



Full wwPDB EM Validation Report ⓘ

Apr 1, 2025 – 08:37 pm BST

PDB ID : 6ZKT / pdb_00006zkt
EMDB ID : EMD-11261
Title : Deactive complex I, open2
Authors : Kampjut, D.; Sazanov, L.A.
Deposited on : 2020-06-30
Resolution : 2.80 Å(reported)
Based on initial model : 5LNK

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev117
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

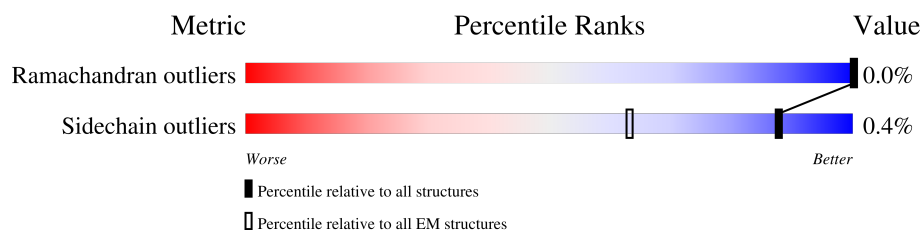
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

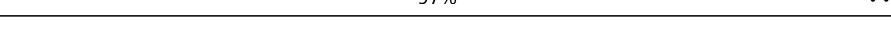
The reported resolution of this entry is 2.80 Å.

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



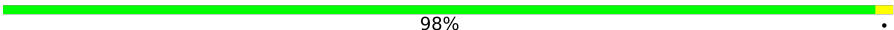
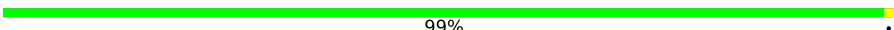
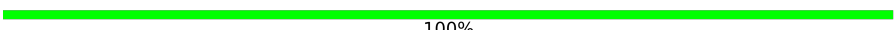
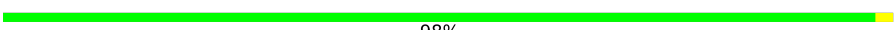






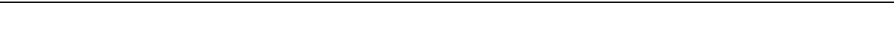

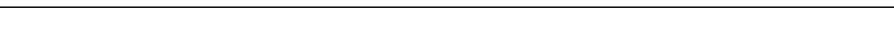
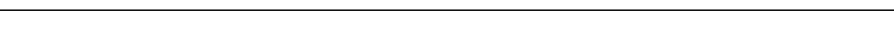


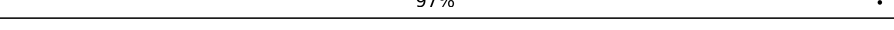


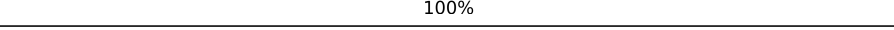

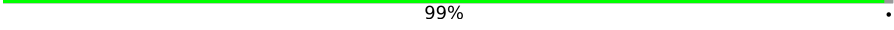
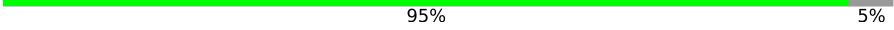

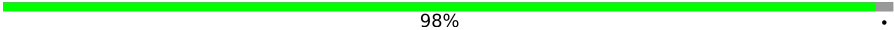
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	1	464	 92% 7%
2	2	246	 86% 13%
3	3	727	 94% • 5%
4	4	463	 90% • 9%
5	5	266	 78% 22%
6	6	223	 69% • 30%
7	9	217	 81% 19%
8	A	115	 95% • •
9	H	318	 97% • •
10	J	175	 99% •

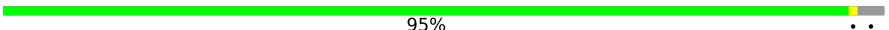


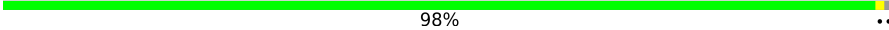




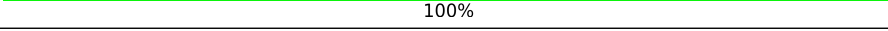
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Mol	Chain	Length	Quality of chain
11	K	98	 98% .
12	L	606	 99% .
13	M	459	 100%
14	N	347	 98% .
15	V	141	 34% 66%
16	W	189	 74% 26%
17	X	157	 55% 45%
17	j	157	 52% 48%
18	Y	172	 99% ..
19	Z	175	 98% .
20	a	109	 40% 60%
21	b	124	 77% 23%
22	c	170	 74% 26%
23	d	380	 78% 22%
24	e	99	 87% 13%
25	f	116	 97% .
26	g	140	 81% 19%
27	h	114	 83% . 16%
28	i	145	 100%
29	k	355	 90% . 10%
30	l	106	 99% .
31	m	84	 95% 5%
32	n	98	 81% 19%
33	o	122	 98% .
34	p	130	 98% .

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Mol	Chain	Length	Quality of chain
35	q	144	 95% . .
36	r	128	 77% 23%
37	s	137	 88% . 11%
38	t	179	 98% ..
39	u	108	 60% 40%
40	v	186	 83% 17%
41	w	154	 65% . 34%
42	x	76	 64% 36%
43	y	58	 86% 14%
44	z	70	 100%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
51	CDL	L	1003	X	-	-	-
51	CDL	M	502	X	-	-	-
51	CDL	o	201	X	-	-	-

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 66294 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 dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	430	Total	C	N	O	S	0	0
			3312	2086	593	613	20		

- Molecule 2 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	213	Total	C	N	O	S	0	0
			1655	1058	278	309	10		

- Molecule 3 is a protein called NADH:ubiquinone oxidoreductase core subunit S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	688	Total	C	N	O	S	0	0
			5275	3301	922	1011	41		

- Molecule 4 is a protein called Mitochondrial complex I, 49 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	420	Total	C	N	O	S	0	0
			3381	2159	579	618	25		

- Molecule 5 is a protein called NADH:ubiquinone oxidoreductase core subunit S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	208	Total	C	N	O	S	0	0
			1726	1112	296	315	3		

- Molecule 6 is a protein called Mitochondrial complex I, PSST subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	156	Total	C	N	O	S	0	0
			1247	795	225	213	14		

- Molecule 7 is a protein called Mitochondrial complex I, TYKY subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	9	176	Total	C	N	O	S	0	0
			1414	889	243	270	12		

- Molecule 8 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	110	Total	C	N	O	S	0	0
			880	593	128	153	6		

- Molecule 9 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	311	Total	C	N	O	S	0	0
			2479	1675	377	408	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	175	Total	C	N	O	S	0	0
			1344	904	192	235	13		

- Molecule 11 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	98	Total	C	N	O	S	0	0
			749	490	112	132	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	606	Total	C	N	O	S	0	0
			4807	3188	746	829	44		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	459	Total	C	N	O	S	0	0
			3647	2429	571	607	40		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	347	Total	C	N	O	S	0	0
			2723	1808	416	459	40		

- Molecule 15 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	V	48	Total	C	N	O	S	0	0
			336	220	54	58	4		

- Molecule 16 is a protein called NADH:ubiquinone oxidoreductase subunit B5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	W	139	Total	C	N	O	S	0	0
			1155	761	194	198	2		

- Molecule 17 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	87	Total	C	N	O	S	0	0
			701	451	103	142	5		
17	j	82	Total	C	N	O	S	0	0
			660	425	98	132	5		

- Molecule 18 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Y	171	Total	C	N	O	S	0	0
			1403	889	253	251	10		

- Molecule 19 is a protein called Mitochondrial complex I, PDSW subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Z	171	Total	C	N	O	S	0	0
			1441	905	266	262	8		

- Molecule 20 is a protein called Mitochondrial complex I, 10 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	a	44	Total	C	N	O	S	0	0
			371	233	66	71	1		

- Molecule 21 is a protein called Mitochondrial complex I, 13 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	b	95	Total	C	N	O	S	0	0
			737	451	139	144	3		

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	c	126	Total	C	N	O	S	0	0
			1024	646	182	193	3		

- Molecule 23 is a protein called NADH:ubiquinone oxidoreductase subunit A9.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	d	297	Total	C	N	O	S	0	0
			2372	1516	432	419	5		

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	e	86	Total	C	N	O	S	0	0
			691	434	129	126	2		

- Molecule 25 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	f	113	Total	C	N	O	S	0	0
			917	595	153	167	2		

- Molecule 26 is a protein called NADH:ubiquinone oxidoreductase subunit A6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	g	114	Total	C	N	O	S	0	0
			969	619	180	166	4		

- Molecule 27 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	h	96	Total	C	N	O	S	0	0
			769	480	146	140	3		

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	i	145	Total	C	N	O	S	0	0
			1209	778	216	210	5		

- Molecule 29 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	k	320	Total	C	N	O	P S	0	0
			2596	1659	432	494	1 10		

- Molecule 30 is a protein called NADH:ubiquinone oxidoreductase subunit S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	l	105	Total	C	N	O	S	0	0
			874	551	164	153	6		

- Molecule 31 is a protein called NADH:ubiquinone oxidoreductase subunit A3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	m	80	Total	C	N	O	S	0	0
			626	411	103	110	2		

- Molecule 32 is a protein called NADH:ubiquinone oxidoreductase subunit B3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	n	79	Total	C	N	O	S	0	0
			634	415	106	111	2		

- Molecule 33 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	o	120	Total	C	N	O	S	0	0
			1004	652	175	172	5		

- Molecule 34 is a protein called NADH:ubiquinone oxidoreductase subunit B4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	p	128	Total	C	N	O	S	0	0
			1059	675	189	194	1		

- Molecule 35 is a protein called Mitochondrial complex I, B16.6 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	q	139	Total	C	N	O	S	0	0
			1142	733	200	200	9		

- Molecule 36 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	r	99	Total	C	N	O	S	0	0
			846	554	149	142	1		

- Molecule 37 is a protein called NADH:ubiquinone oxidoreductase subunit B7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	s	122	Total	C	N	O	S	0	0
			1047	653	199	186	9		

- Molecule 38 is a protein called NADH:ubiquinone oxidoreductase subunit B9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	t	177	Total	C	N	O	S	0	0
			1520	973	279	262	6		

- Molecule 39 is a protein called NADH:ubiquinone oxidoreductase subunit B2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	u	65	Total	C	N	O	S	0	0
			563	372	93	97	1		

- Molecule 40 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	v	155	Total	C	N	O	S	0	0
			1307	846	213	239	9		

- Molecule 41 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	w	101	Total	C	N	O	S	0	0
			846	542	140	160	4		

- Molecule 42 is a protein called Mitochondrial complex I, KFYI subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	x	49	Total	C	N	O	0	0
			412	271	70	71		

- Molecule 43 is a protein called Mitochondrial complex I, MNLL subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	y	50	Total	C	N	O	0	0
			436	287	77	72		

- Molecule 44 is a protein called Mitochondrial complex I, MWFE subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	z	70	Total	C	N	O	S	0	0
			576	369	106	96	5		

- Molecule 45 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			AltConf
45	1	1	Total	Fe	S	0
			8	4	4	
45	3	1	Total	Fe	S	0
			8	4	4	
45	3	1	Total	Fe	S	0
			8	4	4	
45	6	1	Total	Fe	S	0
			8	4	4	

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Mol	Chain	Residues	Atoms			AltConf
45	9	1	Total	Fe	S	0
			8	4	4	
45	9	1	Total	Fe	S	0
			8	4	4	

- Molecule 46 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



Mol	Chain	Residues	Atoms					AltConf
46	1	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 47 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).

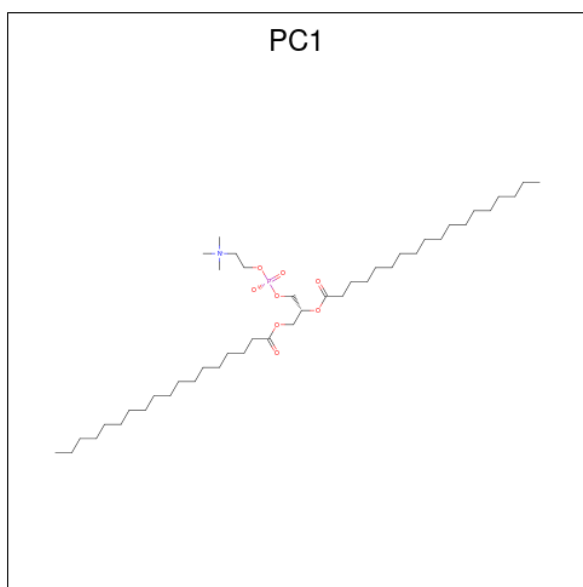


Mol	Chain	Residues	Atoms			AltConf
47	2	1	Total	Fe	S	0
			4	2	2	
47	3	1	Total	Fe	S	0
			4	2	2	

- Molecule 48 is POTASSIUM ION (CCD ID: K) (formula: K).

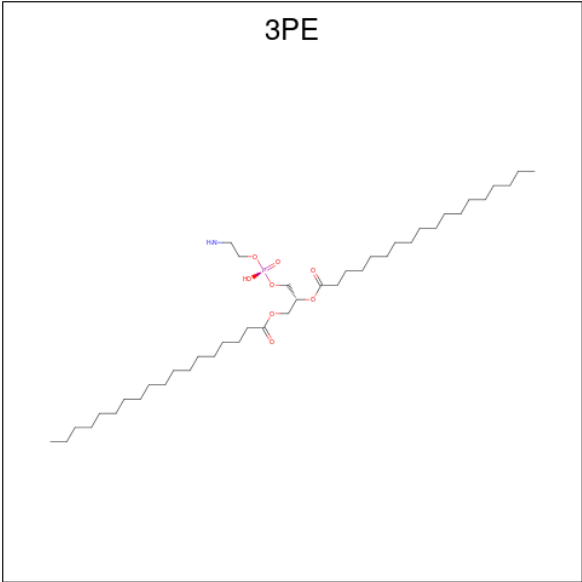
Mol	Chain	Residues	Atoms		AltConf
48	3	1	Total	K	0
			1	1	

- Molecule 49 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: C₄₄H₈₈NO₈P).



Mol	Chain	Residues	Atoms					AltConf
49	6	1	Total	C	N	O	P	0
			46	36	1	8	1	
49	A	1	Total	C	N	O	P	0
			37	27	1	8	1	
49	H	1	Total	C	N	O	P	0
			54	44	1	8	1	
49	L	1	Total	C	N	O	P	0
			54	44	1	8	1	
49	M	1	Total	C	N	O	P	0
			36	26	1	8	1	
49	w	1	Total	C	N	O	P	0
			54	44	1	8	1	

- Molecule 50 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$).



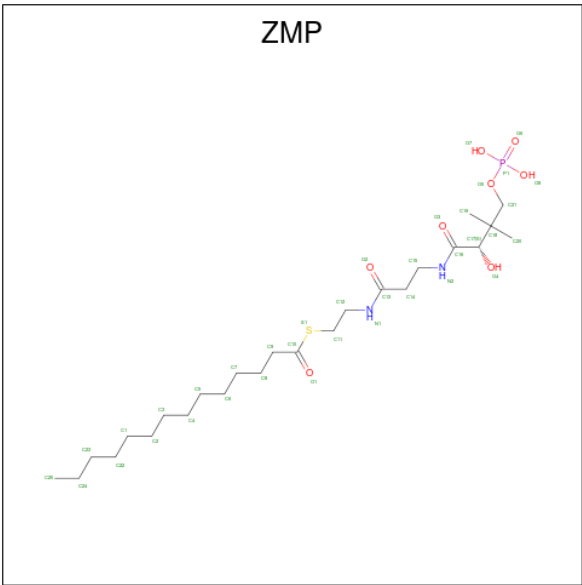
Mol	Chain	Residues	Atoms					AltConf
50	6	1	Total	C	N	O	P	0
			51	41	1	8	1	
50	H	1	Total	C	N	O	P	0
			51	41	1	8	1	
50	L	1	Total	C	N	O	P	0
			51	41	1	8	1	
50	L	1	Total	C	N	O	P	0
			31	21	1	8	1	
50	N	1	Total	C	N	O	P	0
			51	41	1	8	1	
50	N	1	Total	C	N	O	P	0
			31	21	1	8	1	
50	i	1	Total	C	N	O	P	0
			51	41	1	8	1	
50	m	1	Total	C	N	O	P	0
			51	41	1	8	1	

- Molecule 51 is CARDIOLIPIN (CCD ID: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).



Mol	Chain	Residues	Atoms				AltConf
51	L	1	Total	C	O	P	0
			100	81	17	2	
51	M	1	Total	C	O	P	0
			100	81	17	2	
51	M	1	Total	C	O	P	0
			90	71	17	2	
51	W	1	Total	C	O	P	0
			100	81	17	2	
51	h	1	Total	C	O	P	0
			58	39	17	2	
51	o	1	Total	C	O	P	0
			75	56	17	2	

- Molecule 52 is S-[2-({N-[(2S)-2-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-beta-alanyl}amino)ethyl] tetradecanethioate (CCD ID: ZMP) (formula: C₂₅H₄₉N₂O₈PS).

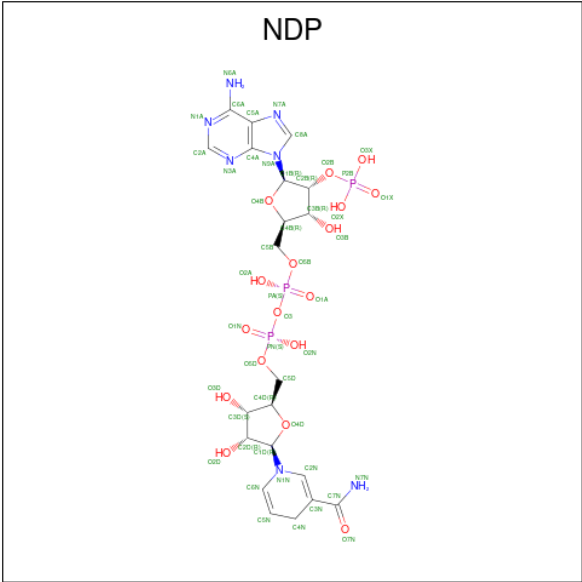


Mol	Chain	Residues	Atoms					AltConf
52	X	1	Total	C	N	O	P	S
			31	20	2	7	1	1
52	g	1	Total	C	N	O	P	S
			34	23	2	7	1	1

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

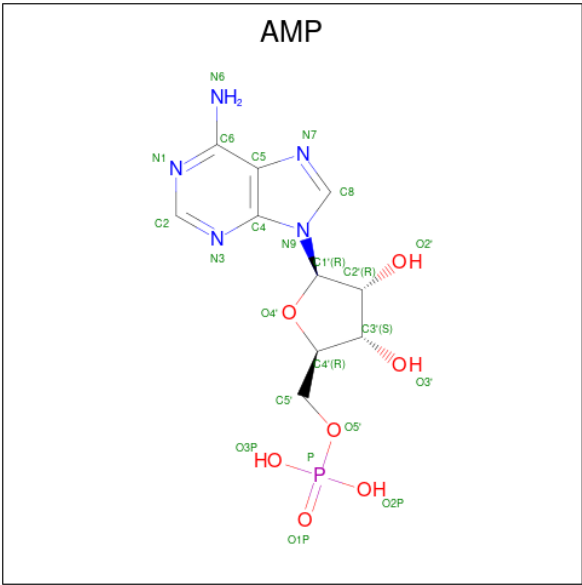
Mol	Chain	Residues	Atoms		AltConf
53	b	1	Total	Zn	0
			1	1	

- Molecule 54 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



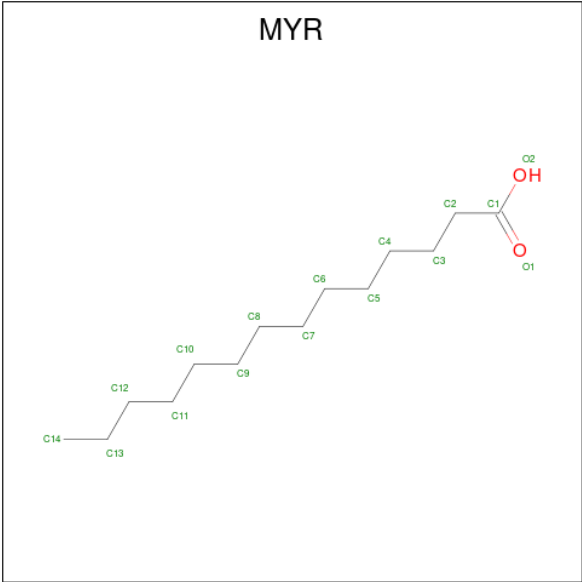
Mol	Chain	Residues	Atoms					AltConf
54	d	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 55 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					AltConf
55	k	1	Total	C	N	O	P	0
			23	10	5	7	1	

- Molecule 56 is MYRISTIC ACID (CCD ID: MYR) (formula: $C_{14}H_{28}O_2$).



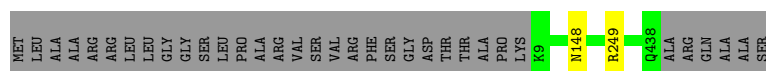
Mol	Chain	Residues	Atoms			AltConf
56	s	1	Total	C	O	0
			15	14	1	

3 Residue-property plots


These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

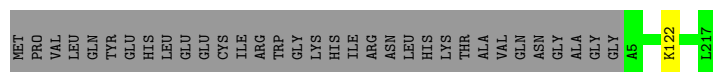
- Molecule 1: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial

Chain 1:  92% 7%



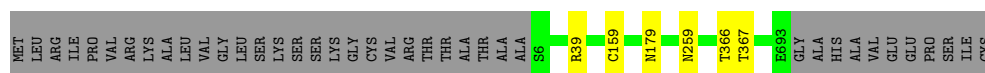
- Molecule 2: Uncharacterized protein

Chain 2:  86% 13%



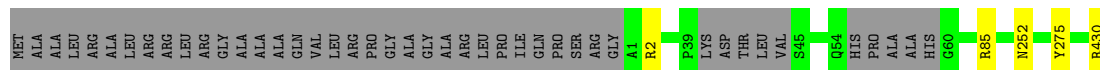
- Molecule 3: NADH:ubiquinone oxidoreductase core subunit S1

Chain 3:  94% 5%




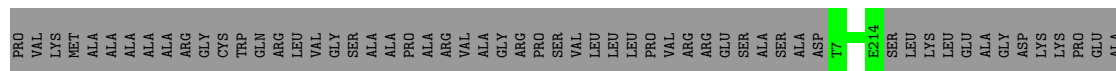
- Molecule 4: Mitochondrial complex I, 49 kDa subunit

Chain 4:  90% 9%



- Molecule 5: NADH:ubiquinone oxidoreductase core subunit S3

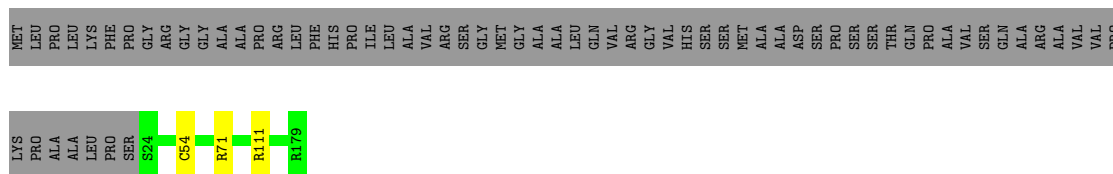
Chain 5:  78% 22%




LYS

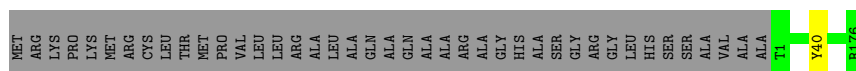
- Molecule 6: Mitochondrial complex I, PSST subunit

Chain 6:  69% 30%



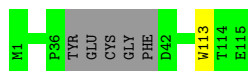
- Molecule 7: Mitochondrial complex I, TYKY subunit

Chain 9:  81% 19%



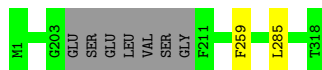
- Molecule 8: NADH-ubiquinone oxidoreductase chain 3

Chain A:  95%



- Molecule 9: NADH-ubiquinone oxidoreductase chain 1

Chain H:  97%



- Molecule 10: NADH-ubiquinone oxidoreductase chain 6

Chain J:  99%



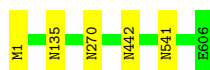
- Molecule 11: NADH-ubiquinone oxidoreductase chain 4L

Chain K:  98%



- Molecule 12: NADH-ubiquinone oxidoreductase chain 5

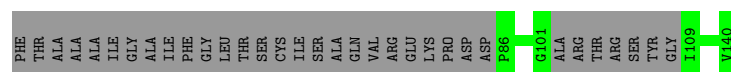
Chain L:  99%



-
- M1 N144 L458 Y459

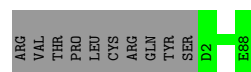
-
- | Data Type | Number of Samples |
|-----------|-------------------|
| M1 | 100 |
| L146 | 100 |
| L170 | 100 |
| M240 | 100 |
| L288 | 100 |
| L302 | 100 |
| F305 | 100 |
| E347 | 100 |

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| NET | LYS | LYS | THR | LEU | LEU | HIS | GLN | TYR | TRP | ASP | ILE | PRO | PRO | GLY | GLU | THR | GLU | CYS | HIS | ARG | ARG | LYS | THR | TYR | ALA | ALA | ALA | THR | SER | THR | ILE | GLY | GLY | ALA | SER | SER | GLY | LEU | VAL | VAL | SER | VAL | LEU | LYS | THR | THR | THR | SER | PHE | LEU | LEU | GLY | GLY | VAL | VAL | ALA | ALA | ARG | THR | THR | GLY | ARG | ARG | TYR |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|
| MET | ALA | ALA | MET | SER | LEU | LEU | HIS | ARG | ALA | ALA | SER | SER | SER | VAL | VAL | ALA | VAL | VAL | ALA | ALA | LEU | SER | SER | GLY | ARG | ARG | ARG | LEU | PHE | GLY | GLY | PHE | LEU | THR | THR | ARG | ASP | PHE | PRO | LYS | THR | VAL | ALA | PRO | VAL | VAL | ARG | HIS | SER | GLY | ASP | HIS | G6 | Val |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| VAL | GLU | VAL | LYS | ASP | PHE | THR | THR | ASN | TYR | GLN | THR | ALA | ALA | VAL | SER | SER | PRO | PRO | GLY | LEU | PRO | MET | MET | SER | SER | LEU | LEU | MET | ALA | VAL | VAL | PRO | VAL | LYS | SER | SER | GLY | ALA | ASN | VAL | VAL | PRO | PRO | ARG | ARG | GLU | GLU | SER | ARG | VAL | VAL | VAL | LEU | THR | GLN | ARG | ARG | LYS | VAL | VAL | PRO | PRO |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

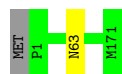


- [illegible]

ARG	VAL	THR	PRO	LEU	CYS	ARG	GLN	TYR	SER	ASP	ALA	PRO	P5	V86	TYR	GLU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	-----	-----	-----

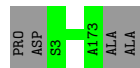
- Molecule 18: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8

Chain Y:  99%



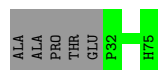
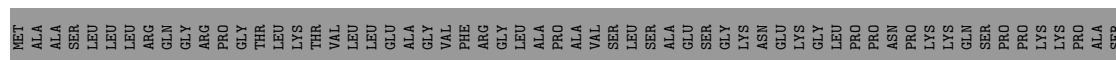
- Molecule 19: Mitochondrial complex I, PDSW subunit

Chain Z:  98%



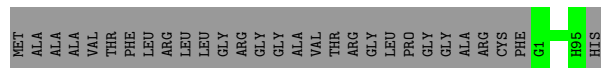
- Molecule 20: Mitochondrial complex I, 10 kDa subunit

Chain a:  40%



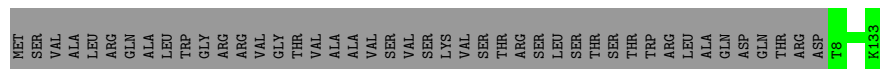
- Molecule 21: Mitochondrial complex I, 13 kDa subunit

Chain b:  77%




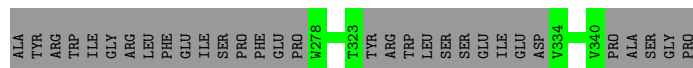
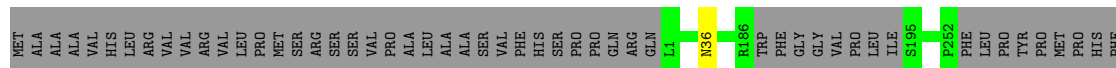
- Molecule 22: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

Chain c:  74%




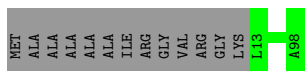
- Molecule 23: NADH:ubiquinone oxidoreductase subunit A9

Chain d:  78%



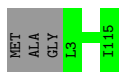
- Molecule 24: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2

Chain e:  87% 13%




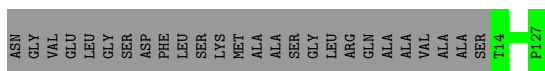
- Molecule 25: Uncharacterized protein

Chain f:  97% .




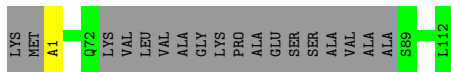
- Molecule 26: NADH:ubiquinone oxidoreductase subunit A6

Chain g:  81% 19%



- Molecule 27: Uncharacterized protein

Chain h:  83% 16%



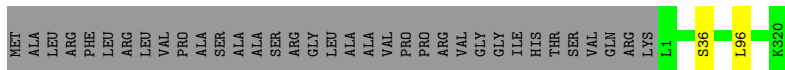
- Molecule 28: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

Chain i:  100%

There are no outlier residues recorded for this chain.

- Molecule 29: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial

Chain k:  90% 10%



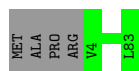
- Molecule 30: NADH:ubiquinone oxidoreductase subunit S5

Chain l:  99% .



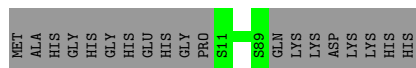
- Molecule 31: NADH:ubiquinone oxidoreductase subunit A3

Chain m:  95% 5%



- Molecule 32: NADH:ubiquinone oxidoreductase subunit B3

Chain n: 81% 19%



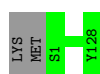
- Molecule 33: NADH dehydrogenase [ubiquinone] 1 subunit C2

Chain o: 98% .



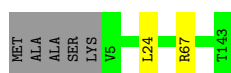
- Molecule 34: NADH:ubiquinone oxidoreductase subunit B4

Chain p: 98% .



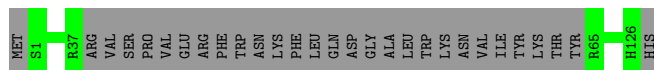
- Molecule 35: Mitochondrial complex I, B16.6 subunit

Chain q: 95% ..



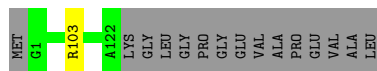
- Molecule 36: Uncharacterized protein

Chain r: 77% 23%



- Molecule 37: NADH:ubiquinone oxidoreductase subunit B7

Chain s: 88% . 11%



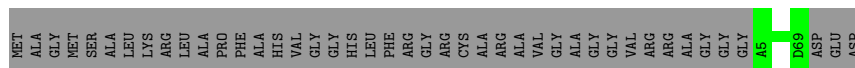
- Molecule 38: NADH:ubiquinone oxidoreductase subunit B9

Chain t: 98% ..



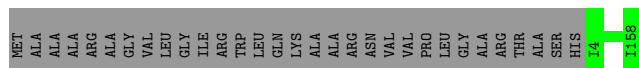
- Molecule 39: NADH:ubiquinone oxidoreductase subunit B2

Chain u: 60% 40%



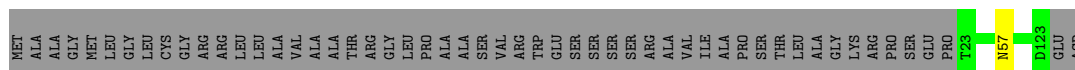
- Molecule 40: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

Chain v: 83% 17%



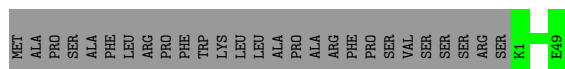
- Molecule 41: Uncharacterized protein

Chain w: 65% 34%



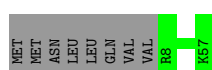
- Molecule 42: Mitochondrial complex I, KFYI subunit

Chain x: 64% 36%



- Molecule 43: Mitochondrial complex I, MNLL subunit

Chain y: 86% 14%



- Molecule 44: Mitochondrial complex I, MWFE subunit

Chain z: 100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	76479	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 ($e^-/\text{\AA}^2$)	100	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MYR, SEP, SF4, NDP, CDL, FME, AMP, ZMP, 3PE, FMN, FES, 2MR, AYA, ZN, K, PC1

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	1	0.40	0/3386	0.57	0/4575
2	2	0.37	0/1695	0.58	0/2306
3	3	0.40	1/5362 (0.0%)	0.58	0/7266
4	4	0.42	0/3454	0.58	0/4676
5	5	0.40	0/1776	0.56	0/2417
6	6	0.47	0/1278	0.55	0/1728
7	9	0.49	0/1445	0.60	1/1956 (0.1%)
8	A	0.34	0/902	0.63	0/1234
9	H	0.39	0/2553	0.65	0/3492
10	J	0.40	0/1378	0.63	0/1868
11	K	0.34	0/749	0.66	0/1014
12	L	0.33	0/4925	0.57	0/6700
13	M	0.36	0/3731	0.61	1/5085 (0.0%)
14	N	0.38	0/2787	0.65	3/3795 (0.1%)
15	V	0.25	0/341	0.57	0/458
16	W	0.33	0/1188	0.49	0/1607
17	X	0.29	0/713	0.49	0/963
17	j	0.31	0/670	0.52	0/902
18	Y	0.35	0/1440	0.53	0/1942
19	Z	0.32	0/1475	0.48	0/1989
20	a	0.32	0/383	0.48	0/518
21	b	0.36	0/749	0.50	0/1009
22	c	0.37	0/1047	0.53	0/1415
23	d	0.34	0/2424	0.53	0/3276
24	e	0.31	0/702	0.52	0/945
25	f	0.33	0/937	0.51	0/1271
26	g	0.35	0/993	0.53	0/1336
27	h	0.37	0/779	0.55	0/1053
28	i	0.37	0/1250	0.50	0/1698
29	k	0.33	0/2646	0.50	1/3579 (0.0%)
30	l	0.34	0/896	0.54	0/1200
31	m	0.31	0/647	0.51	0/890

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	n	0.29	0/653	0.44	0/882
33	o	0.36	0/1035	0.51	0/1398
34	p	0.28	0/1085	0.47	0/1467
35	q	0.33	0/1171	0.52	0/1579
36	r	0.31	0/874	0.53	0/1188
37	s	0.28	0/1072	0.48	0/1436
38	t	0.31	0/1573	0.49	0/2130
39	u	0.29	0/590	0.46	0/810
40	v	0.31	0/1361	0.51	0/1861
41	w	0.34	0/872	0.53	0/1185
42	x	0.28	0/425	0.41	0/576
43	y	0.30	0/449	0.51	0/605
44	z	0.36	0/591	0.57	0/795
All	All	0.36	1/66452 (0.0%)	0.56	6/90075 (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
3	3	0	2
4	4	0	1
8	A	0	1
10	J	0	1
14	N	0	2
35	q	0	1
All	All	0	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	3	159	CYS	CB-SG	-7.62	1.69	1.82

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	288	LEU	CA-CB-CG	7.23	131.93	115.30
14	N	170	LEU	CA-CB-CG	5.83	128.72	115.30
13	M	458	LEU	CA-CB-CG	5.83	128.71	115.30
29	k	96	LEU	CA-CB-CG	5.42	127.77	115.30
7	9	40	TYR	CB-CG-CD2	-5.40	117.76	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	146	LEU	CA-CB-CG	5.34	127.57	115.30

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	3	259	ASN	Peptide
3	3	366	THR	Peptide
4	4	275	TYR	Peptide
8	A	113	TRP	Peptide
10	J	85	SER	Peptide
14	N	302	LEU	Peptide
14	N	305	PHE	Peptide
35	q	24	LEU	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	428/464 (92%)	409 (96%)	19 (4%)	0	100	100
2	2	211/246 (86%)	197 (93%)	14 (7%)	0	100	100
3	3	686/727 (94%)	658 (96%)	27 (4%)	1 (0%)	48	77
4	4	413/463 (89%)	399 (97%)	14 (3%)	0	100	100
5	5	206/266 (77%)	196 (95%)	10 (5%)	0	100	100
6	6	154/223 (69%)	148 (96%)	6 (4%)	0	100	100
7	9	174/217 (80%)	167 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	A	106/115 (92%)	96 (91%)	10 (9%)	0	100	100
9	H	307/318 (96%)	298 (97%)	9 (3%)	0	100	100
10	J	173/175 (99%)	156 (90%)	17 (10%)	0	100	100
11	K	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
12	L	604/606 (100%)	574 (95%)	30 (5%)	0	100	100
13	M	457/459 (100%)	445 (97%)	12 (3%)	0	100	100
14	N	345/347 (99%)	332 (96%)	13 (4%)	0	100	100
15	V	44/141 (31%)	43 (98%)	1 (2%)	0	100	100
16	W	137/189 (72%)	135 (98%)	2 (2%)	0	100	100
17	X	85/157 (54%)	83 (98%)	2 (2%)	0	100	100
17	j	80/157 (51%)	79 (99%)	1 (1%)	0	100	100
18	Y	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
19	Z	169/175 (97%)	165 (98%)	4 (2%)	0	100	100
20	a	42/109 (38%)	40 (95%)	2 (5%)	0	100	100
21	b	93/124 (75%)	91 (98%)	2 (2%)	0	100	100
22	c	124/170 (73%)	122 (98%)	2 (2%)	0	100	100
23	d	289/380 (76%)	283 (98%)	6 (2%)	0	100	100
24	e	84/99 (85%)	82 (98%)	2 (2%)	0	100	100
25	f	111/116 (96%)	109 (98%)	2 (2%)	0	100	100
26	g	112/140 (80%)	106 (95%)	6 (5%)	0	100	100
27	h	92/114 (81%)	87 (95%)	5 (5%)	0	100	100
28	i	143/145 (99%)	140 (98%)	3 (2%)	0	100	100
29	k	317/355 (89%)	296 (93%)	21 (7%)	0	100	100
30	l	103/106 (97%)	99 (96%)	4 (4%)	0	100	100
31	m	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
32	n	77/98 (79%)	73 (95%)	4 (5%)	0	100	100
33	o	118/122 (97%)	117 (99%)	1 (1%)	0	100	100
34	p	126/130 (97%)	122 (97%)	4 (3%)	0	100	100
35	q	137/144 (95%)	134 (98%)	3 (2%)	0	100	100
36	r	95/128 (74%)	90 (95%)	5 (5%)	0	100	100
37	s	120/137 (88%)	116 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	t	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
39	u	63/108 (58%)	59 (94%)	4 (6%)	0	100	100
40	v	153/186 (82%)	143 (94%)	10 (6%)	0	100	100
41	w	99/154 (64%)	93 (94%)	6 (6%)	0	100	100
42	x	47/76 (62%)	47 (100%)	0	0	100	100
43	y	48/58 (83%)	47 (98%)	1 (2%)	0	100	100
44	z	68/70 (97%)	68 (100%)	0	0	100	100
All	All	7958/9247 (86%)	7645 (96%)	312 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	3	367	THR

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	1	344/368 (94%)	342 (99%)	2 (1%)	84	95
2	2	183/210 (87%)	182 (100%)	1 (0%)	86	95
3	3	578/608 (95%)	576 (100%)	2 (0%)	91	97
4	4	362/391 (93%)	359 (99%)	3 (1%)	79	93
5	5	189/230 (82%)	189 (100%)	0	100	100
6	6	132/181 (73%)	129 (98%)	3 (2%)	45	78
7	9	151/179 (84%)	151 (100%)	0	100	100
8	A	99/103 (96%)	99 (100%)	0	100	100
9	H	272/278 (98%)	270 (99%)	2 (1%)	81	94
10	J	144/144 (100%)	144 (100%)	0	100	100
11	K	86/86 (100%)	84 (98%)	2 (2%)	45	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	L	538/538 (100%)	534 (99%)	4 (1%)	81	94
13	M	411/411 (100%)	410 (100%)	1 (0%)	92	97
14	N	315/315 (100%)	314 (100%)	1 (0%)	91	97
15	V	31/102 (30%)	31 (100%)	0	100	100
16	W	122/160 (76%)	122 (100%)	0	100	100
17	X	80/141 (57%)	80 (100%)	0	100	100
17	j	76/141 (54%)	76 (100%)	0	100	100
18	Y	154/155 (99%)	153 (99%)	1 (1%)	84	95
19	Z	155/157 (99%)	155 (100%)	0	100	100
20	a	43/93 (46%)	43 (100%)	0	100	100
21	b	79/97 (81%)	79 (100%)	0	100	100
22	c	113/150 (75%)	113 (100%)	0	100	100
23	d	255/326 (78%)	254 (100%)	1 (0%)	89	96
24	e	76/82 (93%)	76 (100%)	0	100	100
25	f	101/102 (99%)	101 (100%)	0	100	100
26	g	107/124 (86%)	107 (100%)	0	100	100
27	h	84/96 (88%)	84 (100%)	0	100	100
28	i	131/131 (100%)	131 (100%)	0	100	100
29	k	283/309 (92%)	283 (100%)	0	100	100
30	l	94/95 (99%)	94 (100%)	0	100	100
31	m	69/72 (96%)	69 (100%)	0	100	100
32	n	61/76 (80%)	61 (100%)	0	100	100
33	o	107/109 (98%)	107 (100%)	0	100	100
34	p	114/116 (98%)	114 (100%)	0	100	100
35	q	119/122 (98%)	118 (99%)	1 (1%)	79	93
36	r	95/122 (78%)	95 (100%)	0	100	100
37	s	110/120 (92%)	109 (99%)	1 (1%)	75	92
38	t	159/161 (99%)	158 (99%)	1 (1%)	84	95
39	u	59/84 (70%)	59 (100%)	0	100	100
40	v	140/160 (88%)	140 (100%)	0	100	100
41	w	92/130 (71%)	91 (99%)	1 (1%)	70	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	x	44/67 (66%)	44 (100%)	0	100	100
43	y	46/54 (85%)	46 (100%)	0	100	100
44	z	59/59 (100%)	59 (100%)	0	100	100
All	All	7062/7955 (89%)	7035 (100%)	27 (0%)	88	96

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	148	ASN
1	1	249	ARG
2	2	122	LYS
3	3	39	ARG
3	3	179	ASN
4	4	2	ARG
4	4	252	ASN
4	4	430	ARG
6	6	54	CYS
6	6	71	ARG
6	6	111	ARG
9	H	259	PHE
9	H	285	LEU
11	K	4	VAL
11	K	50	ASN
12	L	135	ASN
12	L	270	ASN
12	L	442	ASN
12	L	541	ASN
13	M	144	ASN
14	N	240	MET
18	Y	63	ASN
23	d	36	ASN
35	q	67	ARG
37	s	103	ARG
38	t	128	ARG
41	w	57	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	361	GLN

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Mol	Chain	Res	Type
1	1	373	ASN
1	1	437	HIS
4	4	149	ASN
4	4	252	ASN
9	H	124	ASN
11	K	50	ASN
11	K	92	ASN
12	L	446	ASN
13	M	144	ASN
13	M	169	ASN
16	W	143	ASN
18	Y	15	GLN
18	Y	29	HIS
19	Z	114	GLN
21	b	36	ASN
23	d	180	ASN
23	d	184	ASN
25	f	49	GLN
26	g	125	HIS
29	k	107	GLN
29	k	180	GLN
29	k	204	ASN
29	k	287	HIS
30	l	97	HIS
34	p	47	GLN
34	p	74	ASN
34	p	78	ASN
39	u	13	GLN
40	v	66	HIS
41	w	57	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
13	FME	M	1	13	8,9,10	0.90	0	7,9,11	1.00	0
4	2MR	4	85	4	10,12,13	2.30	3 (30%)	5,13,15	1.95	1 (20%)
11	FME	K	1	11	8,9,10	0.91	0	7,9,11	0.84	0
29	SEP	k	36	29	8,9,10	1.56	1 (12%)	8,12,14	1.42	2 (25%)
27	AYA	h	1	27	6,7,8	1.34	1 (16%)	5,8,10	1.37	1 (20%)
12	FME	L	1	12	8,9,10	1.01	1 (12%)	7,9,11	0.98	0

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
13	FME	M	1	13	-	3/7/9/11	-
4	2MR	4	85	4	-	0/10/13/15	-
11	FME	K	1	11	-	4/7/9/11	-
29	SEP	k	36	29	-	5/5/8/10	-
27	AYA	h	1	27	-	0/4/6/8	-
12	FME	L	1	12	-	2/7/9/11	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	4	85	2MR	CZ-NH2	4.64	1.43	1.33
4	4	85	2MR	CZ-NE	4.32	1.43	1.34
29	k	36	SEP	P-O1P	3.37	1.61	1.50
27	h	1	AYA	CA-N	-2.78	1.43	1.46
4	4	85	2MR	CQ1-NH1	-2.35	1.41	1.46
12	L	1	FME	CA-N	-2.05	1.43	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	4	85	2MR	NE-CZ-NH2	-3.65	116.13	119.48
27	h	1	AYA	CB-CA-N	2.86	112.79	109.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	k	36	SEP	P-OG-CB	-2.81	110.56	118.30
29	k	36	SEP	OG-CB-CA	2.13	110.22	108.14

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	K	1	FME	O1-CN-N-CA
12	L	1	FME	CA-CB-CG-SD
13	M	1	FME	CB-CA-N-CN
13	M	1	FME	C-CA-CB-CG
29	k	36	SEP	CB-OG-P-O2P
29	k	36	SEP	CB-OG-P-O3P
11	K	1	FME	N-CA-CB-CG
12	L	1	FME	N-CA-CB-CG
29	k	36	SEP	CB-OG-P-O1P
29	k	36	SEP	CA-CB-OG-P
11	K	1	FME	CB-CA-N-CN
29	k	36	SEP	N-CA-CB-OG
11	K	1	FME	C-CA-CB-CG
13	M	1	FME	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 36 ligands modelled in this entry, 2 are monoatomic - leaving 34 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
55	AMP	k	501	-	22,25,25	0.89	1 (4%)	25,38,38	1.14	2 (8%)
45	SF4	9	201	7	0,12,12	-	-	-		
56	MYR	s	201	37	14,14,15	0.21	0	13,13,15	0.17	0
49	PC1	w	801	-	53,53,53	0.28	0	59,61,61	0.39	0
45	SF4	6	201	6	0,12,12	-	-	-		
49	PC1	M	501	-	35,35,53	0.37	0	41,43,61	0.37	0
52	ZMP	X	101	17	24,30,36	0.80	1 (4%)	29,37,45	1.00	2 (6%)
54	NDP	d	401	-	45,52,52	0.57	0	53,80,80	0.60	1 (1%)
50	3PE	N	402	-	30,30,50	0.38	0	33,35,55	0.35	0
49	PC1	6	202	-	45,45,53	0.31	0	51,53,61	0.33	0
50	3PE	i	201	-	50,50,50	0.30	0	53,55,55	0.29	0
51	CDL	o	201	-	74,74,99	0.31	0	80,86,111	0.46	1 (1%)
50	3PE	6	203	-	50,50,50	0.30	0	53,55,55	0.31	0
47	FES	2	300	2	0,4,4	-	-	-		
51	CDL	M	503	-	89,89,99	0.28	0	95,101,111	0.41	0
49	PC1	H	401	-	53,53,53	0.31	0	59,61,61	0.50	1 (1%)
47	FES	3	803	3	0,4,4	-	-	-		
50	3PE	H	402	-	50,50,50	0.31	0	53,55,55	0.43	0
50	3PE	m	101	-	50,50,50	0.31	0	53,55,55	0.39	0
45	SF4	3	801	3	0,12,12	-	-	-		
52	ZMP	g	201	-	27,33,36	0.60	0	32,40,45	1.21	4 (12%)
50	3PE	L	1004	-	30,30,50	0.40	0	33,35,55	0.70	1 (3%)
51	CDL	M	502	-	99,99,99	0.27	0	105,111,111	0.32	0
45	SF4	3	802	3	0,12,12	-	-	-		
45	SF4	1	500	1	0,12,12	-	-	-		
49	PC1	A	201	-	36,36,53	0.37	0	42,44,61	0.60	2 (4%)
51	CDL	L	1003	-	99,99,99	0.27	0	105,111,111	0.29	0
51	CDL	W	201	-	99,99,99	0.28	0	105,111,111	0.30	0
50	3PE	L	1001	-	50,50,50	0.30	0	53,55,55	0.32	0
50	3PE	N	401	-	50,50,50	0.32	0	53,55,55	0.53	2 (3%)
46	FMN	1	501	-	33,33,33	1.13	1 (3%)	48,50,50	1.30	7 (14%)
49	PC1	L	1002	-	53,53,53	0.32	0	59,61,61	0.60	2 (3%)
45	SF4	9	202	7	0,12,12	-	-	-		
51	CDL	h	201	-	57,57,99	0.36	0	63,69,111	0.33	0

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
55	AMP	k	501	-	-	5/6/26/26	0/3/3/3
45	SF4	9	201	7	-	-	0/6/5/5
56	MYR	s	201	37	-	2/11/12/13	-
49	PC1	w	801	-	-	14/57/57/57	-
52	ZMP	X	101	17	-	9/35/37/43	-
49	PC1	M	501	-	-	13/39/39/57	-
45	SF4	6	201	6	-	-	0/6/5/5
54	NDP	d	401	-	-	6/30/77/77	0/5/5/5
50	3PE	N	402	-	-	5/34/34/54	-
49	PC1	6	202	-	-	13/49/49/57	-
51	CDL	o	201	-	2/2/9/9	25/85/85/110	-
50	3PE	i	201	-	-	11/54/54/54	-
50	3PE	6	203	-	-	11/54/54/54	-
51	CDL	M	503	-	-	28/100/100/110	-
47	FES	2	300	2	-	-	0/1/1/1
49	PC1	H	401	-	-	14/57/57/57	-
47	FES	3	803	3	-	-	0/1/1/1
50	3PE	H	402	-	-	10/54/54/54	-
50	3PE	m	101	-	-	11/54/54/54	-
52	ZMP	g	201	-	-	14/38/40/43	-
45	SF4	3	801	3	-	-	0/6/5/5
50	3PE	L	1004	-	-	11/34/34/54	-
51	CDL	M	502	-	1/1/9/9	26/110/110/110	-
45	SF4	3	802	3	-	-	0/6/5/5
51	CDL	L	1003	-	1/1/9/9	37/110/110/110	-
49	PC1	A	201	-	-	7/40/40/57	-
45	SF4	1	500	1	-	-	0/6/5/5
51	CDL	W	201	-	-	21/110/110/110	-
50	3PE	L	1001	-	-	10/54/54/54	-
50	3PE	N	401	-	-	17/54/54/54	-
46	FMN	1	501	-	-	10/18/18/18	0/3/3/3
49	PC1	L	1002	-	-	17/57/57/57	-
45	SF4	9	202	7	-	-	0/6/5/5
51	CDL	h	201	-	-	24/68/68/110	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	1	501	FMN	C4A-N5	3.27	1.37	1.30
55	k	501	AMP	C5-C4	2.51	1.47	1.40
52	X	101	ZMP	C9-C10	2.46	1.53	1.50

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	1	501	FMN	C4-N3-C2	-3.66	118.87	125.64
55	k	501	AMP	N3-C2-N1	-3.23	123.63	128.68
46	1	501	FMN	O4-C4-C4A	-3.02	118.59	126.60
52	g	201	ZMP	O1-C10-C9	-2.97	120.48	123.99
52	g	201	ZMP	C15-C14-C13	-2.88	107.56	112.36
46	1	501	FMN	C4A-C10-N10	2.87	120.68	116.48
46	1	501	FMN	C4A-C4-N3	2.83	120.37	113.19
52	X	101	ZMP	O1-C10-C9	-2.68	120.82	123.99
46	1	501	FMN	C4A-C10-N1	-2.67	118.54	124.73
49	L	1002	PC1	C2-O21-C21	2.64	124.30	117.79
54	d	401	NDP	C5A-C6A-N6A	2.36	123.94	120.35
52	g	201	ZMP	C14-C15-N2	-2.36	107.14	111.90
46	1	501	FMN	C4-C4A-C10	2.32	120.69	116.79
50	L	1004	3PE	C2-O21-C21	2.30	123.46	117.79
49	L	1002	PC1	O21-C2-C1	2.30	116.71	108.40
49	A	201	PC1	O21-C2-C3	2.22	116.45	108.40
49	A	201	PC1	C2-O21-C21	2.21	123.23	117.79
52	X	101	ZMP	C8-C9-C10	-2.18	107.50	112.33
50	N	401	3PE	O21-C2-C1	2.11	116.05	108.40
49	H	401	PC1	C2-O21-C21	2.11	122.98	117.79
50	N	401	3PE	C2-O21-C21	2.08	122.91	117.79
55	k	501	AMP	C4-C5-N7	-2.07	107.24	109.40
52	g	201	ZMP	C9-C10-S1	2.02	115.81	113.46
51	o	201	CDL	CB4-OB6-CB5	2.01	122.75	117.79
46	1	501	FMN	C10-C4A-N5	-2.00	120.61	124.86

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
51	L	1003	CDL	CB4
51	M	502	CDL	CB4
51	o	201	CDL	CA4
51	o	201	CDL	CB4

All (371) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
46	1	501	FMN	N10-C1'-C2'-O2'
46	1	501	FMN	N10-C1'-C2'-C3'
46	1	501	FMN	C5'-O5'-P-O2P
46	1	501	FMN	C5'-O5'-P-O3P
49	6	202	PC1	C11-O13-P-O12
49	6	202	PC1	C1-O11-P-O14
49	H	401	PC1	C11-O13-P-O12
49	H	401	PC1	C11-O13-P-O14
49	H	401	PC1	C11-O13-P-O11
49	L	1002	PC1	C11-O13-P-O14
49	L	1002	PC1	C1-O11-P-O12
49	M	501	PC1	C11-O13-P-O12
49	M	501	PC1	C11-O13-P-O14
49	w	801	PC1	C11-O13-P-O12
49	w	801	PC1	C11-O13-P-O14
49	w	801	PC1	C11-O13-P-O11
50	6	203	3PE	C1-O11-P-O12
50	6	203	3PE	O13-C11-C12-N
50	H	402	3PE	C11-O13-P-O14
50	H	402	3PE	O13-C11-C12-N
50	L	1001	3PE	O13-C11-C12-N
50	L	1004	3PE	C11-O13-P-O12
50	L	1004	3PE	C11-O13-P-O14
50	L	1004	3PE	C2-C1-O11-P
50	N	401	3PE	C1-O11-P-O12
50	N	402	3PE	C11-O13-P-O12
50	N	402	3PE	C11-O13-P-O14
50	i	201	3PE	C1-O11-P-O12
50	i	201	3PE	O13-C11-C12-N
50	m	101	3PE	C11-O13-P-O11
50	m	101	3PE	C11-O13-P-O12
50	m	101	3PE	C11-O13-P-O14
51	L	1003	CDL	CA3-OA5-PA1-OA2
51	L	1003	CDL	CA3-OA5-PA1-OA3
51	L	1003	CDL	CA3-OA5-PA1-OA4
51	L	1003	CDL	CB3-OB5-PB2-OB3
51	M	502	CDL	O1-C1-CB2-OB2
51	M	502	CDL	CB3-OB5-PB2-OB2
51	M	502	CDL	CB3-OB5-PB2-OB3
51	M	503	CDL	O1-C1-CB2-OB2
51	M	503	CDL	CA2-OA2-PA1-OA4
51	M	503	CDL	CA3-OA5-PA1-OA3
51	M	503	CDL	CB2-OB2-PB2-OB3

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Mol	Chain	Res	Type	Atoms
51	W	201	CDL	CA2-OA2-PA1-OA3
51	W	201	CDL	CA2-OA2-PA1-OA4
51	W	201	CDL	CB3-OB5-PB2-OB3
51	h	201	CDL	CA2-OA2-PA1-OA5
51	h	201	CDL	CB2-OB2-PB2-OB3
51	h	201	CDL	CB2-OB2-PB2-OB4
51	h	201	CDL	CB3-OB5-PB2-OB3
51	o	201	CDL	CA2-OA2-PA1-OA3
51	o	201	CDL	CA2-OA2-PA1-OA4
51	o	201	CDL	CA2-OA2-PA1-OA5
51	o	201	CDL	CA3-OA5-PA1-OA2
51	o	201	CDL	CA3-OA5-PA1-OA3
51	o	201	CDL	CA3-OA5-PA1-OA4
51	o	201	CDL	OA6-CA4-CA6-OA8
51	o	201	CDL	CB2-OB2-PB2-OB5
51	o	201	CDL	CB3-OB5-PB2-OB2
51	o	201	CDL	CB3-OB5-PB2-OB3
51	o	201	CDL	CB3-OB5-PB2-OB4
52	X	101	ZMP	C16-C17-C18-C21
52	X	101	ZMP	O3-C16-C17-O4
52	X	101	ZMP	C17-C16-N2-C15
52	g	201	ZMP	S1-C11-C12-N1
52	g	201	ZMP	C7-C8-C9-C10
54	d	401	NDP	C2N-C3N-C7N-O7N
55	k	501	AMP	C5'-O5'-P-O2P
55	k	501	AMP	C5'-O5'-P-O3P
55	k	501	AMP	C3'-C4'-C5'-O5'
51	h	201	CDL	O1-C1-CB2-OB2
52	X	101	ZMP	O3-C16-N2-C15
51	M	502	CDL	CA2-C1-CB2-OB2
51	M	503	CDL	CA2-C1-CB2-OB2
51	h	201	CDL	CA2-C1-CB2-OB2
49	L	1002	PC1	C21-C22-C23-C24
51	L	1003	CDL	CB7-C71-C72-C73
51	M	503	CDL	CB5-C51-C52-C53
55	k	501	AMP	O4'-C4'-C5'-O5'
49	6	202	PC1	C11-C12-N-C14
49	M	501	PC1	C11-C12-N-C13
49	M	501	PC1	C11-C12-N-C15
51	M	503	CDL	CB7-C71-C72-C73
46	1	501	FMN	O3'-C3'-C4'-C5'
49	M	501	PC1	C11-O13-P-O11

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Mol	Chain	Res	Type	Atoms
50	H	402	3PE	C11-O13-P-O11
50	L	1004	3PE	C1-O11-P-O13
50	L	1004	3PE	C11-O13-P-O11
50	N	401	3PE	C11-O13-P-O11
50	N	402	3PE	C11-O13-P-O11
50	i	201	3PE	C11-O13-P-O11
51	L	1003	CDL	CB2-OB2-PB2-OB5
51	L	1003	CDL	CB3-OB5-PB2-OB2
51	M	503	CDL	CA2-OA2-PA1-OA5
51	M	503	CDL	CB2-OB2-PB2-OB5
51	W	201	CDL	CA2-OA2-PA1-OA5
51	h	201	CDL	CA3-OA5-PA1-OA2
51	h	201	CDL	CB2-OB2-PB2-OB5
51	L	1003	CDL	C21-C22-C23-C24
51	L	1003	CDL	C41-C42-C43-C44
51	M	503	CDL	C78-C79-C80-C81
51	L	1003	CDL	C17-C18-C19-C20
51	L	1003	CDL	C56-C57-C58-C59
51	M	503	CDL	C81-C82-C83-C84
46	1	501	FMN	C2'-C3'-C4'-O4'
51	M	502	CDL	C57-C58-C59-C60
51	M	502	CDL	C63-C64-C65-C66
49	L	1002	PC1	C2-C1-O11-P
49	L	1002	PC1	C36-C37-C38-C39
49	L	1002	PC1	C37-C38-C39-C3A
51	L	1003	CDL	C82-C83-C84-C85
51	M	502	CDL	C52-C53-C54-C55
51	M	503	CDL	OA6-CA4-CA6-OA8
49	H	401	PC1	C3C-C3D-C3E-C3F
51	M	502	CDL	C81-C82-C83-C84
51	L	1003	CDL	C77-C78-C79-C80
51	W	201	CDL	C35-C36-C37-C38
50	m	101	3PE	C3A-C3B-C3C-C3D
49	H	401	PC1	C3B-C3C-C3D-C3E
51	W	201	CDL	CB5-C51-C52-C53
51	M	503	CDL	C56-C57-C58-C59
49	6	202	PC1	C11-C12-N-C15
50	L	1001	3PE	C26-C27-C28-C29
51	M	502	CDL	C12-C13-C14-C15
50	N	401	3PE	C21-C22-C23-C24
52	g	201	ZMP	C3-C4-C5-C6
51	M	502	CDL	C32-C33-C34-C35

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Mol	Chain	Res	Type	Atoms
46	1	501	FMN	C2'-C3'-C4'-C5'
49	L	1002	PC1	C38-C39-C3A-C3B
46	1	501	FMN	O3'-C3'-C4'-O4'
49	H	401	PC1	C2C-C2D-C2E-C2F
49	6	202	PC1	C11-C12-N-C13
51	L	1003	CDL	CB5-C51-C52-C53
51	L	1003	CDL	C32-C33-C34-C35
51	M	502	CDL	CB5-C51-C52-C53
49	L	1002	PC1	C33-C34-C35-C36
50	m	101	3PE	C2C-C2D-C2E-C2F
50	m	101	3PE	C2E-C2F-C2G-C2H
51	W	201	CDL	CA5-C11-C12-C13
50	L	1001	3PE	C35-C36-C37-C38
51	M	502	CDL	C37-C38-C39-C40
49	M	501	PC1	C11-C12-N-C14
49	6	202	PC1	C23-C24-C25-C26
49	6	202	PC1	C11-O13-P-O11
49	6	202	PC1	C1-O11-P-O13
49	L	1002	PC1	C11-O13-P-O11
50	i	201	3PE	C1-O11-P-O13
51	W	201	CDL	CB3-OB5-PB2-OB2
51	h	201	CDL	CB3-OB5-PB2-OB2
49	L	1002	PC1	O11-C1-C2-C3
50	H	402	3PE	O11-C1-C2-C3
51	M	503	CDL	C71-C72-C73-C74
50	N	401	3PE	C1-C2-C3-O31
51	M	502	CDL	CA3-CA4-CA6-OA8
51	M	503	CDL	CA3-CA4-CA6-OA8
49	6	202	PC1	C3B-C3C-C3D-C3E
51	M	502	CDL	C11-C12-C13-C14
46	1	501	FMN	C5'-O5'-P-O1P
50	L	1001	3PE	C34-C35-C36-C37
49	A	201	PC1	O11-C1-C2-O21
50	L	1004	3PE	O11-C1-C2-O21
51	W	201	CDL	OB5-CB3-CB4-OB6
49	6	202	PC1	C3C-C3D-C3E-C3F
49	w	801	PC1	C3E-C3F-C3G-C3H
52	g	201	ZMP	O4-C17-C18-C19
52	g	201	ZMP	O4-C17-C18-C20
50	N	401	3PE	C32-C33-C34-C35
49	w	801	PC1	C27-C28-C29-C2A
51	L	1003	CDL	OB5-CB3-CB4-CB6

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Mol	Chain	Res	Type	Atoms
51	M	503	CDL	OB5-CB3-CB4-CB6
51	o	201	CDL	CA4-CA3-OA5-PA1
55	k	501	AMP	C4'-C5'-O5'-P
50	6	203	3PE	C3A-C3B-C3C-C3D
51	W	201	CDL	CA3-CA4-CA6-OA8
51	o	201	CDL	CA3-CA4-CA6-OA8
51	h	201	CDL	CB7-C71-C72-C73
50	N	401	3PE	C2B-C2C-C2D-C2E
50	N	401	3PE	C2C-C2D-C2E-C2F
49	L	1002	PC1	C1-O11-P-O13
51	M	502	CDL	C15-C16-C17-C18
49	L	1002	PC1	C3E-C3F-C3G-C3H
51	M	502	CDL	OA6-CA4-CA6-OA8
50	6	203	3PE	C23-C24-C25-C26
51	L	1003	CDL	CA4-CA3-OA5-PA1
51	M	503	CDL	CB4-CB3-OB5-PB2
50	6	203	3PE	C33-C34-C35-C36
52	g	201	ZMP	O1-C10-S1-C11
50	i	201	3PE	C36-C37-C38-C39
49	A	201	PC1	O11-C1-C2-C3
49	M	501	PC1	O11-C1-C2-C3
51	W	201	CDL	OB5-CB3-CB4-CB6
51	L	1003	CDL	C22-C23-C24-C25
49	w	801	PC1	C29-C2A-C2B-C2C
54	d	401	NDP	C2B-O2B-P2B-O1X
49	M	501	PC1	O31-C31-C32-C33
52	g	201	ZMP	C9-C10-S1-C11
51	h	201	CDL	CA3-CA4-CA6-OA8
51	W	201	CDL	C13-C14-C15-C16
49	w	801	PC1	C39-C3A-C3B-C3C
52	X	101	ZMP	C16-C17-C18-C20
52	g	201	ZMP	C16-C17-C18-C19
52	g	201	ZMP	C16-C17-C18-C20
51	M	503	CDL	C80-C81-C82-C83
50	m	101	3PE	C38-C39-C3A-C3B
51	W	201	CDL	OA6-CA4-CA6-OA8
51	o	201	CDL	C14-C15-C16-C17
50	6	203	3PE	C37-C38-C39-C3A
49	H	401	PC1	C1-O11-P-O13
50	6	203	3PE	C11-O13-P-O11
50	m	101	3PE	C1-O11-P-O13
51	M	503	CDL	CA3-OA5-PA1-OA2

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Mol	Chain	Res	Type	Atoms
49	H	401	PC1	C3A-C3B-C3C-C3D
46	1	501	FMN	C4'-C5'-O5'-P
50	H	402	3PE	C2-C1-O11-P
51	h	201	CDL	CB4-CB3-OB5-PB2
49	6	202	PC1	C11-O13-P-O14
49	6	202	PC1	C1-O11-P-O12
49	H	401	PC1	C1-O11-P-O12
49	L	1002	PC1	C11-O13-P-O12
49	L	1002	PC1	C1-O11-P-O14
50	H	402	3PE	C11-O13-P-O12
50	L	1004	3PE	C1-O11-P-O14
50	N	401	3PE	C1-O11-P-O14
50	N	401	3PE	C11-O13-P-O14
50	i	201	3PE	C1-O11-P-O14
50	i	201	3PE	C11-O13-P-O14
51	L	1003	CDL	CB2-OB2-PB2-OB3
51	L	1003	CDL	CB3-OB5-PB2-OB4
51	M	503	CDL	CA2-OA2-PA1-OA3
51	M	503	CDL	CB2-OB2-PB2-OB4
51	W	201	CDL	CB3-OB5-PB2-OB4
51	h	201	CDL	CA2-OA2-PA1-OA4
51	h	201	CDL	CA3-OA5-PA1-OA3
51	h	201	CDL	CA3-OA5-PA1-OA4
51	h	201	CDL	CB3-OB5-PB2-OB4
51	o	201	CDL	CB2-OB2-PB2-OB4
54	d	401	NDP	C2N-C3N-C7N-N7N
51	h	201	CDL	C52-C53-C54-C55
51	o	201	CDL	C52-C51-CB5-OB6
50	L	1001	3PE	C23-C24-C25-C26
50	6	203	3PE	C3D-C3E-C3F-C3G
52	X	101	ZMP	C2-C3-C4-C5
49	M	501	PC1	C12-C11-O13-P
51	M	502	CDL	C14-C15-C16-C17
49	L	1002	PC1	O11-C1-C2-O21
49	M	501	PC1	O11-C1-C2-O21
49	w	801	PC1	C31-C32-C33-C34
51	L	1003	CDL	OA5-CA3-CA4-OA6
51	L	1003	CDL	OB5-CB3-CB4-OB6
51	o	201	CDL	CA7-C31-C32-C33
51	o	201	CDL	OB5-CB3-CB4-OB6
51	L	1003	CDL	C31-C32-C33-C34
49	H	401	PC1	O13-C11-C12-N

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Mol	Chain	Res	Type	Atoms
49	w	801	PC1	O13-C11-C12-N
52	g	201	ZMP	O4-C17-C18-C21
56	s	201	MYR	C1-C2-C3-C4
49	H	401	PC1	C2-C1-O11-P
51	h	201	CDL	C1-CB2-OB2-PB2
49	M	501	PC1	C34-C35-C36-C37
49	H	401	PC1	C3-C2-O21-C21
49	L	1002	PC1	C1-C2-O21-C21
50	L	1001	3PE	C3B-C3C-C3D-C3E
51	L	1003	CDL	CB4-CB3-OB5-PB2
50	H	402	3PE	O11-C1-C2-O21
50	N	401	3PE	O11-C1-C2-O21
51	h	201	CDL	OA5-CA3-CA4-OA6
50	N	401	3PE	O21-C2-C3-O31
51	h	201	CDL	OA6-CA4-CA6-OA8
49	A	201	PC1	C11-O13-P-O11
50	H	402	3PE	C1-O11-P-O13
50	L	1001	3PE	C11-O13-P-O11
51	W	201	CDL	CA3-OA5-PA1-OA2
50	i	201	3PE	C38-C39-C3A-C3B
54	d	401	NDP	O4D-C1D-N1N-C6N
50	H	402	3PE	C27-C28-C29-C2A
54	d	401	NDP	C2D-C1D-N1N-C6N
51	L	1003	CDL	C34-C35-C36-C37
51	W	201	CDL	CA7-C31-C32-C33
51	o	201	CDL	C12-C13-C14-C15
51	M	503	CDL	C1-CA2-OA2-PA1
51	M	503	CDL	CA4-CA3-OA5-PA1
49	A	201	PC1	O31-C31-C32-C33
49	w	801	PC1	C2C-C2D-C2E-C2F
50	i	201	3PE	C29-C2A-C2B-C2C
50	N	401	3PE	C38-C39-C3A-C3B
51	h	201	CDL	CB3-CB4-CB6-OB8
51	o	201	CDL	CB3-CB4-CB6-OB8
50	m	101	3PE	C2D-C2E-C2F-C2G
51	h	201	CDL	CA5-C11-C12-C13
49	6	202	PC1	C3E-C3F-C3G-C3H
50	N	401	3PE	C1-O11-P-O13
51	M	502	CDL	C1-CB2-OB2-PB2
51	o	201	CDL	O1-C1-CB2-OB2
51	M	503	CDL	C12-C13-C14-C15
52	g	201	ZMP	C12-C11-S1-C10

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Mol	Chain	Res	Type	Atoms
50	m	101	3PE	O21-C2-C3-O31
51	W	201	CDL	CB7-C71-C72-C73
51	L	1003	CDL	CA2-C1-CB2-OB2
51	L	1003	CDL	C58-C59-C60-C61
51	M	503	CDL	C64-C65-C66-C67
51	M	502	CDL	C80-C81-C82-C83
49	w	801	PC1	C2B-C2C-C2D-C2E
51	L	1003	CDL	C15-C16-C17-C18
49	w	801	PC1	C26-C27-C28-C29
50	6	203	3PE	C35-C36-C37-C38
49	H	401	PC1	O22-C21-O21-C2
51	M	502	CDL	C12-C11-CA5-OA6
52	X	101	ZMP	N2-C16-C17-O4
52	g	201	ZMP	N2-C16-C17-O4
50	i	201	3PE	O21-C21-C22-C23
49	A	201	PC1	O21-C21-C22-C23
49	M	501	PC1	C24-C25-C26-C27
50	L	1004	3PE	C1-C2-O21-C21
51	M	503	CDL	CB3-CB4-OB6-CB5
51	L	1003	CDL	C72-C71-CB7-OB8
51	W	201	CDL	C12-C11-CA5-OA6
52	g	201	ZMP	C2-C1-C22-C23
51	M	502	CDL	C59-C60-C61-C62
50	N	401	3PE	O31-C31-C32-C33
51	M	502	CDL	C61-C62-C63-C64
51	L	1003	CDL	C72-C73-C74-C75
51	h	201	CDL	C52-C51-CB5-OB6
51	M	502	CDL	C13-C14-C15-C16
50	N	402	3PE	C25-C26-C27-C28
52	X	101	ZMP	C16-C17-C18-C19
51	L	1003	CDL	OA5-CA3-CA4-CA6
51	o	201	CDL	C72-C71-CB7-OB8
49	H	401	PC1	C22-C21-O21-C2
51	L	1003	CDL	C40-C41-C42-C43
52	X	101	ZMP	C5-C6-C7-C8
50	N	402	3PE	C32-C33-C34-C35
51	o	201	CDL	C18-C19-C20-C21
49	w	801	PC1	C3A-C3B-C3C-C3D
49	A	201	PC1	C32-C33-C34-C35
50	N	401	3PE	O32-C31-C32-C33
50	i	201	3PE	O22-C21-C22-C23
51	M	502	CDL	C12-C11-CA5-OA7

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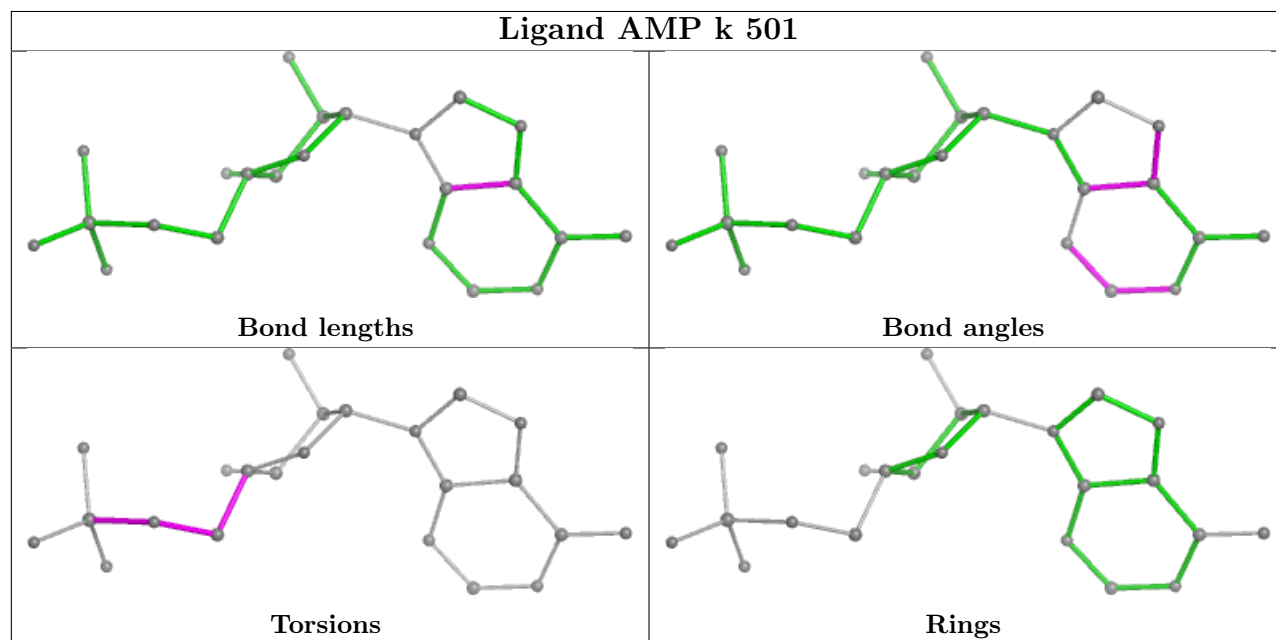
Mol	Chain	Res	Type	Atoms
50	L	1004	3PE	C33-C34-C35-C36
51	L	1003	CDL	C72-C71-CB7-OB9
51	W	201	CDL	C12-C11-CA5-OA7
51	M	502	CDL	C79-C80-C81-C82
51	h	201	CDL	C52-C51-CB5-OB7
51	L	1003	CDL	C79-C80-C81-C82
51	L	1003	CDL	C54-C55-C56-C57
56	s	201	MYR	C11-C10-C9-C8
50	6	203	3PE	C1-O11-P-O14
50	6	203	3PE	C11-O13-P-O12
50	L	1001	3PE	C11-O13-P-O14
51	L	1003	CDL	CA2-OA2-PA1-OA3
54	d	401	NDP	O4B-C4B-C5B-O5B
50	L	1004	3PE	O21-C21-C22-C23
51	M	503	CDL	C76-C77-C78-C79
50	m	101	3PE	C24-C25-C26-C27
50	L	1004	3PE	C12-C11-O13-P
50	N	401	3PE	C3-C2-O21-C21
51	o	201	CDL	CB6-CB4-OB6-CB5
51	o	201	CDL	C72-C71-CB7-OB9
51	M	503	CDL	C31-C32-C33-C34
50	L	1001	3PE	O31-C31-C32-C33
50	L	1001	3PE	O21-C21-C22-C23
49	A	201	PC1	C22-C23-C24-C25
51	W	201	CDL	C22-C23-C24-C25
49	L	1002	PC1	C3A-C3B-C3C-C3D
52	g	201	ZMP	C16-C17-C18-C21
50	H	402	3PE	O31-C31-C32-C33
49	w	801	PC1	C37-C38-C39-C3A
50	N	401	3PE	C3C-C3D-C3E-C3F
51	W	201	CDL	C44-C45-C46-C47
49	M	501	PC1	O32-C31-C32-C33
51	L	1003	CDL	O1-C1-CB2-OB2
51	M	502	CDL	C72-C71-CB7-OB8

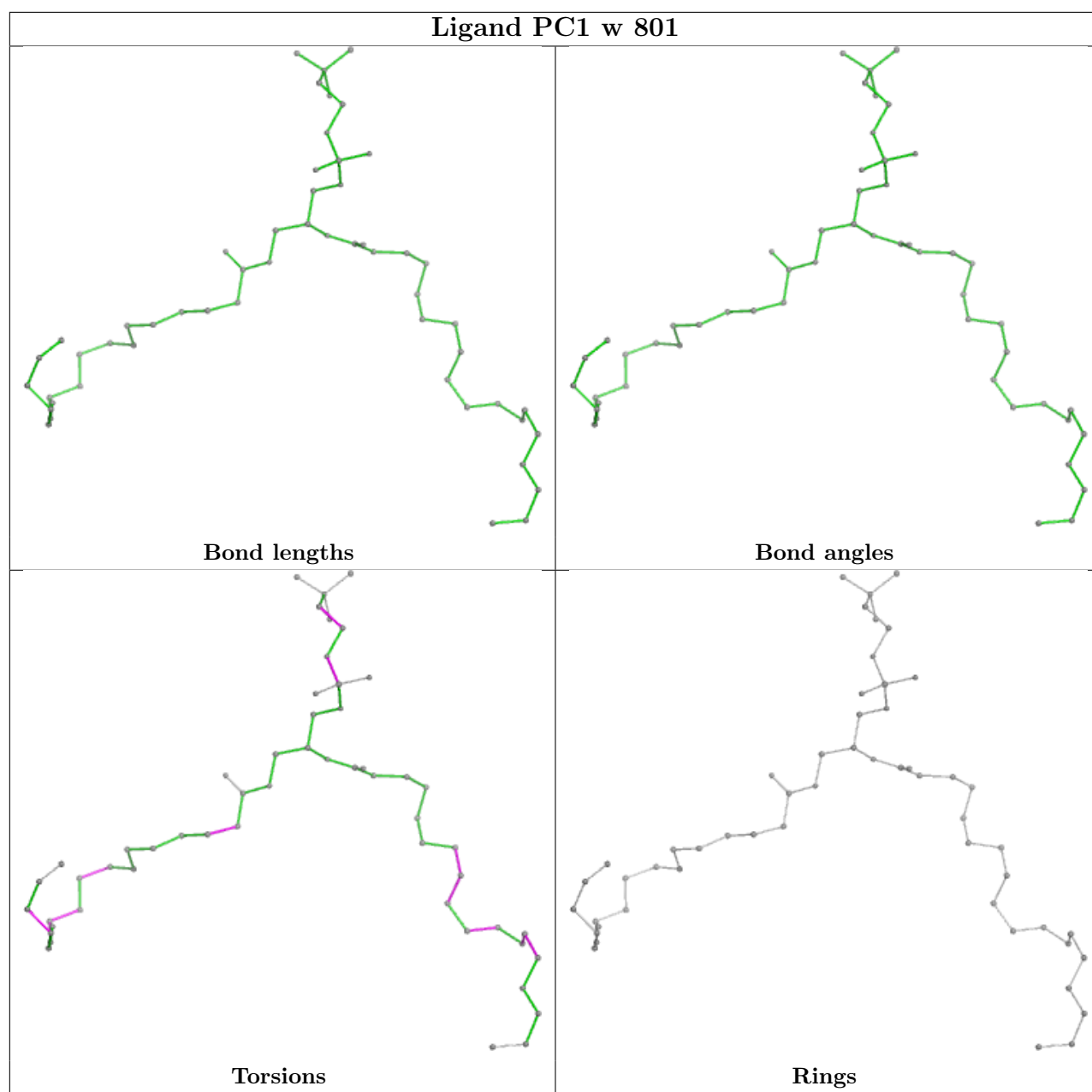
There are no ring outliers.

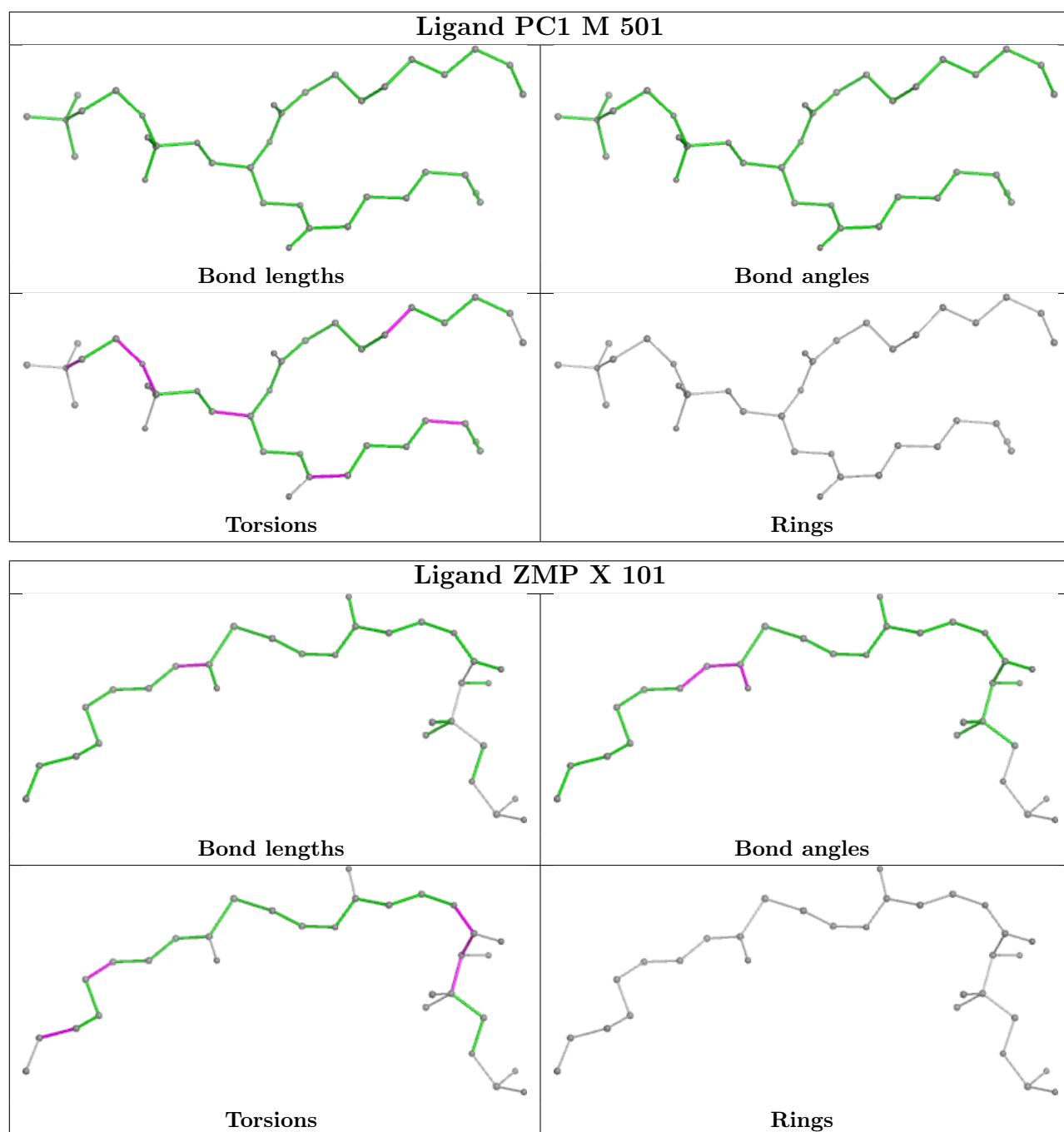
No monomer is involved in short contacts.

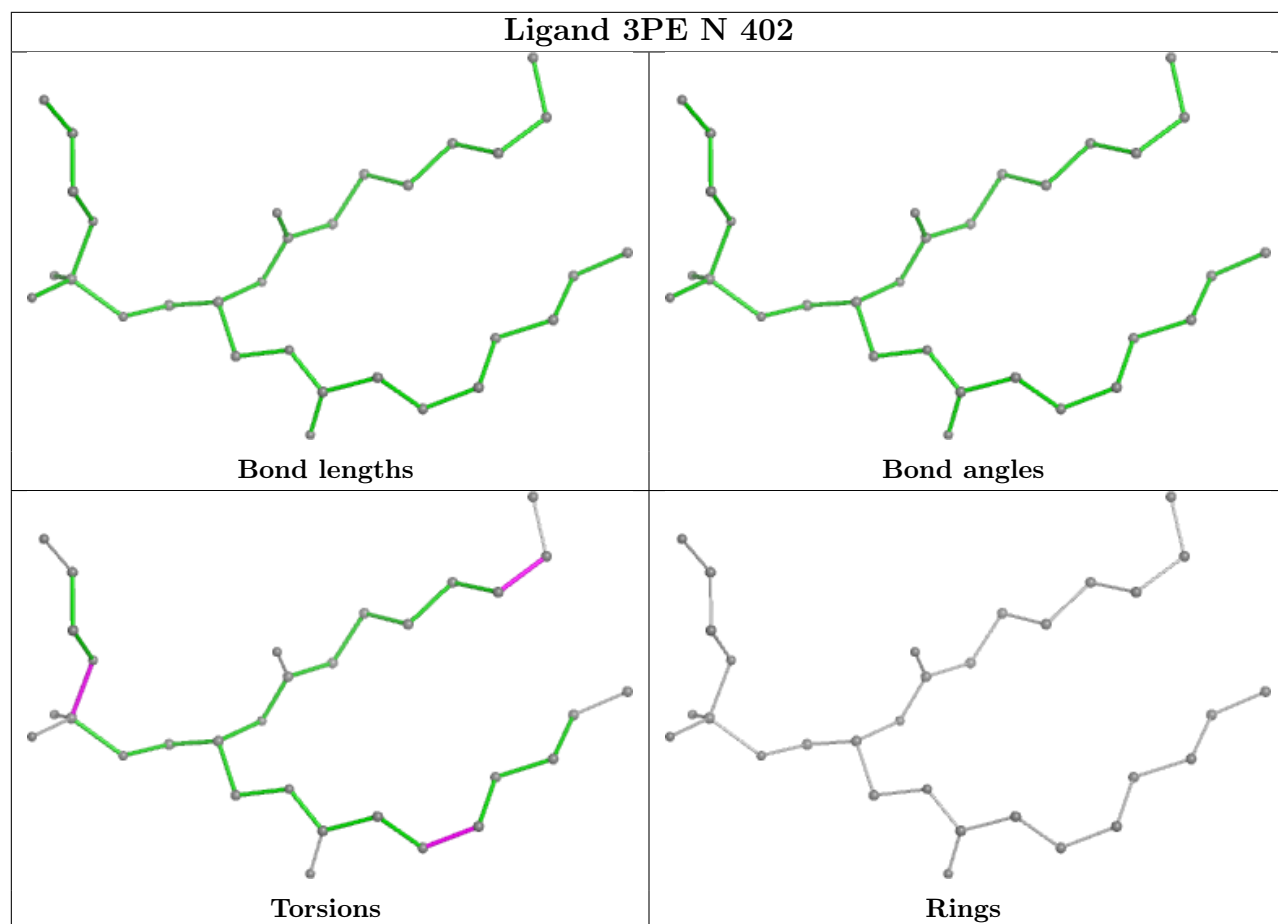
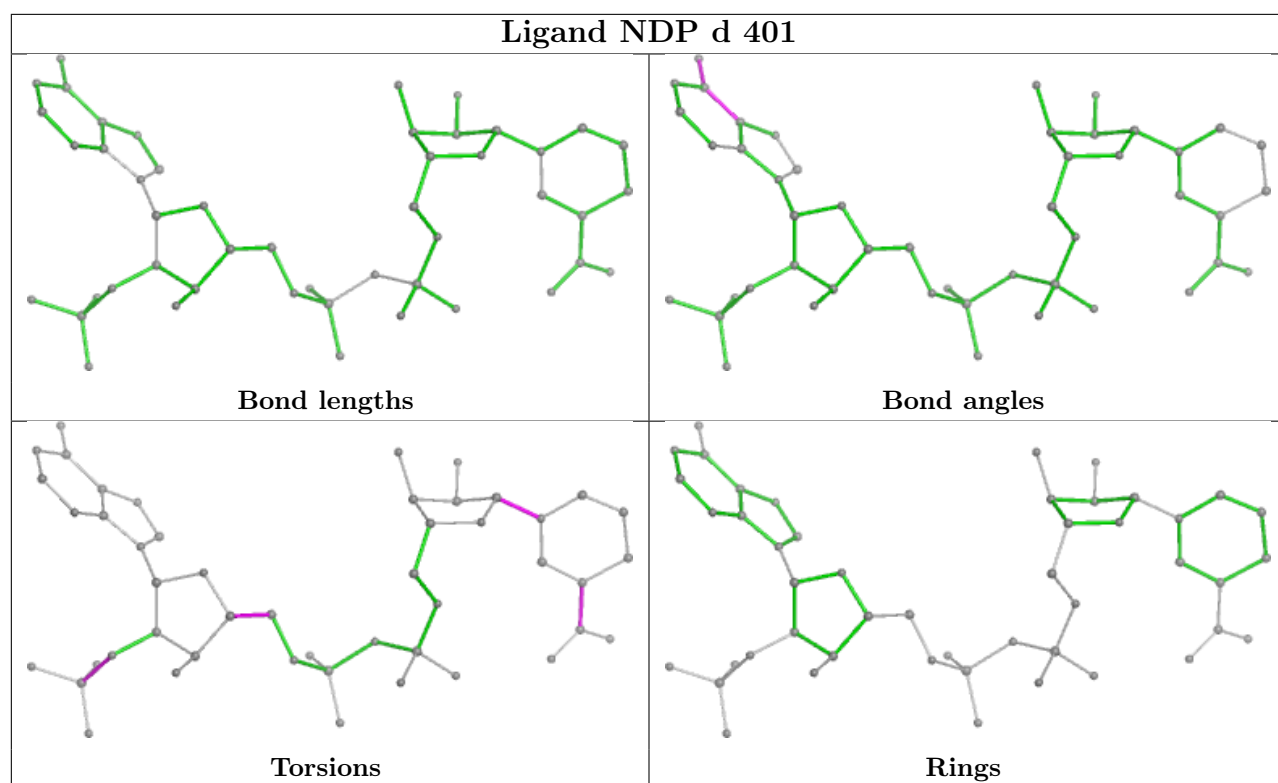
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

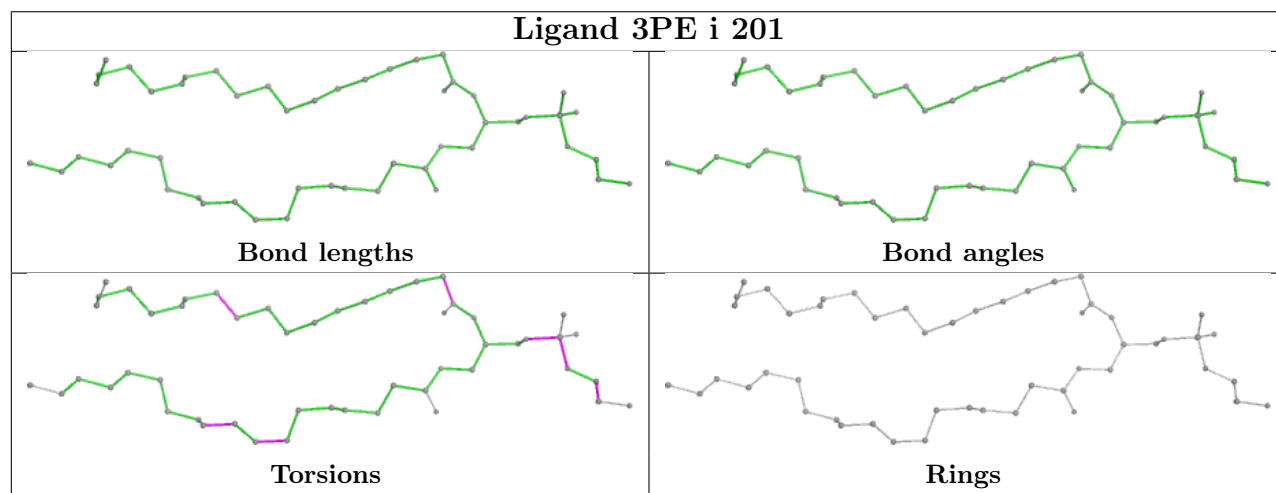
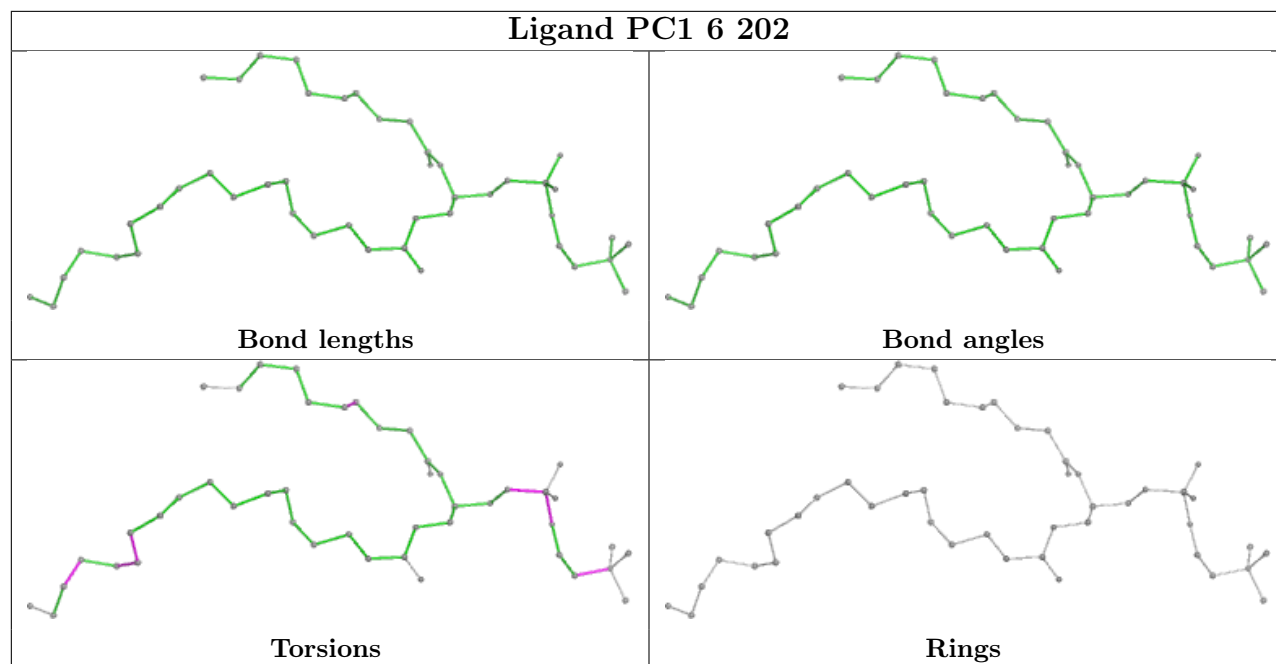
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD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

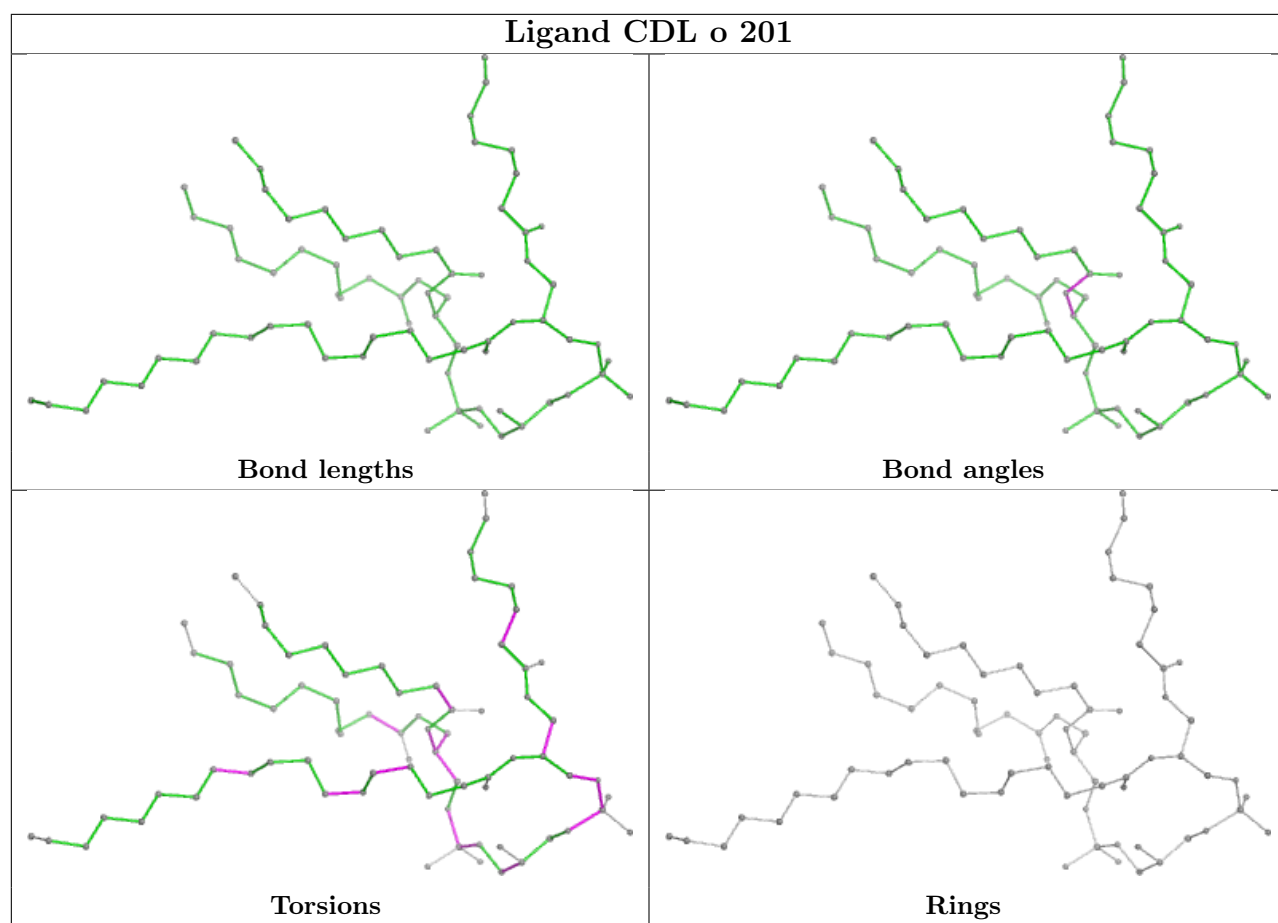


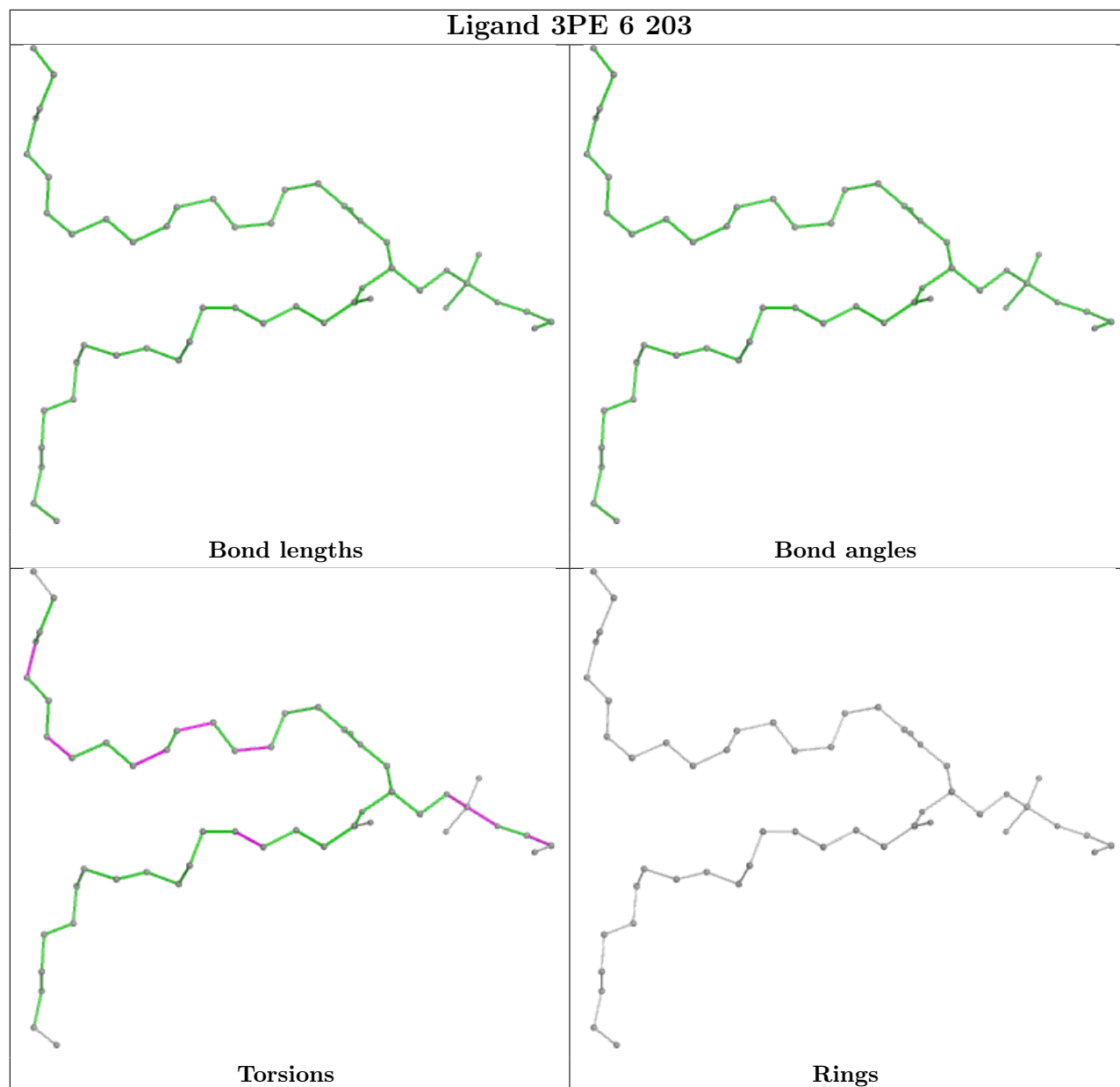


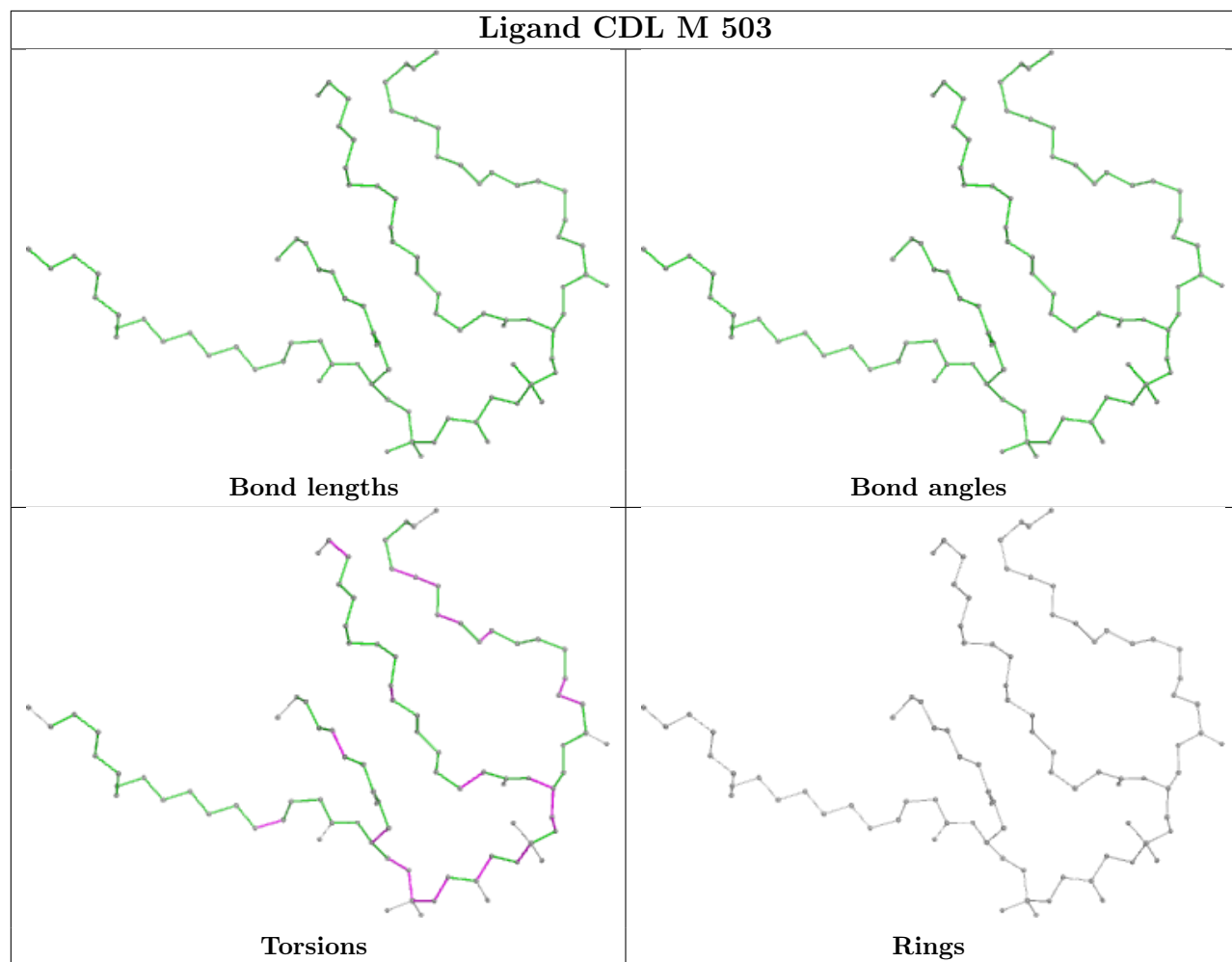


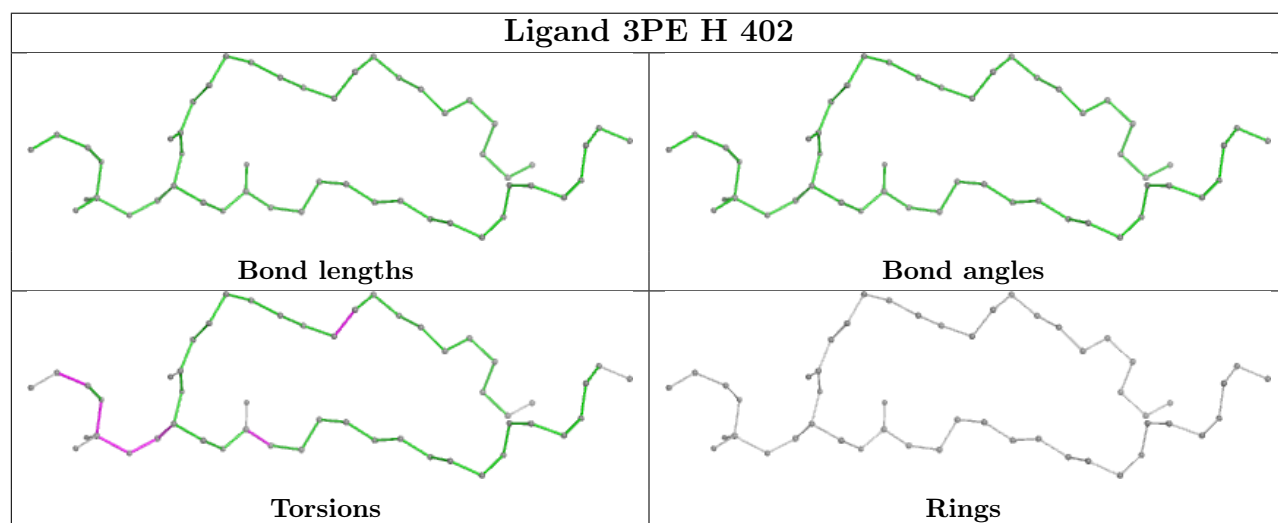
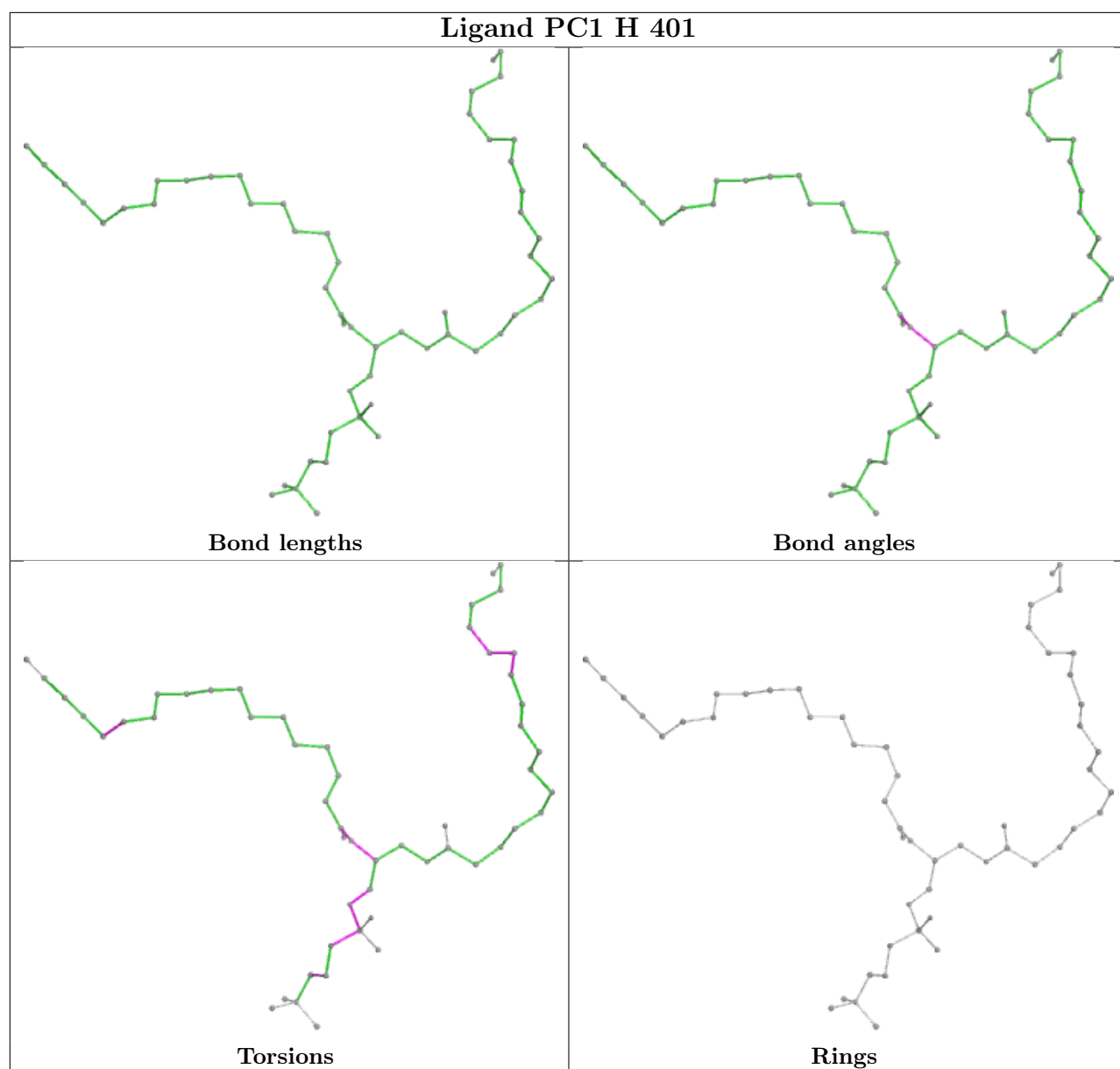


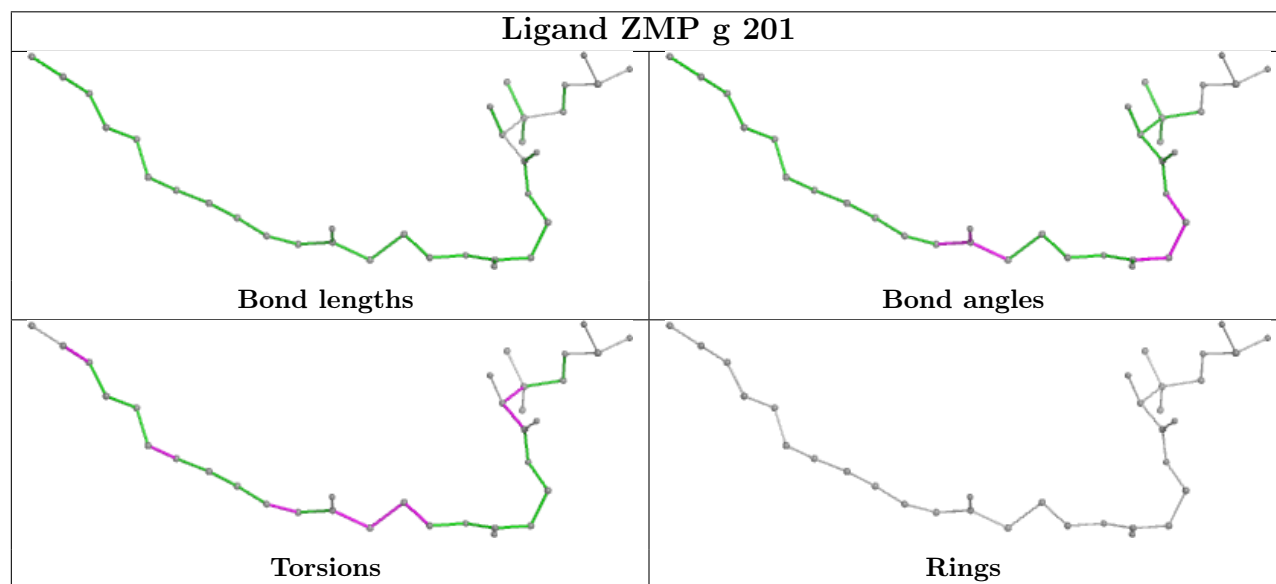
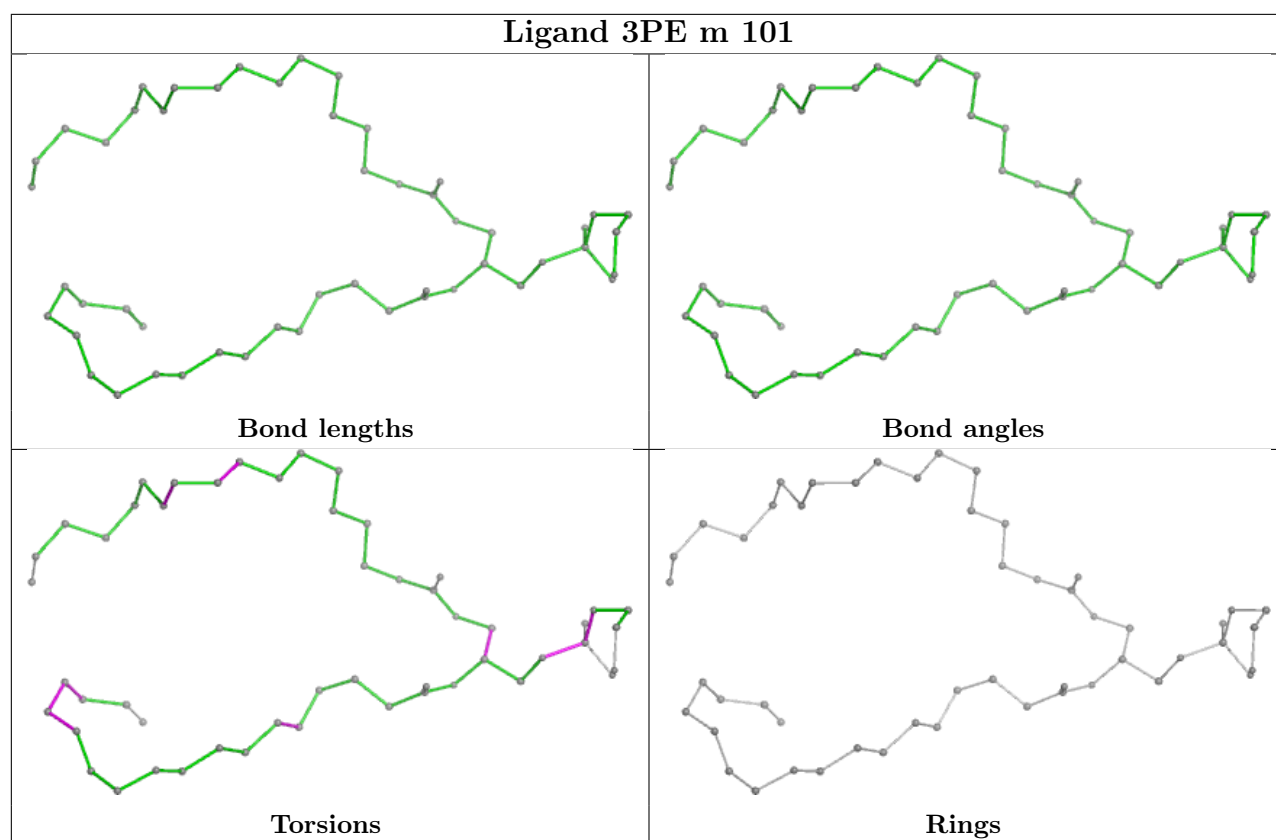


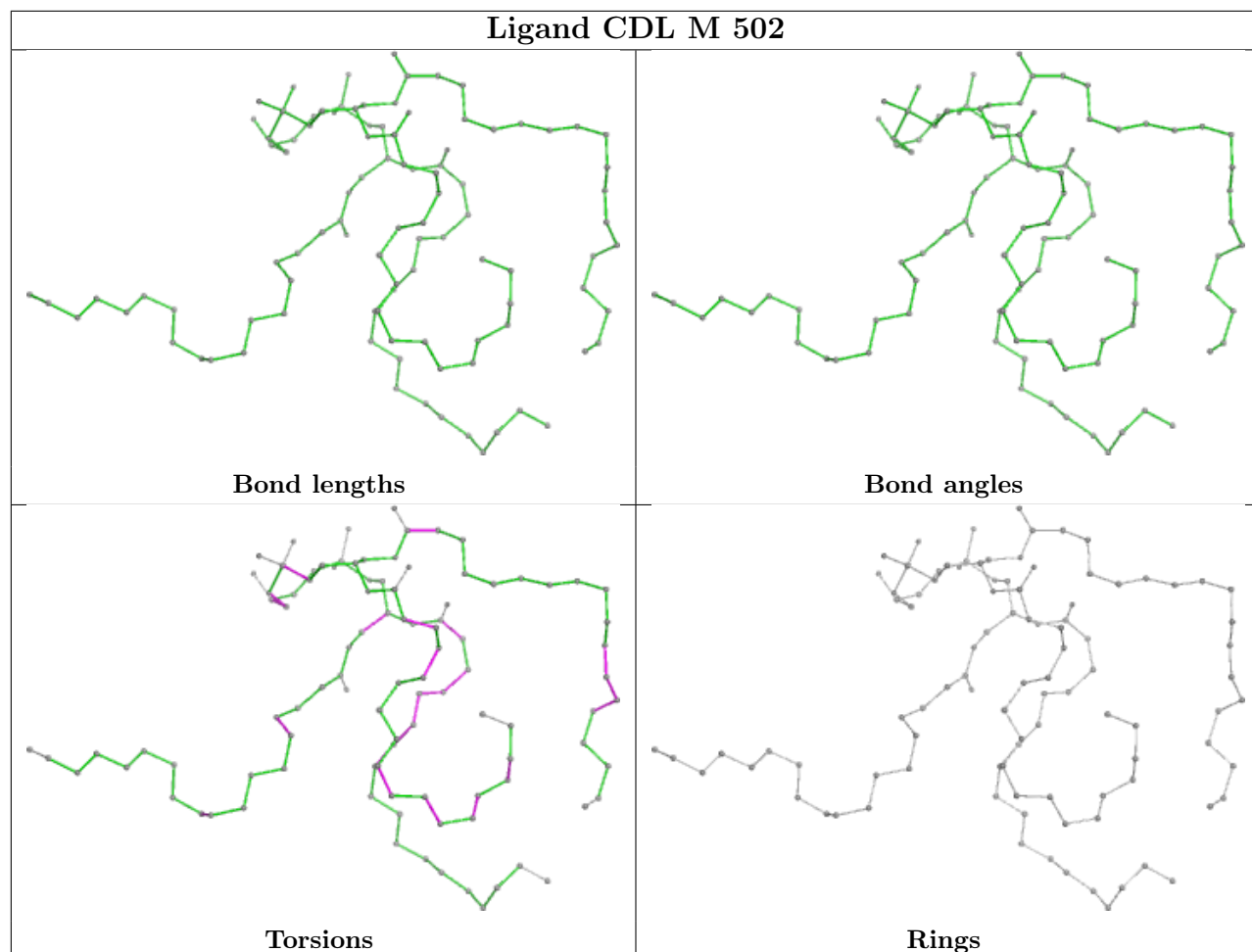
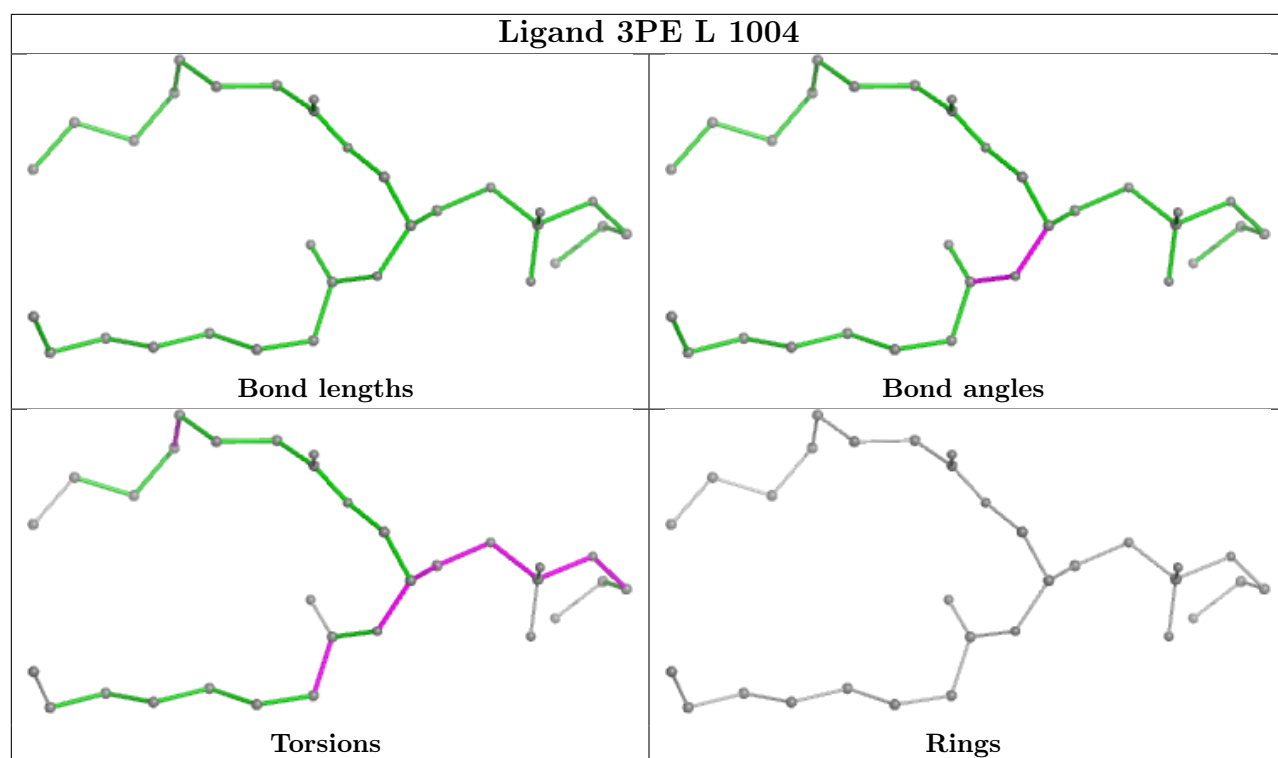


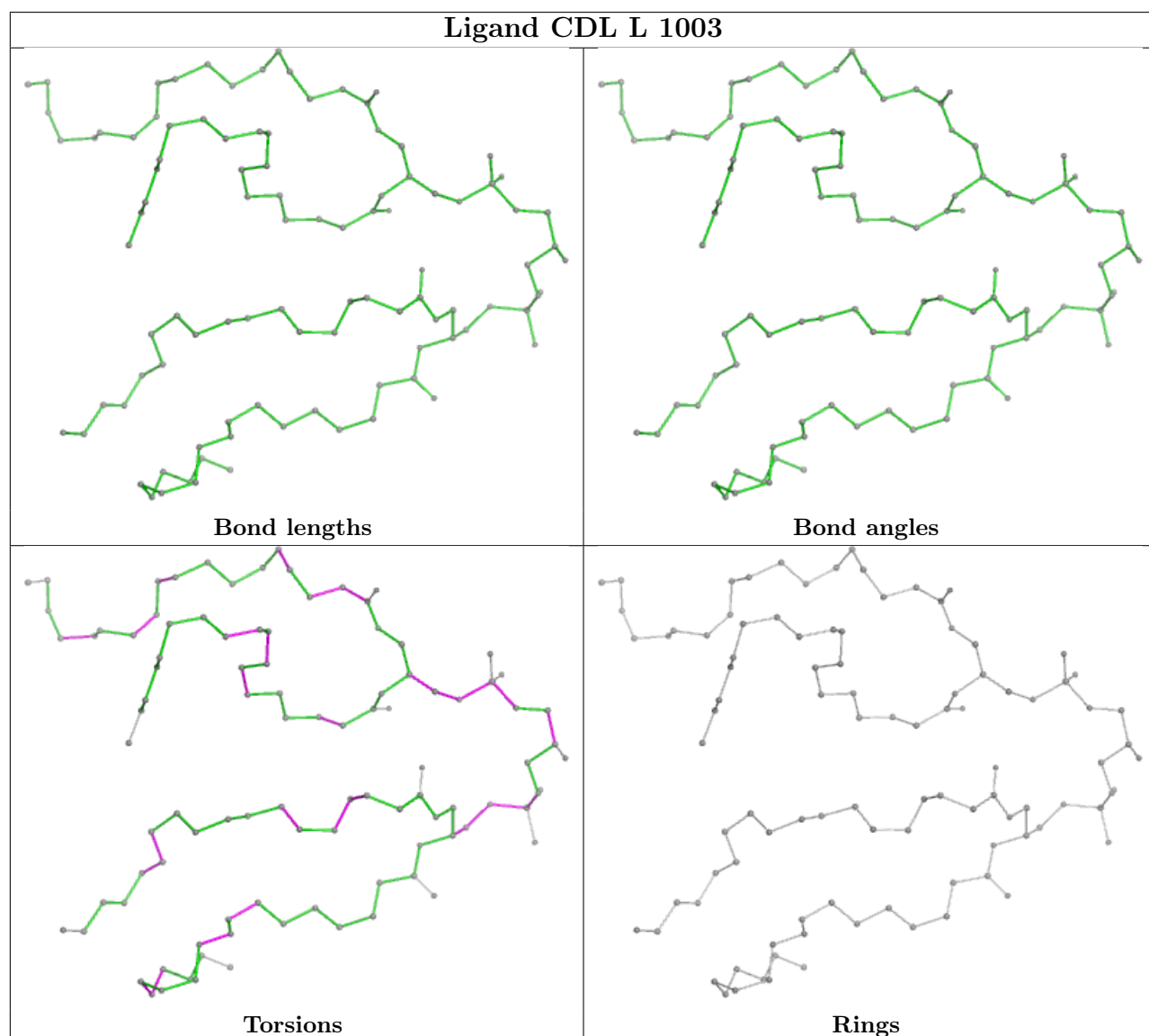
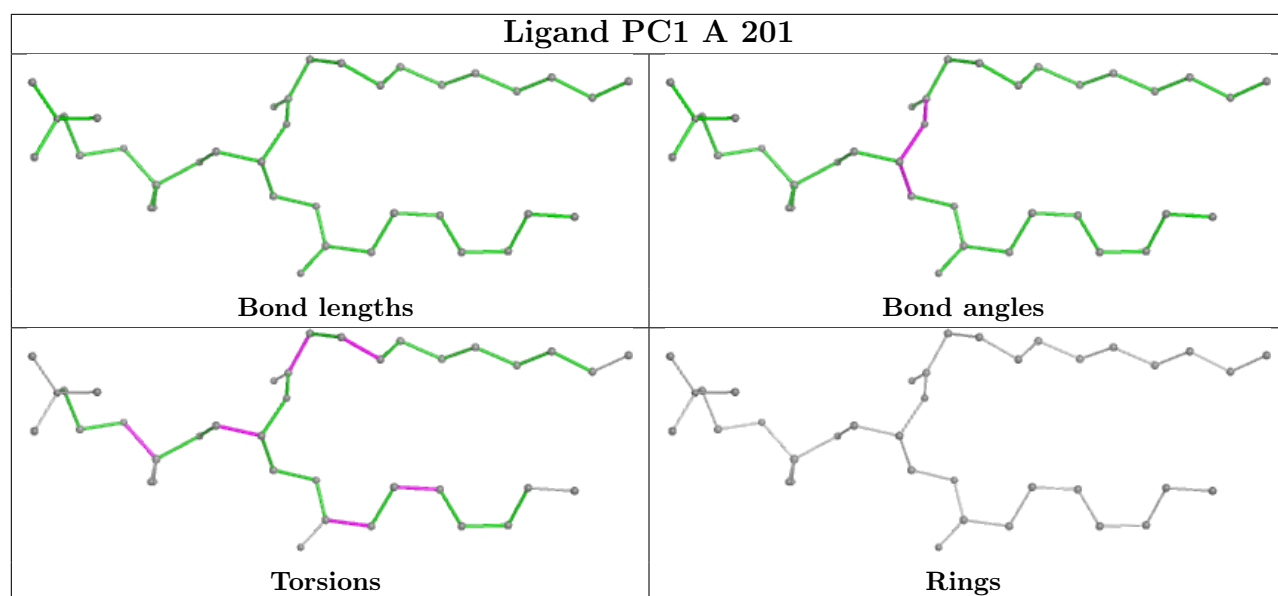


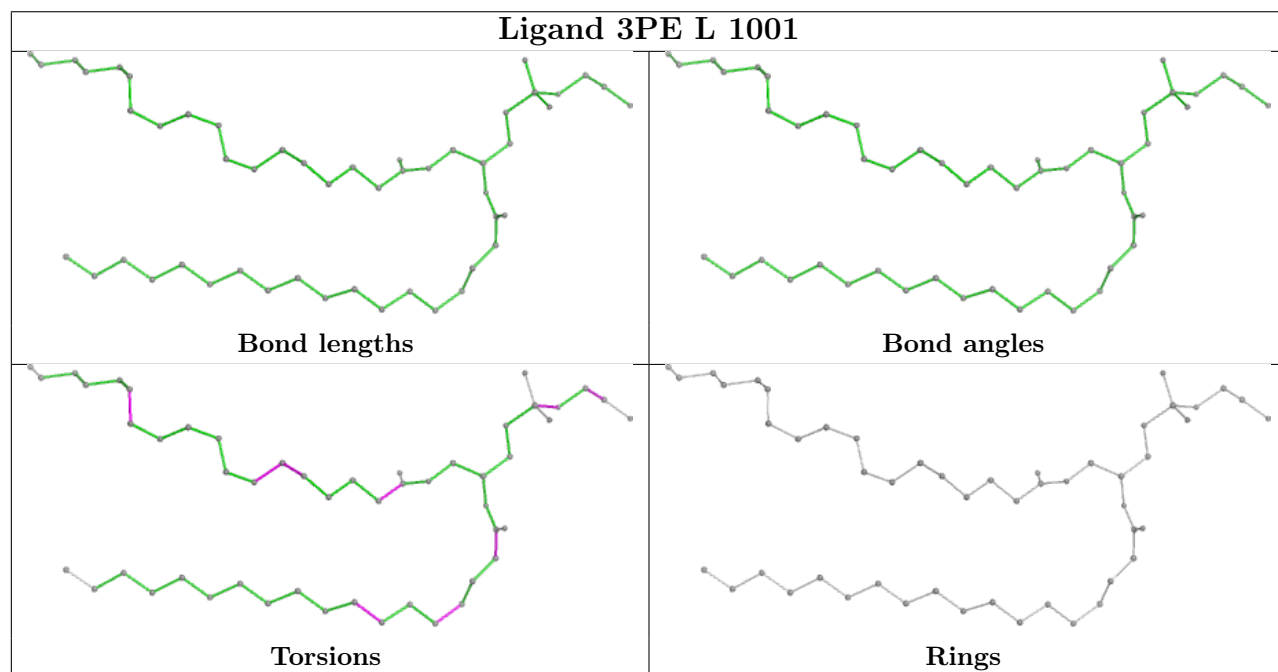
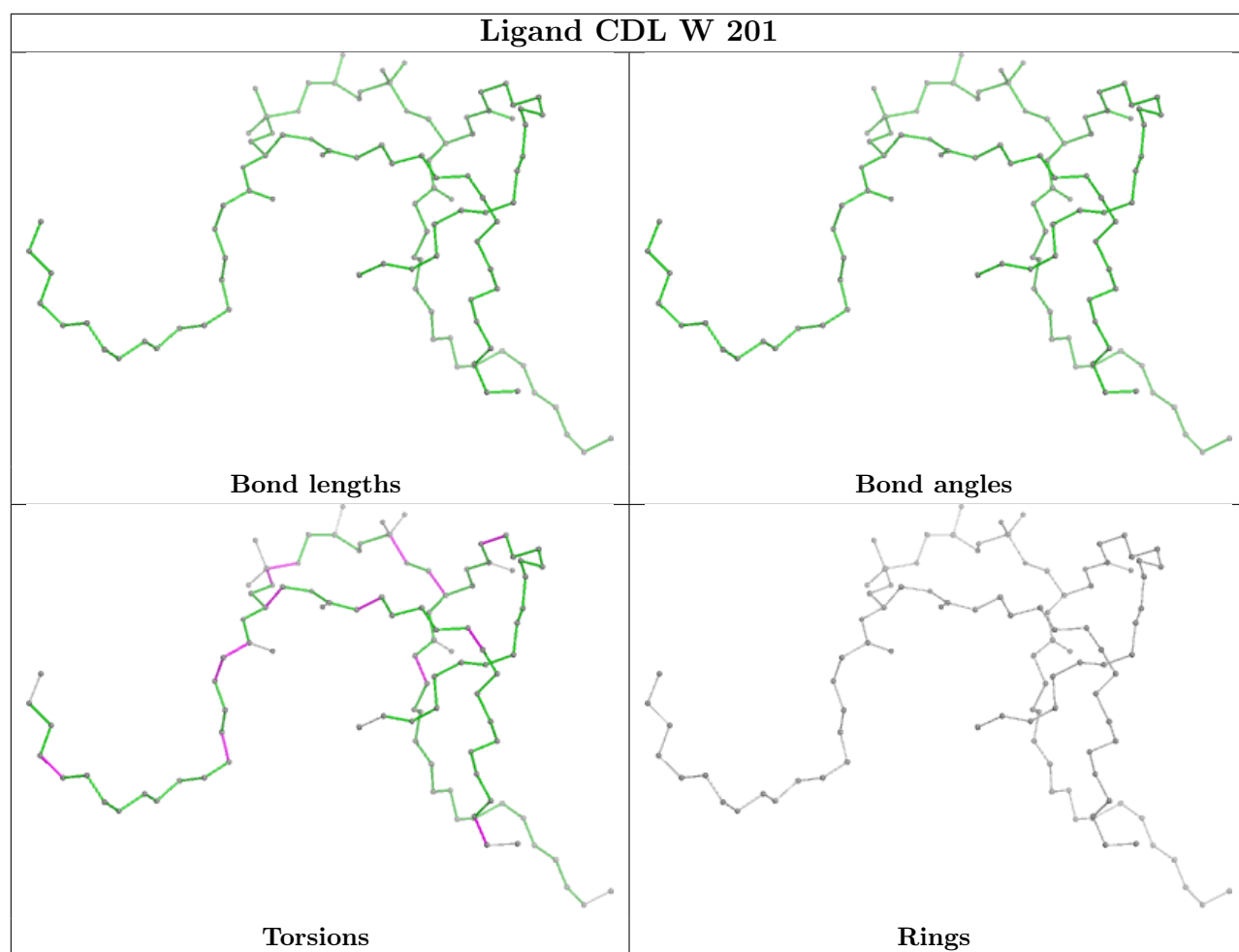


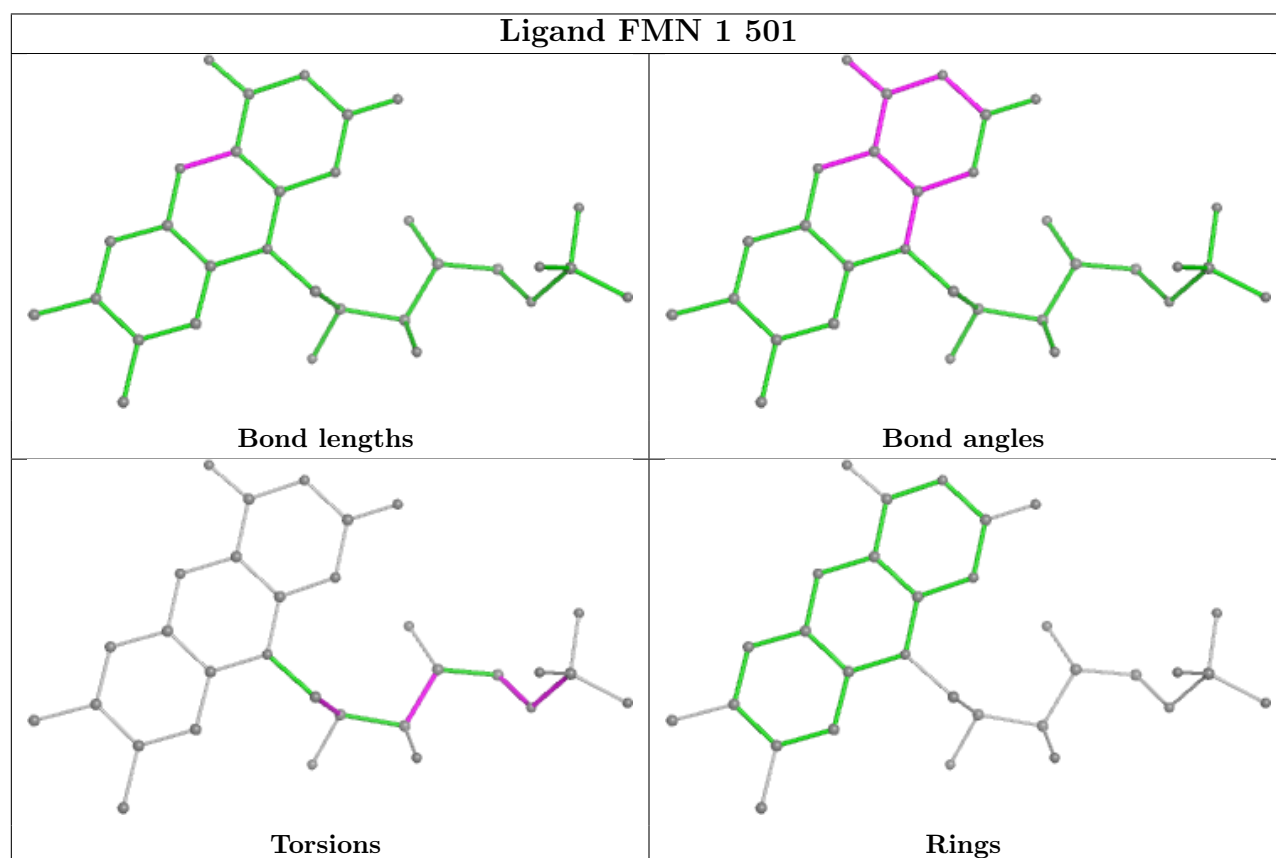
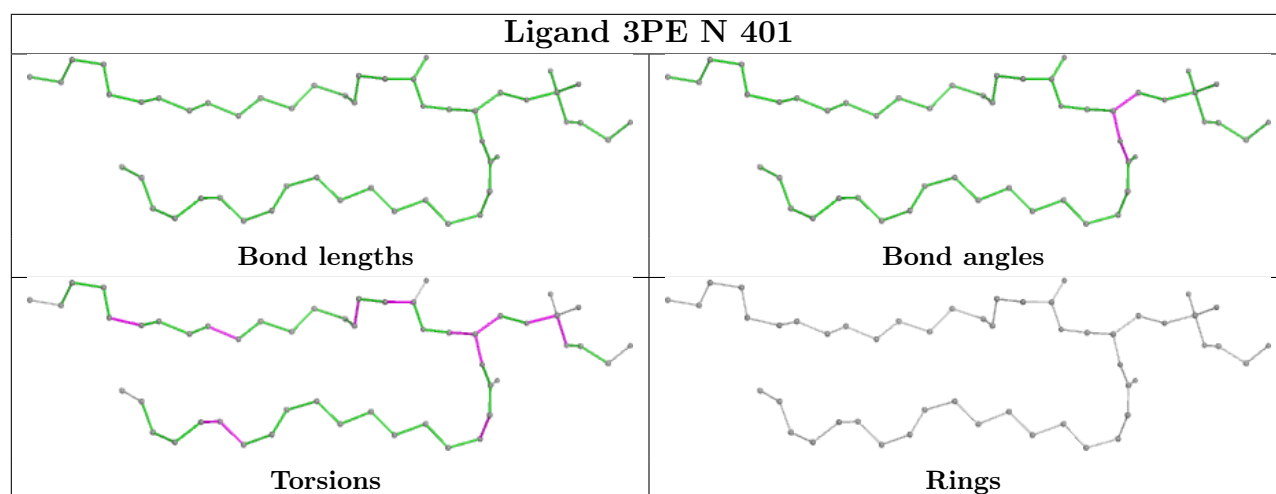


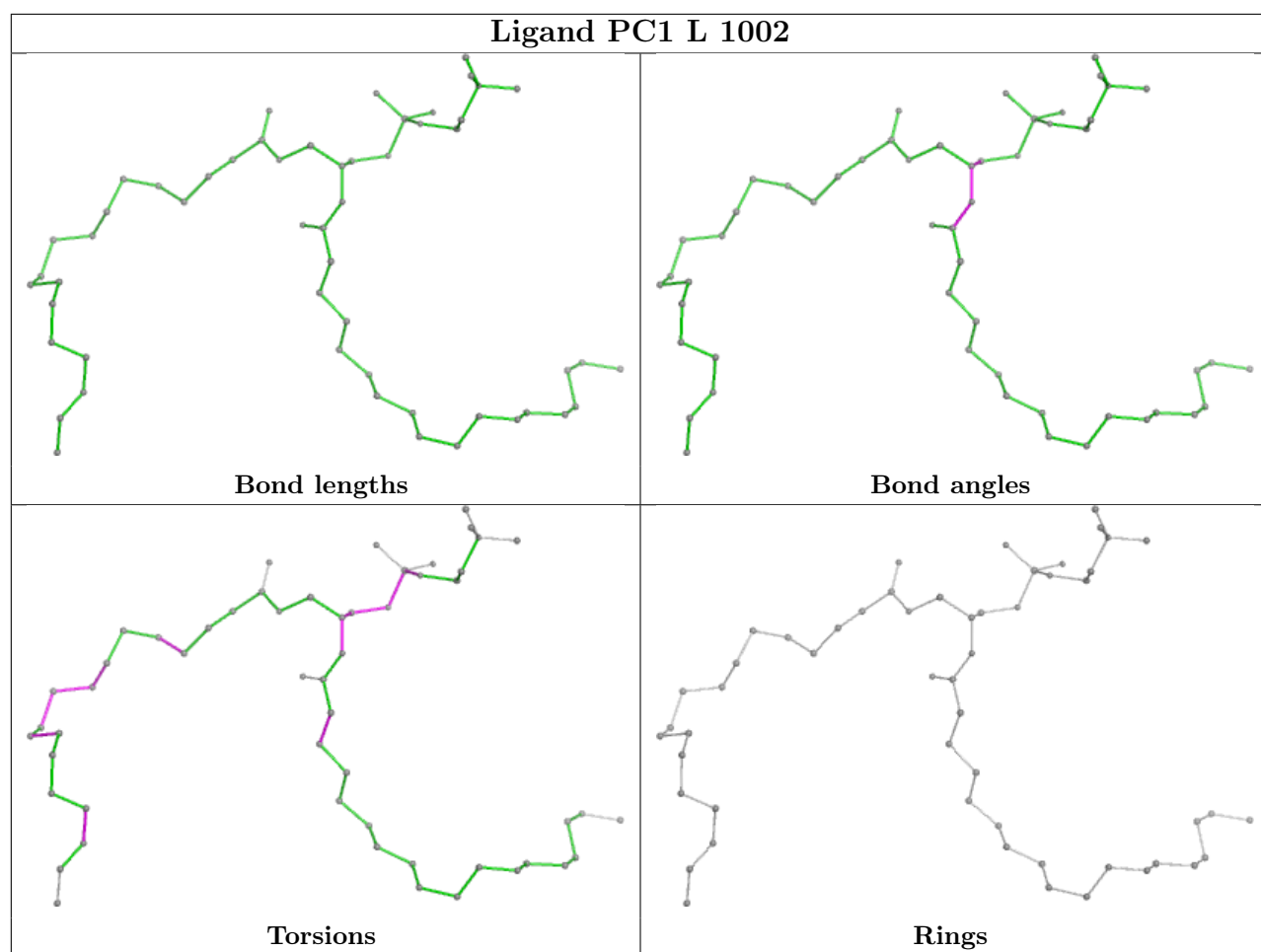


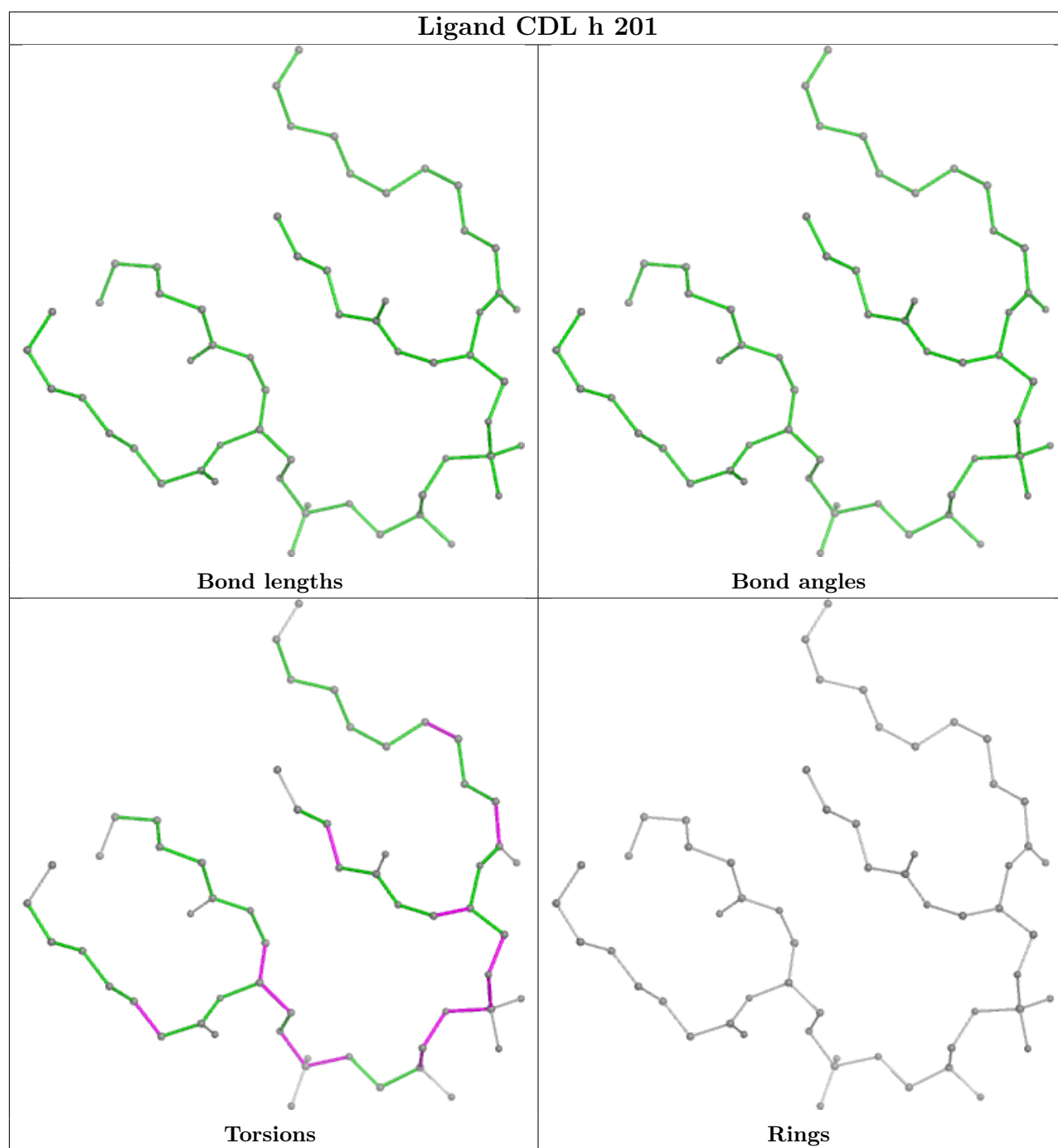












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-11261. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.