



wwPDB EM Validation Summary Report ⓘ

Dec 17, 2024 – 03:19 PM EST

PDB ID : 8UGI
EMDB ID : EMD-42226
Title : High resolution in-situ structure of typeA supercomplex in respiratory chain (I1III2IV1,composite)
Authors : Zheng, W.; Zhang, K.; Zhu, J.
Deposited on : 2023-10-05
Resolution : 2.10 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:

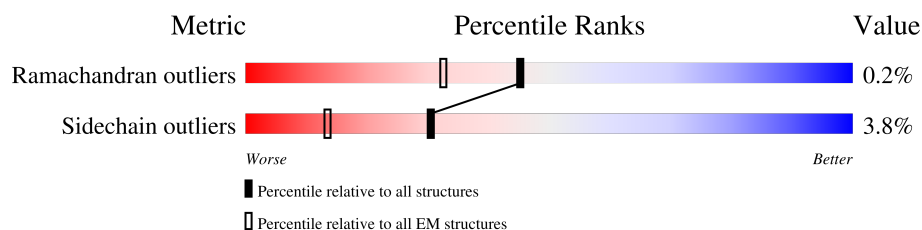
| | | |
|--------------------------------|---|--|
| EMDB validation analysis | : | 0.0.1.dev113 |
| Mogul | : | 2022.3.0, CSD as543be (2022) |
| MolProbity | : | 4.02b-467 |
| buster-report | : | 1.1.7 (2018) |
| Percentile statistics | : | 20231227.v01 (using entries in the PDB archive December 27th 2023) |
| MapQ | : | 1.9.13 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.40 |

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 2.10 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 $\leq 5\%$. 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 | 1A | 115 | <div> <div>37%</div> <div>92%</div> <div>8%</div> </div> |
| 2 | 1B | 258 | <div> <div>55%</div> <div>5%</div> <div>40%</div> </div> |
| 3 | 1C | 264 | <div> <div>78%</div> <div>21%</div> </div> |
| 4 | 1D | 476 | <div> <div>9%</div> <div>87%</div> <div>10%</div> </div> |
| 5 | 1E | 249 | <div> <div>23%</div> <div>80%</div> <div>6%</div> <div>14%</div> </div> |
| 6 | 1F | 464 | <div> <div>8%</div> <div>89%</div> <div>7%</div> </div> |
| 7 | 1G | 727 | <div> <div>7%</div> <div>92%</div> <div>5%</div> </div> |
| 8 | 1H | 318 | <div> <div>12%</div> <div>96%</div> </div> |
| 9 | 1I | 239 | <div> <div>72%</div> <div>26%</div> </div> |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 10 | 1J | 175 | |
| 11 | 1K | 98 | |
| 12 | 1L | 606 | |
| 13 | 1M | 459 | |
| 14 | 1N | 347 | |
| 15 | 1O | 357 | |
| 16 | 1P | 377 | |
| 17 | 1Q | 175 | |
| 18 | 1R | 123 | |
| 19 | 1S | 99 | |
| 20 | 1T | 156 | |
| 20 | 1U | 156 | |
| 21 | 1V | 116 | |
| 22 | 1W | 128 | |
| 23 | 1X | 172 | |
| 24 | 1Y | 141 | |
| 25 | 1Z | 144 | |
| 26 | 1a | 70 | |
| 27 | 1b | 84 | |
| 28 | 1c | 76 | |
| 29 | 1d | 122 | |
| 30 | 1e | 106 | |
| 31 | 1f | 135 | |
| 32 | 1g | 154 | |
| 33 | 1h | 189 | |











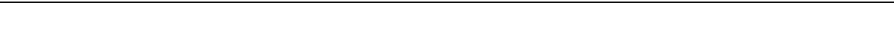

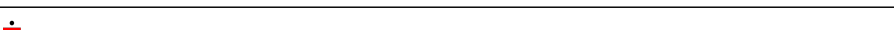
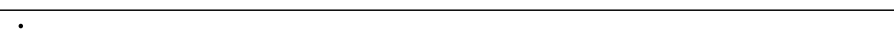








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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 34 | 1i | 128 | |
| 35 | 1j | 105 | |
| 36 | 1k | 98 | |
| 37 | 1l | 186 | |
| 38 | 1m | 129 | |
| 39 | 1n | 179 | |
| 40 | 1o | 137 | |
| 41 | 1p | 176 | |
| 42 | 1q | 145 | |
| 43 | 1r | 113 | |
| 44 | 1s | 471 | |
| 45 | 3A | 480 | |
| 45 | 3N | 480 | |
| 46 | 3B | 453 | |
| 46 | 3O | 453 | |
| 47 | 3C | 379 | |
| 47 | 3P | 379 | |
| 48 | 3D | 325 | |
| 48 | 3Q | 325 | |
| 49 | 3E | 274 | |
| 49 | 3I | 274 | |
| 49 | 3R | 274 | |
| 49 | 3V | 274 | |
| 50 | 3F | 111 | |
| 50 | 3S | 111 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 51 | 3G | 82 |  90% 10% |
| 51 | 3T | 82 |  88% 10% |
| 52 | 3H | 91 |  69% 29% |
| 52 | 3U | 91 |  70% 29% |
| 53 | 3J | 64 |  81% 12% |
| 53 | 3W | 64 |  88% 12% |
| 54 | 3X | 56 |  91% 7% |
| 54 | 3Y | 56 |  89% 9% |
| 55 | 4A | 514 |  98% |
| 56 | 4B | 227 |  97% |
| 57 | 4C | 261 |  97% |
| 58 | 4D | 169 |  78% 5% 18% |
| 59 | 4E | 152 |  66% 31% |
| 60 | 4F | 129 |  72% 25% |
| 61 | 4G | 97 |  8% 68% 9% 23% |
| 62 | 4H | 86 |  92% 5% |
| 63 | 4I | 75 |  85% 11% |
| 64 | 4J | 80 |  70% 28% |
| 65 | 4K | 80 |  61% 39% |
| 66 | 4L | 63 |  71% 27% |
| 67 | 4M | 70 |  60% 39% |
| 68 | 4N | 82 |  6% 94% 5% |

2 Entry composition

There are 93 unique types of molecules in this entry. The entry contains 124291 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called NADH-ubiquinone oxidoreductase chain 3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 1 | 1A | 115 | Total | C | N | O | S | 0 | 0 |
| | | | 916 | 616 | 134 | 159 | 7 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 2 | 1B | 155 | Total | C | N | O | S | 0 | 0 |
| | | | 1242 | 791 | 226 | 211 | 14 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 3 | 1C | 209 | Total | C | N | O | S | 0 | 0 |
| | | | 1740 | 1125 | 297 | 316 | 2 | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|----------------|
| 1C | 104 | GLN | ARG | conflict | UNP A0A286ZNN4 |
| 1C | 154 | GLY | ASP | conflict | UNP A0A286ZNN4 |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 4 | 1D | 429 | Total | C | N | O | S | 0 | 0 |
| | | | 3452 | 2207 | 593 | 628 | 24 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|----------------|
| 1D | 0 | GLY | GLU | conflict | UNP A0A8D0QM68 |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 5 | 1E | 214 | Total | C | N | O | S | 0 | 0 |
| | | | 1658 | 1058 | 278 | 312 | 10 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 6 | 1F | 432 | Total | C | N | O | S | 0 | 0 |
| | | | 3325 | 2100 | 592 | 613 | 20 | | |

- Molecule 7 is a protein called NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|----|---------|-------|
| 7 | 1G | 699 | Total | C | N | O | S | 0 | 0 |
| | | | 5362 | 3360 | 933 | 1029 | 40 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 8 | 1H | 318 | Total | C | N | O | S | 0 | 0 |
| | | | 2504 | 1673 | 385 | 425 | 21 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 9 | 1I | 176 | Total | C | N | O | S | 0 | 0 |
| | | | 1412 | 887 | 243 | 269 | 13 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 10 | 1J | 174 | Total | C | N | O | S | 0 | 0 |
| | | | 1329 | 892 | 189 | 236 | 12 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 11 | 1K | 98 | Total | C | N | O | S | 0 | 0 |
| | | | 750 | 494 | 113 | 129 | 14 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 12 | 1L | 606 | Total | C | N | O | S | 0 | 0 |
| | | | 4818 | 3195 | 746 | 826 | 51 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 13 | 1M | 459 | Total | C | N | O | S | 0 | 0 |
| | | | 3632 | 2411 | 572 | 610 | 39 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 14 | 1N | 347 | Total | C | N | O | S | 0 | 0 |
| | | | 2712 | 1783 | 420 | 463 | 46 | | |

- Molecule 15 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 15 | 1O | 320 | Total | C | N | O | S | 0 | 0 |
| | | | 2590 | 1649 | 440 | 491 | 10 | | |

- Molecule 16 is a protein called NADH:ubiquinone oxidoreductase subunit A9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 16 | 1P | 342 | Total | C | N | O | S | 0 | 0 |
| | | | 2751 | 1783 | 481 | 478 | 9 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17 | 1Q | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1047 | 659 | 186 | 199 | 3 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 18 | 1R | 96 | Total | C | N | O | S | 0 | 0 |
| | | | 741 | 452 | 140 | 146 | 3 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19 | 1S | 87 | Total | C | N | O | S | 0 | 0 |
| | | | 700 | 440 | 131 | 127 | 2 | | |

- Molecule 20 is a protein called NADH:ubiquinone oxidoreductase subunit AB1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20 | 1T | 85 | Total | C | N | O | S | 0 | 0 |
| | | | 689 | 445 | 101 | 138 | 5 | | |
| 20 | 1U | 86 | Total | C | N | O | S | 0 | 0 |
| | | | 694 | 448 | 102 | 139 | 5 | | |

- Molecule 21 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 isoform X1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21 | 1V | 115 | Total | C | N | O | S | 0 | 0 |
| | | | 927 | 599 | 157 | 168 | 3 | | |

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 22 | 1W | 115 | Total | C | N | O | S | 0 | 0 |
| | | | 971 | 619 | 179 | 168 | 5 | | |

- Molecule 23 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 23 | 1X | 171 | Total | C | N | O | S | 0 | 0 |
| | | | 1398 | 887 | 250 | 251 | 10 | | |

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24 | 1Y | 139 | Total | C | N | O | S | 0 | 0 |
| | | | 1016 | 648 | 173 | 189 | 6 | | |

- Molecule 25 is a protein called NADH:ubiquinone oxidoreductase subunit A13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25 | 1Z | 141 | Total | C | N | O | S | 0 | 0 |
| | | | 1168 | 752 | 202 | 205 | 9 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 26 | 1a | 70 | Total | C | N | O | S | 0 | 0 |
| | | | 562 | 361 | 101 | 94 | 6 | | |

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27 | 1b | 83 | Total | C | N | O | S | 0 | 0 |
| | | | 643 | 417 | 110 | 115 | 1 | | |

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 28 | 1c | 49 | Total | C | N | O | 0 | 0 |
| | | | 417 | 276 | 71 | 70 | | |

- Molecule 29 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29 | 1d | 119 | Total | C | N | O | S | 0 | 0 |
| | | | 985 | 641 | 171 | 168 | 5 | | |

- Molecule 30 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 30 | 1e | 99 | Total | C | N | O | S | 0 | 0 |
| | | | 816 | 519 | 151 | 140 | 6 | | |

- Molecule 31 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit

1 [Sus scrofa].

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 31 | 1f | 57 | Total | C | N | O | S | 0 | 0 |
| | | | 487 | 316 | 89 | 80 | 2 | | |

There are 29 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------------------|----------------|
| 1f | -77 | MET | - | initiating methionine | UNP A0A8D1IZ33 |
| 1f | -76 | ALA | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -75 | ALA | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -74 | ALA | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -73 | ILE | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -72 | LEU | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -71 | LYS | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -70 | LEU | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -69 | GLU | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -68 | GLU | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -67 | THR | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -66 | ARG | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -65 | GLY | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -64 | GLY | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -63 | GLY | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -62 | GLU | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -61 | LYS | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -60 | CYS | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -59 | ASP | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -58 | LYS | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -57 | ASN | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -56 | GLN | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -55 | GLY | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -54 | VAL | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -53 | LYS | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -52 | GLY | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -51 | ARG | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -50 | ARG | - | expression tag | UNP A0A8D1IZ33 |
| 1f | -49 | PHE | - | expression tag | UNP A0A8D1IZ33 |

- Molecule 32 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32 | 1g | 100 | Total | C | N | O | S | 0 | 0 |
| | | | 835 | 535 | 138 | 158 | 4 | | |

- Molecule 33 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33 | 1h | 138 | Total | C | N | O | S | 0 | 0 |
| | | | 1151 | 754 | 195 | 199 | 3 | | |

- Molecule 34 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 34 | 1i | 128 | Total | C | N | O | S | 0 | 0 |
| | | | 1100 | 723 | 194 | 181 | 2 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-------------|----------------|
| 1i | 0 | ACE | - | acetylation | UNP A0A4X1UIV8 |

- Molecule 35 is a protein called NADH:ubiquinone oxidoreductase subunit B2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|---|---------|-------|
| 35 | 1j | 71 | Total | C | N | O | S | 0 | 0 |
| | | | 601 | 394 | 99 | 107 | 1 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 36 | 1k | 81 | Total | C | N | O | S | 0 | 0 |
| | | | 649 | 422 | 110 | 116 | 1 | | |

- Molecule 37 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 37 | 1l | 156 | Total | C | N | O | S | 0 | 0 |
| | | | 1310 | 847 | 213 | 242 | 8 | | |

- Molecule 38 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit

4.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 38 | 1m | 128 | Total | C | N | O | 0 | 0 |
| | | | 1062 | 691 | 182 | 189 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 39 | 1n | 172 | Total | C | N | O | S | 0 | 0 |
| | | | 1495 | 956 | 273 | 258 | 8 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 40 | 1o | 122 | Total | C | N | O | S | 0 | 0 |
| | | | 1045 | 650 | 198 | 187 | 10 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------|------------|
| 1o | 0 | MYR | - | insertion | UNP F1SCH1 |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 41 | 1p | 173 | Total | C | N | O | S | 0 | 0 |
| | | | 1449 | 908 | 263 | 270 | 8 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42 | 1q | 145 | Total | C | N | O | S | 0 | 0 |
| | | | 1212 | 775 | 219 | 213 | 5 | | |

- Molecule 43 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 43 | 1r | 94 | Total | C | N | O | S | 0 | 0 |
| | | | 759 | 478 | 143 | 135 | 3 | | |

- Molecule 44 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 44 | 1s | 45 | Total | C | N | O | S | 0 | 0 |
| | | | 382 | 238 | 70 | 73 | 1 | | |

- Molecule 45 is a protein called Cytochrome b-c1 complex subunit 1, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 45 | 3A | 440 | Total | C | N | O | S | 0 | 0 |
| | | | 3411 | 2131 | 599 | 662 | 19 | | |
| 45 | 3N | 445 | Total | C | N | O | S | 1 | 0 |
| | | | 3424 | 2162 | 606 | 637 | 19 | | |

- Molecule 46 is a protein called Cytochrome b-c1 complex subunit 2, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 46 | 3B | 418 | Total | C | N | O | S | 0 | 0 |
| | | | 3138 | 1965 | 555 | 610 | 8 | | |
| 46 | 3O | 417 | Total | C | N | O | S | 0 | 0 |
| | | | 3124 | 1960 | 554 | 602 | 8 | | |

- Molecule 47 is a protein called Cytochrome b.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 47 | 3C | 379 | Total | C | N | O | S | 0 | 0 |
| | | | 3025 | 2031 | 471 | 502 | 21 | | |
| 47 | 3P | 379 | Total | C | N | O | S | 0 | 0 |
| | | | 3024 | 2031 | 471 | 501 | 21 | | |

- Molecule 48 is a protein called Cytochrome c1, heme protein, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 48 | 3D | 237 | Total | C | N | O | S | 0 | 0 |
| | | | 1888 | 1205 | 325 | 342 | 16 | | |
| 48 | 3Q | 239 | Total | C | N | O | S | 0 | 0 |
| | | | 1904 | 1215 | 327 | 346 | 16 | | |

- Molecule 49 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 49 | 3E | 196 | Total | C | N | O | S | 0 | 0 |
| | | | 1518 | 955 | 265 | 291 | 7 | | |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 49 | 3I | 47 | Total | C | N | O | S | 0 | 0 |
| | | | 337 | 210 | 62 | 64 | 1 | | |
| 49 | 3R | 196 | Total | C | N | O | S | 0 | 0 |
| | | | 1518 | 955 | 265 | 291 | 7 | | |
| 49 | 3V | 31 | Total | C | N | O | S | 0 | 0 |
| | | | 223 | 137 | 45 | 40 | 1 | | |

- Molecule 50 is a protein called Cytochrome b-c1 complex subunit 7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 50 | 3F | 98 | Total | C | N | O | S | 0 | 0 |
| | | | 868 | 557 | 152 | 157 | 2 | | |
| 50 | 3S | 98 | Total | C | N | O | S | 0 | 0 |
| | | | 868 | 557 | 152 | 157 | 2 | | |

- Molecule 51 is a protein called Cytochrome b-c1 complex subunit 8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 51 | 3G | 74 | Total | C | N | O | S | 0 | 0 |
| | | | 628 | 411 | 116 | 99 | 2 | | |
| 51 | 3T | 74 | Total | C | N | O | S | 0 | 0 |
| | | | 628 | 411 | 116 | 99 | 2 | | |

- Molecule 52 is a protein called Cytochrome b-c1 complex subunit 6, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|---|---------|-------|
| 52 | 3H | 65 | Total | C | N | O | S | 0 | 0 |
| | | | 533 | 325 | 97 | 106 | 5 | | |
| 52 | 3U | 65 | Total | C | N | O | S | 0 | 0 |
| | | | 533 | 325 | 97 | 106 | 5 | | |

- Molecule 53 is a protein called Ubiquinol-cytochrome c reductase complex 7.2 kDa protein.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 53 | 3J | 56 | Total | C | N | O | 0 | 0 |
| | | | 464 | 305 | 82 | 77 | | |
| 53 | 3W | 56 | Total | C | N | O | 0 | 0 |
| | | | 464 | 305 | 82 | 77 | | |

- Molecule 54 is a protein called Cytochrome b-c1 complex subunit 10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 54 | 3X | 52 | Total | C | N | O | S | 0 | 0 |
| | | | 429 | 286 | 75 | 66 | 2 | | |
| 54 | 3Y | 51 | Total | C | N | O | S | 0 | 0 |
| | | | 421 | 281 | 74 | 65 | 1 | | |

- Molecule 55 is a protein called Cytochrome c oxidase subunit 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 55 | 4A | 513 | Total | C | N | O | S | 1 | 0 |
| | | | 4025 | 2692 | 625 | 677 | 31 | | |

- Molecule 56 is a protein called Cytochrome c oxidase subunit 2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 56 | 4B | 227 | Total | C | N | O | S | 0 | 0 |
| | | | 1829 | 1190 | 281 | 340 | 18 | | |

- Molecule 57 is a protein called Cytochrome c oxidase subunit 3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 57 | 4C | 259 | Total | C | N | O | S | 0 | 0 |
| | | | 2096 | 1399 | 336 | 351 | 10 | | |

- Molecule 58 is a protein called Cytochrome c oxidase subunit 4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 58 | 4D | 139 | Total | C | N | O | S | 0 | 0 |
| | | | 1163 | 757 | 190 | 212 | 4 | | |

- Molecule 59 is a protein called Cytochrome c oxidase subunit 5A, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 59 | 4E | 105 | Total | C | N | O | S | 0 | 0 |
| | | | 852 | 544 | 144 | 162 | 2 | | |

- Molecule 60 is a protein called Cytochrome c oxidase subunit 5B, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 60 | 4F | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 734 | 455 | 130 | 143 | 6 | | |

- Molecule 61 is a protein called Cytochrome c oxidase subunit 6A2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 61 | 4G | 75 | Total | C | N | O | S | 0 | 0 |
| | | | 617 | 398 | 118 | 100 | 1 | | |

- Molecule 62 is a protein called Cytochrome c oxidase subunit 6B1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 62 | 4H | 82 | Total | C | N | O | S | 0 | 0 |
| | | | 687 | 434 | 125 | 123 | 5 | | |

- Molecule 63 is a protein called Cytochrome c oxidase subunit 6C.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 63 | 4I | 67 | Total | C | N | O | S | 0 | 0 |
| | | | 550 | 359 | 97 | 91 | 3 | | |

- Molecule 64 is a protein called Cytochrome c oxidase subunit 7A1, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 64 | 4J | 58 | Total | C | N | O | S | 0 | 0 |
| | | | 456 | 293 | 78 | 82 | 3 | | |

- Molecule 65 is a protein called Cytochrome c oxidase subunit 7B.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 65 | 4K | 49 | Total | C | N | O | S | 0 | 0 |
| | | | 383 | 249 | 65 | 68 | 1 | | |

- Molecule 66 is a protein called Cytochrome c oxidase subunit 7C, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 66 | 4L | 46 | Total | C | N | O | S | 0 | 0 |
| | | | 381 | 254 | 64 | 61 | 2 | | |

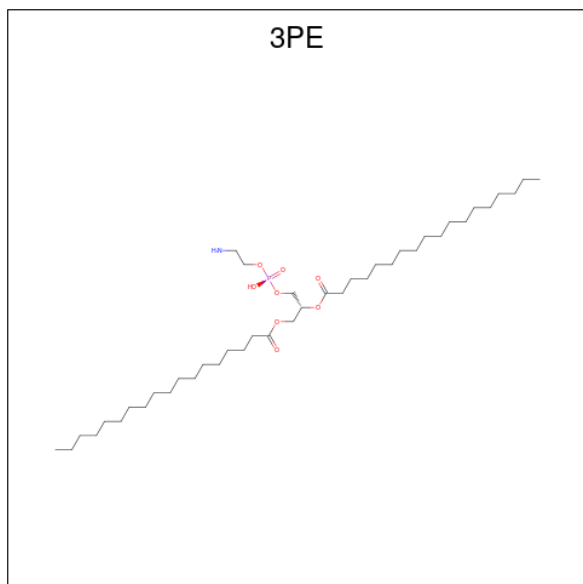
- Molecule 67 is a protein called Cytochrome c oxidase subunit 8.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 67 | 4M | 43 | Total | C | N | O | 0 | 0 |
| | | | 338 | 222 | 57 | 59 | | |

- Molecule 68 is a protein called Cytochrome c oxidase subunit NDUFA4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 68 | 4N | 82 | Total | C | N | O | S | 0 | 0 |
| | | | 660 | 432 | 112 | 114 | 2 | | |

- Molecule 69 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (three-letter code: 3PE) (formula: $C_{41}H_{82}NO_8P$).



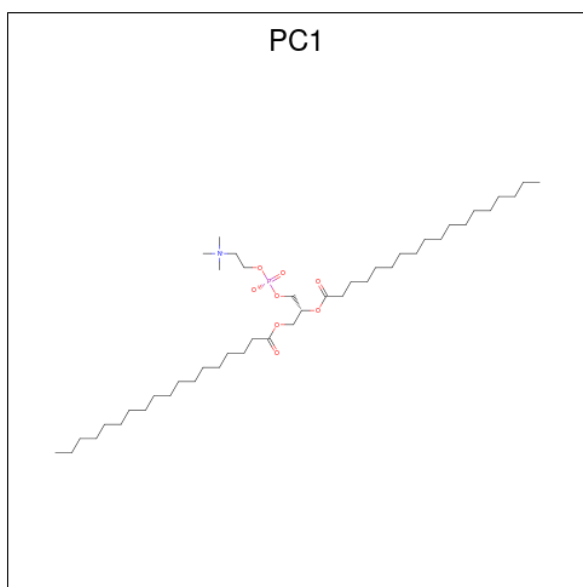
| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---|---------|
| 69 | 1A | 1 | Total | C | N | O | P | 0 |
| | | | 47 | 37 | 1 | 8 | 1 | |
| 69 | 1J | 1 | Total | C | N | O | P | 0 |
| | | | 44 | 34 | 1 | 8 | 1 | |
| 69 | 1L | 1 | Total | C | N | O | P | 0 |
| | | | 46 | 36 | 1 | 8 | 1 | |
| 69 | 1L | 1 | Total | C | N | O | P | 0 |
| | | | 45 | 35 | 1 | 8 | 1 | |
| 69 | 1L | 1 | Total | C | N | O | P | 0 |
| | | | 31 | 21 | 1 | 8 | 1 | |
| 69 | 1M | 1 | Total | C | N | O | P | 0 |
| | | | 45 | 35 | 1 | 8 | 1 | |
| 69 | 1M | 1 | Total | C | N | O | P | 0 |
| | | | 51 | 41 | 1 | 8 | 1 | |
| 69 | 1M | 1 | Total | C | N | O | P | 0 |
| | | | 50 | 40 | 1 | 8 | 1 | |
| 69 | 1N | 1 | Total | C | N | O | P | 0 |
| | | | 49 | 39 | 1 | 8 | 1 | |
| 69 | 1N | 1 | Total | C | N | O | P | 0 |
| | | | 33 | 23 | 1 | 8 | 1 | |

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| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---|---------|
| 69 | 1Y | 1 | Total | C | N | O | P | 0 |
| | | | 40 | 30 | 1 | 8 | 1 | |
| 69 | 1Y | 1 | Total | C | N | O | P | 0 |
| | | | 30 | 20 | 1 | 8 | 1 | |
| 69 | 1Y | 1 | Total | C | N | O | P | 0 |
| | | | 27 | 17 | 1 | 8 | 1 | |
| 69 | 1Y | 1 | Total | C | N | O | P | 0 |
| | | | 41 | 31 | 1 | 8 | 1 | |
| 69 | 1d | 1 | Total | C | N | O | P | 0 |
| | | | 48 | 38 | 1 | 8 | 1 | |
| 69 | 1j | 1 | Total | C | N | O | P | 0 |
| | | | 44 | 34 | 1 | 8 | 1 | |
| 69 | 3A | 1 | Total | C | N | O | P | 0 |
| | | | 27 | 17 | 1 | 8 | 1 | |
| 69 | 3A | 1 | Total | C | N | O | P | 0 |
| | | | 32 | 22 | 1 | 8 | 1 | |
| 69 | 3C | 1 | Total | C | N | O | P | 0 |
| | | | 35 | 25 | 1 | 8 | 1 | |
| 69 | 3C | 1 | Total | C | N | O | P | 0 |
| | | | 34 | 24 | 1 | 8 | 1 | |
| 69 | 3D | 1 | Total | C | N | O | P | 0 |
| | | | 33 | 23 | 1 | 8 | 1 | |
| 69 | 3G | 1 | Total | C | N | O | P | 0 |
| | | | 29 | 19 | 1 | 8 | 1 | |
| 69 | 3N | 1 | Total | C | N | O | P | 0 |
| | | | 33 | 23 | 1 | 8 | 1 | |
| 69 | 3N | 1 | Total | C | N | O | P | 0 |
| | | | 25 | 15 | 1 | 8 | 1 | |
| 69 | 3P | 1 | Total | C | N | O | P | 0 |
| | | | 33 | 23 | 1 | 8 | 1 | |
| 69 | 3R | 1 | Total | C | N | O | P | 0 |
| | | | 47 | 37 | 1 | 8 | 1 | |
| 69 | 3Y | 1 | Total | C | N | O | P | 0 |
| | | | 30 | 20 | 1 | 8 | 1 | |

- Molecule 70 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PC1) (formula: C₄₄H₈₈NO₈P).



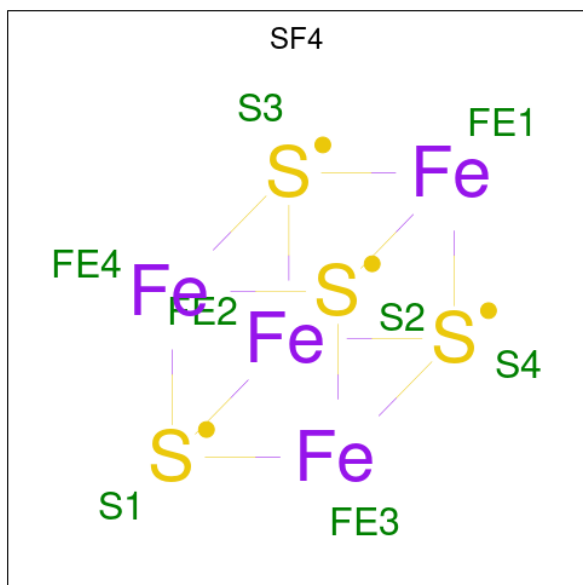
| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---|---------|
| 70 | 1A | 1 | Total | C | N | O | P | 0 |
| | | | 35 | 25 | 1 | 8 | 1 | |
| 70 | 1B | 1 | Total | C | N | O | P | 0 |
| | | | 46 | 36 | 1 | 8 | 1 | |
| 70 | 1B | 1 | Total | C | N | O | P | 0 |
| | | | 48 | 38 | 1 | 8 | 1 | |
| 70 | 1H | 1 | Total | C | N | O | P | 0 |
| | | | 48 | 38 | 1 | 8 | 1 | |
| 70 | 1I | 1 | Total | C | N | O | P | 0 |
| | | | 54 | 44 | 1 | 8 | 1 | |
| 70 | 1M | 1 | Total | C | N | O | P | 0 |
| | | | 44 | 34 | 1 | 8 | 1 | |
| 70 | 1P | 1 | Total | C | N | O | P | 0 |
| | | | 33 | 23 | 1 | 8 | 1 | |
| 70 | 1Y | 1 | Total | C | N | O | P | 0 |
| | | | 35 | 25 | 1 | 8 | 1 | |
| 70 | 1Z | 1 | Total | C | N | O | P | 0 |
| | | | 44 | 34 | 1 | 8 | 1 | |
| 70 | 1h | 1 | Total | C | N | O | P | 0 |
| | | | 47 | 37 | 1 | 8 | 1 | |
| 70 | 1m | 1 | Total | C | N | O | P | 0 |
| | | | 46 | 36 | 1 | 8 | 1 | |
| 70 | 1q | 1 | Total | C | N | O | P | 0 |
| | | | 49 | 39 | 1 | 8 | 1 | |
| 70 | 3E | 1 | Total | C | N | O | P | 0 |
| | | | 47 | 37 | 1 | 8 | 1 | |
| 70 | 3R | 1 | Total | C | N | O | P | 0 |
| | | | 45 | 35 | 1 | 8 | 1 | |

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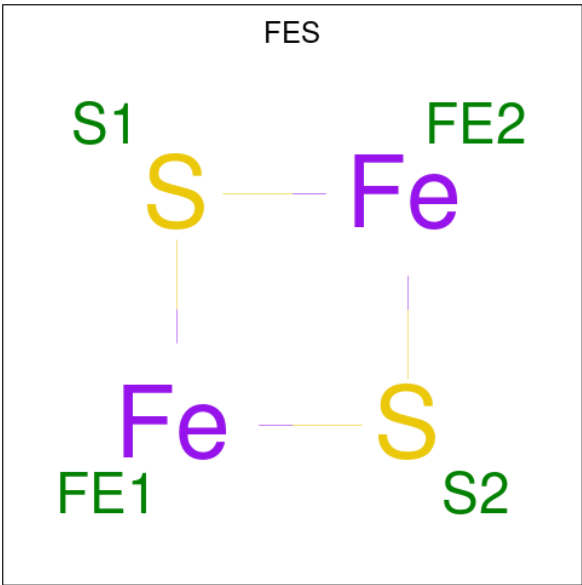
| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---|---------|
| 70 | 3X | 1 | Total | C | N | O | P | 0 |
| | | | 29 | 19 | 1 | 8 | 1 | |

- Molecule 71 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).



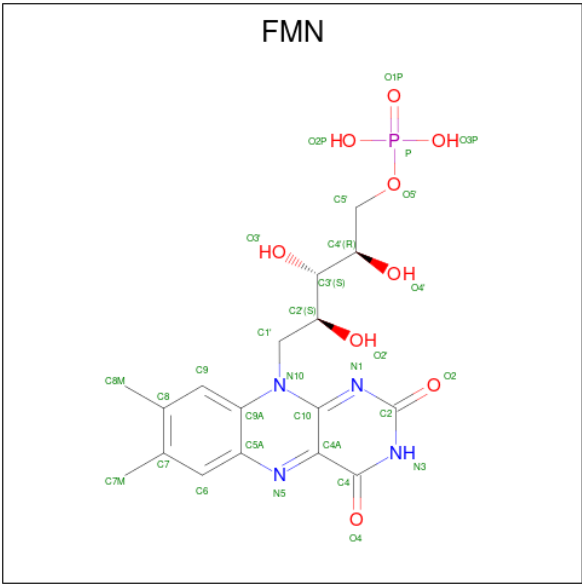
| Mol | Chain | Residues | Atoms | | | AltConf |
|-----|-------|----------|-------|----|---|---------|
| 71 | 1B | 1 | Total | Fe | S | 0 |
| | | | 8 | 4 | 4 | |
| 71 | 1F | 1 | Total | Fe | S | 0 |
| | | | 8 | 4 | 4 | |
| 71 | 1G | 1 | Total | Fe | S | 0 |
| | | | 8 | 4 | 4 | |
| 71 | 1G | 1 | Total | Fe | S | 0 |
| | | | 8 | 4 | 4 | |
| 71 | 1I | 1 | Total | Fe | S | 0 |
| | | | 8 | 4 | 4 | |
| 71 | 1I | 1 | Total | Fe | S | 0 |
| | | | 8 | 4 | 4 | |

- Molecule 72 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



| Mol | Chain | Residues | Atoms | | | AltConf |
|-----|-------|----------|-------|----|---|---------|
| 72 | 1E | 1 | Total | Fe | S | 0 |
| | | | 4 | 2 | 2 | |
| 72 | 1G | 1 | Total | Fe | S | 0 |
| | | | 4 | 2 | 2 | |
| 72 | 3E | 1 | Total | Fe | S | 0 |
| | | | 4 | 2 | 2 | |
| 72 | 3R | 1 | Total | Fe | S | 0 |
| | | | 4 | 2 | 2 | |

- Molecule 73 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P).

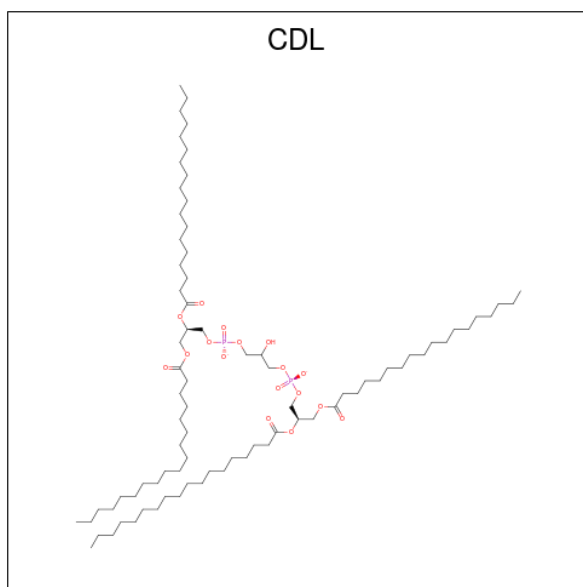


| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---|---------|
| 73 | 1F | 1 | Total | C | N | O | P | 0 |
| | | | 31 | 17 | 4 | 9 | 1 | |

- Molecule 74 is POTASSIUM ION (three-letter code: K) (formula: K).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|---|---------|
| 74 | 1G | 1 | Total | K | 0 |
| | | | 1 | 1 | |

- Molecule 75 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



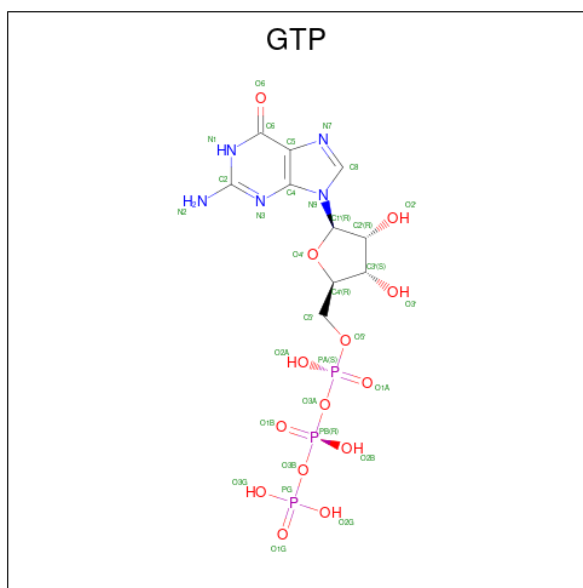
| Mol | Chain | Residues | Atoms | | | | AltConf |
|-----|-------|----------|-------|----|----|---|---------|
| 75 | 1L | 1 | Total | C | O | P | 0 |
| | | | 76 | 57 | 17 | 2 | |
| 75 | 1N | 1 | Total | C | O | P | 0 |
| | | | 62 | 43 | 17 | 2 | |
| 75 | 1X | 1 | Total | C | O | P | 0 |
| | | | 86 | 67 | 17 | 2 | |
| 75 | 1d | 1 | Total | C | O | P | 0 |
| | | | 65 | 46 | 17 | 2 | |
| 75 | 1h | 1 | Total | C | O | P | 0 |
| | | | 80 | 61 | 17 | 2 | |
| 75 | 1q | 1 | Total | C | O | P | 0 |
| | | | 61 | 42 | 17 | 2 | |
| 75 | 3A | 1 | Total | C | O | P | 0 |
| | | | 58 | 39 | 17 | 2 | |
| 75 | 3G | 1 | Total | C | O | P | 0 |
| | | | 52 | 33 | 17 | 2 | |

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| Mol | Chain | Residues | Atoms | | | | AltConf |
|-----|-------|----------|-------|----|----|---|---------|
| 75 | 3G | 1 | Total | C | O | P | 0 |
| | | | 56 | 37 | 17 | 2 | |
| 75 | 3N | 1 | Total | C | O | P | 0 |
| | | | 43 | 24 | 17 | 2 | |
| 75 | 3P | 1 | Total | C | O | P | 0 |
| | | | 56 | 37 | 17 | 2 | |
| 75 | 3T | 1 | Total | C | O | P | 0 |
| | | | 57 | 38 | 17 | 2 | |
| 75 | 4B | 1 | Total | C | O | P | 0 |
| | | | 100 | 81 | 17 | 2 | |
| 75 | 4C | 1 | Total | C | O | P | 0 |
| | | | 100 | 81 | 17 | 2 | |
| 75 | 4D | 1 | Total | C | O | P | 0 |
| | | | 100 | 81 | 17 | 2 | |

- Molecule 76 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|----|---|---------|
| 76 | 1O | 1 | Total | C | N | O | P | 0 |
| | | | 32 | 10 | 5 | 14 | 3 | |

- Molecule 77 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

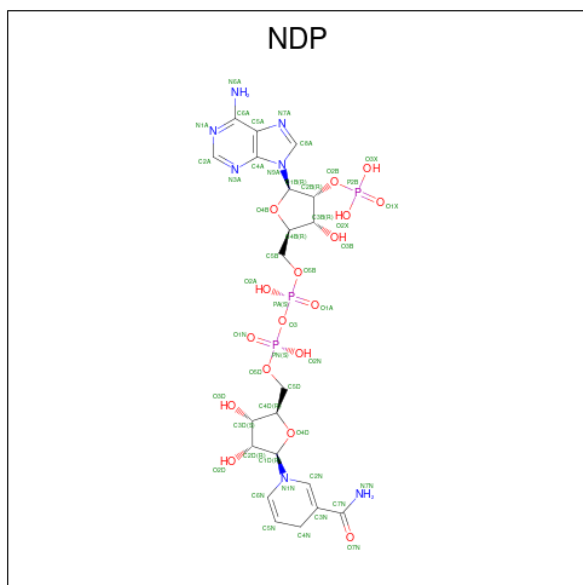
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 77 | 1O | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |

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| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 77 | 4A | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |

- Molecule 78 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).

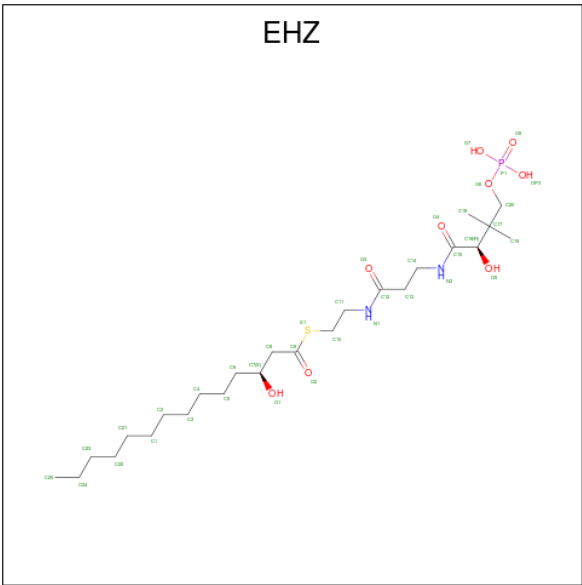


| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|----|---|---------|
| 78 | 1P | 1 | Total | C | N | O | P | 0 |
| | | | 48 | 21 | 7 | 17 | 3 | |

- Molecule 79 is ZINC ION (three-letter code: ZN) (formula: Zn).

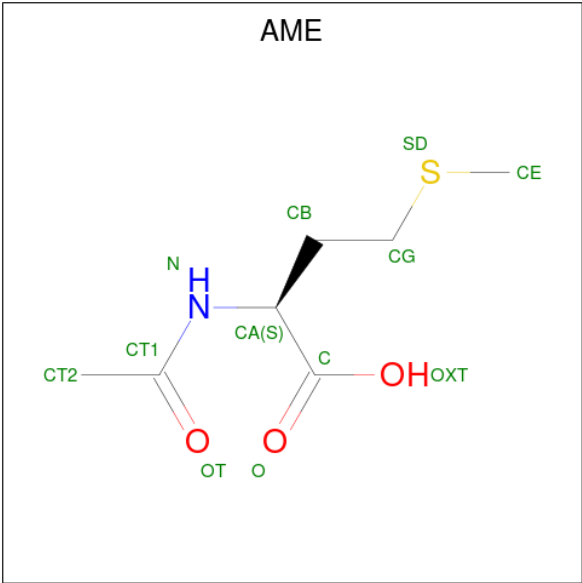
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 79 | 1R | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 79 | 4F | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |

- Molecule 80 is {S}-[2-[3-[(2 {R})-3,3-dimethyl-2-oxidanyl-4-phosphonooxy-butanoyl]amino]propanoylamino]ethyl] (3 {S})-3-oxidanyltetradecanethioate (three-letter code: EHZ) (formula: $C_{25}H_{49}N_2O_9PS$).



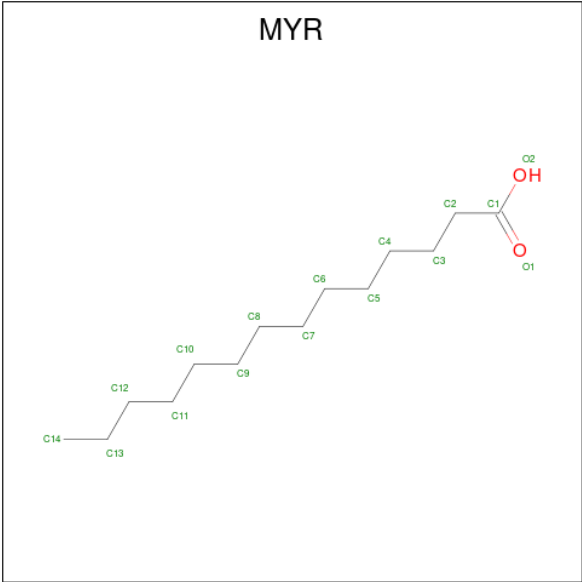
| Mol | Chain | Residues | Atoms | | | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---|---|---------|
| 80 | 1T | 1 | Total | C | N | O | P | S | 0 |
| | | | 37 | 25 | 2 | 8 | 1 | 1 | |
| 80 | 1n | 1 | Total | C | N | O | P | S | 0 |
| | | | 37 | 25 | 2 | 8 | 1 | 1 | |

- Molecule 81 is N-ACETYLMETHIONINE (three-letter code: AME) (formula: C₇H₁₃NO₃S).



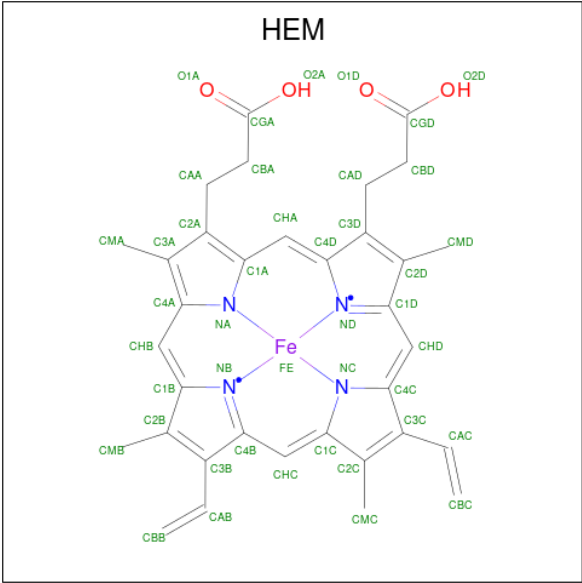
| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|---|---|---|---|---------|
| 81 | 1h | 1 | Total | C | N | O | S | 0 |
| | | | 11 | 7 | 1 | 2 | 1 | |

- Molecule 82 is MYRISTIC ACID (three-letter code: MYR) (formula: C₁₄H₂₈O₂).



| Mol | Chain | Residues | Atoms | | | | AltConf |
|-----|-------|----------|-------|----|---|--|---------|
| 82 | 1l | 1 | Total | C | O | | 0 |
| | | | 15 | 14 | 1 | | |

- Molecule 83 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



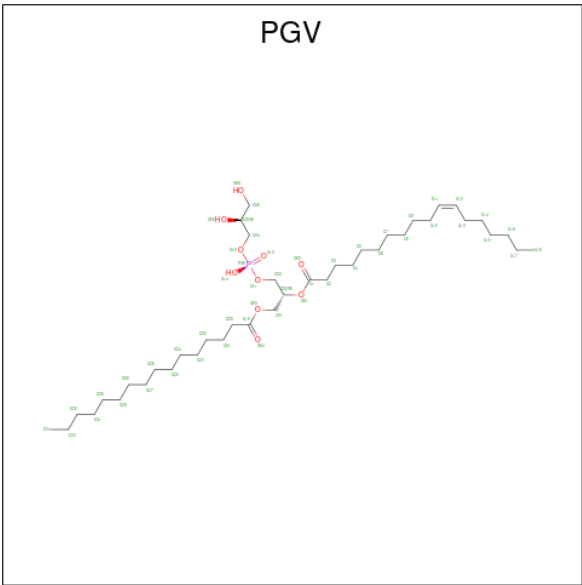
| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|----|---|---|---------|
| 83 | 3C | 1 | Total | C | Fe | N | O | 0 |
| | | | 43 | 34 | 1 | 4 | 4 | |
| 83 | 3C | 1 | Total | C | Fe | N | O | 0 |
| | | | 43 | 34 | 1 | 4 | 4 | |

Continued on next page...

| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------------|---------|---------|--------|--------|---------|
| 83 | 3P | 1 | Total 43 | C 34 | Fe 1 | N 4 | O 4 | 0 |
| 83 | 3P | 1 | Total 43 | C 34 | Fe 1 | N 4 | O 4 | 0 |

-
- The chemical structure of HEC (Hexaethylcobalamin) is shown. It features a central iron atom (Fe) coordinated by four nitrogen atoms (N) in a corrin ring. The structure includes two propionate side chains (top) and two ethyl side chains (bottom). The atoms are labeled with green text: O1A, O2A, O1D, O2D for the carboxylate oxygens; CAA, CBA, CAD, CBD for the propionate chain carbons; CMA, C3A, C4A, C3B, C4B, C2B, C1B, C4C, C3C, C2C, C1C, C4D, C3D, C2D, C1D, C4C, C3C, C2C, C1C, C4D, C3D, C2D, C1D for the corrin ring and side chain carbons; and CAA, CBA, CAD, CBD for the propionate chain carbons. The central iron atom is labeled 'FE' and the nitrogen atoms are labeled 'NA', 'NB', 'NC', 'ND'.

- Molecule 85 is (1R)-2-[[{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (three-letter code: PGV) (formula: C₄₀H₇₇O₁₀P).



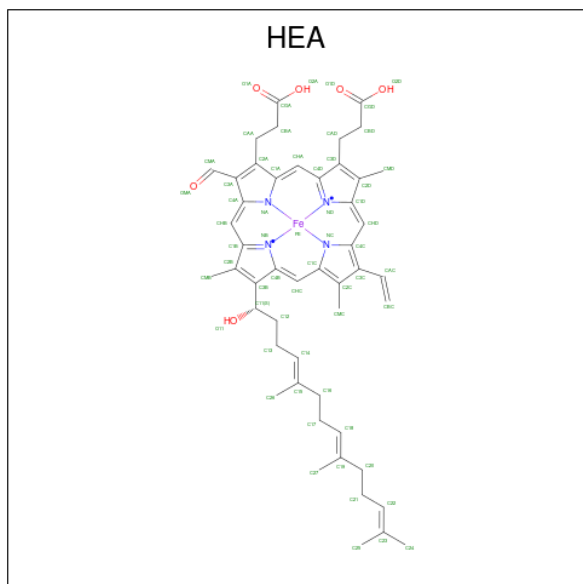
| Mol | Chain | Residues | Atoms | | | | AltConf |
|-----|-------|----------|-------|----|----|---|---------|
| 85 | 4A | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |
| 85 | 4A | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |
| 85 | 4A | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |
| 85 | 4B | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |
| 85 | 4C | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |
| 85 | 4C | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |
| 85 | 4C | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |
| 85 | 4C | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |
| 85 | 4C | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |
| 85 | 4G | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |
| 85 | 4J | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |
| 85 | 4K | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |
| 85 | 4L | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |

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| Mol | Chain | Residues | Atoms | | | | AltConf |
|-----|-------|----------|-------|----|----|---|---------|
| 85 | 4M | 1 | Total | C | O | P | 0 |
| | | | 51 | 40 | 10 | 1 | |

- Molecule 86 is HEME-A (three-letter code: HEA) (formula: $C_{49}H_{56}FeN_4O_6$).



| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|----|---|---|---------|
| 86 | 4A | 1 | Total | C | Fe | N | O | 0 |
| | | | 60 | 49 | 1 | 4 | 6 | |
| 86 | 4A | 1 | Total | C | Fe | N | O | 0 |
| | | | 60 | 49 | 1 | 4 | 6 | |

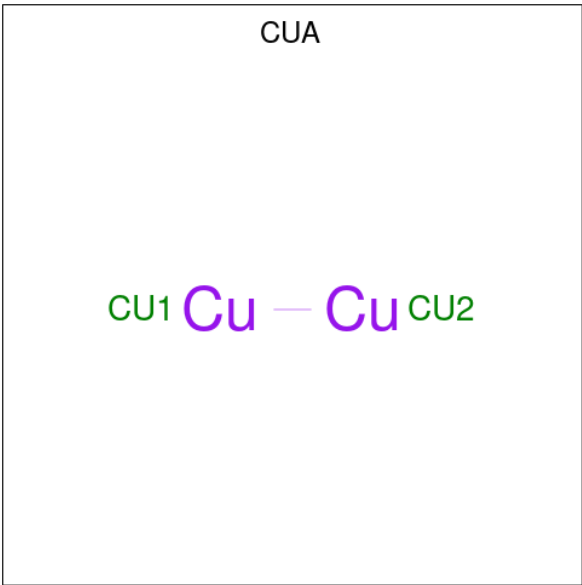
- Molecule 87 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 87 | 4A | 1 | Total | Cu | 0 |
| | | | 1 | 1 | |

- Molecule 88 is SODIUM ION (three-letter code: NA) (formula: Na).

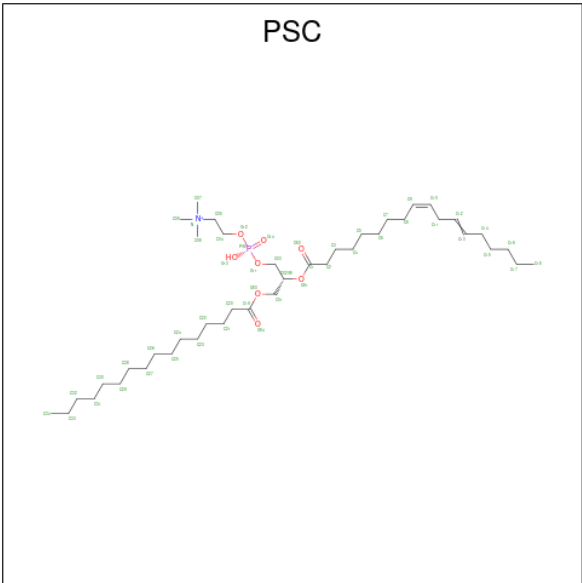
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 88 | 4A | 1 | Total | Na | 0 |
| | | | 1 | 1 | |

- Molecule 89 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu_2).



| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 89 | 4B | 1 | Total | Cu | 0 |
| | | | 2 | 2 | |

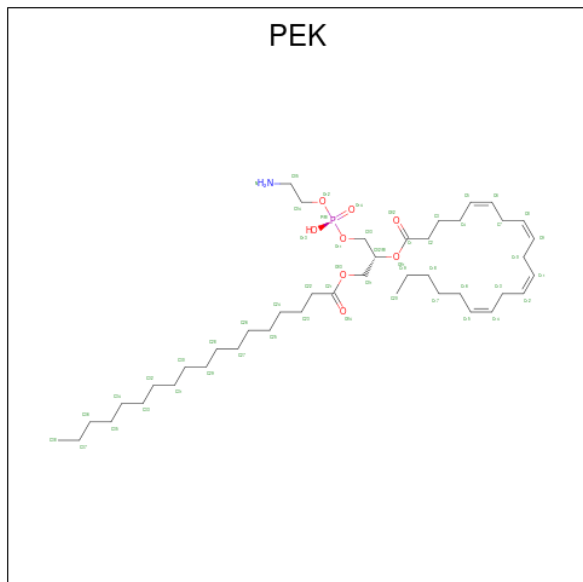
- Molecule 90 is (7R,17E,20E)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITOYLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSA-17,20-DIEN-1-AMINIUM 4-OXIDE (three-letter code: PSC) (formula: C₄₂H₈₁NO₈P).



| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---|---------|
| 90 | 4B | 1 | Total | C | N | O | P | 0 |
| | | | 52 | 42 | 1 | 8 | 1 | |

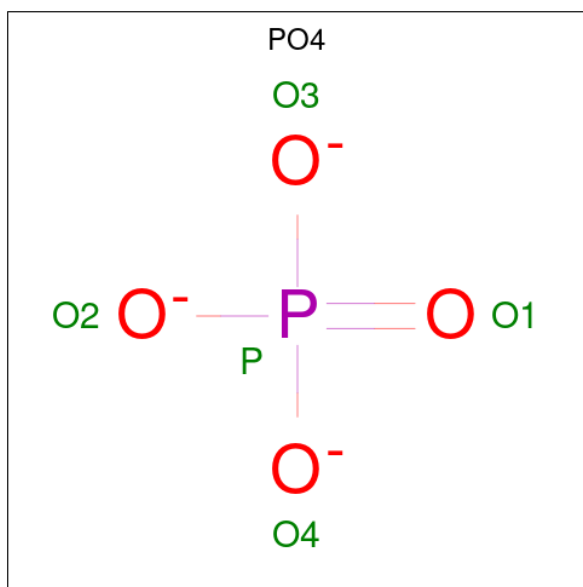
- Molecule 91 is (1S)-2-{[(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(ST

EAROYLOXY)METHYL]ETHYL (5E,8E,11E,14E)-ICOSA-5,8,11,14-TETRAENOATE
(three-letter code: PEK) (formula: C₄₃H₇₈NO₈P).



| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---|---------|
| 91 | 4G | 1 | Total | C | N | O | P | 0 |
| | | | 53 | 43 | 1 | 8 | 1 | |
| 91 | 4G | 1 | Total | C | N | O | P | 0 |
| | | | 52 | 42 | 1 | 8 | 1 | |

- Molecule 92 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



| Mol | Chain | Residues | Atoms | | | AltConf |
|-----|-------|----------|-------|---|---|---------|
| 92 | 4H | 1 | Total | O | P | 0 |
| | | | 5 | 4 | 1 | |

- Molecule 93 is water.

| Mol | Chain | Residues | Atoms | | | AltConf |
|-----|-------|----------|-------|-----|--|---------|
| 93 | 1A | 21 | Total | O | | 0 |
| | | | 21 | 21 | | |
| 93 | 1B | 53 | Total | O | | 0 |
| | | | 53 | 53 | | |
| 93 | 1C | 96 | Total | O | | 0 |
| | | | 96 | 96 | | |
| 93 | 1D | 138 | Total | O | | 0 |
| | | | 138 | 138 | | |
| 93 | 1E | 55 | Total | O | | 0 |
| | | | 55 | 55 | | |
| 93 | 1F | 113 | Total | O | | 0 |
| | | | 113 | 113 | | |
| 93 | 1G | 255 | Total | O | | 0 |
| | | | 255 | 255 | | |
| 93 | 1H | 80 | Total | O | | 0 |
| | | | 80 | 80 | | |
| 93 | 1I | 75 | Total | O | | 0 |
| | | | 75 | 75 | | |
| 93 | 1J | 56 | Total | O | | 0 |
| | | | 56 | 56 | | |
| 93 | 1K | 38 | Total | O | | 0 |
| | | | 38 | 38 | | |
| 93 | 1L | 228 | Total | O | | 0 |
| | | | 228 | 228 | | |
| 93 | 1M | 201 | Total | O | | 0 |
| | | | 201 | 201 | | |
| 93 | 1N | 154 | Total | O | | 0 |
| | | | 154 | 154 | | |
| 93 | 1O | 150 | Total | O | | 0 |
| | | | 150 | 150 | | |
| 93 | 1P | 118 | Total | O | | 0 |
| | | | 118 | 118 | | |
| 93 | 1Q | 63 | Total | O | | 0 |
| | | | 63 | 63 | | |
| 93 | 1R | 41 | Total | O | | 0 |
| | | | 41 | 41 | | |
| 93 | 1S | 56 | Total | O | | 0 |
| | | | 56 | 56 | | |

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| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|--------------|----------|---------|
| 93 | 1T | 12 | Total 12 | O 12 | 0 |
| 93 | 1U | 26 | Total 26 | O 26 | 0 |
| 93 | 1V | 20 | Total 20 | O 20 | 0 |
| 93 | 1W | 37 | Total 37 | O 37 | 0 |
| 93 | 1X | 106 | Total 106 | O 106 | 0 |
| 93 | 1Y | 39 | Total 39 | O 39 | 0 |
| 93 | 1Z | 83 | Total 83 | O 83 | 0 |
| 93 | 1a | 30 | Total 30 | O 30 | 0 |
| 93 | 1b | 35 | Total 35 | O 35 | 0 |
| 93 | 1c | 23 | Total 23 | O 23 | 0 |
| 93 | 1d | 95 | Total 95 | O 95 | 0 |
| 93 | 1e | 91 | Total 91 | O 91 | 0 |
| 93 | 1f | 43 | Total 43 | O 43 | 0 |
| 93 | 1g | 76 | Total 76 | O 76 | 0 |
| 93 | 1h | 116 | Total 116 | O 116 | 0 |
| 93 | 1i | 48 | Total 48 | O 48 | 0 |
| 93 | 1j | 37 | Total 37 | O 37 | 0 |
| 93 | 1k | 35 | Total 35 | O 35 | 0 |
| 93 | 1l | 97 | Total 97 | O 97 | 0 |
| 93 | 1m | 78 | Total 78 | O 78 | 0 |
| 93 | 1n | 122 | Total 122 | O 122 | 0 |

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| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|--------------|----------|---------|
| 93 | 1o | 101 | Total 101 | O 101 | 0 |
| 93 | 1p | 141 | Total 141 | O 141 | 0 |
| 93 | 1q | 47 | Total 47 | O 47 | 0 |
| 93 | 1r | 25 | Total 25 | O 25 | 0 |
| 93 | 1s | 15 | Total 15 | O 15 | 0 |
| 93 | 3A | 184 | Total 184 | O 184 | 0 |
| 93 | 3B | 110 | Total 110 | O 110 | 0 |
| 93 | 3C | 222 | Total 222 | O 222 | 0 |
| 93 | 3D | 131 | Total 131 | O 131 | 0 |
| 93 | 3E | 45 | Total 45 | O 45 | 0 |
| 93 | 3F | 115 | Total 115 | O 115 | 0 |
| 93 | 3G | 78 | Total 78 | O 78 | 0 |
| 93 | 3H | 26 | Total 26 | O 26 | 0 |
| 93 | 3I | 5 | Total 5 | O 5 | 0 |
| 93 | 3J | 27 | Total 27 | O 27 | 0 |
| 93 | 3N | 231 | Total 231 | O 231 | 0 |
| 93 | 3O | 184 | Total 184 | O 184 | 0 |
| 93 | 3P | 152 | Total 152 | O 152 | 0 |
| 93 | 3Q | 98 | Total 98 | O 98 | 0 |
| 93 | 3R | 47 | Total 47 | O 47 | 0 |
| 93 | 3S | 71 | Total 71 | O 71 | 0 |

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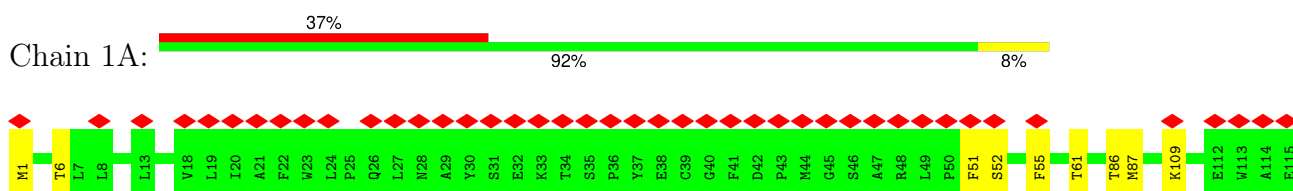
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| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|--------------|----------|---------|
| 93 | 3T | 40 | Total 40 | O 40 | 0 |
| 93 | 3U | 110 | Total 110 | O 110 | 0 |
| 93 | 3V | 7 | Total 7 | O 7 | 0 |
| 93 | 3W | 31 | Total 31 | O 31 | 0 |
| 93 | 3X | 25 | Total 25 | O 25 | 0 |
| 93 | 3Y | 16 | Total 16 | O 16 | 0 |
| 93 | 4A | 110 | Total 110 | O 110 | 0 |
| 93 | 4B | 115 | Total 115 | O 115 | 0 |
| 93 | 4C | 103 | Total 103 | O 103 | 0 |
| 93 | 4D | 81 | Total 81 | O 81 | 0 |
| 93 | 4E | 55 | Total 55 | O 55 | 0 |
| 93 | 4F | 67 | Total 67 | O 67 | 0 |
| 93 | 4G | 39 | Total 39 | O 39 | 0 |
| 93 | 4H | 43 | Total 43 | O 43 | 0 |
| 93 | 4I | 25 | Total 25 | O 25 | 0 |
| 93 | 4J | 34 | Total 34 | O 34 | 0 |
| 93 | 4K | 27 | Total 27 | O 27 | 0 |
| 93 | 4L | 23 | Total 23 | O 23 | 0 |
| 93 | 4M | 28 | Total 28 | O 28 | 0 |
| 93 | 4N | 53 | Total 53 | O 53 | 0 |

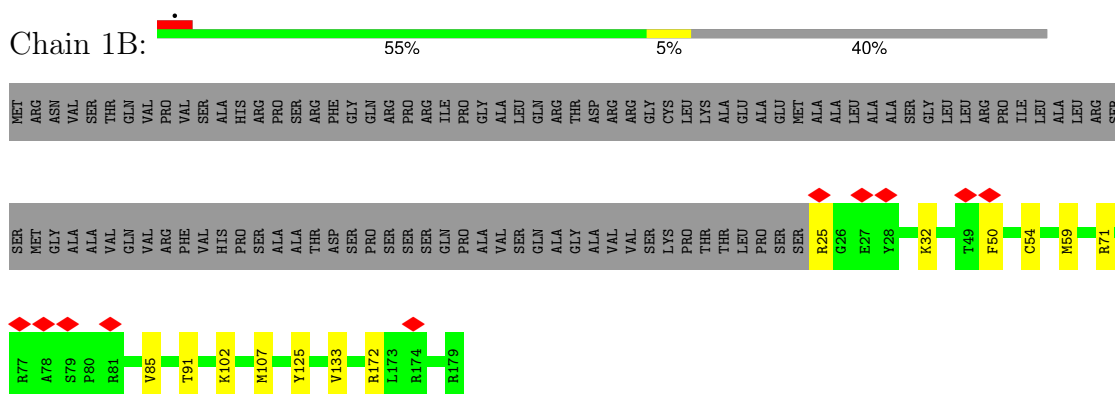
3 Residue-property plots

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

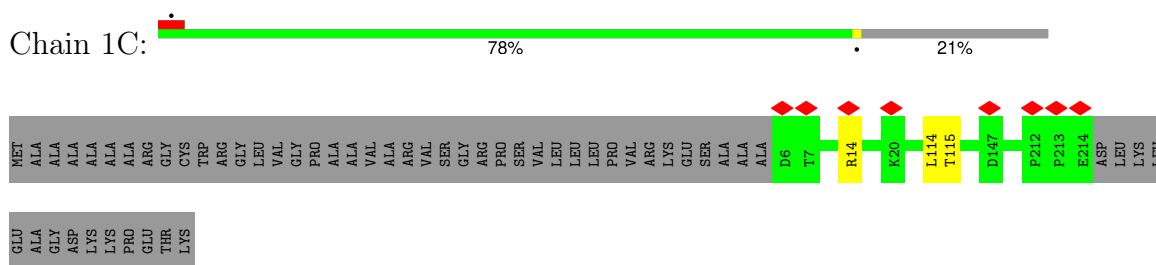
- Molecule 1: NADH-ubiquinone oxidoreductase chain 3



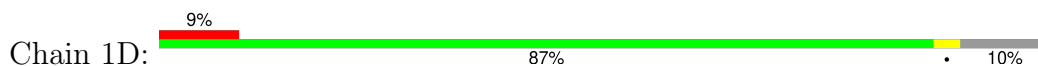
- Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial

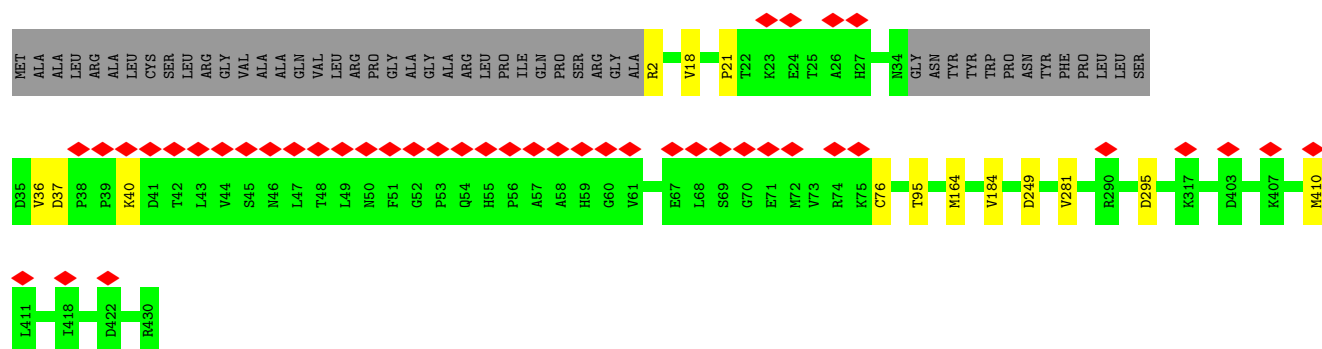


- Molecule 3: NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial

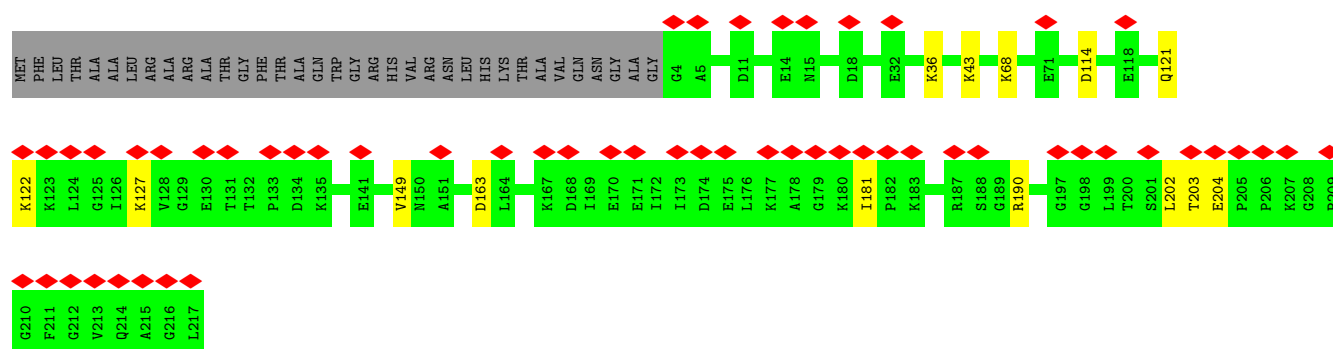
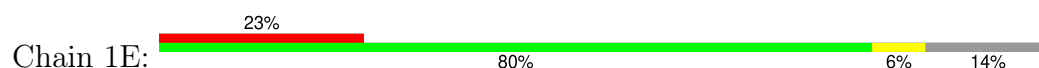


- Molecule 4: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial

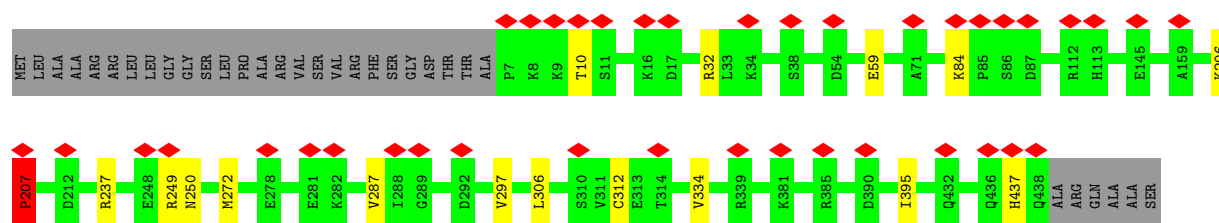
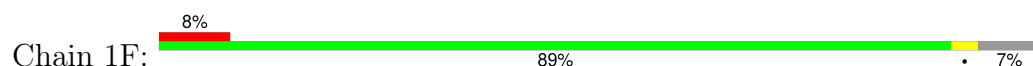




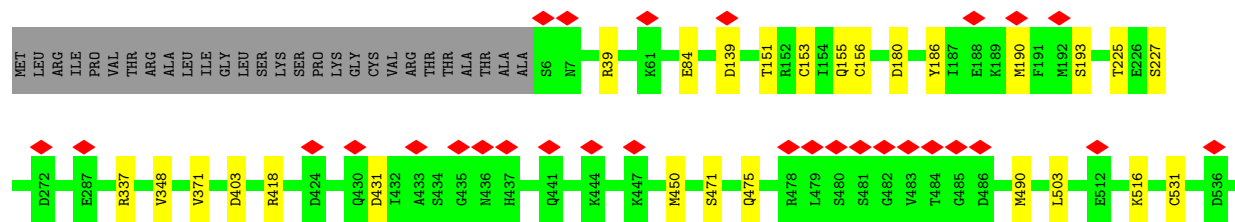
- Molecule 5: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial

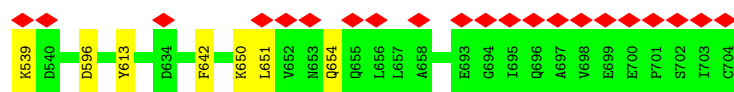


- Molecule 6: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial

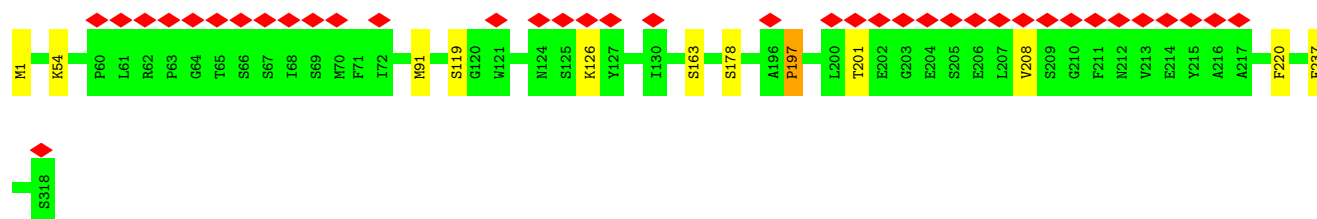


- Molecule 7: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial

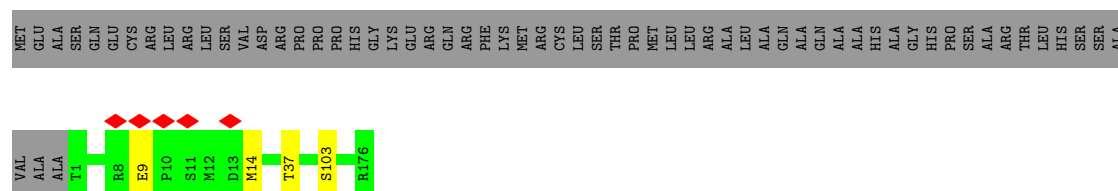




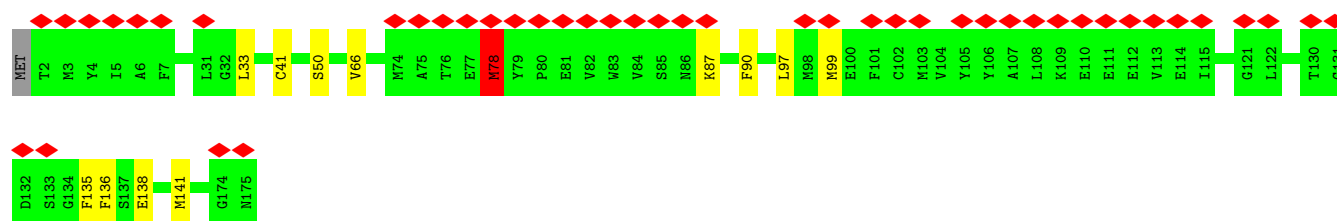
- Molecule 8: NADH-ubiquinone oxidoreductase chain 1



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



- Molecule 10: NADH-ubiquinone oxidoreductase chain 6



- Molecule 11: NADH-ubiquinone oxidoreductase chain 4L



- Molecule 12: NADH-ubiquinone oxidoreductase chain 5



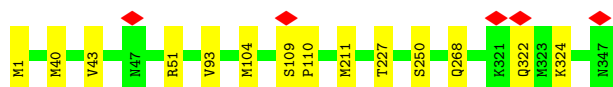
- Molecule 13: NADH-ubiquinone oxidoreductase chain 4

Chain 1M:  97%




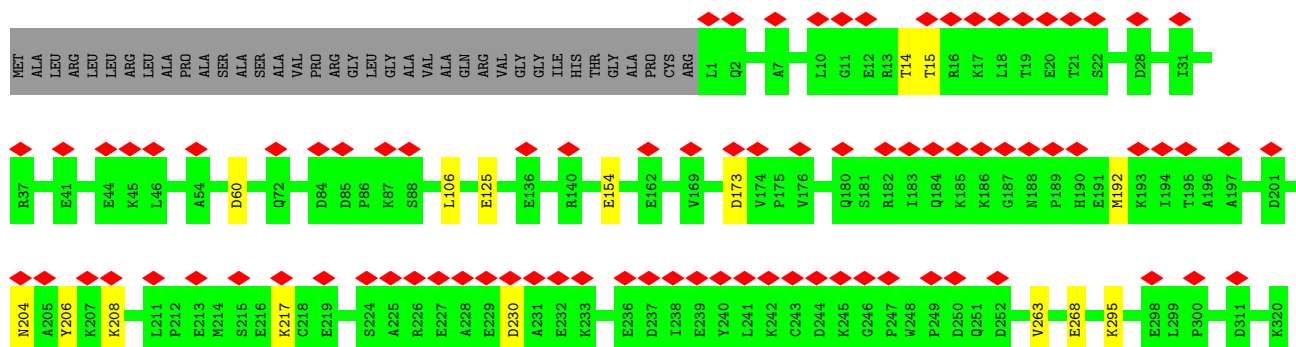
- Molecule 14: NADH-ubiquinone oxidoreductase chain 2

Chain 1N:  96%




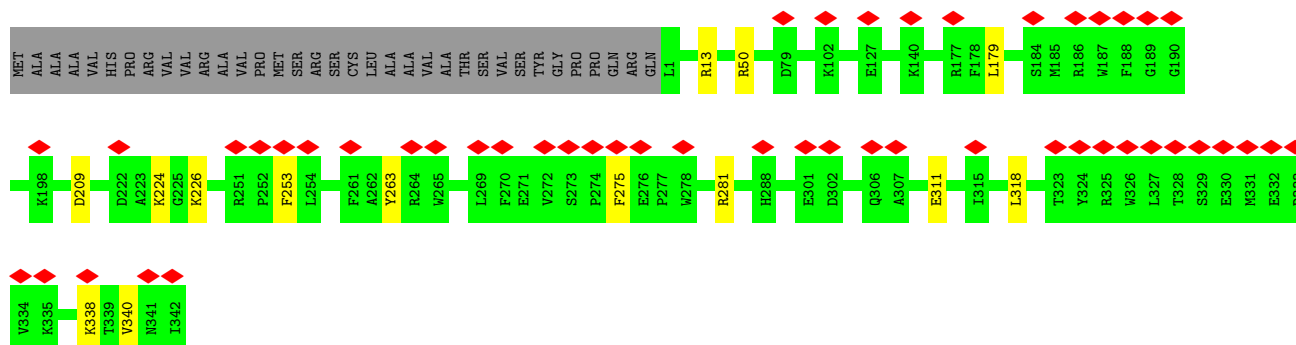
- Molecule 15: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial

Chain 1O:  24% 85% 10%



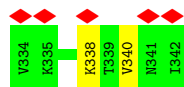
- Molecule 16: NADH:ubiquinone oxidoreductase subunit A9

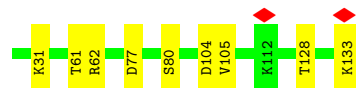
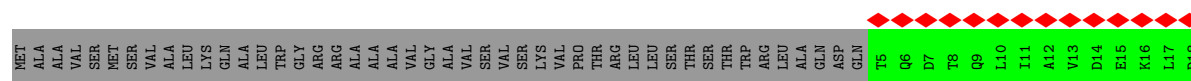
Chain 1P:  13% 87% 9%



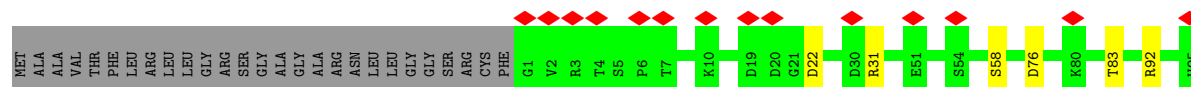
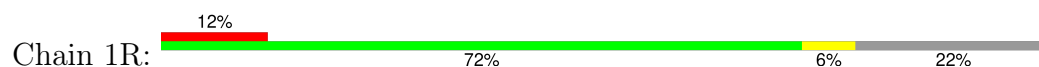
- Molecule 17: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

Chain 1Q:  9% 69% 5% 26%

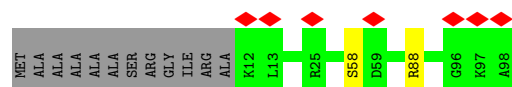
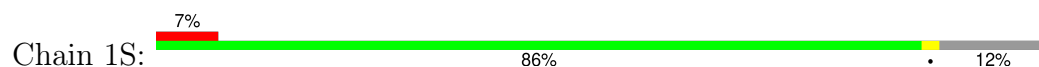




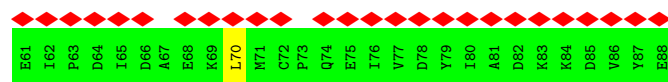
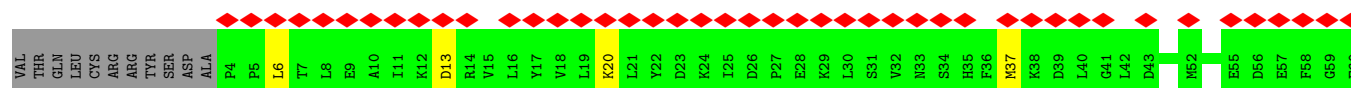
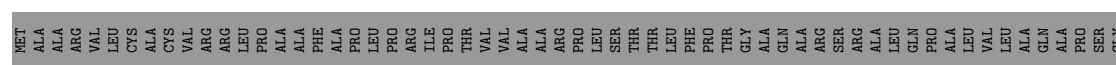
- Molecule 18: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial



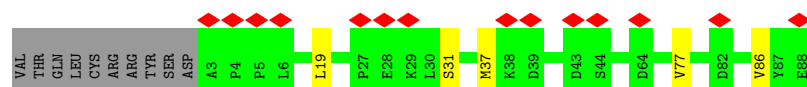
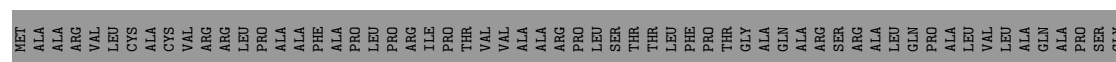
- Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2



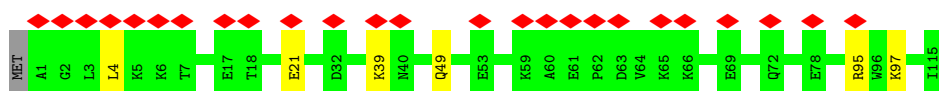
- Molecule 20: NADH:ubiquinone oxidoreductase subunit AB1



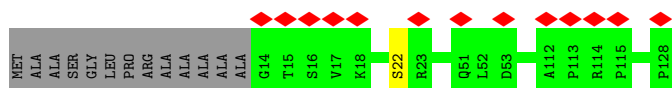
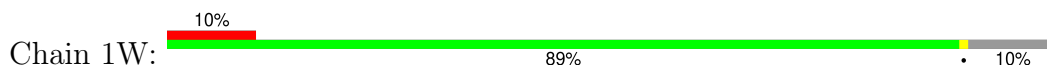
- Molecule 20: NADH:ubiquinone oxidoreductase subunit AB1



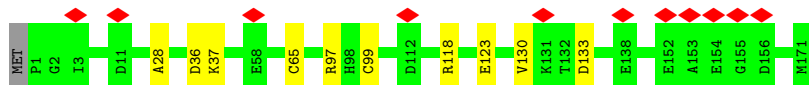
- Molecule 21: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 isoform X1



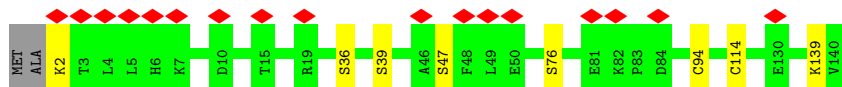
- Molecule 22: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6



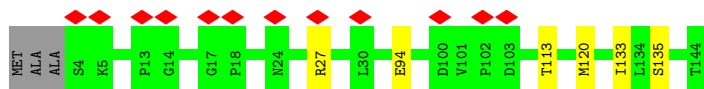
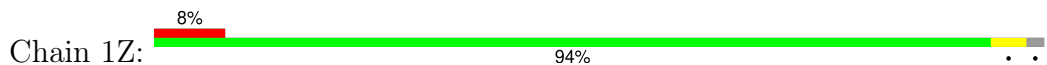
- Molecule 23: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8



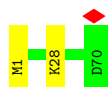
- Molecule 24: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11



- Molecule 25: NADH:ubiquinone oxidoreductase subunit A13

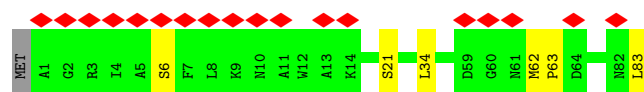


- Molecule 26: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1

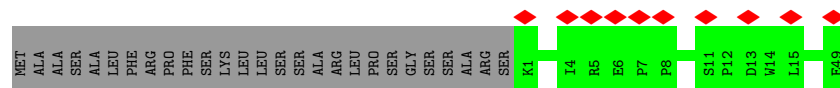


- Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3

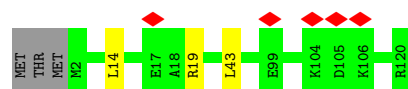




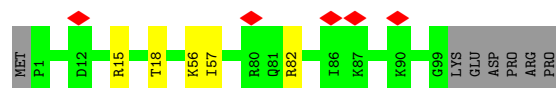
- Molecule 28: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial



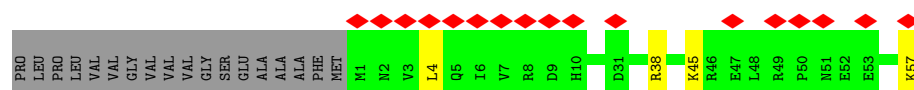
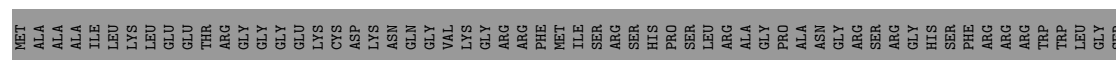
- Molecule 29: NADH dehydrogenase [ubiquinone] 1 subunit C2



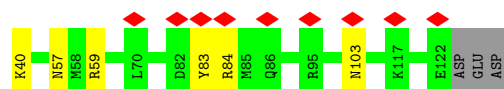
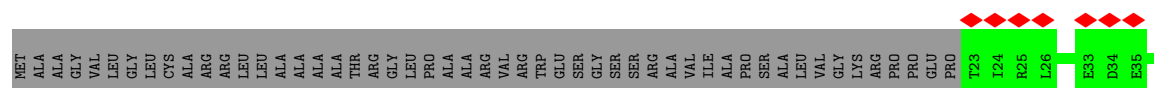
- Molecule 30: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5



- Molecule 31: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1 [Sus scrofa]

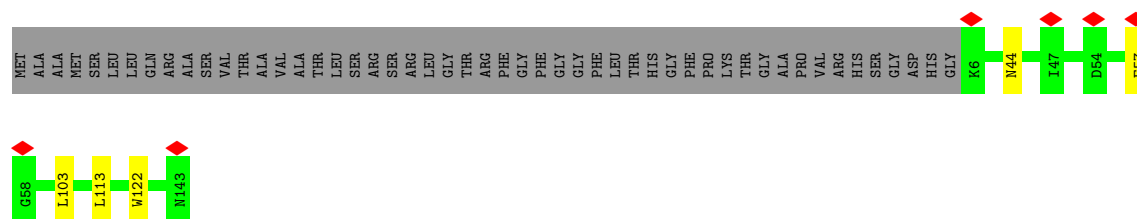


- Molecule 32: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial

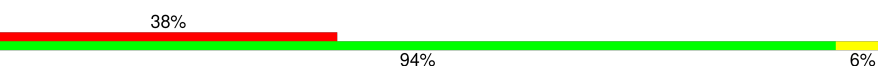


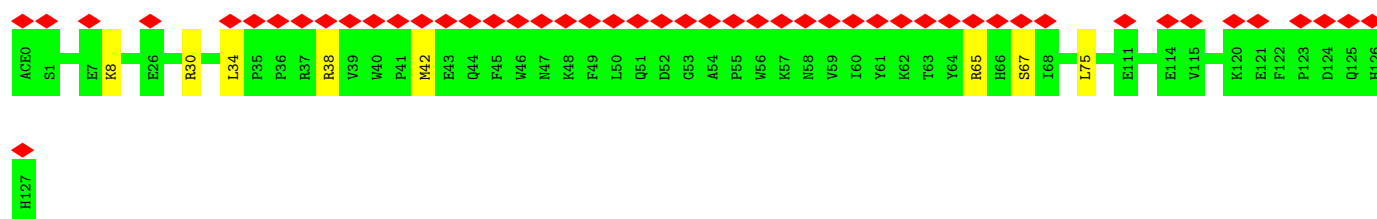
- Molecule 33: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial

Chain 1h: 



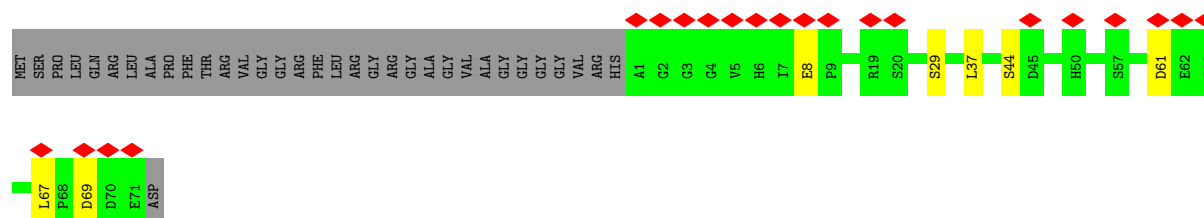
- Molecule 34: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6

Chain 1i: 




- Molecule 35: NADH:ubiquinone oxidoreductase subunit B2

Chain 1j: 




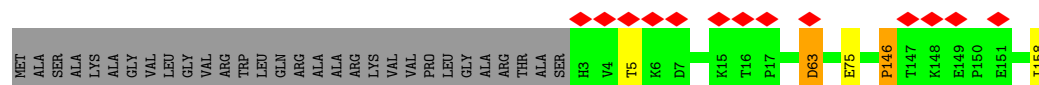
- Molecule 36: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3

Chain 1k: 



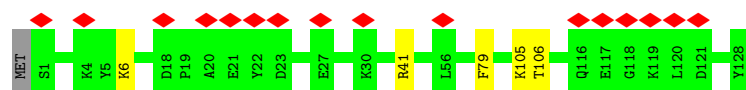
- Molecule 37: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial

Chain 1l: 



- Molecule 38: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4

Chain 1m:  12% 95%




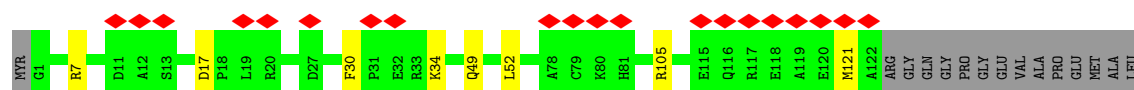
- Molecule 39: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9

Chain 1n:  6% 93%




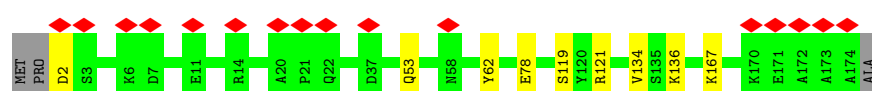
- Molecule 40: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7

Chain 1o:  15% 83% 6% 11%



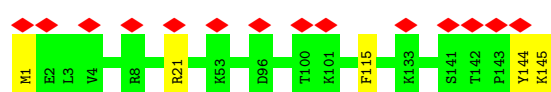
- Molecule 41: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10

Chain 1p:  9% 93% 5%




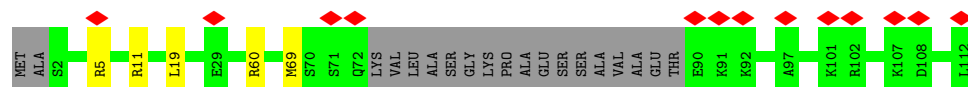
- Molecule 42: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

Chain 1q:  10% 97%



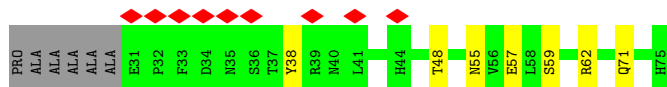
- Molecule 43: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7

Chain 1r:  12% 79% 17%

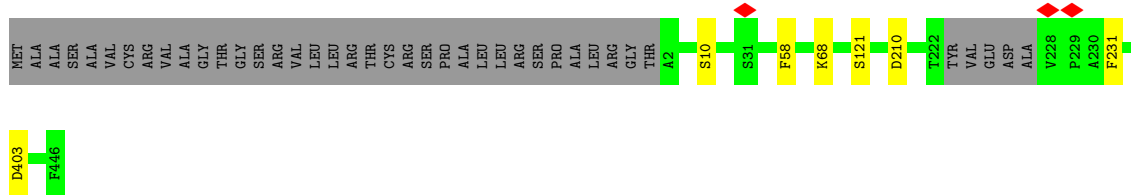


- Molecule 44: NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial

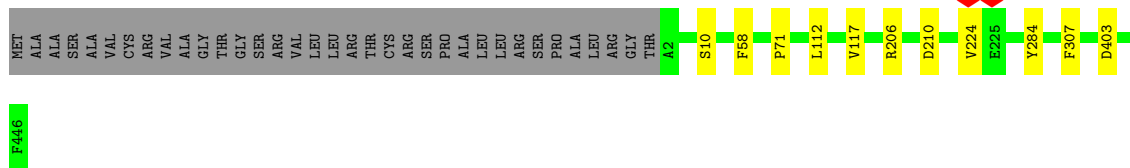
Chain 1s:  8% 90%



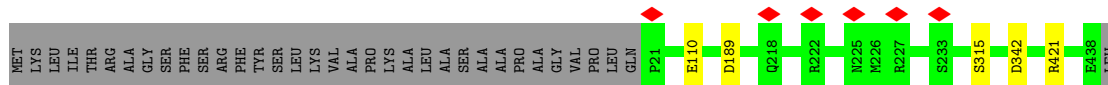
- Chain 3A: 90% 8%



- Chain 3N: 90% • 7%

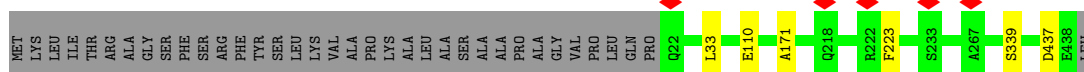


- Chain 3B:  91% • 8%



- 

Chain 3O:  91% 8%



- Molecule 47: Cytochrome b

Chain 3C:  98%



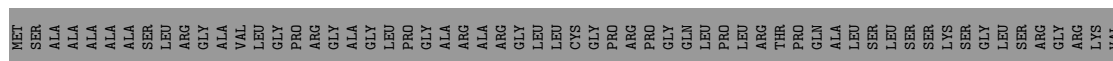
- Molecule 47: Cytochrome b

Chain 3P:  99%



- Molecule 48: Cytochrome c1, heme protein, mitochondrial

Chain 3D:  70% 27%



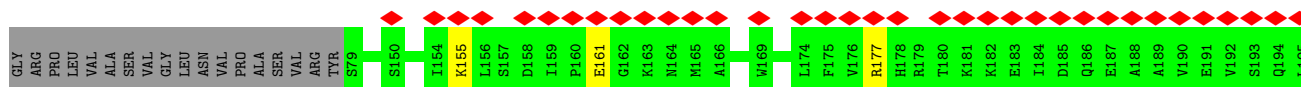
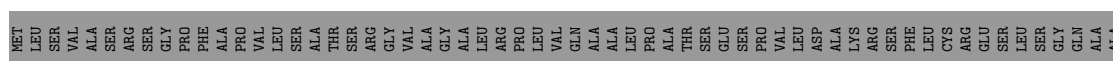
- Molecule 48: Cytochrome c1, heme protein, mitochondrial

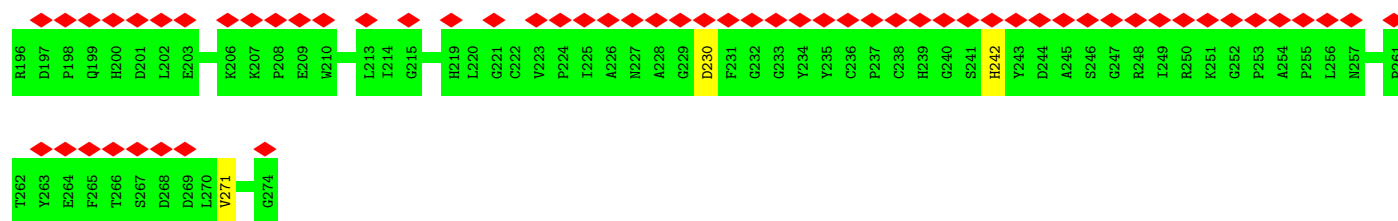
Chain 3Q:  73% 26%



- Molecule 49: Cytochrome b-c1 complex subunit Rieske, mitochondrial

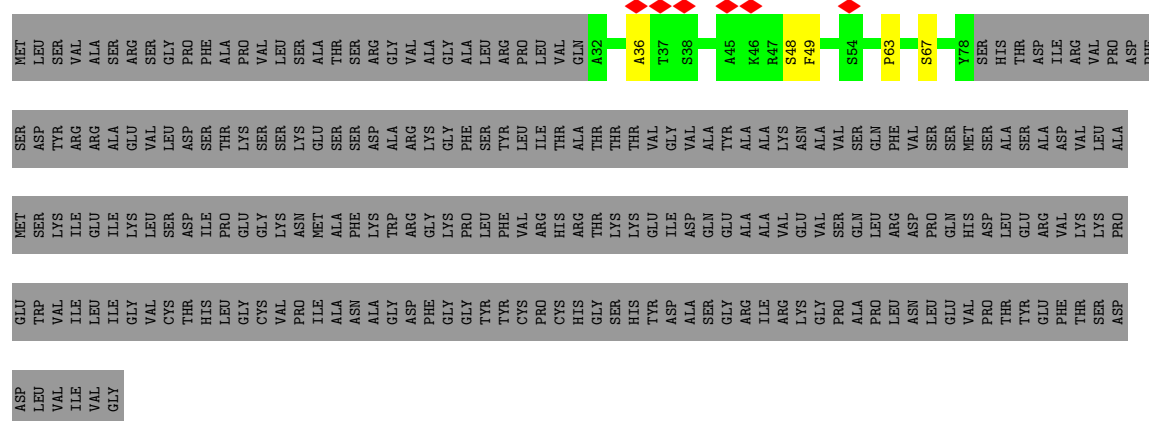
Chain 3E:  35% 69% 28%





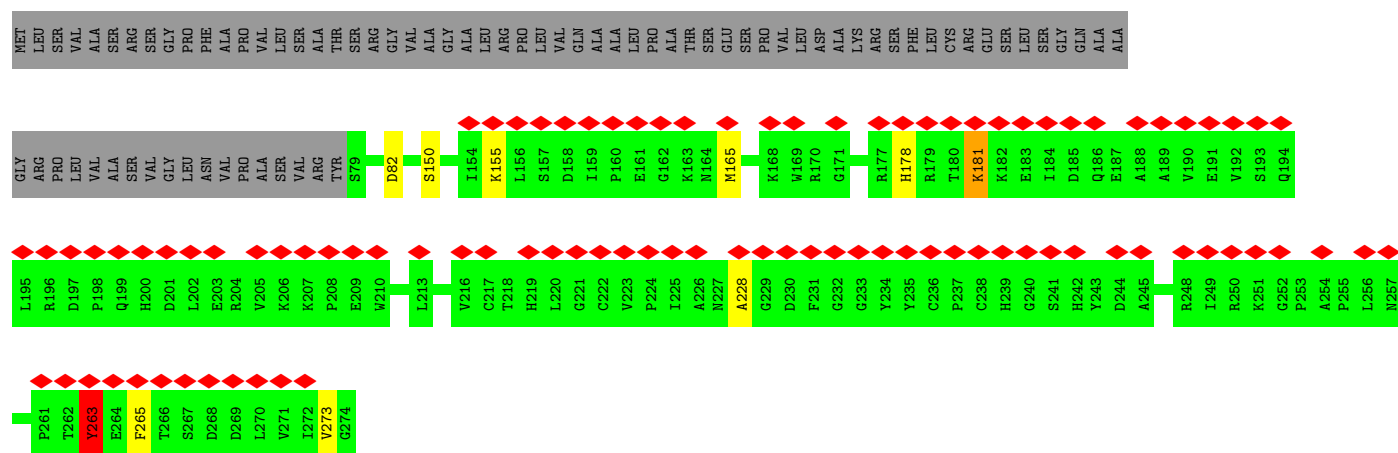
- Molecule 49: Cytochrome b-c1 complex subunit Rieske, mitochondrial

Chain 3I: 15% 83%



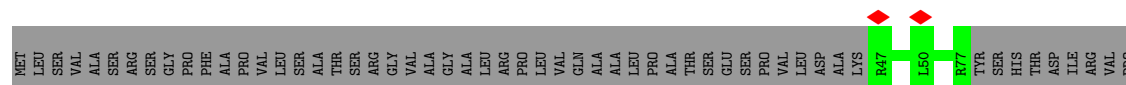
- Molecule 49: Cytochrome b-c1 complex subunit Rieske, mitochondrial

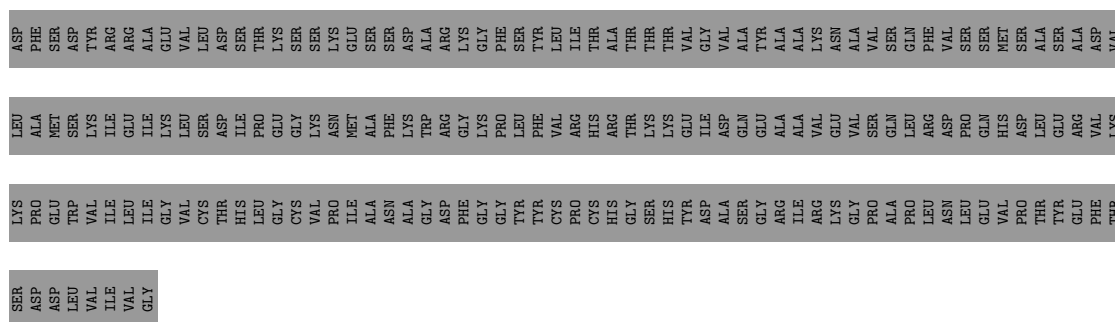
Chain 3R: 34% 68% 28%



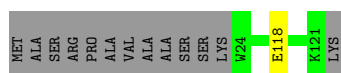
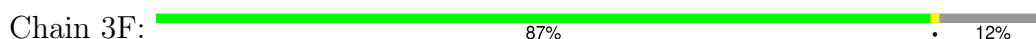
- Molecule 49: Cytochrome b-c1 complex subunit Rieske, mitochondrial

Chain 3V: 11% 89%

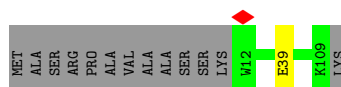




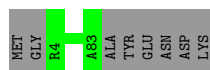
- Molecule 50: Cytochrome b-c1 complex subunit 7



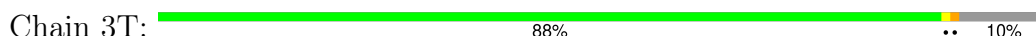
- Molecule 50: Cytochrome b-c1 complex subunit 7



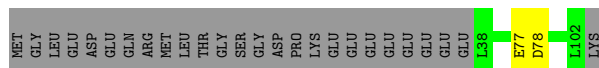
- Molecule 51: Cytochrome b-c1 complex subunit 8



- Molecule 51: Cytochrome b-c1 complex subunit 8

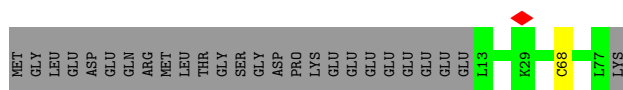


- Molecule 52: Cytochrome b-c1 complex subunit 6, mitochondrial



- Molecule 52: Cytochrome b-c1 complex subunit 6, mitochondrial





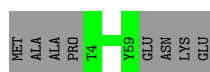
- Molecule 53: Ubiquinol-cytochrome c reductase complex 7.2 kDa protein

Chain 3J: 81% 12%



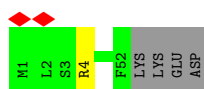
- Molecule 53: Ubiquinol-cytochrome c reductase complex 7.2 kDa protein

Chain 3W: 88% 12%



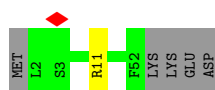
- Molecule 54: Cytochrome b-c1 complex subunit 10

Chain 3X: 91% 7%



- Molecule 54: Cytochrome b-c1 complex subunit 10

Chain 3Y: 89% 9%



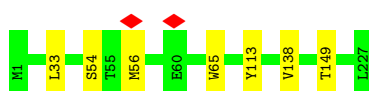
- Molecule 55: Cytochrome c oxidase subunit 1

Chain 4A: 98%



- Molecule 56: Cytochrome c oxidase subunit 2

Chain 4B: 97%




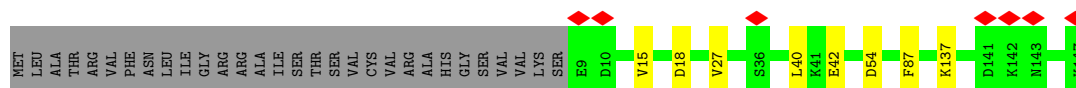
- Molecule 57: Cytochrome c oxidase subunit 3

Chain 4C:  97%



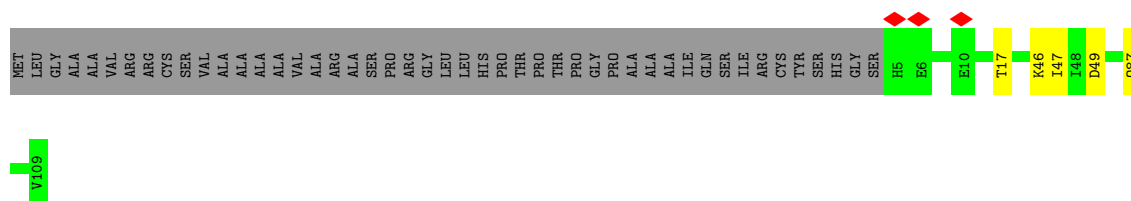
- Molecule 58: Cytochrome c oxidase subunit 4

Chain 4D:  78% 5% 18%



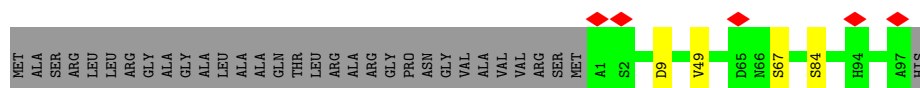
- Molecule 59: Cytochrome c oxidase subunit 5A, mitochondrial

Chain 4E:  66% 31%



- Molecule 60: Cytochrome c oxidase subunit 5B, mitochondrial

Chain 4F:  72% 25%



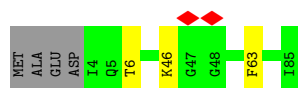
- Molecule 61: Cytochrome c oxidase subunit 6A2

Chain 4G:  8% 68% 9% 23%



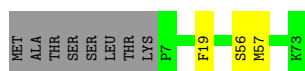
- Molecule 62: Cytochrome c oxidase subunit 6B1

Chain 4H:  92% 5%

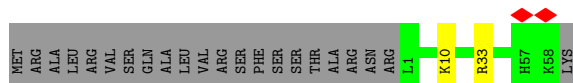


- Molecule 63: Cytochrome c oxidase subunit 6C

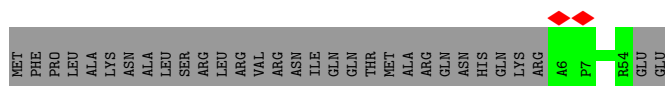
Chain 4I:  85% 11%



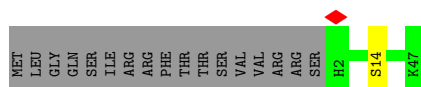
- Molecule 64: Cytochrome c oxidase subunit 7A1, mitochondrial



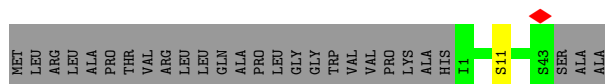
- Molecule 65: Cytochrome c oxidase subunit 7B



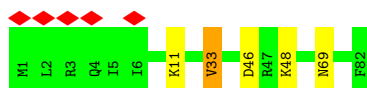
- Molecule 66: Cytochrome c oxidase subunit 7C, mitochondrial



- Molecule 67: Cytochrome c oxidase subunit 8



- Molecule 68: Cytochrome c oxidase subunit NDUF4



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 400000 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 50 | Depositor |
| Minimum defocus (nm) | 1300 | Depositor |
| Maximum defocus (nm) | 3000 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K3 BIOQUANTUM (6k x 4k) | Depositor |
| Maximum map value | 1.632 | Depositor |
| Minimum map value | -0.000 | Depositor |
| Average map value | 0.005 | Depositor |
| Map value standard deviation | 0.030 | Depositor |
| Recommended contour level | 0.12 | Depositor |
| Map size (Å) | 370.296, 370.296, 370.296 | wwPDB |
| Map dimensions | 888, 888, 888 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 0.417, 0.417, 0.417 | Depositor |

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SF4, AME, CU, MYR, FES, GTP, HEA, CDL, FME, PEK, HEC, NA, MG, ACE, FMN, NDP, PGV, K, 3PE, CUA, PC1, HEM, PO4, EH2, PSC

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 | 1A | 0.25 | 0/930 | 0.49 | 0/1271 |
| 2 | 1B | 0.27 | 0/1273 | 0.54 | 0/1722 |
| 3 | 1C | 0.26 | 0/1791 | 0.51 | 0/2439 |
| 4 | 1D | 0.36 | 2/3545 (0.1%) | 0.65 | 4/4806 (0.1%) |
| 5 | 1E | 0.27 | 0/1698 | 0.51 | 1/2311 (0.0%) |
| 6 | 1F | 0.36 | 1/3401 (0.0%) | 0.62 | 3/4595 (0.1%) |
| 7 | 1G | 0.26 | 0/5451 | 0.51 | 0/7387 |
| 8 | 1H | 0.27 | 0/2566 | 0.54 | 3/3509 (0.1%) |
| 9 | 1I | 0.26 | 0/1443 | 0.51 | 0/1952 |
| 10 | 1J | 0.28 | 0/1364 | 0.56 | 1/1850 (0.1%) |
| 11 | 1K | 0.26 | 0/751 | 0.47 | 0/1018 |
| 12 | 1L | 0.27 | 0/4939 | 0.45 | 0/6718 |
| 13 | 1M | 0.26 | 0/3713 | 0.47 | 0/5063 |
| 14 | 1N | 0.26 | 0/2765 | 0.46 | 0/3758 |
| 15 | 1O | 0.27 | 0/2650 | 0.51 | 0/3588 |
| 16 | 1P | 0.26 | 0/2828 | 0.50 | 0/3834 |
| 17 | 1Q | 0.26 | 0/1070 | 0.51 | 0/1446 |
| 18 | 1R | 0.25 | 0/755 | 0.51 | 0/1018 |
| 19 | 1S | 0.27 | 0/711 | 0.54 | 0/956 |
| 20 | 1T | 0.26 | 0/701 | 0.45 | 0/946 |
| 20 | 1U | 0.26 | 0/706 | 0.42 | 0/954 |
| 21 | 1V | 0.25 | 0/946 | 0.43 | 0/1281 |
| 22 | 1W | 0.26 | 0/995 | 0.51 | 0/1340 |
| 23 | 1X | 0.27 | 0/1436 | 0.51 | 0/1938 |
| 24 | 1Y | 0.41 | 2/1037 (0.2%) | 0.55 | 1/1404 (0.1%) |
| 25 | 1Z | 0.27 | 0/1199 | 0.52 | 0/1617 |
| 26 | 1a | 0.26 | 0/577 | 0.45 | 0/777 |
| 27 | 1b | 1.12 | 3/664 (0.5%) | 1.23 | 6/912 (0.7%) |
| 28 | 1c | 0.25 | 0/430 | 0.47 | 0/581 |
| 29 | 1d | 0.28 | 0/1016 | 0.49 | 0/1374 |
| 30 | 1e | 0.27 | 0/836 | 0.52 | 0/1118 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------------|-------------|----------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 31 | 1f | 0.25 | 0/499 | 0.54 | 0/673 |
| 32 | 1g | 0.27 | 0/858 | 0.53 | 0/1165 |
| 33 | 1h | 0.27 | 0/1184 | 0.52 | 0/1603 |
| 34 | 1i | 0.25 | 0/1138 | 0.49 | 0/1551 |
| 35 | 1j | 0.24 | 0/627 | 0.46 | 0/858 |
| 36 | 1k | 0.26 | 0/668 | 0.44 | 0/903 |
| 37 | 1l | 0.41 | 1/1365 (0.1%) | 0.72 | 4/1867 (0.2%) |
| 38 | 1m | 0.27 | 0/1092 | 0.54 | 0/1481 |
| 39 | 1n | 0.26 | 0/1549 | 0.52 | 0/2098 |
| 40 | 1o | 0.26 | 0/1069 | 0.52 | 0/1430 |
| 41 | 1p | 0.26 | 0/1481 | 0.52 | 0/1997 |
| 42 | 1q | 0.25 | 0/1253 | 0.50 | 0/1704 |
| 43 | 1r | 0.27 | 0/777 | 0.51 | 0/1051 |
| 44 | 1s | 0.27 | 0/394 | 0.51 | 0/533 |
| 45 | 3A | 0.30 | 0/3481 | 0.54 | 0/4722 |
| 45 | 3N | 0.31 | 0/3496 | 0.55 | 0/4723 |
| 46 | 3B | 0.30 | 0/3190 | 0.52 | 0/4317 |
| 46 | 3O | 0.30 | 0/3175 | 0.54 | 1/4292 (0.0%) |
| 47 | 3C | 0.60 | 4/3123 (0.1%) | 0.74 | 8/4269 (0.2%) |
| 47 | 3P | 0.29 | 0/3122 | 0.48 | 0/4269 |
| 48 | 3D | 0.83 | 6/1946 (0.3%) | 1.00 | 11/2641 (0.4%) |
| 48 | 3Q | 0.60 | 3/1962 (0.2%) | 0.80 | 4/2663 (0.2%) |
| 49 | 3E | 0.30 | 0/1551 | 0.56 | 0/2098 |
| 49 | 3I | 0.79 | 2/342 (0.6%) | 1.38 | 7/465 (1.5%) |
| 49 | 3R | 0.42 | 2/1551 (0.1%) | 0.59 | 0/2098 |
| 49 | 3V | 0.29 | 0/225 | 0.61 | 0/303 |
| 50 | 3F | 0.32 | 0/888 | 0.55 | 0/1193 |
| 50 | 3S | 0.30 | 0/888 | 0.53 | 0/1193 |
| 51 | 3G | 0.32 | 0/649 | 0.57 | 0/878 |
| 51 | 3T | 1.17 | 4/649 (0.6%) | 1.38 | 7/878 (0.8%) |
| 52 | 3H | 0.32 | 0/539 | 0.67 | 1/724 (0.1%) |
| 52 | 3U | 0.43 | 1/539 (0.2%) | 0.60 | 0/724 |
| 53 | 3J | 0.51 | 0/476 | 0.65 | 0/641 |
| 53 | 3W | 0.31 | 0/476 | 0.54 | 0/641 |
| 54 | 3X | 0.29 | 0/445 | 0.53 | 0/608 |
| 54 | 3Y | 0.29 | 0/437 | 0.54 | 0/598 |
| 55 | 4A | 0.33 | 2/4165 (0.0%) | 0.59 | 4/5691 (0.1%) |
| 56 | 4B | 0.24 | 0/1866 | 0.46 | 0/2544 |
| 57 | 4C | 0.24 | 0/2179 | 0.39 | 0/2981 |
| 58 | 4D | 0.25 | 0/1197 | 0.42 | 0/1617 |
| 59 | 4E | 0.24 | 0/871 | 0.48 | 0/1182 |
| 60 | 4F | 0.24 | 0/749 | 0.49 | 0/1016 |
| 61 | 4G | 0.24 | 0/644 | 0.51 | 0/881 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|------------------|-------------|------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 62 | 4H | 0.25 | 0/708 | 0.48 | 0/956 |
| 63 | 4I | 0.25 | 0/563 | 0.46 | 0/748 |
| 64 | 4J | 0.24 | 0/466 | 0.42 | 0/631 |
| 65 | 4K | 0.23 | 0/396 | 0.42 | 0/543 |
| 66 | 4L | 0.25 | 0/394 | 0.41 | 0/528 |
| 67 | 4M | 0.23 | 0/349 | 0.42 | 0/477 |
| 68 | 4N | 0.25 | 0/680 | 0.44 | 0/921 |
| All | All | 0.35 | 33/116518 (0.0%) | 0.57 | 66/158051 (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 |
|-----|-------|---------------------|---------------------|
| 6 | 1F | 0 | 2 |
| 8 | 1H | 0 | 1 |
| 49 | 3R | 0 | 2 |
| All | All | 0 | 5 |

The worst 5 of 33 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|--------|-------------|----------|
| 48 | 3D | 265 | PRO | CG-CD | -22.86 | 0.75 | 1.50 |
| 51 | 3T | 74 | PRO | CG-CD | -21.57 | 0.79 | 1.50 |
| 27 | 1b | 63 | PRO | CB-CG | 20.89 | 2.54 | 1.50 |
| 47 | 3C | 270 | PRO | CB-CG | 19.83 | 2.49 | 1.50 |
| 48 | 3Q | 74 | PRO | CG-CD | -19.53 | 0.86 | 1.50 |

The worst 5 of 66 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|--------|-------------|----------|
| 47 | 3C | 270 | PRO | CB-CG-CD | -25.58 | 6.74 | 106.50 |
| 27 | 1b | 63 | PRO | CB-CG-CD | -25.44 | 7.28 | 106.50 |
| 48 | 3Q | 74 | PRO | N-CD-CG | -23.27 | 68.30 | 103.20 |
| 51 | 3T | 74 | PRO | N-CD-CG | -22.38 | 69.62 | 103.20 |
| 48 | 3D | 265 | PRO | N-CD-CG | -20.79 | 72.01 | 103.20 |

There are no chirality outliers.

All (5) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|-----------|
| 6 | 1F | 206 | LYS | Peptide |
| 6 | 1F | 207 | PRO | Peptide |
| 8 | 1H | 91 | MET | Peptide |
| 49 | 3R | 263 | TYR | Sidechain |
| 49 | 3R | 265 | PHE | Sidechain |

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 | 1A | 113/115 (98%) | 105 (93%) | 6 (5%) | 2 (2%) | 7 | 3 |
| 2 | 1B | 153/258 (59%) | 145 (95%) | 8 (5%) | 0 | 100 | 100 |
| 3 | 1C | 207/264 (78%) | 204 (99%) | 3 (1%) | 0 | 100 | 100 |
| 4 | 1D | 427/476 (90%) | 408 (96%) | 19 (4%) | 0 | 100 | 100 |
| 5 | 1E | 212/249 (85%) | 198 (93%) | 14 (7%) | 0 | 100 | 100 |
| 6 | 1F | 430/464 (93%) | 410 (95%) | 18 (4%) | 2 (0%) | 25 | 23 |
| 7 | 1G | 697/727 (96%) | 672 (96%) | 22 (3%) | 3 (0%) | 30 | 29 |
| 8 | 1H | 316/318 (99%) | 297 (94%) | 18 (6%) | 1 (0%) | 37 | 37 |
| 9 | 1I | 174/239 (73%) | 169 (97%) | 5 (3%) | 0 | 100 | 100 |
| 10 | 1J | 172/175 (98%) | 157 (91%) | 13 (8%) | 2 (1%) | 11 | 7 |
| 11 | 1K | 96/98 (98%) | 93 (97%) | 3 (3%) | 0 | 100 | 100 |
| 12 | 1L | 604/606 (100%) | 572 (95%) | 30 (5%) | 2 (0%) | 37 | 37 |
| 13 | 1M | 457/459 (100%) | 450 (98%) | 6 (1%) | 1 (0%) | 44 | 45 |
| 14 | 1N | 345/347 (99%) | 334 (97%) | 10 (3%) | 1 (0%) | 37 | 37 |
| 15 | 1O | 318/357 (89%) | 308 (97%) | 10 (3%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 16 | 1P | 340/377 (90%) | 324 (95%) | 16 (5%) | 0 | 100 | 100 |
| 17 | 1Q | 127/175 (73%) | 120 (94%) | 7 (6%) | 0 | 100 | 100 |
| 18 | 1R | 94/123 (76%) | 88 (94%) | 6 (6%) | 0 | 100 | 100 |
| 19 | 1S | 85/99 (86%) | 81 (95%) | 4 (5%) | 0 | 100 | 100 |
| 20 | 1T | 83/156 (53%) | 83 (100%) | 0 | 0 | 100 | 100 |
| 20 | 1U | 84/156 (54%) | 83 (99%) | 1 (1%) | 0 | 100 | 100 |
| 21 | 1V | 113/116 (97%) | 111 (98%) | 2 (2%) | 0 | 100 | 100 |
| 22 | 1W | 113/128 (88%) | 109 (96%) | 4 (4%) | 0 | 100 | 100 |
| 23 | 1X | 169/172 (98%) | 161 (95%) | 7 (4%) | 1 (1%) | 22 | 19 |
| 24 | 1Y | 137/141 (97%) | 136 (99%) | 1 (1%) | 0 | 100 | 100 |
| 25 | 1Z | 139/144 (96%) | 138 (99%) | 1 (1%) | 0 | 100 | 100 |
| 26 | 1a | 68/70 (97%) | 68 (100%) | 0 | 0 | 100 | 100 |
| 27 | 1b | 81/84 (96%) | 77 (95%) | 4 (5%) | 0 | 100 | 100 |
| 28 | 1c | 47/76 (62%) | 47 (100%) | 0 | 0 | 100 | 100 |
| 29 | 1d | 117/122 (96%) | 116 (99%) | 1 (1%) | 0 | 100 | 100 |
| 30 | 1e | 97/106 (92%) | 93 (96%) | 4 (4%) | 0 | 100 | 100 |
| 31 | 1f | 55/135 (41%) | 51 (93%) | 4 (7%) | 0 | 100 | 100 |
| 32 | 1g | 98/154 (64%) | 87 (89%) | 11 (11%) | 0 | 100 | 100 |
| 33 | 1h | 136/189 (72%) | 134 (98%) | 2 (2%) | 0 | 100 | 100 |
| 34 | 1i | 126/128 (98%) | 123 (98%) | 3 (2%) | 0 | 100 | 100 |
| 35 | 1j | 69/105 (66%) | 65 (94%) | 4 (6%) | 0 | 100 | 100 |
| 36 | 1k | 79/98 (81%) | 76 (96%) | 3 (4%) | 0 | 100 | 100 |
| 37 | 1l | 154/186 (83%) | 149 (97%) | 5 (3%) | 0 | 100 | 100 |
| 38 | 1m | 126/129 (98%) | 121 (96%) | 5 (4%) | 0 | 100 | 100 |
| 39 | 1n | 170/179 (95%) | 163 (96%) | 7 (4%) | 0 | 100 | 100 |
| 40 | 1o | 120/137 (88%) | 117 (98%) | 3 (2%) | 0 | 100 | 100 |
| 41 | 1p | 171/176 (97%) | 170 (99%) | 1 (1%) | 0 | 100 | 100 |
| 42 | 1q | 143/145 (99%) | 141 (99%) | 2 (1%) | 0 | 100 | 100 |
| 43 | 1r | 90/113 (80%) | 86 (96%) | 4 (4%) | 0 | 100 | 100 |
| 44 | 1s | 43/471 (9%) | 41 (95%) | 2 (5%) | 0 | 100 | 100 |
| 45 | 3A | 436/480 (91%) | 423 (97%) | 12 (3%) | 1 (0%) | 44 | 45 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|----------|-------------|-----|
| 45 | 3N | 444/480 (92%) | 424 (96%) | 18 (4%) | 2 (0%) | 25 | 23 |
| 46 | 3B | 414/453 (91%) | 397 (96%) | 17 (4%) | 0 | 100 | 100 |
| 46 | 3O | 413/453 (91%) | 402 (97%) | 10 (2%) | 1 (0%) | 44 | 45 |
| 47 | 3C | 377/379 (100%) | 370 (98%) | 6 (2%) | 1 (0%) | 37 | 37 |
| 47 | 3P | 377/379 (100%) | 369 (98%) | 8 (2%) | 0 | 100 | 100 |
| 48 | 3D | 235/325 (72%) | 232 (99%) | 3 (1%) | 0 | 100 | 100 |
| 48 | 3Q | 237/325 (73%) | 228 (96%) | 9 (4%) | 0 | 100 | 100 |
| 49 | 3E | 194/274 (71%) | 169 (87%) | 24 (12%) | 1 (0%) | 25 | 23 |
| 49 | 3I | 45/274 (16%) | 40 (89%) | 4 (9%) | 1 (2%) | 5 | 2 |
| 49 | 3R | 194/274 (71%) | 167 (86%) | 23 (12%) | 4 (2%) | 5 | 2 |
| 49 | 3V | 29/274 (11%) | 28 (97%) | 1 (3%) | 0 | 100 | 100 |
| 50 | 3F | 96/111 (86%) | 95 (99%) | 1 (1%) | 0 | 100 | 100 |
| 50 | 3S | 96/111 (86%) | 95 (99%) | 1 (1%) | 0 | 100 | 100 |
| 51 | 3G | 72/82 (88%) | 70 (97%) | 2 (3%) | 0 | 100 | 100 |
| 51 | 3T | 72/82 (88%) | 71 (99%) | 0 | 1 (1%) | 9 | 5 |
| 52 | 3H | 63/91 (69%) | 61 (97%) | 1 (2%) | 1 (2%) | 8 | 4 |
| 52 | 3U | 63/91 (69%) | 62 (98%) | 1 (2%) | 0 | 100 | 100 |
| 53 | 3J | 54/64 (84%) | 51 (94%) | 1 (2%) | 2 (4%) | 2 | 1 |
| 53 | 3W | 54/64 (84%) | 53 (98%) | 1 (2%) | 0 | 100 | 100 |
| 54 | 3X | 50/56 (89%) | 47 (94%) | 3 (6%) | 0 | 100 | 100 |
| 54 | 3Y | 49/56 (88%) | 45 (92%) | 4 (8%) | 0 | 100 | 100 |
| 55 | 4A | 512/514 (100%) | 500 (98%) | 12 (2%) | 0 | 100 | 100 |
| 56 | 4B | 225/227 (99%) | 216 (96%) | 9 (4%) | 0 | 100 | 100 |
| 57 | 4C | 257/261 (98%) | 249 (97%) | 8 (3%) | 0 | 100 | 100 |
| 58 | 4D | 137/169 (81%) | 130 (95%) | 7 (5%) | 0 | 100 | 100 |
| 59 | 4E | 103/152 (68%) | 99 (96%) | 4 (4%) | 0 | 100 | 100 |
| 60 | 4F | 95/129 (74%) | 94 (99%) | 1 (1%) | 0 | 100 | 100 |
| 61 | 4G | 73/97 (75%) | 69 (94%) | 4 (6%) | 0 | 100 | 100 |
| 62 | 4H | 80/86 (93%) | 77 (96%) | 3 (4%) | 0 | 100 | 100 |
| 63 | 4I | 65/75 (87%) | 64 (98%) | 1 (2%) | 0 | 100 | 100 |
| 64 | 4J | 56/80 (70%) | 55 (98%) | 1 (2%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 65 | 4K | 47/80 (59%) | 46 (98%) | 1 (2%) | 0 | 100 | 100 |
| 66 | 4L | 44/63 (70%) | 43 (98%) | 1 (2%) | 0 | 100 | 100 |
| 67 | 4M | 41/70 (59%) | 41 (100%) | 0 | 0 | 100 | 100 |
| 68 | 4N | 80/82 (98%) | 72 (90%) | 7 (9%) | 1 (1%) | 10 | 6 |
| All | All | 14074/17005 (83%) | 13535 (96%) | 508 (4%) | 31 (0%) | 45 | 45 |

5 of 31 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 10 | 1J | 66 | VAL |
| 13 | 1M | 82 | SER |
| 23 | 1X | 28 | ALA |
| 47 | 3C | 270 | PRO |
| 49 | 3E | 271 | VAL |

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 | 1A | 99/99 (100%) | 93 (94%) | 6 (6%) | 15 | 13 |
| 2 | 1B | 131/212 (62%) | 117 (89%) | 14 (11%) | 5 | 3 |
| 3 | 1C | 190/227 (84%) | 187 (98%) | 3 (2%) | 58 | 65 |
| 4 | 1D | 371/405 (92%) | 358 (96%) | 13 (4%) | 31 | 34 |
| 5 | 1E | 183/207 (88%) | 170 (93%) | 13 (7%) | 12 | 10 |
| 6 | 1F | 346/368 (94%) | 332 (96%) | 14 (4%) | 27 | 28 |
| 7 | 1G | 588/610 (96%) | 558 (95%) | 30 (5%) | 20 | 19 |
| 8 | 1H | 274/274 (100%) | 265 (97%) | 9 (3%) | 33 | 36 |
| 9 | 1I | 151/201 (75%) | 147 (97%) | 4 (3%) | 41 | 46 |
| 10 | 1J | 140/141 (99%) | 128 (91%) | 12 (9%) | 8 | 6 |
| 11 | 1K | 84/84 (100%) | 82 (98%) | 2 (2%) | 44 | 49 |
| 12 | 1L | 539/539 (100%) | 516 (96%) | 23 (4%) | 25 | 25 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|-----|
| 13 | 1M | 408/408 (100%) | 394 (97%) | 14 (3%) | 32 | 35 |
| 14 | 1N | 310/310 (100%) | 298 (96%) | 12 (4%) | 27 | 29 |
| 15 | 1O | 283/307 (92%) | 267 (94%) | 16 (6%) | 17 | 15 |
| 16 | 1P | 296/323 (92%) | 282 (95%) | 14 (5%) | 22 | 22 |
| 17 | 1Q | 117/152 (77%) | 108 (92%) | 9 (8%) | 10 | 8 |
| 18 | 1R | 79/97 (81%) | 72 (91%) | 7 (9%) | 8 | 5 |
| 19 | 1S | 77/82 (94%) | 75 (97%) | 2 (3%) | 41 | 46 |
| 20 | 1T | 79/133 (59%) | 74 (94%) | 5 (6%) | 15 | 13 |
| 20 | 1U | 79/133 (59%) | 74 (94%) | 5 (6%) | 15 | 13 |
| 21 | 1V | 100/101 (99%) | 94 (94%) | 6 (6%) | 16 | 14 |
| 22 | 1W | 107/112 (96%) | 106 (99%) | 1 (1%) | 75 | 82 |
| 23 | 1X | 153/154 (99%) | 144 (94%) | 9 (6%) | 16 | 14 |
| 24 | 1Y | 101/102 (99%) | 95 (94%) | 6 (6%) | 16 | 14 |
| 25 | 1Z | 123/124 (99%) | 117 (95%) | 6 (5%) | 21 | 20 |
| 26 | 1a | 58/58 (100%) | 56 (97%) | 2 (3%) | 32 | 35 |
| 27 | 1b | 69/70 (99%) | 65 (94%) | 4 (6%) | 17 | 15 |
| 28 | 1c | 45/66 (68%) | 45 (100%) | 0 | 100 | 100 |
| 29 | 1d | 106/109 (97%) | 103 (97%) | 3 (3%) | 38 | 43 |
| 30 | 1e | 87/94 (93%) | 82 (94%) | 5 (6%) | 17 | 15 |
| 31 | 1f | 54/113 (48%) | 50 (93%) | 4 (7%) | 11 | 9 |
| 32 | 1g | 92/129 (71%) | 86 (94%) | 6 (6%) | 14 | 12 |
| 33 | 1h | 121/158 (77%) | 116 (96%) | 5 (4%) | 26 | 27 |
| 34 | 1i | 120/120 (100%) | 112 (93%) | 8 (7%) | 13 | 11 |
| 35 | 1j | 62/84 (74%) | 55 (89%) | 7 (11%) | 4 | 2 |
| 36 | 1k | 63/76 (83%) | 62 (98%) | 1 (2%) | 58 | 65 |
| 37 | 1l | 141/161 (88%) | 136 (96%) | 5 (4%) | 31 | 34 |
| 38 | 1m | 113/114 (99%) | 108 (96%) | 5 (4%) | 24 | 24 |
| 39 | 1n | 156/160 (98%) | 151 (97%) | 5 (3%) | 34 | 37 |
| 40 | 1o | 110/119 (92%) | 102 (93%) | 8 (7%) | 11 | 9 |
| 41 | 1p | 154/156 (99%) | 145 (94%) | 9 (6%) | 17 | 15 |
| 42 | 1q | 131/131 (100%) | 126 (96%) | 5 (4%) | 28 | 30 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 43 | 1r | 85/98 (87%) | 80 (94%) | 5 (6%) | 16 | 14 |
| 44 | 1s | 44/351 (12%) | 37 (84%) | 7 (16%) | 2 | 1 |
| 45 | 3A | 367/397 (92%) | 361 (98%) | 6 (2%) | 58 | 65 |
| 45 | 3N | 372/397 (94%) | 363 (98%) | 9 (2%) | 44 | 49 |
| 46 | 3B | 328/355 (92%) | 323 (98%) | 5 (2%) | 60 | 67 |
| 46 | 3O | 327/355 (92%) | 323 (99%) | 4 (1%) | 67 | 74 |
| 47 | 3C | 332/332 (100%) | 328 (99%) | 4 (1%) | 67 | 74 |
| 47 | 3P | 332/332 (100%) | 328 (99%) | 4 (1%) | 67 | 74 |
| 48 | 3D | 202/258 (78%) | 197 (98%) | 5 (2%) | 42 | 47 |
| 48 | 3Q | 204/258 (79%) | 204 (100%) | 0 | 100 | 100 |
| 49 | 3E | 166/225 (74%) | 161 (97%) | 5 (3%) | 36 | 40 |
| 49 | 3I | 36/225 (16%) | 35 (97%) | 1 (3%) | 38 | 43 |
| 49 | 3R | 166/225 (74%) | 160 (96%) | 6 (4%) | 30 | 32 |
| 49 | 3V | 24/225 (11%) | 24 (100%) | 0 | 100 | 100 |
| 50 | 3F | 90/99 (91%) | 89 (99%) | 1 (1%) | 70 | 77 |
| 50 | 3S | 90/99 (91%) | 89 (99%) | 1 (1%) | 70 | 77 |
| 51 | 3G | 67/73 (92%) | 67 (100%) | 0 | 100 | 100 |
| 51 | 3T | 67/73 (92%) | 67 (100%) | 0 | 100 | 100 |
| 52 | 3H | 62/85 (73%) | 62 (100%) | 0 | 100 | 100 |
| 52 | 3U | 62/85 (73%) | 62 (100%) | 0 | 100 | 100 |
| 53 | 3J | 46/52 (88%) | 42 (91%) | 4 (9%) | 8 | 6 |
| 53 | 3W | 46/52 (88%) | 46 (100%) | 0 | 100 | 100 |
| 54 | 3X | 42/46 (91%) | 41 (98%) | 1 (2%) | 44 | 49 |
| 54 | 3Y | 41/46 (89%) | 40 (98%) | 1 (2%) | 44 | 49 |
| 55 | 4A | 425/425 (100%) | 418 (98%) | 7 (2%) | 58 | 65 |
| 56 | 4B | 210/210 (100%) | 203 (97%) | 7 (3%) | 33 | 36 |
| 57 | 4C | 223/225 (99%) | 216 (97%) | 7 (3%) | 35 | 39 |
| 58 | 4D | 124/149 (83%) | 116 (94%) | 8 (6%) | 14 | 12 |
| 59 | 4E | 92/124 (74%) | 87 (95%) | 5 (5%) | 18 | 17 |
| 60 | 4F | 80/101 (79%) | 76 (95%) | 4 (5%) | 20 | 20 |
| 61 | 4G | 65/80 (81%) | 56 (86%) | 9 (14%) | 3 | 1 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|-------------|-----|
| 62 | 4H | 73/76 (96%) | 70 (96%) | 3 (4%) | 26 | 27 |
| 63 | 4I | 54/61 (88%) | 51 (94%) | 3 (6%) | 17 | 16 |
| 64 | 4J | 49/68 (72%) | 47 (96%) | 2 (4%) | 26 | 27 |
| 65 | 4K | 38/66 (58%) | 38 (100%) | 0 | 100 | 100 |
| 66 | 4L | 39/55 (71%) | 38 (97%) | 1 (3%) | 41 | 46 |
| 67 | 4M | 37/57 (65%) | 36 (97%) | 1 (3%) | 40 | 44 |
| 68 | 4N | 70/70 (100%) | 65 (93%) | 5 (7%) | 12 | 10 |
| All | All | 12267/14333 (86%) | 11799 (96%) | 468 (4%) | 30 | 30 |

5 of 468 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 21 | 1V | 95 | ARG |
| 60 | 4F | 84 | SER |
| 34 | 1i | 34 | LEU |
| 59 | 4E | 49 | ASP |
| 49 | 3R | 165 | MET |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 47 | 3P | 221 | HIS |
| 67 | 4M | 39 | HIS |
| 48 | 3Q | 105 | ASN |
| 51 | 3T | 64 | GLN |
| 29 | 1d | 97 | HIS |

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

7 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 |
| 56 | FME | 4B | 1 | 56 | 8,9,10 | 0.95 | 0 | 8,9,11 | 0.91 | 0 |
| 8 | FME | 1H | 1 | 8 | 8,9,10 | 0.55 | 0 | 8,9,11 | 1.04 | 1 (12%) |
| 1 | FME | 1A | 1 | 1 | 8,9,10 | 0.55 | 0 | 8,9,11 | 1.02 | 1 (12%) |
| 12 | FME | 1L | 1 | 12 | 8,9,10 | 0.55 | 0 | 8,9,11 | 0.91 | 1 (12%) |
| 11 | FME | 1K | 1 | 11 | 8,9,10 | 0.53 | 0 | 8,9,11 | 0.98 | 1 (12%) |
| 14 | FME | 1N | 1 | 14 | 8,9,10 | 0.56 | 0 | 8,9,11 | 0.96 | 1 (12%) |
| 13 | FME | 1M | 1 | 13 | 8,9,10 | 0.54 | 0 | 8,9,11 | 1.08 | 1 (12%) |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|----------|-------|
| 56 | FME | 4B | 1 | 56 | - | 4/7/9/11 | - |
| 8 | FME | 1H | 1 | 8 | - | 1/7/9/11 | - |
| 1 | FME | 1A | 1 | 1 | - | 1/7/9/11 | - |
| 12 | FME | 1L | 1 | 12 | - | 0/7/9/11 | - |
| 11 | FME | 1K | 1 | 11 | - | 2/7/9/11 | - |
| 14 | FME | 1N | 1 | 14 | - | 0/7/9/11 | - |
| 13 | FME | 1M | 1 | 13 | - | 1/7/9/11 | - |

There are no bond length outliers.

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

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|--------|-------|-------------|----------|
| 11 | 1K | 1 | FME | O-C-CA | -2.67 | 117.91 | 124.77 |
| 8 | 1H | 1 | FME | O-C-CA | -2.66 | 117.93 | 124.77 |
| 13 | 1M | 1 | FME | O-C-CA | -2.65 | 117.94 | 124.77 |
| 14 | 1N | 1 | FME | O-C-CA | -2.62 | 118.04 | 124.77 |
| 1 | 1A | 1 | FME | O-C-CA | -2.46 | 118.44 | 124.77 |

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|------------|
| 8 | 1H | 1 | FME | O1-CN-N-CA |
| 56 | 4B | 1 | FME | O1-CN-N-CA |
| 56 | 4B | 1 | FME | C-CA-CB-CG |
| 11 | 1K | 1 | FME | N-CA-CB-CG |
| 56 | 4B | 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 109 ligands modelled in this entry, 7 are monoatomic - leaving 102 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 | $\# Z > 2$ |
| 70 | PC1 | 3X | 101 | - | 28,28,53 | 0.37 | 0 | 34,36,61 | 0.64 | 1 (2%) |
| 85 | PGV | 4K | 101 | - | 50,50,50 | 0.30 | 0 | 53,56,56 | 0.33 | 0 |
| 83 | HEM | 3P | 502 | 47 | 42,50,50 | 1.31 | 6 (14%) | 46,82,82 | 1.80 | 12 (26%) |
| 70 | PC1 | 1m | 201 | - | 45,45,53 | 0.30 | 0 | 51,53,61 | 1.10 | 3 (5%) |
| 85 | PGV | 4A | 601 | - | 50,50,50 | 0.27 | 0 | 53,56,56 | 0.32 | 0 |
| 73 | FMN | 1F | 501 | - | 33,33,33 | 0.62 | 0 | 48,50,50 | 0.66 | 1 (2%) |
| 71 | SF4 | 1G | 802 | 7 | 0,12,12 | - | - | - | | |
| 72 | FES | 1E | 301 | 5 | 0,4,4 | - | - | - | | |
| 70 | PC1 | 1Z | 201 | - | 43,43,53 | 0.28 | 0 | 49,51,61 | 0.33 | 0 |
| 70 | PC1 | 1B | 202 | - | 45,45,53 | 0.28 | 0 | 51,53,61 | 0.33 | 0 |
| 69 | 3PE | 1Y | 202 | - | 39,39,50 | 0.29 | 0 | 42,44,55 | 0.40 | 0 |
| 69 | 3PE | 3D | 502 | - | 32,32,50 | 0.36 | 0 | 35,37,55 | 0.52 | 0 |
| 69 | 3PE | 1d | 201 | - | 47,47,50 | 0.29 | 0 | 50,52,55 | 0.44 | 0 |
| 85 | PGV | 4G | 101 | - | 50,50,50 | 0.29 | 0 | 53,56,56 | 0.46 | 1 (1%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 69 | 3PE | 1L | 701 | - | 45,45,50 | 0.31 | 0 | 48,50,55 | 0.47 | 0 |
| 75 | CDL | 4D | 201 | - | 99,99,99 | 0.27 | 0 | 105,111,111 | 0.38 | 0 |
| 75 | CDL | 3A | 501 | - | 57,57,99 | 0.34 | 0 | 63,69,111 | 0.55 | 0 |
| 75 | CDL | 3G | 102 | - | 51,51,99 | 0.36 | 0 | 57,63,111 | 0.66 | 1 (1%) |
| 76 | GTP | 1O | 401 | 77 | 29,34,34 | 1.00 | 2 (6%) | 35,54,54 | 1.06 | 1 (2%) |
| 69 | 3PE | 1Y | 203 | - | 29,29,50 | 0.34 | 0 | 32,34,55 | 0.71 | 1 (3%) |
| 80 | EHZ | 1n | 201 | - | 31,36,37 | 0.18 | 0 | 36,44,47 | 1.12 | 1 (2%) |
| 75 | CDL | 1d | 202 | - | 64,64,99 | 0.33 | 0 | 70,76,111 | 0.41 | 0 |
| 80 | EHZ | 1T | 101 | 20 | 31,36,37 | 0.20 | 0 | 36,44,47 | 1.10 | 1 (2%) |
| 69 | 3PE | 3N | 501 | - | 31,31,50 | 0.35 | 0 | 34,36,55 | 0.74 | 1 (2%) |
| 69 | 3PE | 1M | 504 | - | 49,49,50 | 0.27 | 0 | 52,54,55 | 0.36 | 0 |
| 70 | PC1 | 3R | 303 | - | 44,44,53 | 0.30 | 0 | 50,52,61 | 0.42 | 0 |
| 85 | PGV | 4C | 301 | - | 50,50,50 | 0.28 | 0 | 53,56,56 | 0.32 | 0 |
| 69 | 3PE | 1L | 703 | - | 44,44,50 | 0.28 | 0 | 47,49,55 | 0.48 | 0 |
| 69 | 3PE | 3C | 504 | - | 33,33,50 | 0.36 | 0 | 36,38,55 | 0.53 | 0 |
| 75 | CDL | 4B | 302 | - | 99,99,99 | 0.27 | 0 | 105,111,111 | 0.31 | 0 |
| 69 | 3PE | 1J | 201 | - | 43,43,50 | 0.29 | 0 | 46,48,55 | 0.39 | 0 |
| 69 | 3PE | 1j | 101 | - | 43,43,50 | 0.29 | 0 | 46,48,55 | 0.45 | 0 |
| 85 | PGV | 4C | 304 | - | 50,50,50 | 0.30 | 0 | 53,56,56 | 0.39 | 0 |
| 85 | PGV | 4L | 101 | - | 50,50,50 | 0.30 | 0 | 53,56,56 | 0.38 | 0 |
| 71 | SF4 | 1I | 203 | 9 | 0,12,12 | - | - | - | - | - |
| 75 | CDL | 1L | 702 | - | 75,75,99 | 0.29 | 0 | 81,87,111 | 0.39 | 0 |
| 85 | PGV | 4M | 101 | - | 50,50,50 | 0.29 | 0 | 53,56,56 | 0.31 | 0 |
| 75 | CDL | 1q | 202 | - | 60,60,99 | 0.34 | 0 | 66,72,111 | 0.43 | 0 |
| 85 | PGV | 4C | 302 | - | 50,50,50 | 0.30 | 0 | 53,56,56 | 0.68 | 1 (1%) |
| 69 | 3PE | 1Y | 205 | - | 40,40,50 | 0.30 | 0 | 43,45,55 | 0.68 | 1 (2%) |
| 75 | CDL | 1X | 201 | - | 85,85,99 | 0.28 | 0 | 91,97,111 | 0.40 | 0 |
| 70 | PC1 | 1h | 203 | - | 46,46,53 | 0.28 | 0 | 52,54,61 | 0.31 | 0 |
| 70 | PC1 | 1Y | 201 | - | 34,34,53 | 0.33 | 0 | 40,42,61 | 0.43 | 0 |
| 69 | 3PE | 1N | 901 | - | 48,48,50 | 0.32 | 0 | 51,53,55 | 0.41 | 0 |
| 69 | 3PE | 3A | 502 | - | 26,26,50 | 0.37 | 0 | 29,31,55 | 0.68 | 1 (3%) |
| 85 | PGV | 4B | 301 | - | 50,50,50 | 0.28 | 0 | 53,56,56 | 0.34 | 0 |
| 71 | SF4 | 1G | 801 | 7 | 0,12,12 | - | - | - | - | - |
| 69 | 3PE | 3P | 503 | - | 32,32,50 | 0.33 | 0 | 35,37,55 | 0.56 | 0 |
| 81 | AME | 1h | 201 | - | 9,10,11 | 0.52 | 0 | 9,11,13 | 1.10 | 1 (11%) |
| 71 | SF4 | 1I | 202 | 9 | 0,12,12 | - | - | - | - | - |
| 85 | PGV | 4A | 603 | - | 50,50,50 | 0.30 | 0 | 53,56,56 | 0.35 | 0 |
| 69 | 3PE | 1N | 903 | - | 32,32,50 | 0.33 | 0 | 35,37,55 | 0.44 | 0 |
| 69 | 3PE | 3Y | 101 | - | 29,29,50 | 0.36 | 0 | 32,34,55 | 0.46 | 0 |
| 69 | 3PE | 3A | 503 | - | 31,31,50 | 0.35 | 0 | 34,36,55 | 0.42 | 0 |
| 70 | PC1 | 1B | 203 | - | 47,47,53 | 0.28 | 0 | 53,55,61 | 0.45 | 0 |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 69 | 3PE | 3N | 503 | - | 24,24,50 | 0.37 | 0 | 27,29,55 | 0.54 | 0 |
| 71 | SF4 | 1B | 201 | 2 | 0,12,12 | - | - | - | | |
| 85 | PGV | 4C | 303 | - | 50,50,50 | 0.29 | 0 | 53,56,56 | 0.33 | 0 |
| 85 | PGV | 4J | 101 | - | 50,50,50 | 0.29 | 0 | 53,56,56 | 0.36 | 0 |
| 75 | CDL | 3N | 502 | - | 42,42,99 | 0.40 | 0 | 48,54,111 | 0.62 | 0 |
| 83 | HEM | 3C | 502 | 47 | 42,50,50 | 1.30 | 6 (14%) | 46,82,82 | 1.72 | 9 (19%) |
| 85 | PGV | 4C | 307 | - | 50,50,50 | 0.29 | 0 | 53,56,56 | 0.36 | 0 |
| 69 | 3PE | 1M | 502 | - | 50,50,50 | 0.28 | 0 | 53,55,55 | 0.40 | 0 |
| 69 | 3PE | 3R | 302 | - | 46,46,50 | 0.29 | 0 | 49,51,55 | 0.34 | 0 |
| 82 | MYR | 1l | 201 | - | 13,14,15 | 0.31 | 0 | 12,13,15 | 0.29 | 0 |
| 85 | PGV | 4A | 602 | - | 50,50,50 | 0.28 | 0 | 53,56,56 | 0.36 | 0 |
| 75 | CDL | 4C | 306 | - | 99,99,99 | 0.27 | 0 | 105,111,111 | 0.41 | 1 (0%) |
| 72 | FES | 1G | 803 | 7 | 0,4,4 | - | - | - | | |
| 70 | PC1 | 1A | 202 | - | 34,34,53 | 0.32 | 0 | 40,42,61 | 0.40 | 0 |
| 75 | CDL | 1N | 902 | - | 61,61,99 | 0.31 | 0 | 67,73,111 | 0.58 | 1 (1%) |
| 69 | 3PE | 1Y | 204 | - | 26,26,50 | 0.36 | 0 | 29,31,55 | 0.43 | 0 |
| 91 | PEK | 4G | 102 | - | 52,52,52 | 0.47 | 0 | 55,57,57 | 0.46 | 0 |
| 75 | CDL | 1h | 202 | - | 79,79,99 | 0.30 | 0 | 85,91,111 | 0.45 | 0 |
| 71 | SF4 | 1F | 502 | 6 | 0,12,12 | - | - | - | | |
| 72 | FES | 3E | 301 | 49 | 0,4,4 | - | - | - | | |
| 70 | PC1 | 1P | 401 | - | 32,32,53 | 0.33 | 0 | 38,40,61 | 0.47 | 0 |
| 85 | PGV | 4C | 305 | - | 50,50,50 | 0.30 | 0 | 53,56,56 | 0.57 | 1 (1%) |
| 84 | HEC | 3Q | 501 | 48 | 32,50,50 | 2.31 | 12 (37%) | 30,82,82 | 2.45 | 6 (20%) |
| 75 | CDL | 3G | 103 | - | 55,55,99 | 0.35 | 0 | 61,67,111 | 0.48 | 0 |
| 69 | 3PE | 1A | 201 | - | 46,46,50 | 0.28 | 0 | 49,51,55 | 0.34 | 0 |
| 92 | PO4 | 4H | 101 | - | 4,4,4 | 0.97 | 0 | 6,6,6 | 0.44 | 0 |
| 84 | HEC | 3D | 501 | 48 | 30,49,50 | 2.33 | 12 (40%) | 28,80,82 | 2.41 | 5 (17%) |
| 70 | PC1 | 1M | 503 | - | 43,43,53 | 0.32 | 0 | 49,51,61 | 0.37 | 0 |
| 75 | CDL | 3T | 101 | - | 56,56,99 | 0.36 | 0 | 62,68,111 | 0.71 | 2 (3%) |
| 90 | PSC | 4B | 304 | - | 51,51,51 | 0.48 | 0 | 57,59,59 | 0.44 | 0 |
| 72 | FES | 3R | 301 | 49 | 0,4,4 | - | - | - | | |
| 89 | CUA | 4B | 303 | 56 | 0,1,1 | - | - | - | | |
| 69 | 3PE | 3G | 101 | - | 28,28,50 | 0.35 | 0 | 31,33,55 | 0.44 | 0 |
| 75 | CDL | 3P | 504 | - | 55,55,99 | 0.37 | 0 | 61,67,111 | 0.61 | 1 (1%) |
| 91 | PEK | 4G | 103 | - | 51,51,52 | 0.48 | 0 | 54,56,57 | 0.46 | 0 |
| 78 | NDP | 1P | 402 | - | 47,52,52 | 0.66 | 0 | 61,80,80 | 0.92 | 3 (4%) |
| 83 | HEM | 3C | 501 | 47 | 42,50,50 | 1.30 | 6 (14%) | 46,82,82 | 1.80 | 9 (19%) |
| 70 | PC1 | 1q | 201 | - | 48,48,53 | 0.28 | 0 | 54,56,61 | 0.55 | 1 (1%) |
| 69 | 3PE | 1L | 704 | - | 30,30,50 | 0.34 | 0 | 33,35,55 | 0.69 | 1 (3%) |
| 86 | HEA | 4A | 604 | 55 | 58,67,67 | 2.20 | 20 (34%) | 63,103,103 | 2.48 | 25 (39%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 70 | PC1 | 3E | 302 | - | 46,46,53 | 0.28 | 0 | 52,54,61 | 0.39 | 0 |
| 83 | HEM | 3P | 501 | 47 | 42,50,50 | 1.29 | 5 (11%) | 46,82,82 | 1.82 | 9 (19%) |
| 69 | 3PE | 1M | 501 | - | 44,44,50 | 0.29 | 0 | 47,49,55 | 0.37 | 0 |
| 69 | 3PE | 3C | 503 | - | 34,34,50 | 0.36 | 0 | 37,39,55 | 0.55 | 0 |
| 70 | PC1 | 1I | 201 | - | 53,53,53 | 0.27 | 0 | 59,61,61 | 0.38 | 0 |
| 70 | PC1 | 1H | 401 | - | 47,47,53 | 0.29 | 0 | 53,55,61 | 0.38 | 0 |
| 86 | HEA | 4A | 605 | 55 | 58,67,67 | 2.20 | 20 (34%) | 63,103,103 | 2.41 | 27 (42%) |

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 |
|-----|------|-------|-----|------|---------|----------------|---------|
| 70 | PC1 | 3X | 101 | - | - | 4/32/32/57 | - |
| 85 | PGV | 4K | 101 | - | - | 14/55/55/55 | - |
| 83 | HEM | 3P | 502 | 47 | - | 6/12/54/54 | - |
| 70 | PC1 | 1m | 201 | - | - | 11/49/49/57 | - |
| 85 | PGV | 4A | 601 | - | - | 10/55/55/55 | - |
| 73 | FMN | 1F | 501 | - | - | 1/18/18/18 | 0/3/3/3 |
| 71 | SF4 | 1G | 802 | 7 | - | - | 0/6/5/5 |
| 72 | FES | 1E | 301 | 5 | - | - | 0/1/1/1 |
| 70 | PC1 | 1Z | 201 | - | - | 1/47/47/57 | - |
| 70 | PC1 | 1B | 202 | - | - | 8/49/49/57 | - |
| 69 | 3PE | 1Y | 202 | - | - | 9/43/43/54 | - |
| 69 | 3PE | 3D | 502 | - | - | 4/36/36/54 | - |
| 69 | 3PE | 1d | 201 | - | - | 16/51/51/54 | - |
| 85 | PGV | 4G | 101 | - | - | 8/55/55/55 | - |
| 69 | 3PE | 1L | 701 | - | - | 5/49/49/54 | - |
| 75 | CDL | 4D | 201 | - | - | 16/110/110/110 | - |
| 75 | CDL | 3A | 501 | - | - | 5/68/68/110 | - |
| 75 | CDL | 3G | 102 | - | - | 10/62/62/110 | - |
| 76 | GTP | 1O | 401 | 77 | - | 4/18/38/38 | 0/3/3/3 |
| 69 | 3PE | 1Y | 203 | - | - | 13/33/33/54 | - |
| 80 | EHZ | 1n | 201 | - | - | 3/42/44/45 | - |
| 75 | CDL | 1d | 202 | - | - | 22/75/75/110 | - |
| 80 | EHZ | 1T | 101 | 20 | - | 14/42/44/45 | - |
| 69 | 3PE | 3N | 501 | - | - | 10/35/35/54 | - |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|----------------|---------|
| 69 | 3PE | 1M | 504 | - | - | 5/53/53/54 | - |
| 70 | PC1 | 3R | 303 | - | - | 5/48/48/57 | - |
| 85 | PGV | 4C | 301 | - | - | 1/55/55/55 | - |
| 69 | 3PE | 1L | 703 | - | - | 9/48/48/54 | - |
| 69 | 3PE | 3C | 504 | - | - | 9/37/37/54 | - |
| 75 | CDL | 4B | 302 | - | - | 15/110/110/110 | - |
| 69 | 3PE | 1J | 201 | - | - | 10/47/47/54 | - |
| 69 | 3PE | 1j | 101 | - | - | 3/47/47/54 | - |
| 85 | PGV | 4C | 304 | - | - | 15/55/55/55 | - |
| 85 | PGV | 4L | 101 | - | - | 7/55/55/55 | - |
| 71 | SF4 | 1I | 203 | 9 | - | - | 0/6/5/5 |
| 75 | CDL | 1L | 702 | - | - | 11/86/86/110 | - |
| 85 | PGV | 4M | 101 | - | - | 8/55/55/55 | - |
| 75 | CDL | 1q | 202 | - | - | 7/71/71/110 | - |
| 85 | PGV | 4C | 302 | - | - | 6/55/55/55 | - |
| 69 | 3PE | 1Y | 205 | - | - | 15/44/44/54 | - |
| 75 | CDL | 1X | 201 | - | - | 18/96/96/110 | - |
| 70 | PC1 | 1h | 203 | - | - | 12/50/50/57 | - |
| 70 | PC1 | 1Y | 201 | - | - | 8/38/38/57 | - |
| 69 | 3PE | 1N | 901 | - | - | 13/52/52/54 | - |
| 69 | 3PE | 3A | 502 | - | - | 7/30/30/54 | - |
| 85 | PGV | 4B | 301 | - | - | 11/55/55/55 | - |
| 71 | SF4 | 1G | 801 | 7 | - | - | 0/6/5/5 |
| 69 | 3PE | 3P | 503 | - | - | 10/36/36/54 | - |
| 81 | AME | 1h | 201 | - | - | 2/9/10/12 | - |
| 71 | SF4 | 1I | 202 | 9 | - | - | 0/6/5/5 |
| 85 | PGV | 4A | 603 | - | - | 11/55/55/55 | - |
| 69 | 3PE | 1N | 903 | - | - | 3/36/36/54 | - |
| 69 | 3PE | 3Y | 101 | - | - | 2/33/33/54 | - |
| 69 | 3PE | 3A | 503 | - | - | 6/35/35/54 | - |
| 70 | PC1 | 1B | 203 | - | - | 12/51/51/57 | - |
| 69 | 3PE | 3N | 503 | - | - | 7/28/28/54 | - |
| 85 | PGV | 4C | 303 | - | - | 10/55/55/55 | - |
| 71 | SF4 | 1B | 201 | 2 | - | - | 0/6/5/5 |
| 85 | PGV | 4J | 101 | - | - | 10/55/55/55 | - |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|----------------|---------|
| 75 | CDL | 3N | 502 | - | - | 8/53/53/110 | - |
| 83 | HEM | 3C | 502 | 47 | - | 4/12/54/54 | - |
| 85 | PGV | 4C | 307 | - | - | 4/55/55/55 | - |
| 69 | 3PE | 1M | 502 | - | - | 10/54/54/54 | - |
| 69 | 3PE | 3R | 302 | - | - | 9/50/50/54 | - |
| 82 | MYR | 1I | 201 | - | - | 2/12/12/13 | - |
| 85 | PGV | 4A | 602 | - | - | 6/55/55/55 | - |
| 75 | CDL | 4C | 306 | - | - | 24/110/110/110 | - |
| 72 | FES | 1G | 803 | 7 | - | - | 0/1/1/1 |
| 70 | PC1 | 1A | 202 | - | - | 3/38/38/57 | - |
| 75 | CDL | 1N | 902 | - | - | 10/71/71/110 | - |
| 69 | 3PE | 1Y | 204 | - | - | 5/30/30/54 | - |
| 91 | PEK | 4G | 102 | - | - | 10/56/56/56 | - |
| 75 | CDL | 1h | 202 | - | - | 10/90/90/110 | - |
| 71 | SF4 | 1F | 502 | 6 | - | - | 0/6/5/5 |
| 72 | FES | 3E | 301 | 49 | - | - | 0/1/1/1 |
| 70 | PC1 | 1P | 401 | - | - | 10/36/36/57 | - |
| 85 | PGV | 4C | 305 | - | - | 16/55/55/55 | - |
| 84 | HEC | 3Q | 501 | 48 | - | 4/10/54/54 | - |
| 75 | CDL | 3G | 103 | - | - | 11/66/66/110 | - |
| 69 | 3PE | 1A | 201 | - | - | 9/50/50/54 | - |
| 84 | HEC | 3D | 501 | 48 | - | 3/9/53/54 | - |
| 70 | PC1 | 1M | 503 | - | - | 8/47/47/57 | - |
| 75 | CDL | 3T | 101 | - | - | 13/67/67/110 | - |
| 90 | PSC | 4B | 304 | - | - | 17/55/55/55 | - |
| 72 | FES | 3R | 301 | 49 | - | - | 0/1/1/1 |
| 69 | 3PE | 3G | 101 | - | - | 10/32/32/54 | - |
| 75 | CDL | 3P | 504 | - | - | 13/66/66/110 | - |
| 91 | PEK | 4G | 103 | - | - | 9/55/55/56 | - |
| 78 | NDP | 1P | 402 | - | - | 2/30/77/77 | 0/5/5/5 |
| 83 | HEM | 3C | 501 | 47 | - | 5/12/54/54 | - |
| 70 | PC1 | 1q | 201 | - | - | 7/52/52/57 | - |
| 69 | 3PE | 1L | 704 | - | - | 8/34/34/54 | - |
| 86 | HEA | 4A | 604 | 55 | - | 8/32/76/76 | - |
| 70 | PC1 | 3E | 302 | - | - | 2/50/50/57 | - |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|-------------|-------|
| 83 | HEM | 3P | 501 | 47 | - | 6/12/54/54 | - |
| 69 | 3PE | 1M | 501 | - | - | 7/48/48/54 | - |
| 69 | 3PE | 3C | 503 | - | - | 11/38/38/54 | - |
| 70 | PC1 | 1I | 201 | - | - | 9/57/57/57 | - |
| 70 | PC1 | 1H | 401 | - | - | 13/51/51/57 | - |
| 86 | HEA | 4A | 605 | 55 | - | 7/32/76/76 | - |

The worst 5 of 89 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|---------|------|-------------|----------|
| 84 | 3Q | 501 | HEC | C3C-C2C | 6.60 | 1.48 | 1.40 |
| 84 | 3Q | 501 | HEC | C2B-C3B | 6.45 | 1.48 | 1.40 |
| 84 | 3D | 501 | HEC | C3C-C2C | 6.42 | 1.47 | 1.40 |
| 84 | 3D | 501 | HEC | C2B-C3B | 6.23 | 1.47 | 1.40 |
| 86 | 4A | 604 | HEA | C3B-C2B | 5.48 | 1.47 | 1.34 |

The worst 5 of 129 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-------------|-------|-------------|----------|
| 86 | 4A | 605 | HEA | C3D-C4D-ND | 6.71 | 116.84 | 110.35 |
| 86 | 4A | 604 | HEA | C3D-C4D-ND | 6.51 | 116.64 | 110.35 |
| 84 | 3Q | 501 | HEC | C1D-C2D-C3D | -6.38 | 102.56 | 107.00 |
| 84 | 3D | 501 | HEC | C1D-C2D-C3D | -6.22 | 102.67 | 107.00 |
| 80 | 1n | 201 | EHZ | C10-S1-C9 | 6.21 | 120.20 | 101.84 |

There are no chirality outliers.

5 of 775 torsion outliers are listed below:

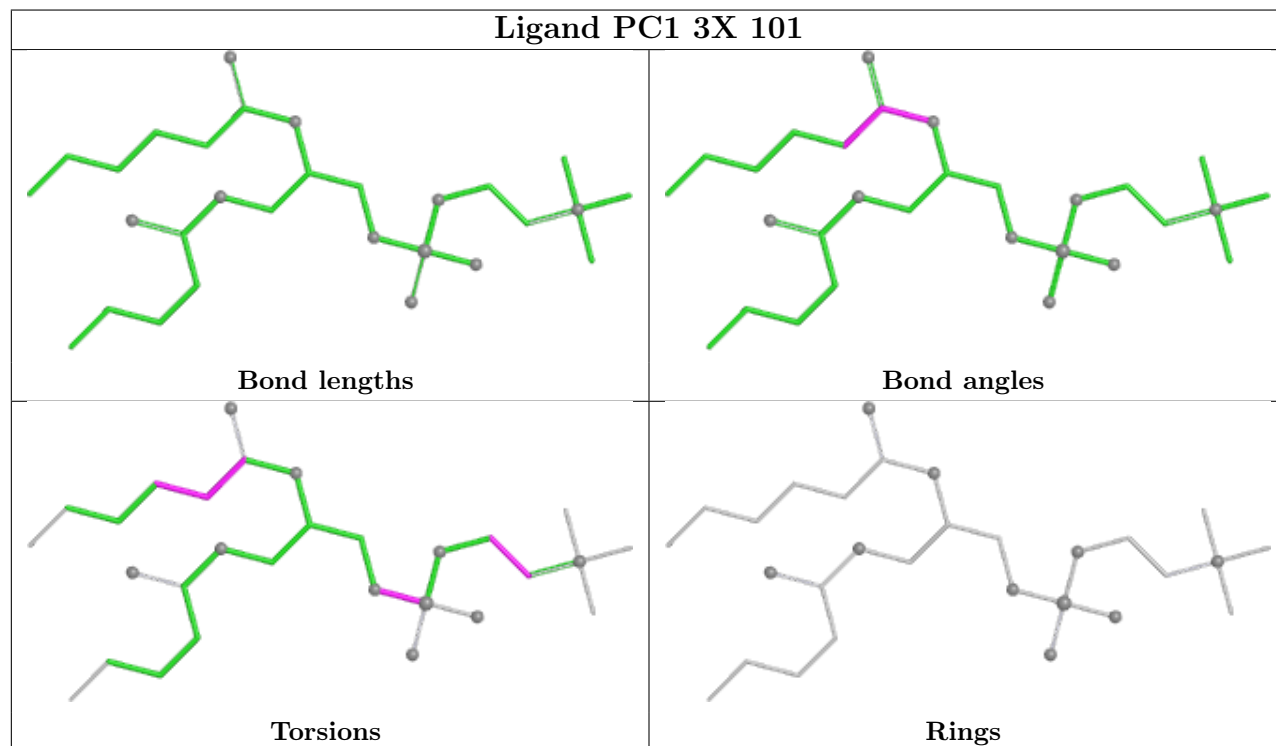
| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|---------------|
| 69 | 1A | 201 | 3PE | C1-O11-P-O13 |
| 69 | 1A | 201 | 3PE | C1-O11-P-O14 |
| 69 | 1J | 201 | 3PE | C1-O11-P-O13 |
| 69 | 1J | 201 | 3PE | C1-O11-P-O14 |
| 69 | 1J | 201 | 3PE | C11-O13-P-O12 |

There are no ring outliers.

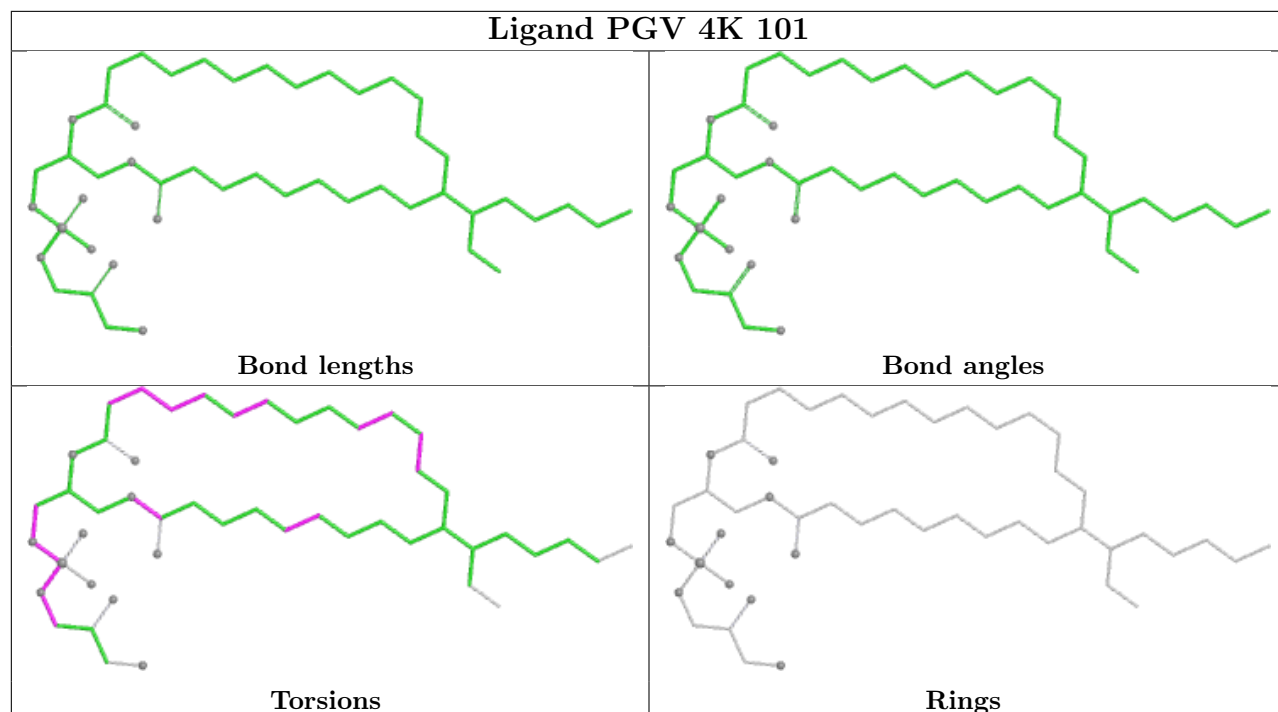
No monomer is involved in short contacts.

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

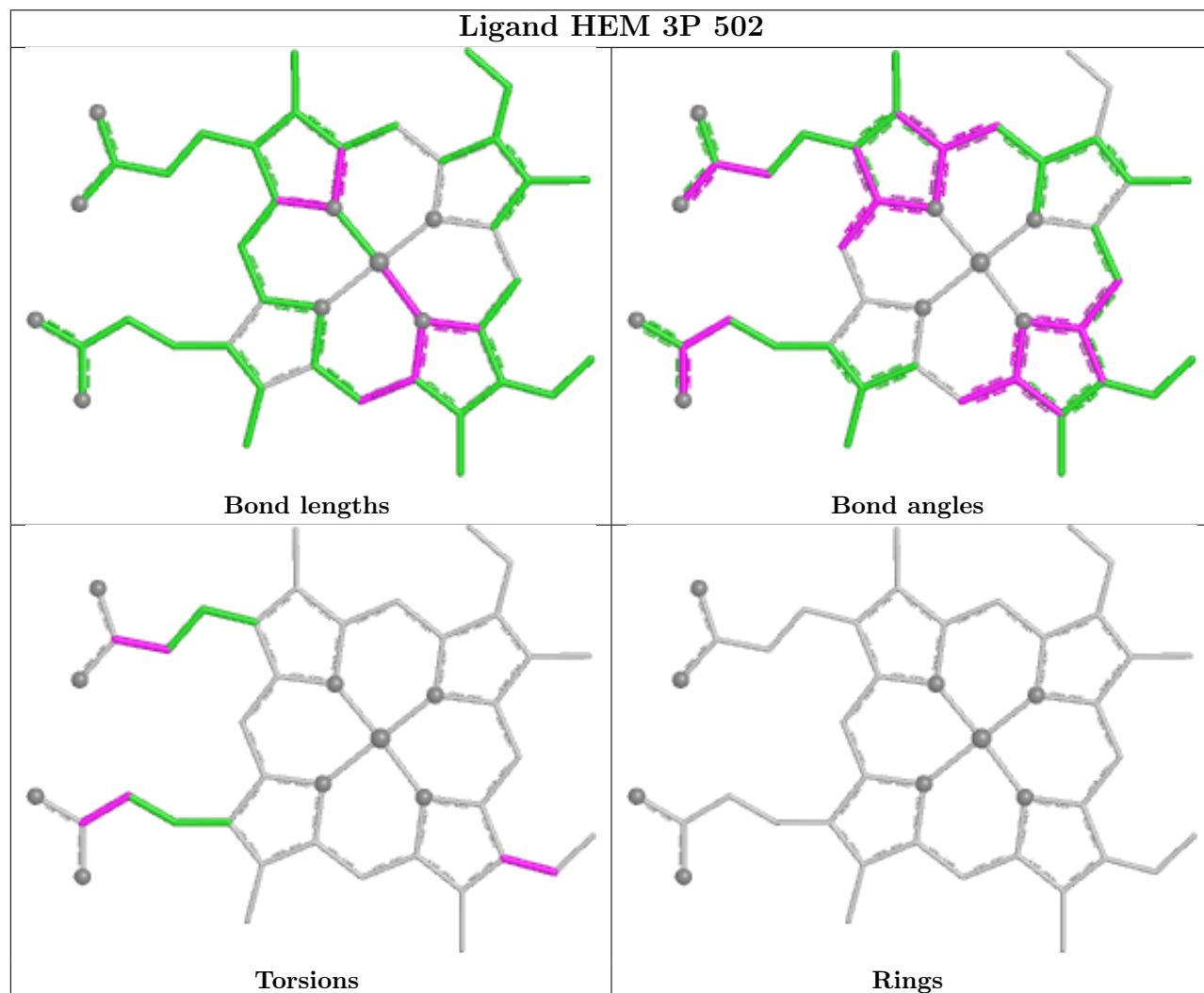
addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. 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.

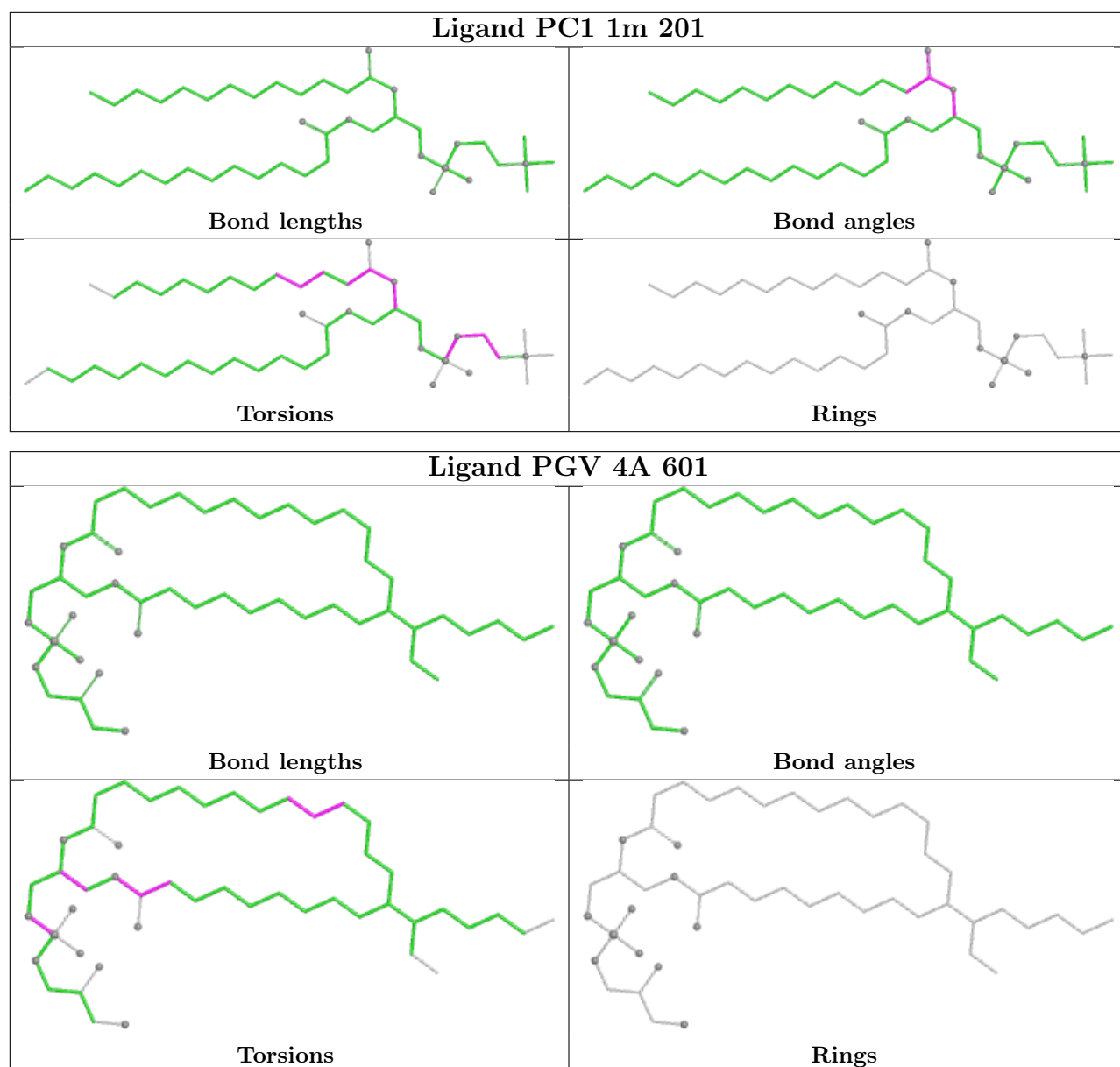


Ligand PGV 4K 101

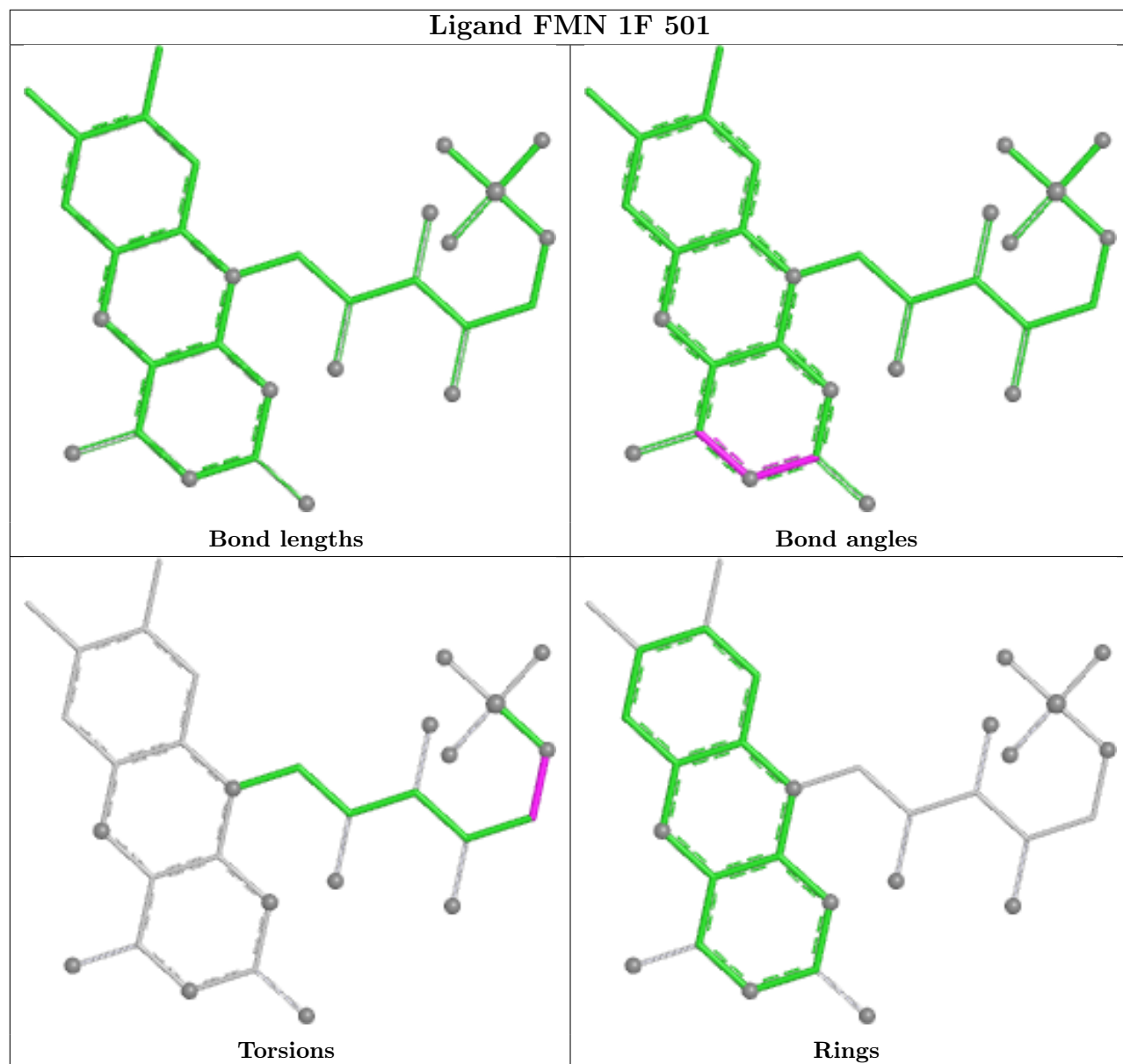


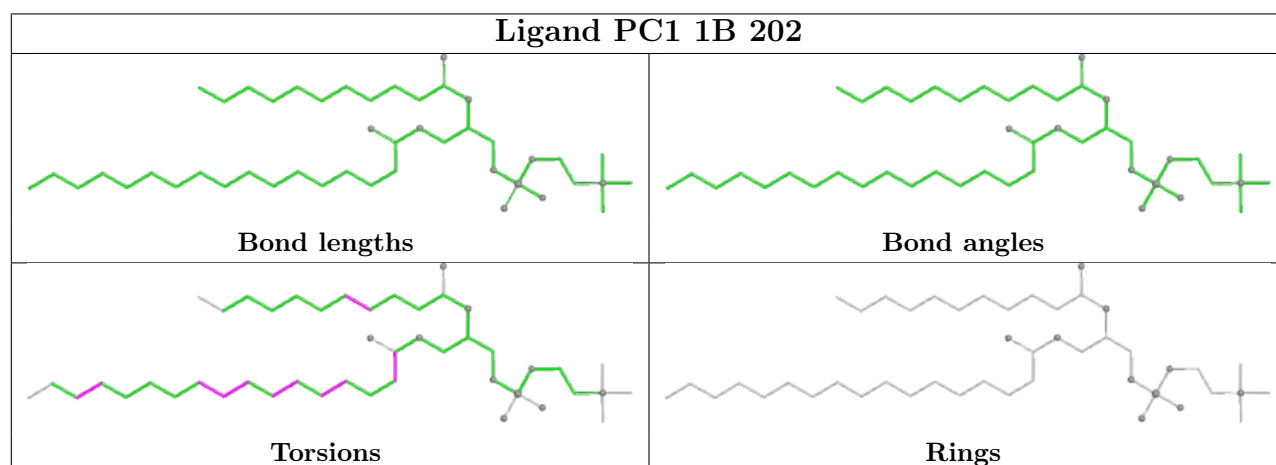
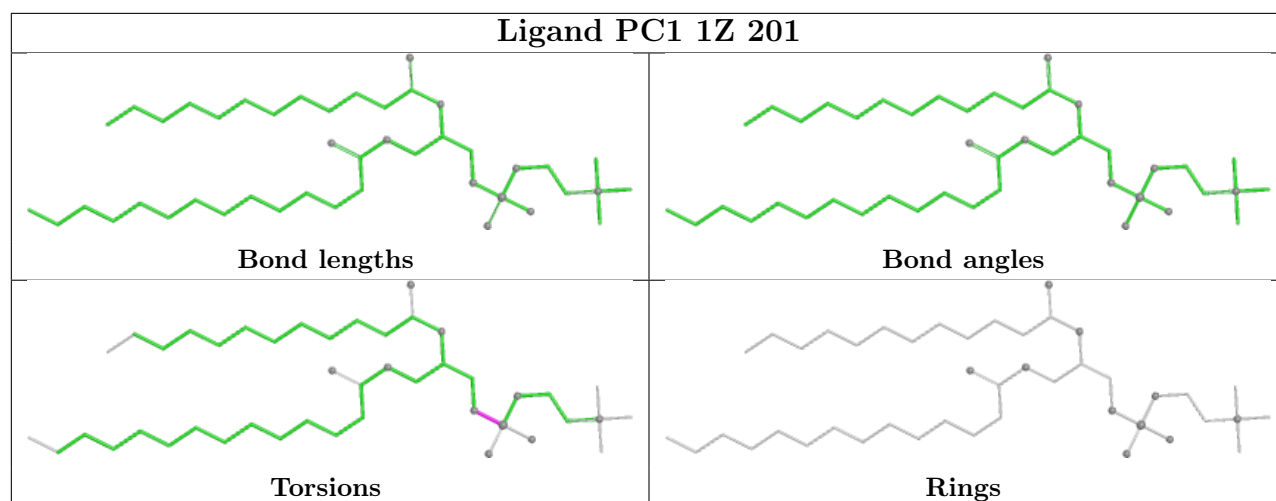
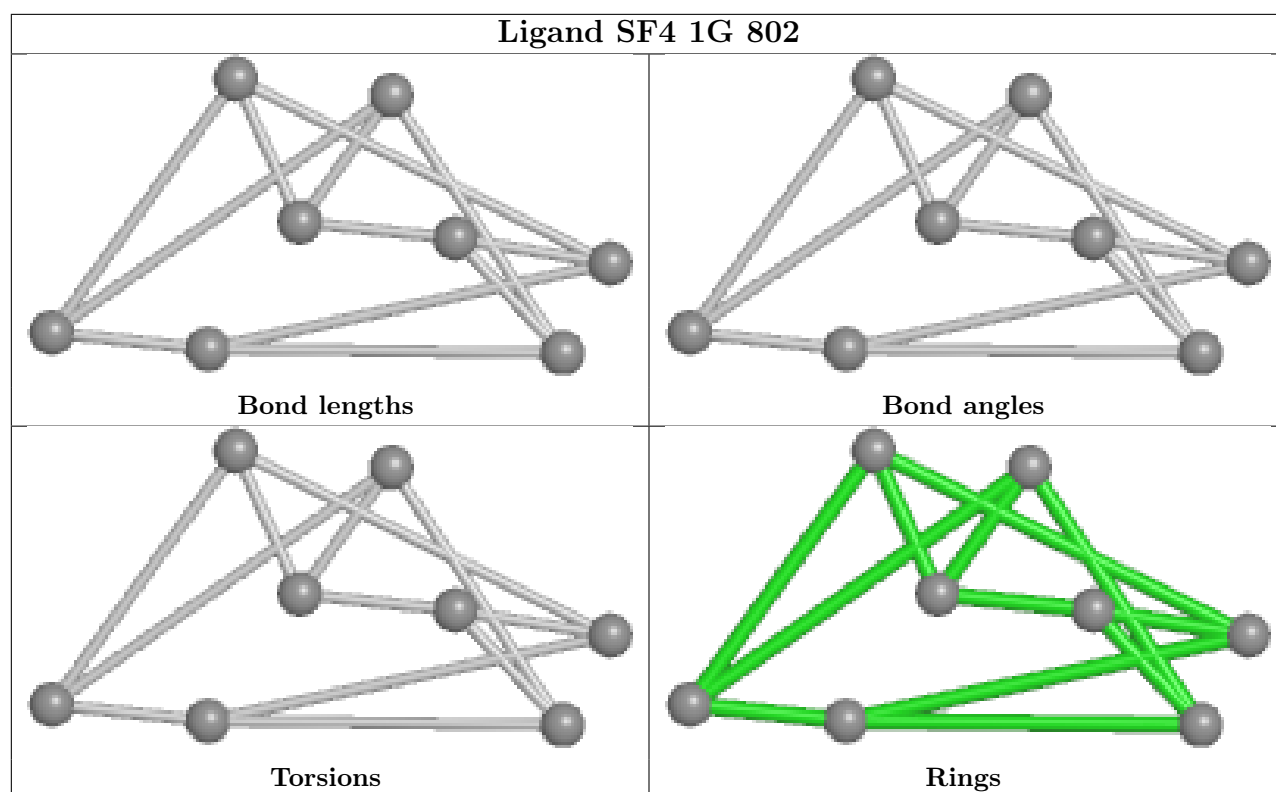
Ligand HEM 3P 502

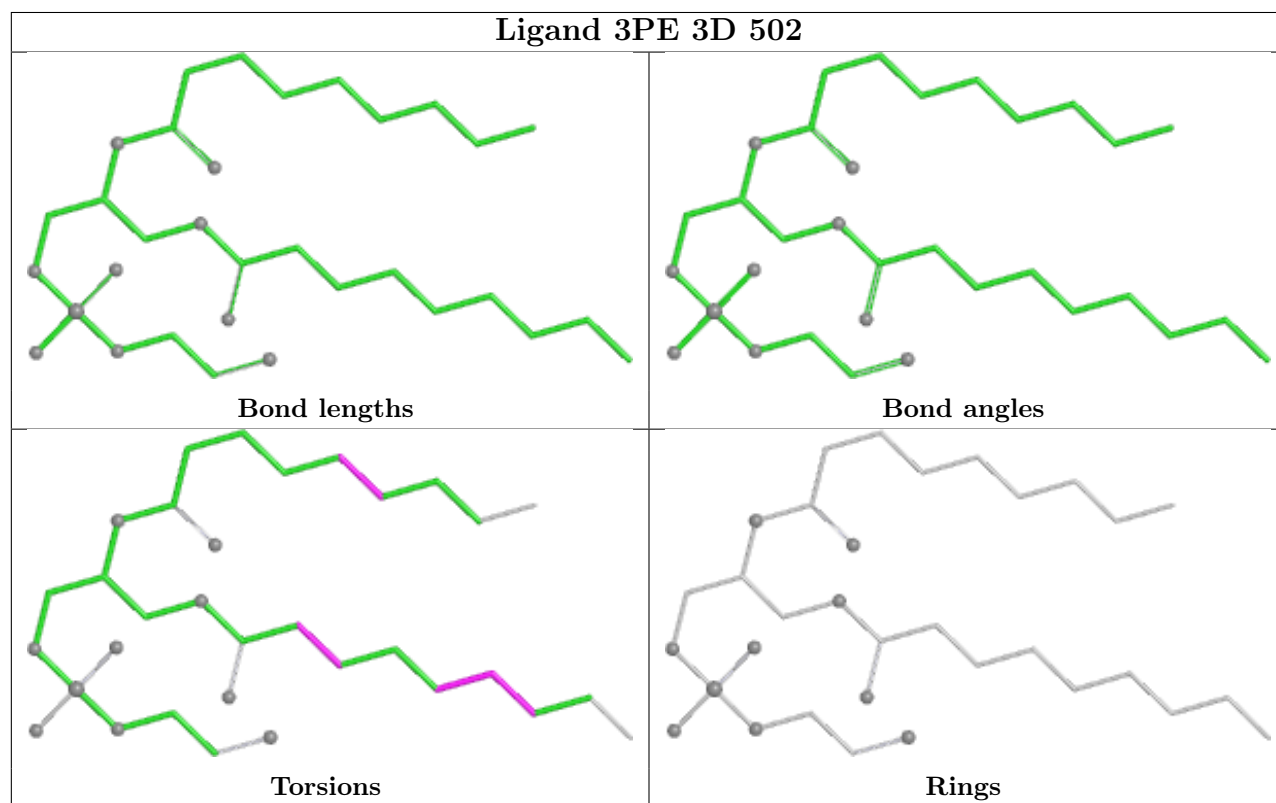
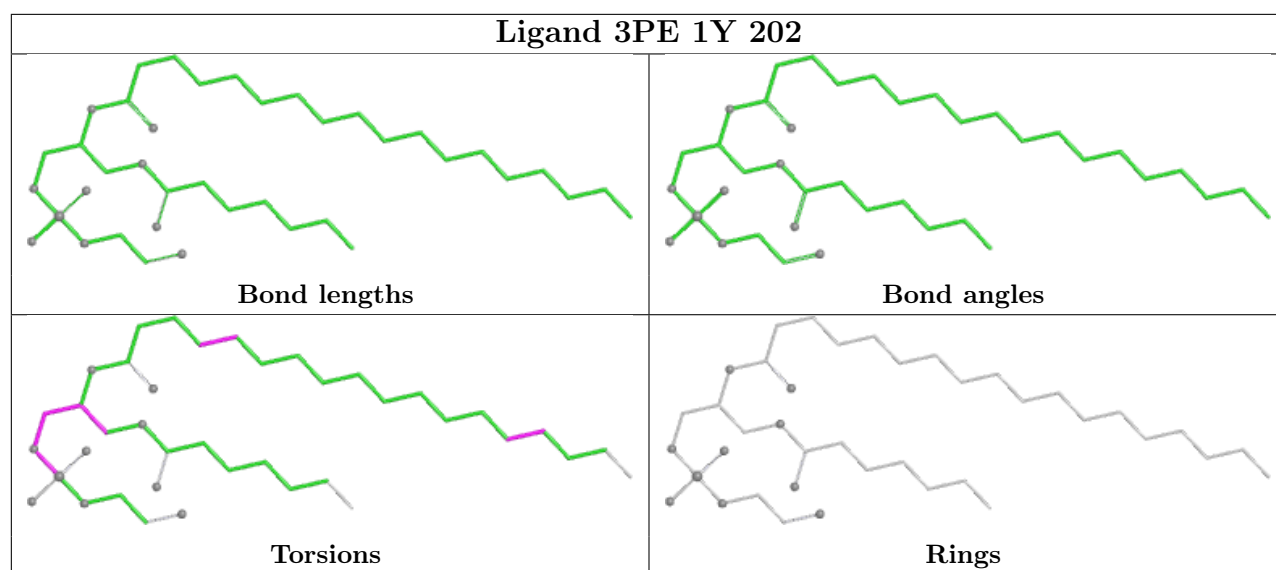


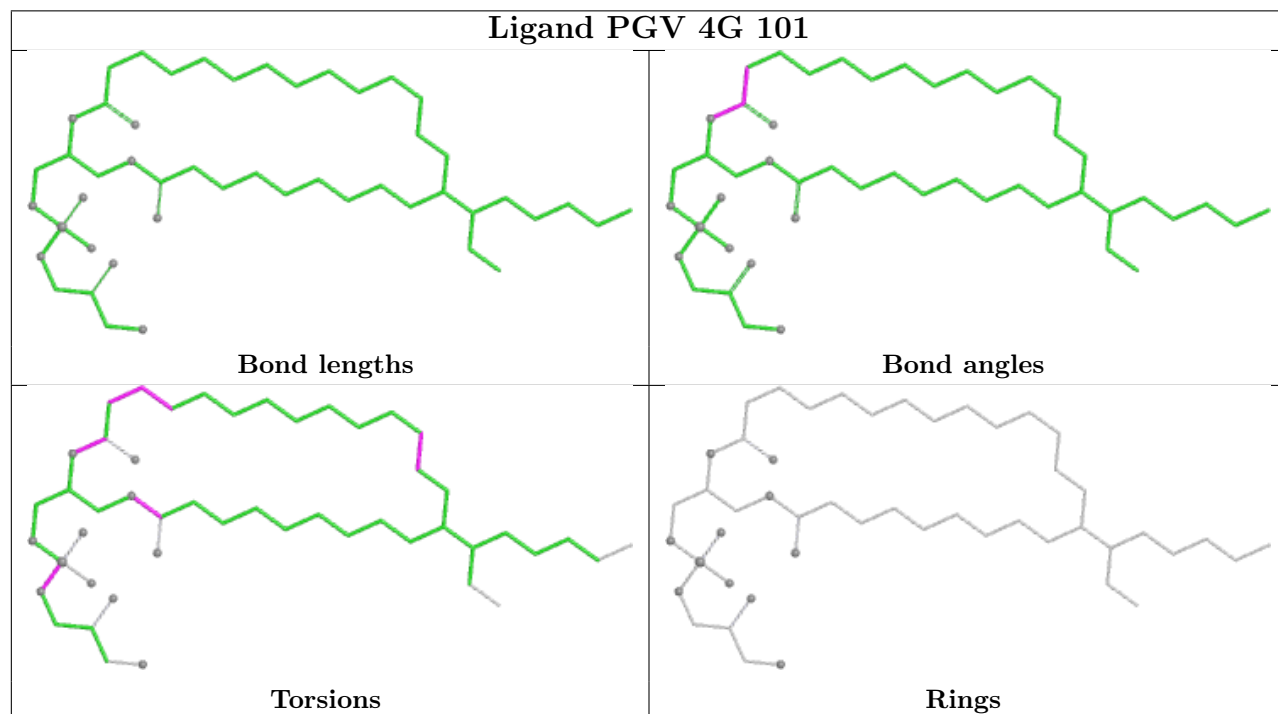
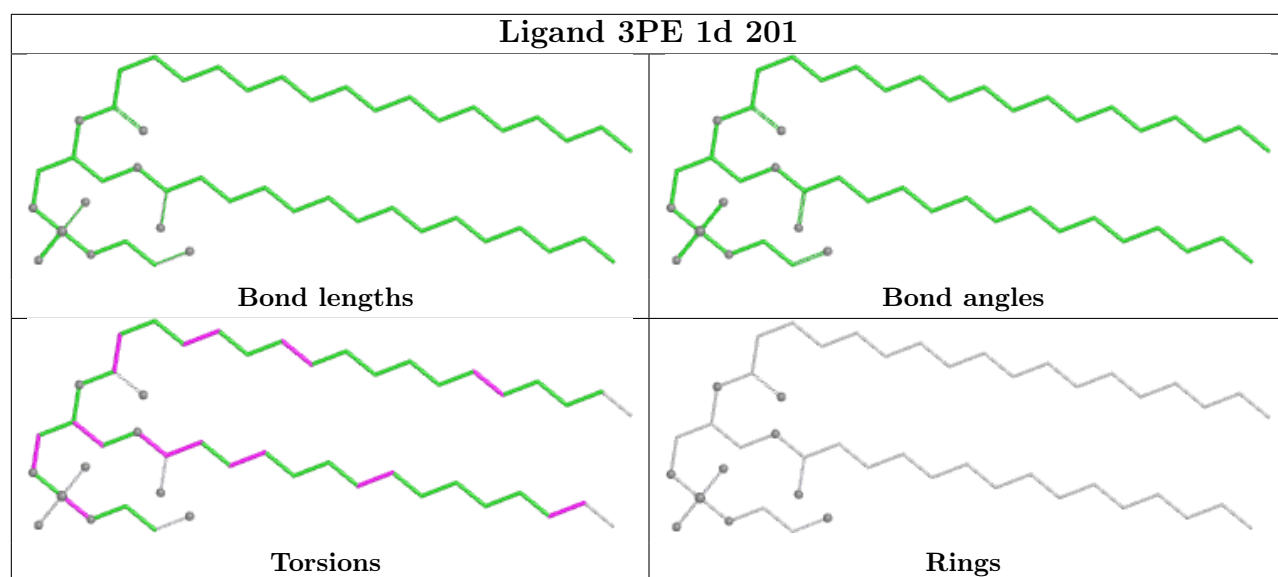


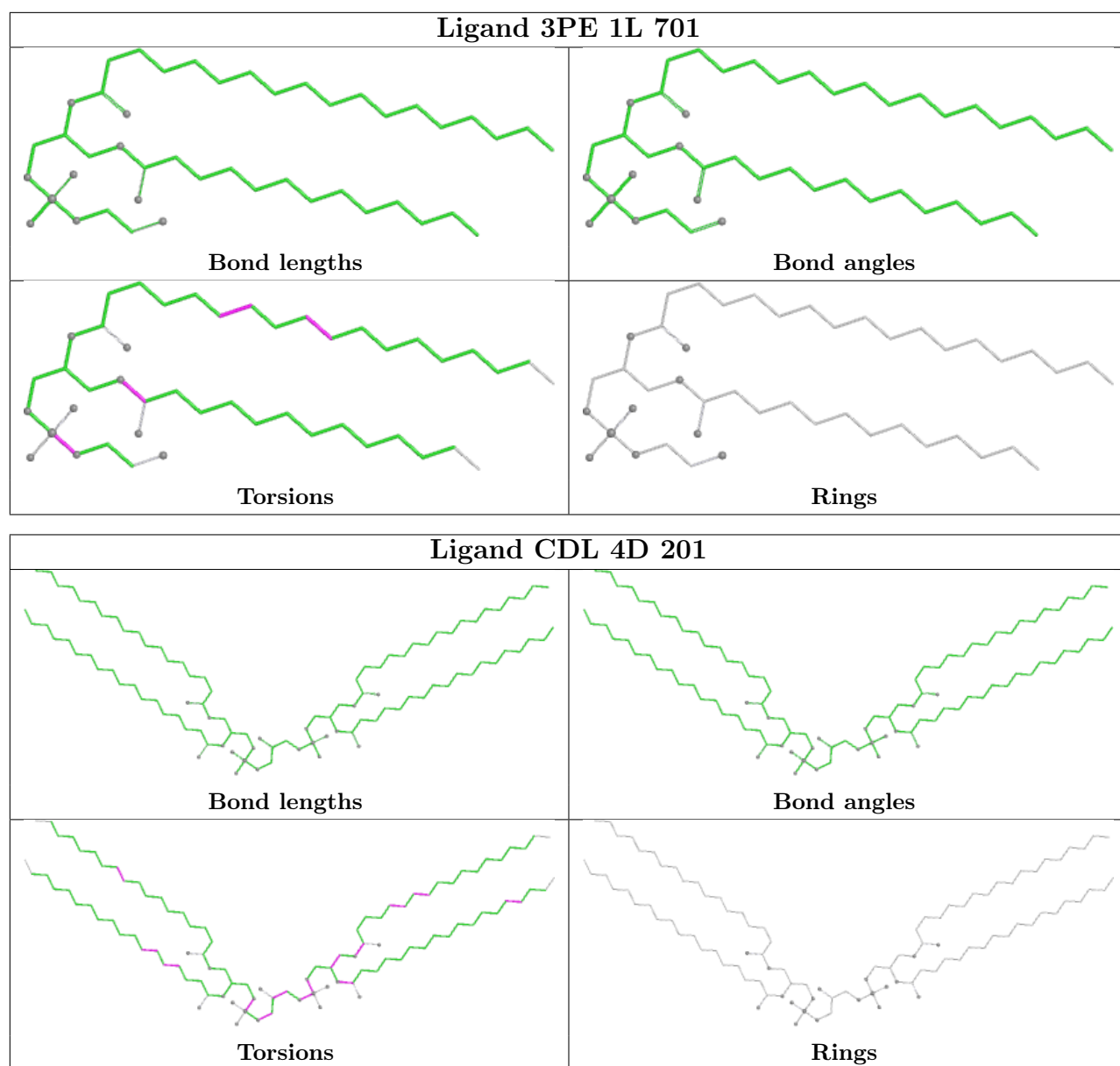
Ligand FMN 1F 501

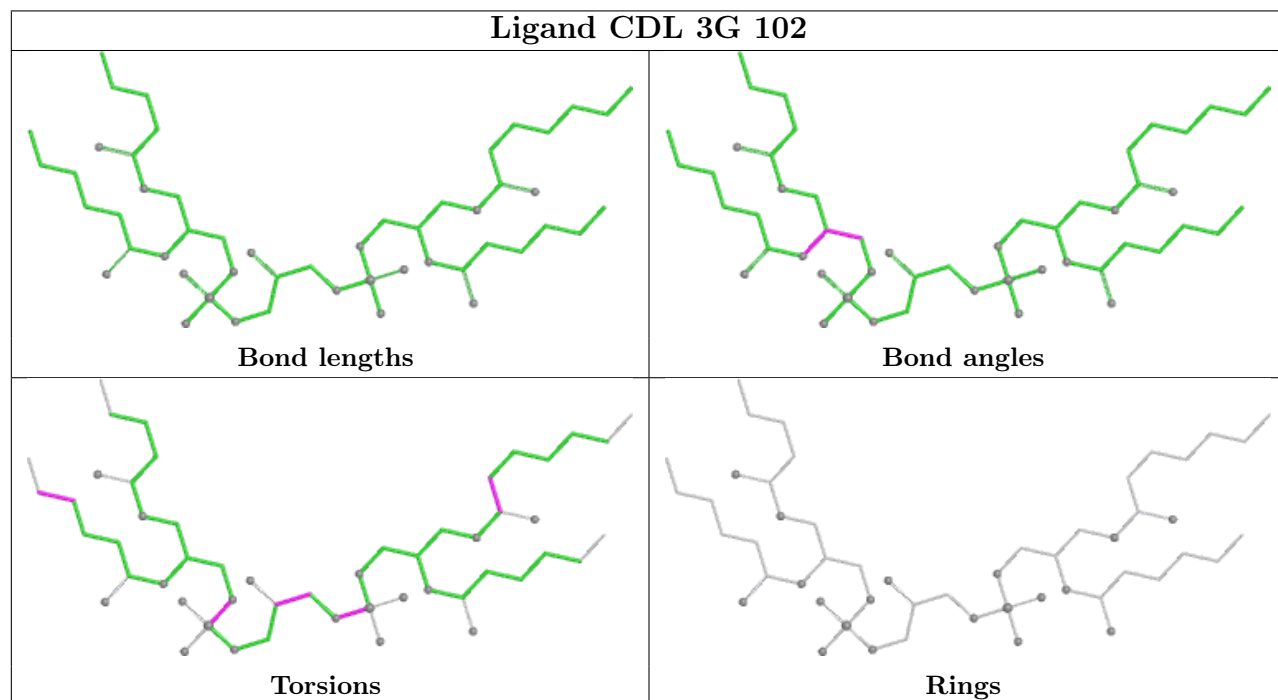
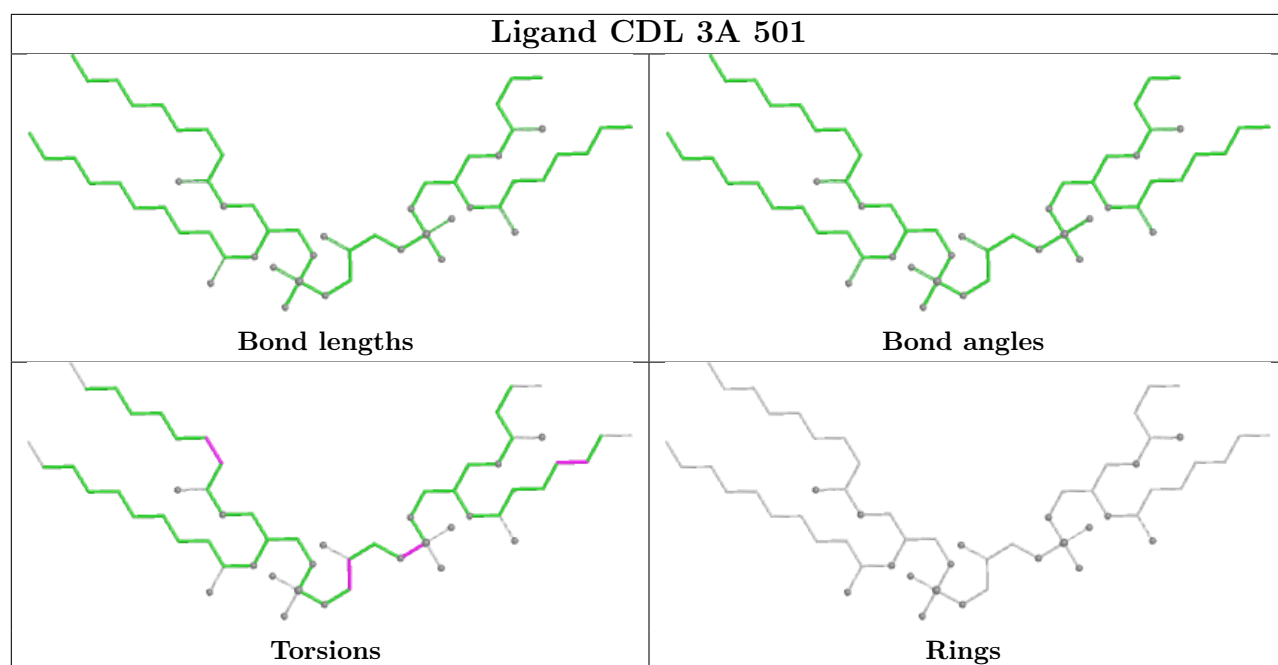


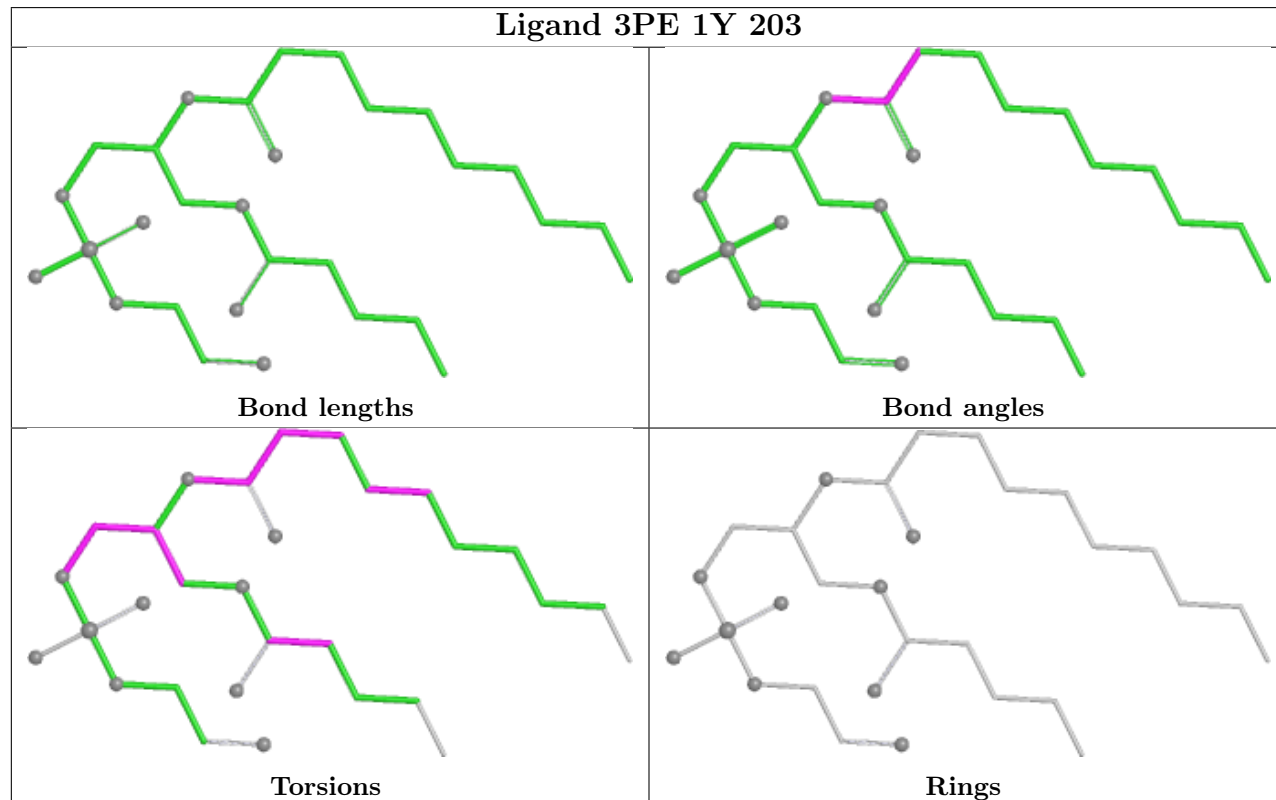
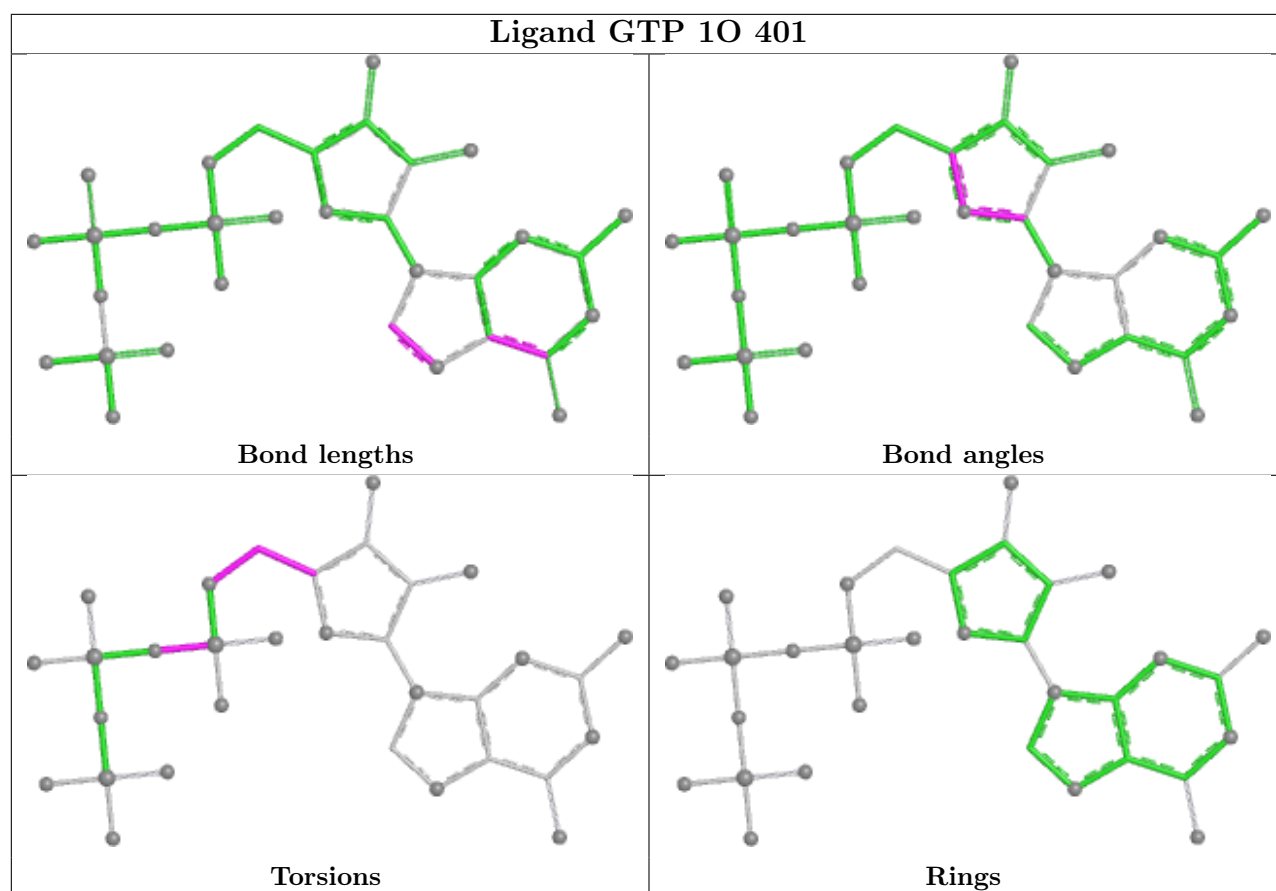


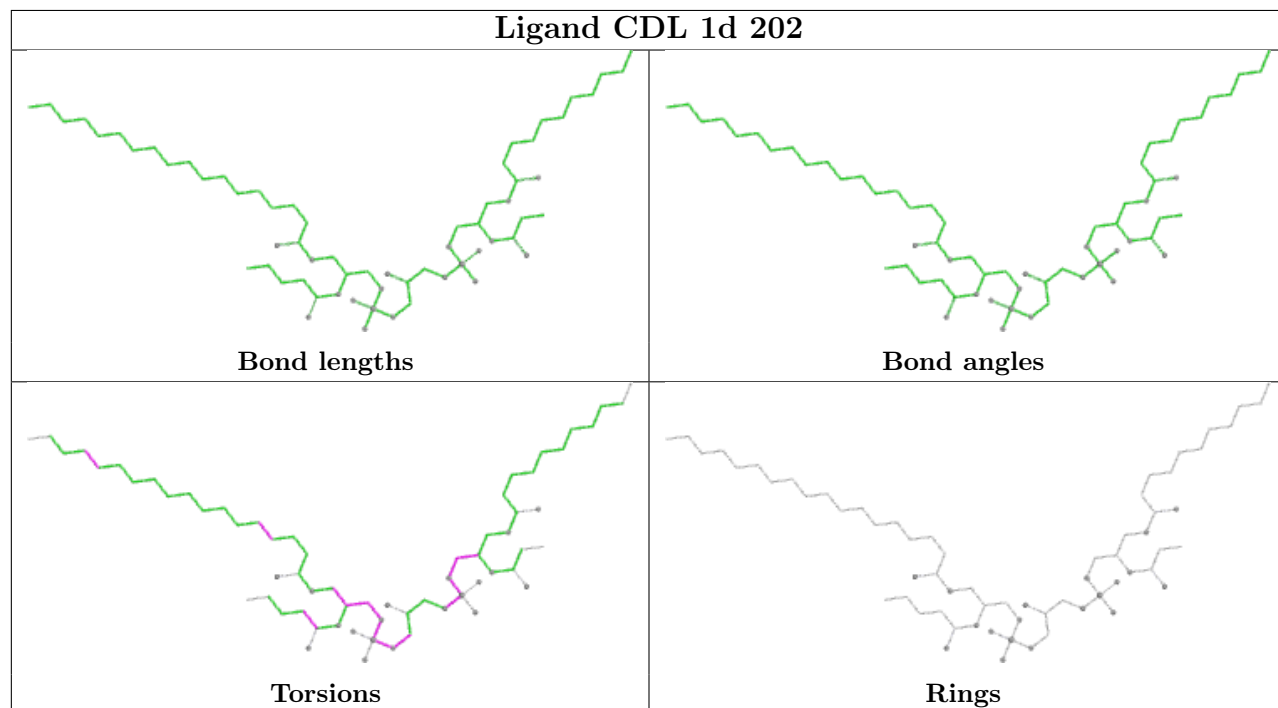
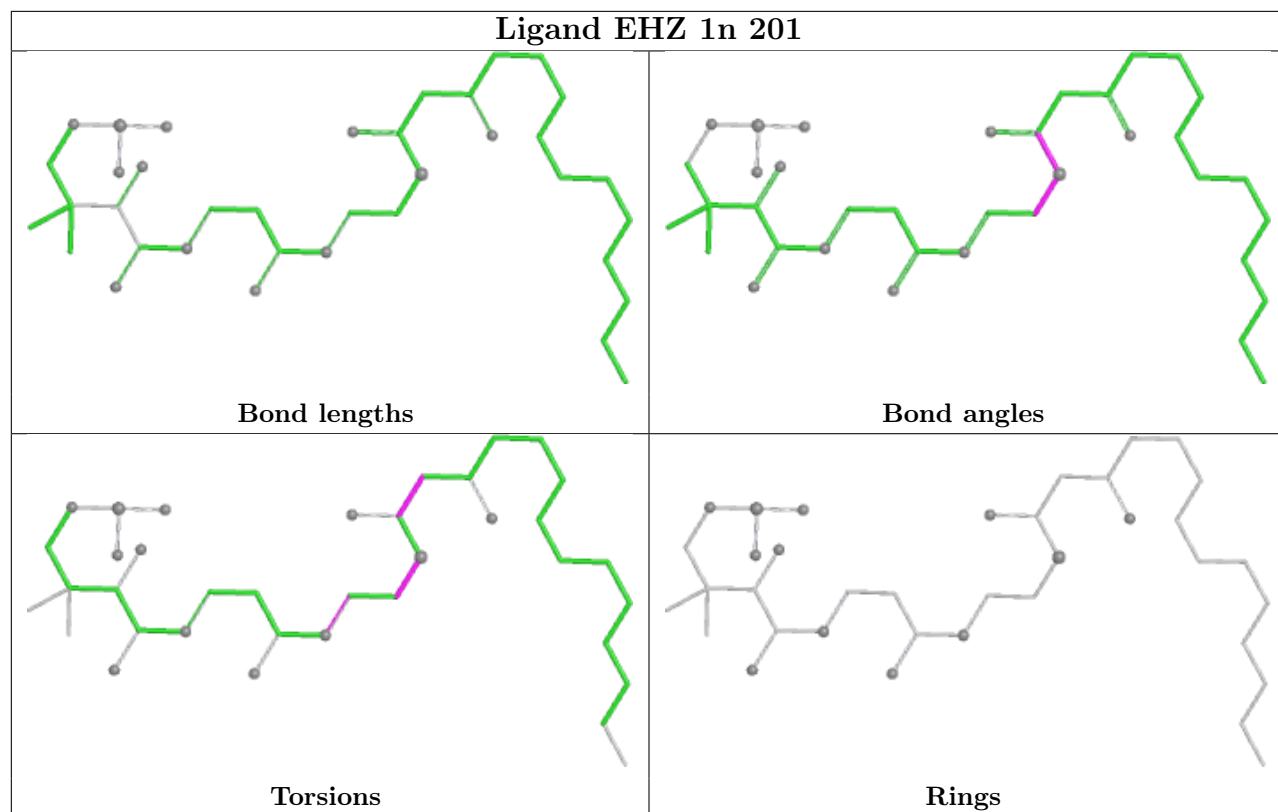


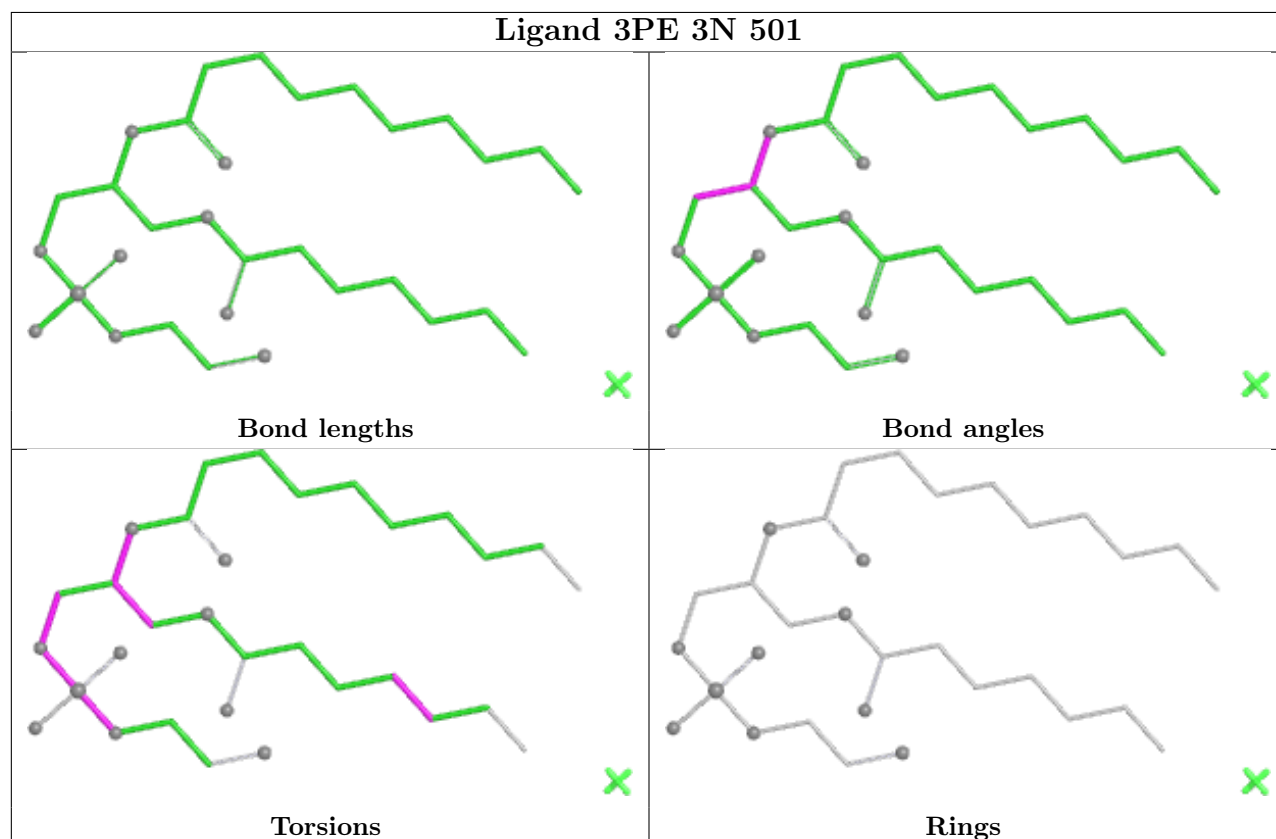
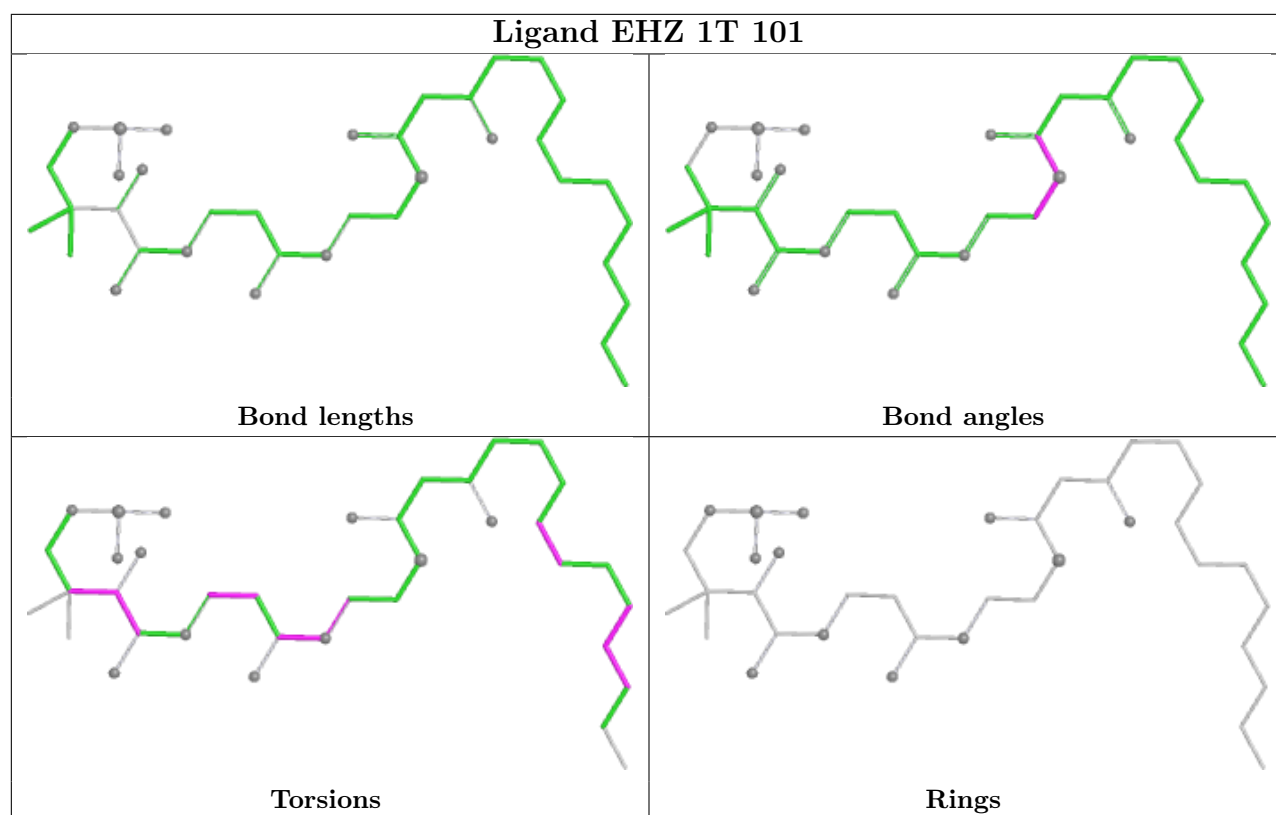


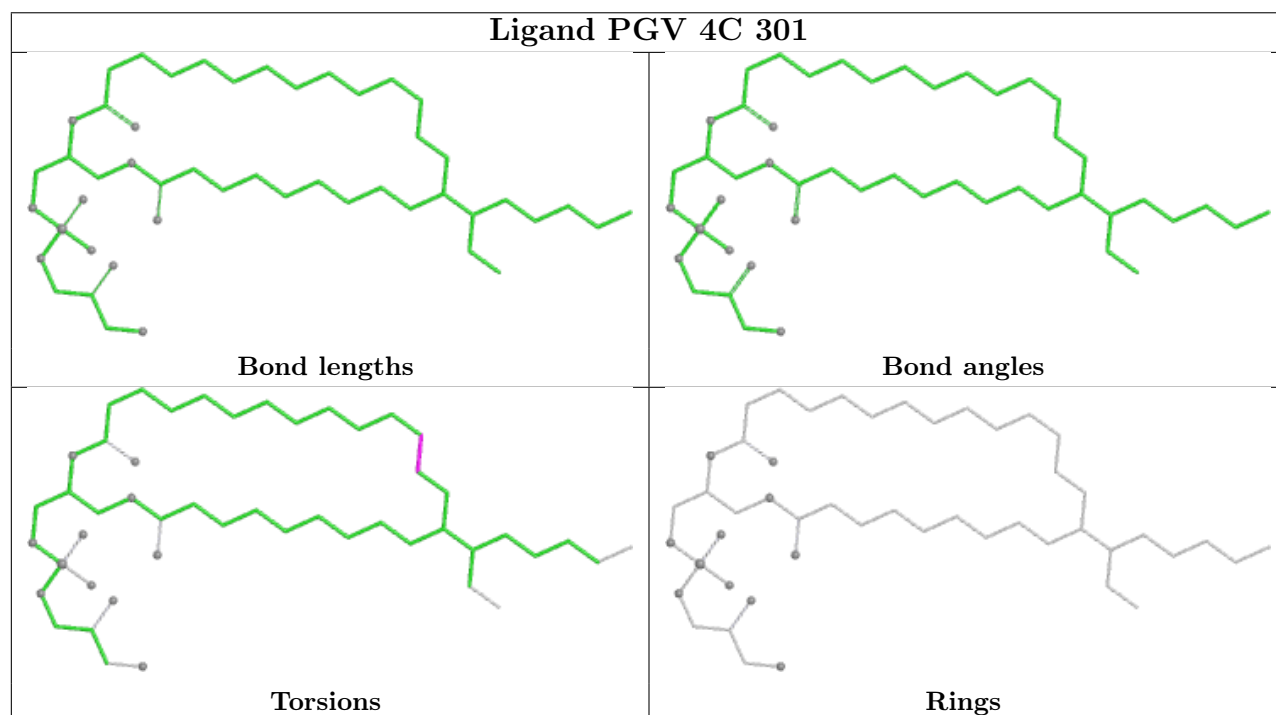
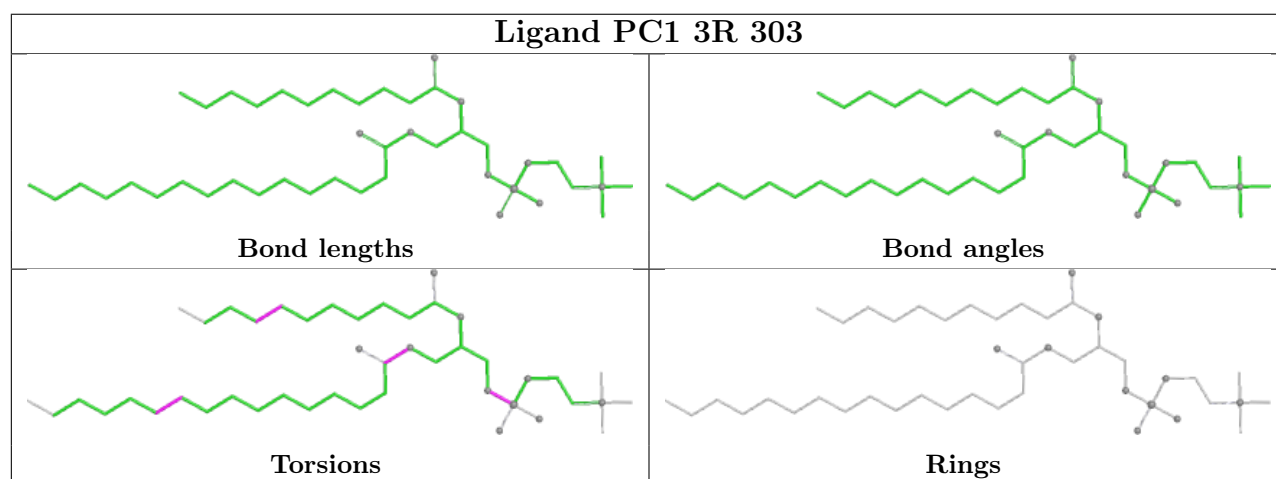
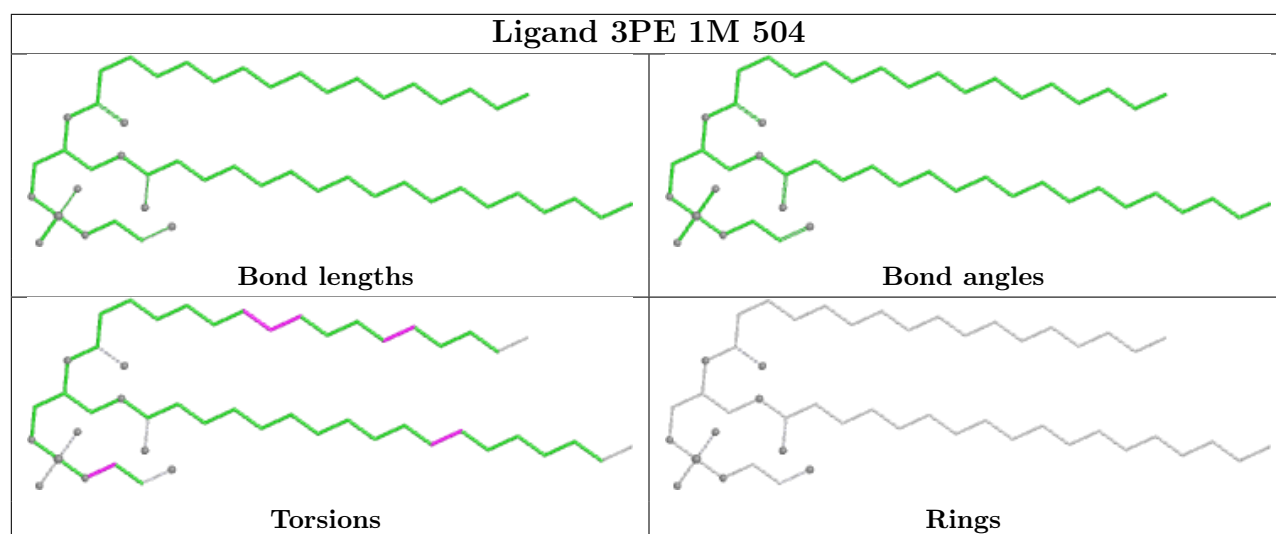


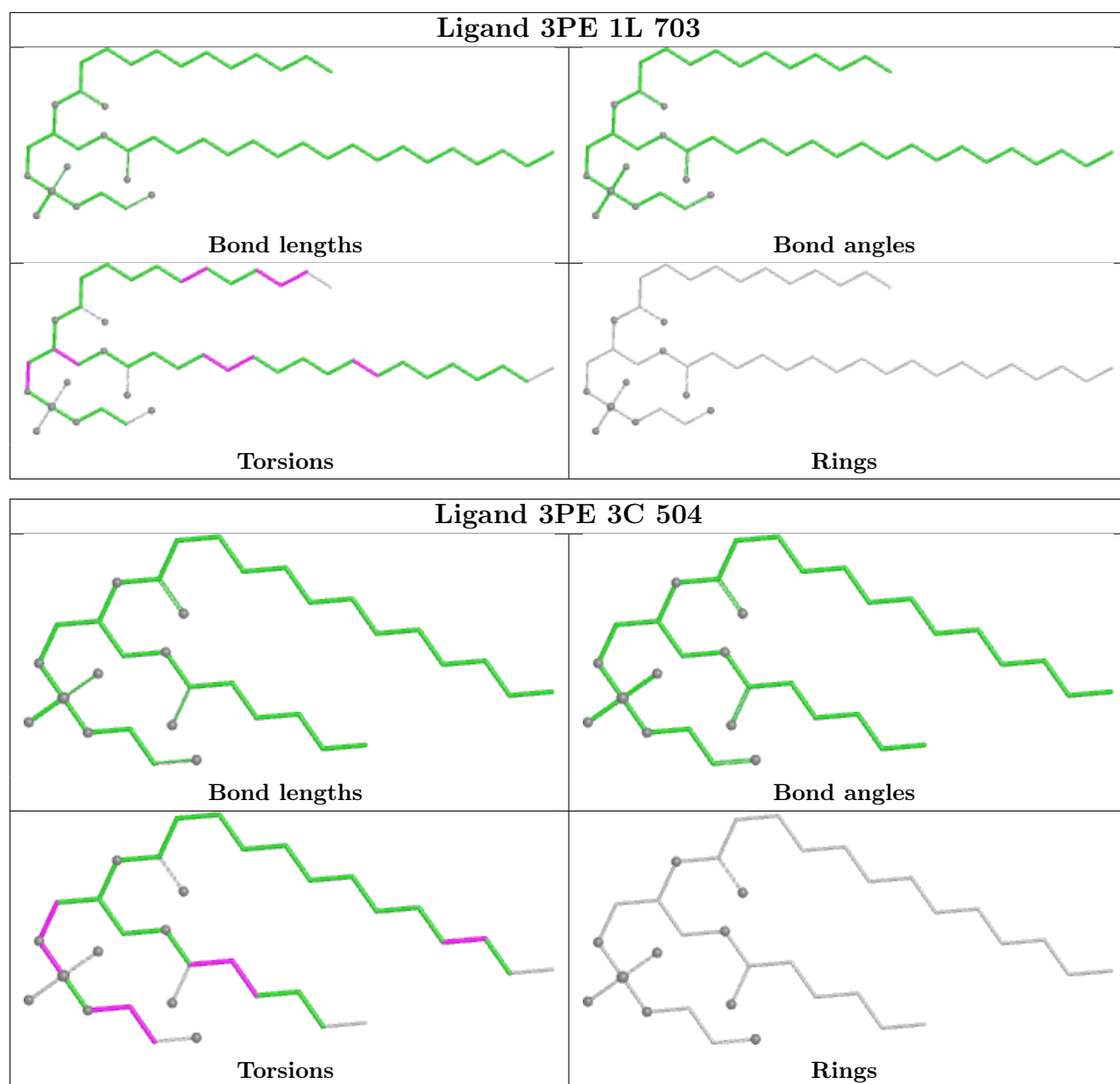


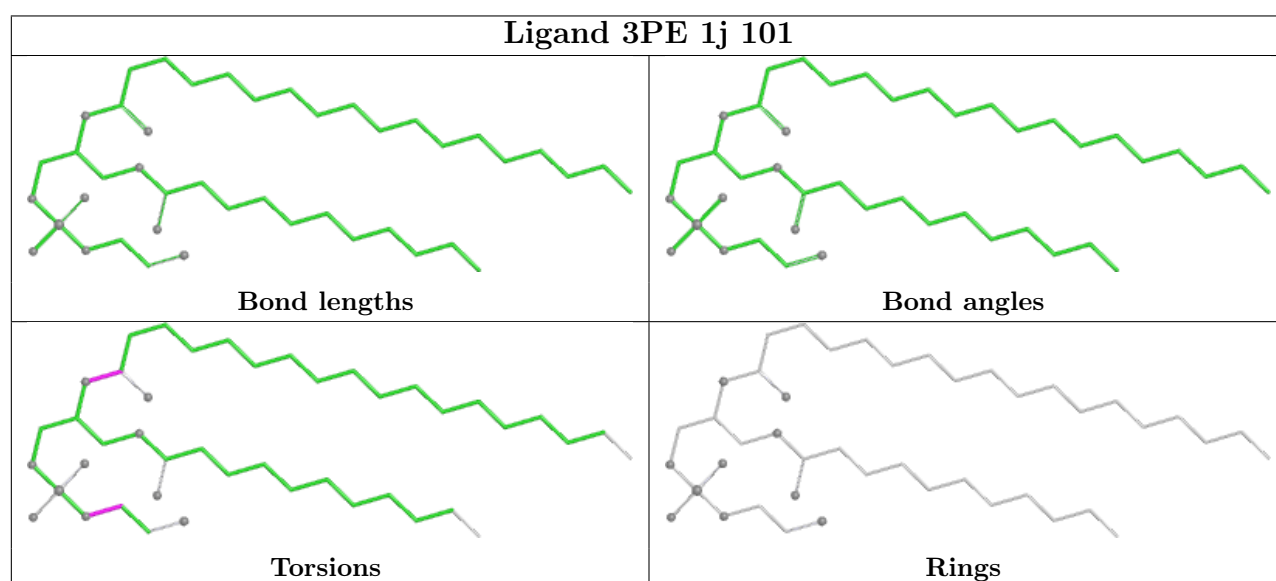
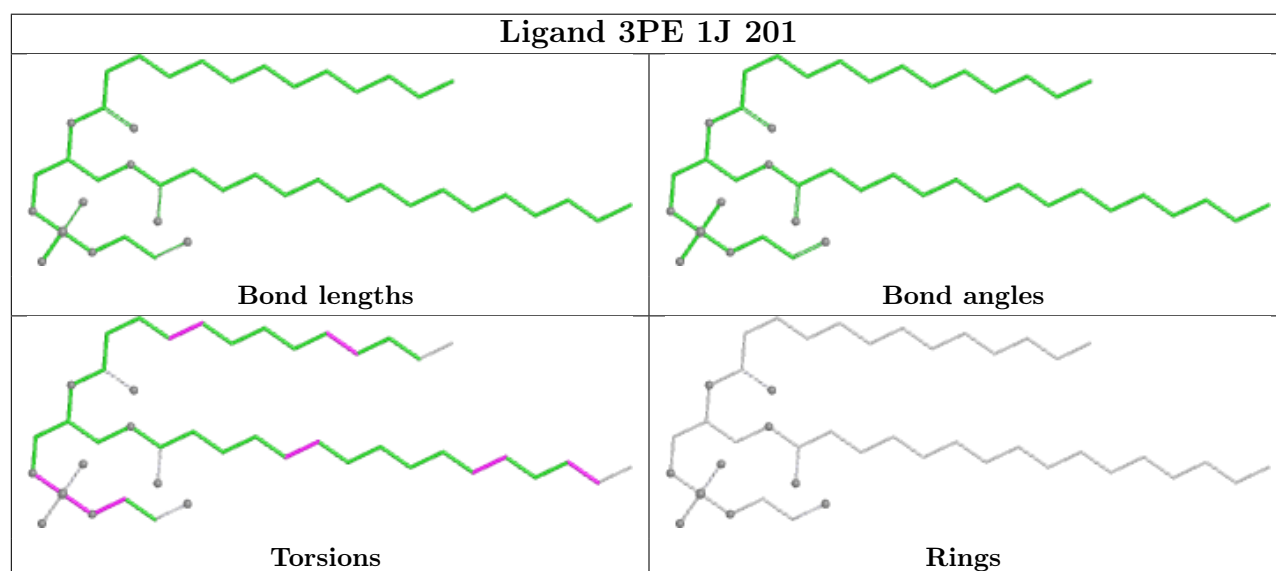
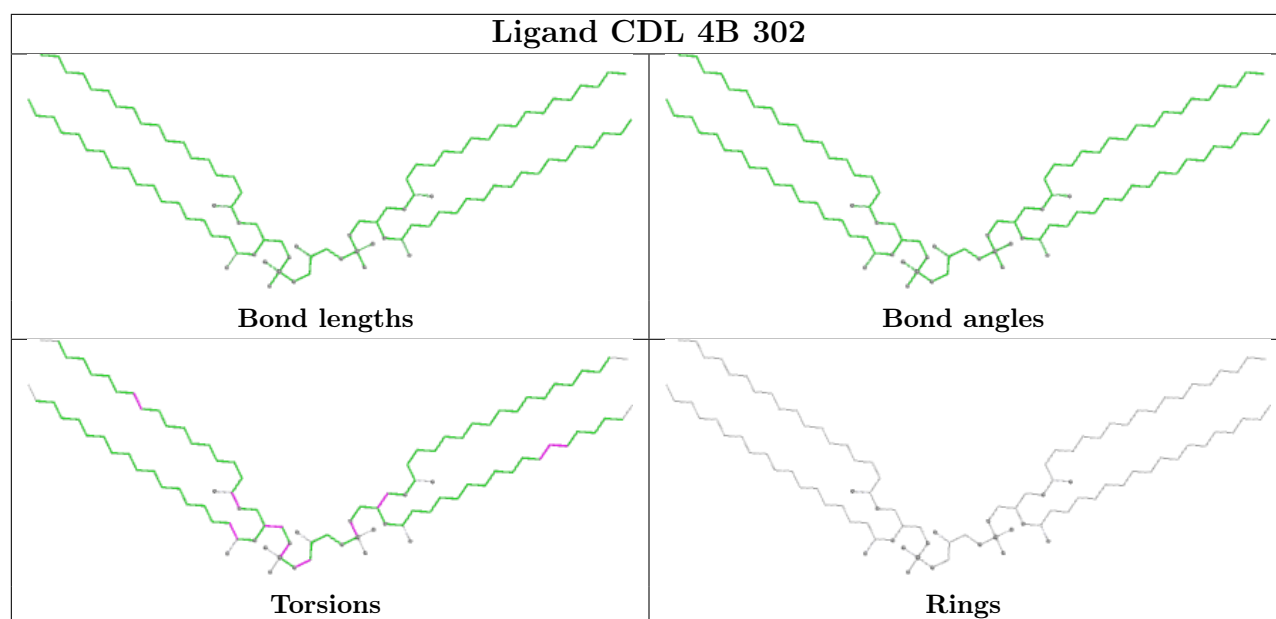


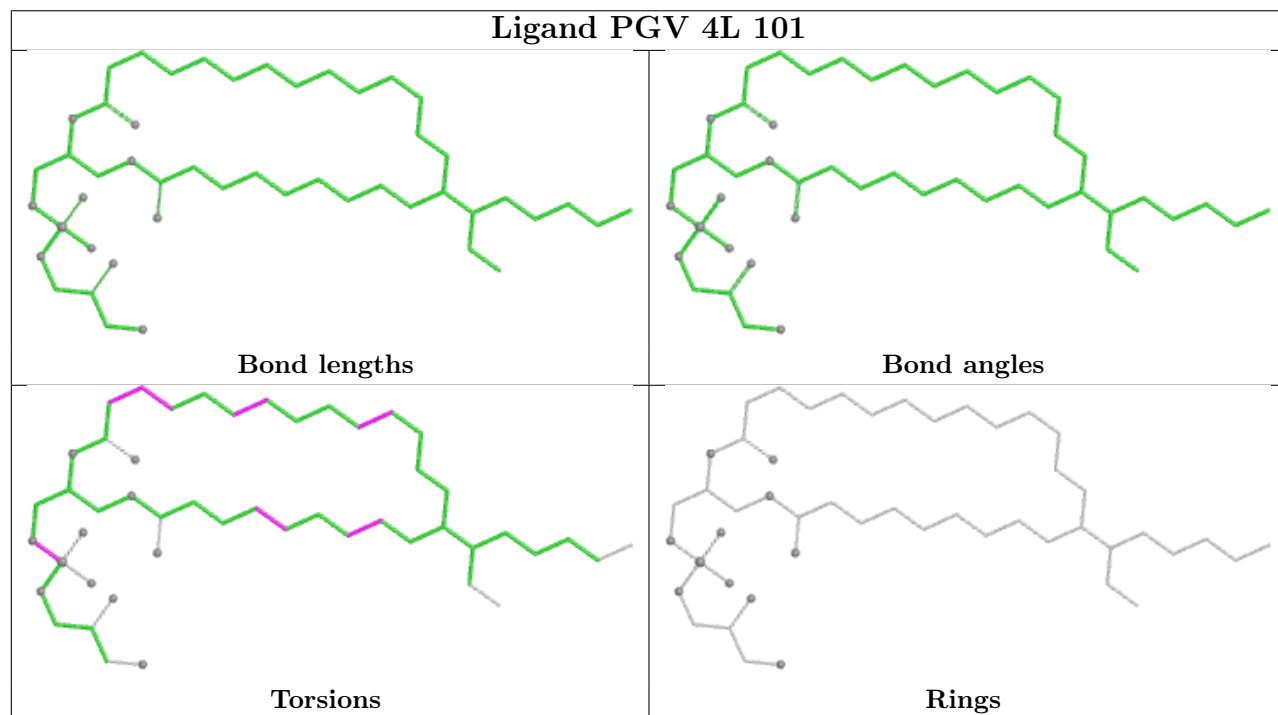
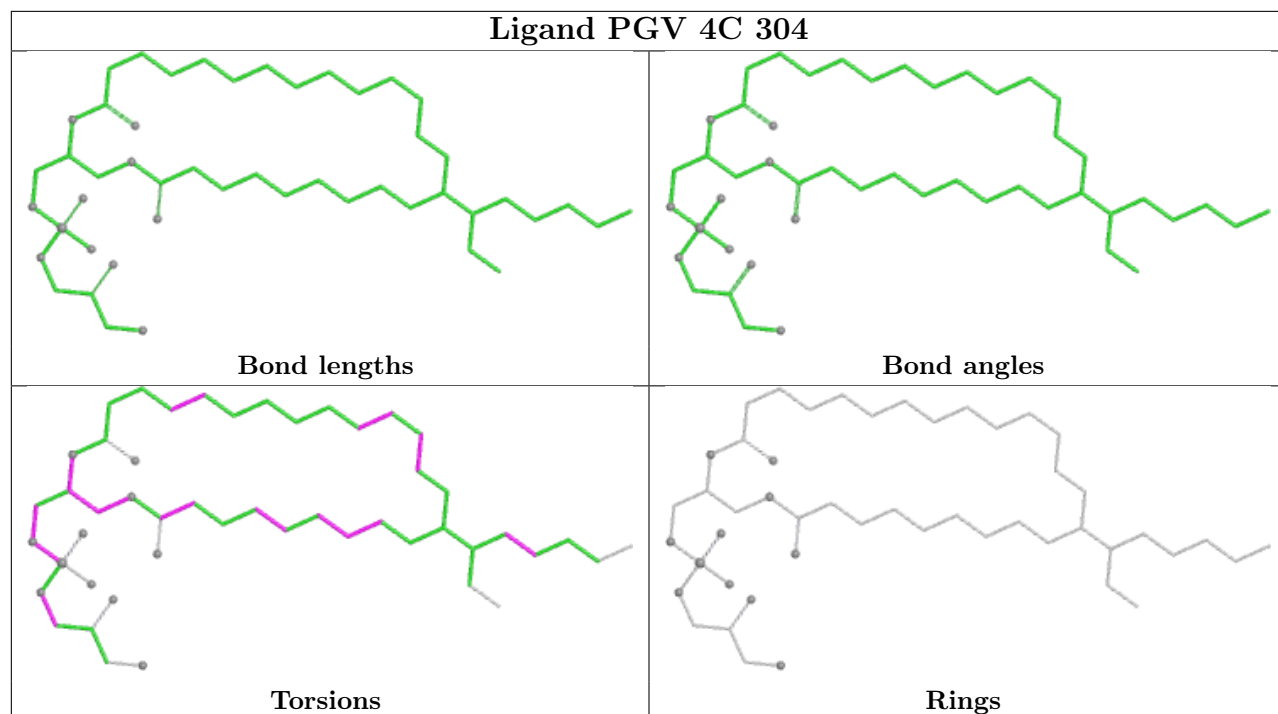


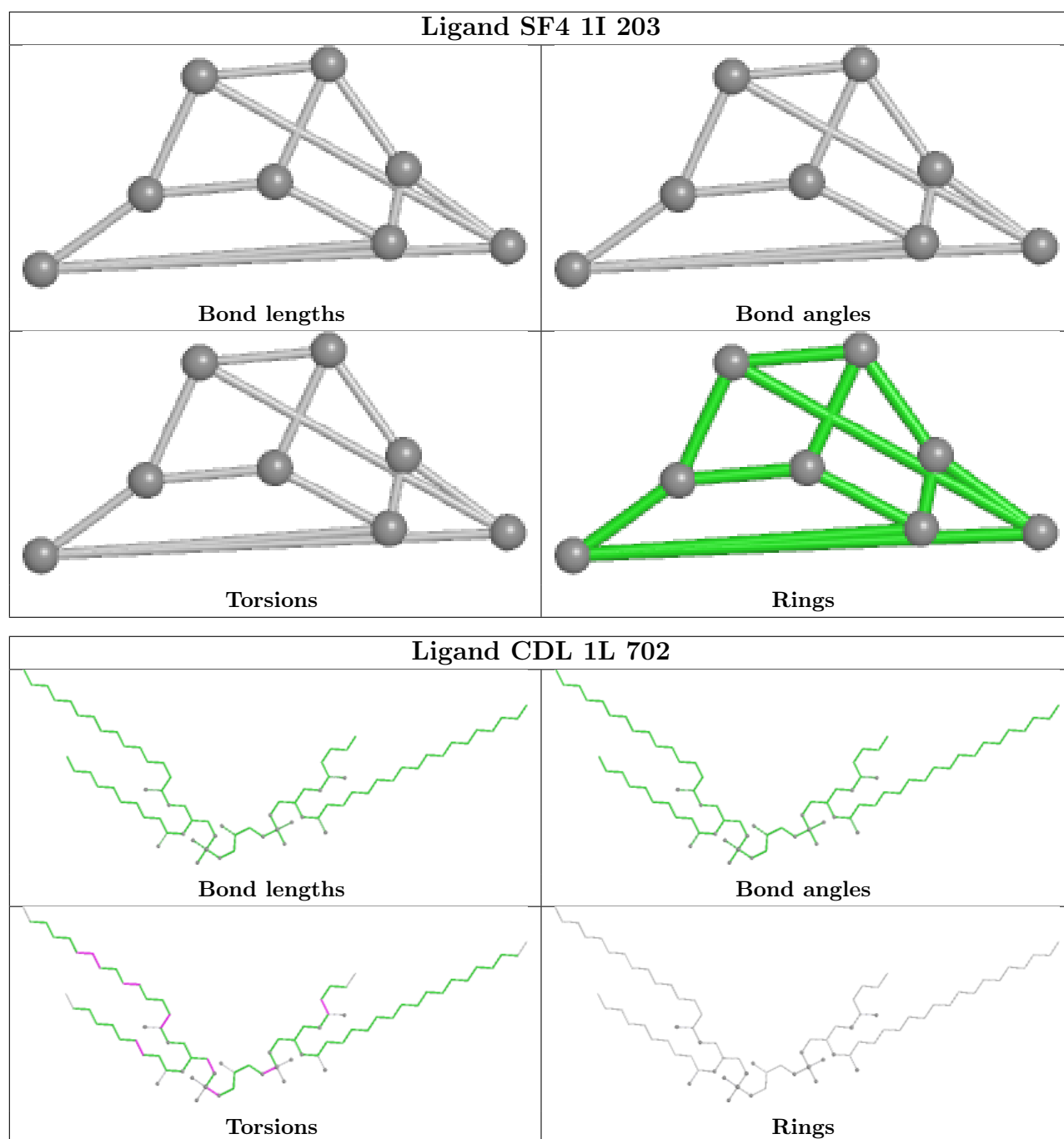


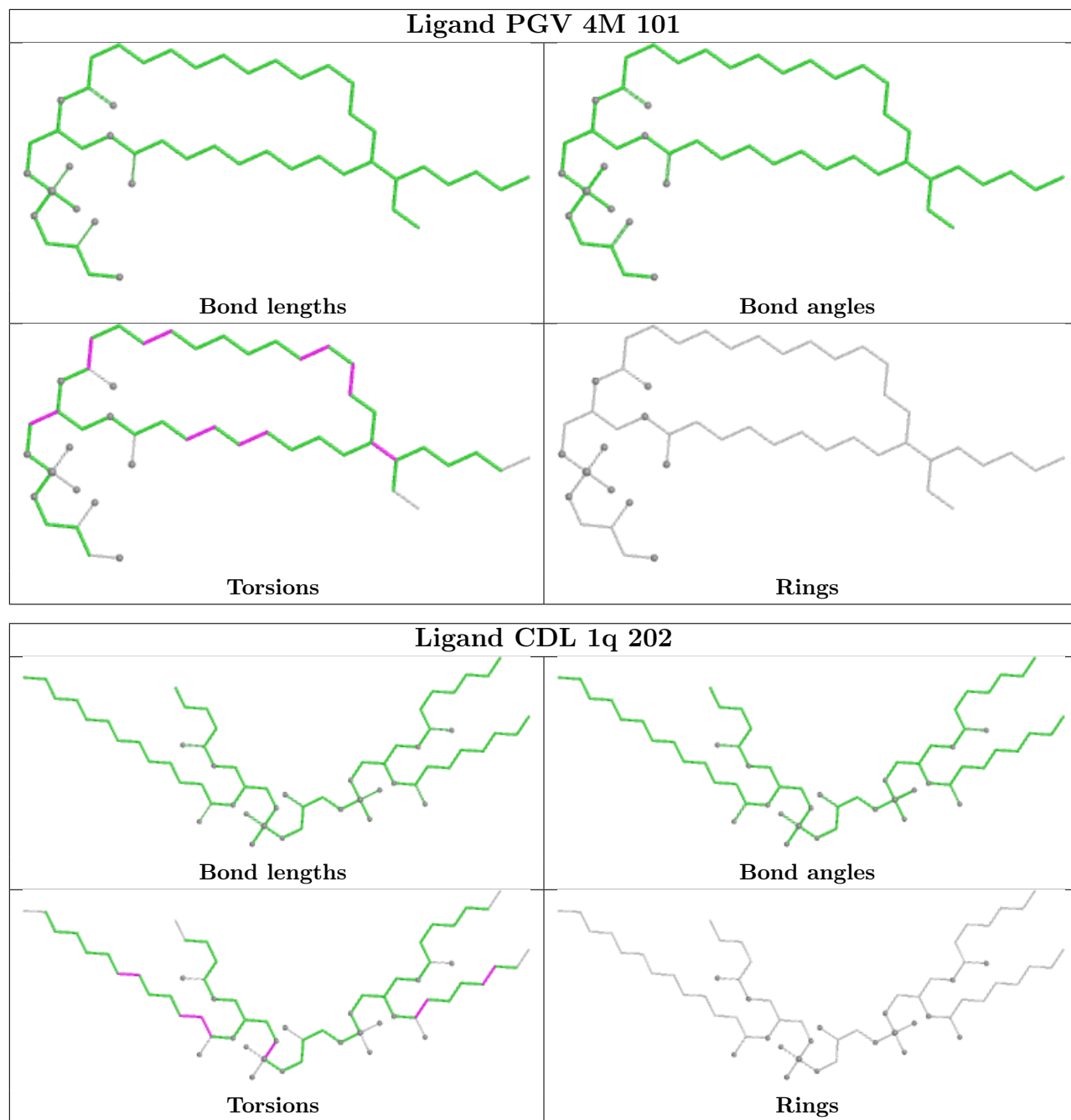


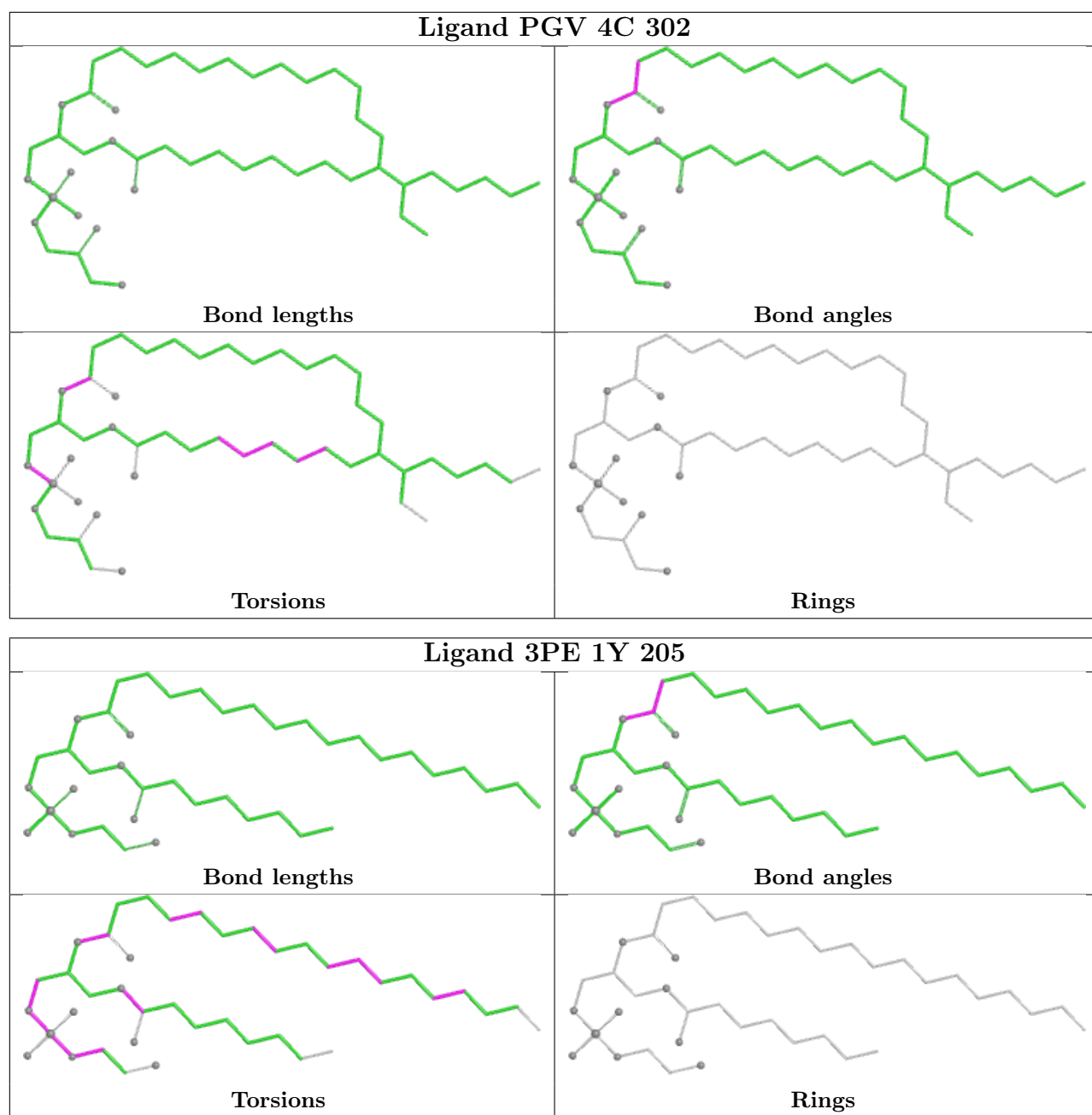


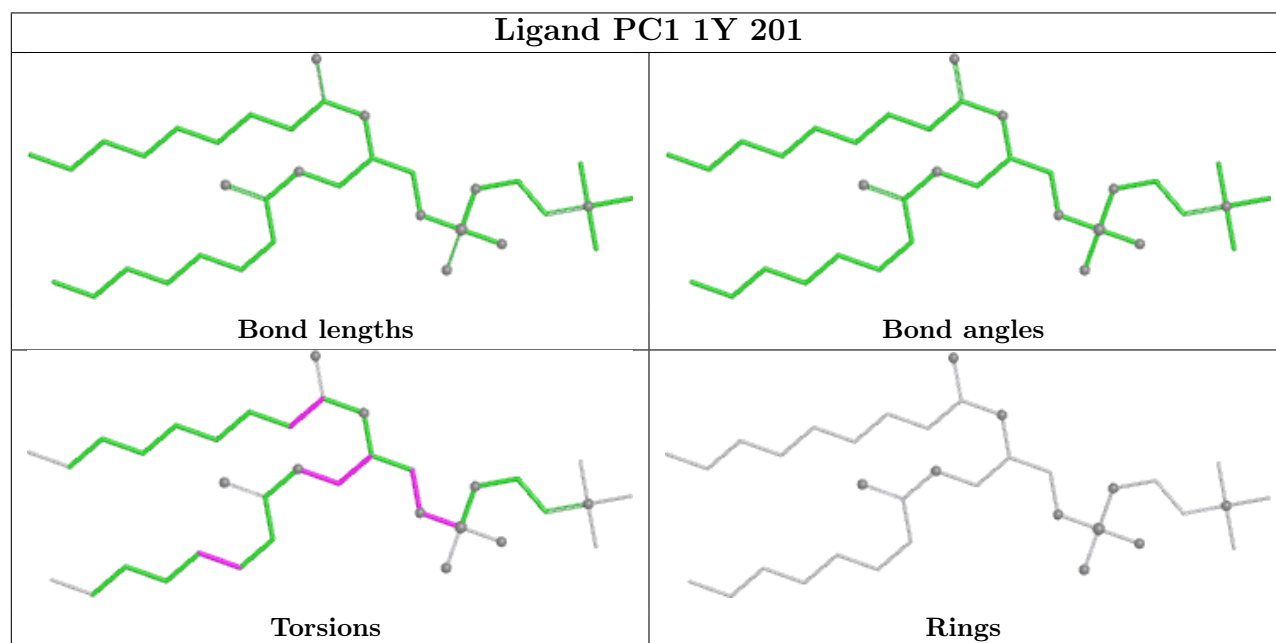
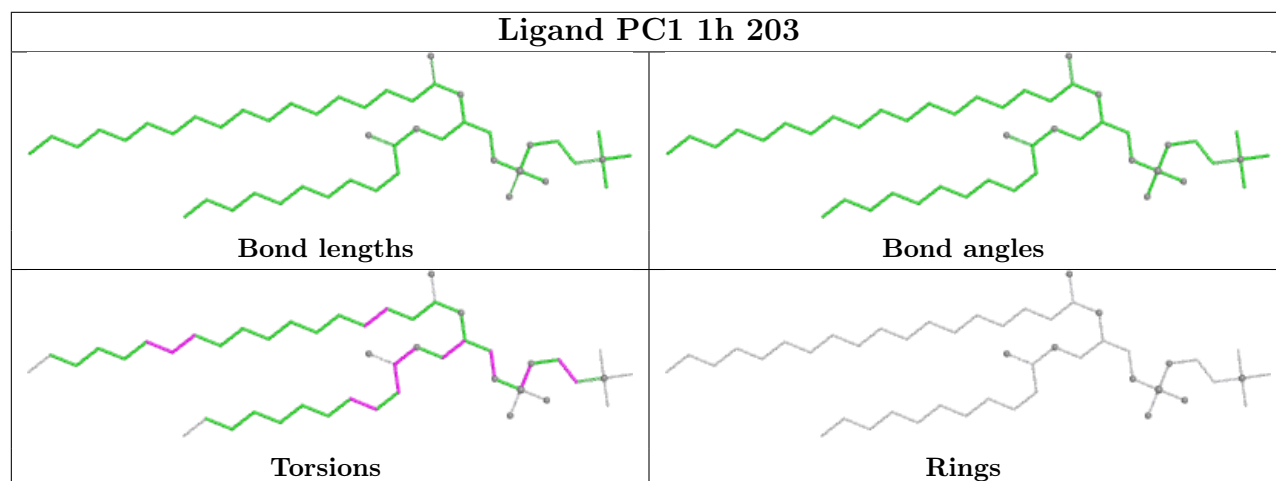
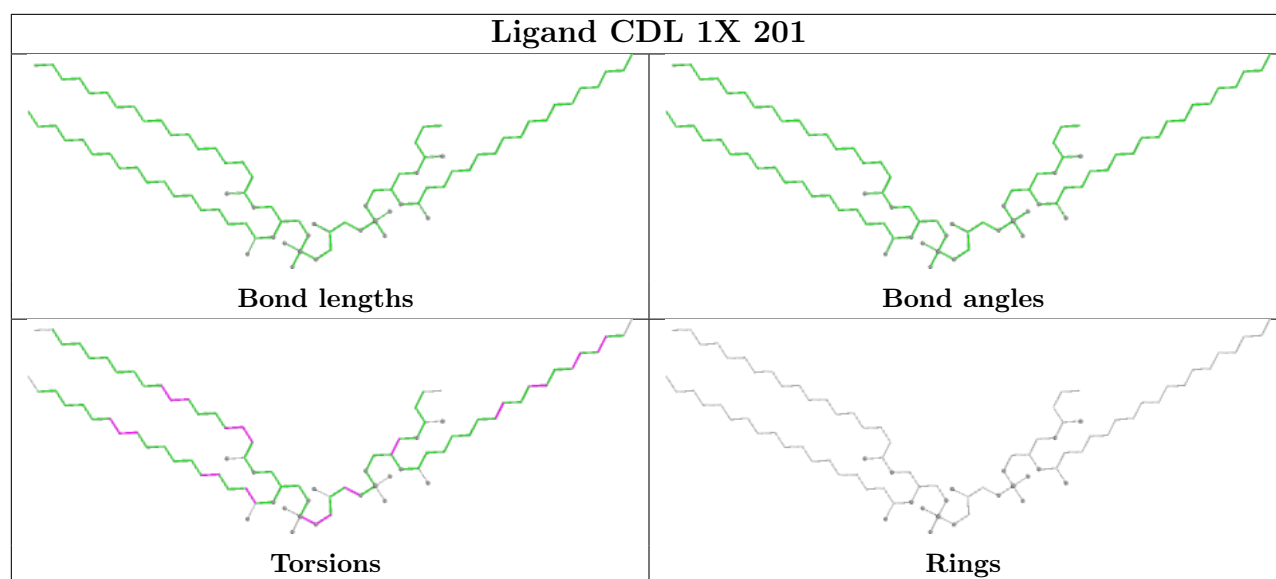


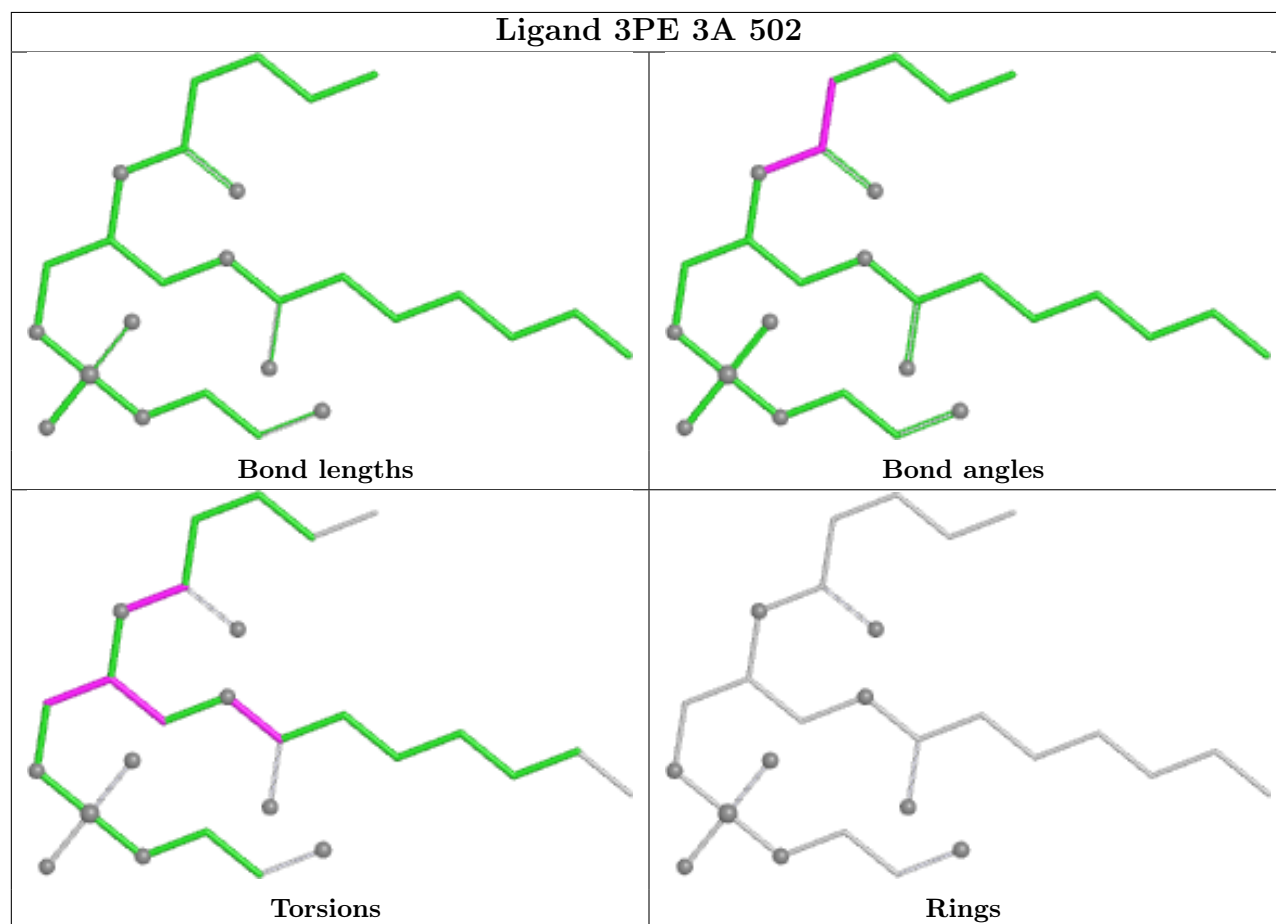
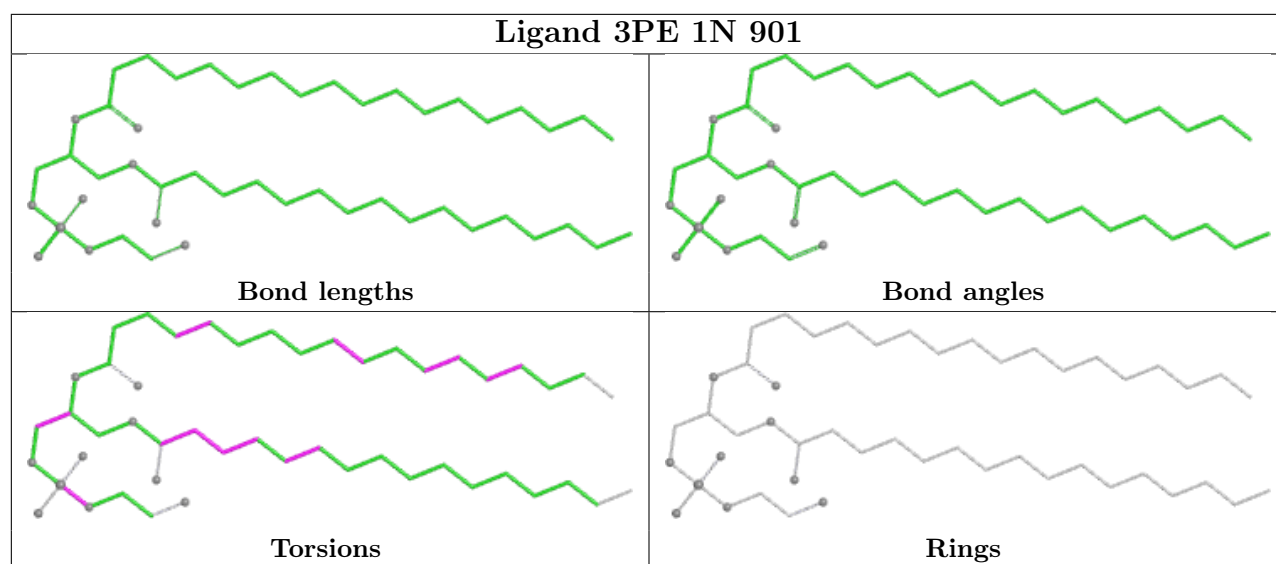


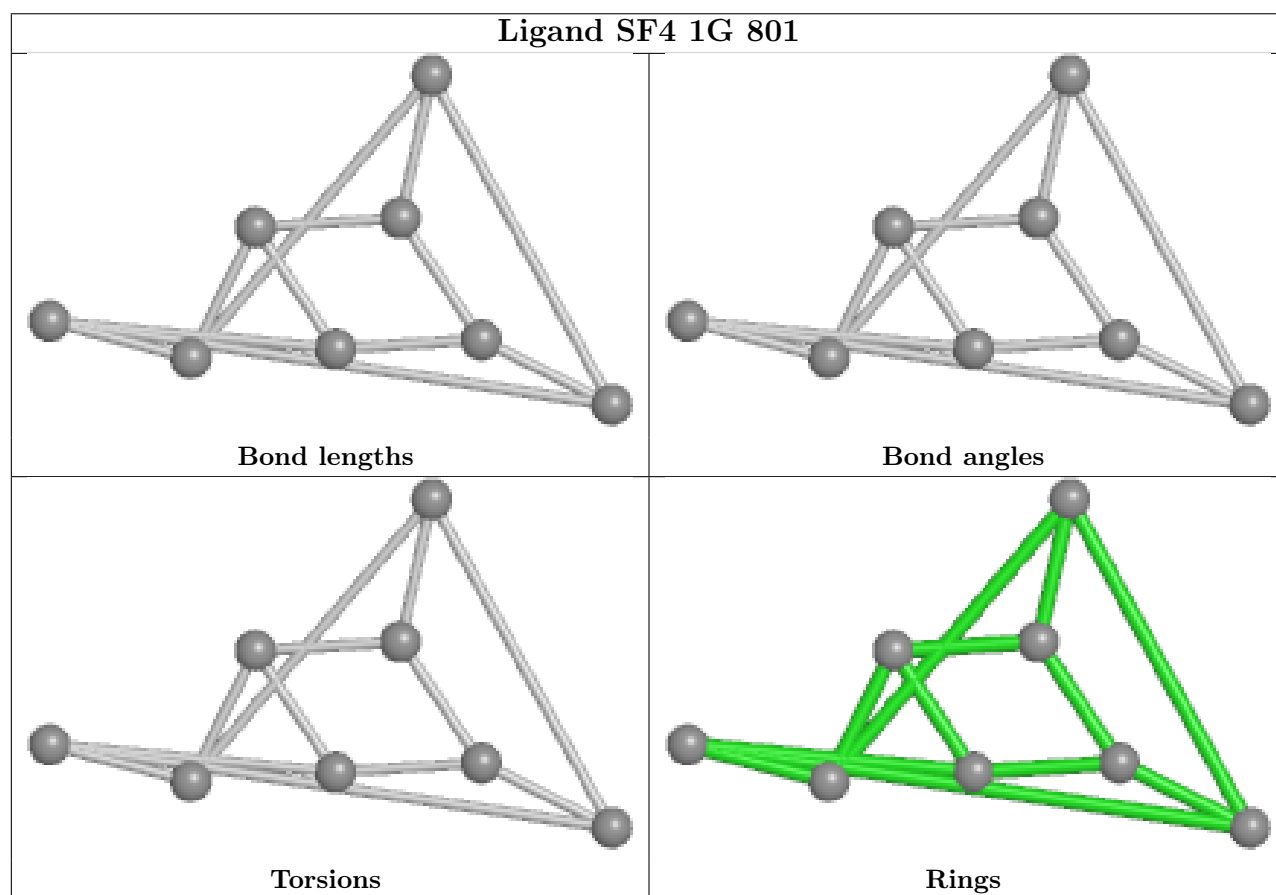
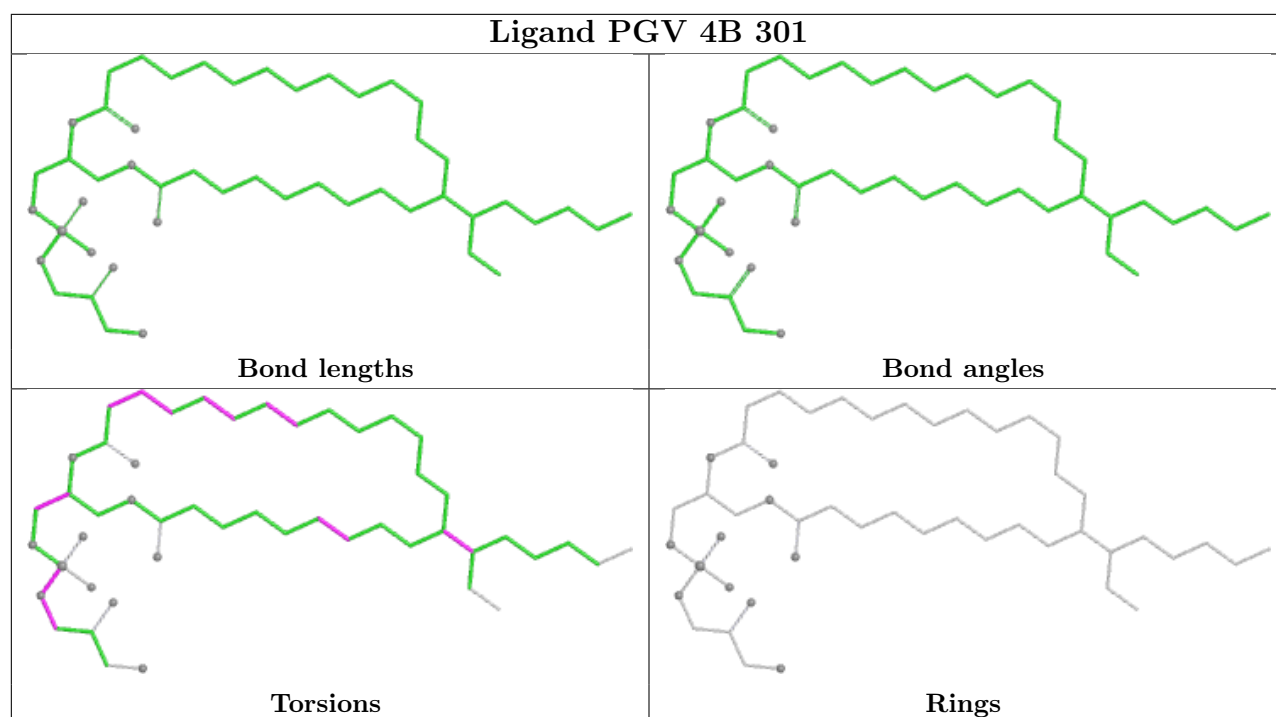


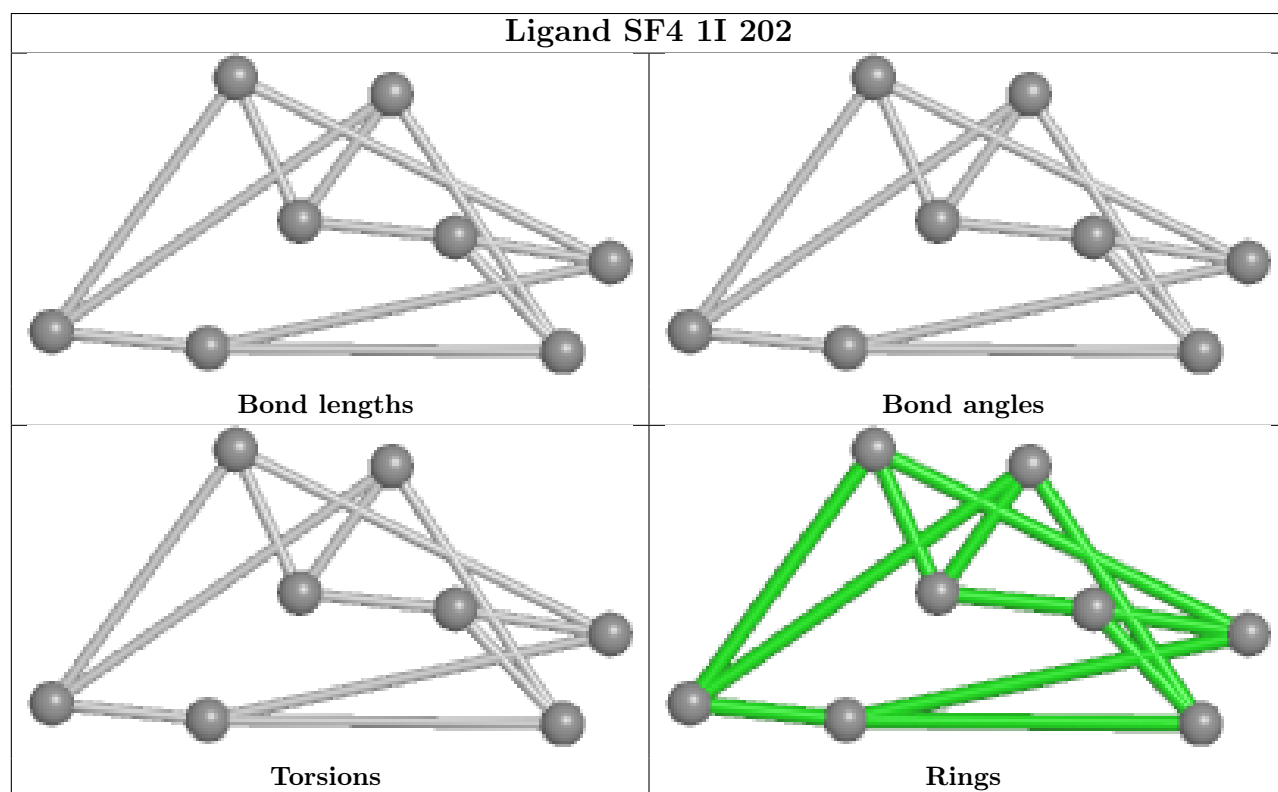
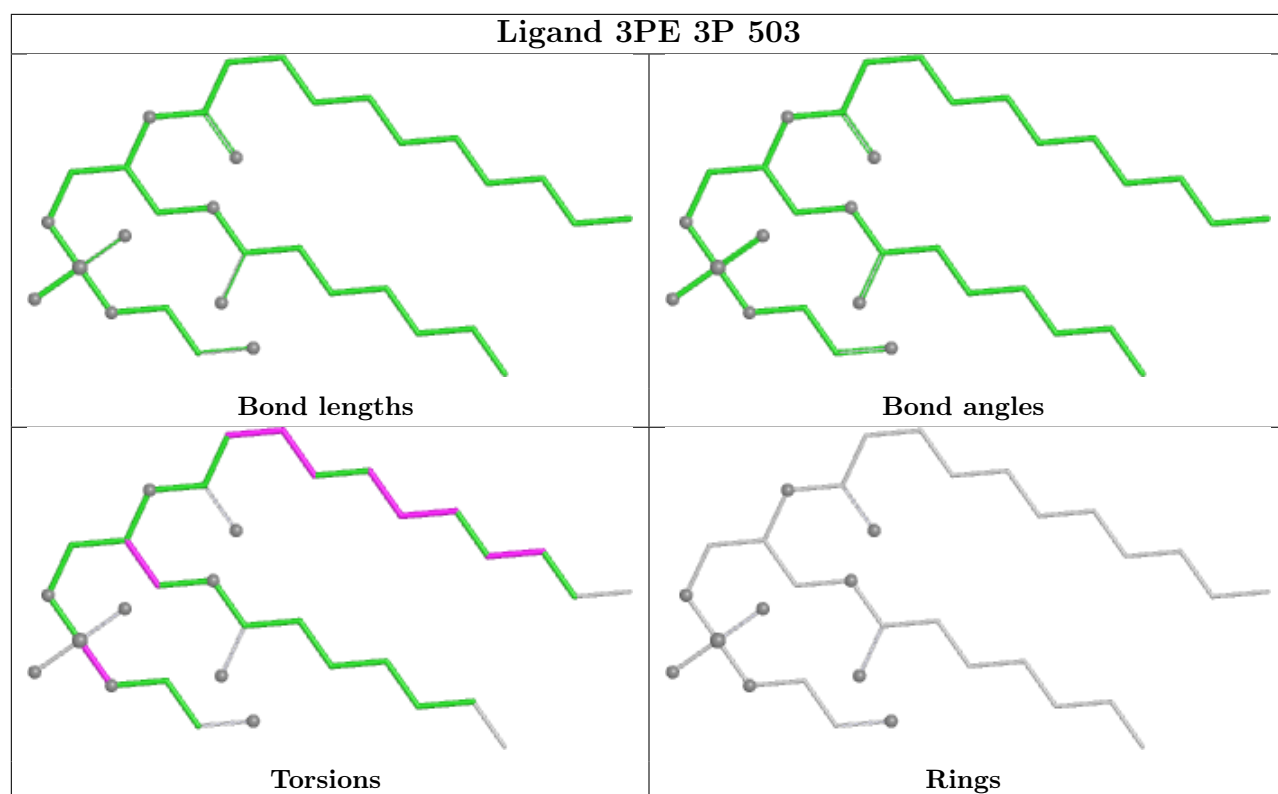


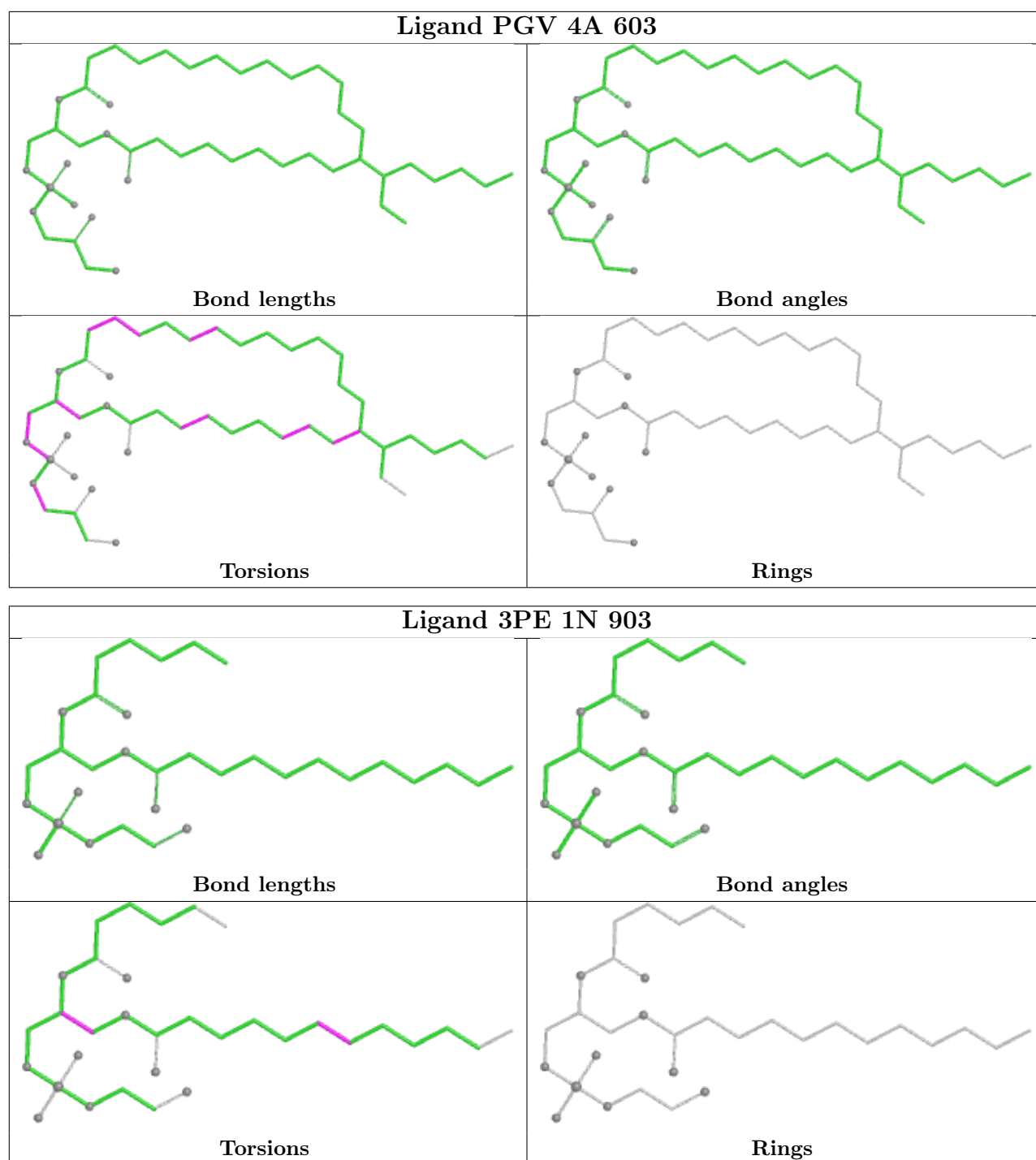


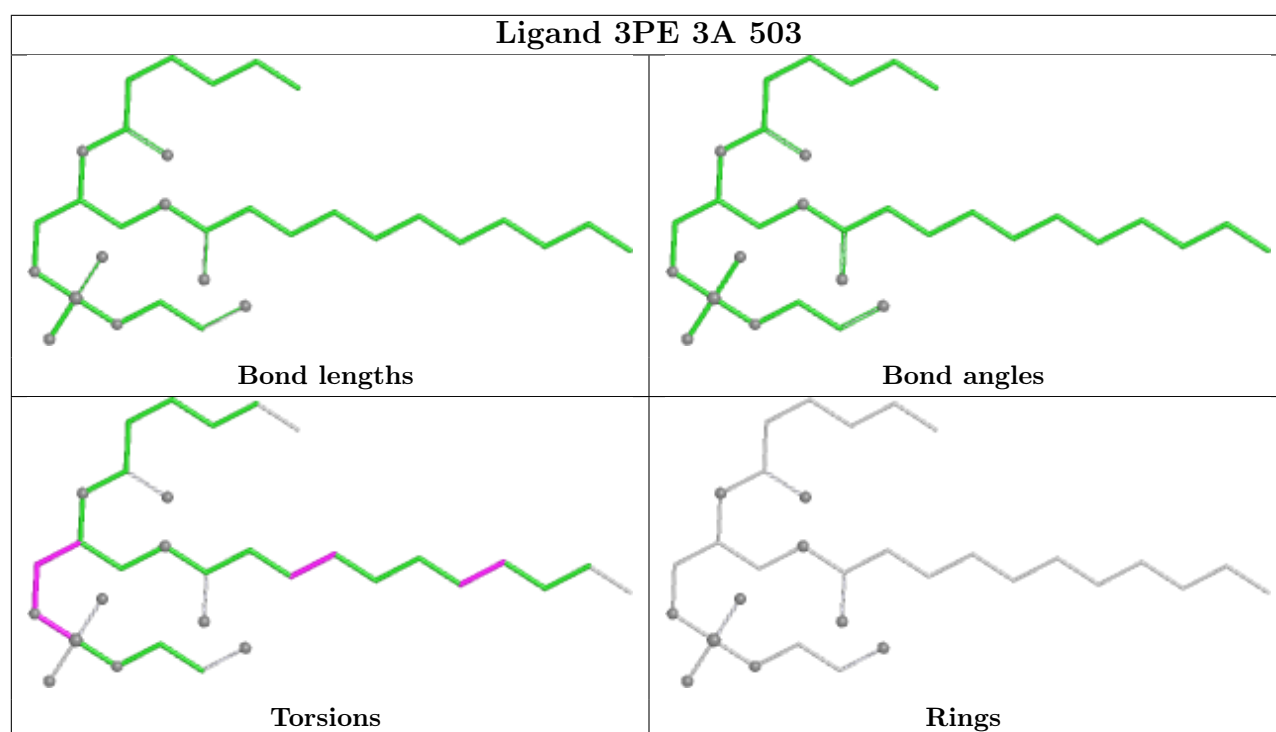
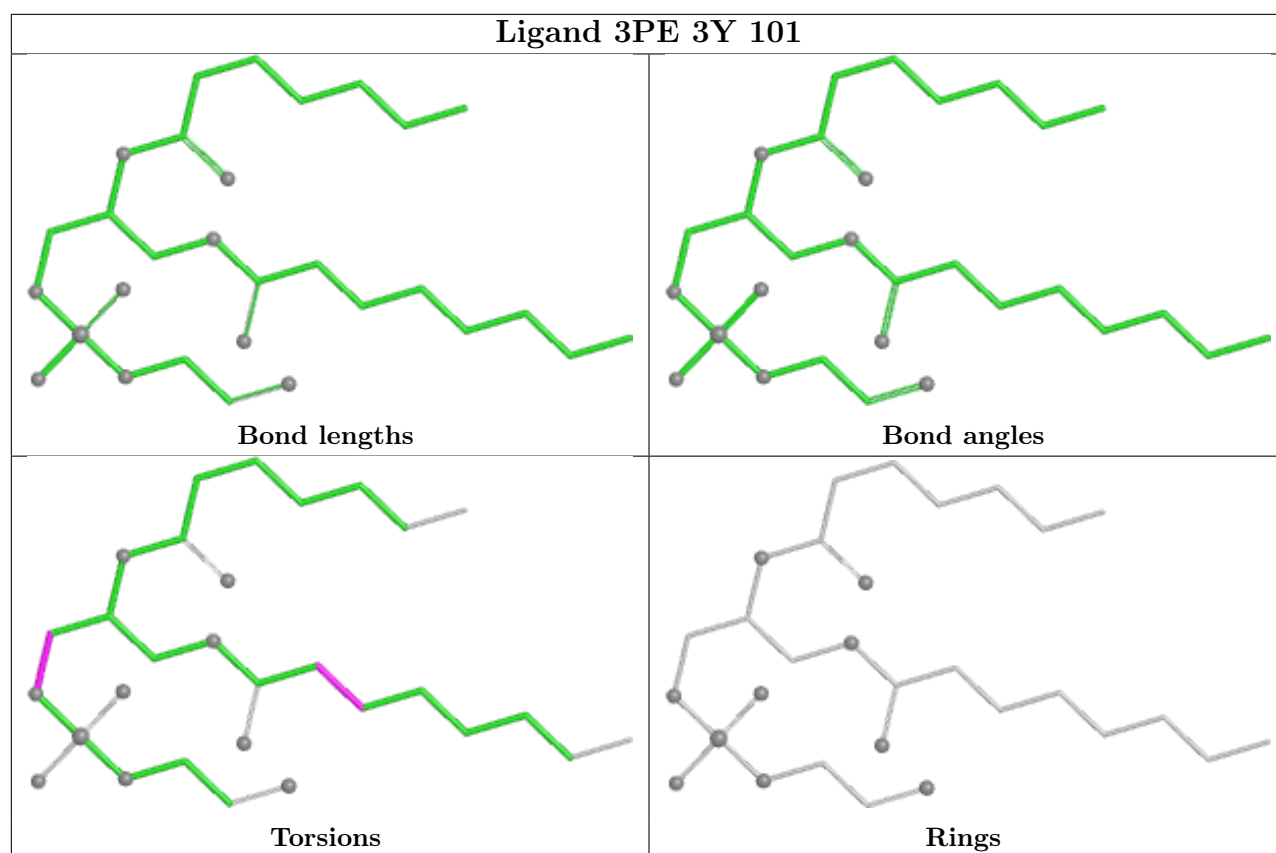


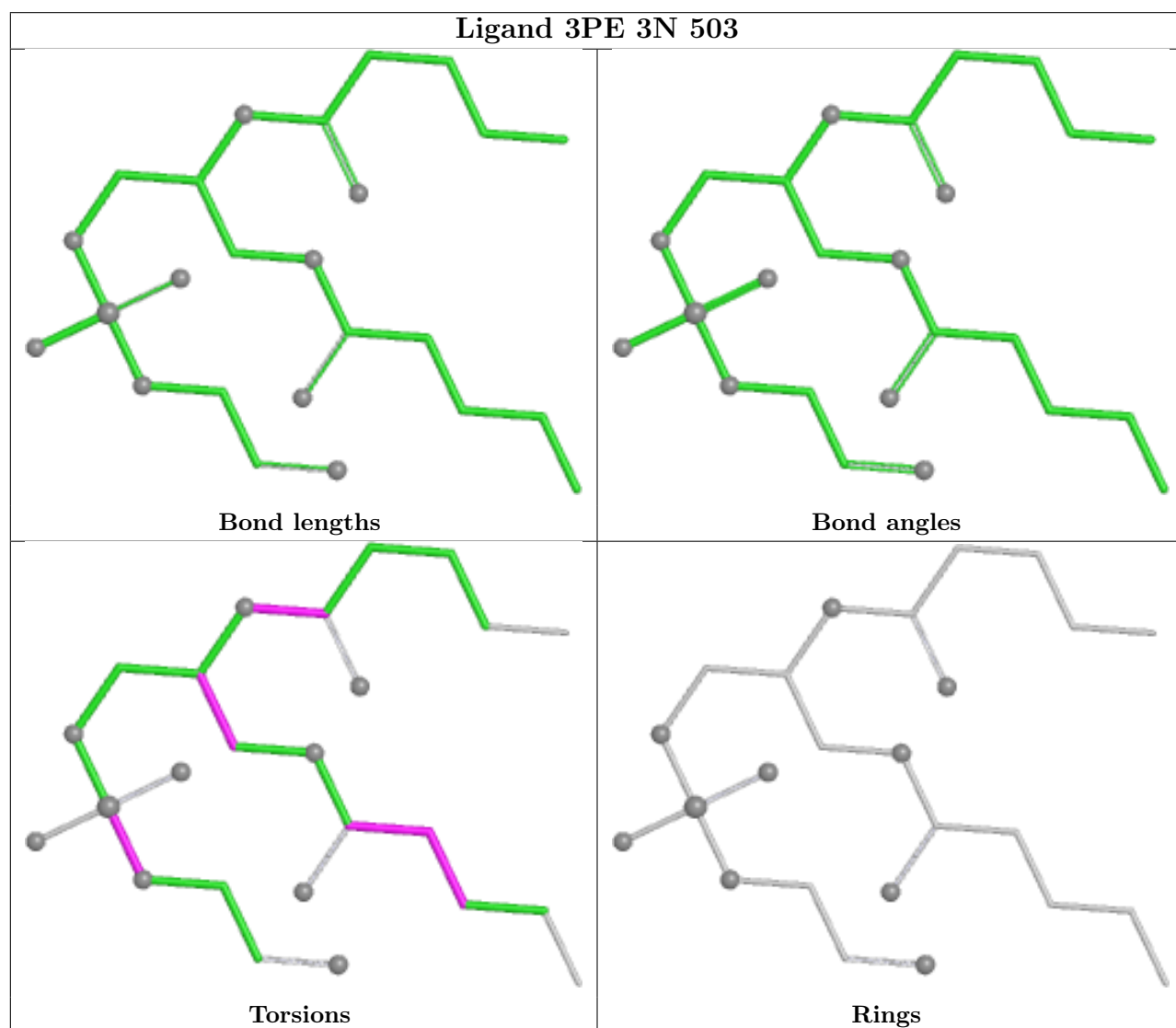
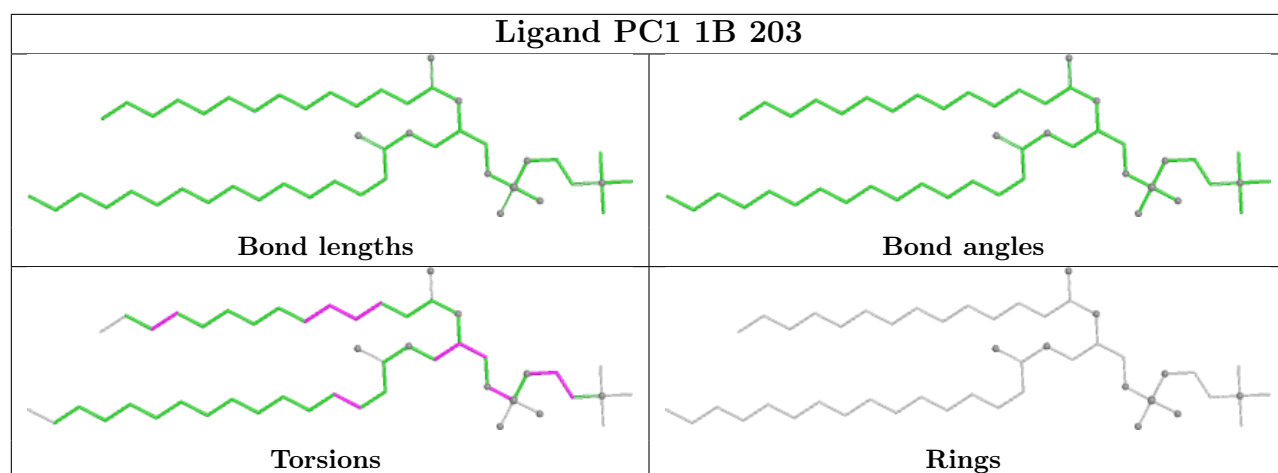


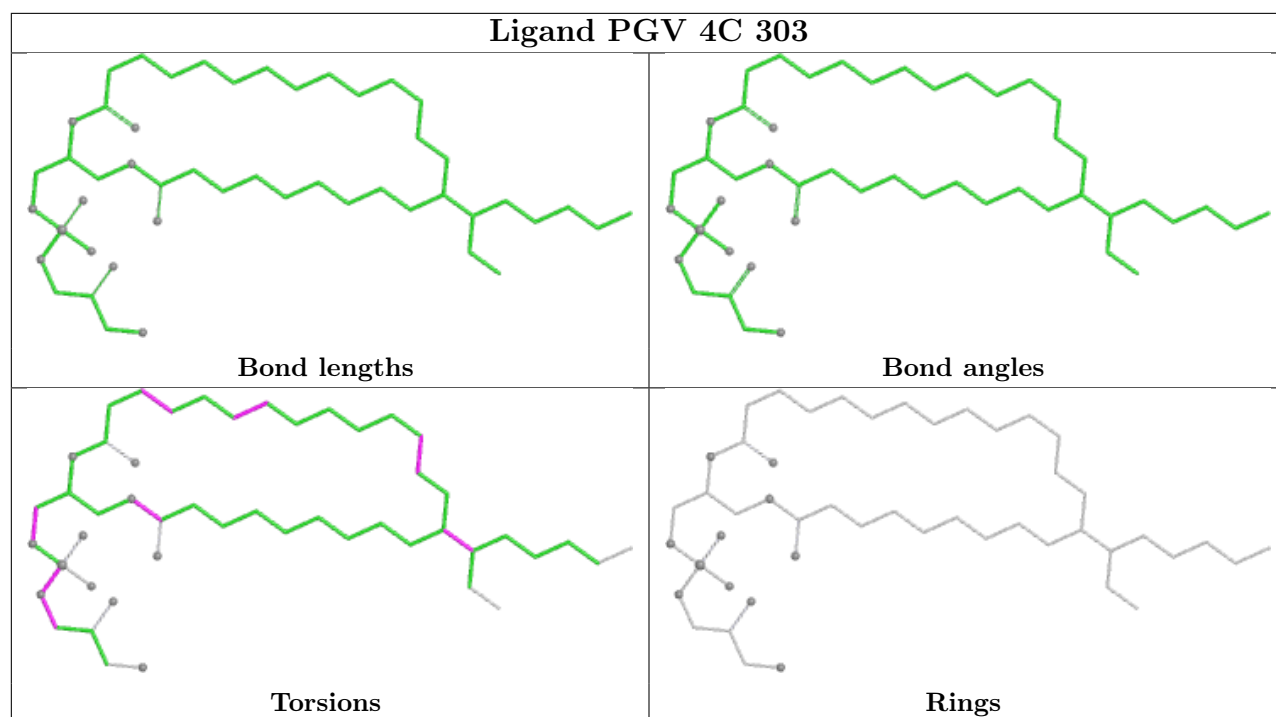
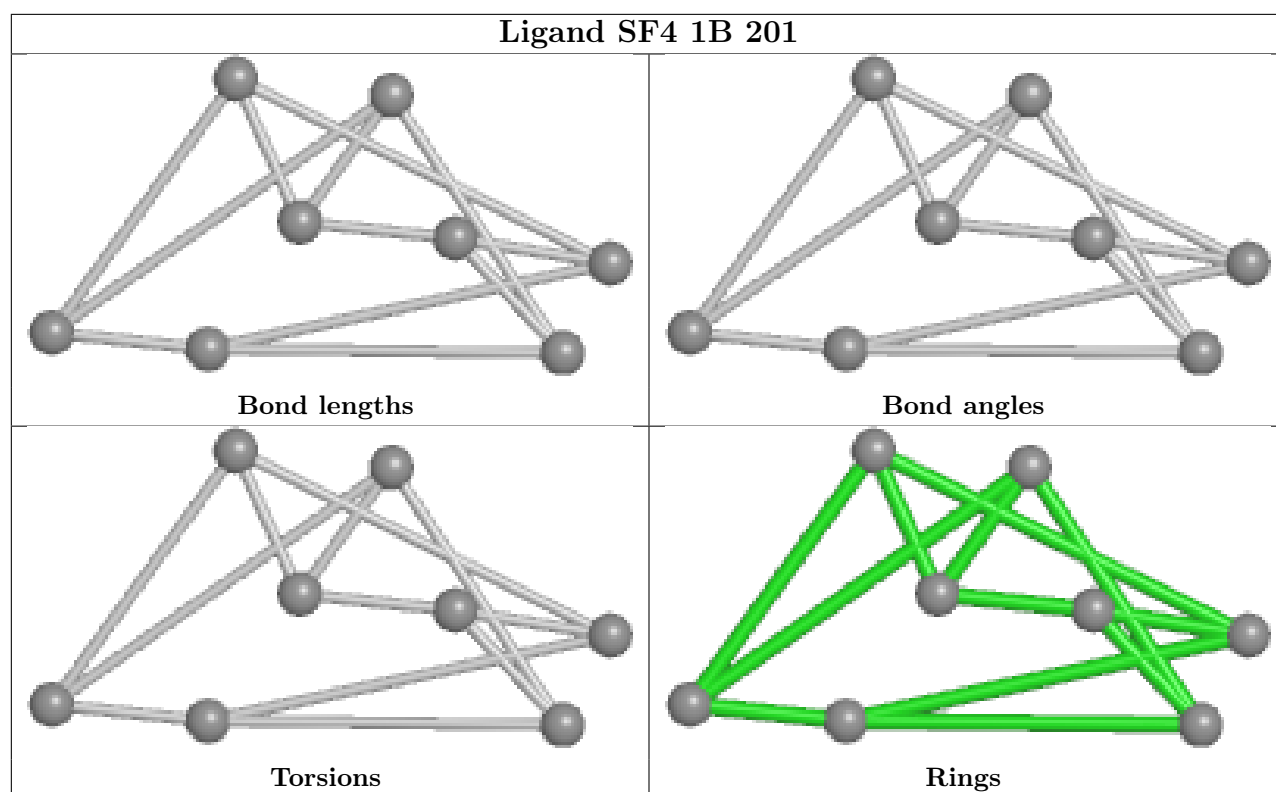


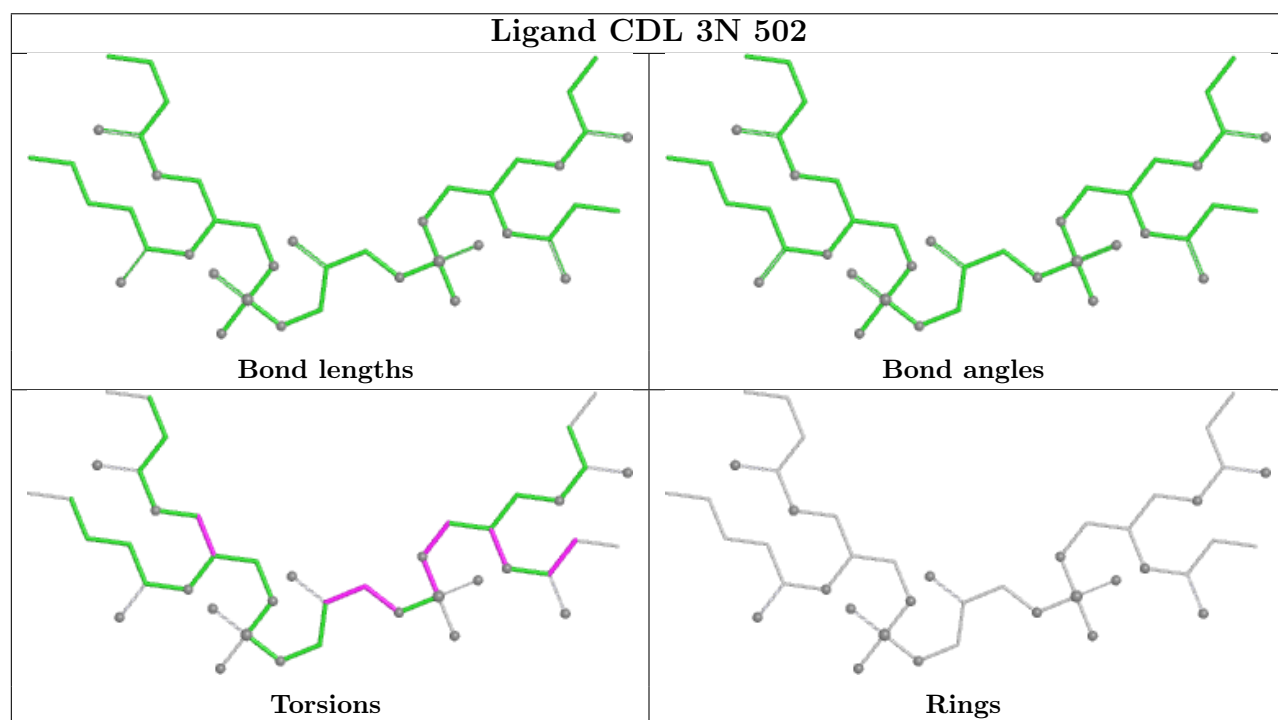
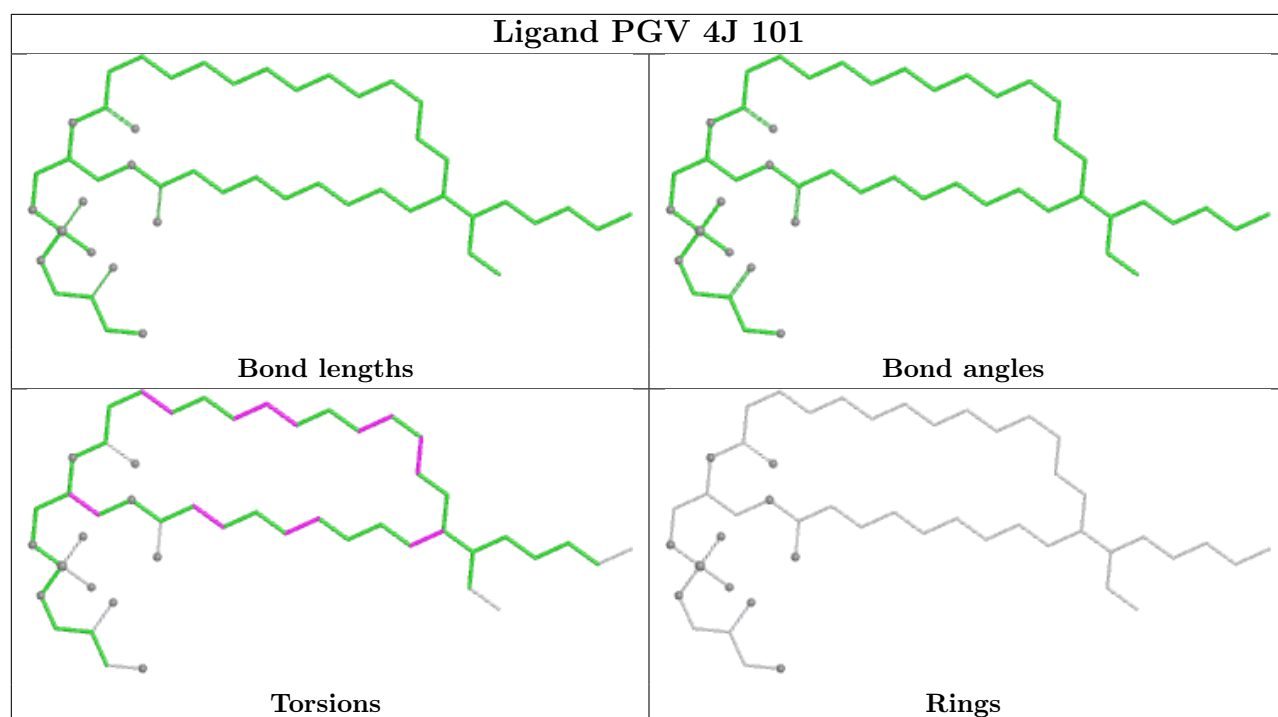




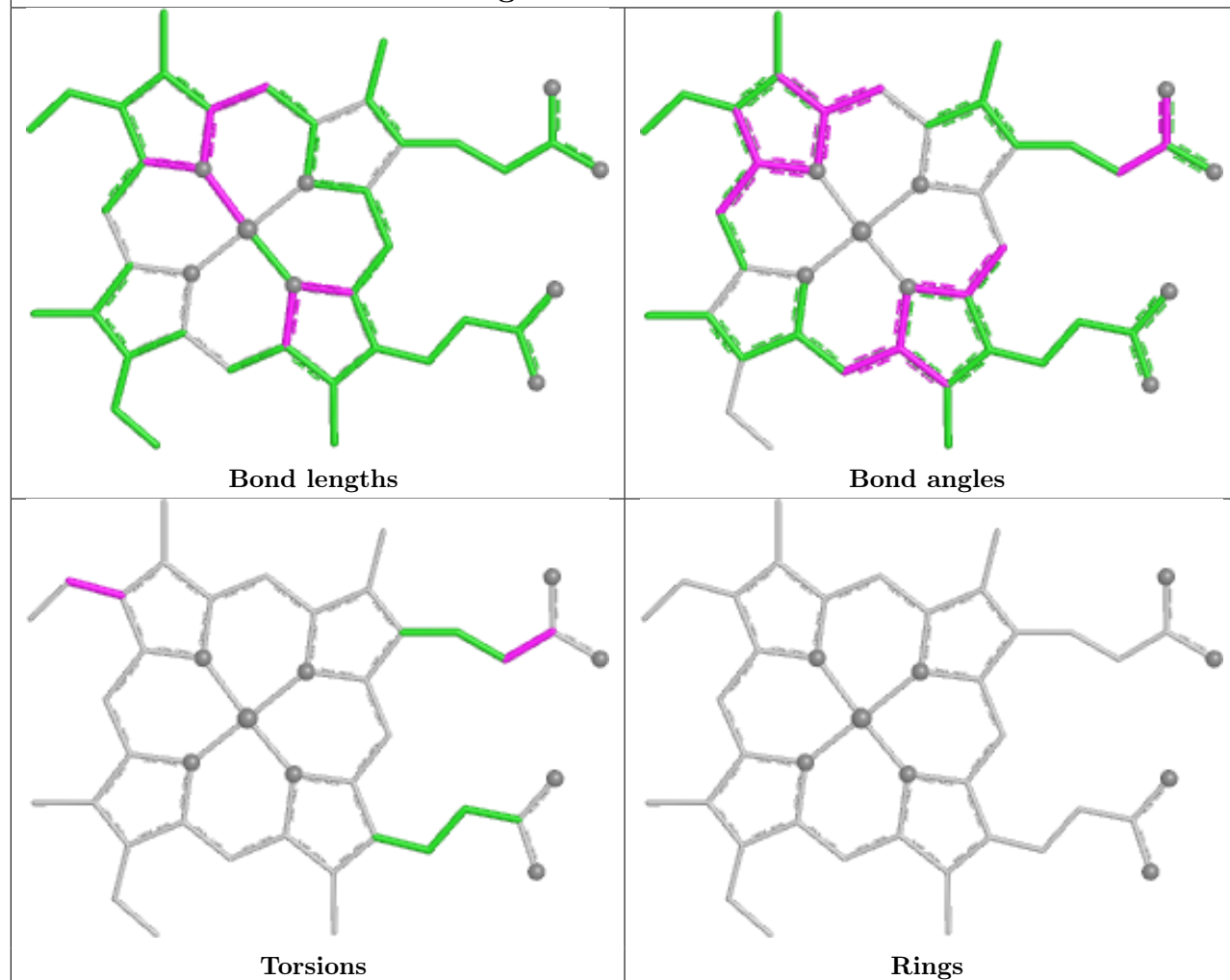




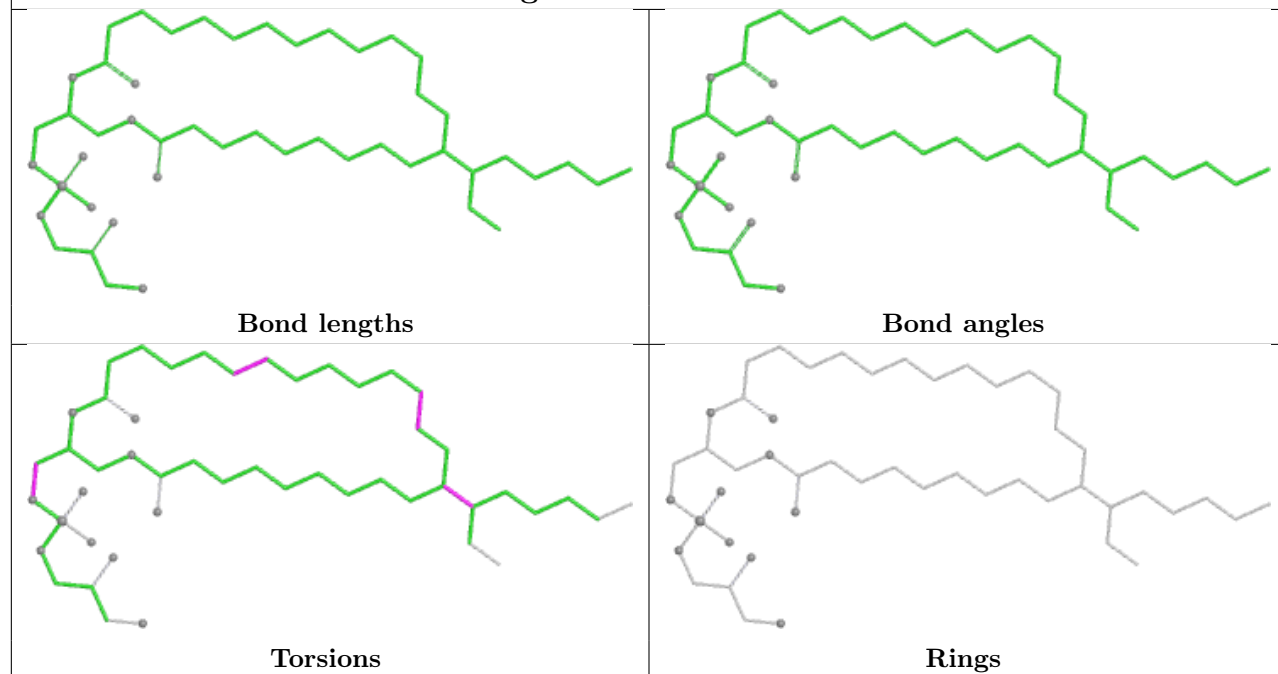


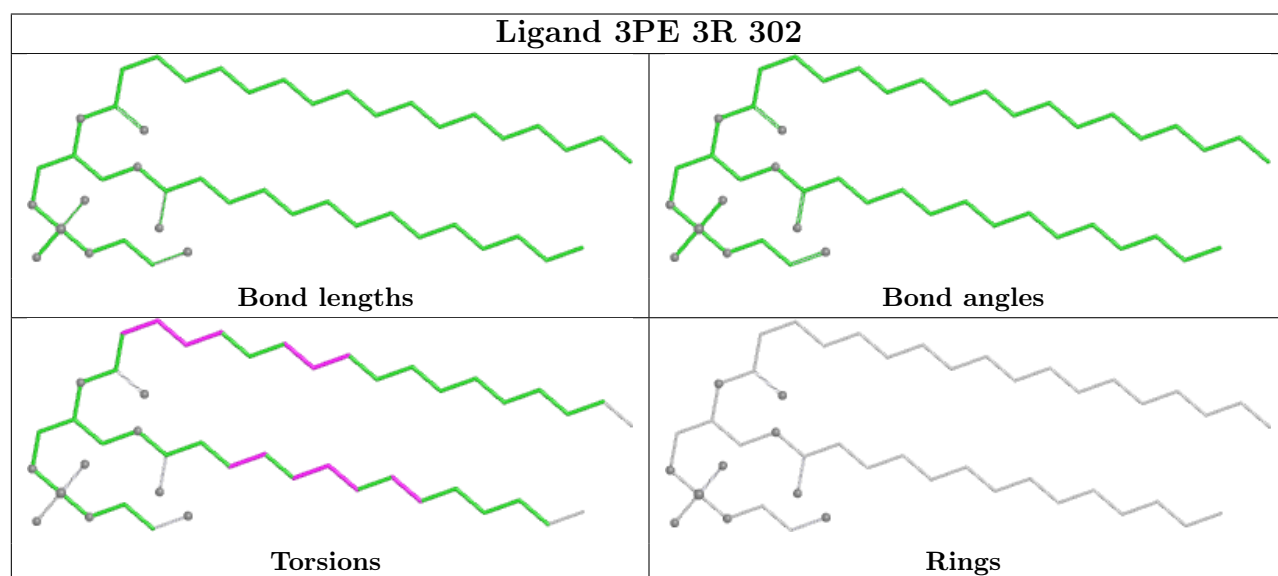
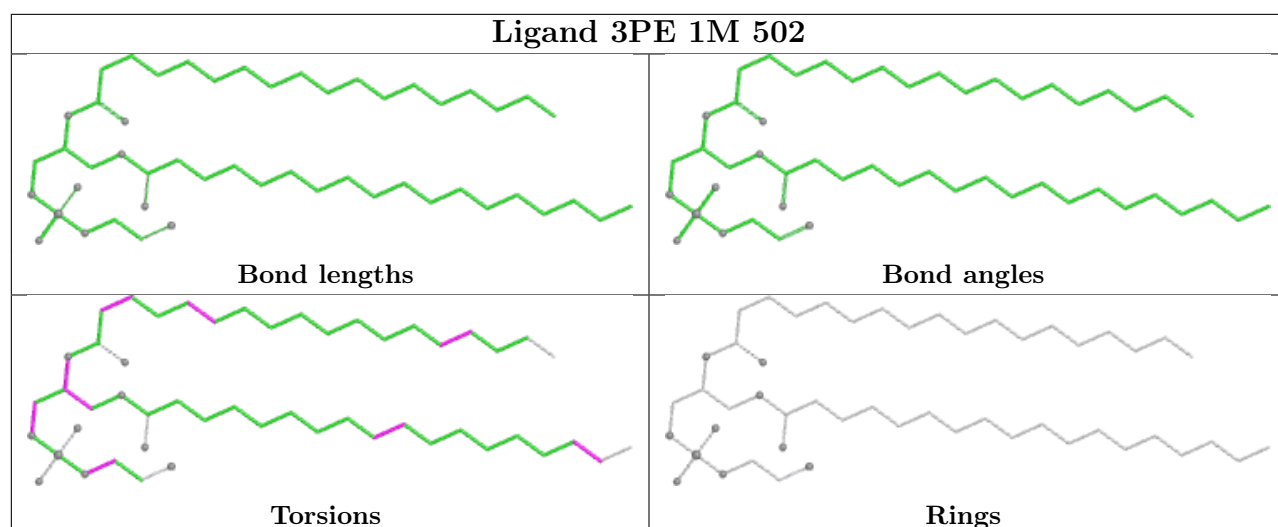


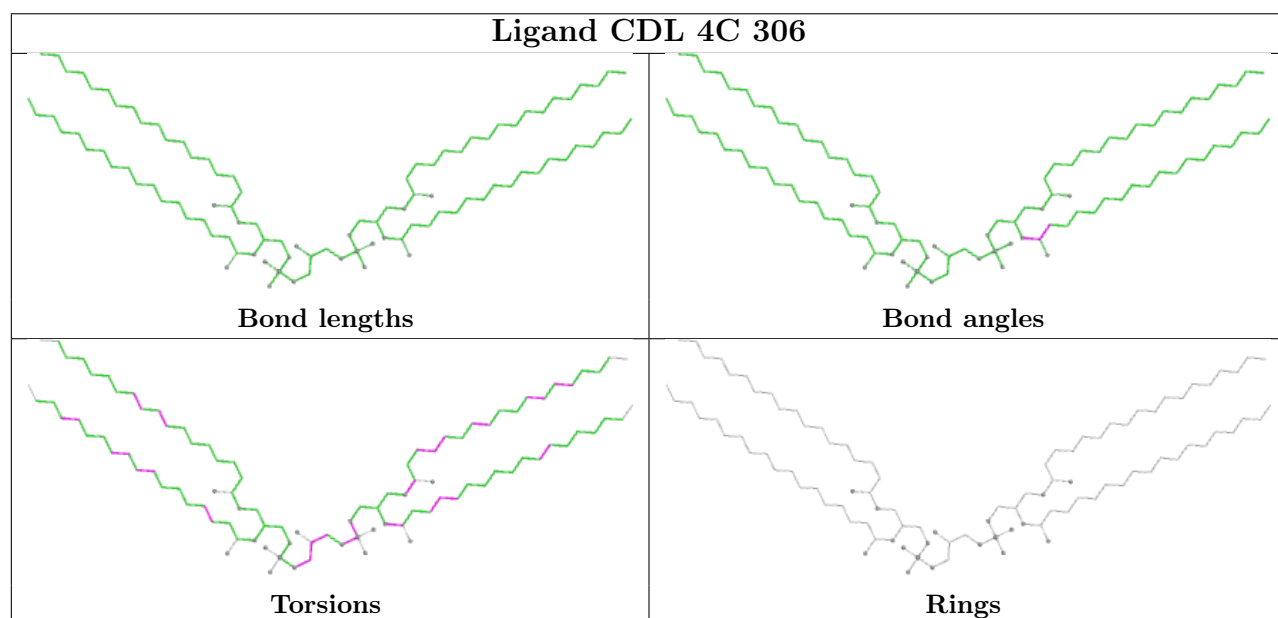
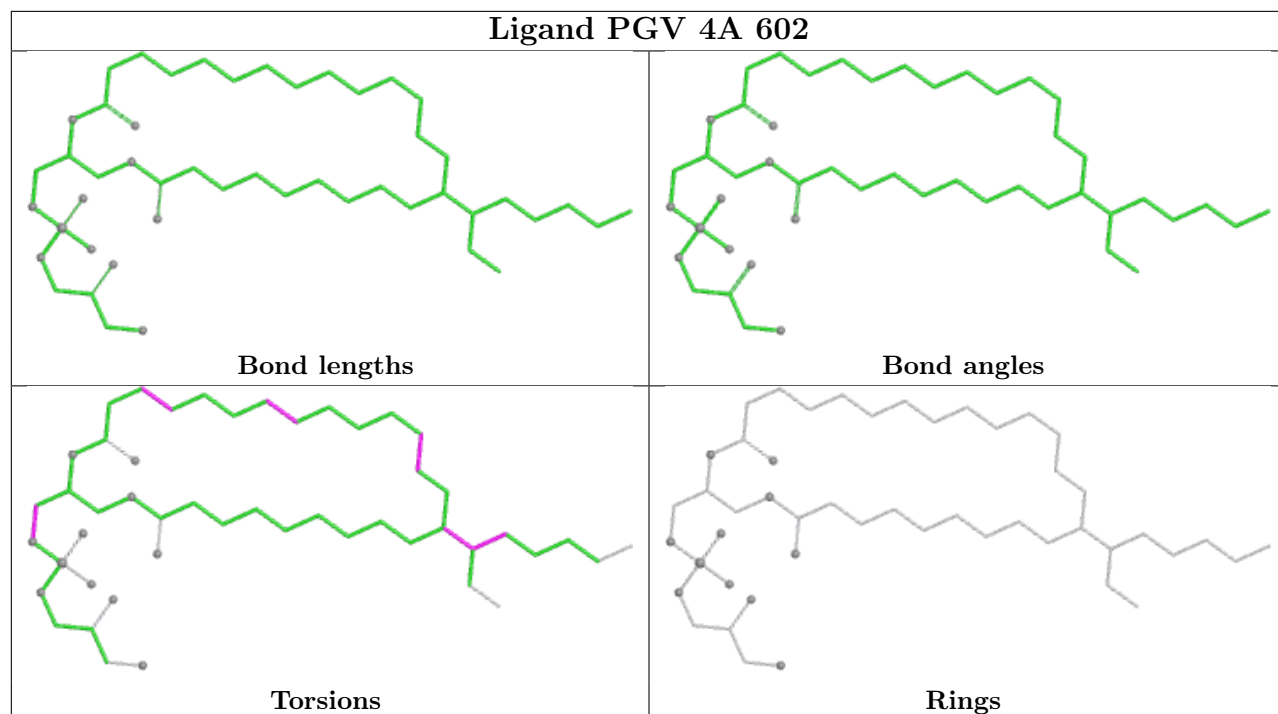
Ligand HEM 3C 502

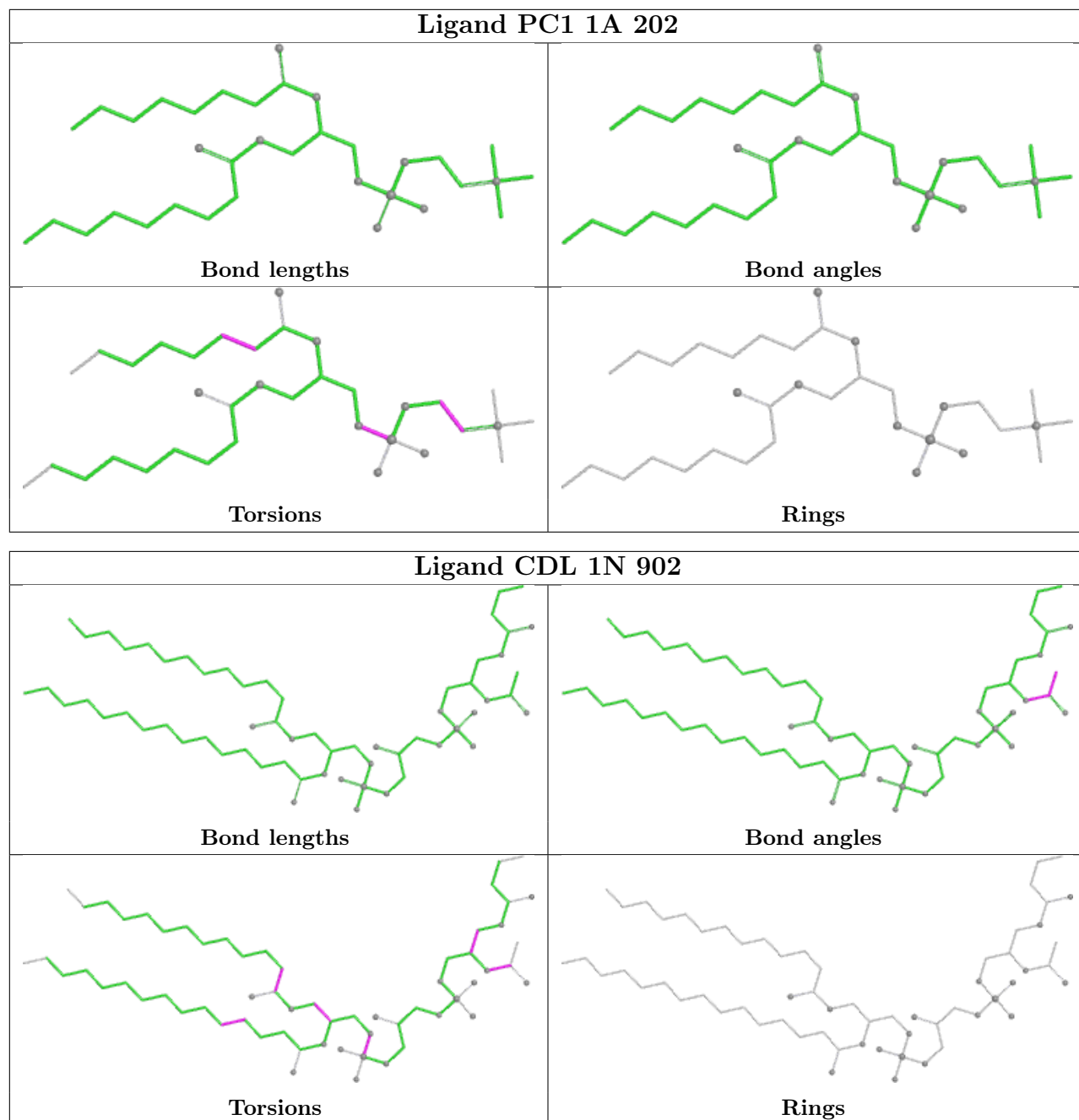


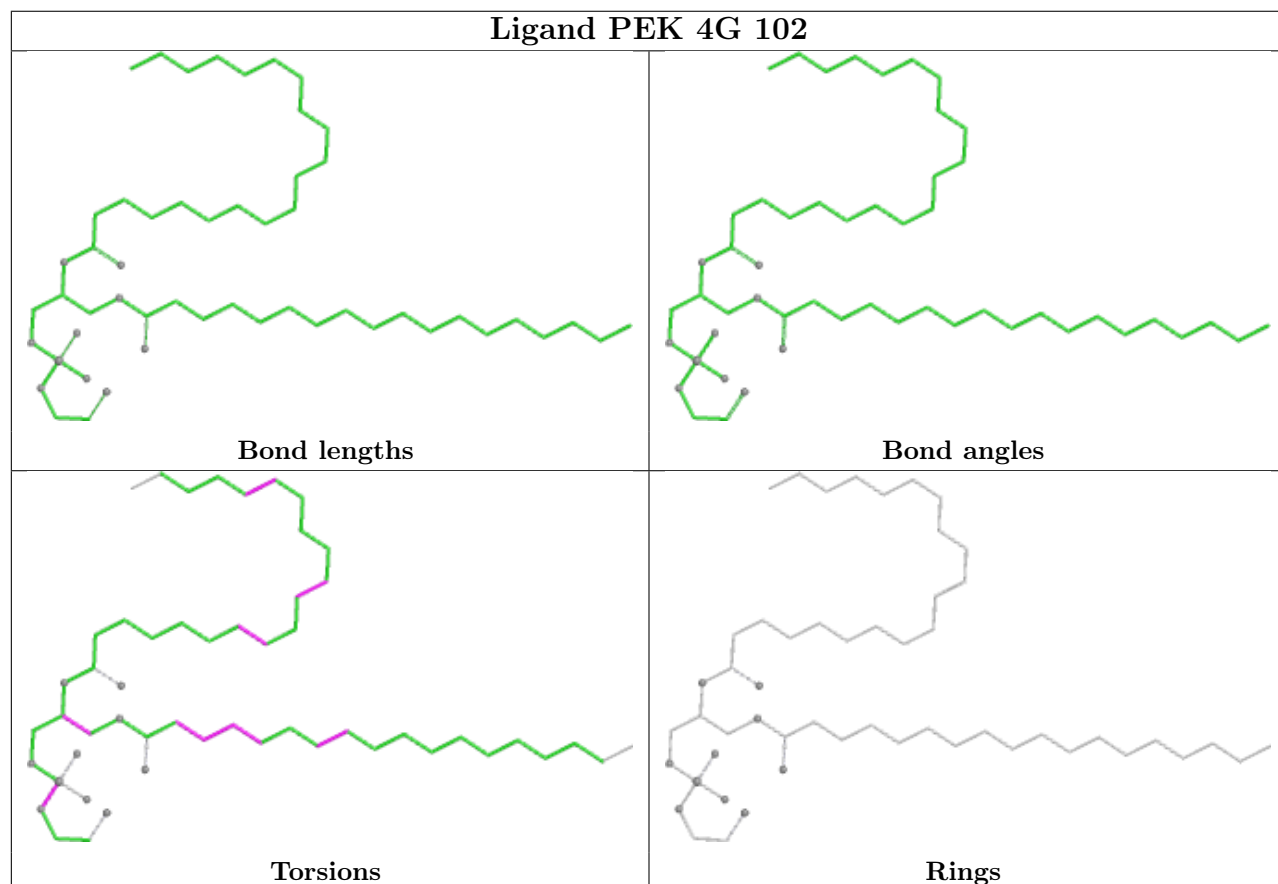
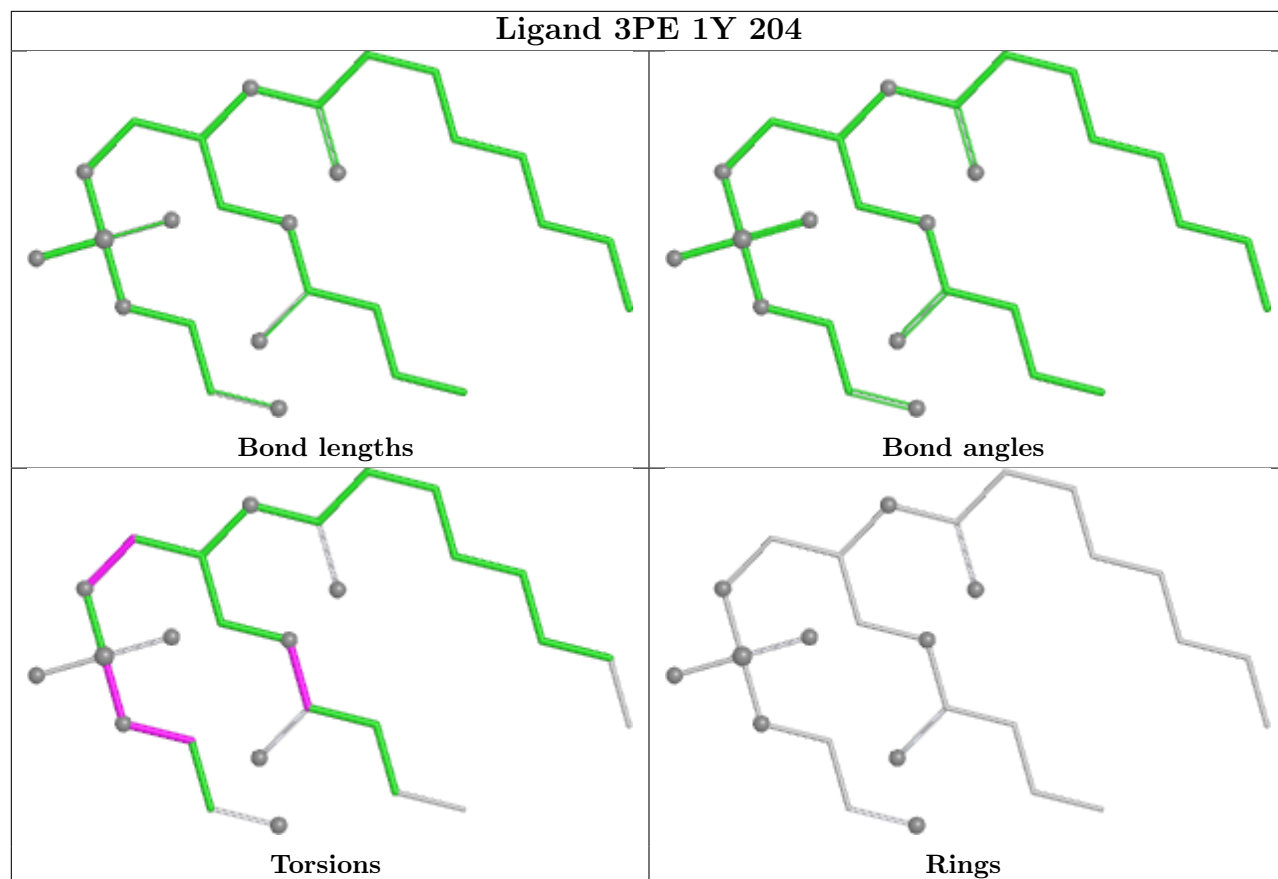
Ligand PGV 4C 307

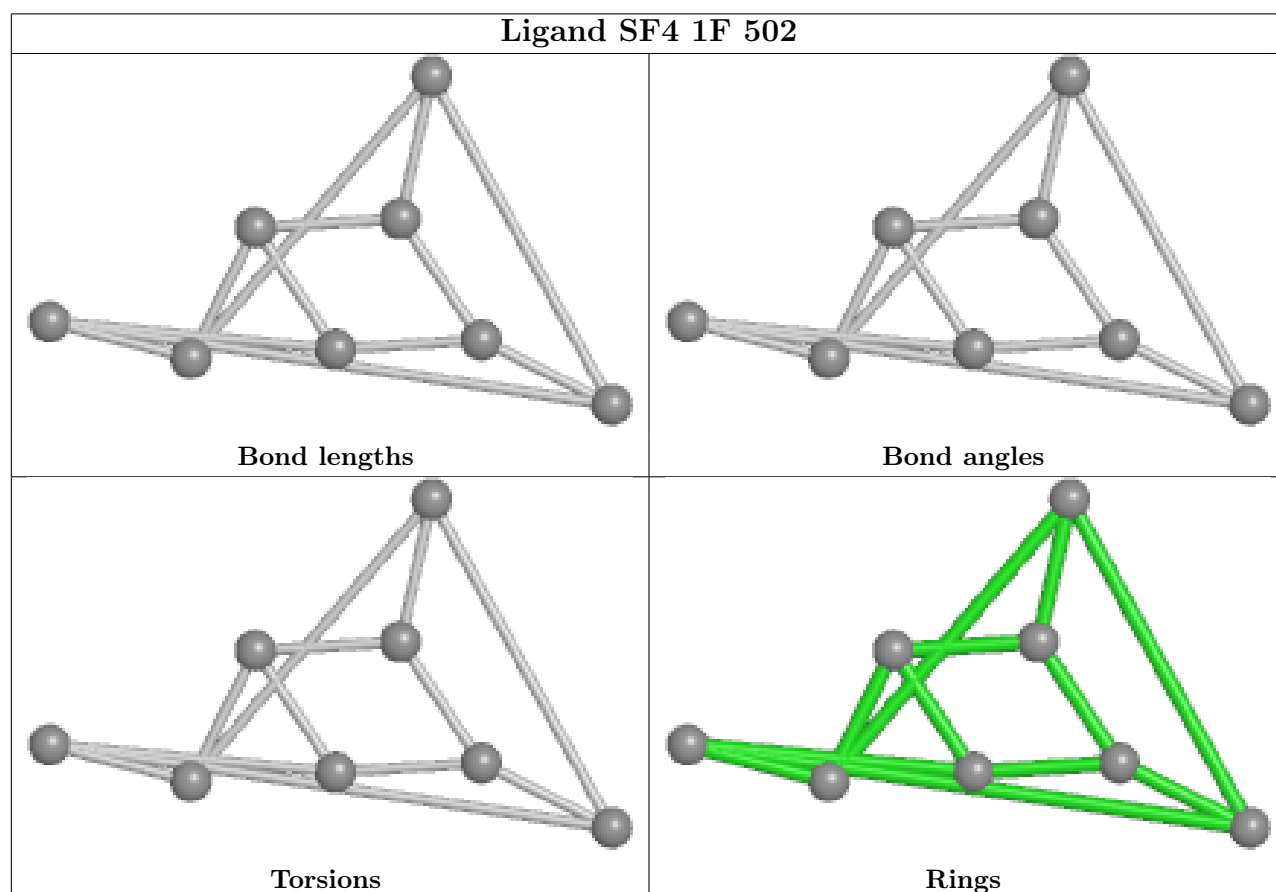
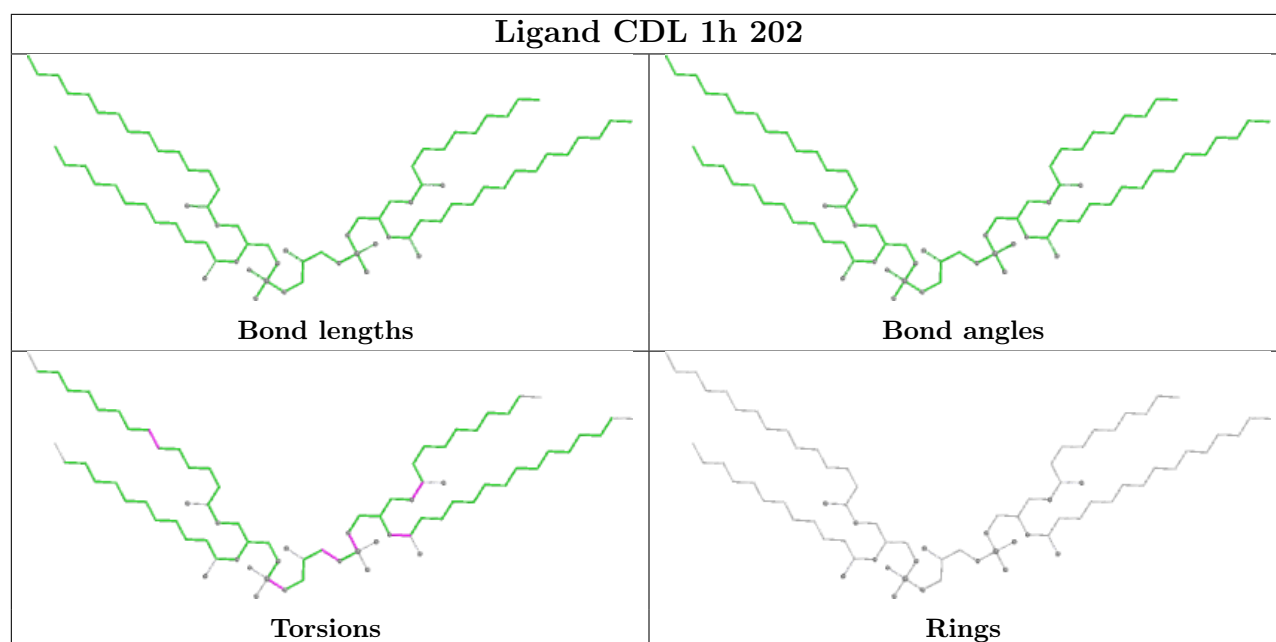


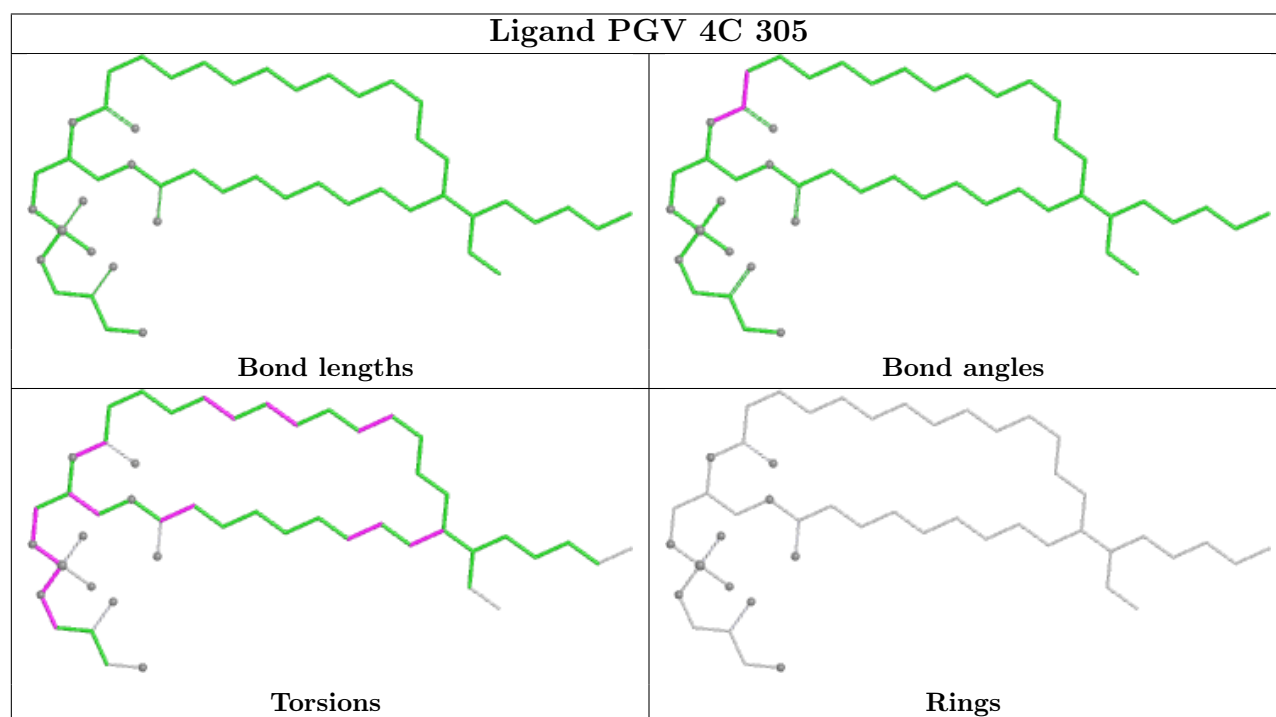
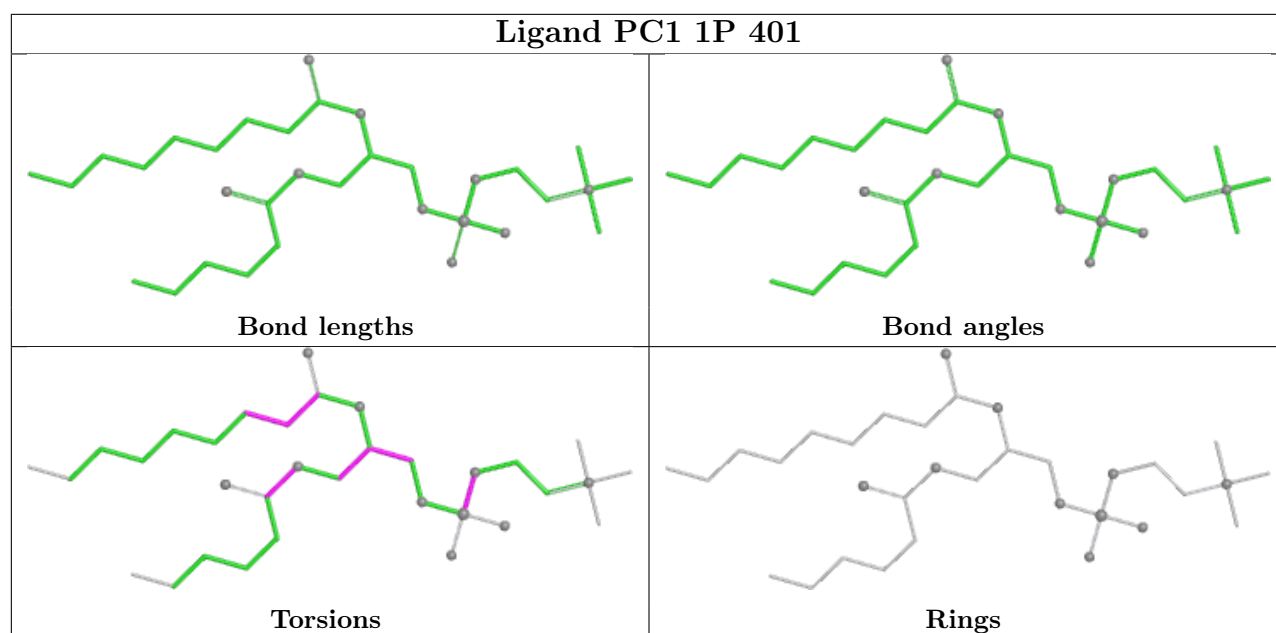




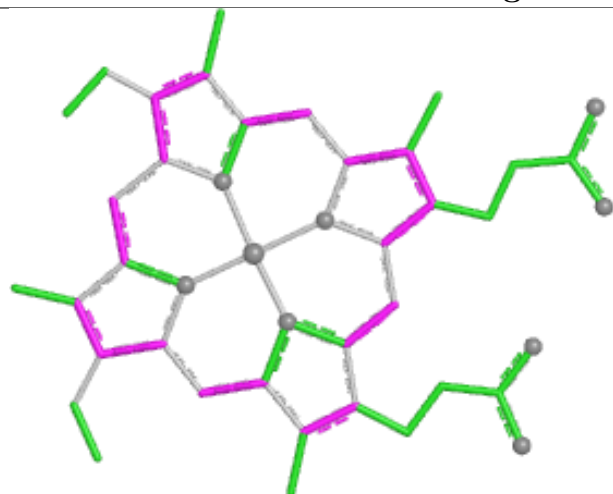




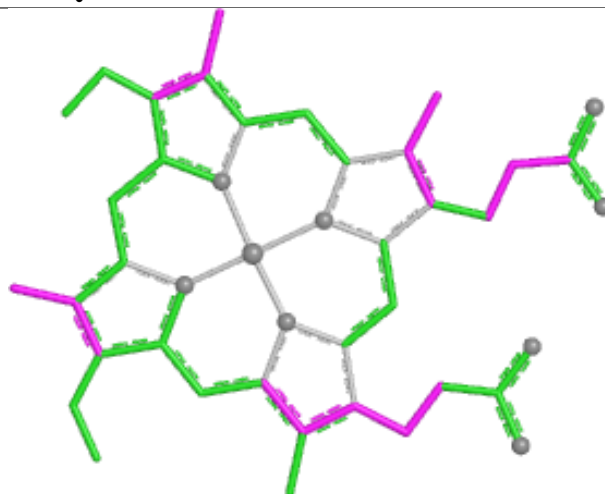




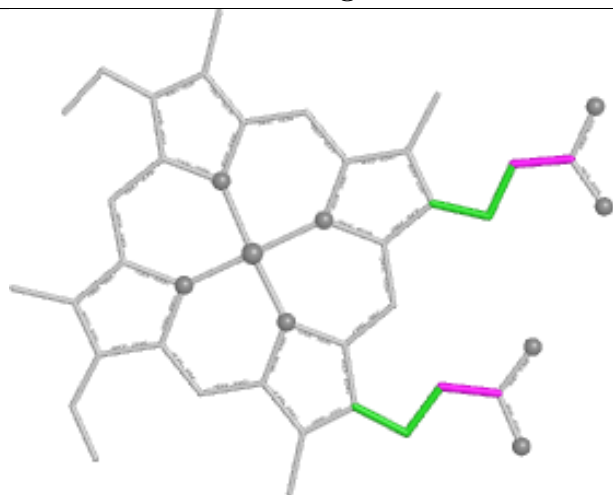
Ligand HEC 3Q 501



Bond lengths



Bond angles

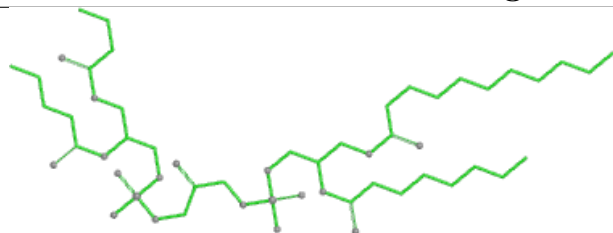


Torsions

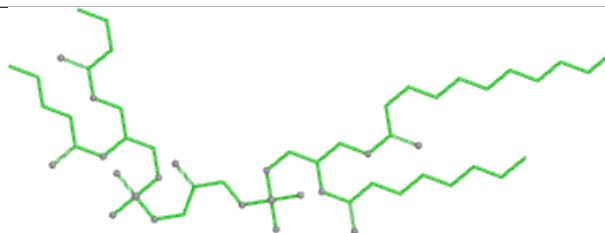


Rings

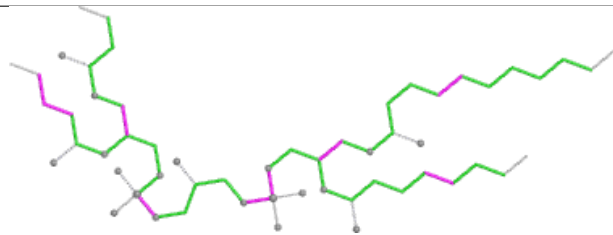
Ligand CDL 3G 103



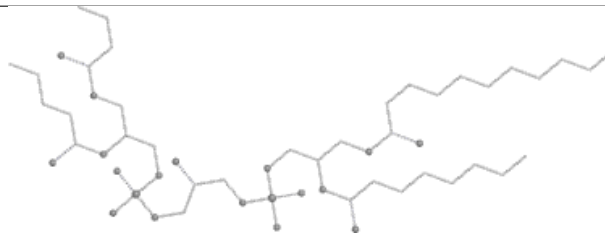
Bond lengths



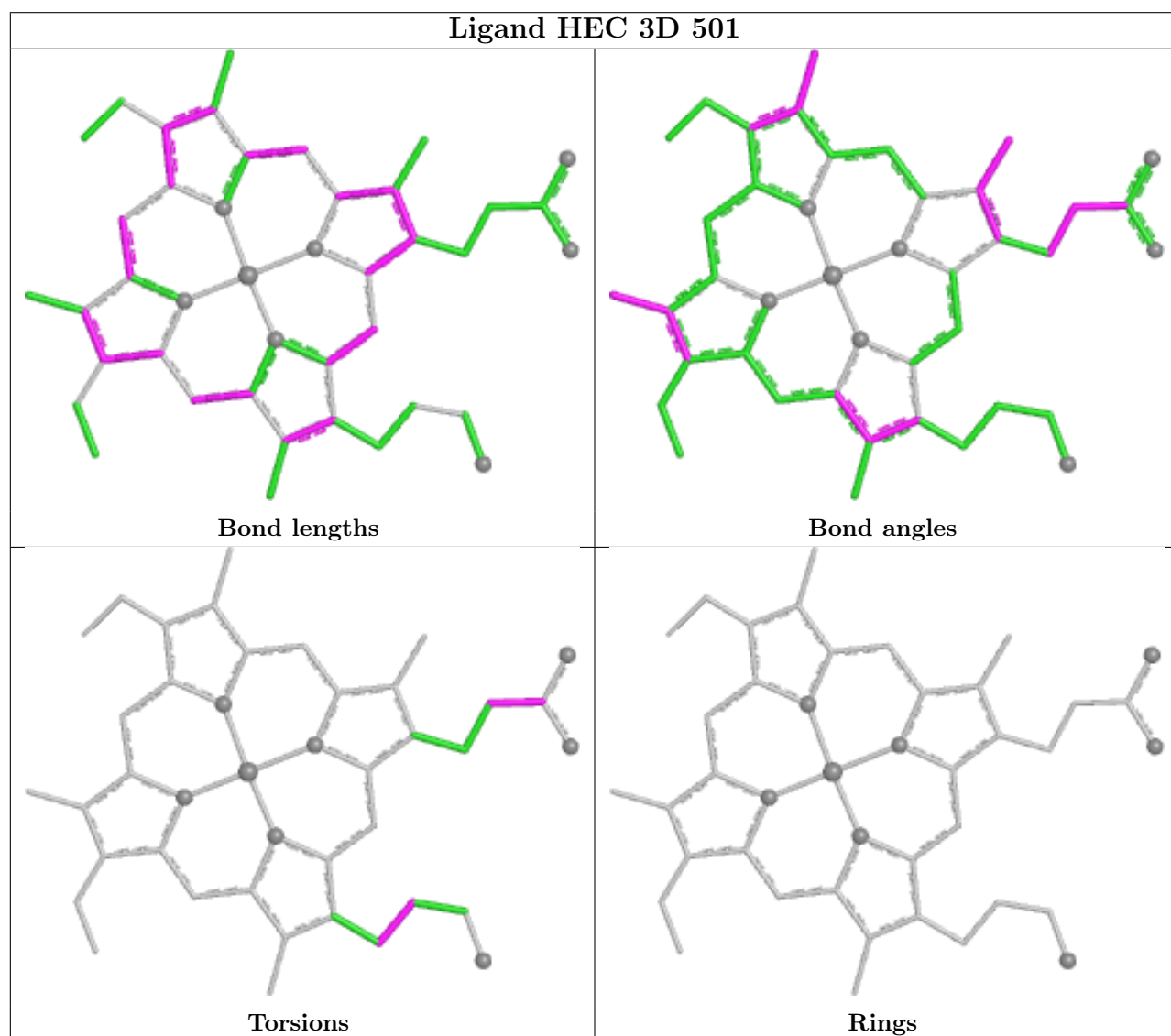
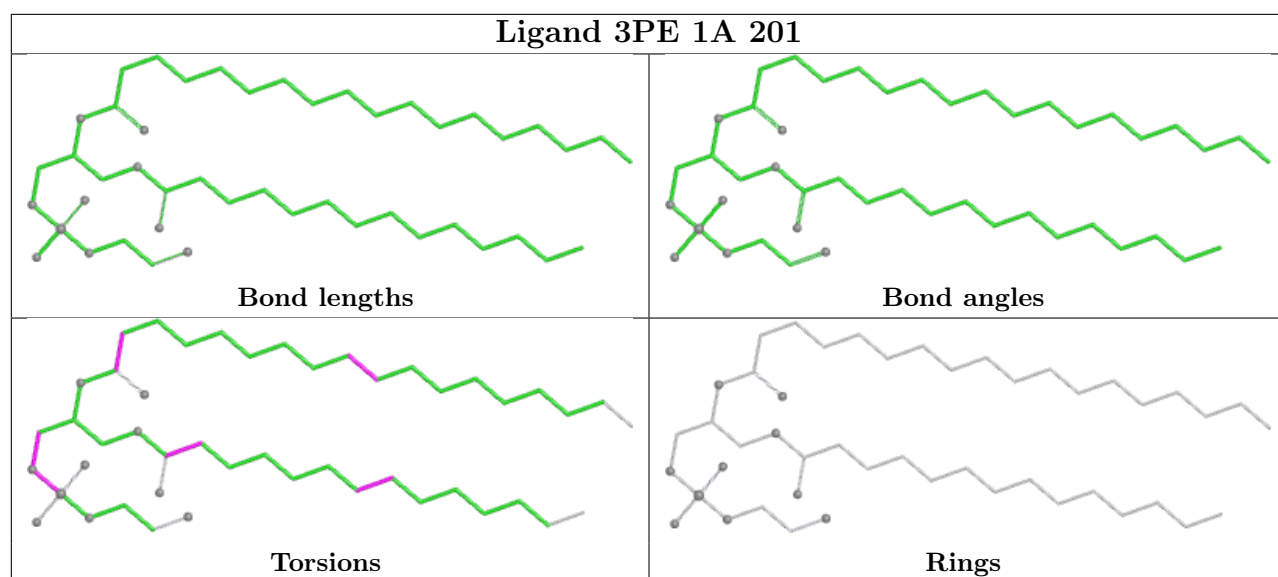
Bond angles

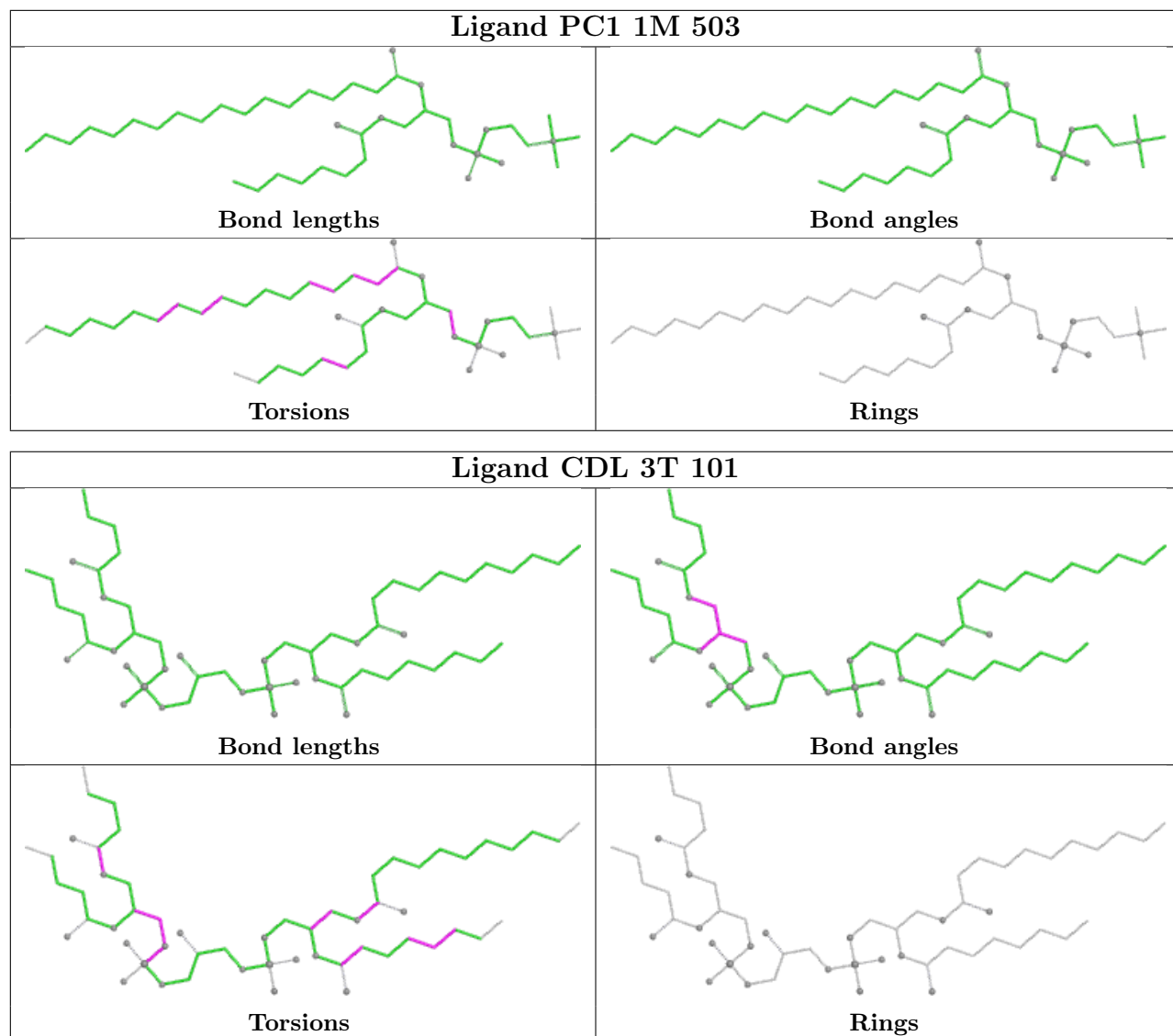


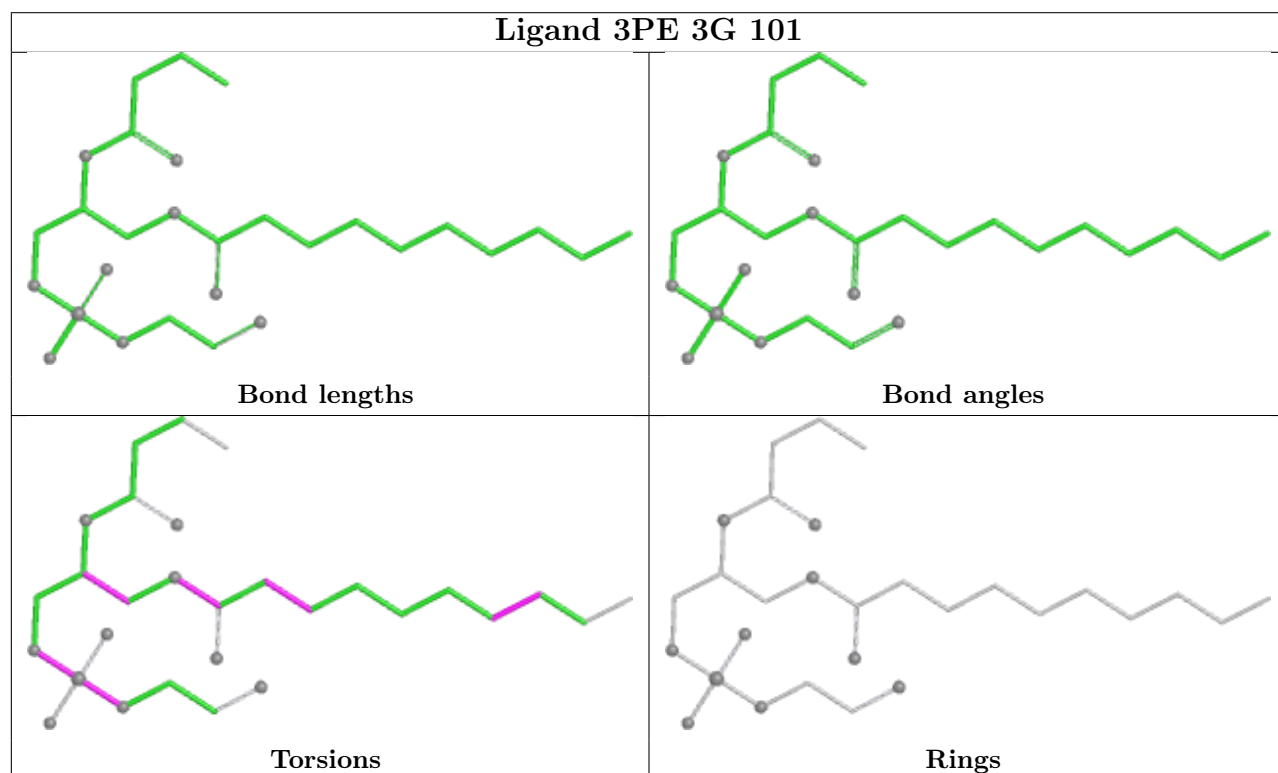
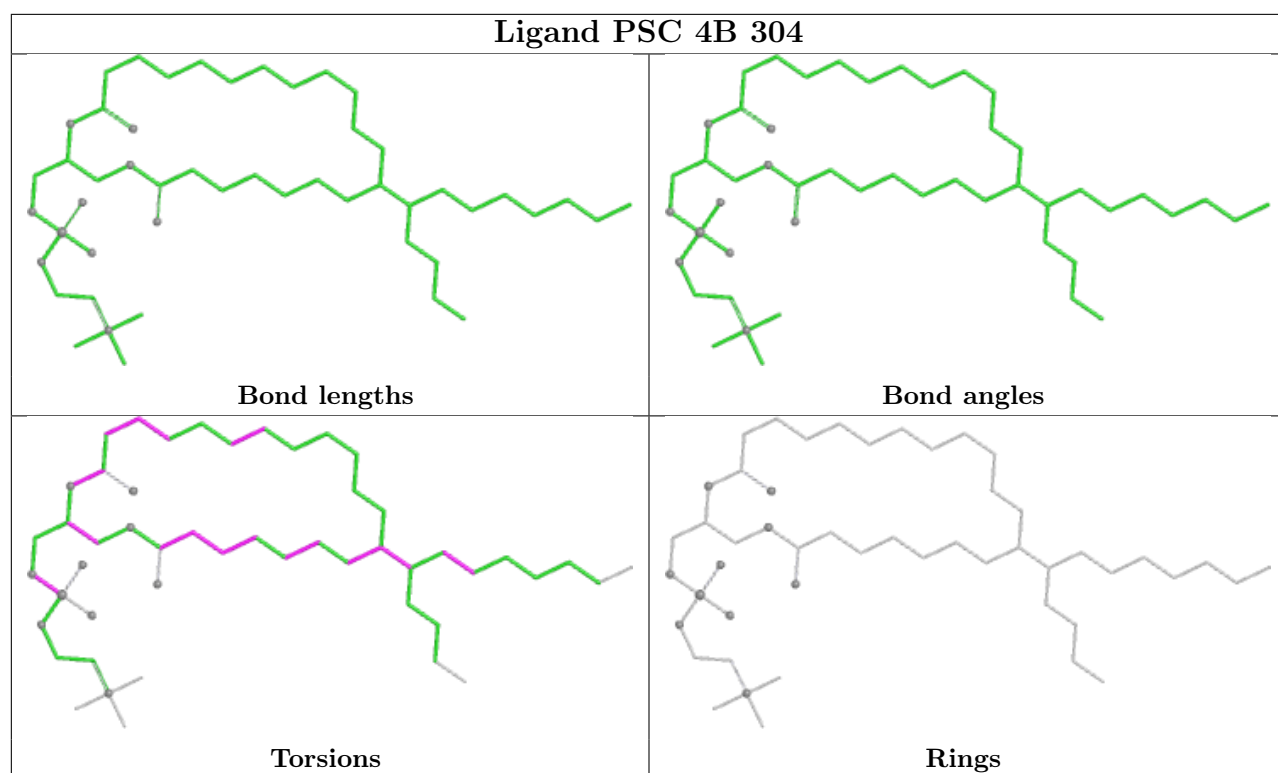
Torsions

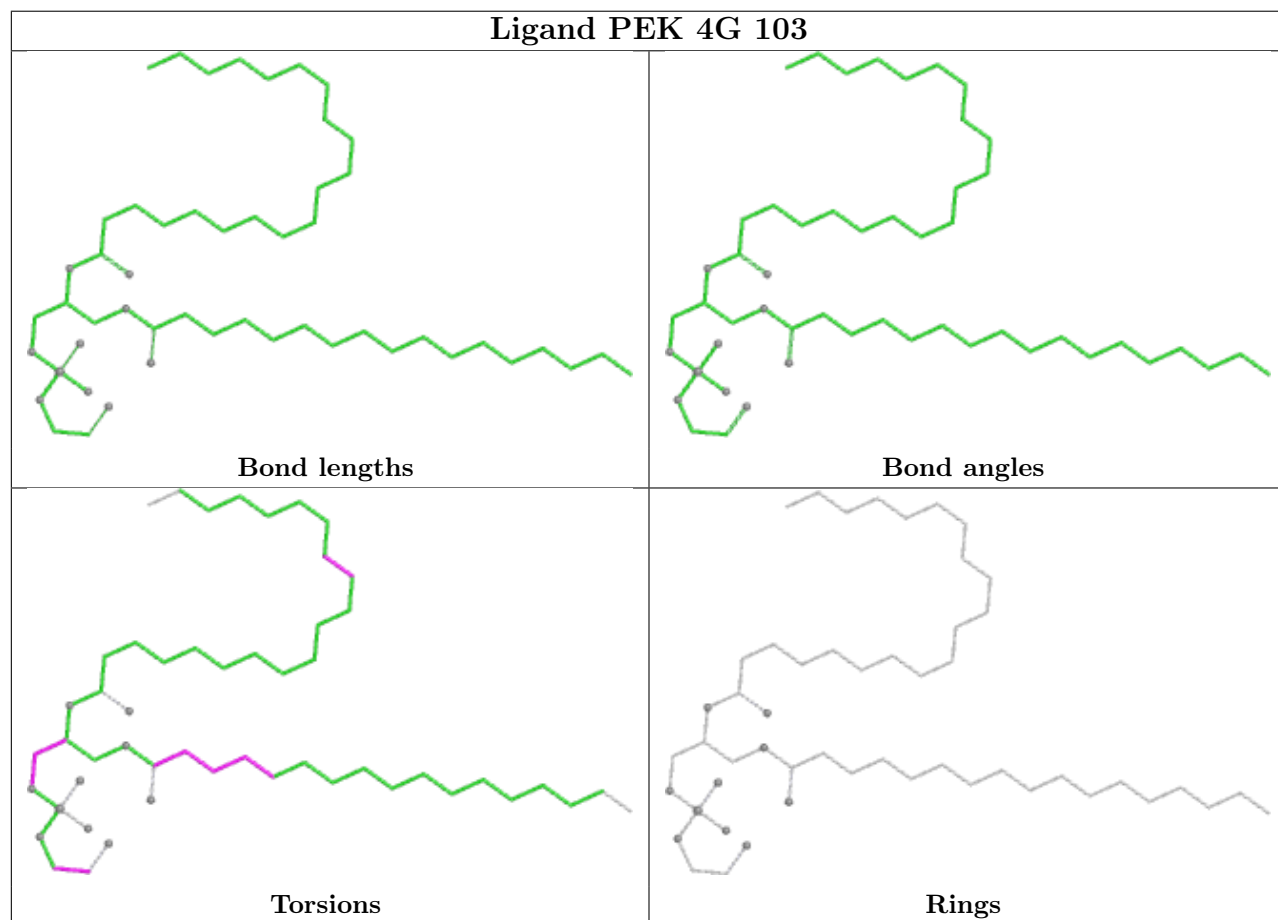
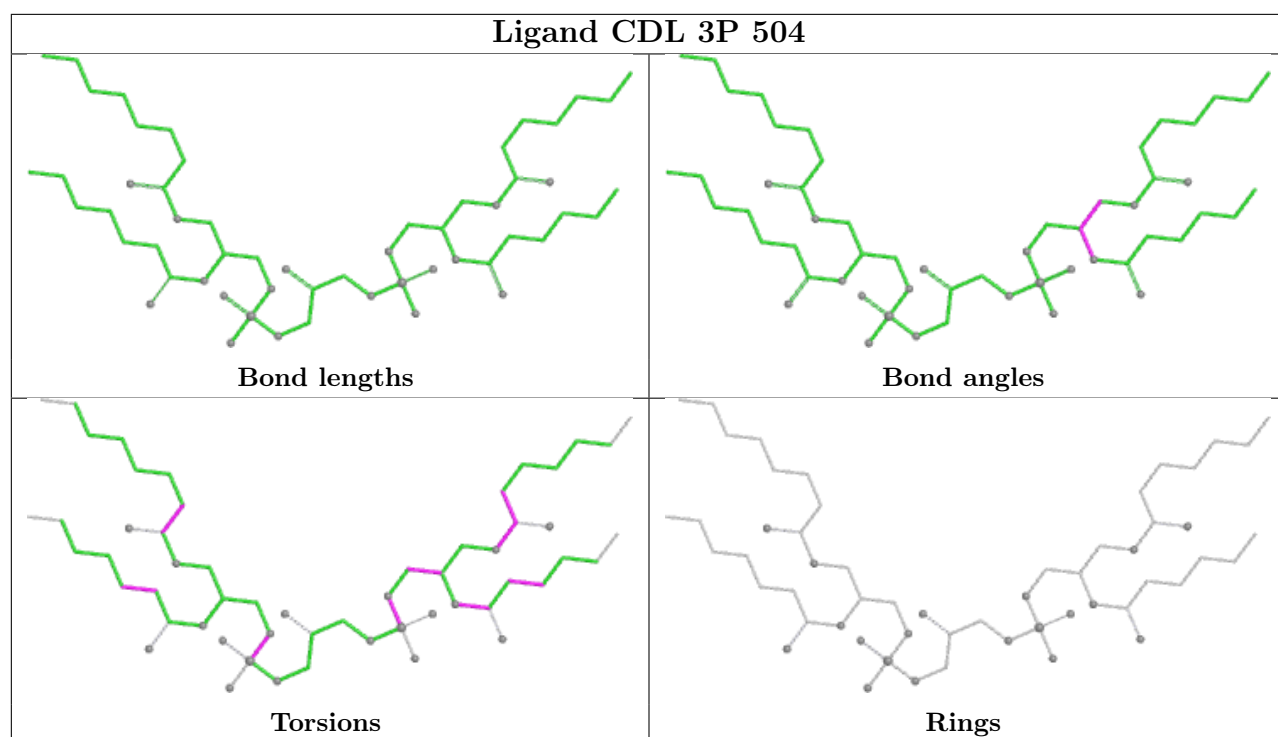


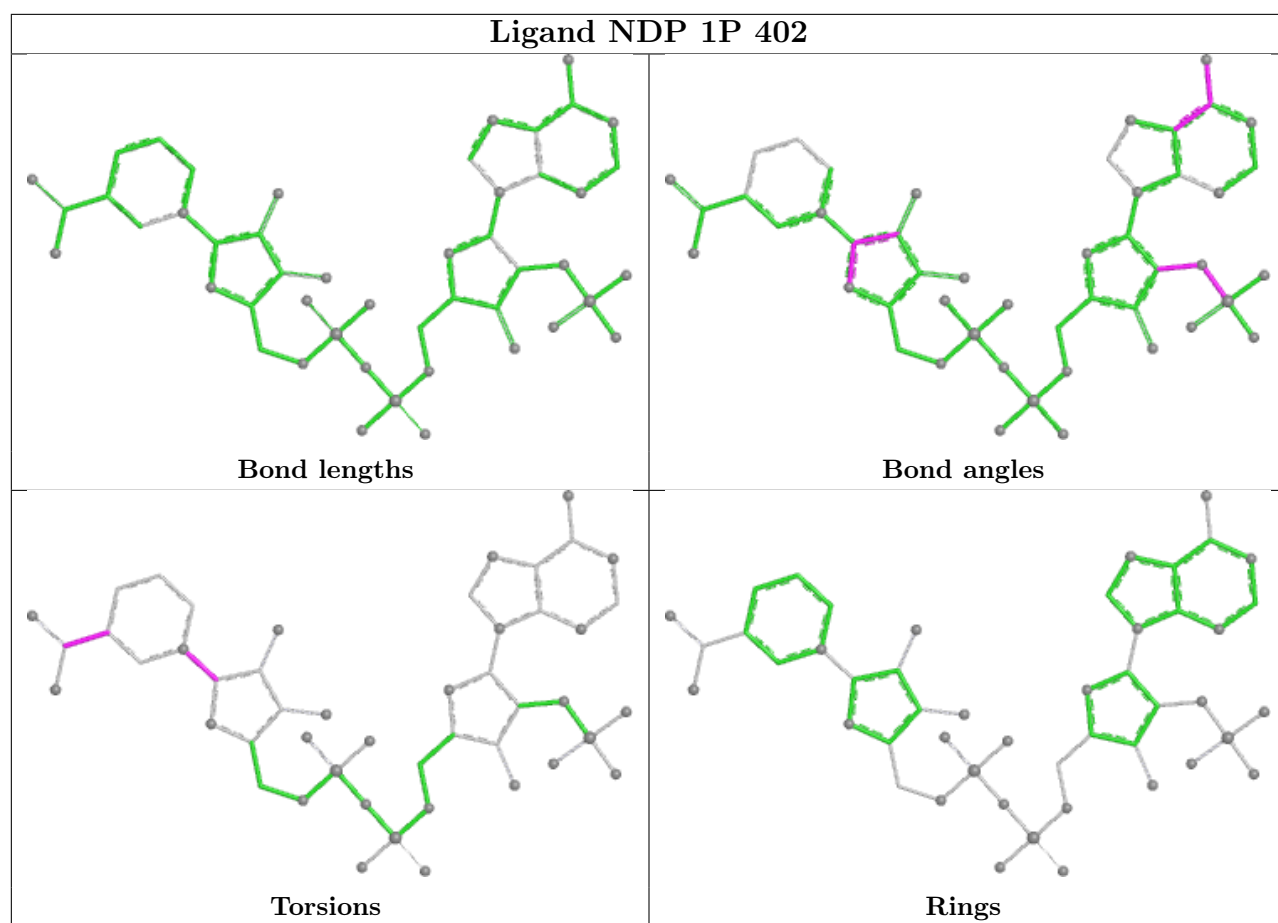
Rings



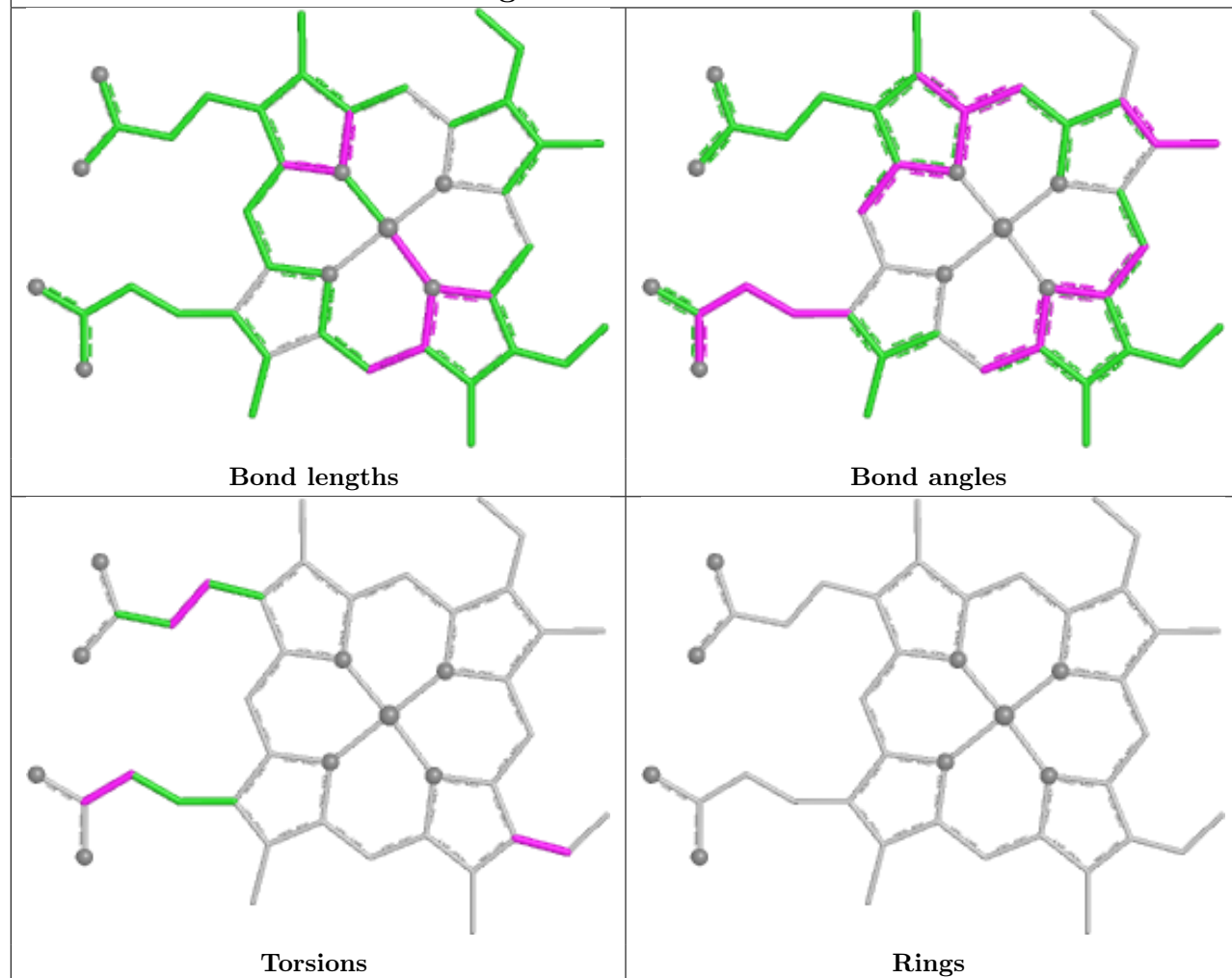




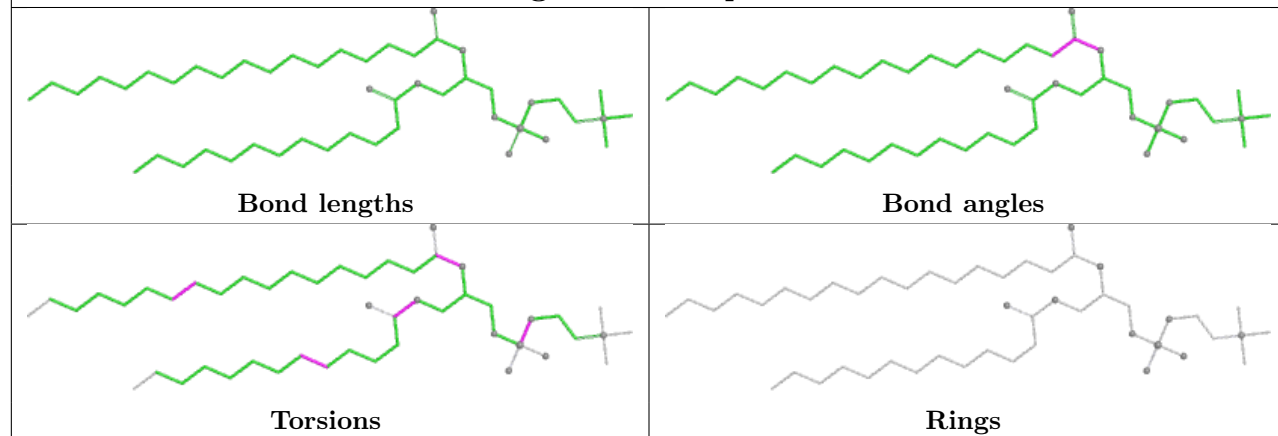


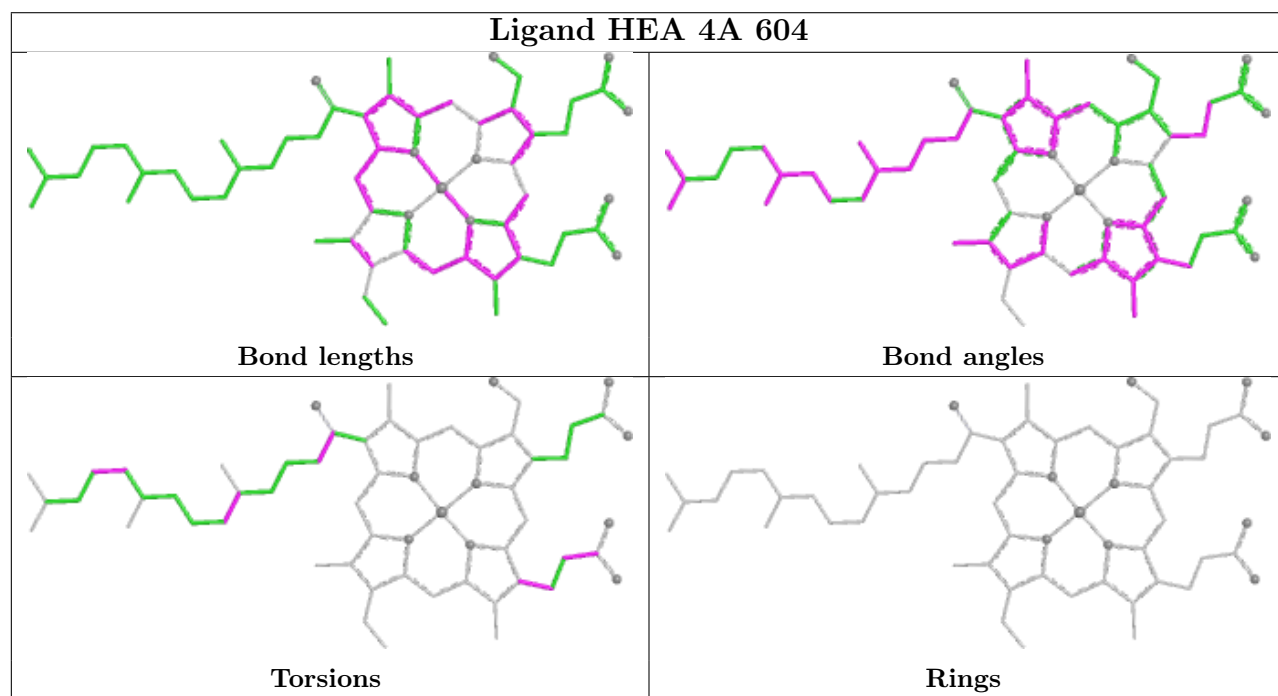
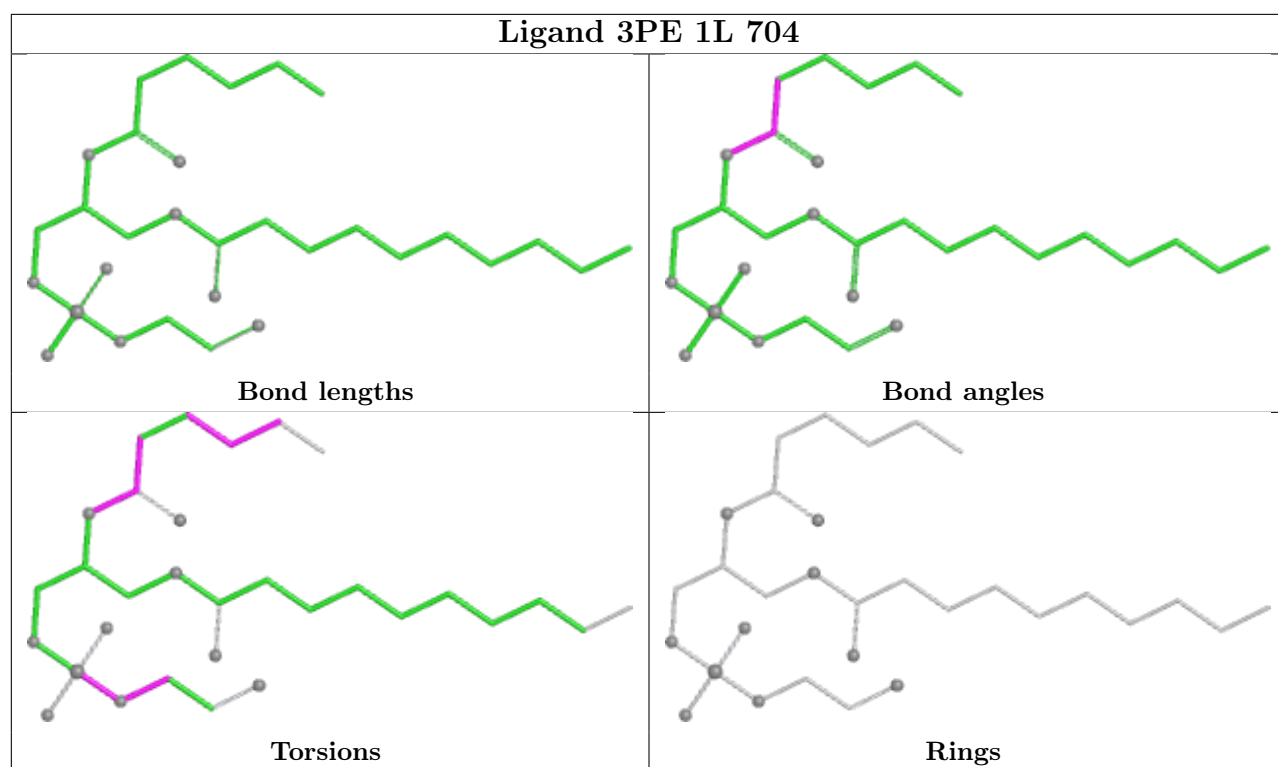


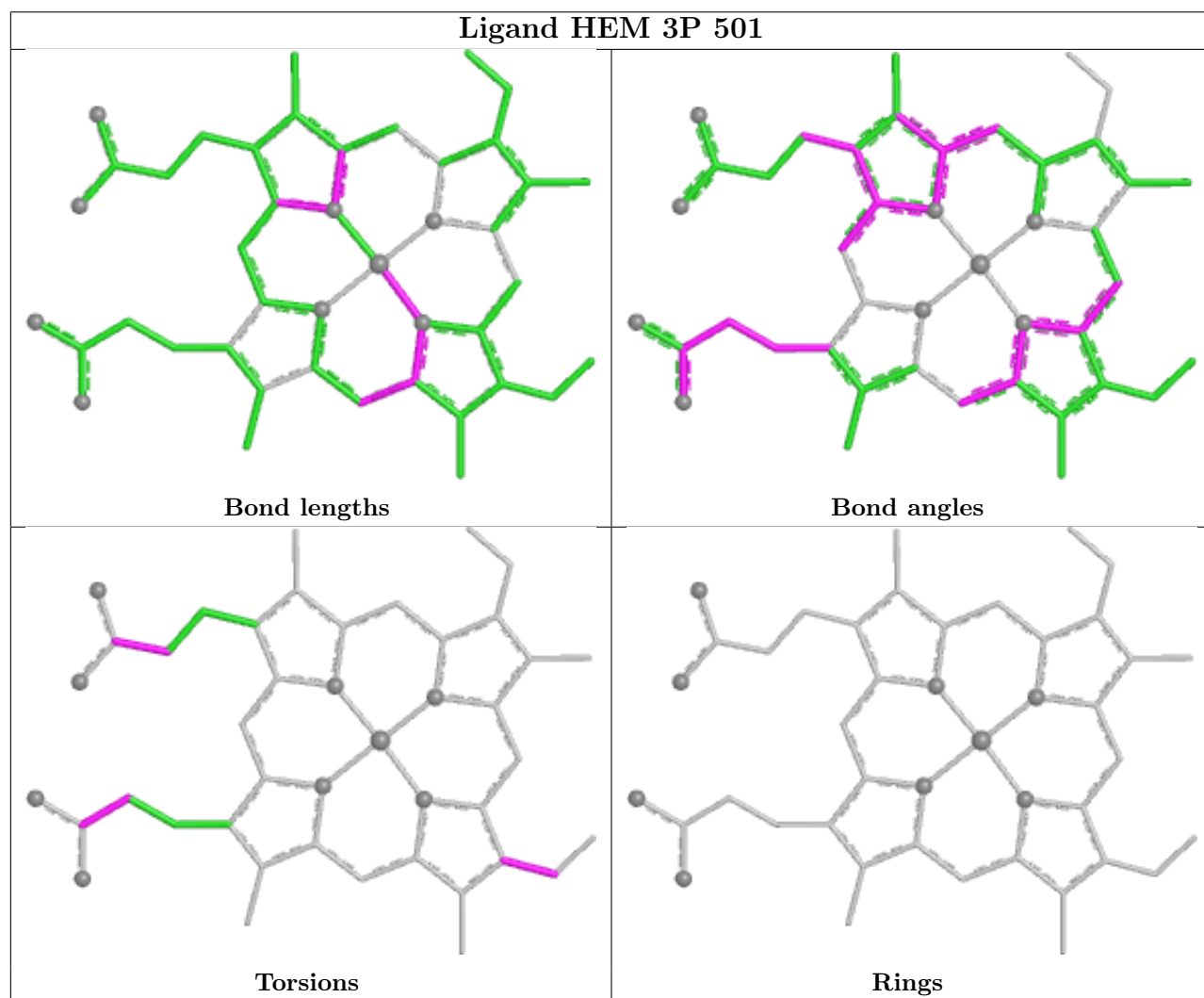
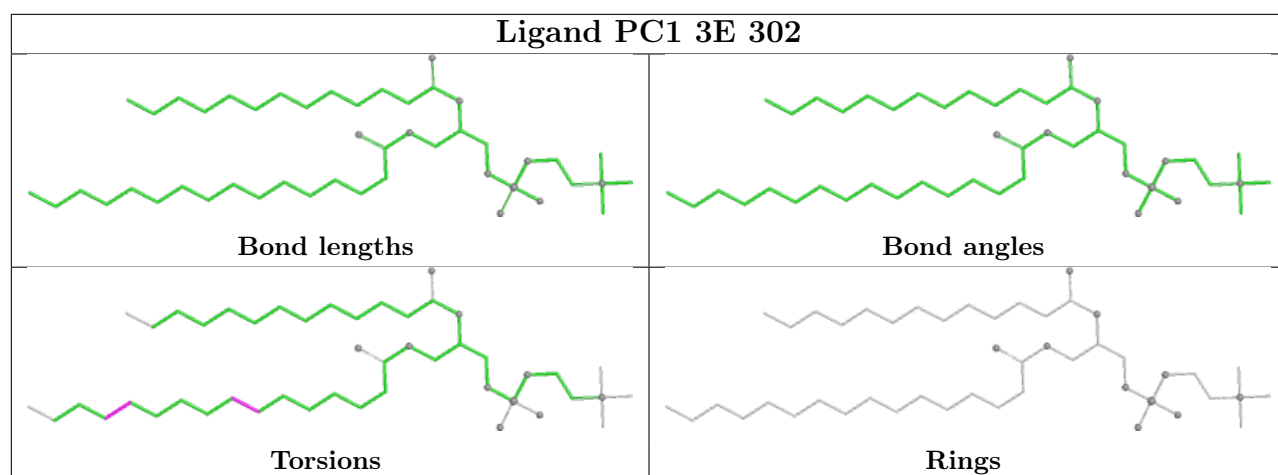
Ligand HEM 3C 501

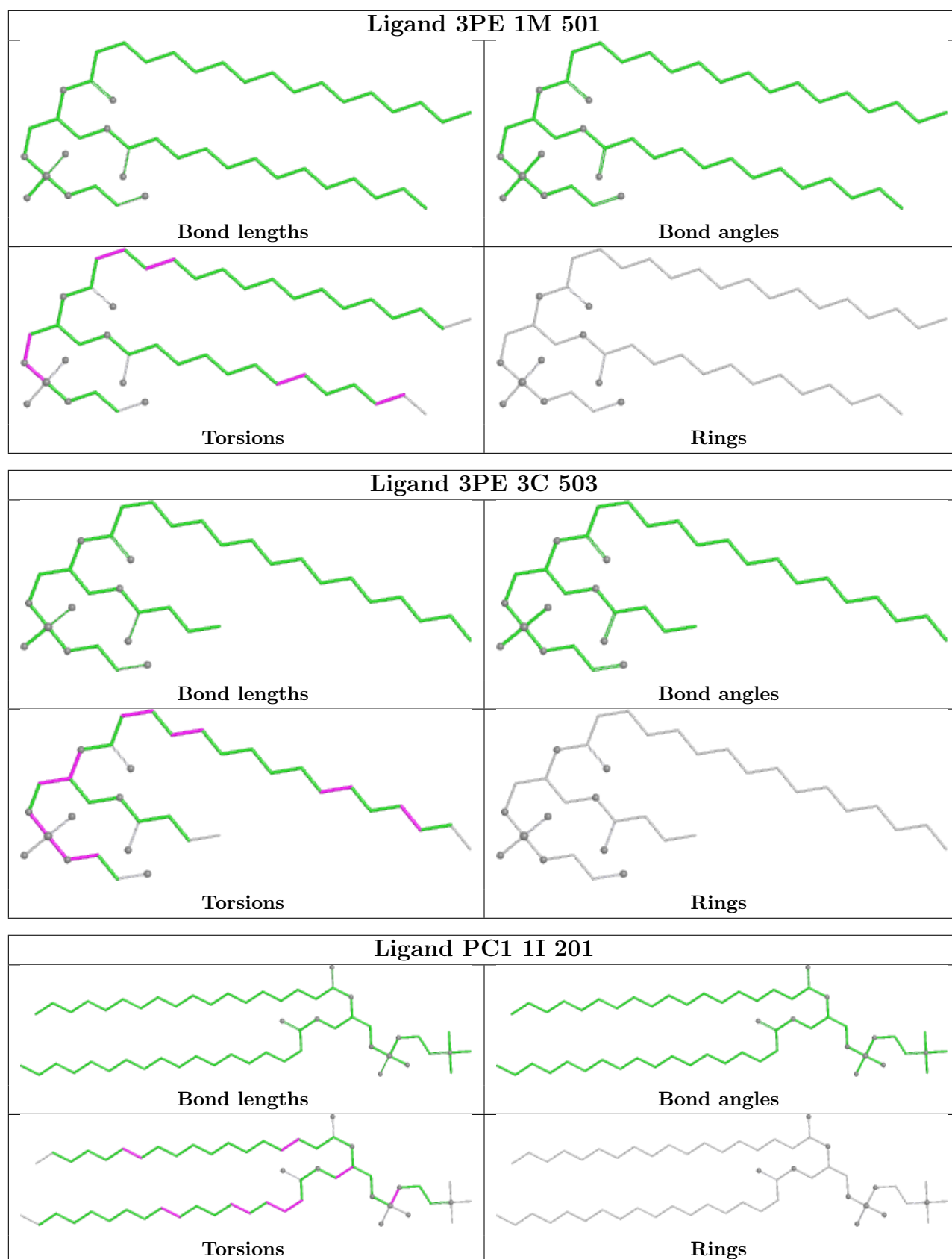


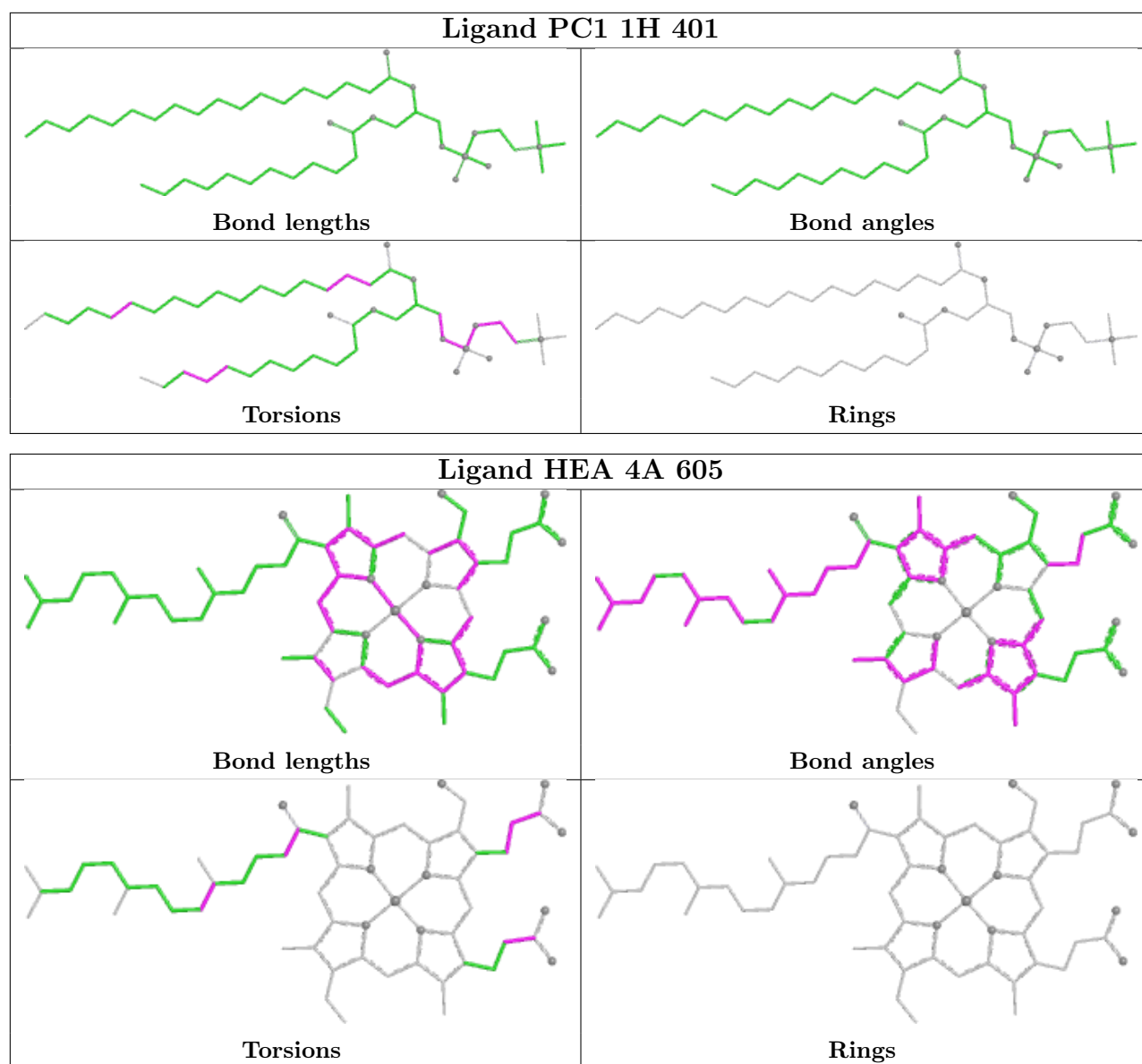
Ligand PC1 1q 201











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 49 | 3I | 1 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | 3I | 48:SER | C | 49:PHE | N | 1.08 |

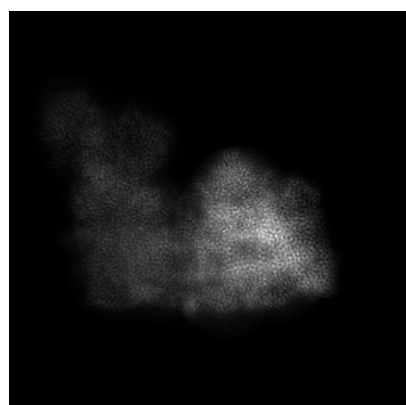
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42226. These allow visual inspection of the internal detail of the map and identification of artifacts.

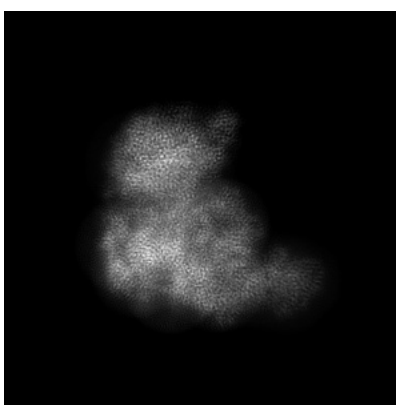
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

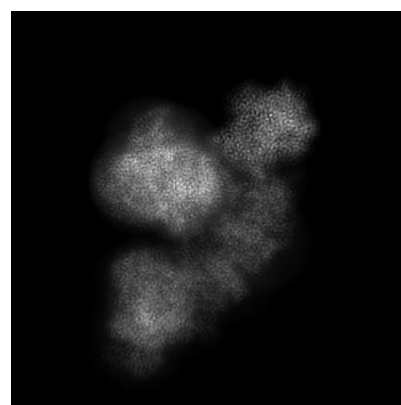
6.1.1 Primary map



X



Y

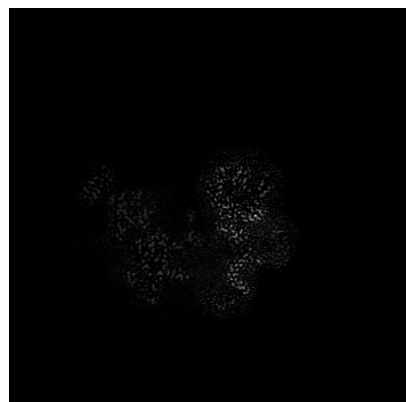


Z

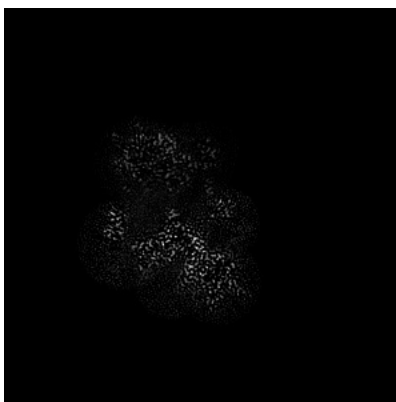
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

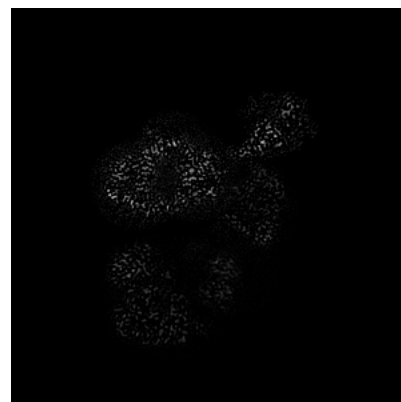
6.2.1 Primary map



X Index: 444



Y Index: 444



Z Index: 444

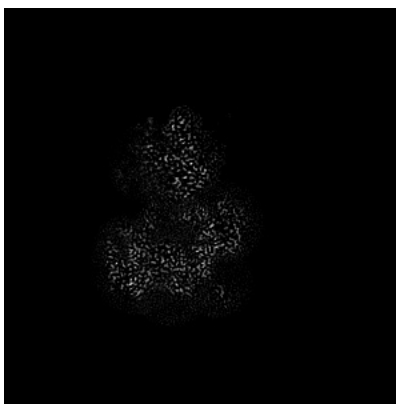
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

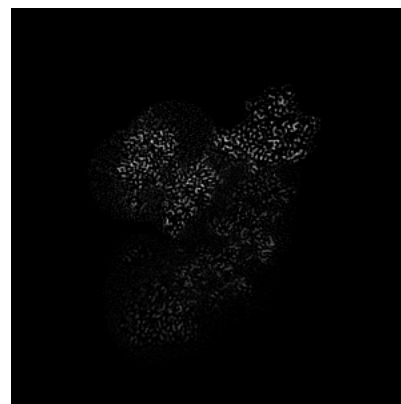
6.3.1 Primary map



X Index: 322



Y Index: 568

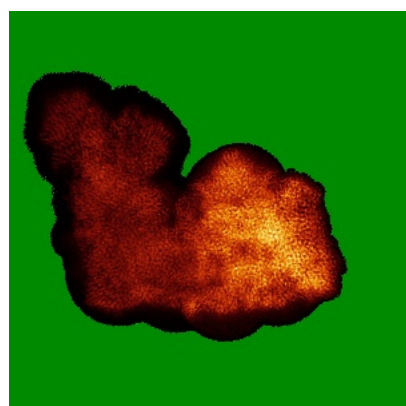


Z Index: 387

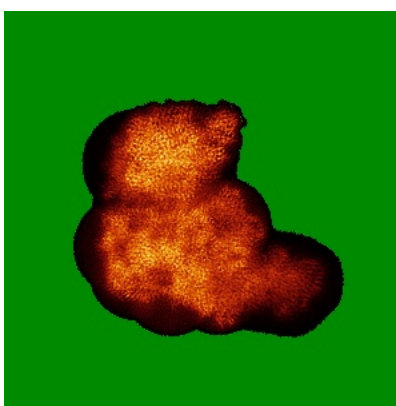
The images above show the largest variance slices of the map in three orthogonal directions.

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

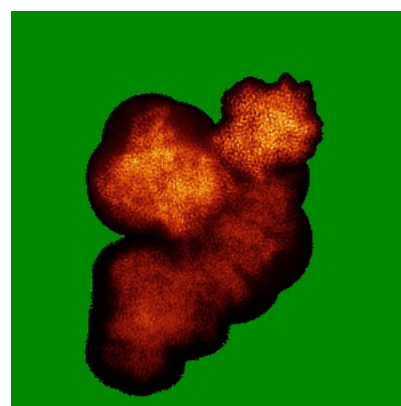
6.4.1 Primary map



X



Y

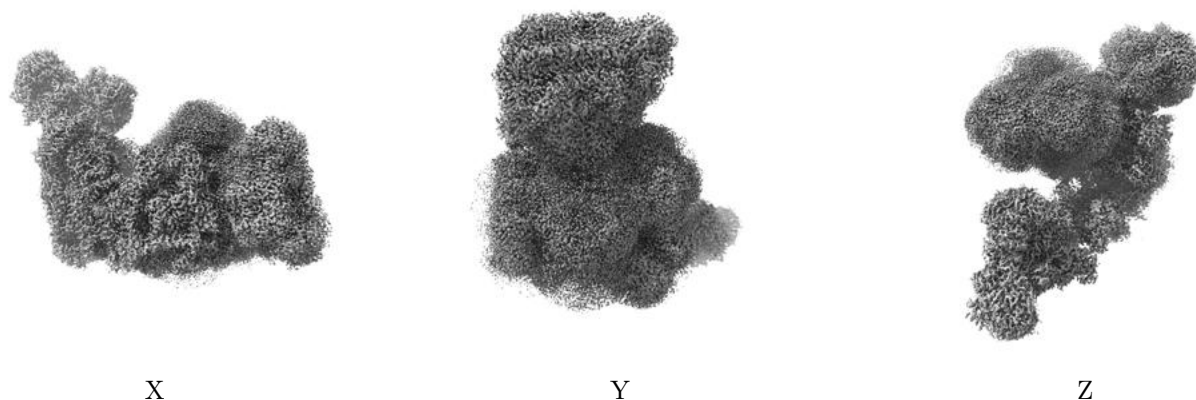


Z

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

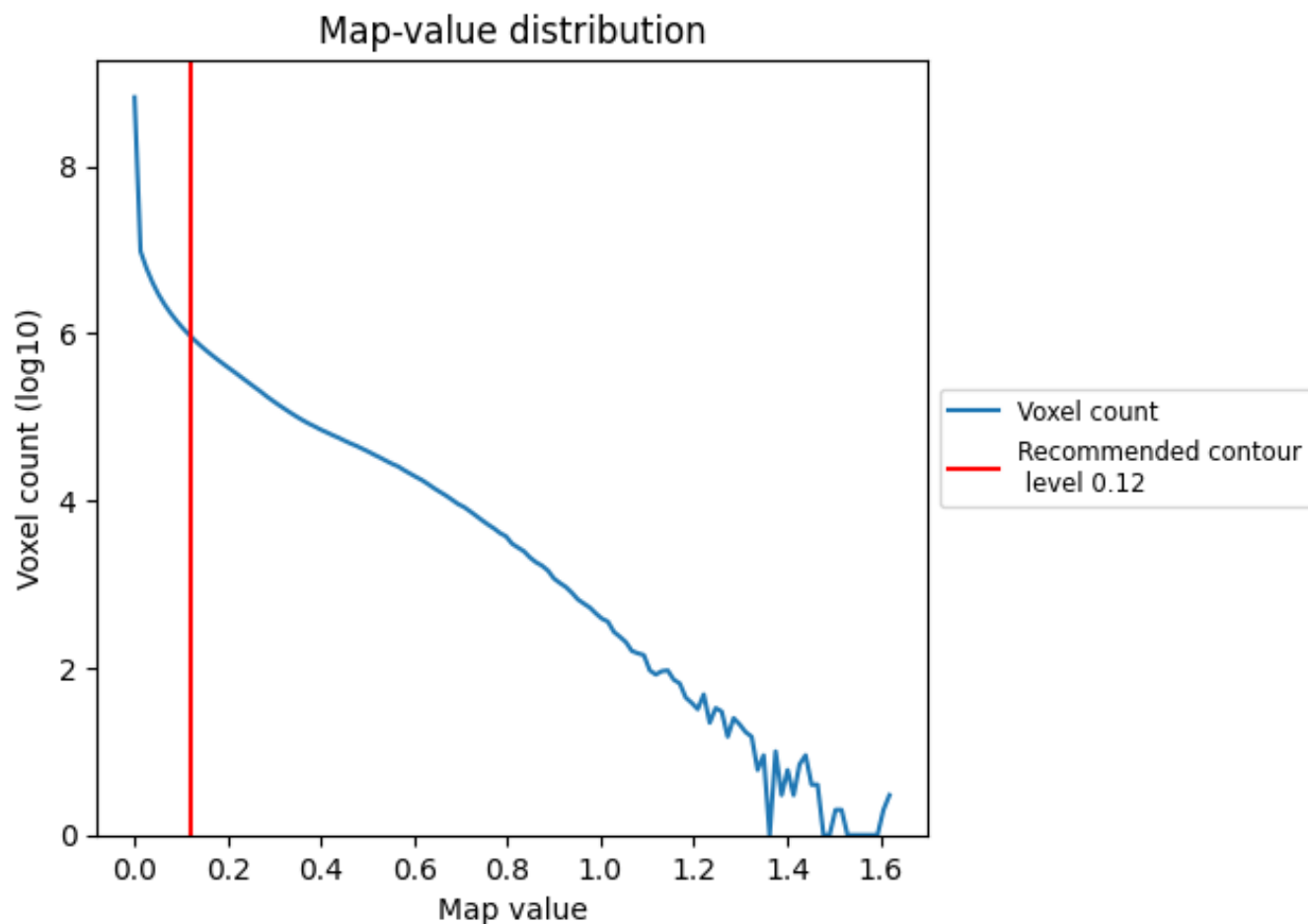
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

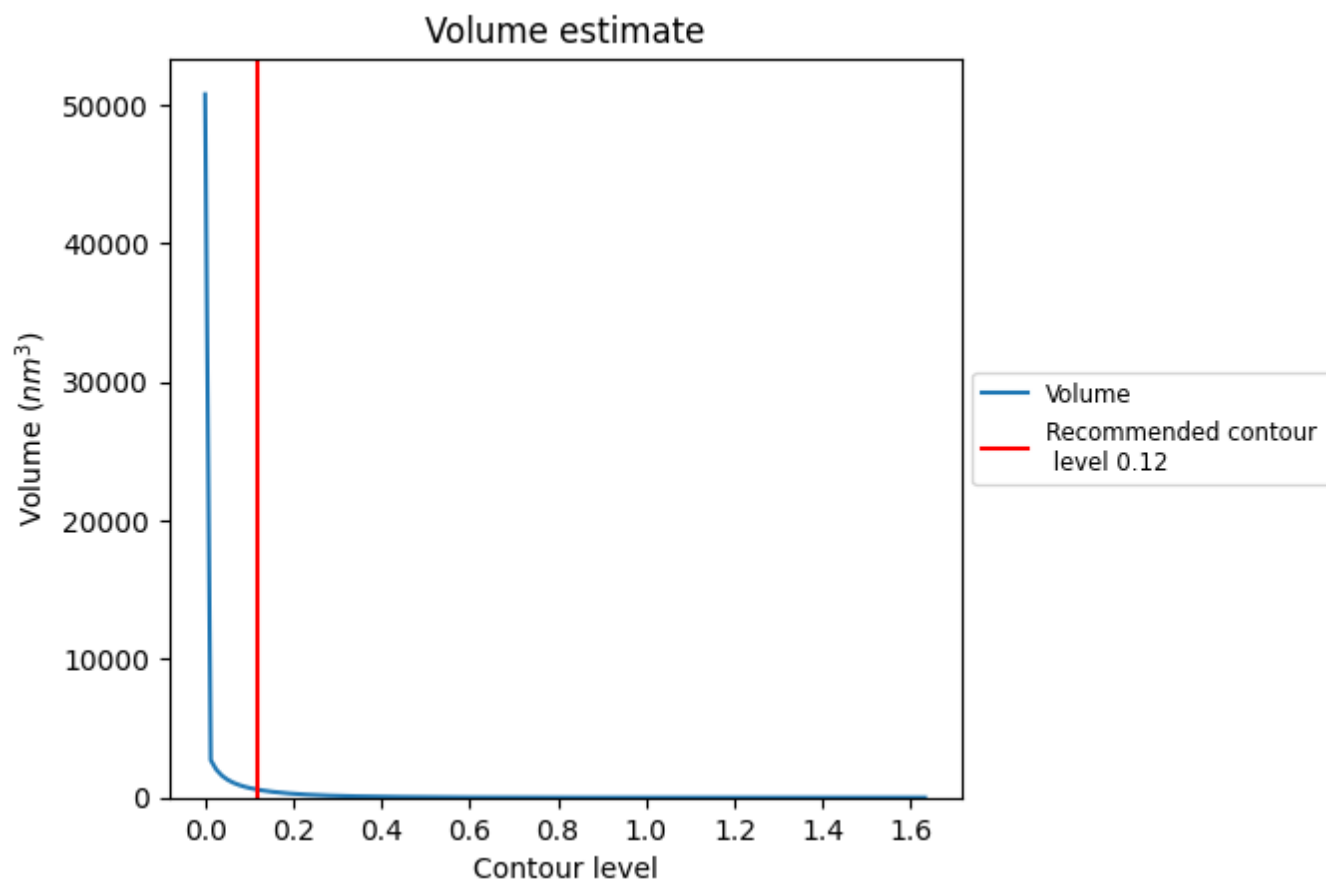
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

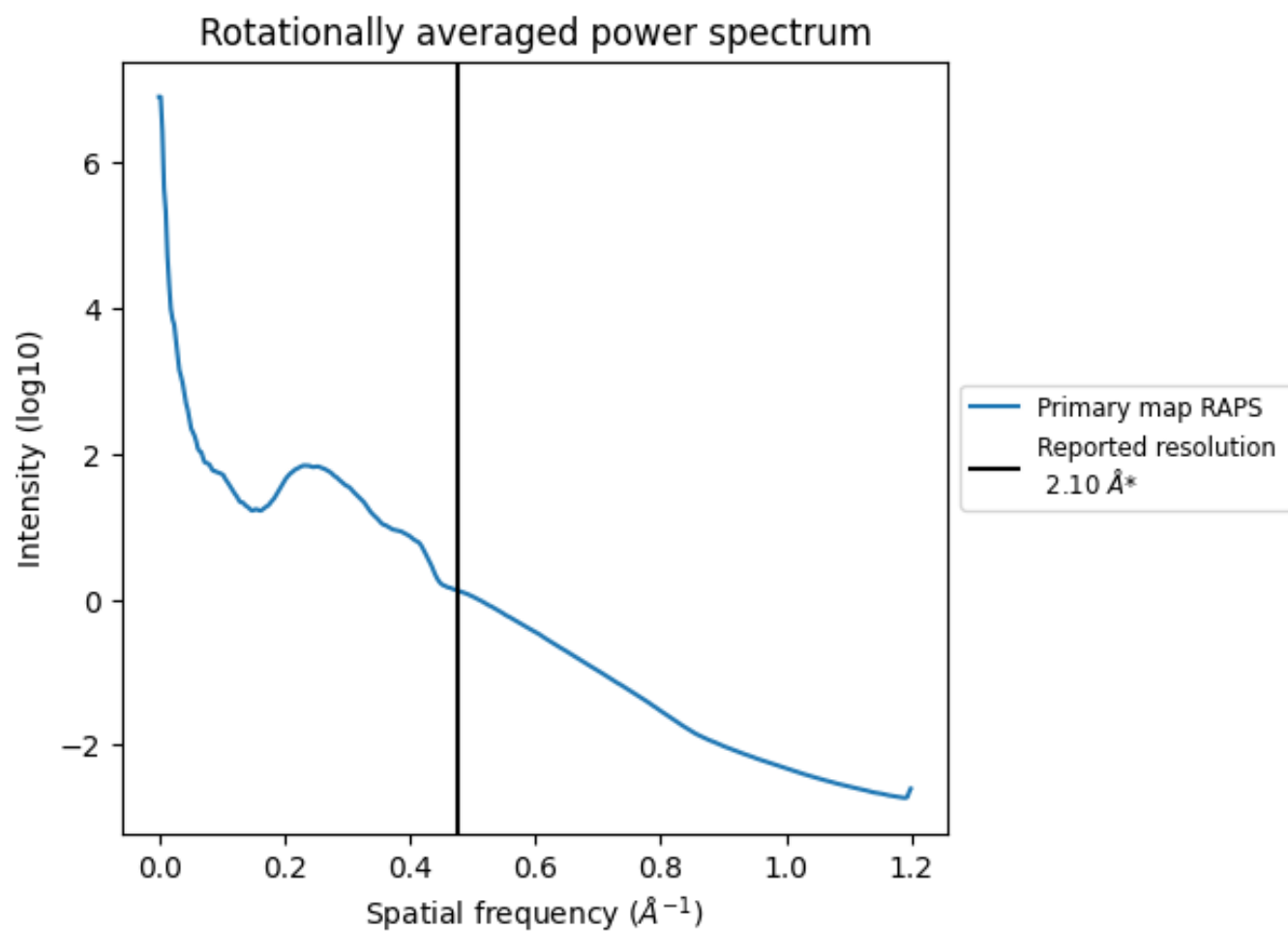
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 569 nm³; this corresponds to an approximate mass of 514 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 0.476 Å⁻¹

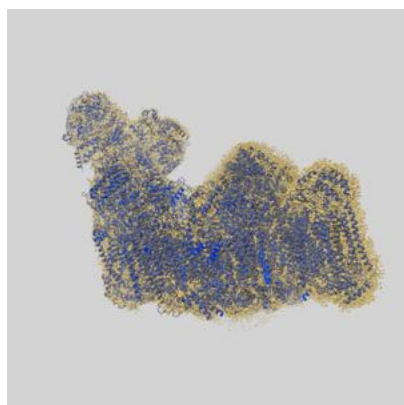
8 Fourier-Shell correlation

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

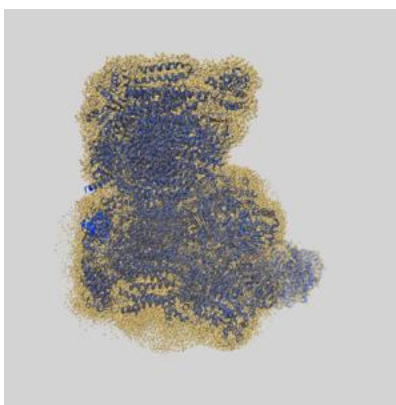
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-42226 and PDB model 8UGI. Per-residue inclusion information can be found in section [3](#) on page [37](#).

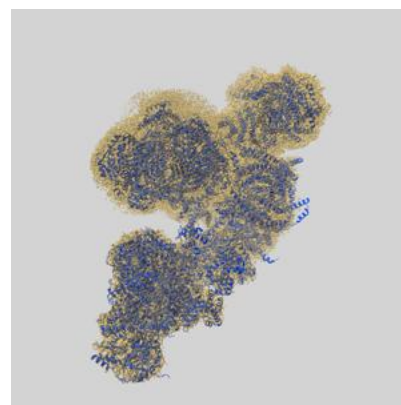
9.1 Map-model overlay [i](#)



X



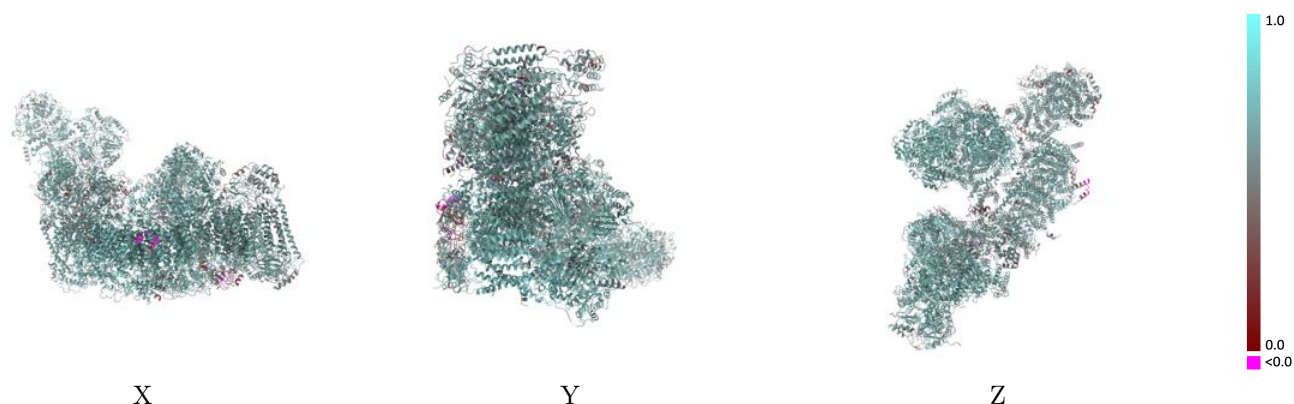
Y



Z

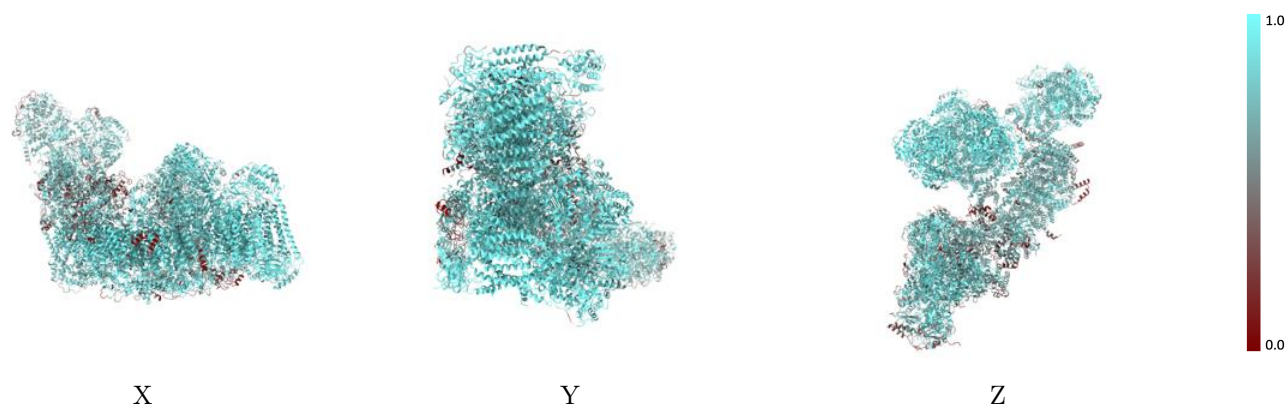
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



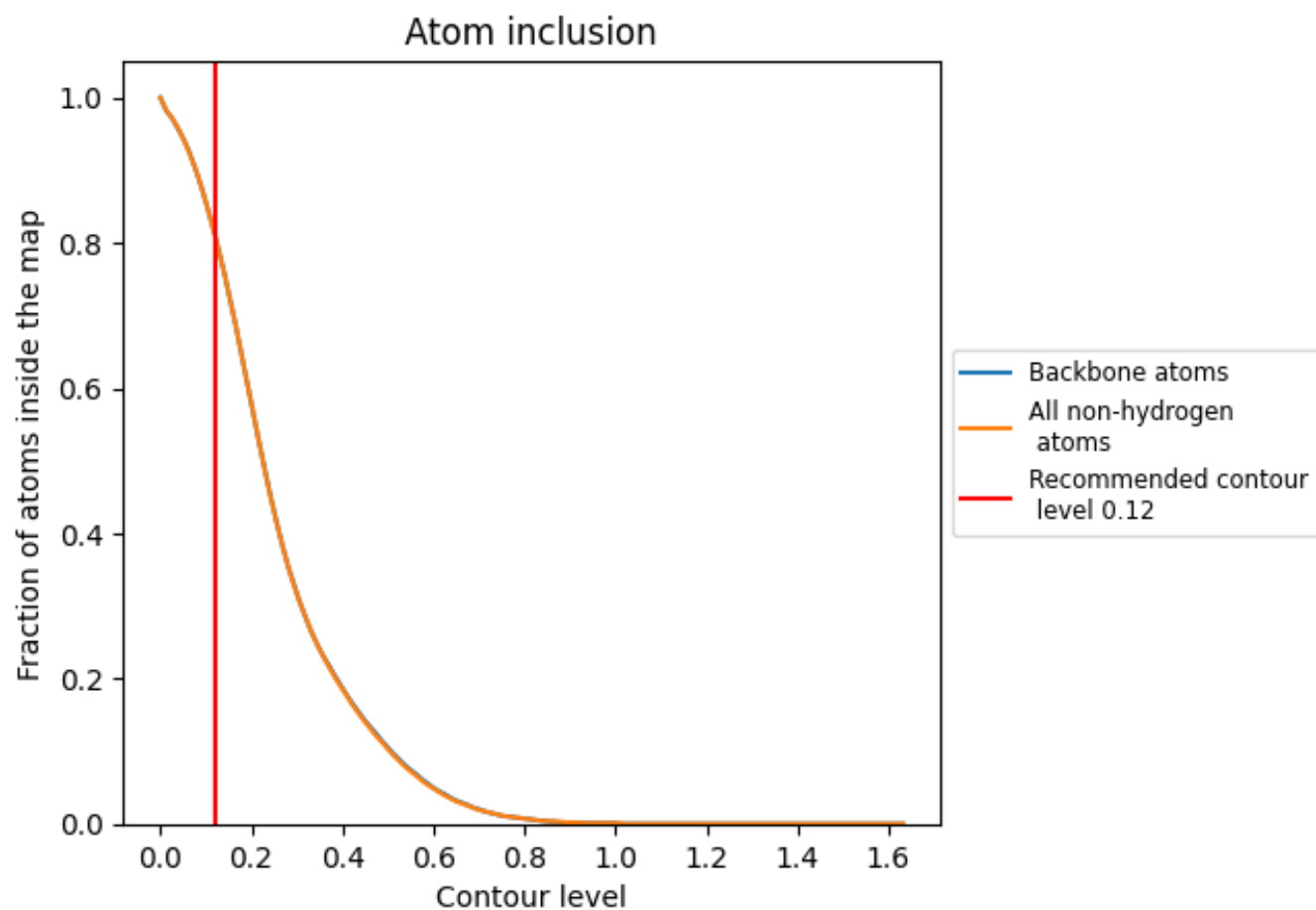
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 81% 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 (0.12) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.8110 |  0.6290 |
| 1A |  0.5190 |  0.5330 |
| 1B |  0.7830 |  0.6630 |
| 1C |  0.8480 |  0.6870 |
| 1D |  0.7960 |  0.6680 |
| 1E |  0.6080 |  0.5860 |
| 1F |  0.7220 |  0.6170 |
| 1G |  0.8100 |  0.6560 |
| 1H |  0.7760 |  0.6240 |
| 1I |  0.8700 |  0.6900 |
| 1J |  0.6170 |  0.5640 |
| 1K |  0.9020 |  0.6730 |
| 1L |  0.8600 |  0.6620 |
| 1M |  0.9120 |  0.6880 |
| 1N |  0.9020 |  0.6860 |
| 1O |  0.6060 |  0.5640 |
| 1P |  0.7150 |  0.6230 |
| 1Q |  0.7540 |  0.6250 |
| 1R |  0.7400 |  0.6380 |
| 1S |  0.7690 |  0.6130 |
| 1T |  0.2250 |  0.4150 |
| 1U |  0.6450 |  0.6190 |
| 1V |  0.5750 |  0.6070 |
| 1W |  0.7400 |  0.6490 |
| 1X |  0.7720 |  0.6300 |
| 1Y |  0.6240 |  0.5950 |
| 1Z |  0.7610 |  0.6400 |
| 1a |  0.8560 |  0.6560 |
| 1b |  0.6820 |  0.6010 |
| 1c |  0.5860 |  0.5910 |
| 1d |  0.7900 |  0.6610 |
| 1e |  0.8390 |  0.6470 |
| 1f |  0.6250 |  0.5700 |
| 1g |  0.7350 |  0.6110 |
| 1h |  0.7890 |  0.6540 |













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| Chain | Atom inclusion | Q-score |
|-------|----------------|---------|
| 1i | 0.5040 | 0.4740 |
| 1j | 0.5840 | 0.5440 |
| 1k | 0.5970 | 0.5710 |
| 1l | 0.7700 | 0.6440 |
| 1m | 0.7570 | 0.6210 |
| 1n | 0.7920 | 0.6340 |
| 1o | 0.6910 | 0.5950 |
| 1p | 0.7720 | 0.6270 |
| 1q | 0.7100 | 0.6630 |
| 1r | 0.6990 | 0.6480 |
| 1s | 0.5900 | 0.5740 |
| 3A | 0.9450 | 0.6800 |
| 3B | 0.9270 | 0.6670 |
| 3C | 0.9880 | 0.7070 |
| 3D | 0.9560 | 0.6770 |
| 3E | 0.5280 | 0.4410 |
| 3F | 0.9730 | 0.6820 |
| 3G | 0.9560 | 0.6510 |
| 3H | 0.8620 | 0.5730 |
| 3I | 0.7010 | 0.5410 |
| 3J | 0.9620 | 0.6820 |
| 3N | 0.9370 | 0.6780 |
| 3O | 0.9260 | 0.6560 |
| 3P | 0.9800 | 0.7090 |
| 3Q | 0.9540 | 0.6850 |
| 3R | 0.5250 | 0.3980 |
| 3S | 0.9570 | 0.6990 |
| 3T | 0.9270 | 0.6610 |
| 3U | 0.8700 | 0.5800 |
| 3V | 0.7210 | 0.5630 |
| 3W | 0.9820 | 0.6920 |
| 3X | 0.9090 | 0.6210 |
| 3Y | 0.9190 | 0.6390 |
| 4A | 0.9490 | 0.6290 |
| 4B | 0.8690 | 0.5720 |
| 4C | 0.8990 | 0.5850 |
| 4D | 0.8030 | 0.5190 |
| 4E | 0.8260 | 0.5190 |
| 4F | 0.8400 | 0.5430 |
| 4G | 0.7930 | 0.5020 |
| 4H | 0.8580 | 0.5360 |
| 4I | 0.8670 | 0.5790 |

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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| 4J |  0.8620 |  0.5620 |
| 4K |  0.7910 |  0.5190 |
| 4L |  0.8730 |  0.5580 |
| 4M |  0.8250 |  0.5480 |
| 4N |  0.8070 |  0.5330 |