



wwPDB EM Validation Summary Report ⓘ

Aug 25, 2026 – 05:05 am BST

PDB ID : 9F5Y / pdb_00009f5y
EMDB ID : EMD-50203
Title : Structure of the Chlamydomonas reinhardtii respiratory complex I from respiratory supercomplex
Authors : Waltz, F.; Righetto, R.; Kotecha, A.; Engel, B.D.
Deposited on : 2024-04-30
Resolution : 2.51 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

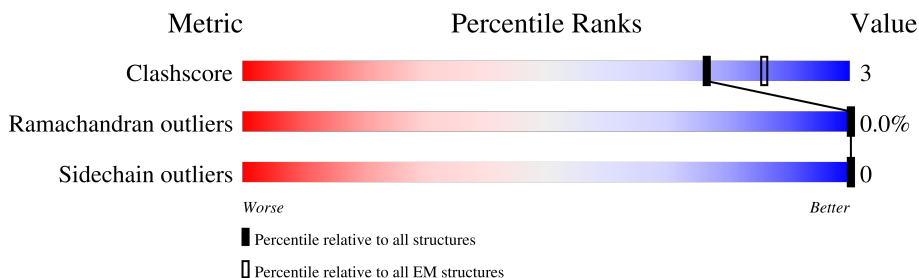
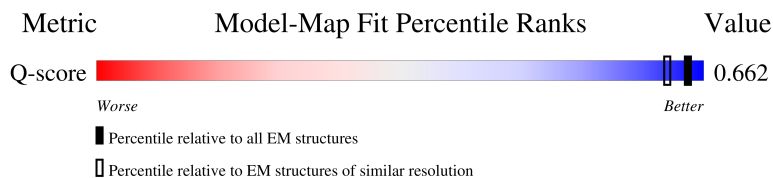
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

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 2.51 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.



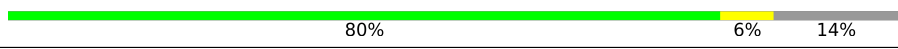
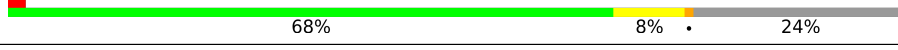
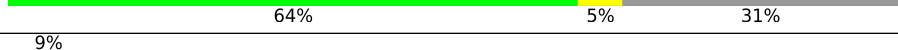
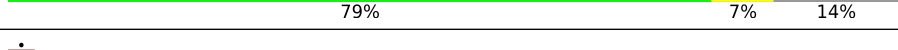
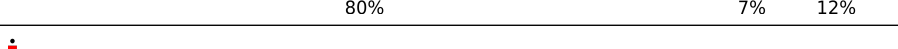
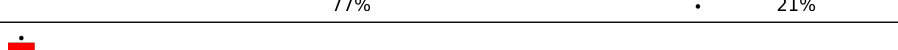
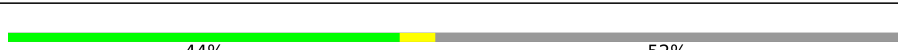
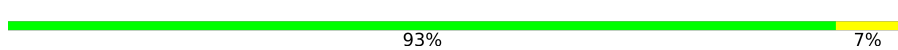
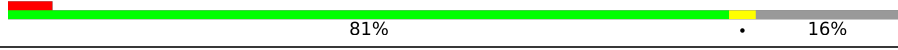
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7159 (2.01 - 3.01)

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	282	
2	B	484	
3	C	733	
4	D	282	

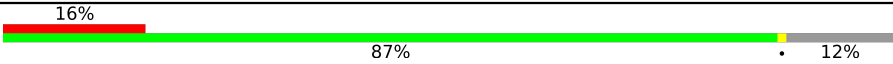
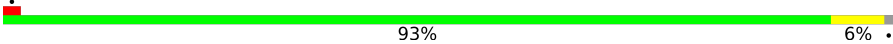
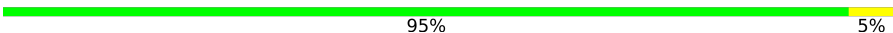
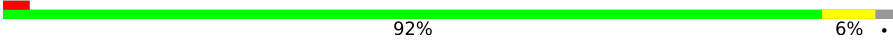
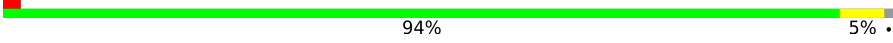
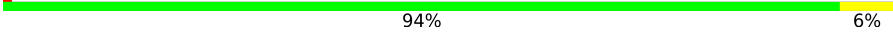
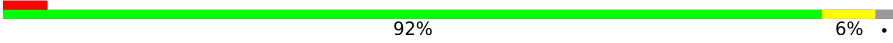
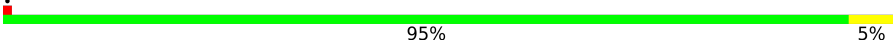
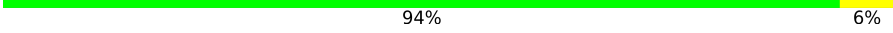
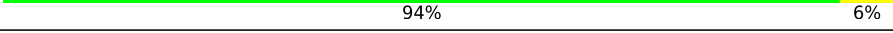
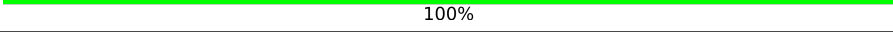
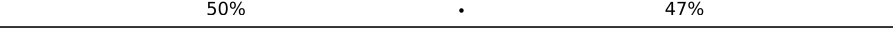
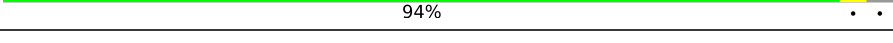
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Mol	Chain	Length	Quality of chain
5	E	467	
6	F	164	
7	G	231	
8	H	118	
9	I	165	
10	J	128	
10	r	128	
11	K	138	
12	L	187	
13	M	154	
14	N	156	
15	O	101	
16	P	397	
17	Q	292	
18	R	387	
19	S	279	
20	T	443	
21	U	227	
22	V	546	
23	W	162	
24	X	149	
25	Y	64	
26	Z	124	
27	a	129	
28	b	172	

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Mol	Chain	Length	Quality of chain
29	c	67	
30	d	86	
31	e	219	
32	f	65	
33	g	55	
34	h	142	
35	i	81	
36	j	86	
37	k	117	
38	l	121	
39	m	142	
40	n	106	
41	o	155	
42	p	130	
43	q	197	
44	s	312	
45	t	279	
46	u	229	
47	v	45	
48	w	109	
49	x	157	
50	y	118	

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 75117 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 24 kD subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	239	Total	C	N	O	S	0	0
			1839	1165	311	352	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	435	Total	C	N	O	S	0	0
			3331	2099	592	614	26		

- Molecule 3 is a protein called NADH:ubiquinone oxidoreductase 78 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	688	Total	C	N	O	S	0	0
			5175	3235	936	972	32		

- Molecule 4 is a protein called NADH:ubiquinone oxidoreductase 30kDa subunit domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	216	Total	C	N	O	S	0	0
			1790	1156	301	325	8		

- Molecule 5 is a protein called NADH:ubiquinone oxidoreductase 49 kD subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	383	Total	C	N	O	S	0	0
			3085	1971	537	554	23		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	157	Total	C	N	O	S	0	0
			1225	787	211	215	12		

- Molecule 7 is a protein called NADH:ubiquinone oxidoreductase subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	199	Total	C	N	O	S	0	0
			1615	1007	281	315	12		

- Molecule 8 is a protein called B14.5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	90	Total	C	N	O	S	0	0
			750	486	129	132	3		

- Molecule 9 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 18 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	135	Total	C	N	O	S	0	0
			1044	661	173	208	2		

- Molecule 10 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	84	Total	C	N	O	S	0	0
			640	404	100	133	3		
10	r	88	Total	C	N	O	S	0	0
			663	419	104	137	3		

- Molecule 11 is a protein called NADH:ubiquinone oxidoreductase B14 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	119	Total	C	N	O	S	0	0
			986	640	173	168	5		

- Molecule 12 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	164	Total	C	N	O	S	0	0
			1275	803	221	245	6		

- Molecule 13 is a protein called NADH:ubiquinone oxidoreductase 13 kD-like subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	121	Total	C	N	O	S	0	0
			913	582	150	178	3		

- Molecule 14 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	150	Total	C	N	O	S	0	0
			1235	791	214	227	3		

- Molecule 15 is a protein called NADH:ubiquinone oxidoreductase B8 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	100	Total	C	N	O	S	0	0
			761	471	138	147	5		

- Molecule 16 is a protein called Putative NADH:ubiquinone oxidoreductase 39 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	363	Total	C	N	O	S	0	0
			2823	1793	489	527	14		

- Molecule 17 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	286	Total	C	N	O	S	0	0
			2179	1448	338	374	19		

- Molecule 18 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	387	Total	C	N	O	S	0	0
			3014	2026	467	496	25		

- Molecule 19 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	134	Total	C	N	O	S	0	0
			1071	715	159	192	5		

- Molecule 20 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	443	Total	C	N	O	S	0	0
			3434	2321	526	557	30		

- Molecule 21 is a protein called NADH dehydrogenase subunit 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	105	Total	C	N	O	S	0	0
			805	524	124	146	11		

- Molecule 22 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	546	Total	C	N	O	S	0	0
			4152	2731	668	716	37		

- Molecule 23 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	157	Total	C	N	O	S	0	0
			1210	820	180	201	9		

- Molecule 24 is a protein called ASH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	125	Total	C	N	O	S	0	0
			1037	685	168	178	6		

- Molecule 25 is a protein called P9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	54	Total	C	N	O	S	0	0
			405	256	74	74	1		

- Molecule 26 is a protein called KFYI.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	107	Total	C	N	O	S	0	0
			861	555	149	152	5		

- Molecule 27 is a protein called AGGG.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	82	Total	C	N	O	S	0	0
			674	440	109	123	2		

- Molecule 28 is a protein called ESSS.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	144	Total	C	N	O	S	0	0
			1169	756	192	214	7		

- Molecule 29 is a protein called B9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	59	Total	C	N	O	S	0	0
			453	298	71	79	5		

- Molecule 30 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 10 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	85	Total	C	N	O	S	0	0
			699	456	120	120	3		

- Molecule 31 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 23 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	218	Total	C	N	O	S	0	0
			1639	1055	279	297	8		

- Molecule 32 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 7.5 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	64	Total	C	N	O	S	0	0
			532	345	93	92	2		

- Molecule 33 is a protein called Mitochondrial putative NADH:ubiquinone oxidoreductase 6.5 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	50	Total	C	N	O	S	0	0
			416	277	73	65	1		

- Molecule 34 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 13 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	108	Total	C	N	O	S	0	0
			915	597	157	159	2		

- Molecule 35 is a protein called NADH:ubiquinone oxidoreductase 15 kDa subunit-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	76	Total	C	N	O	S	0	0
			633	387	122	116	8		

- Molecule 36 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	85	Total	C	N	O	S	0	0
			712	449	131	125	7		

- Molecule 37 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	117	Total	C	N	O	S	0	0
			984	631	176	173	4		

- Molecule 38 is a protein called NADH:ubiquinone oxidoreductase 20,9 kD-like subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	116	Total	C	N	O	S	0	0
			904	589	150	161	4		

- Molecule 39 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	138	Total	C	N	O	S	0	0
			1126	724	205	193	4		

- Molecule 40 is a protein called Putative NADH:ubiquinone oxidoreductase 12.5 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	104	Total	C	N	O	S	0	0
			864	547	152	159	6		

- Molecule 41 is a protein called Putative NADH:ubiquinone oxidoreductase 17.8 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	o	152	Total	C	N	O	S	0	0
			1240	771	238	228	3		

- Molecule 42 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 16 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	p	129	Total	C	N	O	S	0	0
			1069	670	192	204	3		

- Molecule 43 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 19 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	157	Total	C	N	O	S	0	0
			1268	818	217	229	4		

- Molecule 44 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 32 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	312	Total	C	N	O	S	0	0
			2302	1451	407	435	9		

- Molecule 45 is a protein called CAG2 - CA-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	t	253	Total	C	N	O	S	0	0
			1997	1268	357	367	5		

- Molecule 46 is a protein called CAG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	228	Total	C	N	O	S	0	0
			1698	1063	300	327	8		

- Molecule 47 is a protein called P10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	v	45	Total	C	N	O	S	0	0
			361	233	61	66	1		

- Molecule 48 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 9 kDa sub-unit.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	w	64	Total	C	N	O	S	0	0
			508	334	78	91	5		

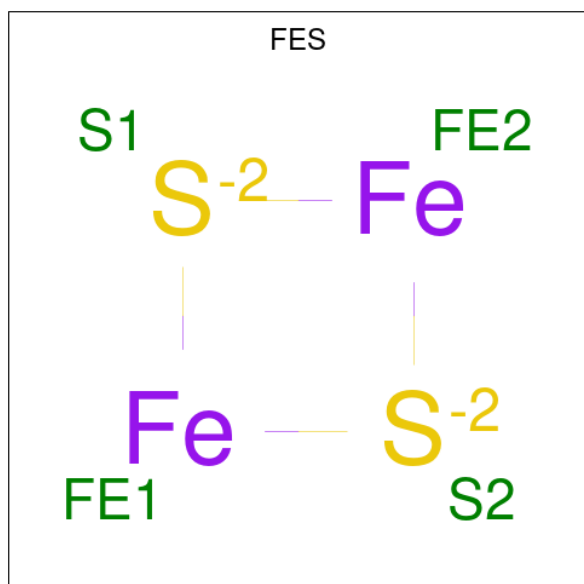
- Molecule 49 is a protein called NUOP8.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	x	83	Total	C	N	O	S	0	0
			699	467	110	121	1		

- Molecule 50 is a protein called NUOP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	114	Total	C	N	O	S	0	0
			932	615	154	161	2		

- Molecule 51 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



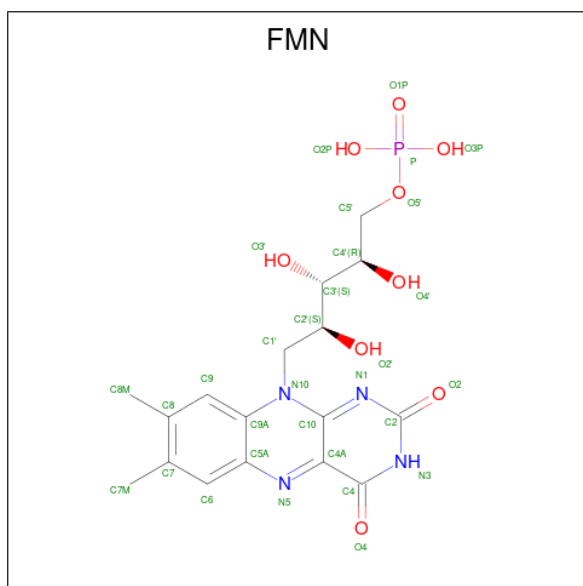
Mol	Chain	Residues	Atoms			AltConf
51	A	1	Total	Fe	S	0
			4	2	2	

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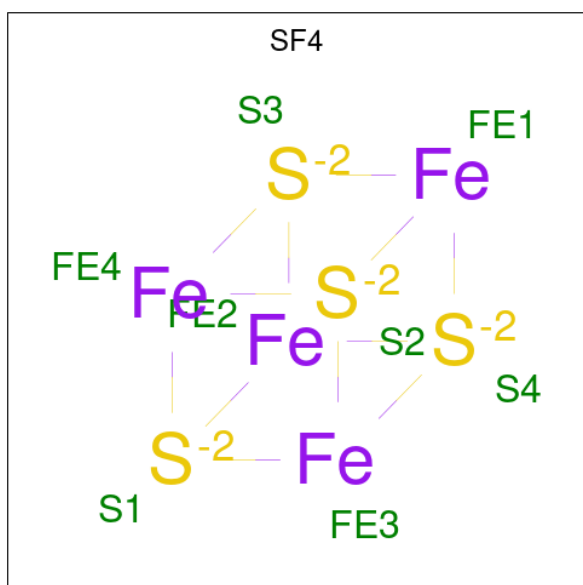
Mol	Chain	Residues	Atoms			AltConf
51	C	1	Total	Fe	S	0
			4	2	2	

- Molecule 52 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



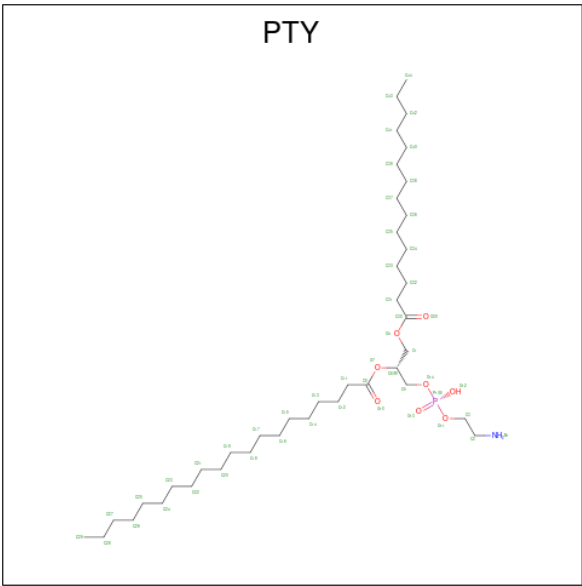
Mol	Chain	Residues	Atoms					AltConf
52	B	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 53 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			AltConf
53	B	1	Total	Fe	S	0
			8	4	4	
53	C	1	Total	Fe	S	0
			8	4	4	
53	C	1	Total	Fe	S	0
			8	4	4	
53	F	1	Total	Fe	S	0
			8	4	4	
53	G	1	Total	Fe	S	0
			8	4	4	
53	G	1	Total	Fe	S	0
			8	4	4	

- Molecule 54 is PHOSPHATIDYLETHANOLAMINE (CCD ID: PTY) (formula: C₄₀H₈₀NO₈P).



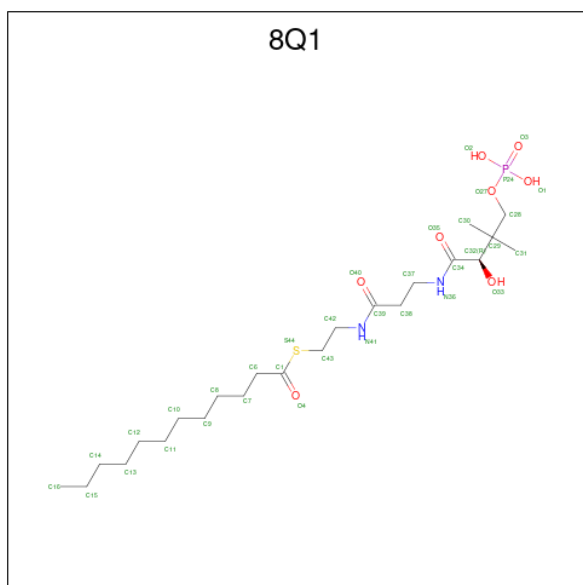
Mol	Chain	Residues	Atoms					AltConf
54	G	1	Total	C	N	O	P	0
			43	33	1	8	1	
54	R	1	Total	C	N	O	P	0
			34	24	1	8	1	
54	R	1	Total	C	N	O	P	0
			44	34	1	8	1	
54	R	1	Total	C	N	O	P	0
			40	30	1	8	1	
54	S	1	Total	C	N	O	P	0
			46	36	1	8	1	
54	T	1	Total	C	N	O	P	0
			50	40	1	8	1	

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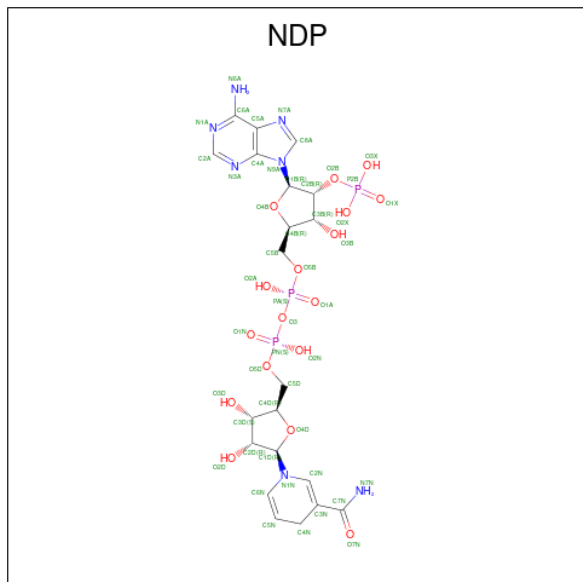
Mol	Chain	Residues	Atoms					AltConf
54	T	1	Total	C	N	O	P	0
			28	18	1	8	1	
54	T	1	Total	C	N	O	P	0
			26	16	1	8	1	
54	V	1	Total	C	N	O	P	0
			40	30	1	8	1	
54	V	1	Total	C	N	O	P	0
			50	40	1	8	1	
54	V	1	Total	C	N	O	P	0
			35	25	1	8	1	
54	e	1	Total	C	N	O	P	0
			25	15	1	8	1	
54	e	1	Total	C	N	O	P	0
			43	33	1	8	1	
54	h	1	Total	C	N	O	P	0
			46	36	1	8	1	
54	x	1	Total	C	N	O	P	0
			50	40	1	8	1	

- Molecule 55 is S-[2-({N-[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-beta-alanyl}amino)ethyl] dodecanethioate (CCD ID: 8Q1) (formula: C₂₃H₄₅N₂O₈PS).



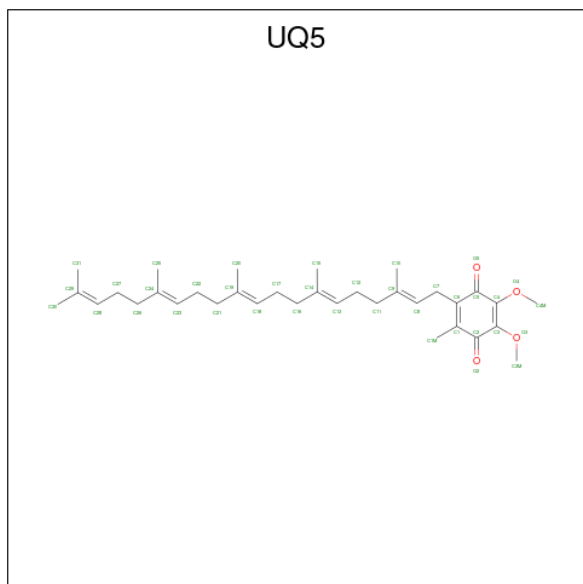
Mol	Chain	Residues	Atoms						AltConf
55	J	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	
55	r	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	

- Molecule 56 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



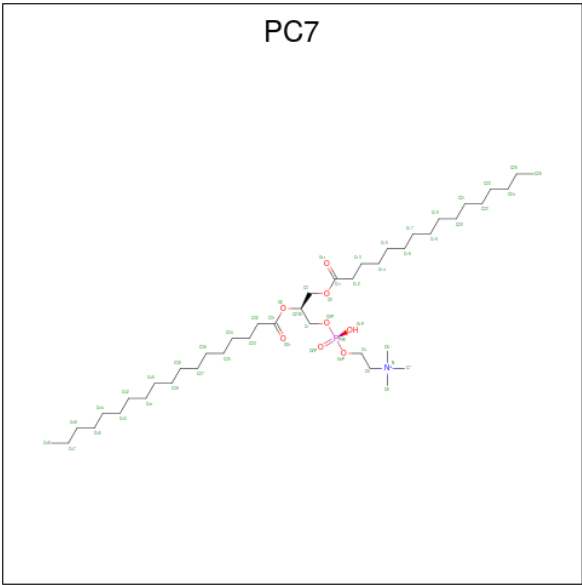
Mol	Chain	Residues	Atoms					AltConf
56	P	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 57 is 2,3-DIMETHOXY-5-METHYL-6-(3,11,15,19-TETRAMETHYL-EICOSA-2,6,10,14,18-PENTAENYL)-[1,4]BENZOQUINONE (CCD ID: UQ5) (formula: $C_{34}H_{50}O_4$).



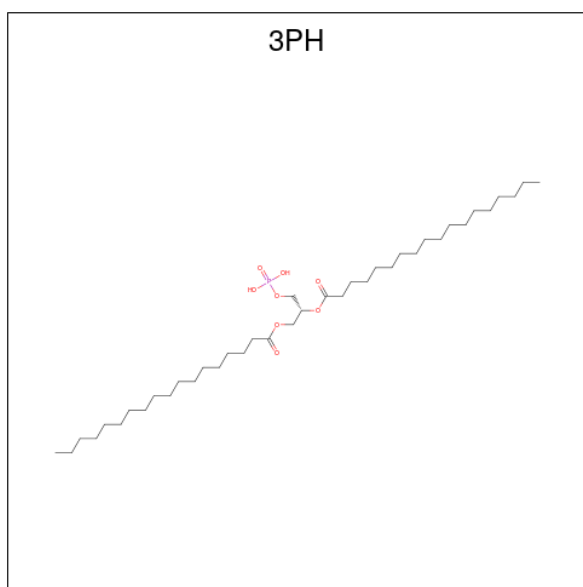
Mol	Chain	Residues	Atoms			AltConf
57	Q	1	Total	C	O	0
			38	34	4	

- Molecule 58 is (7S)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITOYLOXY) METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSAN-1-AMINIUM 4-OXIDE (CCD ID: PC7) (formula: C₄₂H₈₅NO₈P).



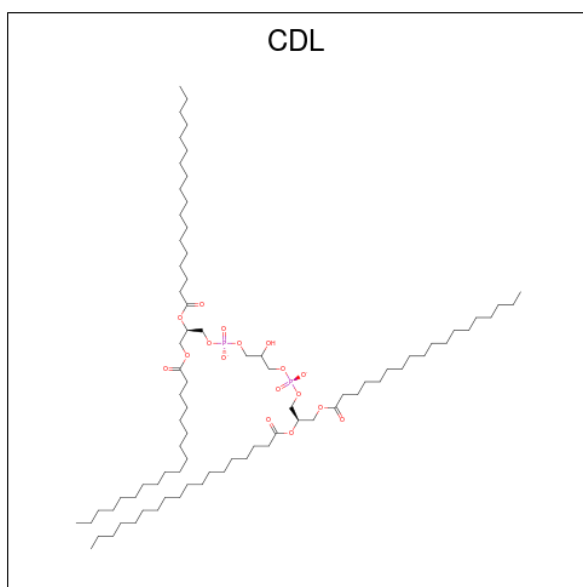
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
58	Q	1	Total 33	23	1	8	1	0
58	R	1	Total 44	34	1	8	1	0
58	T	1	Total 52	42	1	8	1	0
58	u	1	Total 42	32	1	8	1	0

- Molecule 59 is 1,2-DIACYL-GLYCEROL-3-SN-PHOSPHATE (CCD ID: 3PH) (formula: C₃₉H₇₇O₈P).



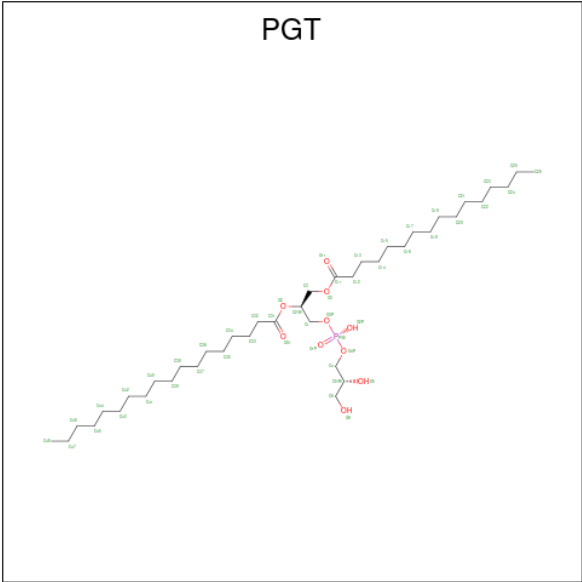
Mol	Chain	Residues	Atoms				AltConf
59	R	1	Total	C	O	P	0
			32	23	8	1	
59	S	1	Total	C	O	P	0
			37	28	8	1	
59	V	1	Total	C	O	P	0
			42	33	8	1	
59	V	1	Total	C	O	P	0
			41	32	8	1	
59	c	1	Total	C	O	P	0
			48	39	8	1	
59	g	1	Total	C	O	P	0
			37	28	8	1	
59	h	1	Total	C	O	P	0
			45	36	8	1	
59	w	1	Total	C	O	P	0
			45	36	8	1	

- Molecule 60 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



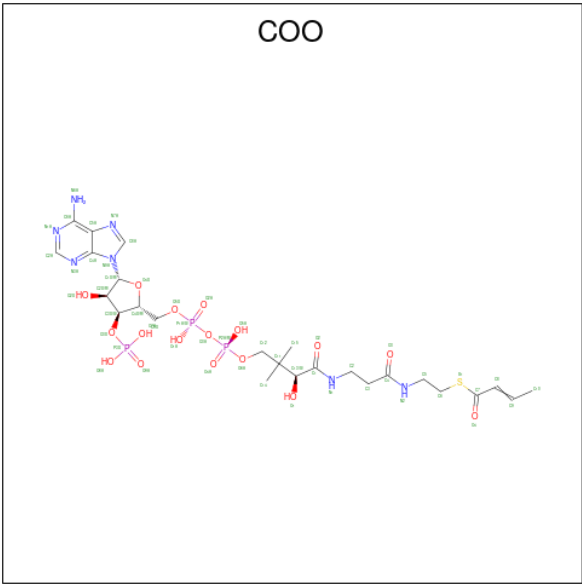
Mol	Chain	Residues	Atoms				AltConf
60	R	1	Total	C	O	P	0
			63	44	17	2	
60	V	1	Total	C	O	P	0
			64	45	17	2	
60	W	1	Total	C	O	P	0
			95	76	17	2	
60	h	1	Total	C	O	P	0
			77	58	17	2	
60	u	1	Total	C	O	P	0
			83	64	17	2	
60	u	1	Total	C	O	P	0
			71	52	17	2	
60	x	1	Total	C	O	P	0
			92	73	17	2	
60	y	1	Total	C	O	P	0
			55	36	17	2	

- Molecule 61 is (1S)-2-[[[(2R)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY-1-[(PALMITOYLOXY)METHYL]ETHYL STEARATE (CCD ID: PGT) (formula: C₄₀H₇₉O₁₀P).



Mol	Chain	Residues	Atoms				AltConf
61	T	1	Total	C	O	P	0
			48	37	10	1	
61	T	1	Total	C	O	P	0
			40	29	10	1	
61	b	1	Total	C	O	P	0
			44	33	10	1	
61	l	1	Total	C	O	P	0
			51	40	10	1	

- Molecule 62 is CROTONYL COENZYME A (CCD ID: COO) (formula: C₂₅H₄₀N₇O₁₇P₃S).



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

- Molecule 63 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
63	s	1	Total	Zn	0
			1	1	

- Molecule 64 is water.

Mol	Chain	Residues	Atoms		AltConf
64	A	24	Total	O	0
			24	24	
64	B	66	Total	O	0
			66	66	
64	C	168	Total	O	0
			168	168	
64	D	66	Total	O	0
			66	66	
64	E	87	Total	O	0
			87	87	
64	F	39	Total	O	0
			39	39	
64	G	62	Total	O	0
			62	62	
64	H	16	Total	O	0
			16	16	
64	I	19	Total	O	0
			19	19	
64	K	16	Total	O	0
			16	16	
64	L	68	Total	O	0
			68	68	
64	M	30	Total	O	0
			30	30	
64	N	53	Total	O	0
			53	53	
64	O	6	Total	O	0
			6	6	
64	P	69	Total	O	0
			69	69	
64	Q	24	Total	O	0
			24	24	

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Mol	Chain	Residues	Atoms		AltConf
64	R	64	Total 64	O 64	0
64	S	22	Total 22	O 22	0
64	T	85	Total 85	O 85	0
64	U	14	Total 14	O 14	0
64	V	99	Total 99	O 99	0
64	W	25	Total 25	O 25	0
64	X	50	Total 50	O 50	0
64	Y	4	Total 4	O 4	0
64	Z	20	Total 20	O 20	0
64	a	6	Total 6	O 6	0
64	b	24	Total 24	O 24	0
64	c	1	Total 1	O 1	0
64	d	12	Total 12	O 12	0
64	e	55	Total 55	O 55	0
64	f	10	Total 10	O 10	0
64	g	7	Total 7	O 7	0
64	h	38	Total 38	O 38	0
64	i	30	Total 30	O 30	0
64	j	29	Total 29	O 29	0
64	k	51	Total 51	O 51	0
64	l	17	Total 17	O 17	0

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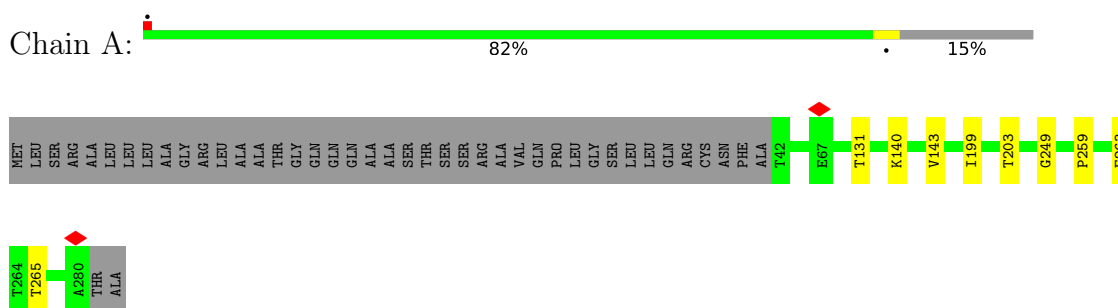
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Mol	Chain	Residues	Atoms		AltConf
64	m	32	Total 32	O 32	0
64	n	7	Total 7	O 7	0
64	o	51	Total 51	O 51	0
64	p	21	Total 21	O 21	0
64	q	24	Total 24	O 24	0
64	r	12	Total 12	O 12	0
64	s	39	Total 39	O 39	0
64	t	55	Total 55	O 55	0
64	u	41	Total 41	O 41	0
64	v	2	Total 2	O 2	0
64	w	16	Total 16	O 16	0
64	x	22	Total 22	O 22	0
64	y	29	Total 29	O 29	0

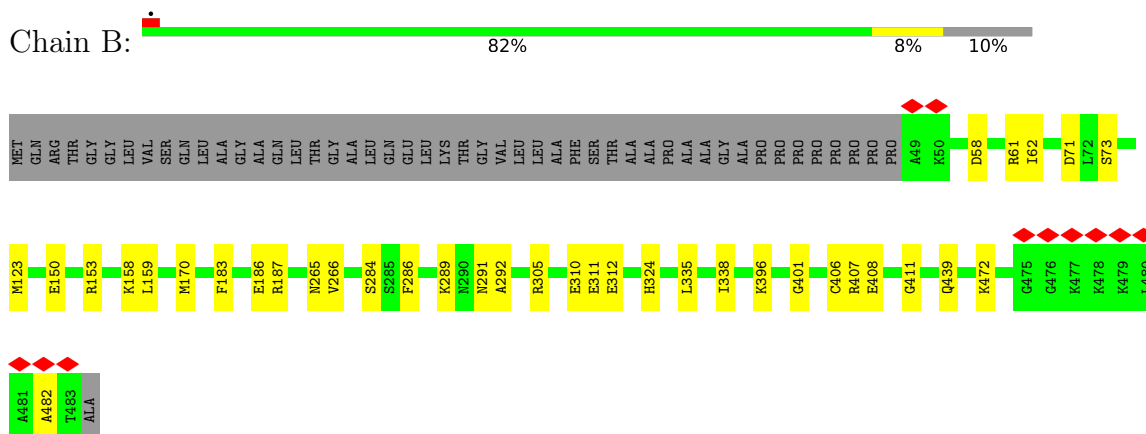
3 Residue-property plots [i](#)

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.

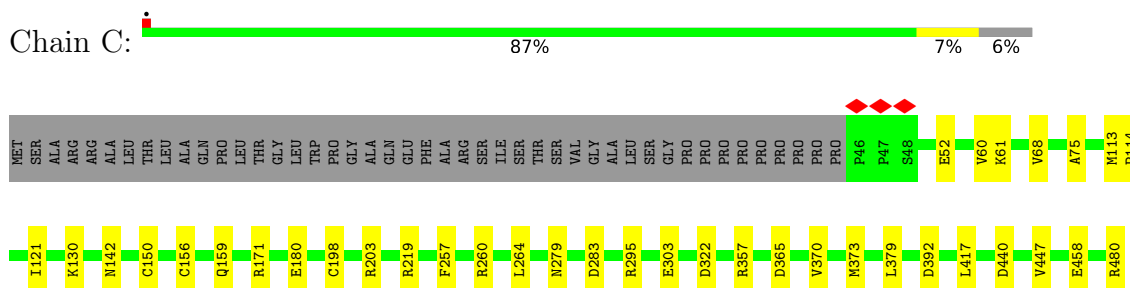
- Molecule 1: NADH:ubiquinone oxidoreductase 24 kD subunit



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

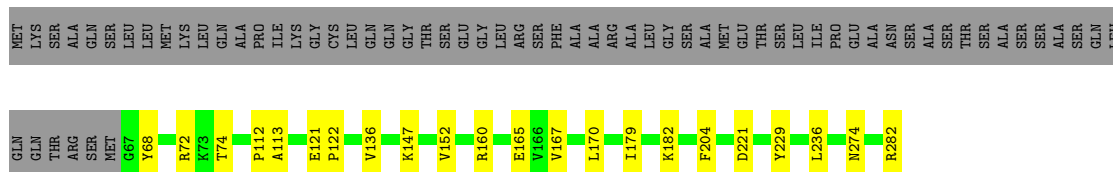


- Molecule 3: NADH:ubiquinone oxidoreductase 78 kDa subunit



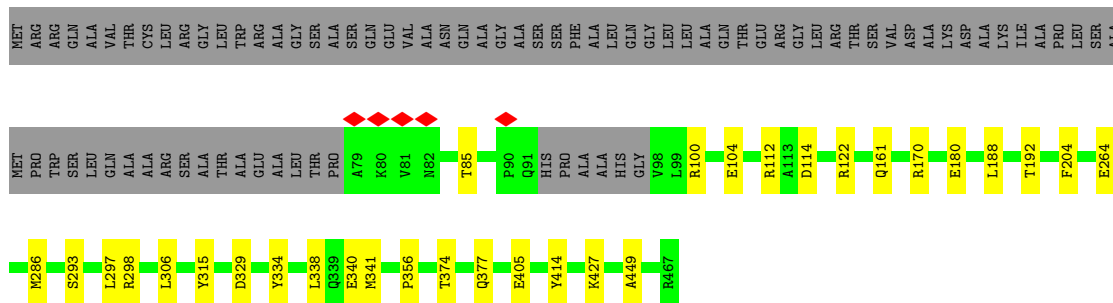
- Molecule 4: NADH:ubiquinone oxidoreductase 30kDa subunit domain-containing protein

Chain D:  69% 8% 23%



- Molecule 5: NADH:ubiquinone oxidoreductase 49 kD subunit

Chain E:  75% 7% 18%



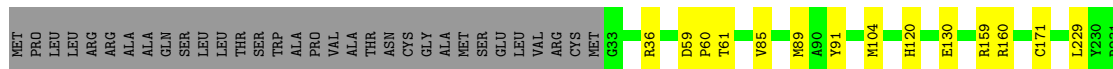
- Molecule 6: NADH:ubiquinone oxidoreductase subunit 10

Chain F: 88% 7% .



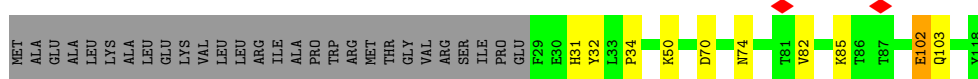
- Molecule 7: NADH:ubiquinone oxidoreductase subunit 8

Chain G:  80% 6% 14%



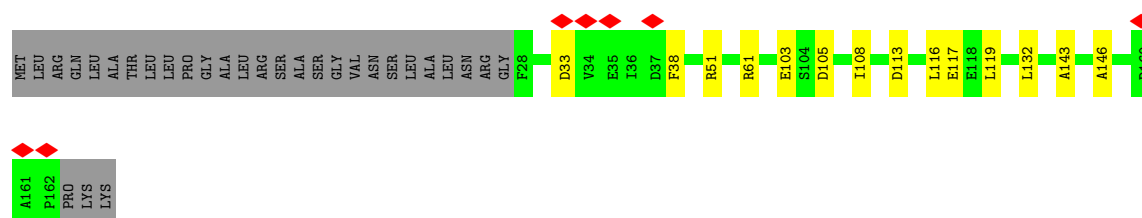
- Molecule 8: B14.5a

Chain H: 68% 8% 24%



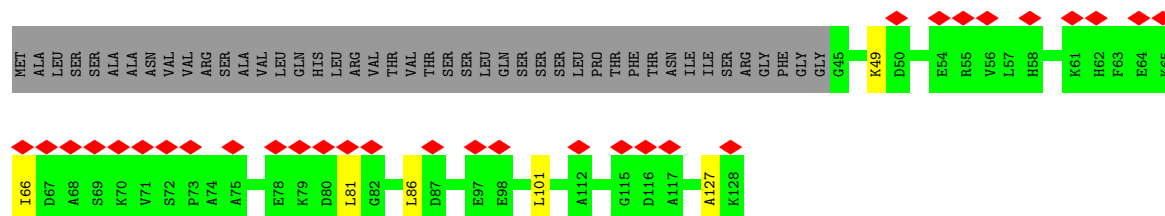
- Molecule 9: Mitochondrial NADH:ubiquinone oxidoreductase 18 kDa subunit

Chain I: 



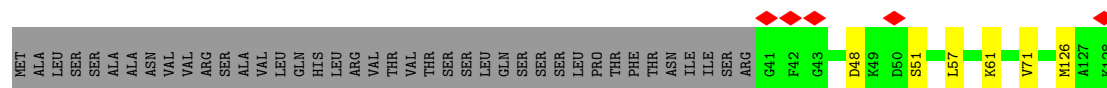
- Molecule 10: Acyl carrier protein

Chain J: 



- Molecule 10: Acyl carrier protein

Chain r: 



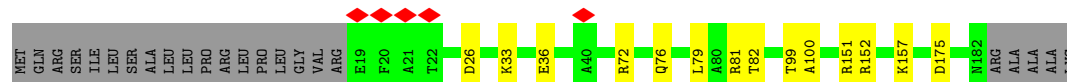
- Molecule 11: NADH:ubiquinone oxidoreductase B14 subunit

Chain K: 



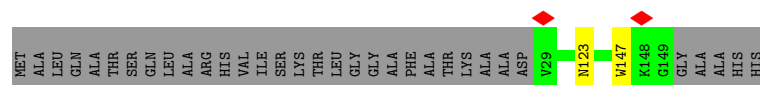
- Molecule 12: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

Chain L: 



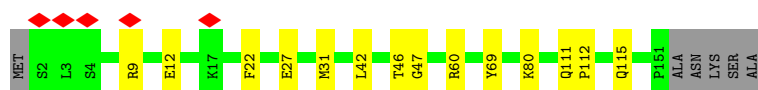
- Molecule 13: NADH:ubiquinone oxidoreductase 13 kD-like subunit

Chain M: 



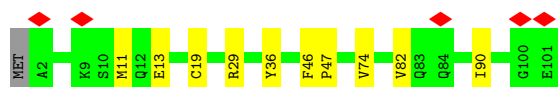
- Molecule 14: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

Chain N:  87% 9%



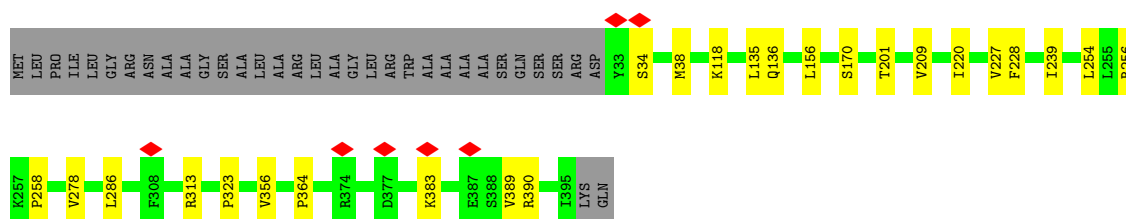
- Molecule 15: NADH:ubiquinone oxidoreductase B8 subunit

Chain O:  5% 89% 10%



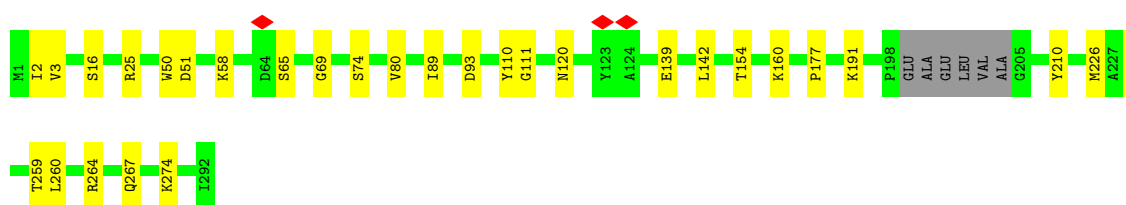
- Molecule 16: Putative NADH:ubiquinone oxidoreductase 39 kDa subunit

Chain P:  85% 6% 9%



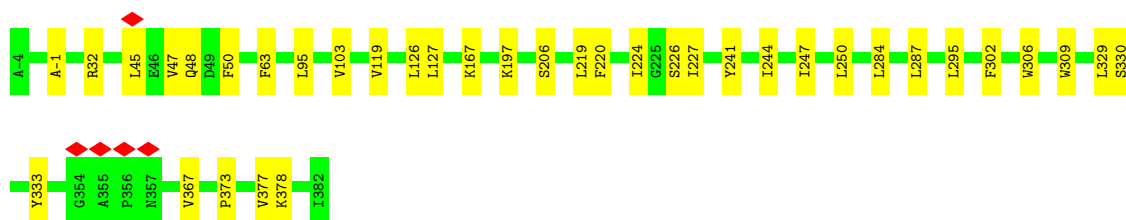
- Molecule 17: NADH-ubiquinone oxidoreductase chain 1

Chain Q:  88% 10%



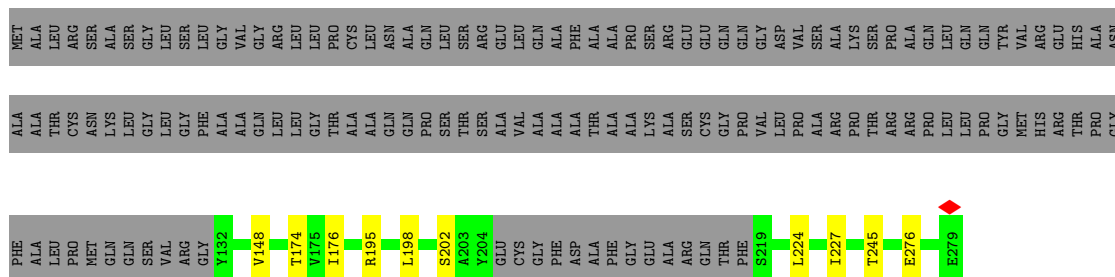
- Molecule 18: NADH-ubiquinone oxidoreductase chain 2

Chain R:  90% 10%



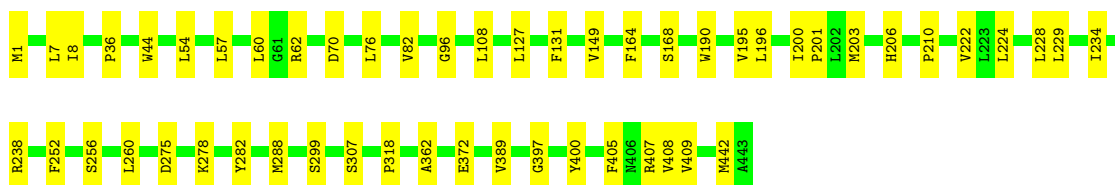
- Molecule 19: NADH-ubiquinone oxidoreductase chain 3

Chain S:  44% 52%



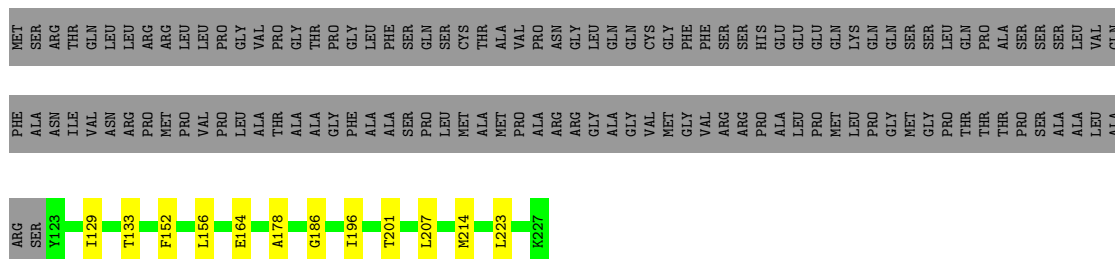
- Molecule 20: NADH-ubiquinone oxidoreductase chain 4

Chain T:  88% 12%



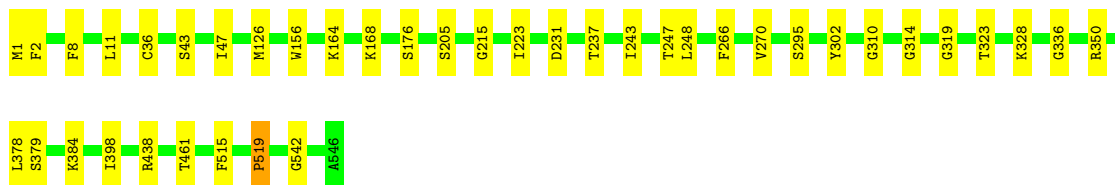
- Molecule 21: NADH dehydrogenase subunit 4L

Chain U:  41% 5% 54%



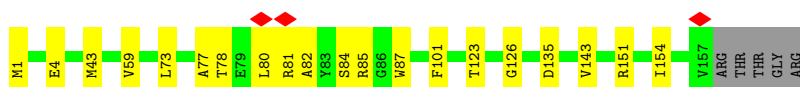
- Molecule 22: NADH-ubiquinone oxidoreductase chain 5

Chain V:  93% 7%



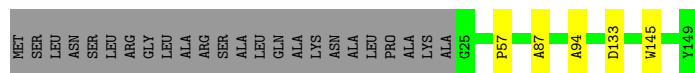
- Molecule 23: NADH-ubiquinone oxidoreductase chain 6

Chain W:  85% 12%



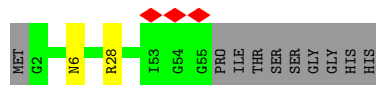
- Molecule 24: ASHI

Chain X:  81% 16%



- Molecule 25: P9

Chain Y:  5% 81% 16%



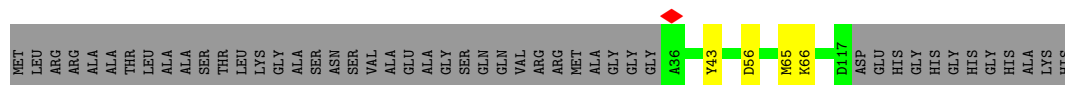
- Molecule 26: KFYI

Chain Z:  83% 14%



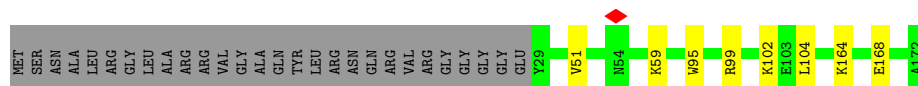
- Molecule 27: AGGG

Chain a:  60% 36%



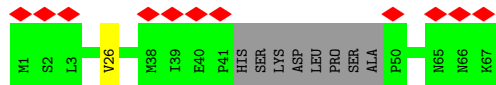
- Molecule 28: ESSS

Chain b:  79% 5% 16%

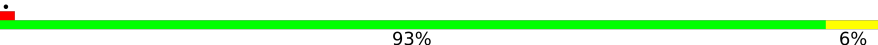


- Molecule 29: B9

Chain c:  16% 87% 12%

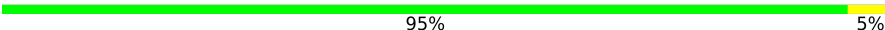


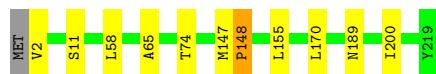
- Molecule 30: Mitochondrial NADH:ubiquinone oxidoreductase 10 kDa subunit

Chain d:  93% 6%



- Molecule 31: Mitochondrial NADH:ubiquinone oxidoreductase 23 kDa subunit

Chain e:  95% 5%



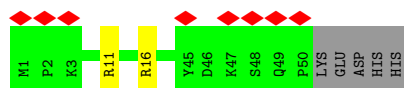
- Molecule 32: Mitochondrial NADH:ubiquinone oxidoreductase 7.5 kDa subunit

Chain f:  92% 6%



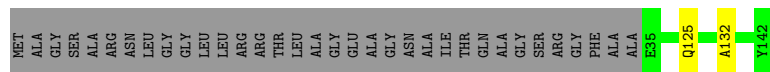
- Molecule 33: Mitochondrial putative NADH:ubiquinone oxidoreductase 6.5 kDa subunit

Chain g:  15% 87% 9%



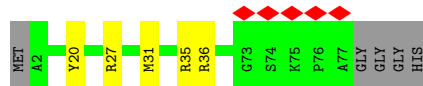
- Molecule 34: Mitochondrial NADH:ubiquinone oxidoreductase 13 kDa subunit

Chain h:  75% 24%

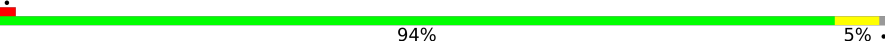


- Molecule 35: NADH:ubiquinone oxidoreductase 15 kDa subunit-like

Chain i:  6% 88% 6% 6%

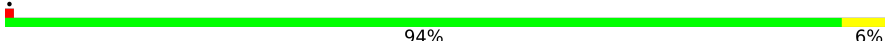


- Molecule 36: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7

Chain j:  94% 5%

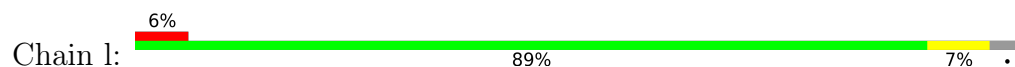


- Molecule 37: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9

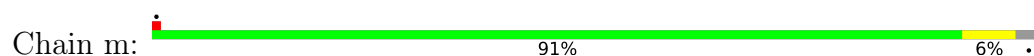
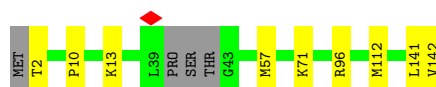
Chain k:  94% 6%



- Molecule 38: NADH:ubiquinone oxidoreductase 20,9 kD-like subunit



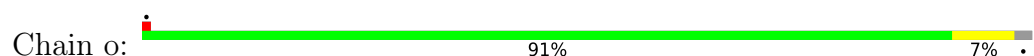
- Molecule 39: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13



- Molecule 40: Putative NADH:ubiquinone oxidoreductase 12.5 kDa subunit



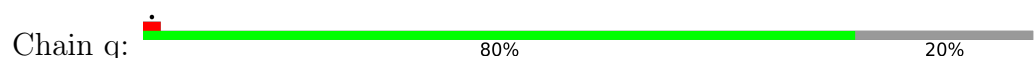
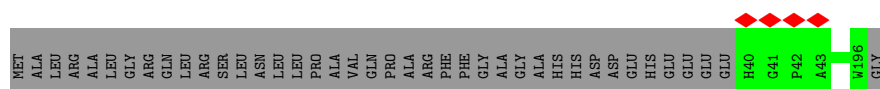
- Molecule 41: Putative NADH:ubiquinone oxidoreductase 17.8 kDa subunit



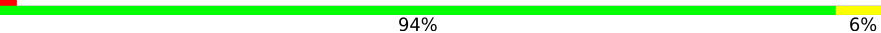
- Molecule 42: Mitochondrial NADH:ubiquinone oxidoreductase 16 kDa subunit



- Molecule 43: Mitochondrial NADH:ubiquinone oxidoreductase 19 kDa subunit



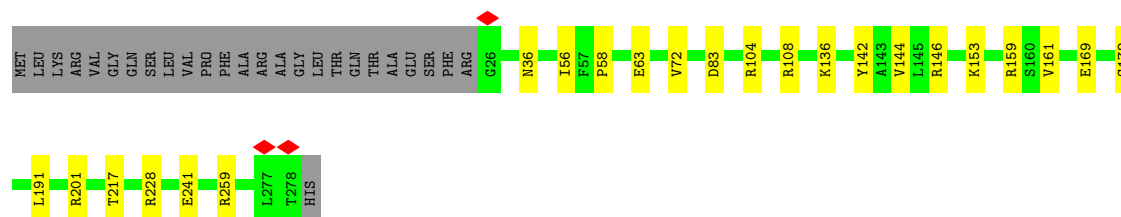
- Molecule 44: Mitochondrial NADH:ubiquinone oxidoreductase 32 kDa subunit

Chain s:  94% 6%

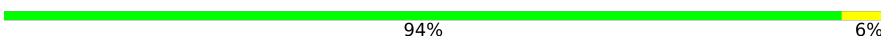


- Molecule 45: CAG2 - CA-like

Chain t:  82% 8% 9%



- Molecule 46: CAG1

Chain u:  94% 6%



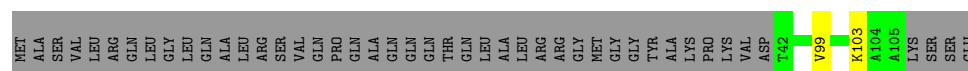
- Molecule 47: P10

Chain v:  100%



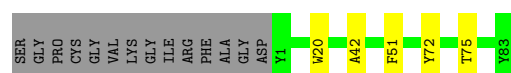
- Molecule 48: Mitochondrial NADH:ubiquinone oxidoreductase 9 kDa subunit

Chain w:  57% 41%

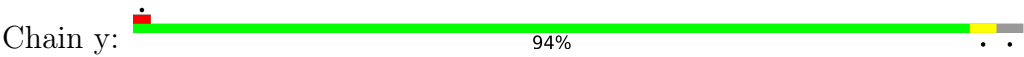
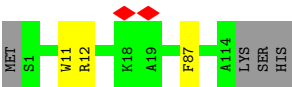


- Molecule 49: NUOP8

Chain x:  50% 47%



- Molecule 50: NUOP7



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83443	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	1.068	Depositor
Minimum map value	0.000	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.141	Depositor
Map size (Å)	589.6, 589.6, 589.6	wwPDB
Map dimensions	588, 588, 588	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0027211, 1.0027211, 1.0027211	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PTY, PGT, PC7, 8Q1, NDP, UQ5, SF4, FES, FMN, 3PH, COO, CDL, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.22	0/1878	0.47	0/2549
2	B	0.24	0/3400	0.45	0/4573
3	C	0.23	0/5272	0.42	0/7143
4	D	0.27	0/1843	0.49	0/2506
5	E	0.29	0/3158	0.49	0/4270
6	F	0.30	0/1258	0.48	0/1706
7	G	0.25	0/1648	0.50	0/2222
8	H	0.24	0/773	0.58	2/1046 (0.2%)
9	I	0.21	0/1061	0.38	0/1441
10	J	0.20	0/649	0.47	0/875
10	r	0.22	0/673	0.40	0/906
11	K	0.24	0/1007	0.54	1/1348 (0.1%)
12	L	0.23	0/1306	0.47	0/1769
13	M	0.23	0/936	0.43	0/1276
14	N	0.21	0/1277	0.37	0/1735
15	O	0.18	0/772	0.45	0/1037
16	P	0.22	0/2879	0.44	0/3905
17	Q	0.29	0/2234	0.52	0/3034
18	R	0.30	0/3100	0.54	0/4226
19	S	0.28	0/1106	0.49	0/1512
20	T	0.31	0/3533	0.55	0/4825
21	U	0.28	0/819	0.48	0/1112
22	V	0.29	0/4258	0.52	0/5792
23	W	0.26	0/1239	0.52	0/1686
24	X	0.27	0/1081	0.51	0/1479
25	Y	0.24	0/411	0.41	0/557
26	Z	0.23	0/894	0.42	0/1218
27	a	0.21	0/698	0.43	0/949
28	b	0.26	0/1201	0.49	0/1623
29	c	0.22	0/463	0.50	0/623
30	d	0.27	0/721	0.41	0/968
31	e	0.27	0/1688	0.46	0/2301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	f	0.25	0/547	0.42	0/740
33	g	0.20	0/433	0.46	0/587
34	h	0.24	0/948	0.49	0/1285
35	i	0.22	0/644	0.40	0/860
36	j	0.23	0/732	0.38	0/983
37	k	0.25	0/1011	0.43	0/1361
38	l	0.25	0/936	0.43	0/1278
39	m	0.27	0/1155	0.41	0/1558
40	n	0.23	0/886	0.39	0/1188
41	o	0.27	0/1265	0.50	0/1705
42	p	0.22	0/1095	0.39	0/1480
43	q	0.23	0/1308	0.38	0/1779
44	s	0.22	0/2353	0.42	0/3202
45	t	0.25	0/2043	0.48	0/2778
46	u	0.25	0/1730	0.47	0/2341
47	v	0.22	0/369	0.37	0/498
48	w	0.24	0/521	0.41	0/702
49	x	0.23	0/727	0.39	0/994
50	y	0.25	0/963	0.48	0/1313
All	All	0.25	0/72902	0.47	3/98844 (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
31	e	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	102	GLU	CA-C-N	7.46	135.79	121.54
8	H	102	GLU	C-N-CA	7.46	135.79	121.54
11	K	85	GLU	N-CA-CB	5.25	118.96	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
31	e	147	MET	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	1839	0	1827	6	0
2	B	3331	0	3328	23	0
3	C	5175	0	5182	32	0
4	D	1790	0	1740	16	0
5	E	3085	0	3058	20	0
6	F	1225	0	1224	11	0
7	G	1615	0	1551	11	0
8	H	750	0	751	8	0
9	I	1044	0	1046	10	0
10	J	640	0	629	5	0
10	r	663	0	647	5	0
11	K	986	0	1017	7	0
12	L	1275	0	1243	12	0
13	M	913	0	909	2	0
14	N	1235	0	1161	9	0
15	O	761	0	759	6	0
16	P	2823	0	2854	14	0
17	Q	2179	0	2241	26	0
18	R	3014	0	3102	31	0
19	S	1071	0	1035	12	0
20	T	3434	0	3590	36	0
21	U	805	0	812	9	0
22	V	4152	0	4212	27	0
23	W	1210	0	1275	19	0
24	X	1037	0	981	5	0
25	Y	405	0	404	2	0
26	Z	861	0	826	3	0
27	a	674	0	620	2	0
28	b	1169	0	1144	6	0
29	c	453	0	475	1	0
30	d	699	0	670	4	0
31	e	1639	0	1618	12	0
32	f	532	0	524	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	g	416	0	402	2	0
34	h	915	0	866	1	0
35	i	633	0	612	3	0
36	j	712	0	684	3	0
37	k	984	0	980	5	0
38	l	904	0	875	4	0
39	m	1126	0	1148	11	0
40	n	864	0	839	6	0
41	o	1240	0	1222	9	0
42	p	1069	0	1014	5	0
43	q	1268	0	1209	0	0
44	s	2302	0	2299	15	0
45	t	1997	0	1985	17	0
46	u	1698	0	1686	9	0
47	v	361	0	359	0	0
48	w	508	0	494	2	0
49	x	699	0	662	4	0
50	y	932	0	950	3	0
51	A	4	0	0	0	0
51	C	4	0	0	0	0
52	B	31	0	19	1	0
53	B	8	0	0	1	0
53	C	16	0	0	0	0
53	F	8	0	0	1	0
53	G	16	0	0	0	0
54	G	43	0	62	2	0
54	R	118	0	161	2	0
54	S	46	0	68	3	0
54	T	104	0	133	1	0
54	V	125	0	175	3	0
54	e	68	0	85	3	0
54	h	46	0	68	1	0
54	x	50	0	79	0	0
55	J	35	0	0	0	0
55	r	35	0	0	0	0
56	P	48	0	26	1	0
57	Q	38	0	50	2	0
58	Q	33	0	40	1	0
58	R	44	0	62	0	0
58	T	52	0	84	3	0
58	u	42	0	58	2	0
59	R	32	0	37	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	S	37	0	47	0	0
59	V	83	0	115	3	0
59	c	48	0	75	2	0
59	g	37	0	50	0	0
59	h	45	0	63	2	0
59	w	45	0	66	3	0
60	R	63	0	70	1	0
60	V	64	0	72	1	0
60	W	95	0	143	8	0
60	h	77	0	98	3	0
60	u	154	0	205	5	0
60	x	92	0	137	9	0
60	y	55	0	54	4	0
61	T	88	0	122	3	0
61	b	44	0	58	1	0
61	l	51	0	78	1	0
62	s	53	0	37	5	0
63	s	1	0	0	0	0
64	A	24	0	0	0	0
64	B	66	0	0	1	0
64	C	168	0	0	1	0
64	D	66	0	0	0	0
64	E	87	0	0	1	0
64	F	39	0	0	0	0
64	G	62	0	0	0	0
64	H	16	0	0	0	0
64	I	19	0	0	0	0
64	K	16	0	0	0	0
64	L	68	0	0	1	0
64	M	30	0	0	0	0
64	N	53	0	0	0	0
64	O	6	0	0	0	0
64	P	69	0	0	0	0
64	Q	24	0	0	0	0
64	R	64	0	0	0	0
64	S	22	0	0	1	0
64	T	85	0	0	1	0
64	U	14	0	0	1	0
64	V	99	0	0	1	0
64	W	25	0	0	0	0
64	X	50	0	0	0	0
64	Y	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	Z	20	0	0	0	0
64	a	6	0	0	0	0
64	b	24	0	0	0	0
64	c	1	0	0	0	0
64	d	12	0	0	0	0
64	e	55	0	0	1	0
64	f	10	0	0	0	0
64	g	7	0	0	1	0
64	h	38	0	0	0	0
64	i	30	0	0	0	0
64	j	29	0	0	0	0
64	k	51	0	0	0	0
64	l	17	0	0	0	0
64	m	32	0	0	1	0
64	n	7	0	0	0	0
64	o	51	0	0	0	0
64	p	21	0	0	0	0
64	q	24	0	0	0	0
64	r	12	0	0	0	0
64	s	39	0	0	0	0
64	t	55	0	0	0	0
64	u	41	0	0	0	0
64	v	2	0	0	0	0
64	w	16	0	0	0	0
64	x	22	0	0	0	0
64	y	29	0	0	0	0
All	All	75117	0	73438	433	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 3.

The worst 5 of 433 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:S:224:LEU:HD12	23:W:151:ARG:HH22	1.57	0.70
33:g:16:ARG:HH12	37:k:33:ARG:HD3	1.58	0.68
40:n:35:CYS:SG	42:p:102:ARG:NH2	2.67	0.67
5:E:122:ARG:HD3	6:F:76:THR:HG21	1.76	0.67
17:Q:69:GLY:HA3	60:W:701:CDL:HB4	1.76	0.65

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	237/282 (84%)	228 (96%)	9 (4%)	0	100	100
2	B	433/484 (90%)	417 (96%)	16 (4%)	0	100	100
3	C	686/733 (94%)	667 (97%)	19 (3%)	0	100	100
4	D	214/282 (76%)	204 (95%)	10 (5%)	0	100	100
5	E	379/467 (81%)	368 (97%)	11 (3%)	0	100	100
6	F	155/164 (94%)	149 (96%)	6 (4%)	0	100	100
7	G	197/231 (85%)	189 (96%)	8 (4%)	0	100	100
8	H	88/118 (75%)	81 (92%)	7 (8%)	0	100	100
9	I	133/165 (81%)	130 (98%)	3 (2%)	0	100	100
10	J	82/128 (64%)	76 (93%)	6 (7%)	0	100	100
10	r	86/128 (67%)	84 (98%)	2 (2%)	0	100	100
11	K	117/138 (85%)	115 (98%)	2 (2%)	0	100	100
12	L	162/187 (87%)	155 (96%)	7 (4%)	0	100	100
13	M	119/154 (77%)	111 (93%)	8 (7%)	0	100	100
14	N	148/156 (95%)	145 (98%)	3 (2%)	0	100	100
15	O	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
16	P	361/397 (91%)	350 (97%)	11 (3%)	0	100	100
17	Q	282/292 (97%)	274 (97%)	8 (3%)	0	100	100
18	R	385/387 (100%)	369 (96%)	16 (4%)	0	100	100
19	S	130/279 (47%)	128 (98%)	2 (2%)	0	100	100
20	T	441/443 (100%)	431 (98%)	10 (2%)	0	100	100
21	U	103/227 (45%)	102 (99%)	1 (1%)	0	100	100
22	V	544/546 (100%)	525 (96%)	18 (3%)	1 (0%)	43	63
23	W	155/162 (96%)	151 (97%)	4 (3%)	0	100	100
24	X	123/149 (83%)	117 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	Y	52/64 (81%)	52 (100%)	0	0	100	100
26	Z	105/124 (85%)	100 (95%)	5 (5%)	0	100	100
27	a	80/129 (62%)	78 (98%)	1 (1%)	1 (1%)	9	18
28	b	142/172 (83%)	139 (98%)	3 (2%)	0	100	100
29	c	55/67 (82%)	52 (94%)	3 (6%)	0	100	100
30	d	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
31	e	216/219 (99%)	214 (99%)	1 (0%)	1 (0%)	24	43
32	f	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
33	g	48/55 (87%)	42 (88%)	6 (12%)	0	100	100
34	h	106/142 (75%)	97 (92%)	9 (8%)	0	100	100
35	i	74/81 (91%)	73 (99%)	1 (1%)	0	100	100
36	j	83/86 (96%)	80 (96%)	3 (4%)	0	100	100
37	k	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
38	l	114/121 (94%)	110 (96%)	4 (4%)	0	100	100
39	m	134/142 (94%)	133 (99%)	1 (1%)	0	100	100
40	n	102/106 (96%)	100 (98%)	2 (2%)	0	100	100
41	o	150/155 (97%)	145 (97%)	5 (3%)	0	100	100
42	p	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
43	q	155/197 (79%)	149 (96%)	6 (4%)	0	100	100
44	s	310/312 (99%)	303 (98%)	7 (2%)	0	100	100
45	t	251/279 (90%)	243 (97%)	8 (3%)	0	100	100
46	u	226/229 (99%)	220 (97%)	6 (3%)	0	100	100
47	v	43/45 (96%)	43 (100%)	0	0	100	100
48	w	62/109 (57%)	61 (98%)	1 (2%)	0	100	100
49	x	81/157 (52%)	81 (100%)	0	0	100	100
50	y	112/118 (95%)	111 (99%)	1 (1%)	0	100	100
All	All	8946/10307 (87%)	8662 (97%)	281 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	a	43	TYR
22	V	519	PRO

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Mol	Chain	Res	Type
31	e	148	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	197/228 (86%)	197 (100%)	0	100	100
2	B	344/377 (91%)	344 (100%)	0	100	100
3	C	537/572 (94%)	537 (100%)	0	100	100
4	D	196/248 (79%)	196 (100%)	0	100	100
5	E	329/388 (85%)	329 (100%)	0	100	100
6	F	129/133 (97%)	129 (100%)	0	100	100
7	G	172/198 (87%)	172 (100%)	0	100	100
8	H	82/105 (78%)	82 (100%)	0	100	100
9	I	111/134 (83%)	111 (100%)	0	100	100
10	J	71/108 (66%)	71 (100%)	0	100	100
10	r	72/108 (67%)	72 (100%)	0	100	100
11	K	106/122 (87%)	106 (100%)	0	100	100
12	L	130/148 (88%)	130 (100%)	0	100	100
13	M	100/121 (83%)	100 (100%)	0	100	100
14	N	128/132 (97%)	128 (100%)	0	100	100
15	O	80/81 (99%)	80 (100%)	0	100	100
16	P	305/327 (93%)	305 (100%)	0	100	100
17	Q	230/234 (98%)	230 (100%)	0	100	100
18	R	321/321 (100%)	321 (100%)	0	100	100
19	S	111/217 (51%)	111 (100%)	0	100	100
20	T	374/374 (100%)	374 (100%)	0	100	100
21	U	84/180 (47%)	84 (100%)	0	100	100
22	V	439/439 (100%)	439 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	W	131/135 (97%)	131 (100%)	0	100	100
24	X	105/122 (86%)	105 (100%)	0	100	100
25	Y	38/46 (83%)	38 (100%)	0	100	100
26	Z	93/102 (91%)	93 (100%)	0	100	100
27	a	68/98 (69%)	68 (100%)	0	100	100
28	b	119/138 (86%)	119 (100%)	0	100	100
29	c	49/56 (88%)	49 (100%)	0	100	100
30	d	63/64 (98%)	63 (100%)	0	100	100
31	e	163/164 (99%)	163 (100%)	0	100	100
32	f	52/53 (98%)	52 (100%)	0	100	100
33	g	40/45 (89%)	40 (100%)	0	100	100
34	h	91/110 (83%)	91 (100%)	0	100	100
35	i	65/67 (97%)	65 (100%)	0	100	100
36	j	72/73 (99%)	72 (100%)	0	100	100
37	k	102/102 (100%)	102 (100%)	0	100	100
38	l	94/99 (95%)	94 (100%)	0	100	100
39	m	118/122 (97%)	118 (100%)	0	100	100
40	n	92/94 (98%)	92 (100%)	0	100	100
41	o	130/132 (98%)	130 (100%)	0	100	100
42	p	109/110 (99%)	109 (100%)	0	100	100
43	q	135/165 (82%)	135 (100%)	0	100	100
44	s	243/243 (100%)	243 (100%)	0	100	100
45	t	212/233 (91%)	212 (100%)	0	100	100
46	u	180/181 (99%)	180 (100%)	0	100	100
47	v	38/38 (100%)	38 (100%)	0	100	100
48	w	55/91 (60%)	55 (100%)	0	100	100
49	x	70/130 (54%)	70 (100%)	0	100	100
50	y	102/106 (96%)	102 (100%)	0	100	100
All	All	7477/8414 (89%)	7477 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57

such sidechains are listed below:

Mol	Chain	Res	Type
18	R	145	GLN
46	u	104	GLN
24	X	119	GLN
46	u	102	ASN
41	o	150	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 54 ligands modelled in this entry, 1 is monoatomic - leaving 53 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	$\# Z > 2$
60	CDL	h	203	-	76,76,99	0.37	0	82,88,111	0.25	0
58	PC7	Q	302	-	32,32,51	0.59	0	38,40,59	0.69	0
61	PGT	T	502	-	47,47,50	0.53	0	50,53,56	0.56	1 (2%)
54	PTY	V	604	-	39,39,49	0.54	0	42,44,54	0.50	0
61	PGT	l	701	-	50,50,50	0.48	0	53,56,56	0.59	1 (1%)
54	PTY	G	303	-	42,42,49	0.49	0	45,47,54	0.44	0
54	PTY	T	501	-	49,49,49	0.46	0	52,54,54	0.62	1 (1%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
54	PTY	R	404	-	43,43,49	0.51	0	46,48,54	0.46	0
59	3PH	V	602	-	40,40,47	0.67	1 (2%)	44,45,52	0.82	1 (2%)
53	SF4	B	502	2	0,12,12	-	-	-	-	-
55	8Q1	J	200	-	31,34,34	1.69	5 (16%)	40,43,43	1.71	5 (12%)
59	3PH	V	601	-	41,41,47	0.66	1 (2%)	45,46,52	0.63	1 (2%)
59	3PH	S	301	-	36,36,47	0.71	1 (2%)	40,41,52	0.70	1 (2%)
54	PTY	S	302	-	45,45,49	0.49	0	48,50,54	0.41	0
57	UQ5	Q	301	-	38,38,38	0.51	0	46,49,49	0.83	3 (6%)
59	3PH	h	201	-	44,44,47	0.65	1 (2%)	48,49,52	3.77	5 (10%)
60	CDL	W	701	-	94,94,99	0.35	0	100,106,111	0.28	0
60	CDL	y	201	-	54,54,99	0.53	1 (1%)	60,66,111	0.32	0
52	FMN	B	501	-	33,33,33	1.09	2 (6%)	48,50,50	1.25	8 (16%)
54	PTY	V	605	-	49,49,49	0.46	0	52,54,54	0.38	0
59	3PH	c	101	-	47,47,47	0.62	1 (2%)	51,52,52	0.63	1 (1%)
54	PTY	x	102	-	49,49,49	0.46	0	52,54,54	0.40	0
60	CDL	V	603	-	63,63,99	0.41	0	69,75,111	0.25	0
60	CDL	R	405	-	62,62,99	0.40	0	68,74,111	0.28	0
53	SF4	G	301	7	0,12,12	-	-	-	-	-
53	SF4	C	803	3	0,12,12	-	-	-	-	-
58	PC7	R	403	-	43,43,51	0.53	0	49,51,59	0.61	0
60	CDL	u	603	-	70,70,99	0.43	0	76,82,111	0.28	0
55	8Q1	r	200	-	31,34,34	1.76	5 (16%)	40,43,43	1.88	10 (25%)
54	PTY	T	504	-	27,27,49	0.65	0	30,32,54	0.48	0
60	CDL	x	101	-	91,91,99	0.40	1 (1%)	97,103,111	0.24	0
58	PC7	T	503	-	51,51,51	0.50	0	57,59,59	0.59	0
54	PTY	T	506	-	25,25,49	0.64	0	28,30,54	0.47	0
61	PGT	b	601	-	43,43,50	0.53	0	46,49,56	0.51	0
53	SF4	G	302	7	0,12,12	-	-	-	-	-
59	3PH	w	201	-	44,44,47	0.64	1 (2%)	48,49,52	0.75	3 (6%)
51	FES	C	801	3	0,4,4	-	-	-	-	-
51	FES	A	301	1	0,4,4	-	-	-	-	-
62	COO	s	401	-	48,55,55	1.10	4 (8%)	68,81,81	4.02	17 (25%)
59	3PH	g	101	-	36,36,47	0.71	1 (2%)	40,41,52	0.70	1 (2%)
54	PTY	e	302	-	42,42,49	0.52	0	45,47,54	0.42	0
54	PTY	h	202	-	45,45,49	0.47	0	48,50,54	0.46	0
54	PTY	V	606	-	34,34,49	0.56	0	37,39,54	0.44	0
53	SF4	C	802	3	0,12,12	-	-	-	-	-
60	CDL	u	602	-	82,82,99	0.38	0	88,94,111	0.30	0
56	NDP	P	401	-	49,52,52	1.20	5 (10%)	66,80,80	1.64	10 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
61	PGT	T	505	-	39,39,50	0.54	0	42,45,56	0.50	0
54	PTY	e	301	-	24,24,49	0.64	0	27,29,54	0.52	0
59	3PH	R	401	-	31,31,47	0.75	1 (3%)	35,36,52	0.73	2 (5%)
53	SF4	F	201	6	0,12,12	-	-	-	-	-
54	PTY	R	406	-	39,39,49	0.53	0	42,44,54	0.51	0
54	PTY	R	402	-	33,33,49	0.53	0	36,38,54	0.43	0
58	PC7	u	601	-	41,41,51	0.55	0	47,49,59	0.68	2 (4%)

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
60	CDL	h	203	-	-	58/87/87/110	-
58	PC7	Q	302	-	-	14/36/36/55	-
61	PGT	T	502	-	-	20/52/52/55	-
54	PTY	V	604	-	-	15/43/43/53	-
61	PGT	l	701	-	-	27/55/55/55	-
54	PTY	G	303	-	-	6/46/46/53	-
54	PTY	T	501	-	-	19/53/53/53	-
54	PTY	R	404	-	-	21/47/47/53	-
59	3PH	V	602	-	-	17/42/42/49	-
55	8Q1	J	200	-	-	11/41/41/41	-
53	SF4	B	502	2	-	-	0/6/5/5
59	3PH	V	601	-	-	18/43/43/49	-
59	3PH	S	301	-	-	13/38/38/49	-
54	PTY	S	302	-	-	21/49/49/53	-
57	UQ5	Q	301	-	-	4/33/57/57	0/1/1/1
59	3PH	h	201	-	-	19/46/46/49	-
60	CDL	W	701	-	-	62/105/105/110	-
60	CDL	y	201	-	-	30/65/65/110	-
52	FMN	B	501	-	-	4/18/18/18	0/3/3/3
54	PTY	V	605	-	-	25/53/53/53	-
59	3PH	c	101	-	-	13/49/49/49	-
54	PTY	x	102	-	-	18/53/53/53	-
60	CDL	V	603	-	-	42/74/74/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	CDL	R	405	-	-	43/73/73/110	-
53	SF4	G	301	7	-	-	0/6/5/5
58	PC7	R	403	-	-	15/47/47/55	-
53	SF4	C	803	3	-	-	0/6/5/5
60	CDL	u	603	-	-	57/81/81/110	-
55	8Q1	r	200	-	-	19/41/41/41	-
54	PTY	T	504	-	-	11/31/31/53	-
60	CDL	x	101	-	-	65/102/102/110	-
58	PC7	T	503	-	-	22/55/55/55	-
54	PTY	T	506	-	-	15/29/29/53	-
61	PGT	b	601	-	-	27/48/48/55	-
53	SF4	G	302	7	-	-	0/6/5/5
59	3PH	w	201	-	-	21/46/46/49	-
51	FES	C	801	3	-	-	0/1/1/1
51	FES	A	301	1	-	-	0/1/1/1
62	COO	s	401	-	-	22/54/70/70	0/3/3/3
59	3PH	g	101	-	-	10/38/38/49	-
54	PTY	e	302	-	-	22/46/46/53	-
54	PTY	h	202	-	-	20/49/49/53	-
54	PTY	V	606	-	-	18/38/38/53	-
61	PGT	T	505	-	-	18/44/44/55	-
60	CDL	u	602	-	-	51/93/93/110	-
56	NDP	P	401	-	-	9/34/77/77	0/5/5/5
53	SF4	C	802	3	-	-	0/6/5/5
54	PTY	e	301	-	-	9/28/28/53	-
59	3PH	R	401	-	-	13/33/33/49	-
53	SF4	F	201	6	-	-	0/6/5/5
54	PTY	R	406	-	-	15/43/43/53	-
54	PTY	R	402	-	-	11/37/37/53	-
58	PC7	u	601	-	-	15/45/45/55	-

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	r	200	8Q1	C34-N36	5.99	1.46	1.33
55	J	200	8Q1	C34-N36	5.48	1.45	1.33
55	r	200	8Q1	C39-N41	5.24	1.45	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	J	200	8Q1	C39-N41	5.13	1.45	1.33
62	s	401	COO	C5A-C4A	4.47	1.47	1.39

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	s	401	COO	C15-C11-C12	-19.13	77.03	108.23
59	h	201	3PH	O31-C31-O32	-17.93	78.33	123.59
62	s	401	COO	C15-C11-C13	-16.74	79.80	108.82
62	s	401	COO	C15-C11-C14	-15.18	78.23	109.17
59	h	201	3PH	O31-C31-C32	14.35	156.94	111.91

There are no chirality outliers.

5 of 1005 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
52	B	501	FMN	C5'-O5'-P-O1P
52	B	501	FMN	C5'-O5'-P-O2P
52	B	501	FMN	C5'-O5'-P-O3P
54	G	303	PTY	C3-O11-P1-O13
54	R	402	PTY	C2-C3-O11-P1

There are no ring outliers.

34 monomers are involved in 75 short contacts:

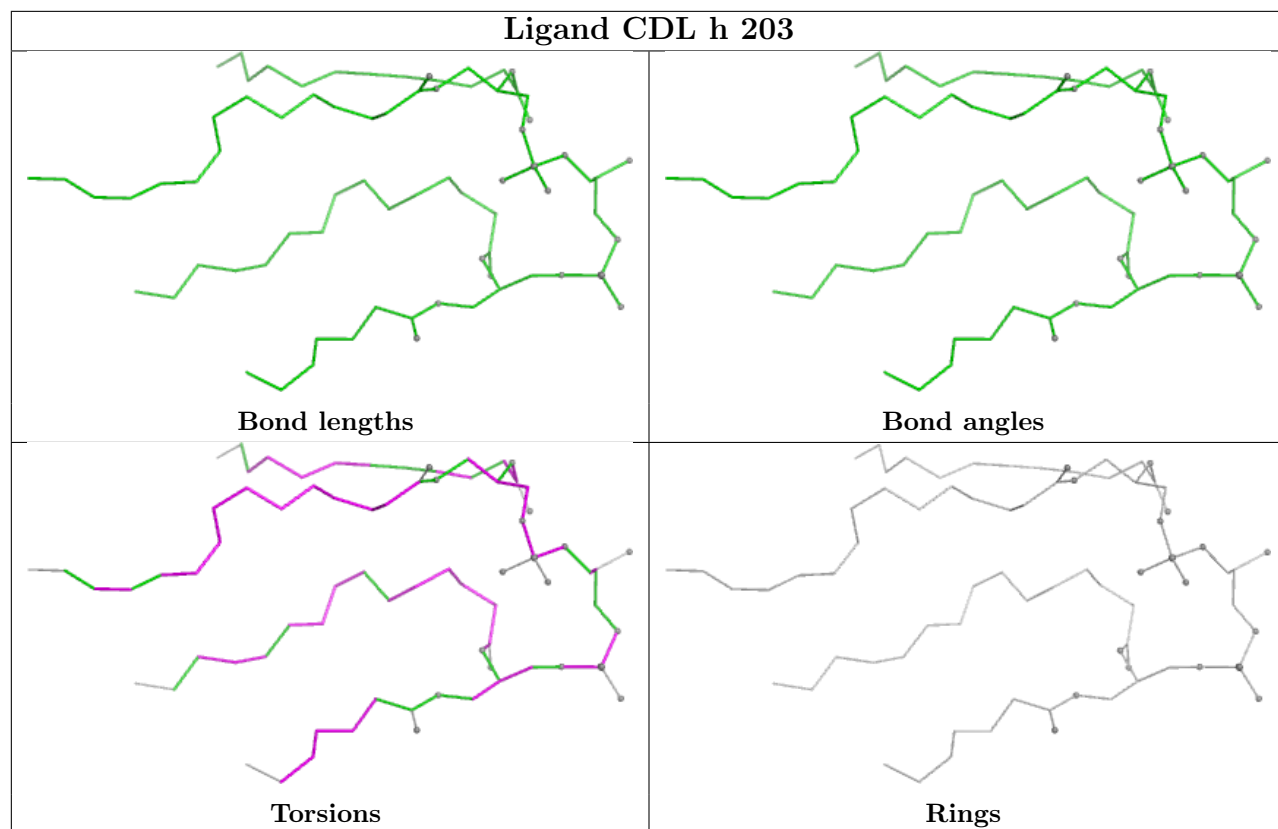
Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	h	203	CDL	3	0
58	Q	302	PC7	1	0
61	T	502	PGT	3	0
61	l	701	PGT	1	0
54	G	303	PTY	2	0
54	T	501	PTY	1	0
54	R	404	PTY	1	0
59	V	602	3PH	3	0
53	B	502	SF4	1	0
54	S	302	PTY	3	0
57	Q	301	UQ5	2	0
59	h	201	3PH	2	0
60	W	701	CDL	8	0
60	y	201	CDL	4	0
52	B	501	FMN	1	0

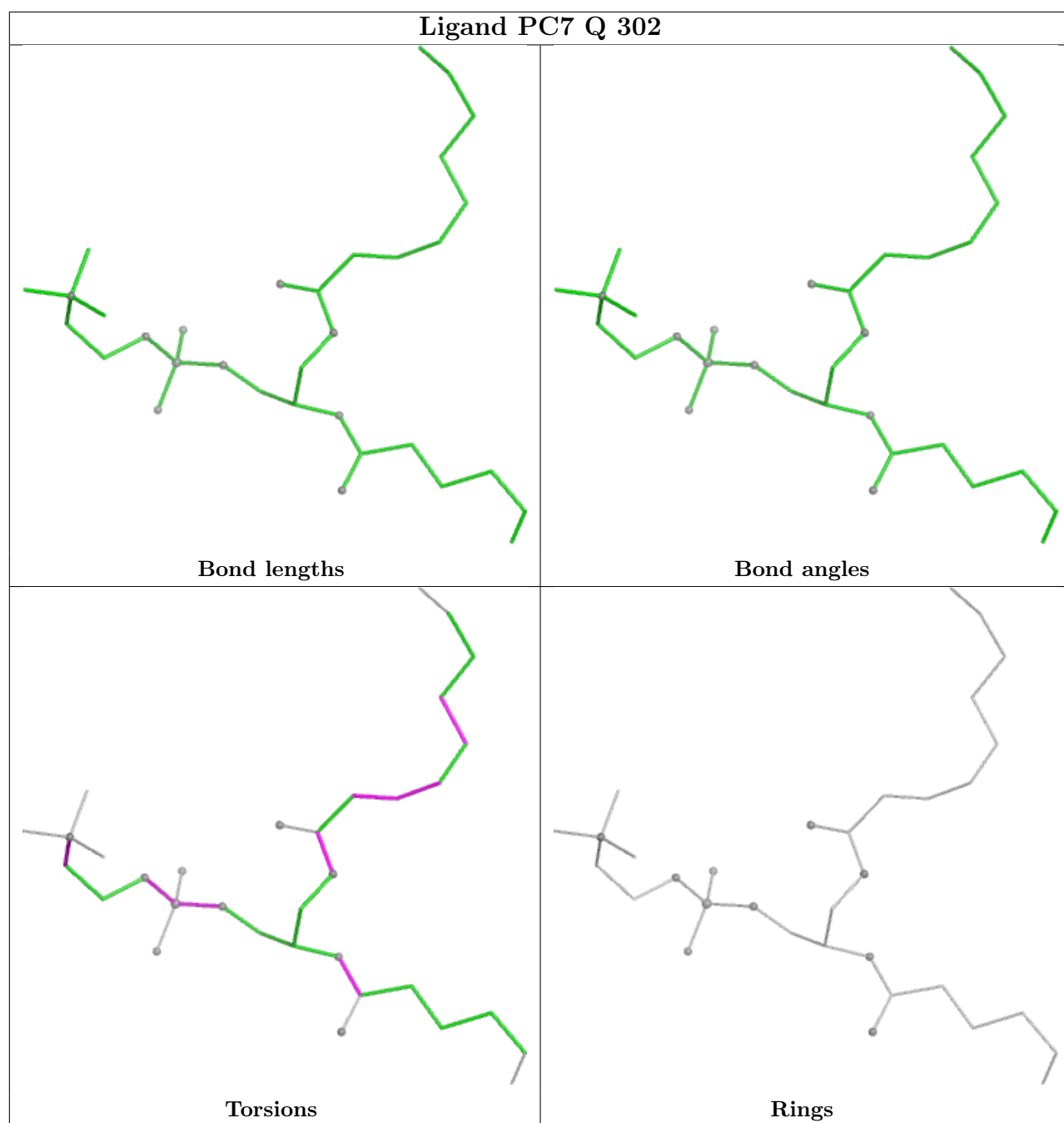
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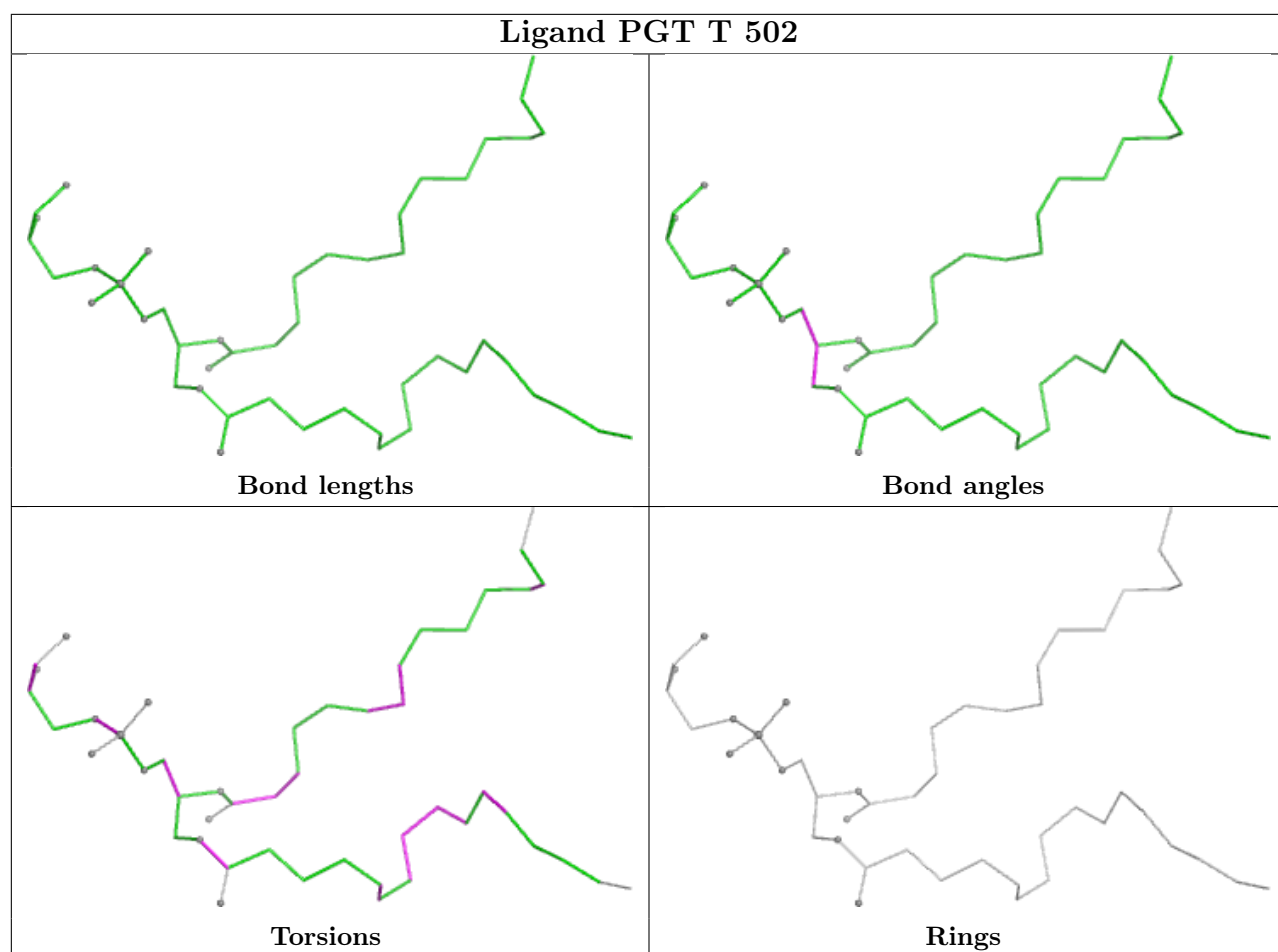
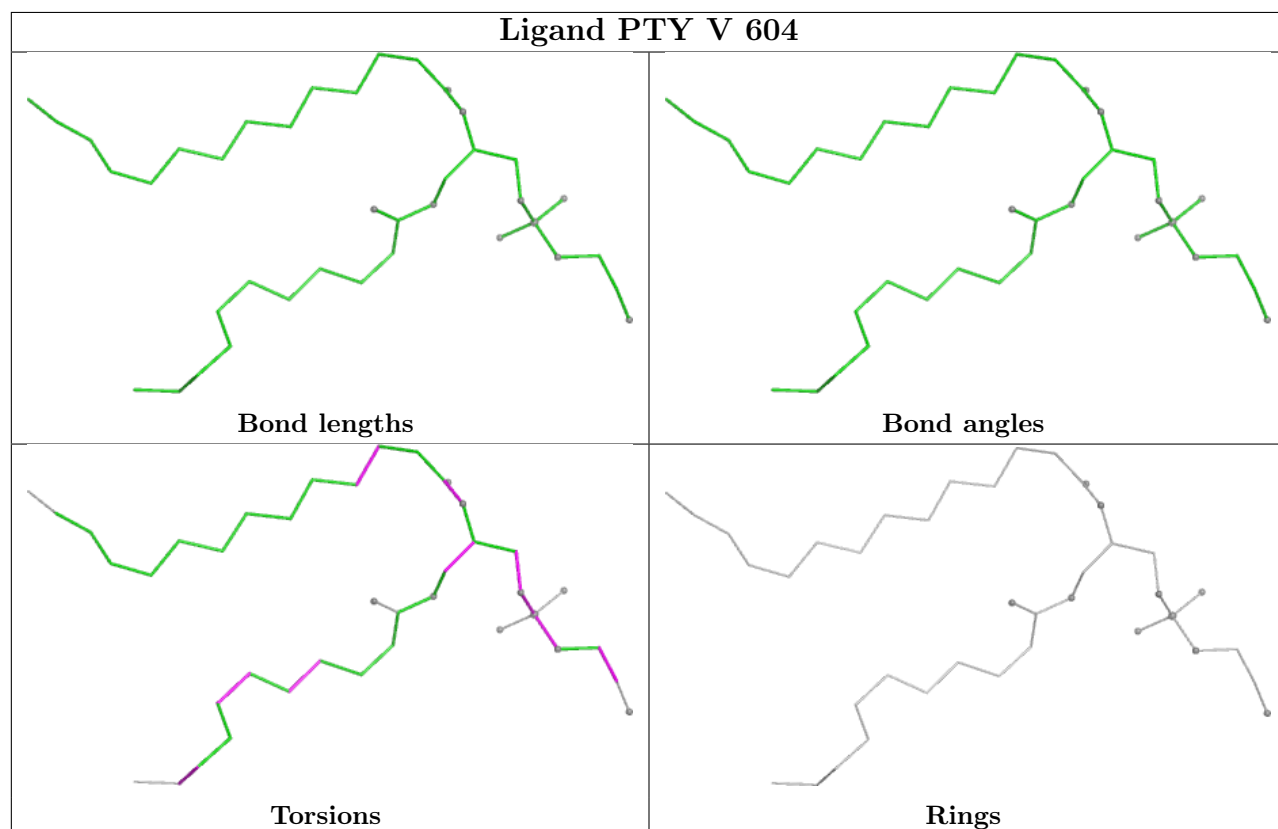
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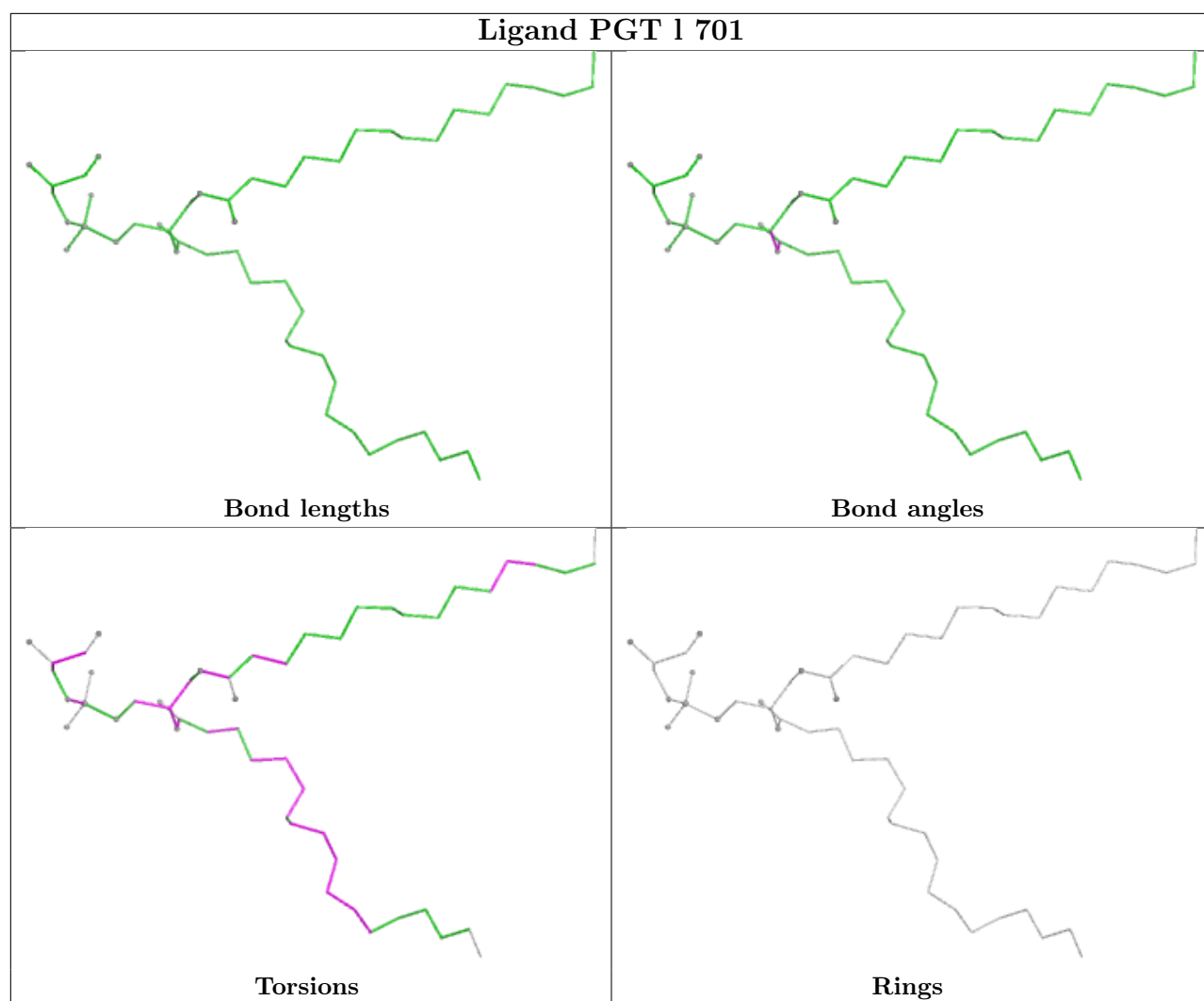
Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	V	605	PTY	2	0
59	c	101	3PH	2	0
60	V	603	CDL	1	0
60	R	405	CDL	1	0
60	u	603	CDL	3	0
60	x	101	CDL	9	0
58	T	503	PC7	3	0
61	b	601	PGT	1	0
59	w	201	3PH	3	0
62	s	401	COO	5	0
54	e	302	PTY	3	0
54	h	202	PTY	1	0
54	V	606	PTY	1	0
60	u	602	CDL	2	0
56	P	401	NDP	1	0
59	R	401	3PH	1	0
53	F	201	SF4	1	0
54	R	406	PTY	1	0
58	u	601	PC7	2	0

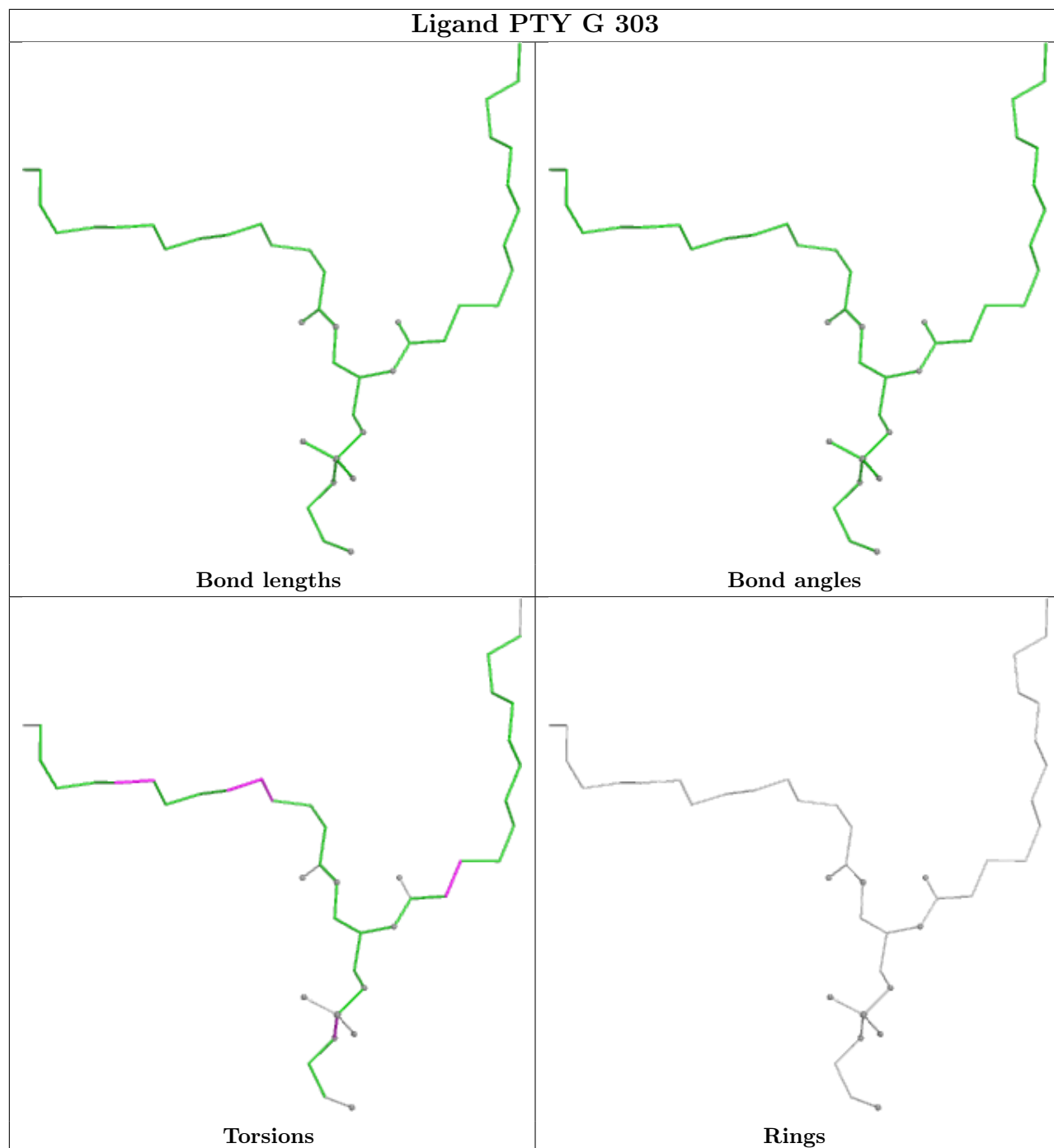
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

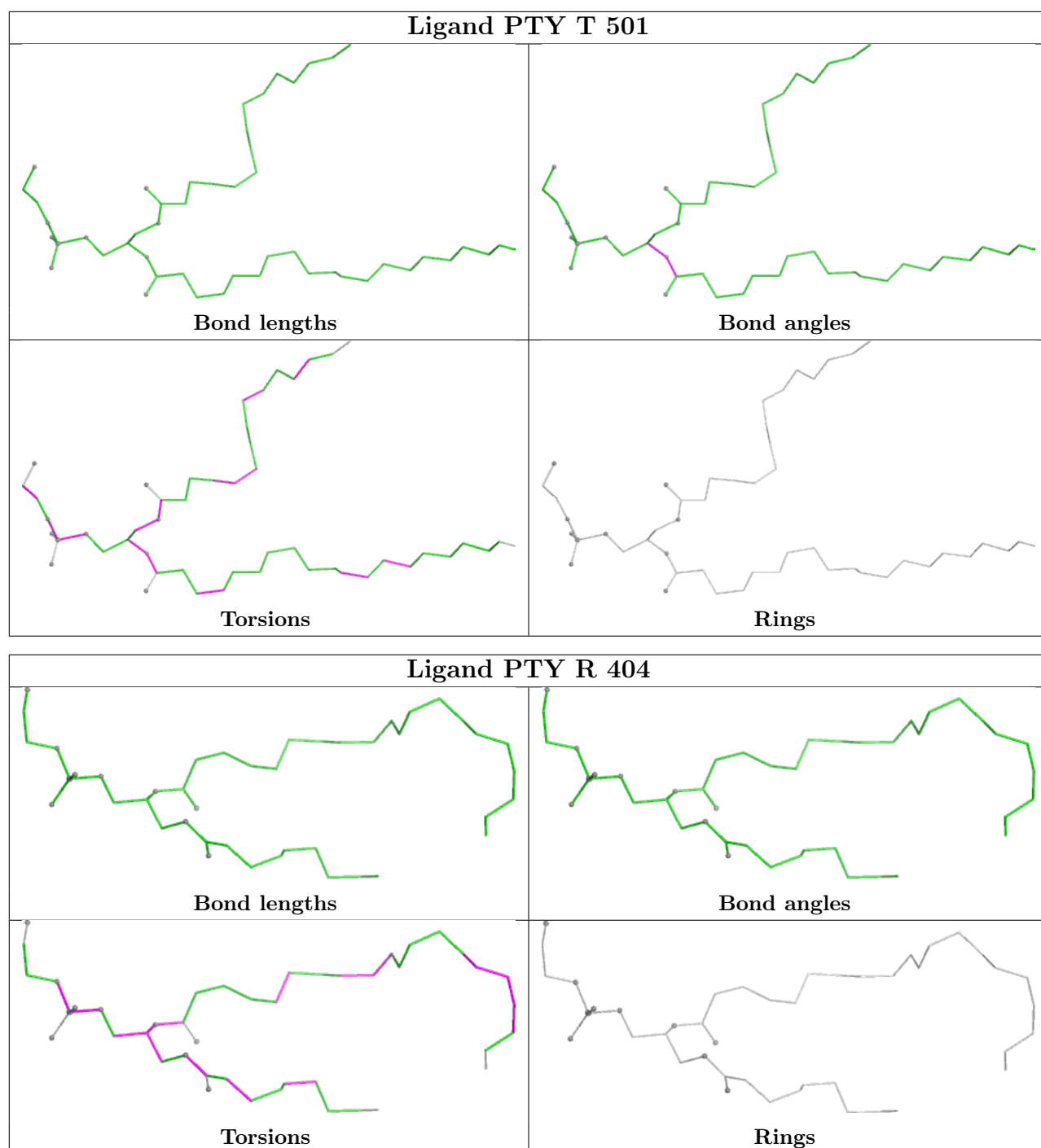


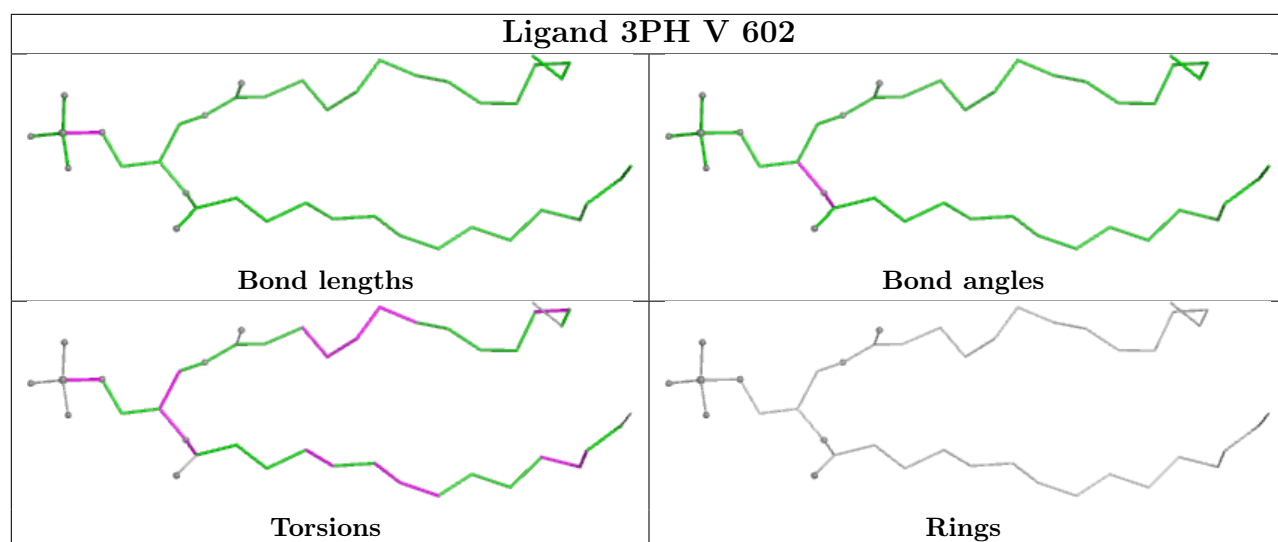
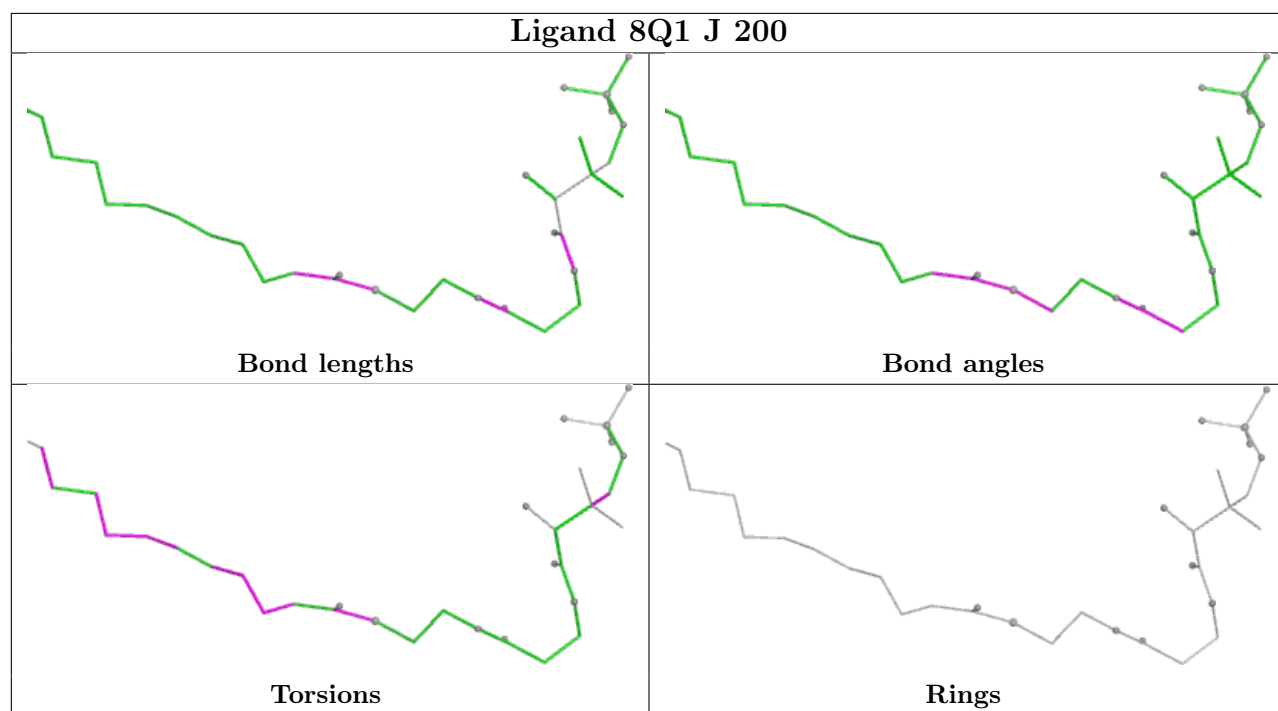


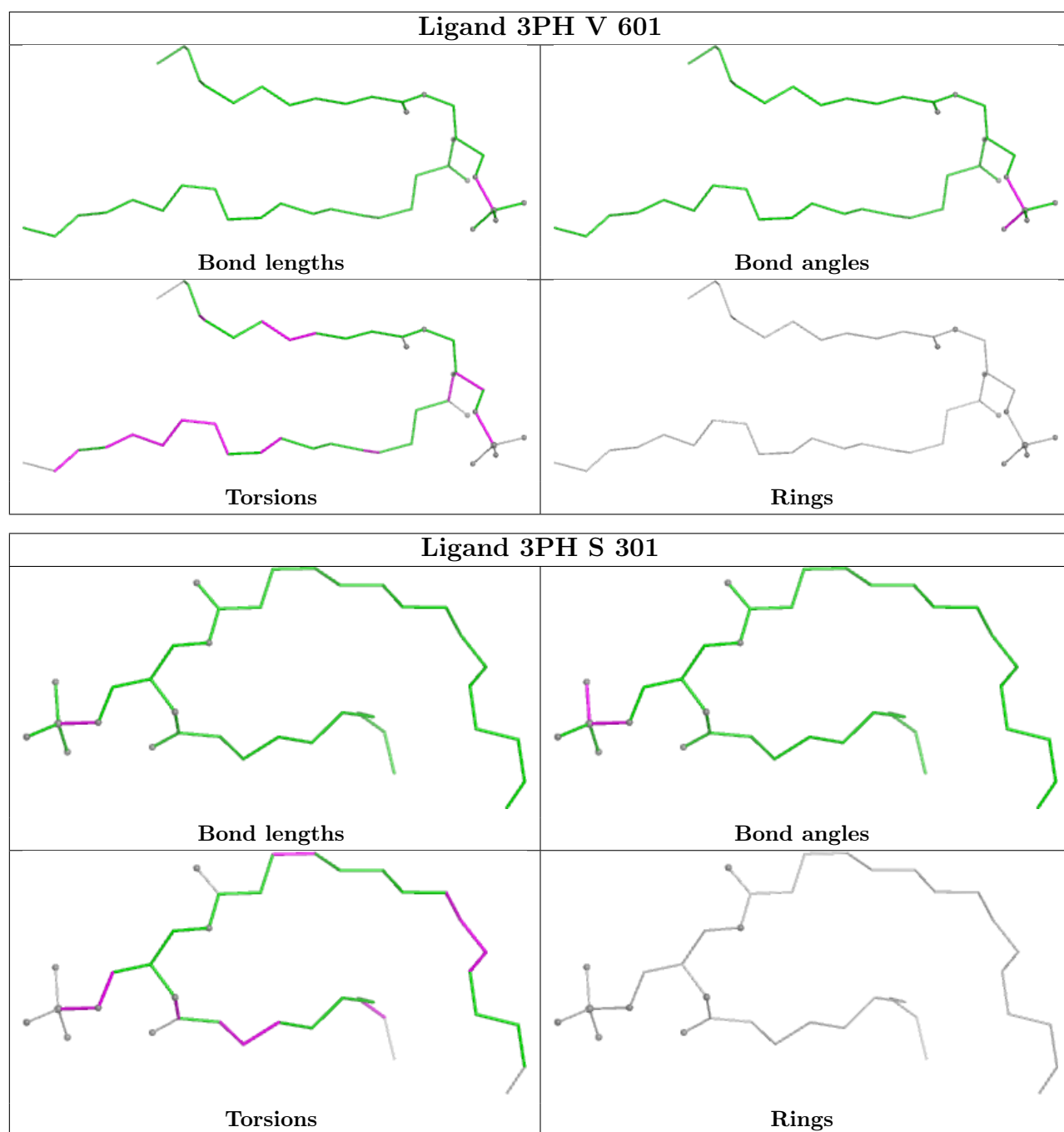


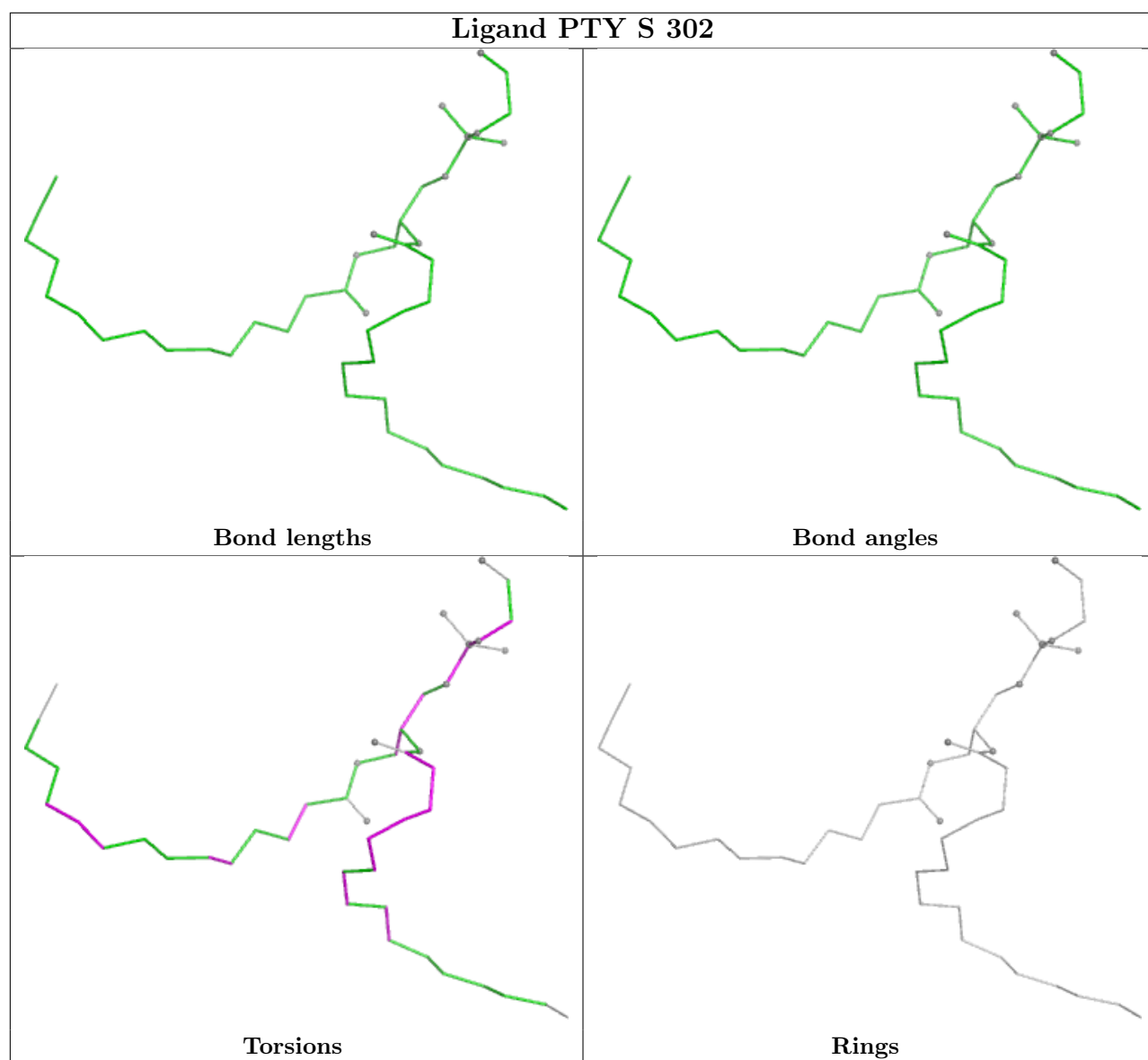
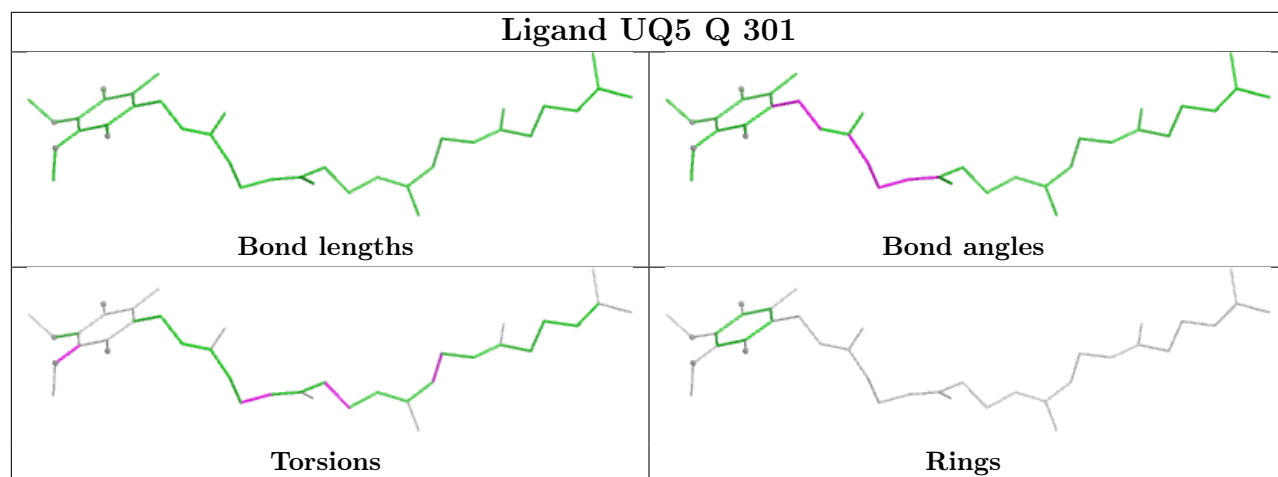


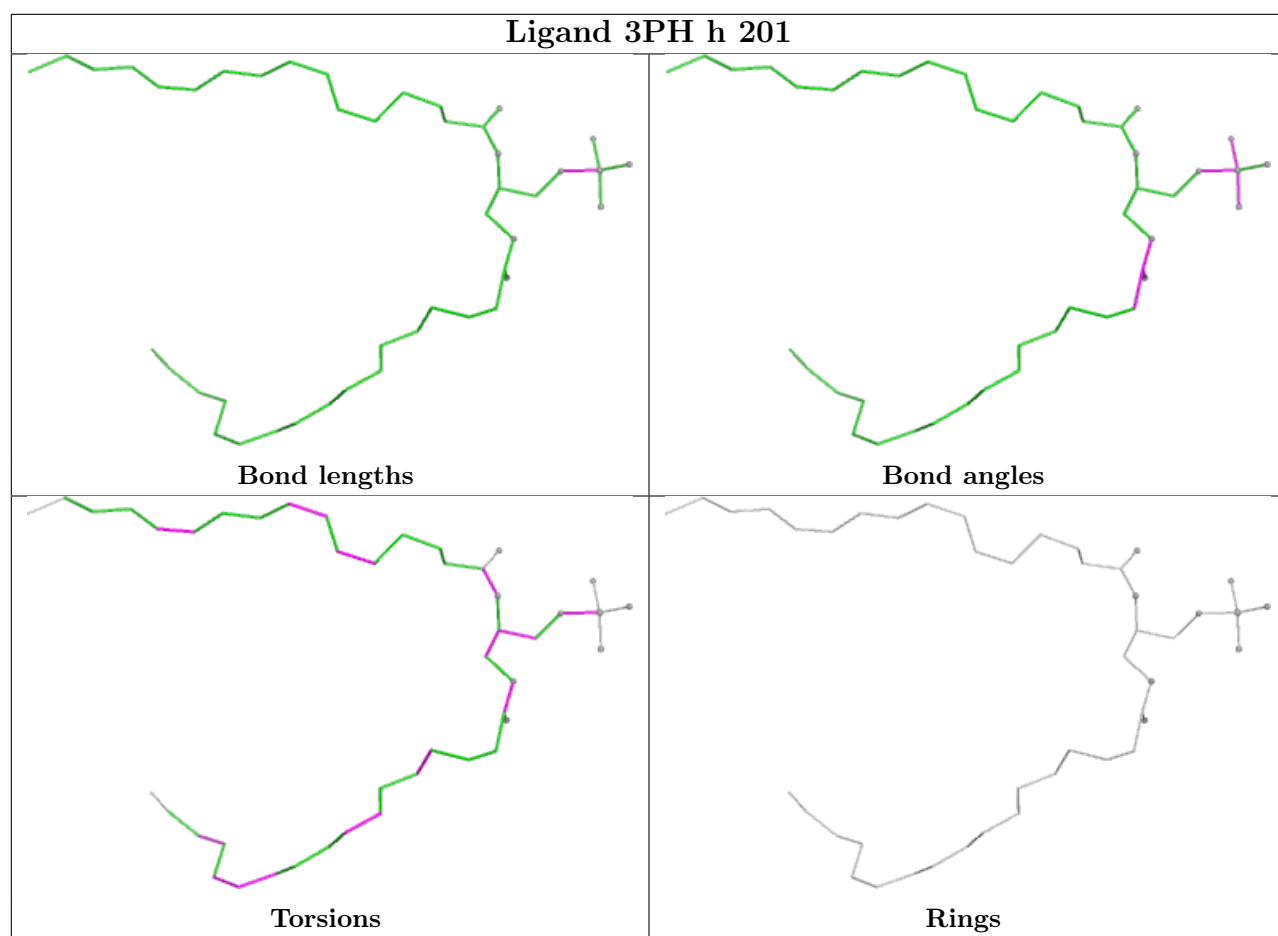


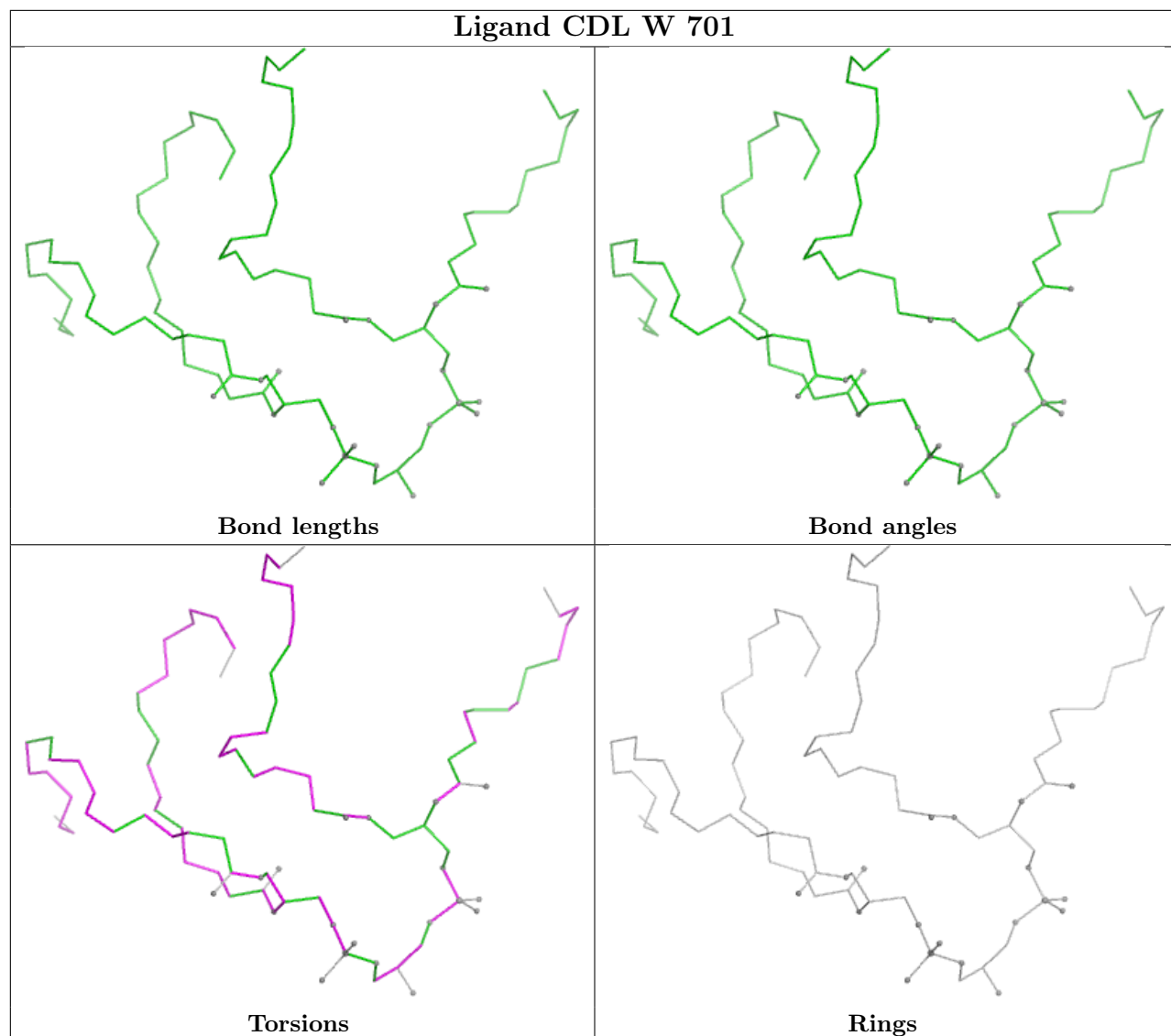


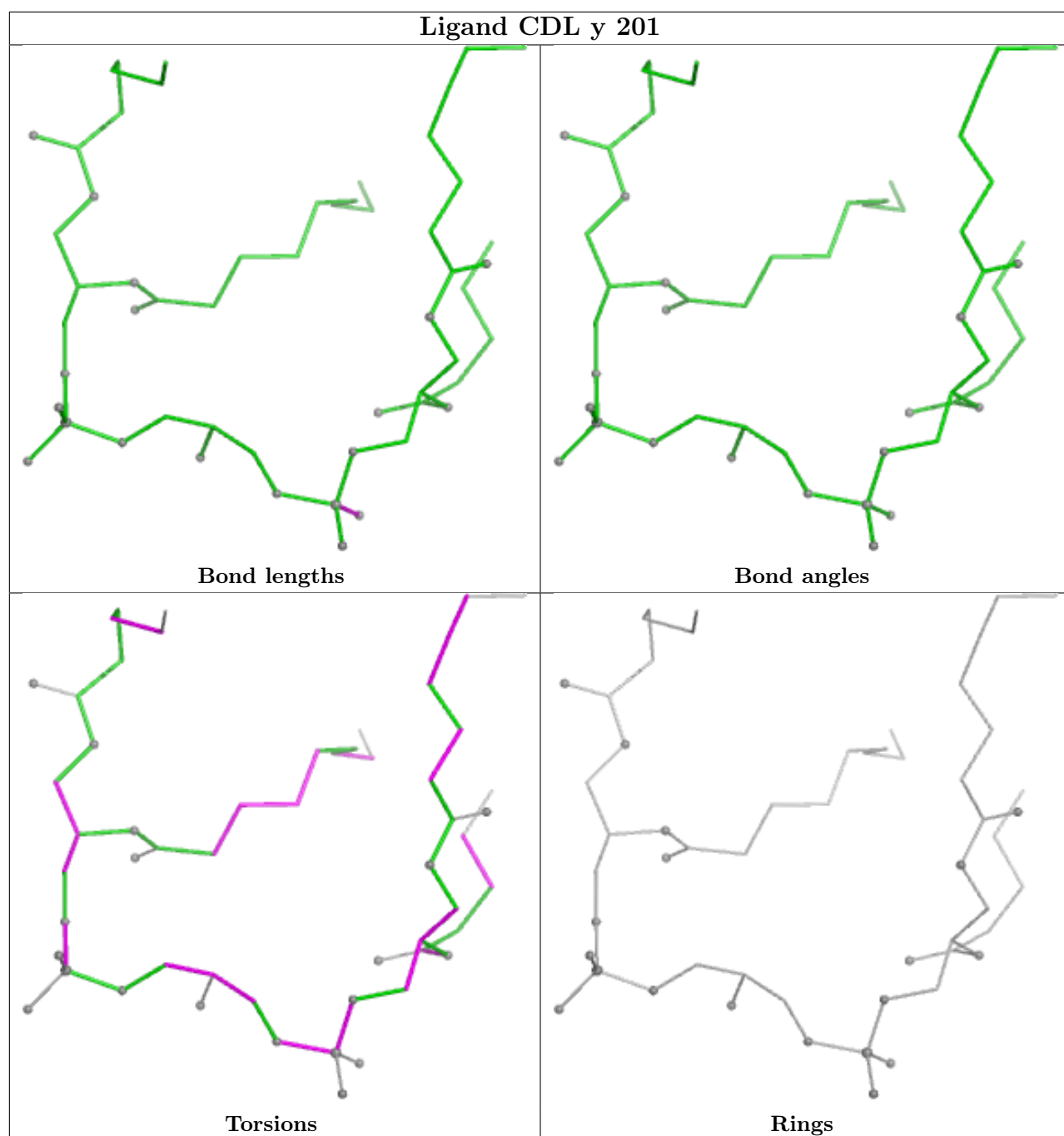


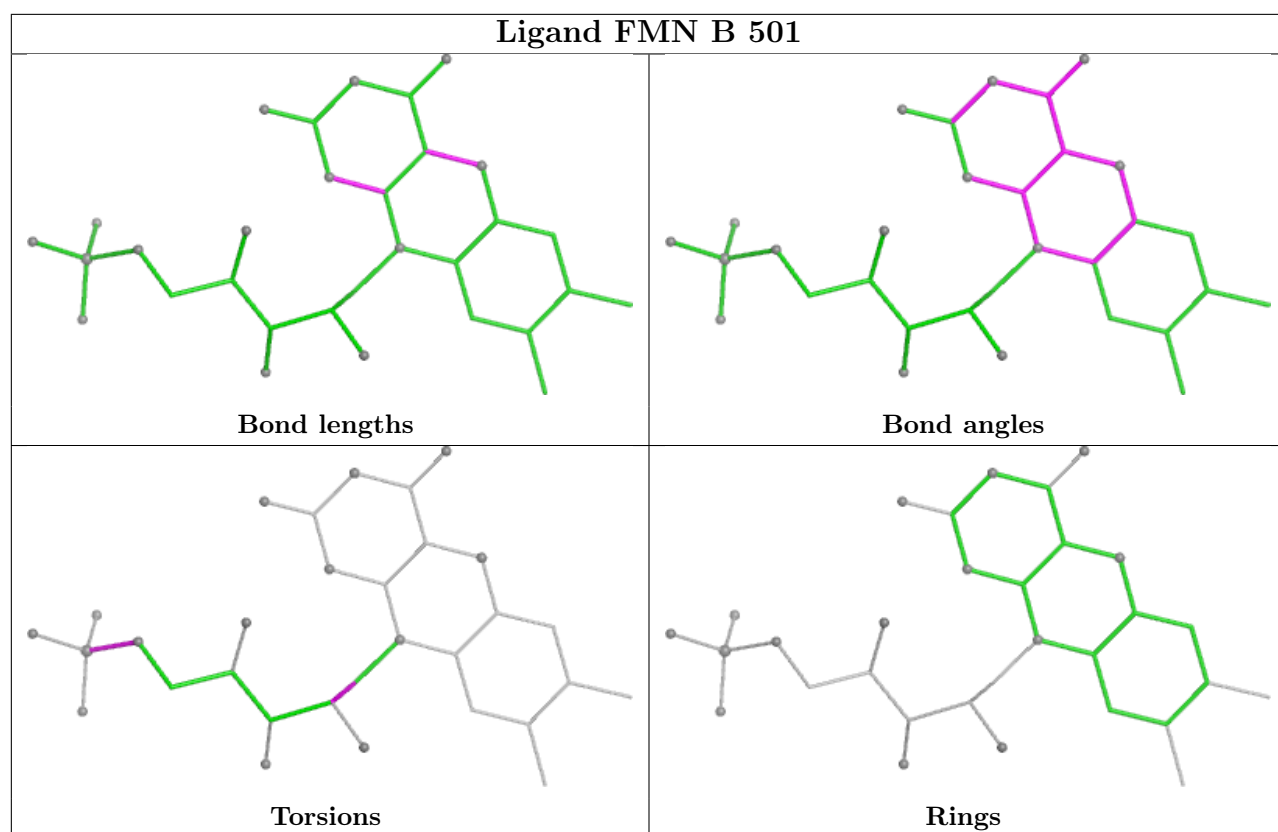
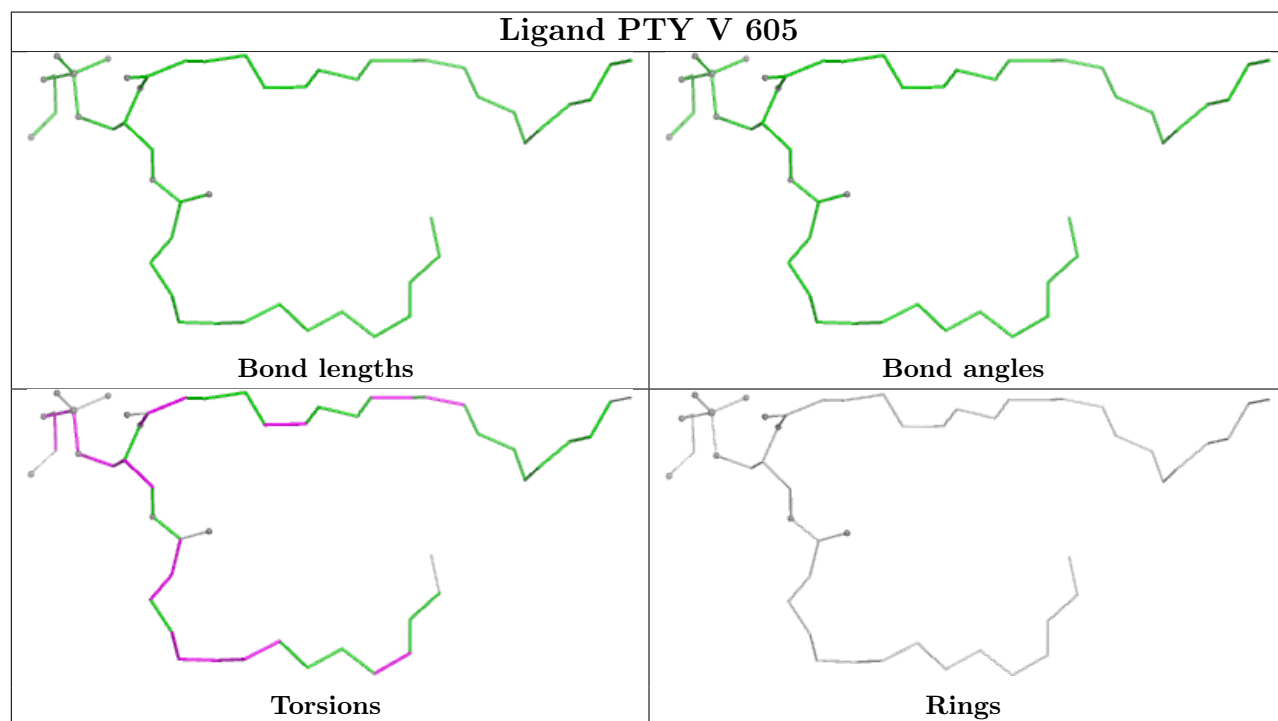


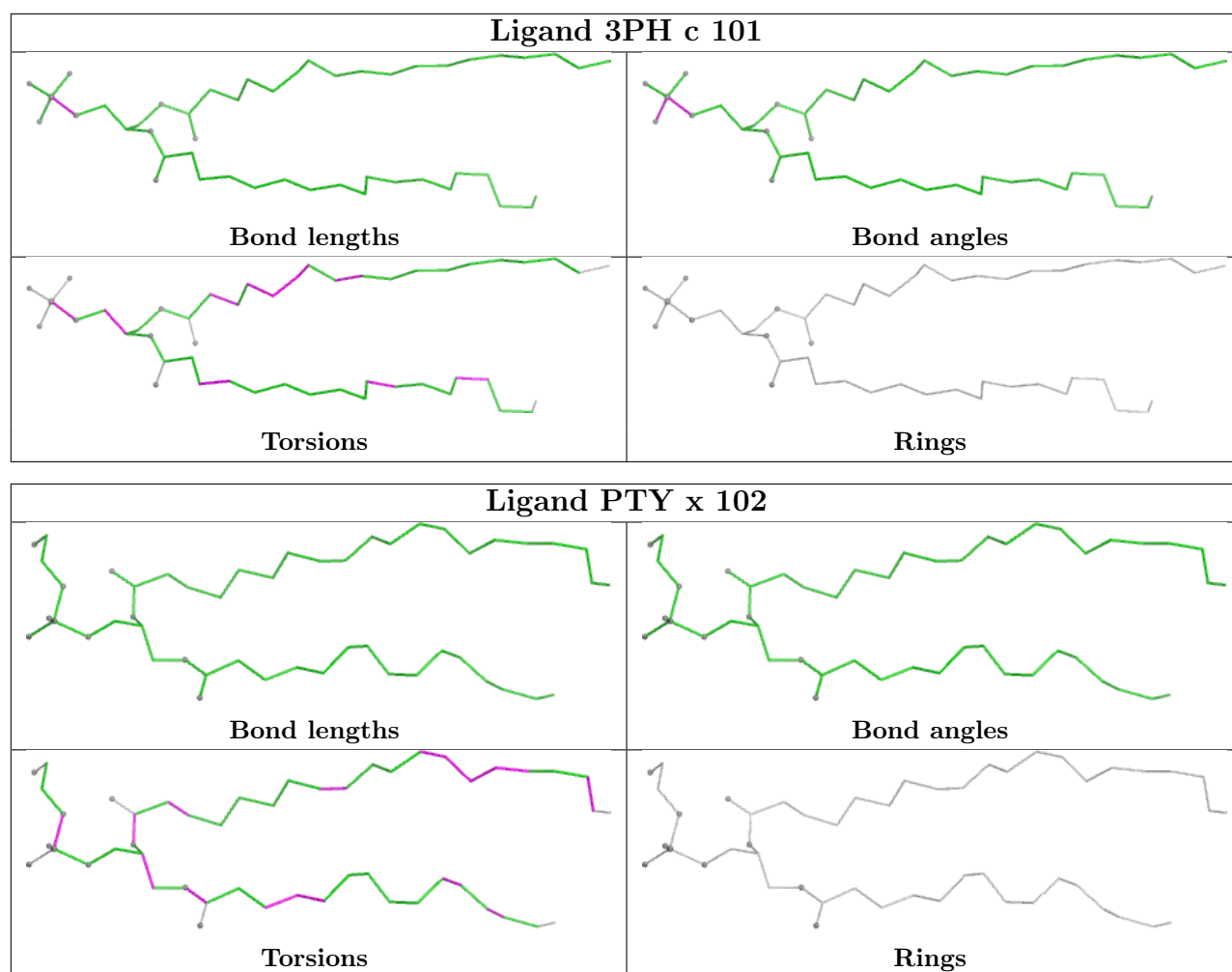


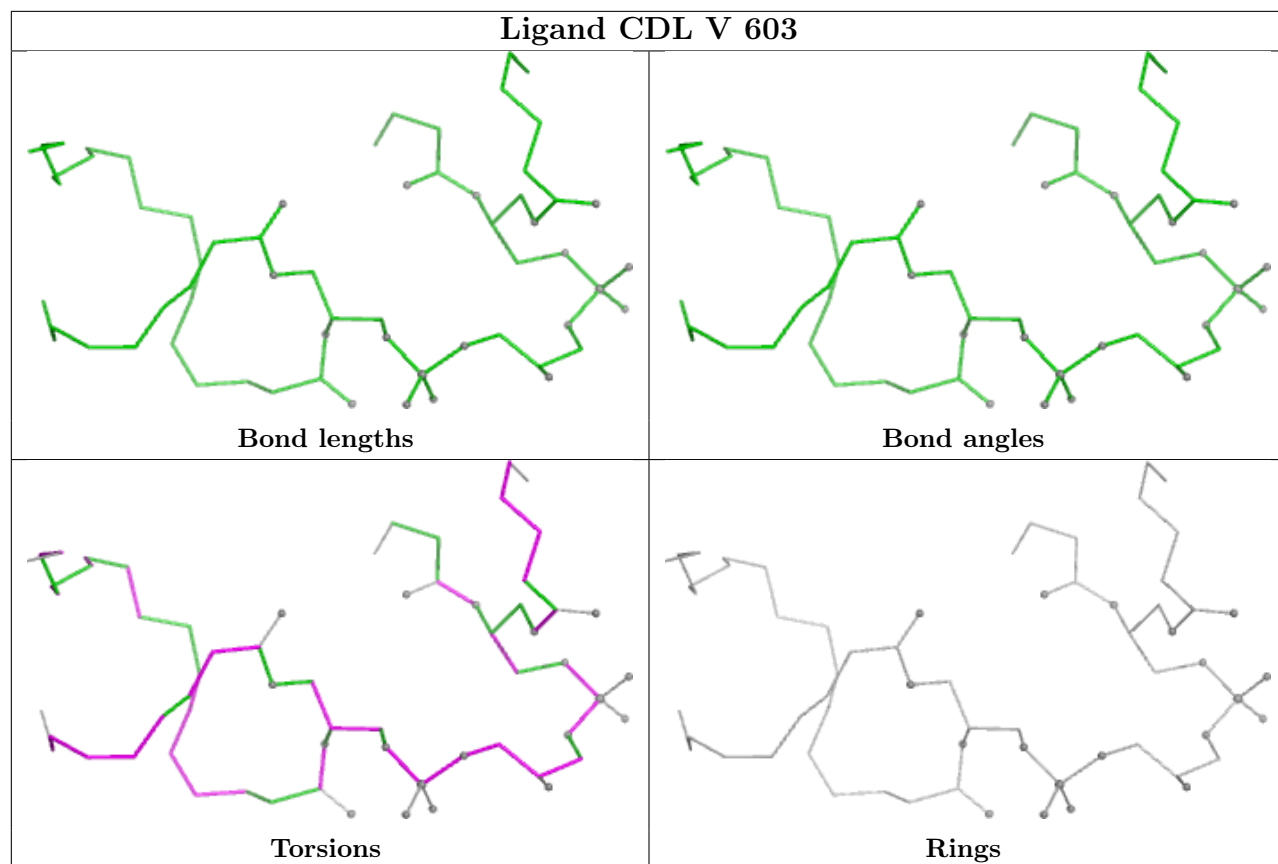


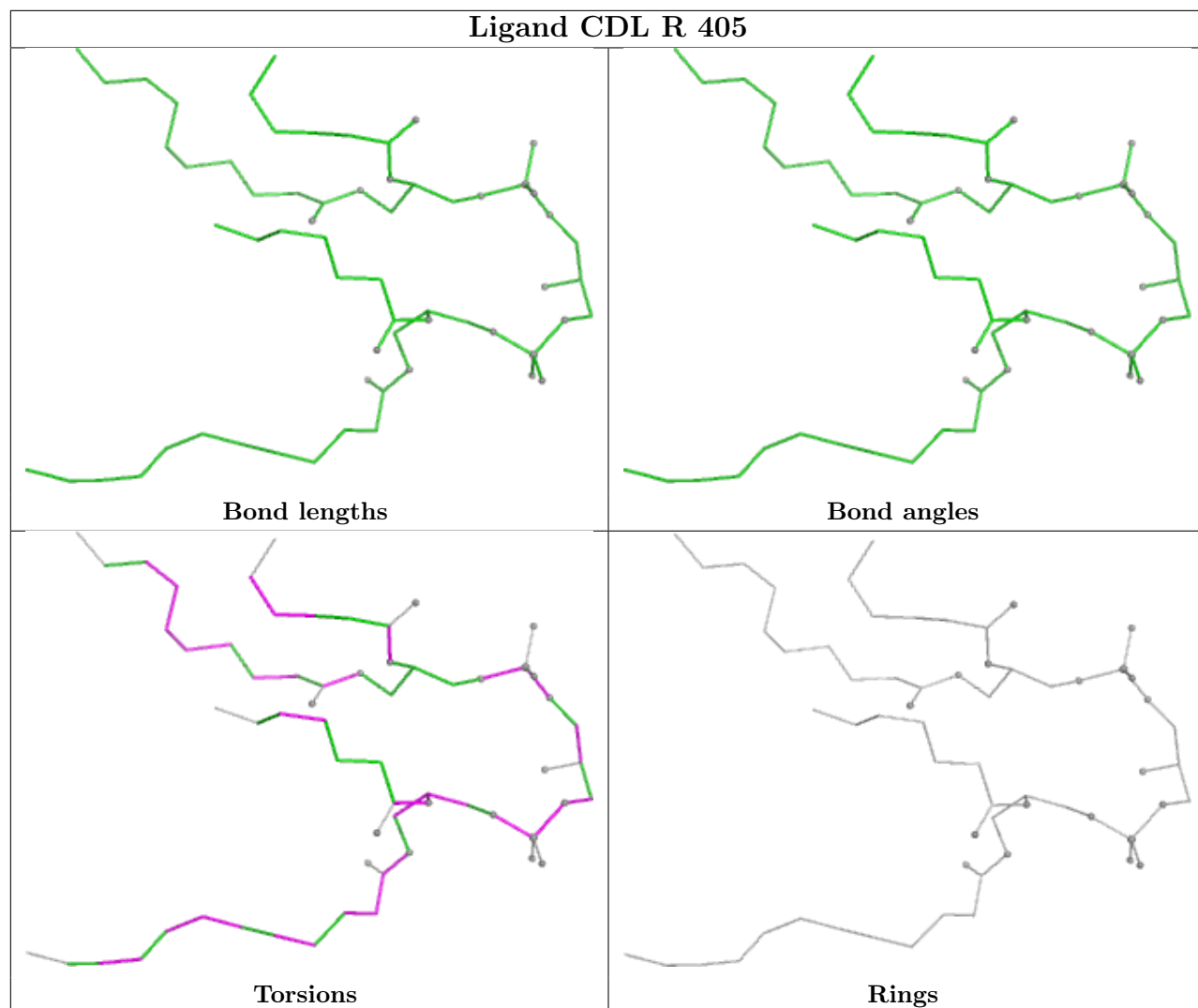


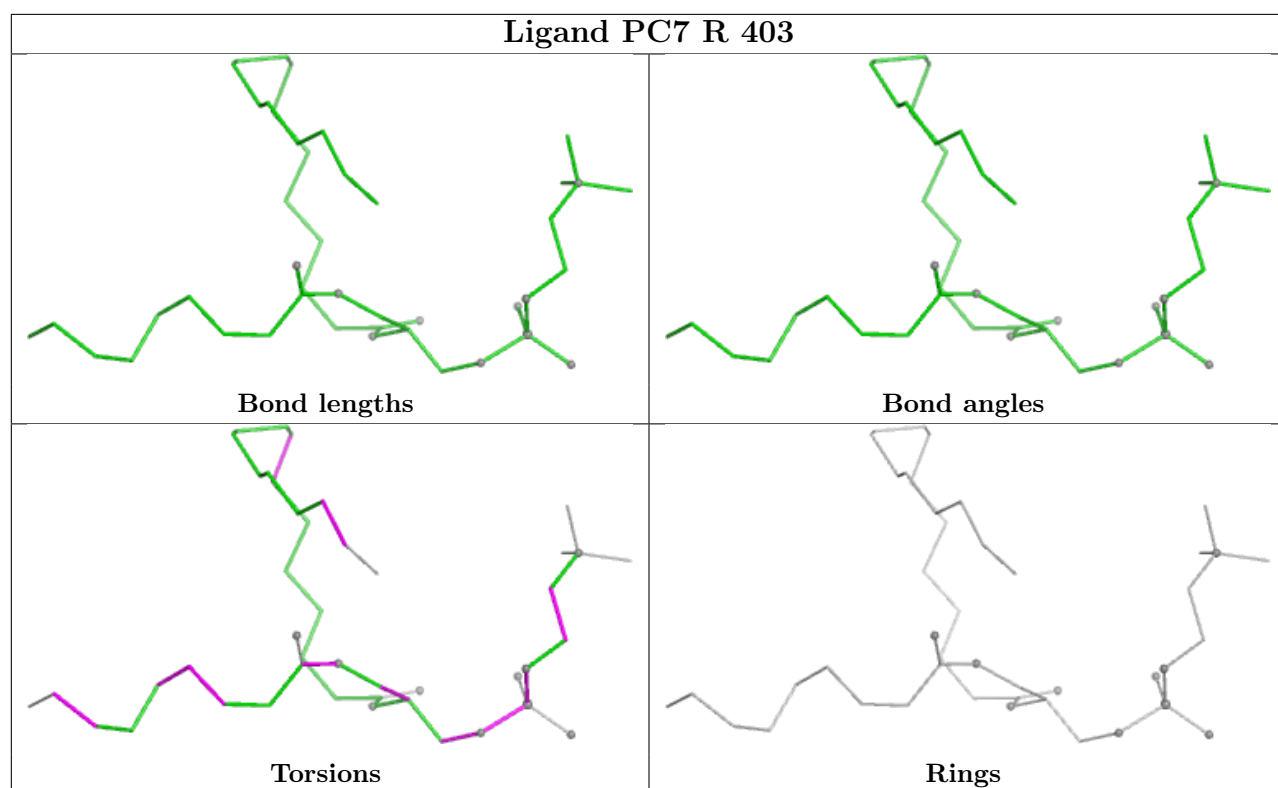
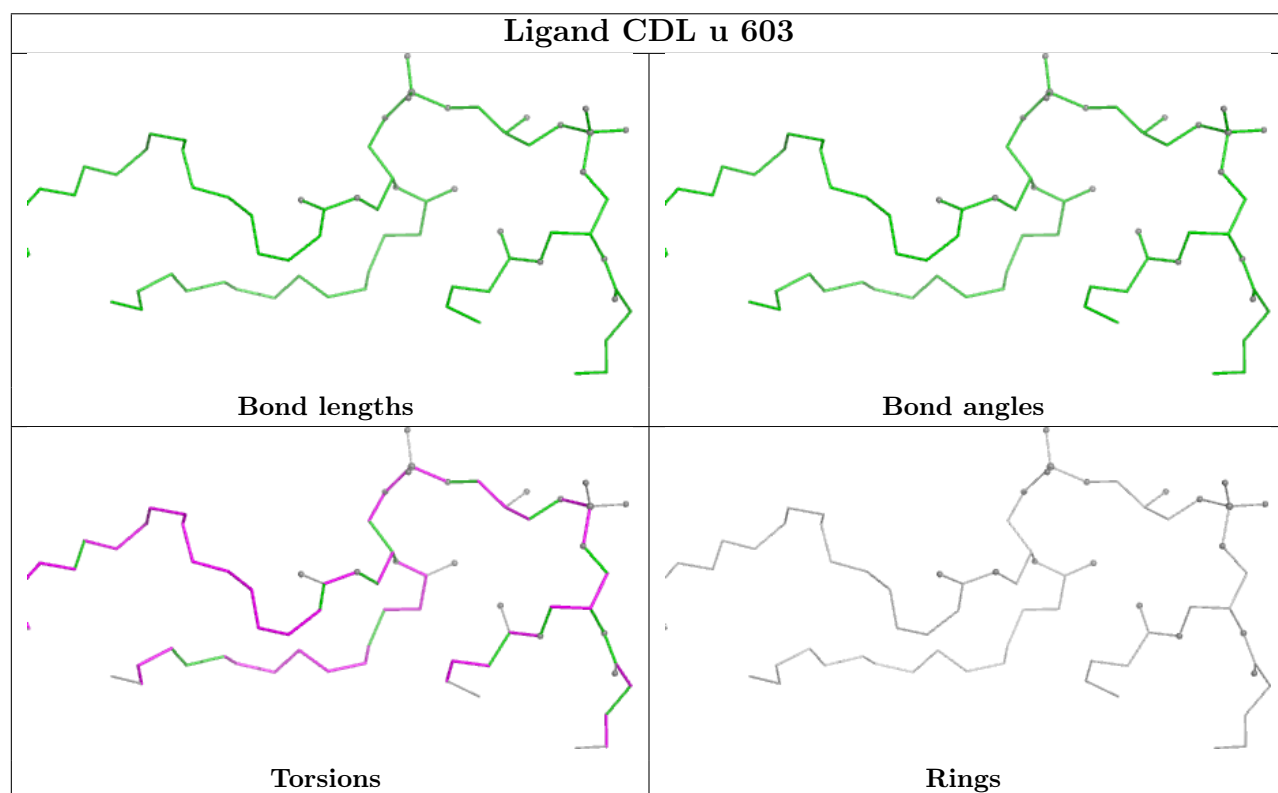


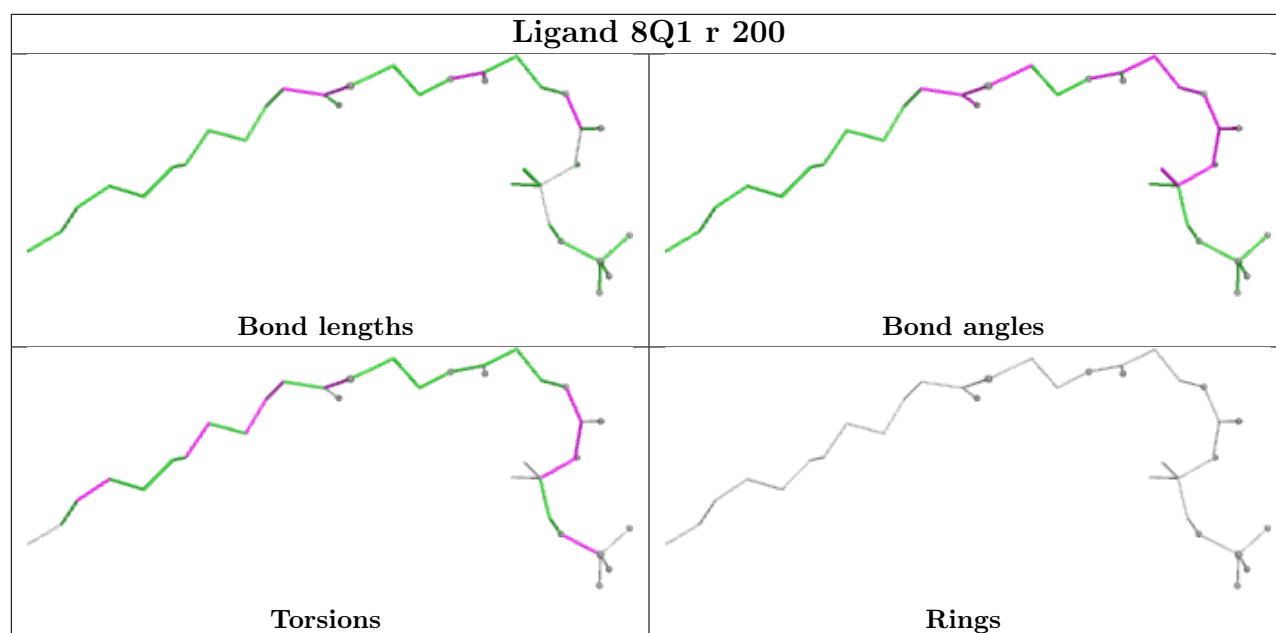
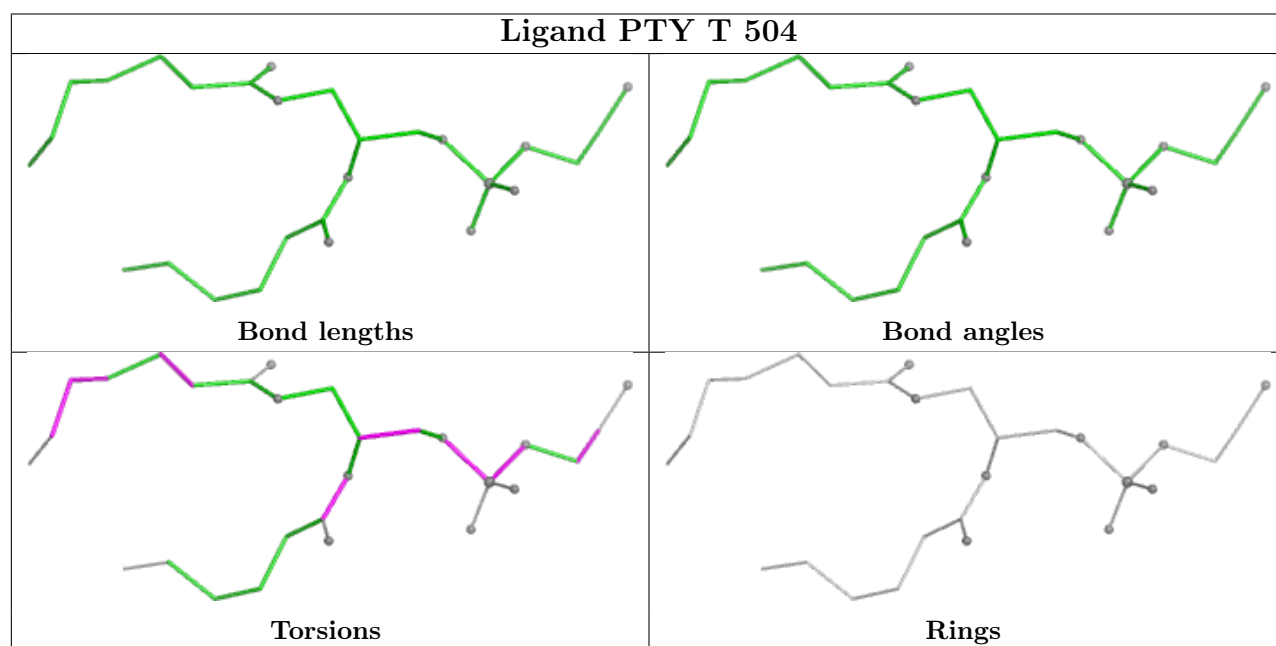


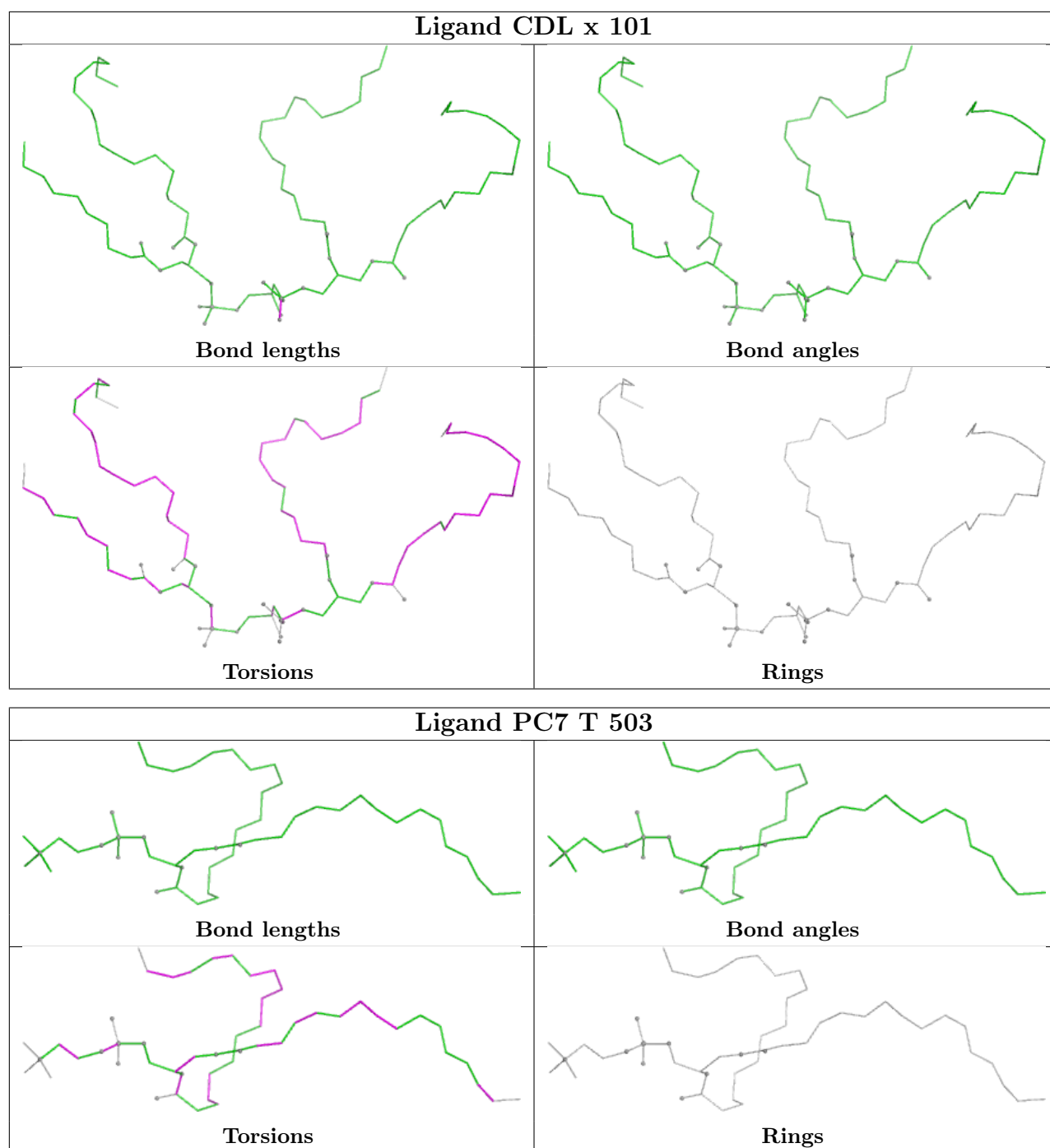


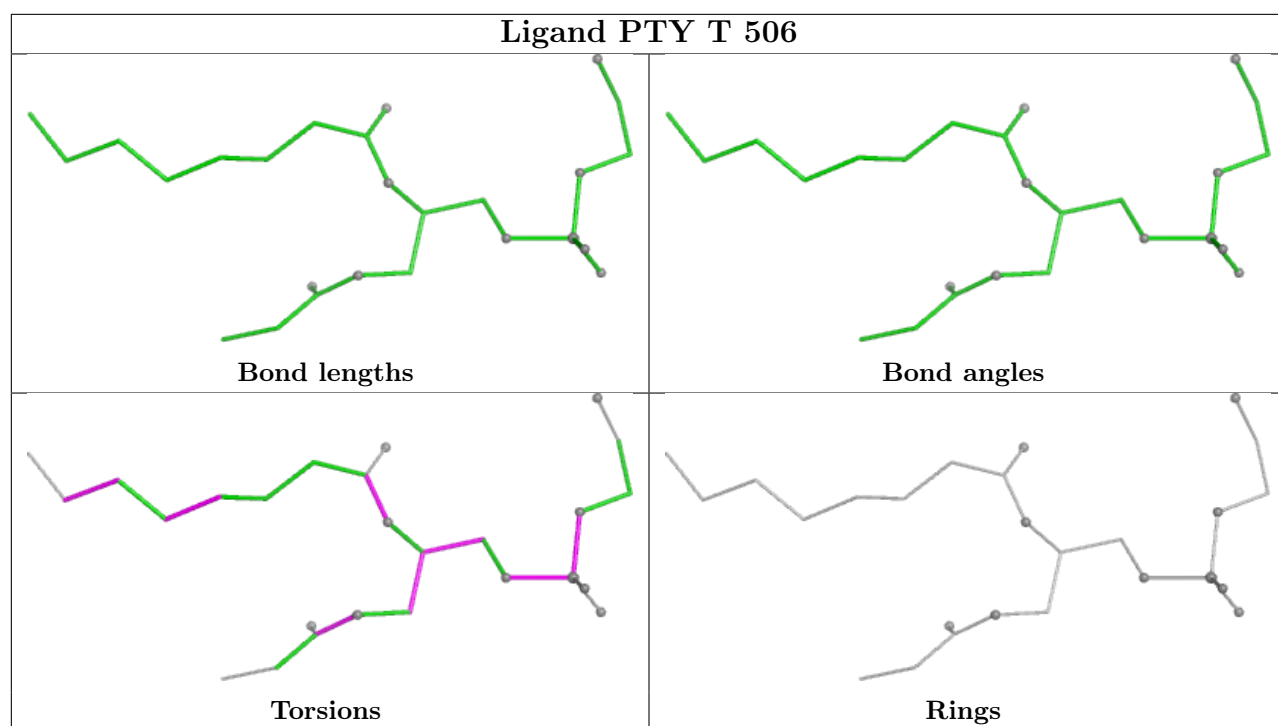
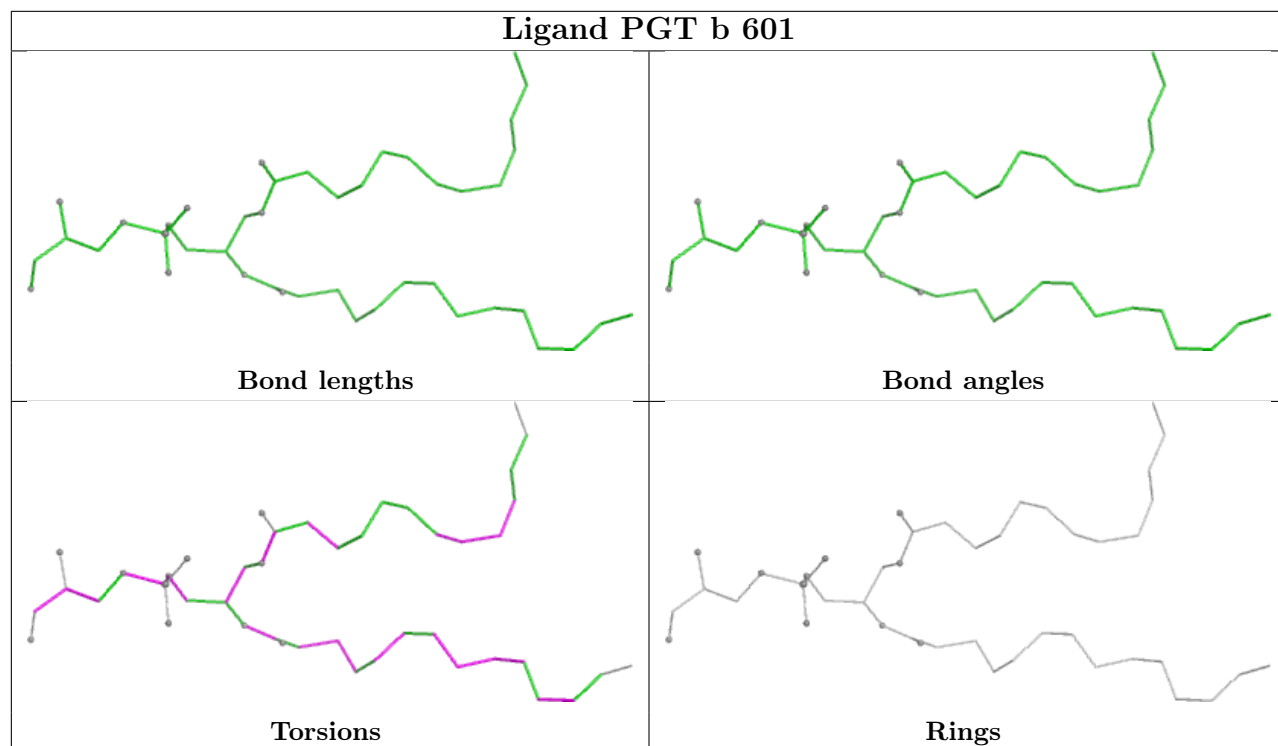


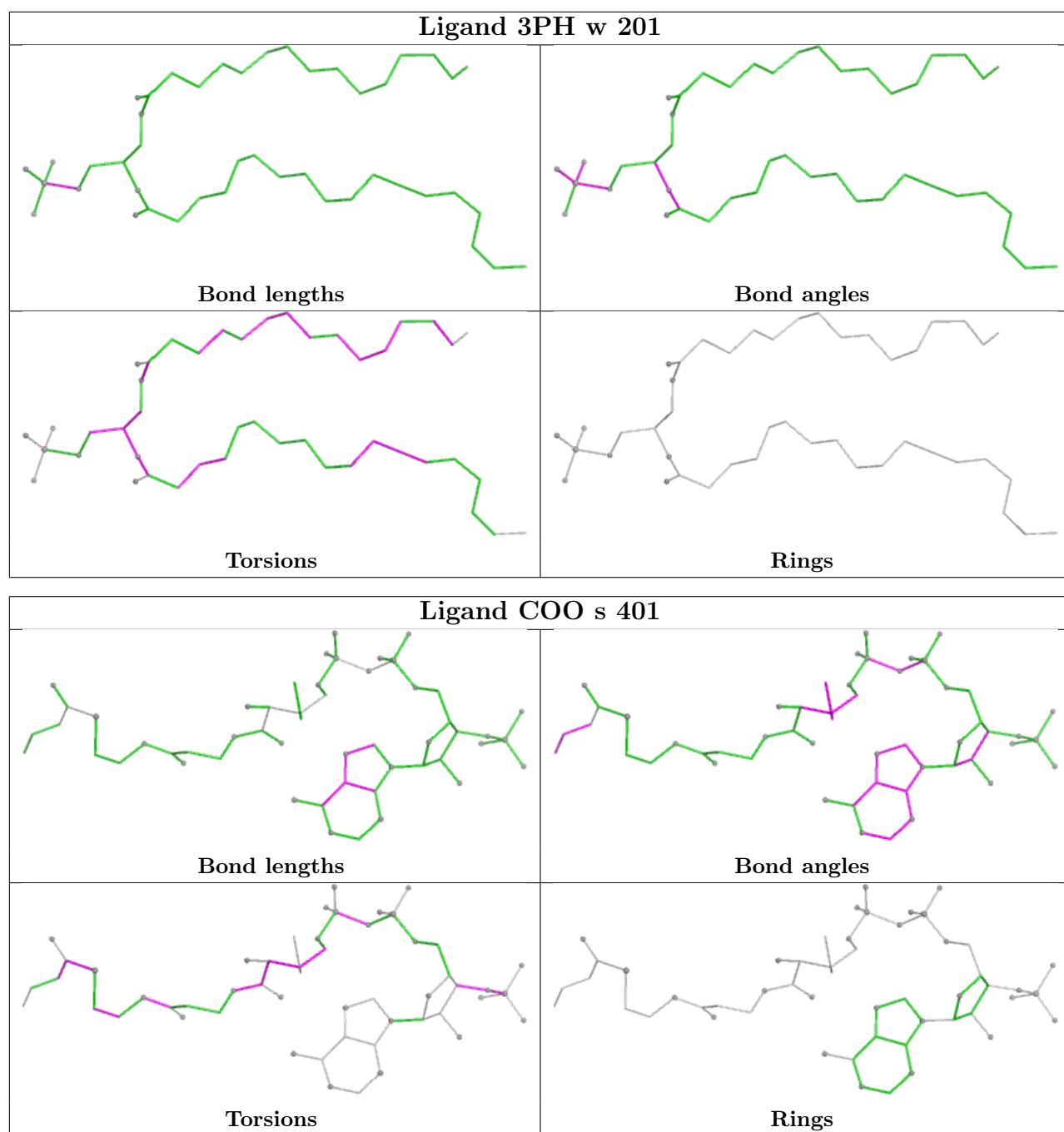


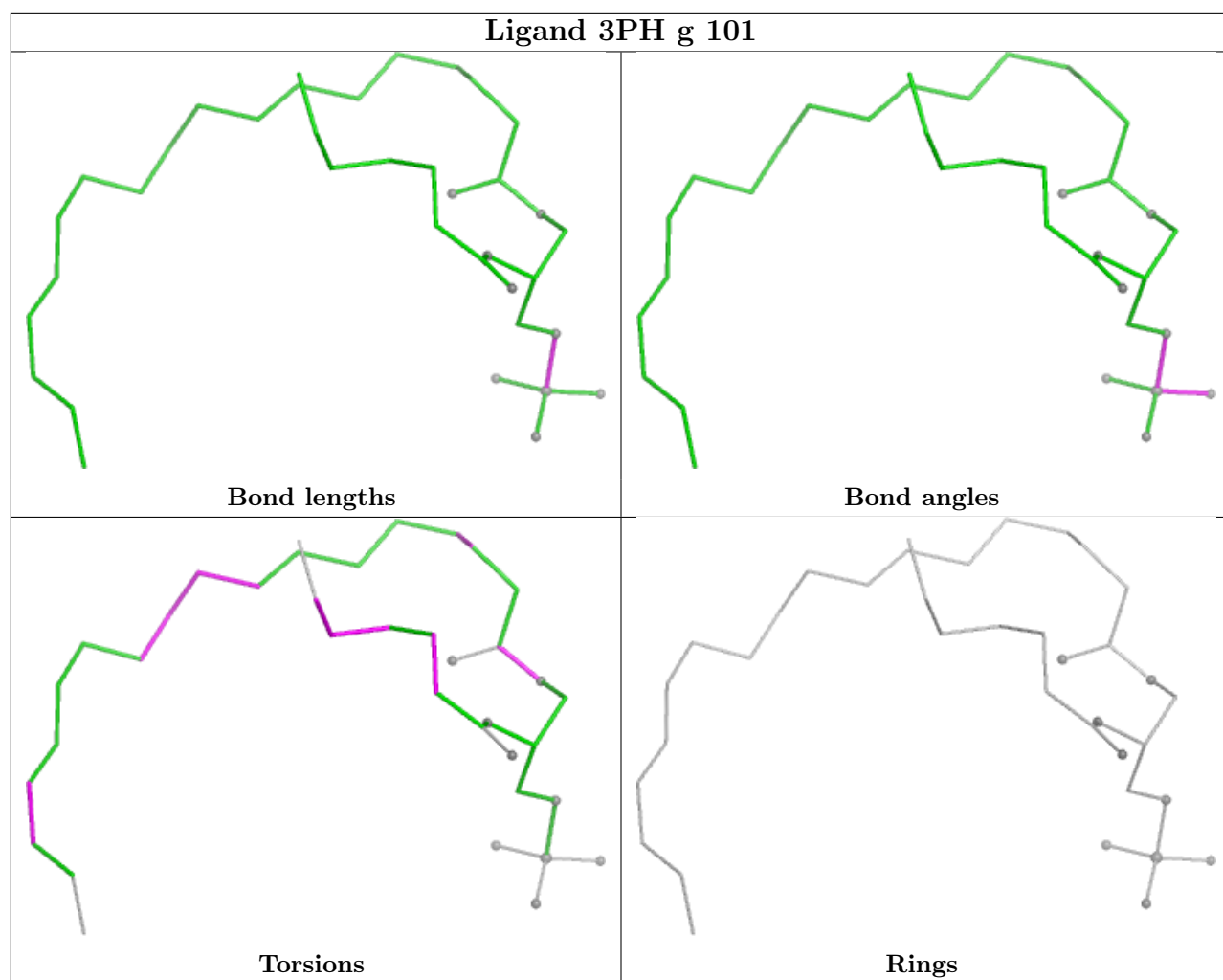
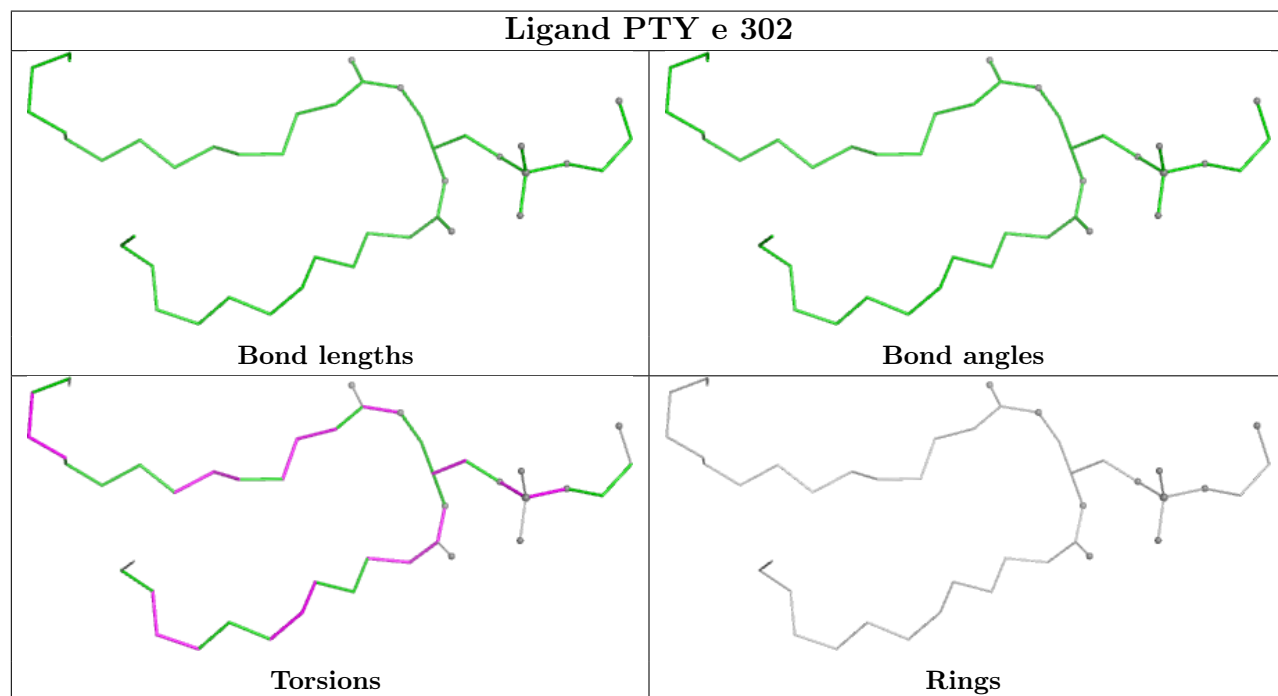


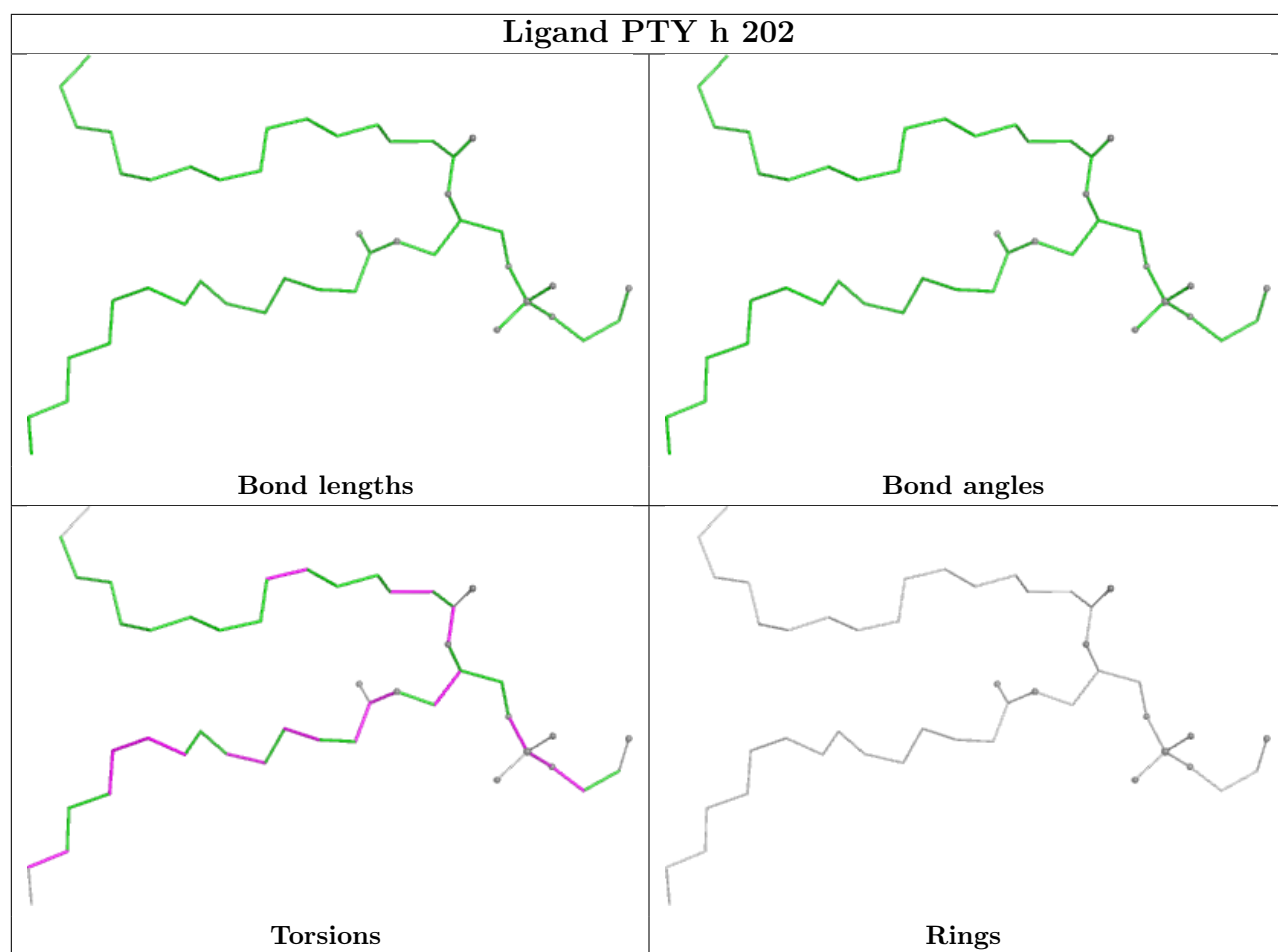


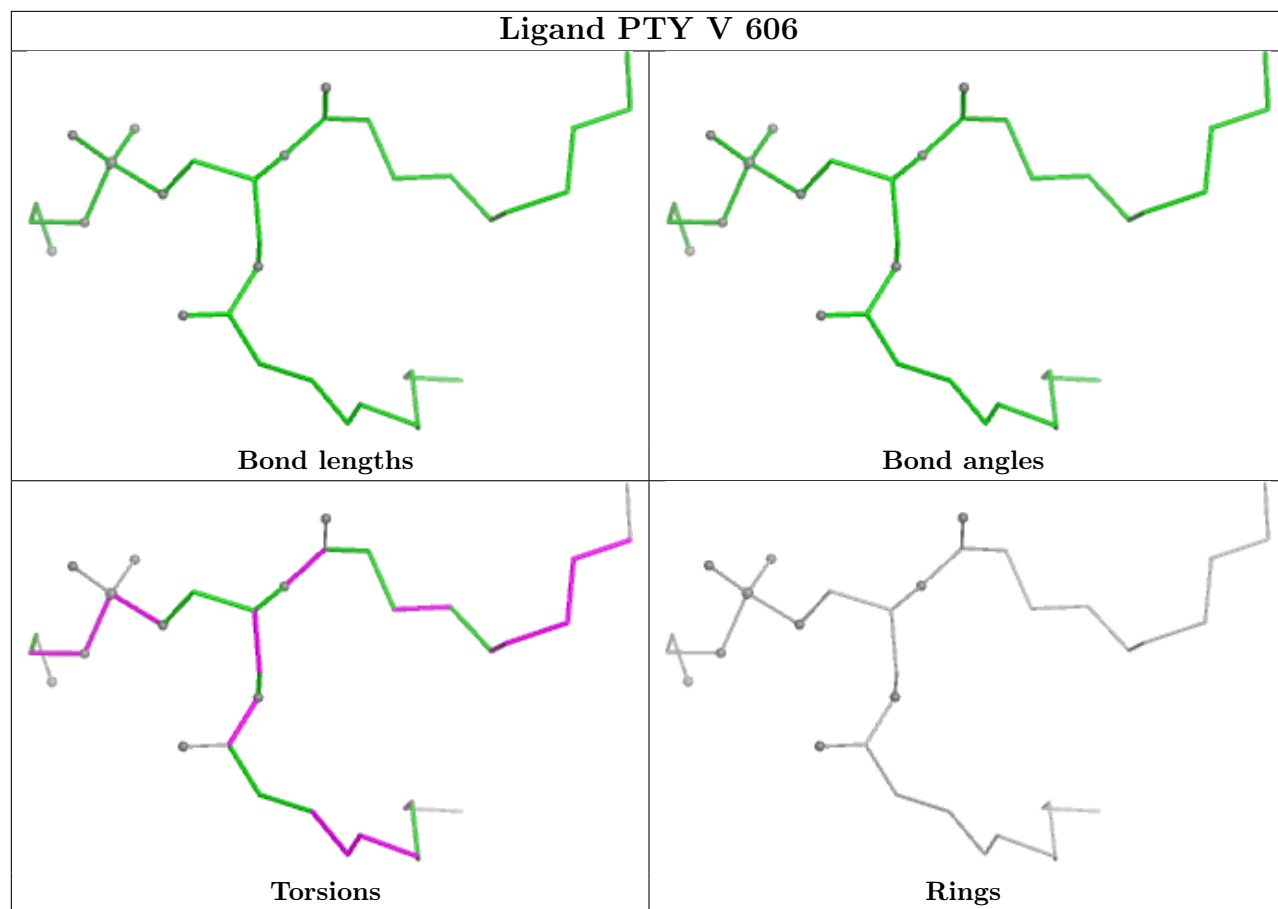


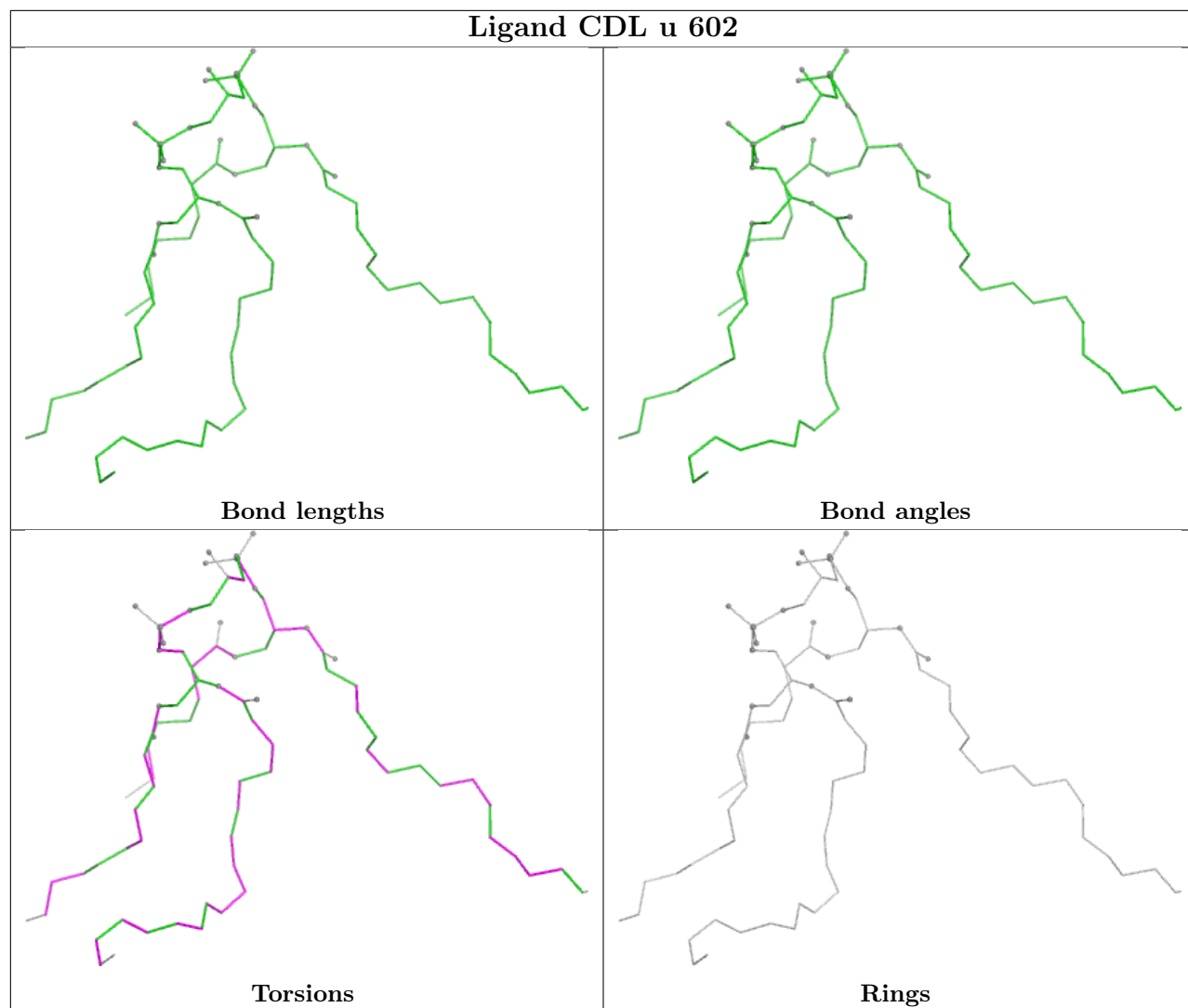


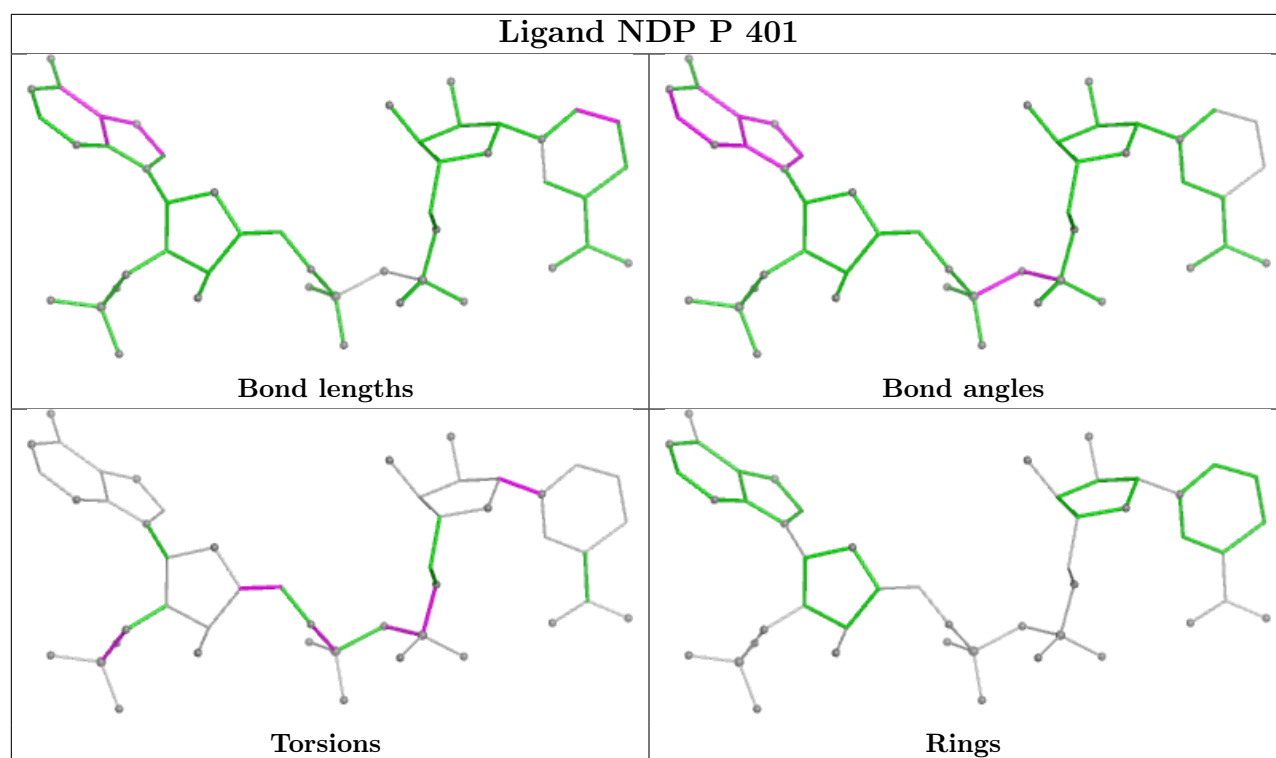
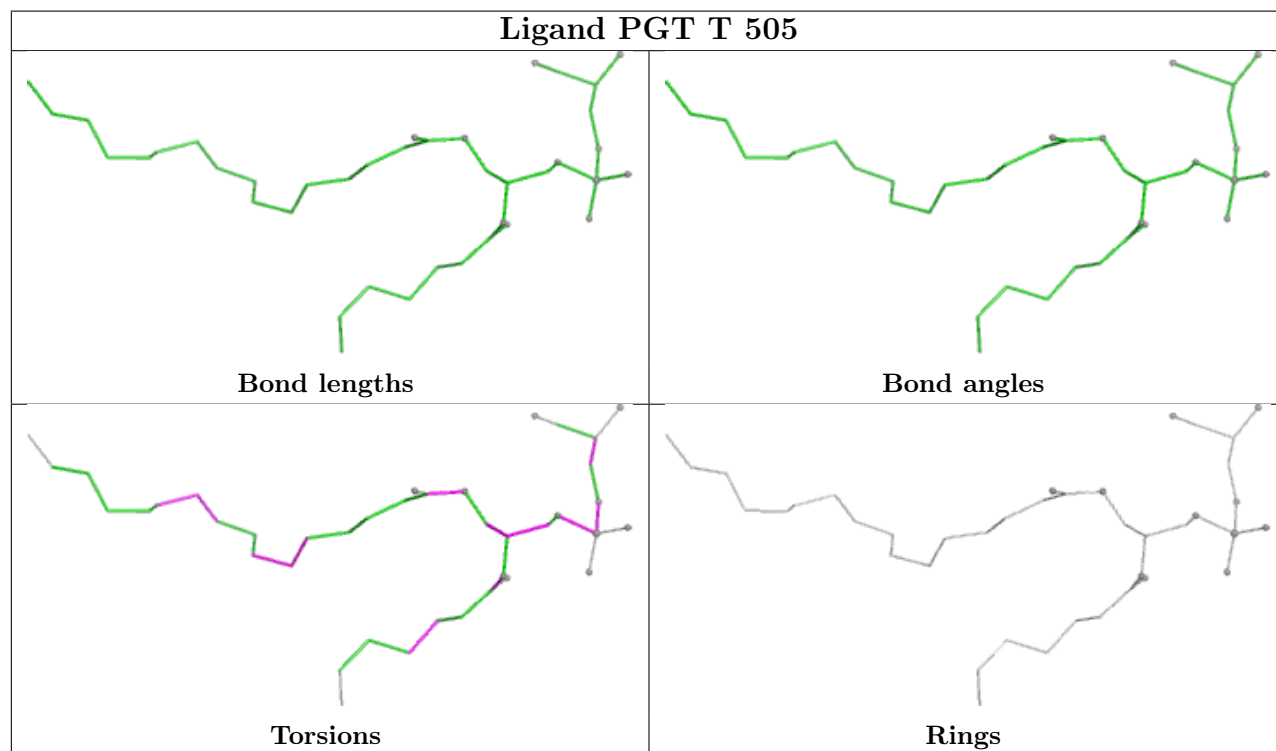


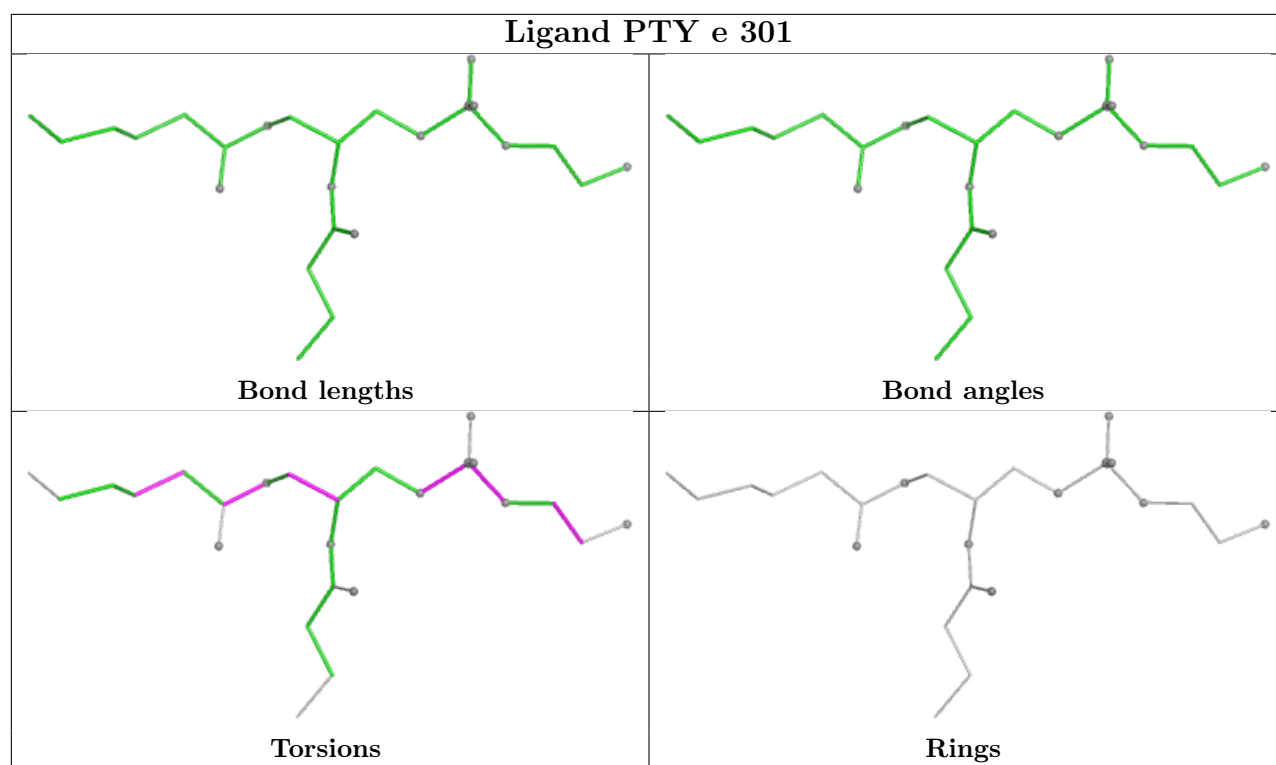
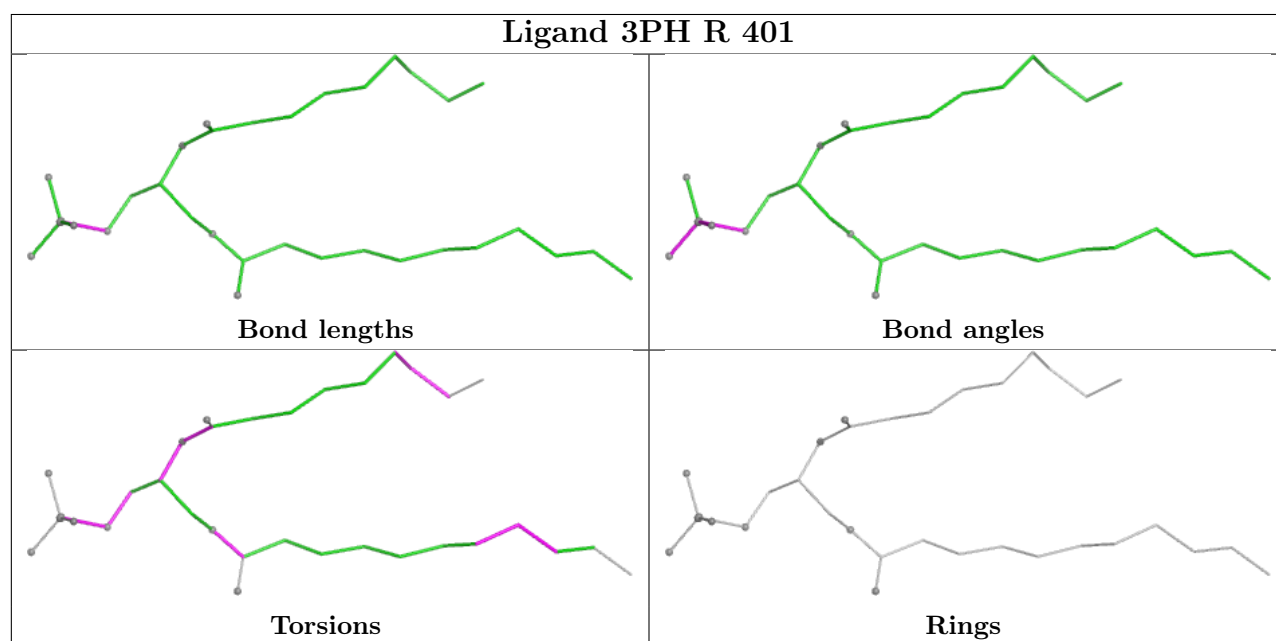


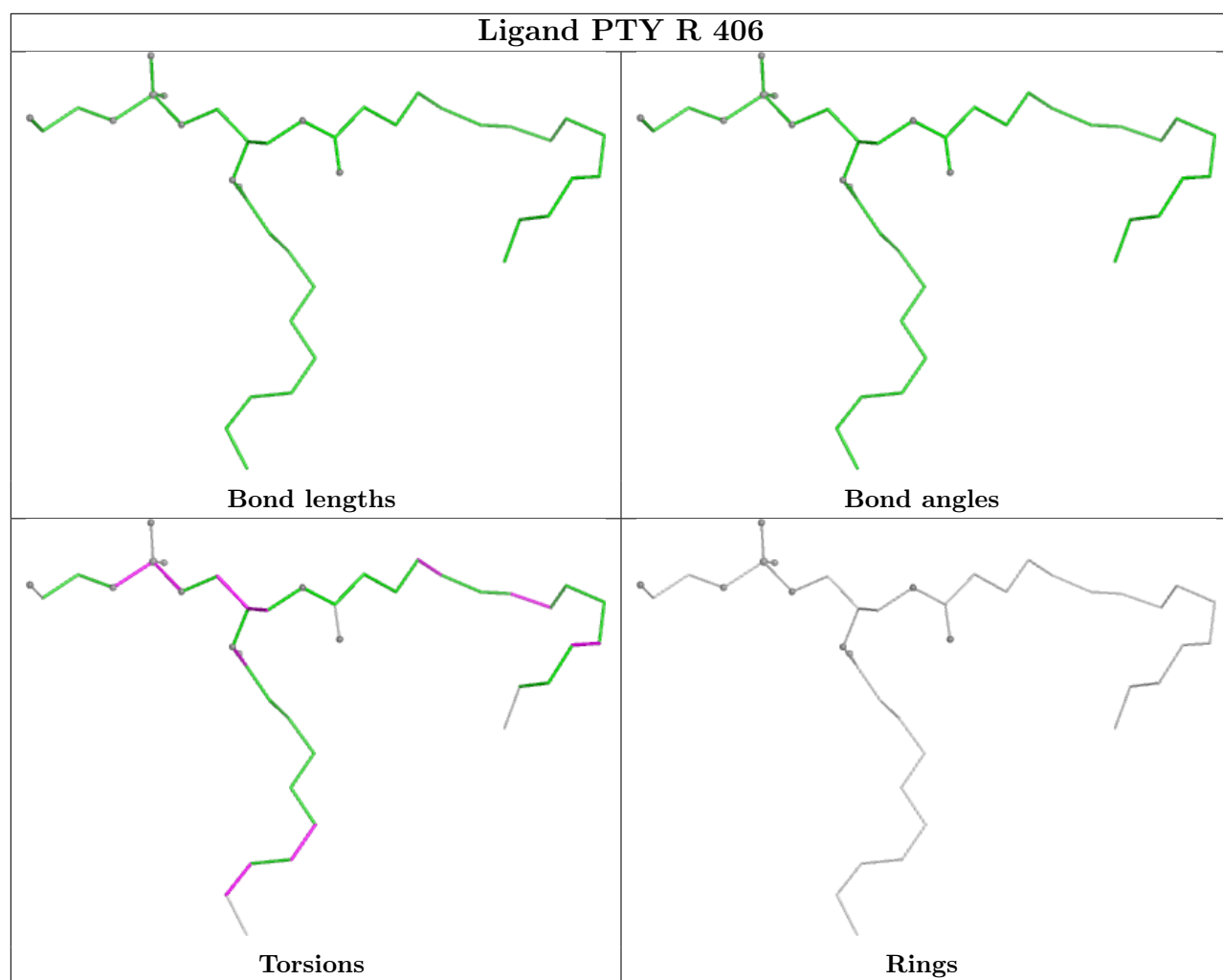
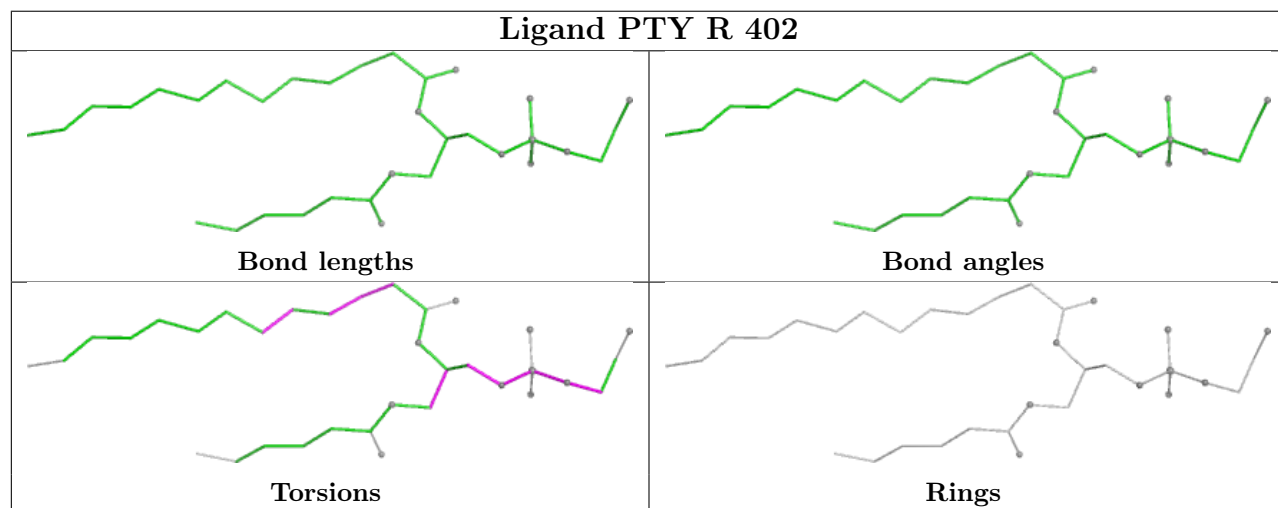


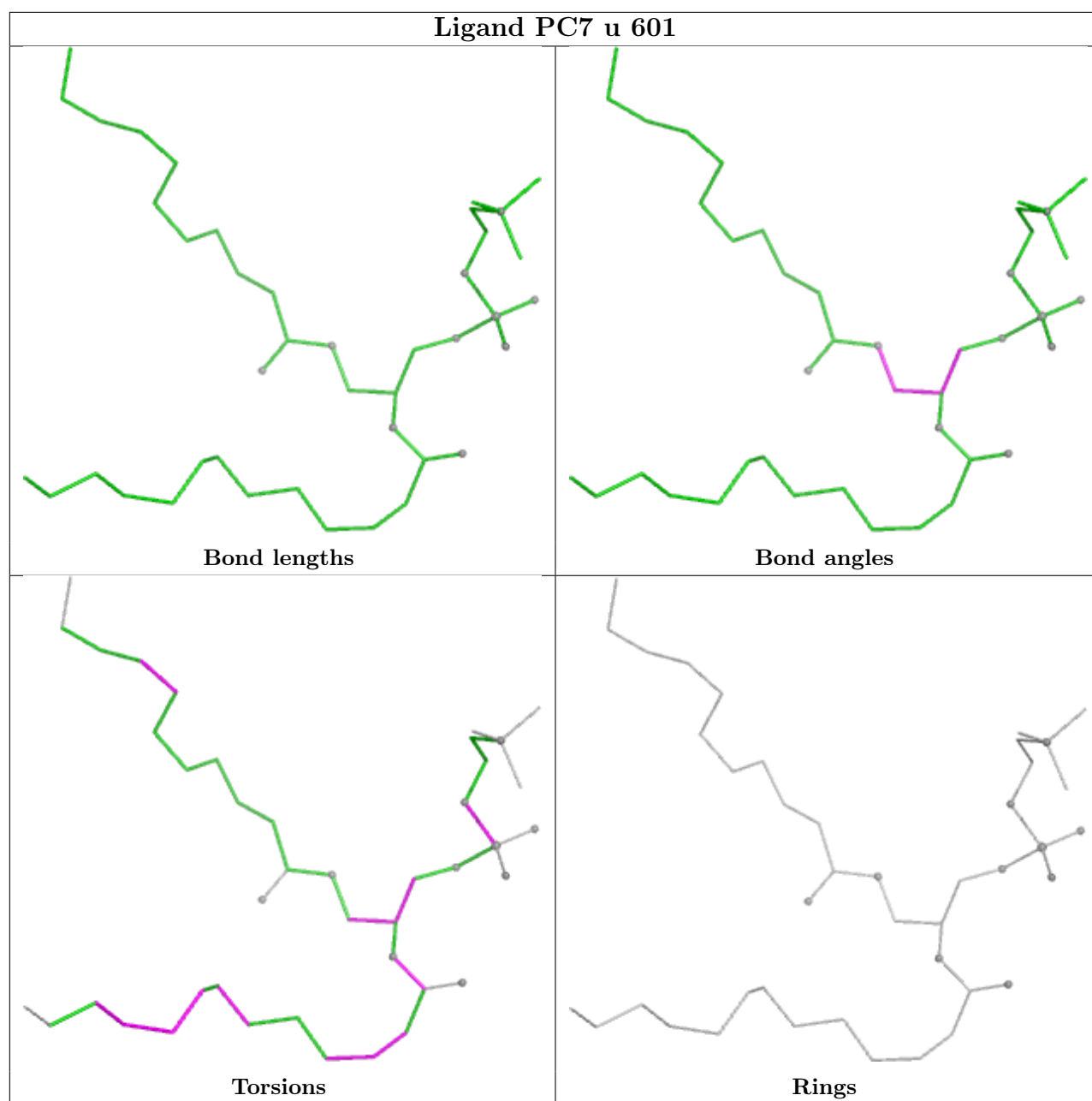












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

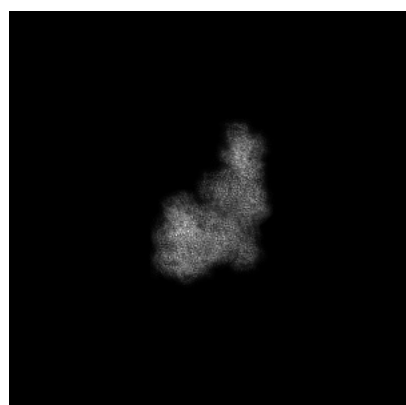
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50203. These allow visual inspection of the internal detail of the map and identification of artifacts.

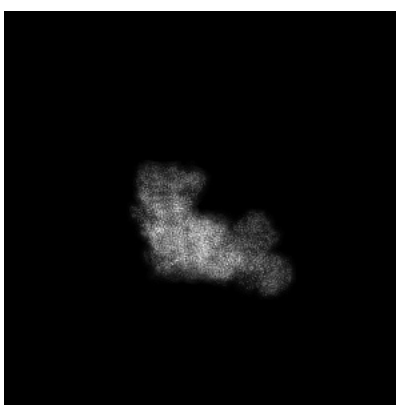
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

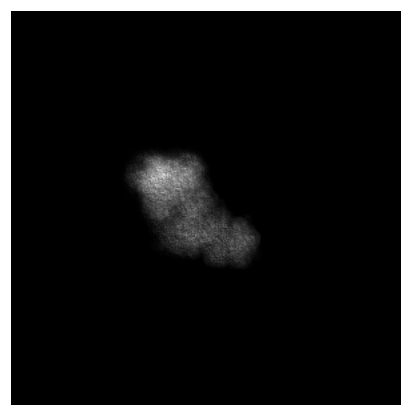
6.1.1 Primary map



X



Y

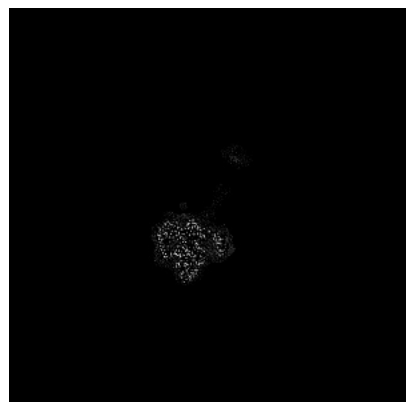


Z

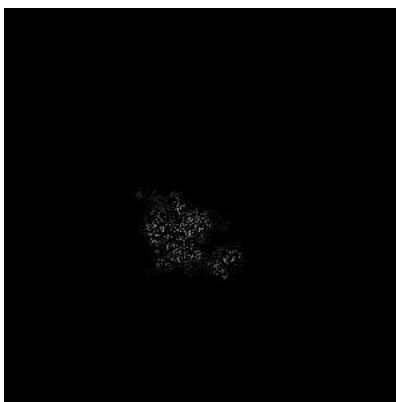
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

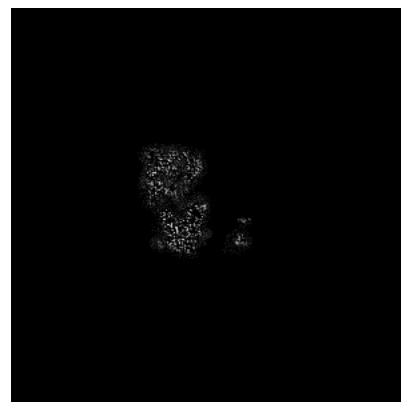
6.2.1 Primary map



X Index: 294



Y Index: 294

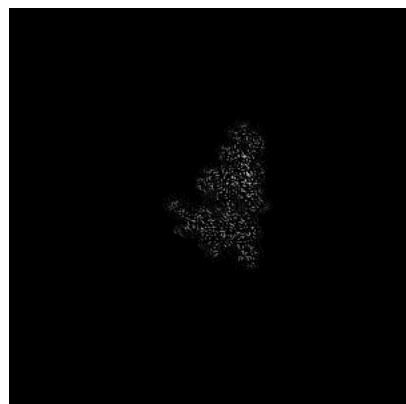


Z Index: 294

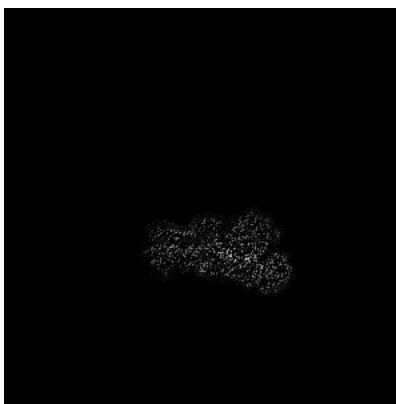
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

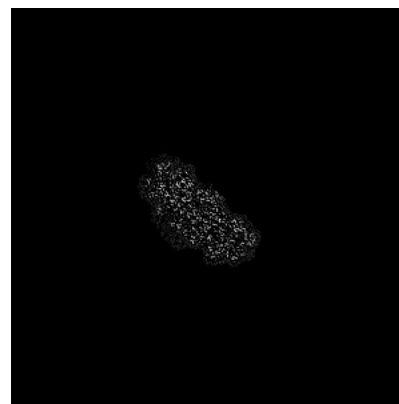
6.3.1 Primary map



X Index: 221



Y Index: 345

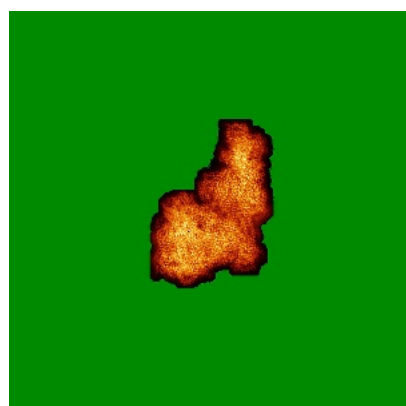


Z Index: 252

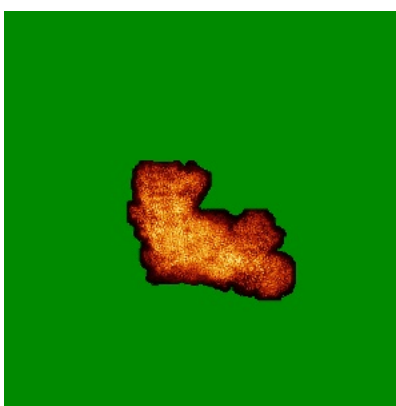
The images above show the largest variance slices of the map in three orthogonal directions.

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

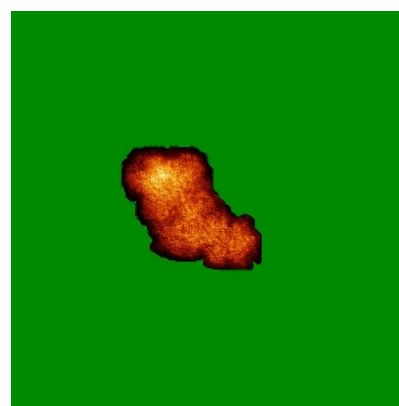
6.4.1 Primary map



X



Y

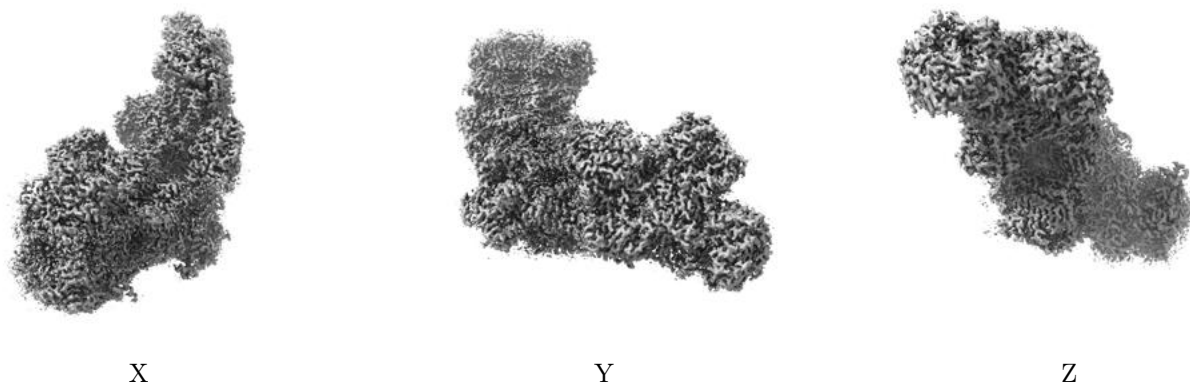


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.141. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

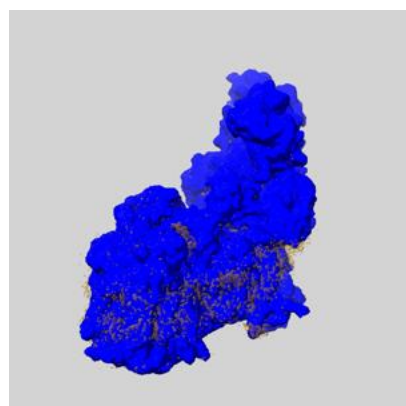
6.6 Mask visualisation [i](#)

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

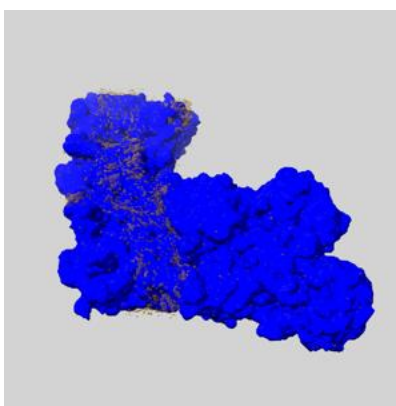
A mask typically either:

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

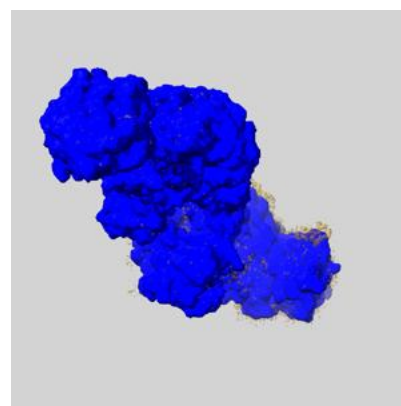
6.6.1 emd_50203_msk_1.map [i](#)



X



Y

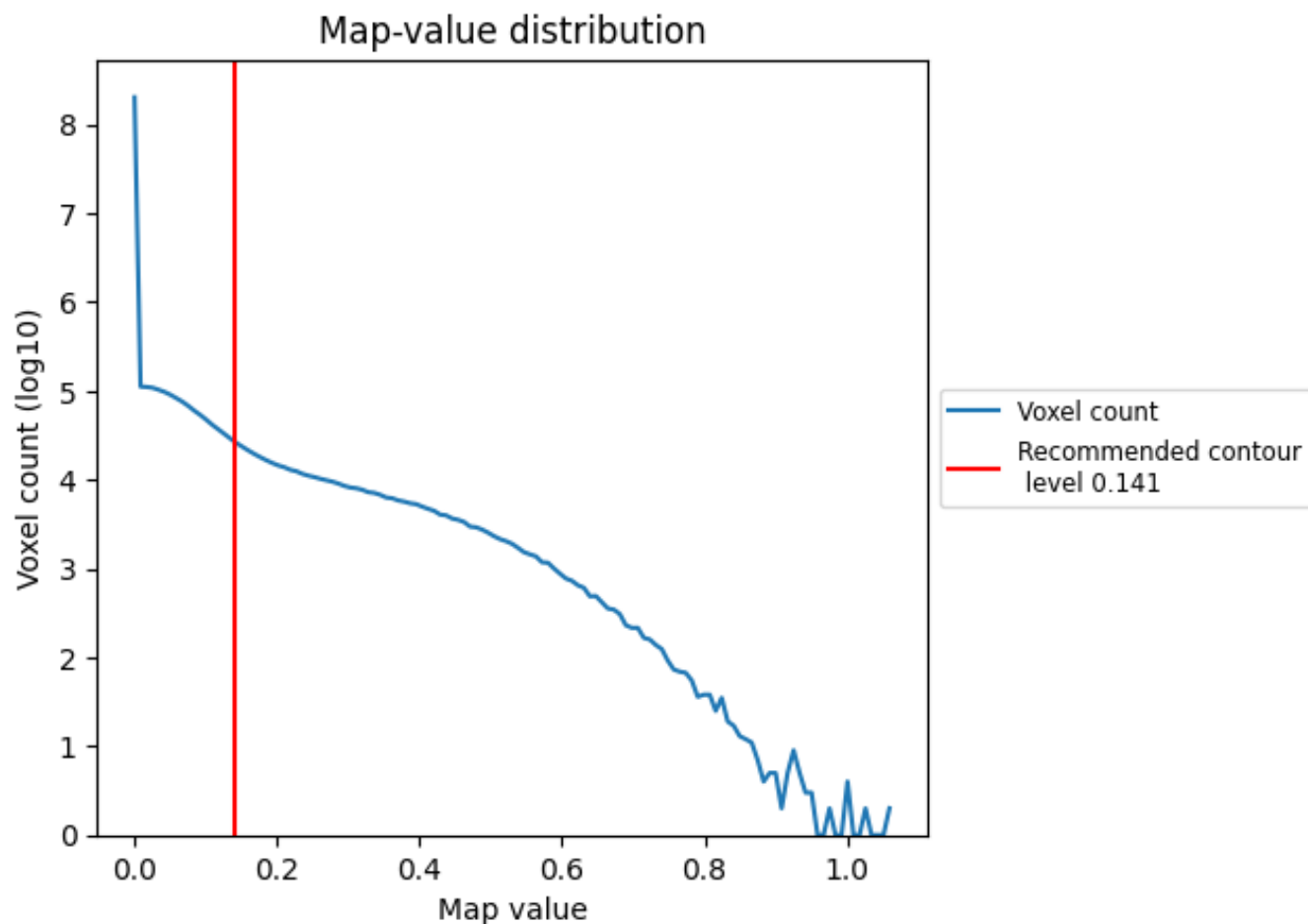


Z

7 Map analysis [i](#)

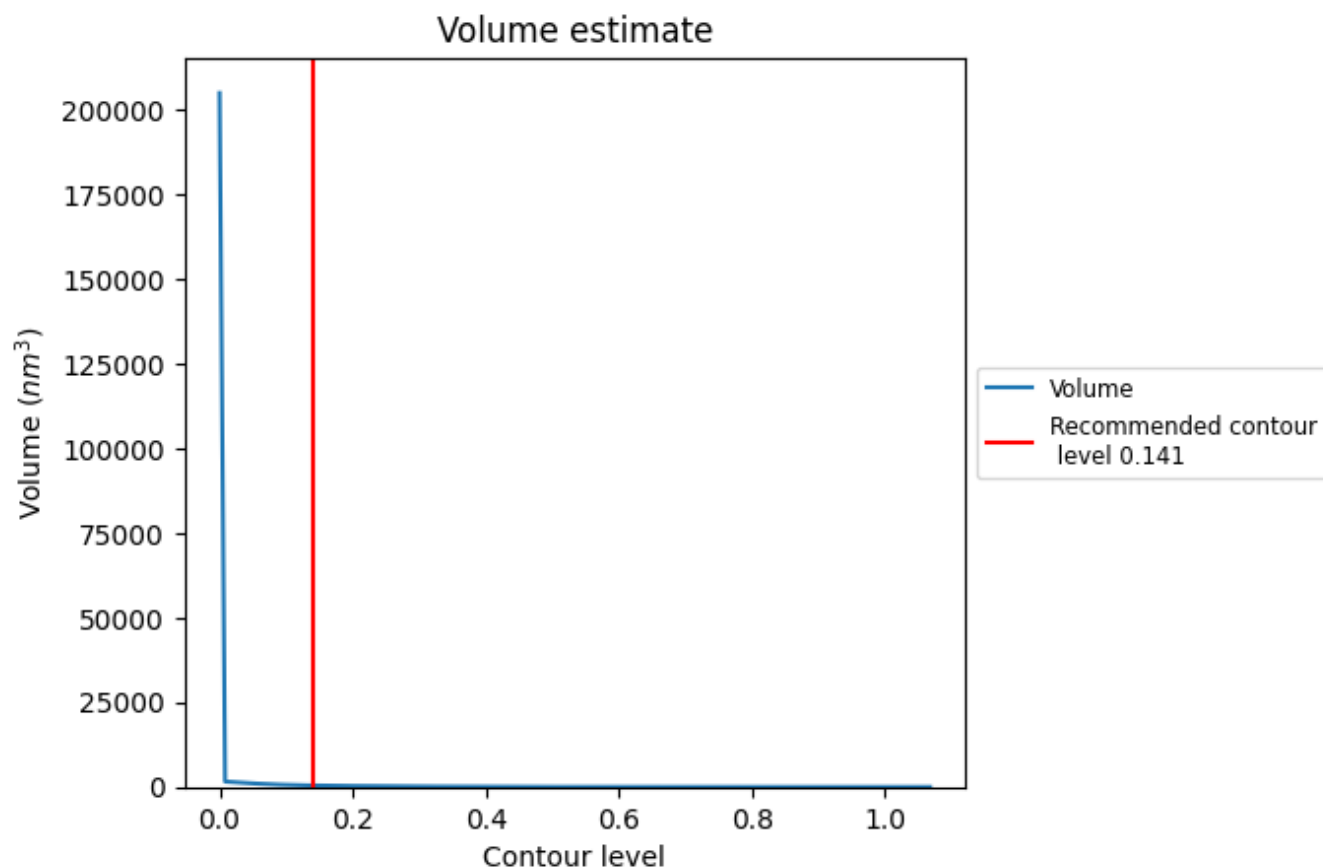
This section contains the results of statistical analysis of the map.

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.

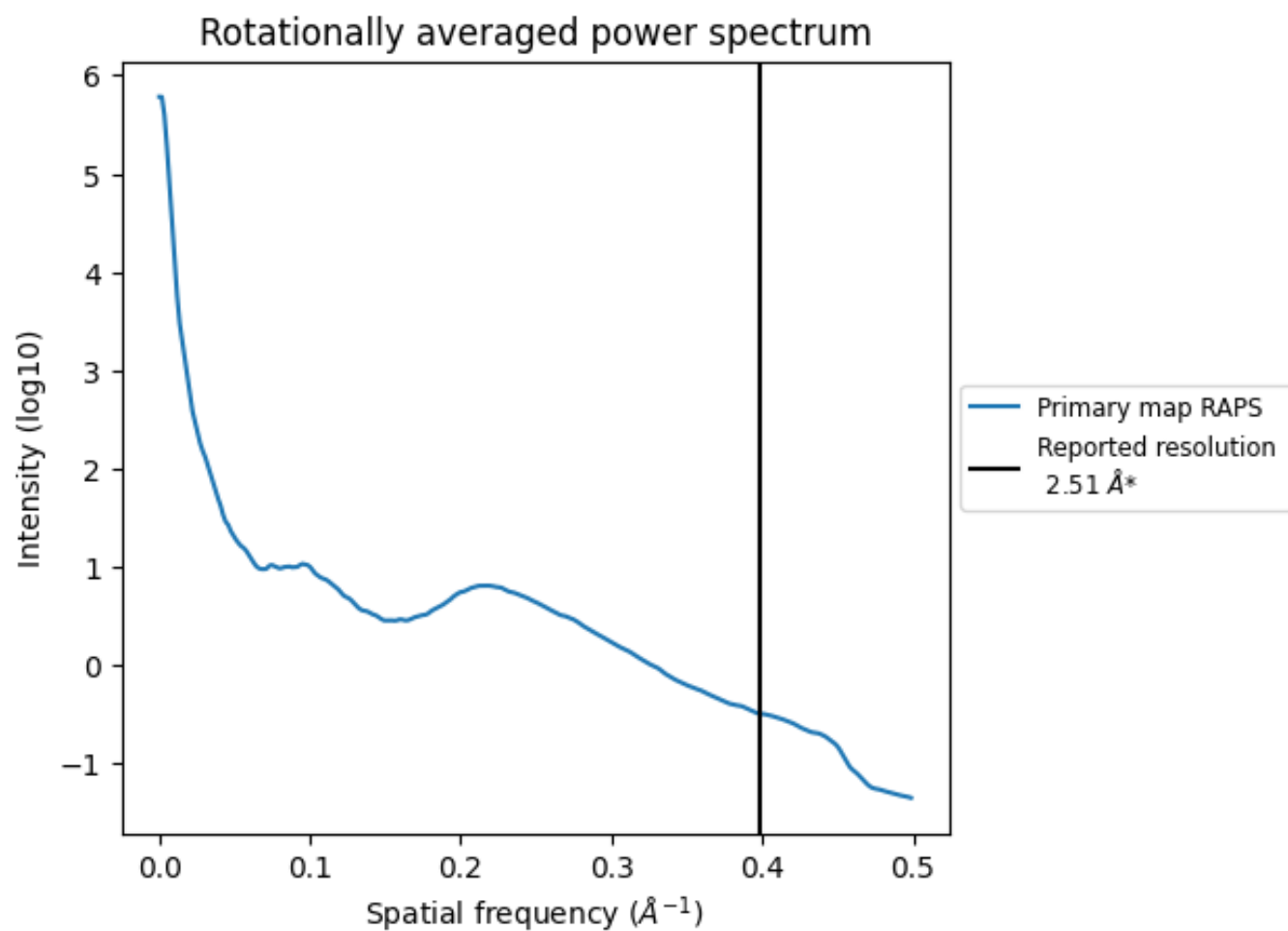
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 434 nm^3 ; this corresponds to an approximate mass of 392 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 ⓘ

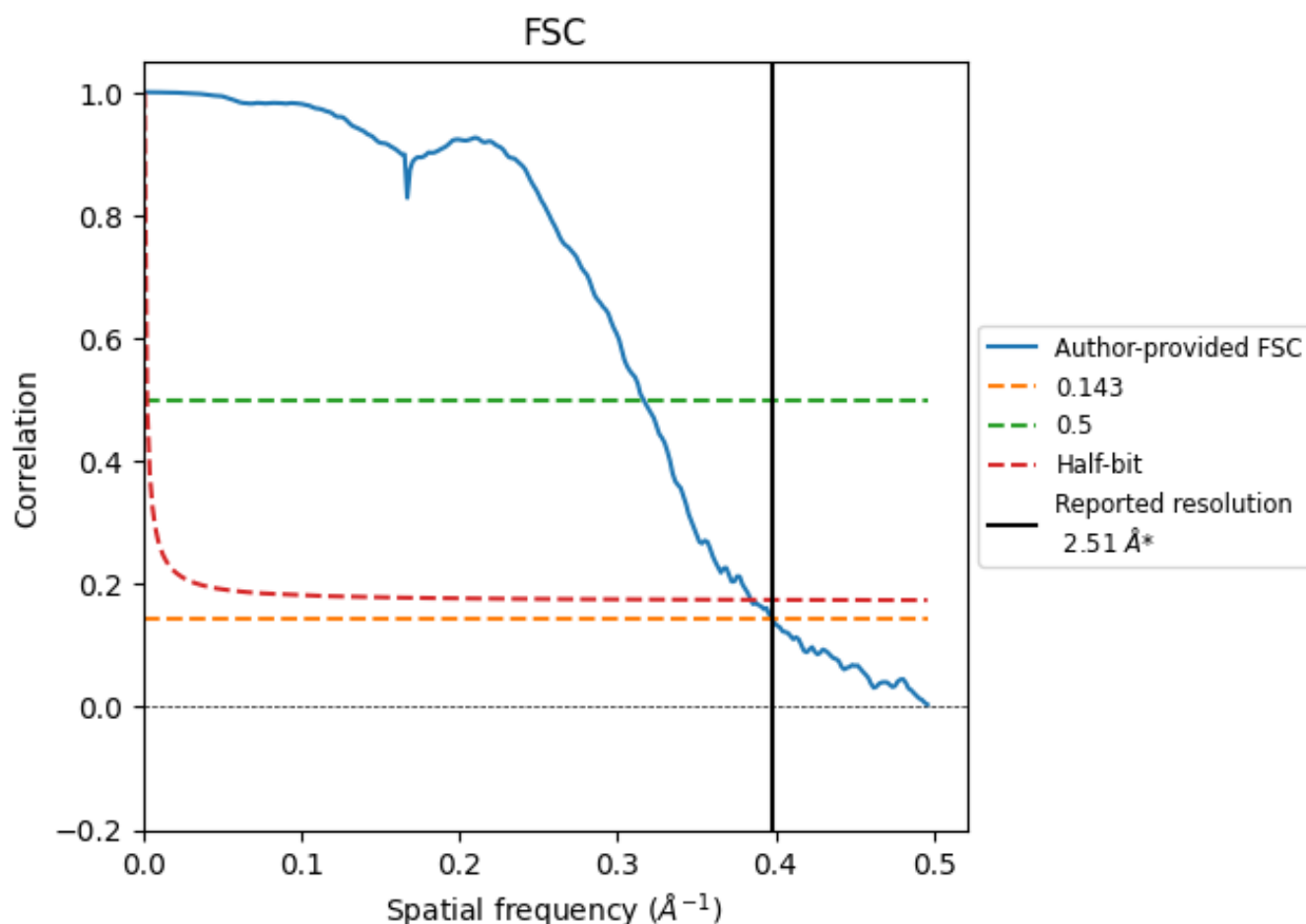


*Reported resolution corresponds to spatial frequency of 0.398 Å⁻¹

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 0.398 Å⁻¹

8.2 Resolution estimates [i](#)

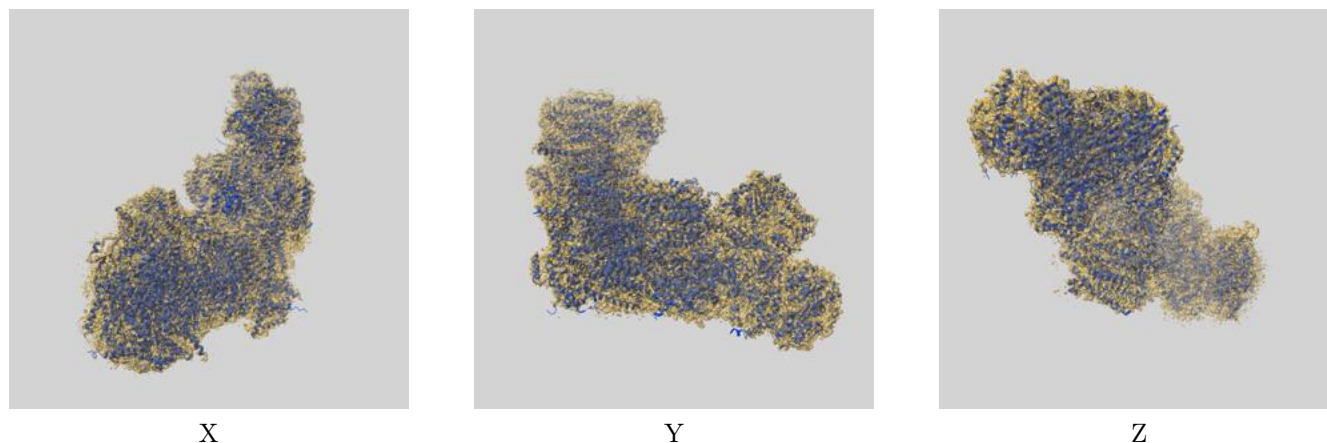
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.51	-	-
Author-provided FSC curve	2.51	3.16	2.60
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

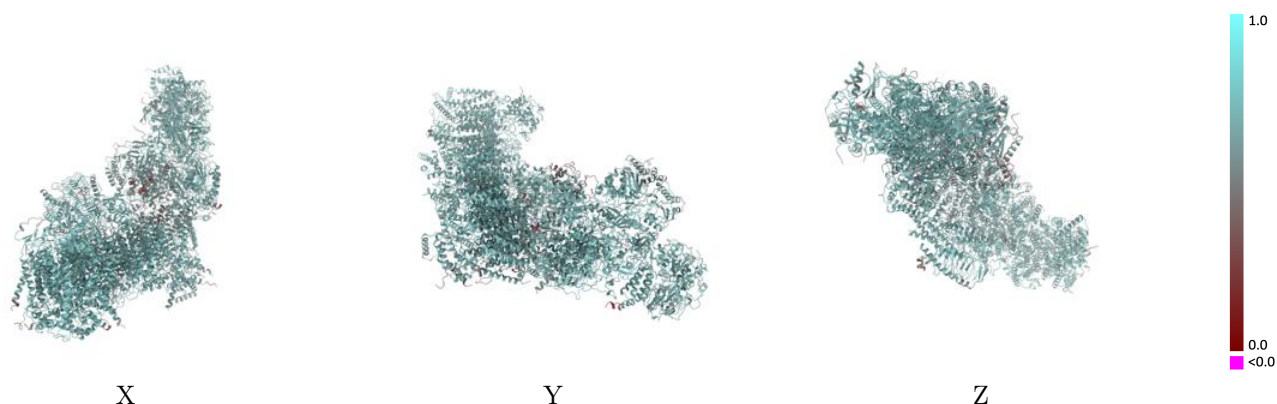
This section contains information regarding the fit between EMDB map EMD-50203 and PDB model 9F5Y. Per-residue inclusion information can be found in section [3](#) on page [24](#).

9.1 Map-model overlay [i](#)



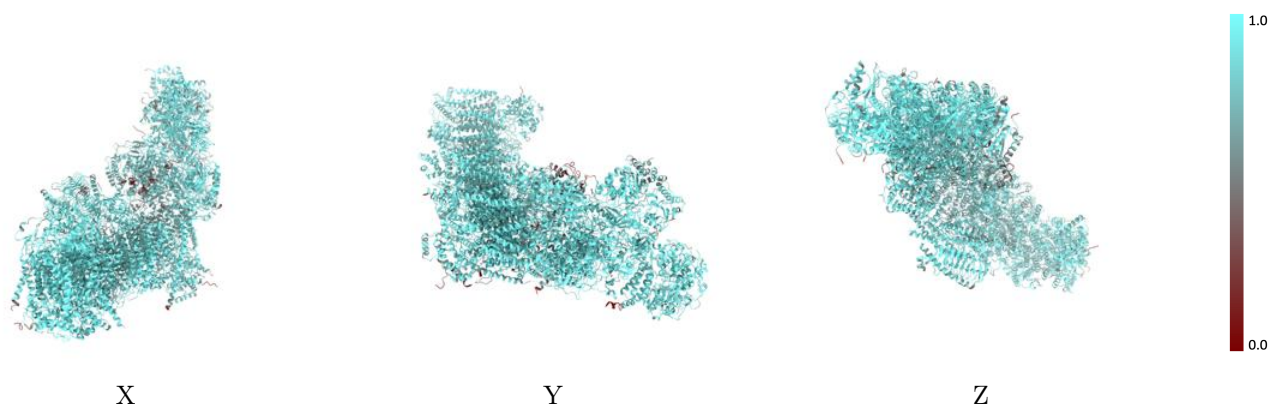
The images above show the 3D surface view of the map at the recommended contour level 0.141 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



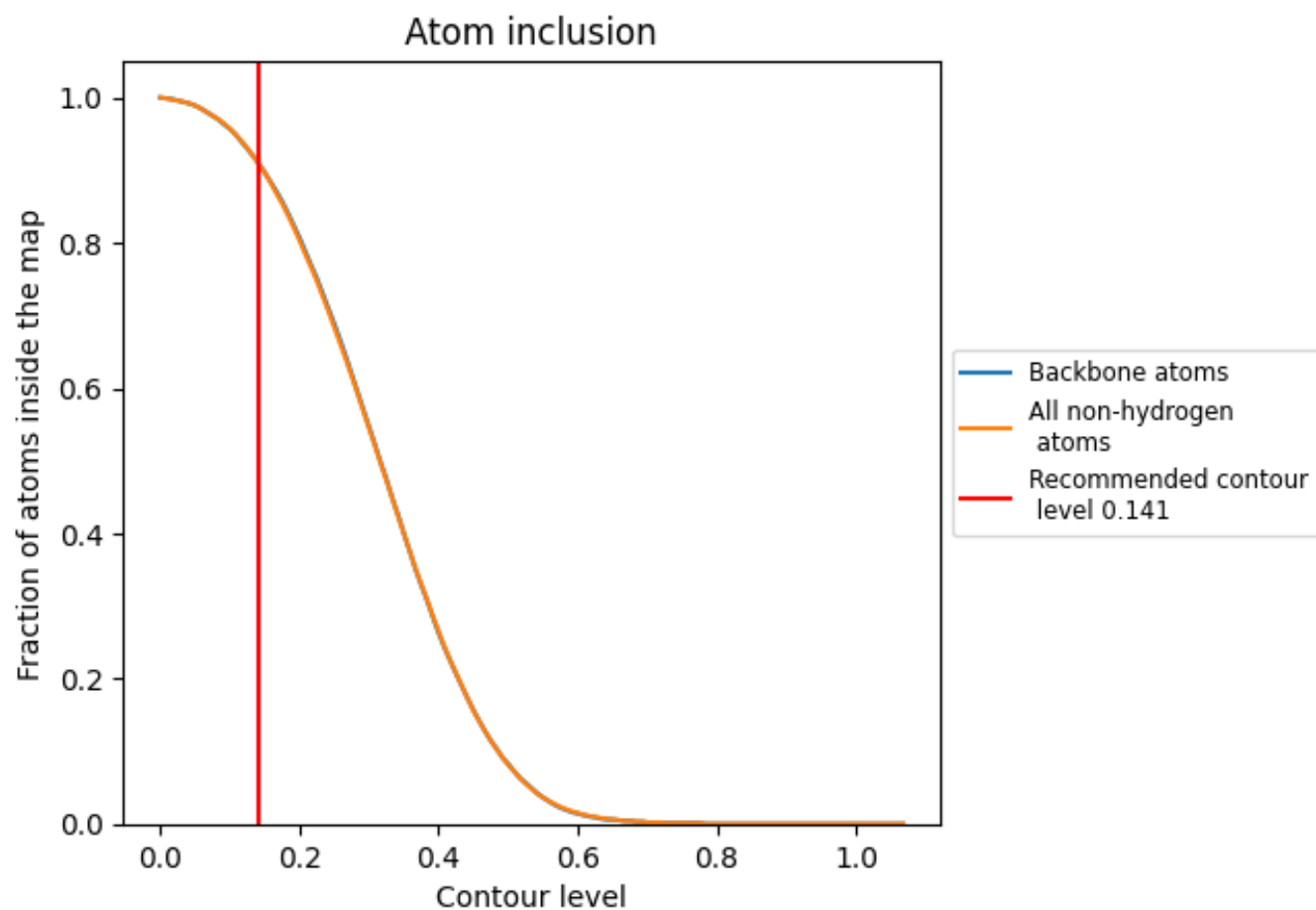
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.141).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 91% 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 (0.141) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9090	 0.6620
A	 0.8780	 0.6380
B	 0.9170	 0.6520
C	 0.9200	 0.6640
D	 0.9500	 0.6840
E	 0.9470	 0.6730
F	 0.9480	 0.6620
G	 0.9390	 0.6720
H	 0.8900	 0.6480
I	 0.8450	 0.6330
J	 0.5040	 0.4580
K	 0.7710	 0.5790
L	 0.8820	 0.6440
M	 0.8960	 0.6650
N	 0.8970	 0.6540
O	 0.7580	 0.5770
P	 0.8800	 0.6270
Q	 0.9240	 0.6520
R	 0.9450	 0.6840
S	 0.9150	 0.6560
T	 0.9710	 0.7050
U	 0.9550	 0.6910
V	 0.9620	 0.6990
W	 0.9190	 0.6630
X	 0.9600	 0.6950
Y	 0.8980	 0.6440
Z	 0.9250	 0.6820
a	 0.8750	 0.6360
b	 0.9210	 0.6870
c	 0.6900	 0.5460
d	 0.9350	 0.6700
e	 0.9500	 0.6790
f	 0.8990	 0.6490
g	 0.7460	 0.5720
h	 0.9030	 0.6750



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Chain	Atom inclusion	Q-score
i	 0.8940	 0.6610
j	 0.9370	 0.6780
k	 0.9370	 0.6800
l	 0.8550	 0.6300
m	 0.8840	 0.6450
n	 0.8340	 0.6300
o	 0.9440	 0.6840
p	 0.9140	 0.6620
q	 0.9200	 0.6730
r	 0.8600	 0.6350
s	 0.8950	 0.6520
t	 0.9480	 0.6940
u	 0.9060	 0.6670
v	 0.8770	 0.6370
w	 0.9070	 0.6680
x	 0.9110	 0.6670
y	 0.9240	 0.6780