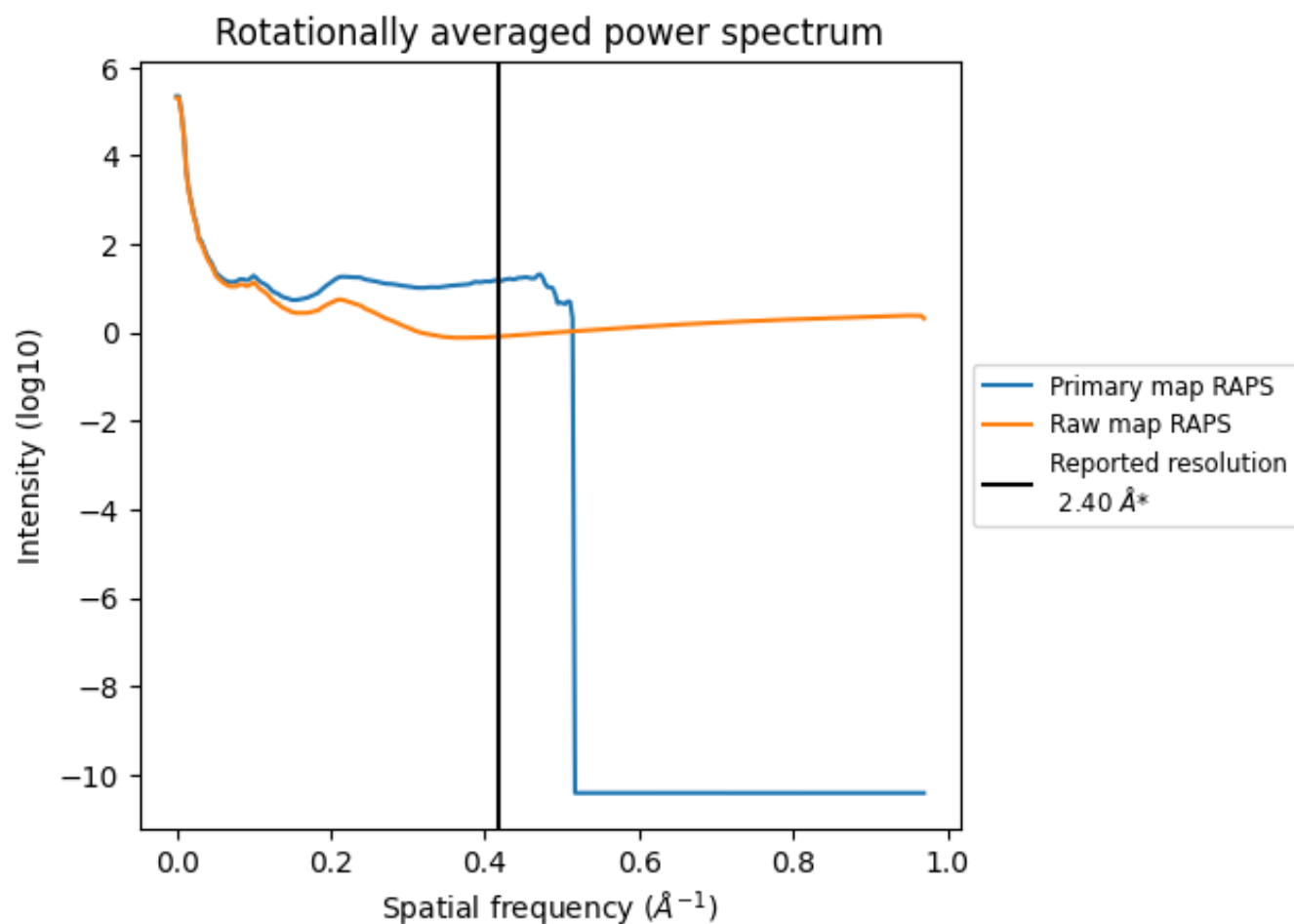
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 112 nm³; this corresponds to an approximate mass of 101 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

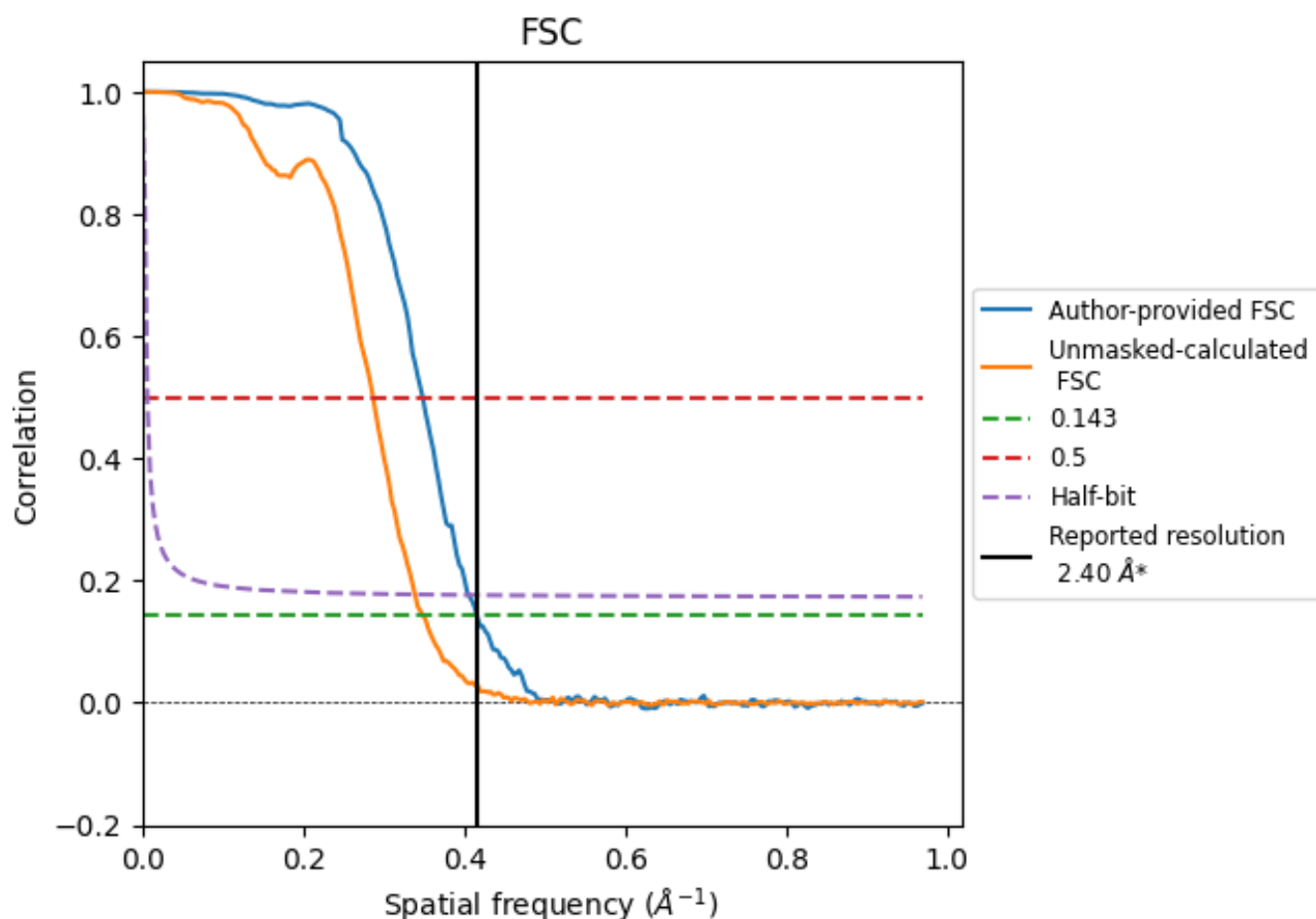


*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8.2 Resolution estimates [i](#)

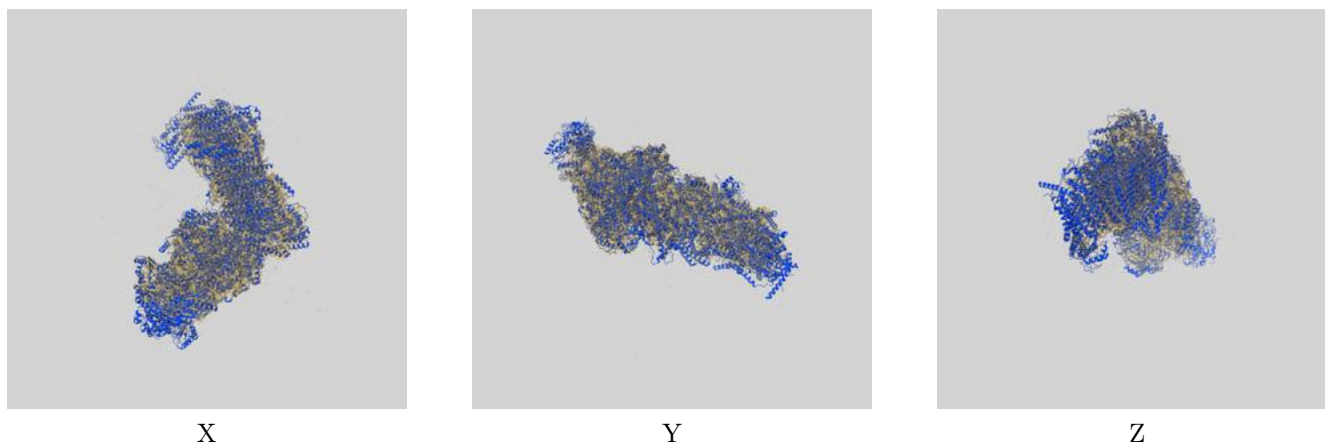
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.41	2.87	2.46
Unmasked-calculated*	2.87	3.49	2.95

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.87 differs from the reported value 2.4 by more than 10 %

9 Map-model fit [i](#)

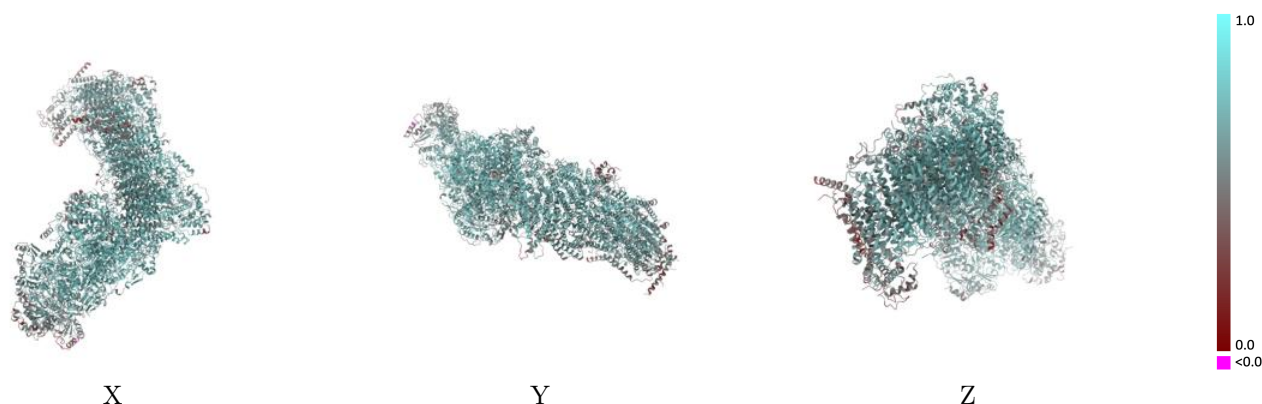
This section contains information regarding the fit between EMDB map EMD-12742 and PDB model 7O71. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

9.1 Map-model overlay [i](#)



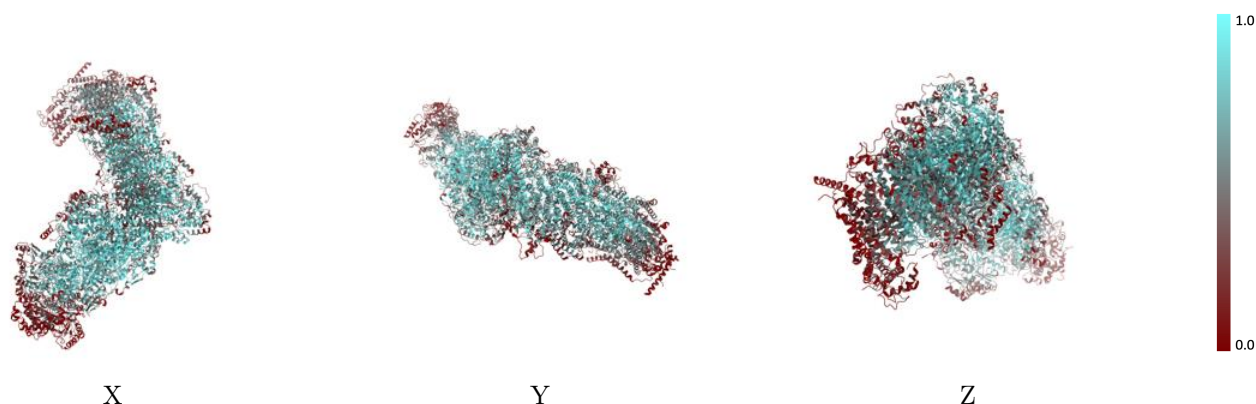
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



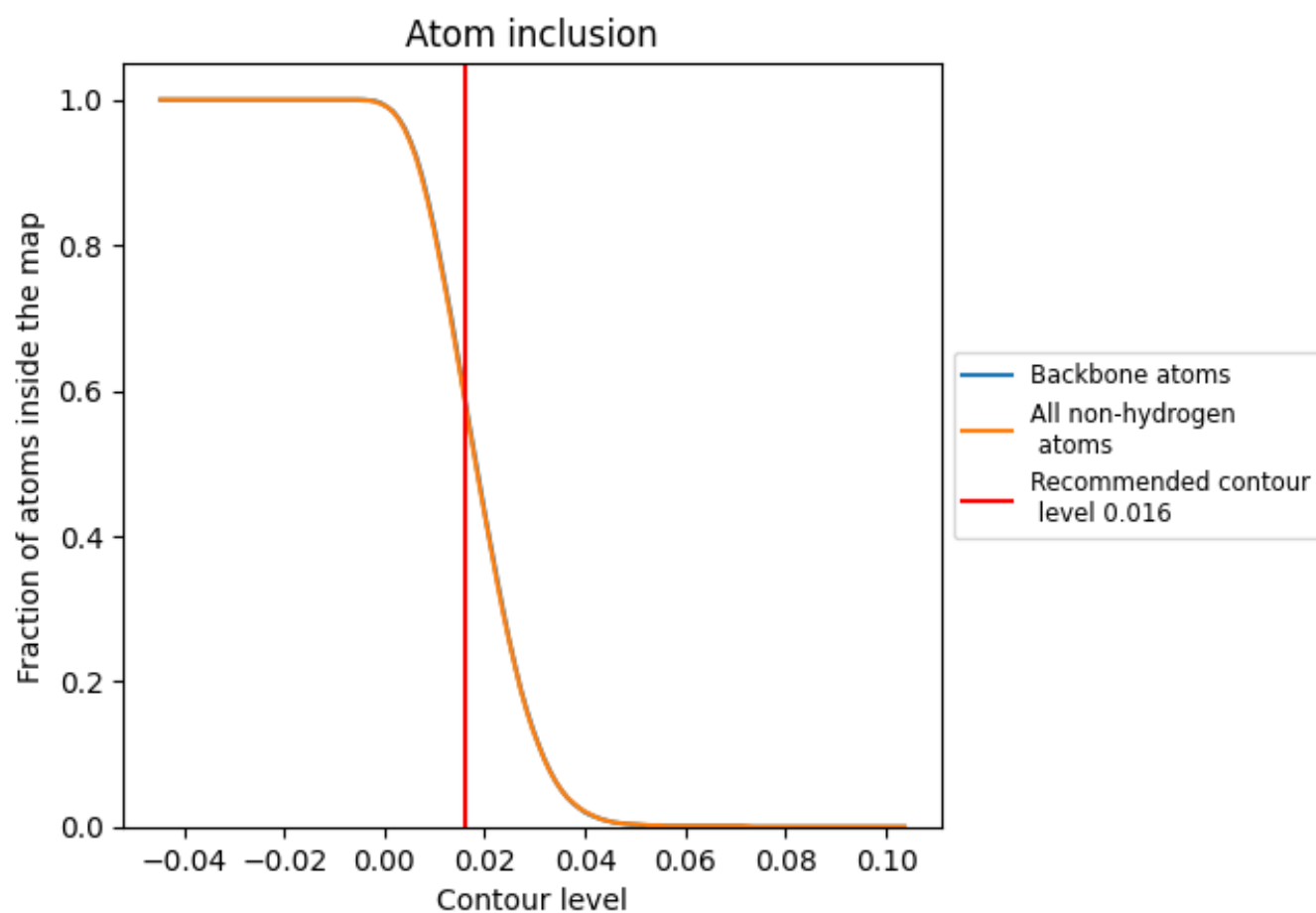
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.016).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 59% of all backbone atoms, 59% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5880	 0.6440
1	 0.7260	 0.6880
2	 0.8590	 0.7290
3	 0.5810	 0.6340
4	 0.7920	 0.7060
5	 0.5100	 0.6360
6	 0.5600	 0.6440
8	 0.1180	 0.4910
9	 0.4610	 0.5950
A	 0.6350	 0.6650
B	 0.3000	 0.5630
C	 0.8160	 0.7170
D	 0.7120	 0.6900
E	 0.5920	 0.6440
F	 0.6100	 0.6600
G	 0.8290	 0.7160
H	 0.2400	 0.5030
I	 0.8610	 0.7310
J	 0.4410	 0.5980
K	 0.8220	 0.7180
L	 0.7590	 0.7020
M	 0.7430	 0.6940
O	 0.0860	 0.3970
P	 0.5850	 0.6400
Q	 0.0900	 0.4420
R	 0.2720	 0.5240
S	 0.2550	 0.4720
U	 0.5590	 0.6450
W	 0.6160	 0.6560
X	 0.6650	 0.6740
Y	 0.7270	 0.6820
Z	 0.6250	 0.6560
a	 0.3340	 0.5810
b	 0.6560	 0.6750
c	 0.1180	 0.4570



Continued on next page...

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Chain	Atom inclusion	Q-score
d	 0.6180	 0.6570
e	 0.1010	 0.4670
f	 0.3030	 0.5590
g	 0.4910	 0.6220
h	 0.7380	 0.6880
i	 0.3720	 0.5910
j	 0.4910	 0.6040
n	 0.5060	 0.6310