



wwPDB EM Validation Summary Report ⓘ

May 27, 2024 – 01:56 AM EDT

PDB ID : 7SOM
EMDB ID : EMD-25361
Title : Ciliary C2 central pair apparatus isolated from *Chlamydomonas reinhardtii*
Authors : Gui, M.; Wang, X.; Dutcher, S.K.; Brown, A.; Zhang, R.
Deposited on : 2021-11-01
Resolution : 3.70 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.dev92
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

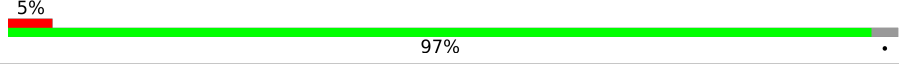
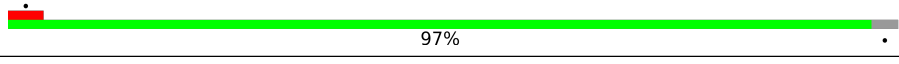
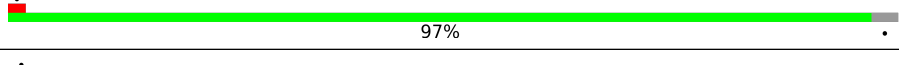
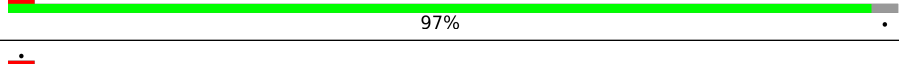
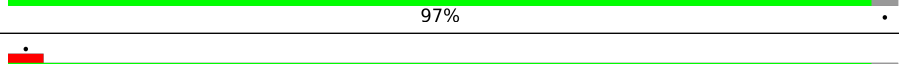
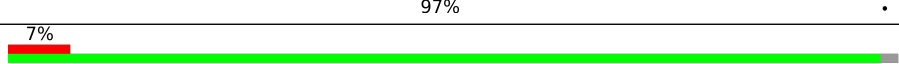
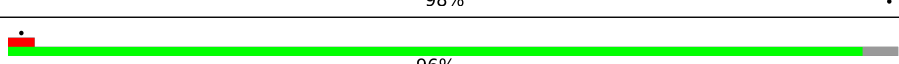
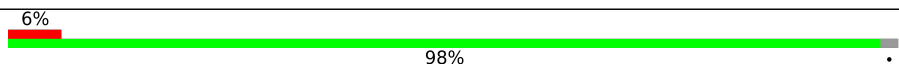
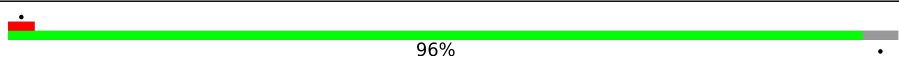
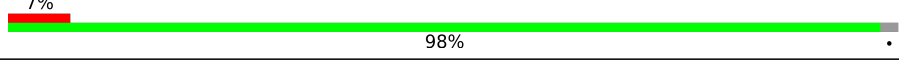
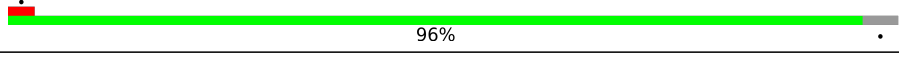
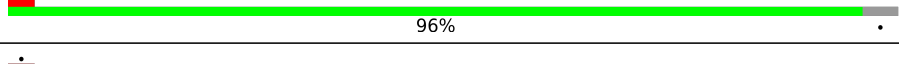
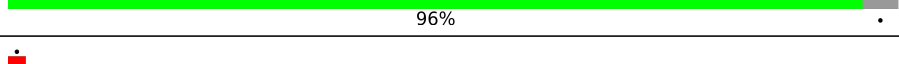
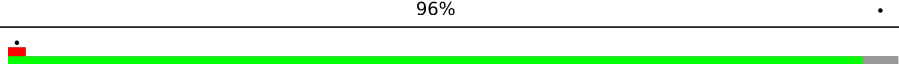
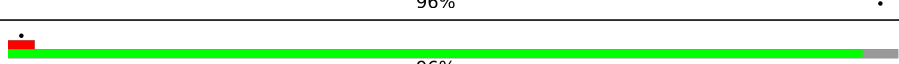


1 Overall quality at a glance

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

The reported resolution of this entry is 3.70 Å.

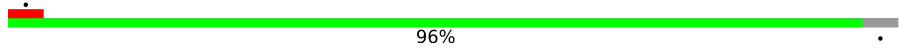
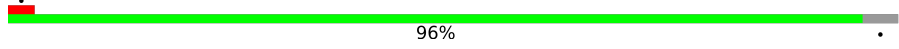
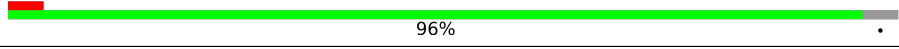
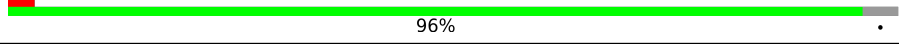
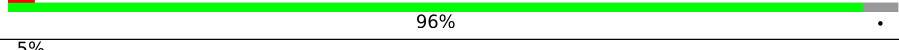
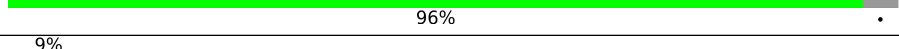
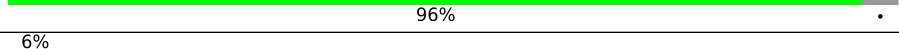
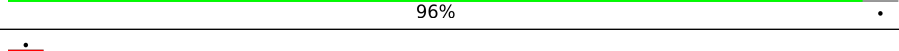
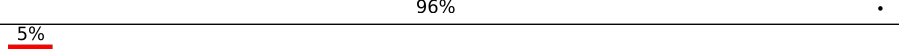
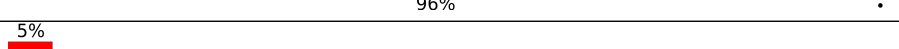
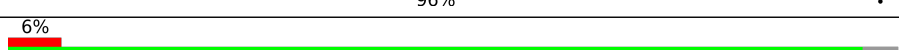
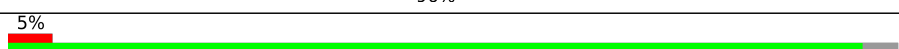
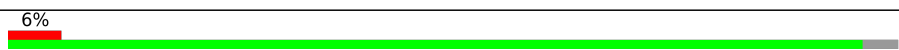
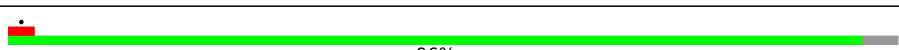
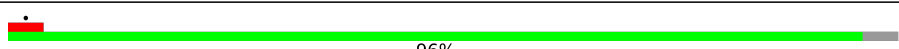
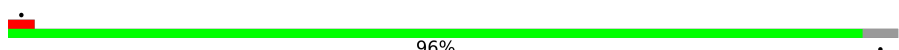
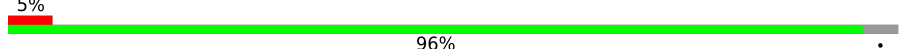
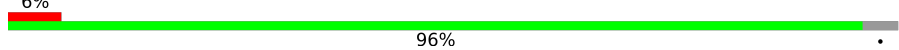
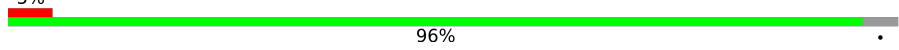
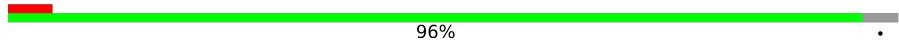
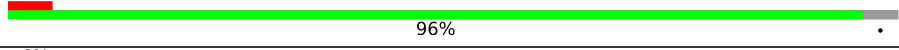
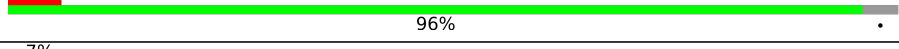
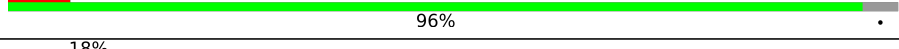
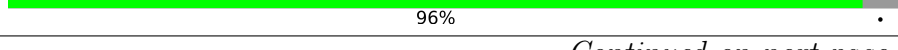

There are no overall percentile quality scores available for this entry.

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 | AA | 443 |  5% 97% |
| 1 | AC | 443 |  1% 97% |
| 1 | AE | 443 |  1% 97% |
| 1 | AG | 443 |  1% 97% |
| 1 | AI | 443 |  1% 97% |
| 1 | AK | 443 |  1% 97% |
| 1 | BA | 443 |  7% 98% |
| 1 | BC | 443 |  1% 96% |
| 1 | BE | 443 |  6% 98% |
| 1 | BG | 443 |  1% 96% |
| 1 | BI | 443 |  7% 98% |
| 1 | BK | 443 |  1% 96% |
| 1 | CA | 443 |  1% 96% |
| 1 | CC | 443 |  1% 96% |
| 1 | CE | 443 |  1% 96% |
| 1 | CG | 443 |  1% 96% |
| 1 | CI | 443 |  1% 96% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 1 | CK | 443 |  96% |
| 1 | DC | 443 |  96% |
| 1 | DE | 443 |  96% |
| 1 | DG | 443 |  96% |
| 1 | DI | 443 |  96% |
| 1 | DK | 443 |  96% |
| 1 | EA | 443 |  96% |
| 1 | EC | 443 |  96% |
| 1 | EE | 443 |  96% |
| 1 | EG | 443 |  96% |
| 1 | EI | 443 |  96% |
| 1 | EK | 443 |  96% |
| 1 | FA | 443 |  96% |
| 1 | FC | 443 |  96% |
| 1 | FE | 443 |  96% |
| 1 | FG | 443 |  96% |
| 1 | FI | 443 |  96% |
| 1 | FK | 443 |  96% |
| 1 | GC | 443 |  96% |
| 1 | GE | 443 |  96% |
| 1 | GG | 443 |  96% |
| 1 | GI | 443 |  96% |
| 1 | GK | 443 |  96% |
| 1 | GM | 443 |  96% |
| 1 | HC | 443 |  96% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | HE | 443 | 18% 96% |
| 1 | HG | 443 | 13% 96% |
| 1 | HI | 443 | 14% 96% |
| 1 | HK | 443 | 16% 96% |
| 1 | HM | 443 | 16% 96% |
| 1 | IC | 443 | 11% 96% |
| 1 | IE | 443 | 11% 96% |
| 1 | IG | 443 | 10% 96% |
| 1 | II | 443 | 10% 96% |
| 1 | IK | 443 | 10% 96% |
| 1 | IM | 443 | 10% 96% |
| 1 | JC | 443 | 6% 96% |
| 1 | JE | 443 | . 96% |
| 1 | JG | 443 | . 96% |
| 1 | JI | 443 | . 96% |
| 1 | JK | 443 | . 96% |
| 1 | JM | 443 | 5% 96% |
| 1 | KC | 443 | . 96% |
| 1 | KE | 443 | 5% 96% |
| 1 | KG | 443 | . 96% |
| 1 | KI | 443 | . 96% |
| 1 | KK | 443 | 5% 96% |
| 1 | LC | 443 | . 96% |
| 1 | LE | 443 | . 96% |
| 1 | LG | 443 | . 96% |

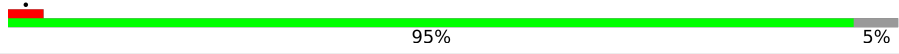
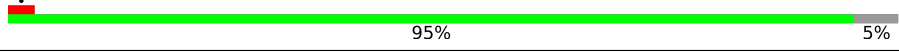
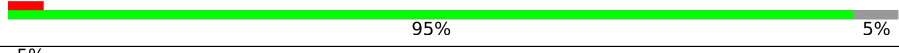
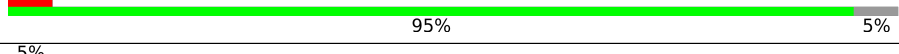
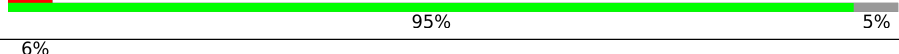
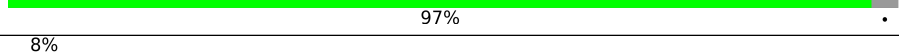
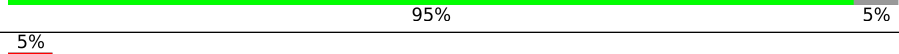
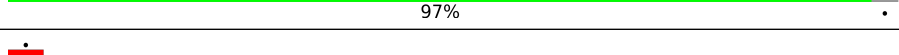
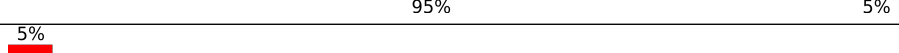
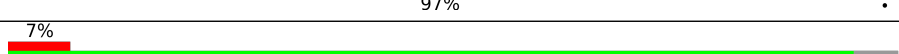
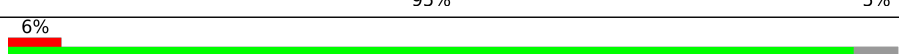
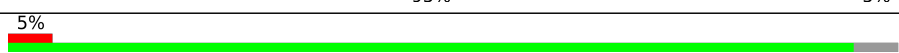
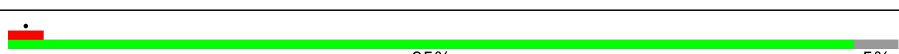
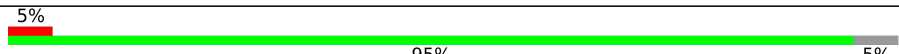
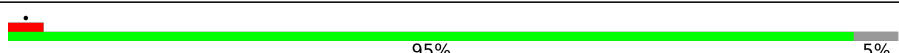
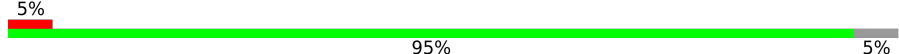
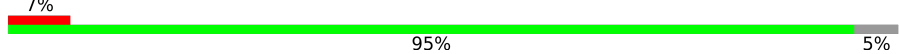
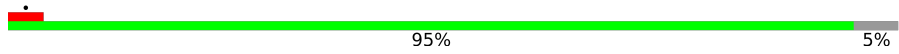
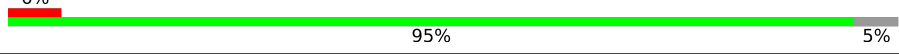
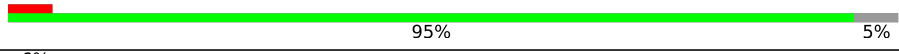
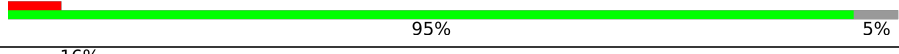
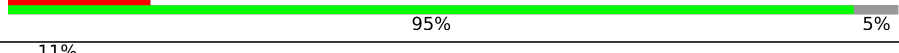
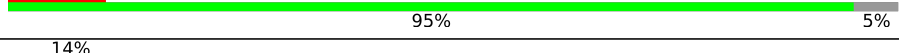
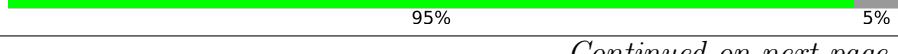

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | LI | 443 | 96% |
| 1 | LK | 443 | 96% |
| 1 | MC | 443 | 97% |
| 1 | ME | 443 | 96% |
| 1 | MG | 443 | 97% |
| 1 | MI | 443 | 96% |
| 1 | MK | 443 | 97% |
| 2 | AB | 451 | 96% |
| 2 | AD | 451 | 96% |
| 2 | AF | 451 | 96% |
| 2 | AH | 451 | 95% 5% |
| 2 | AJ | 451 | 96% |
| 2 | AL | 451 | 95% 5% |
| 2 | BB | 451 | 97% |
| 2 | BD | 451 | 95% 5% |
| 2 | BF | 451 | 97% |
| 2 | BH | 451 | 95% 5% |
| 2 | BJ | 451 | 97% |
| 2 | BL | 451 | 95% 5% |
| 2 | CB | 451 | 95% 5% |
| 2 | CD | 451 | 95% 5% |
| 2 | CF | 451 | 95% 5% |
| 2 | CH | 451 | 95% 5% |
| 2 | CJ | 451 | 95% 5% |
| 2 | DB | 451 | 95% 5% |

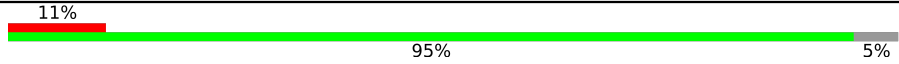
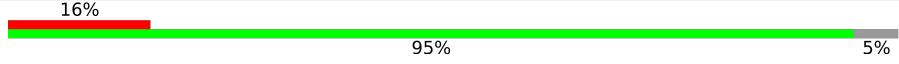
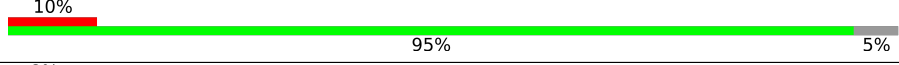
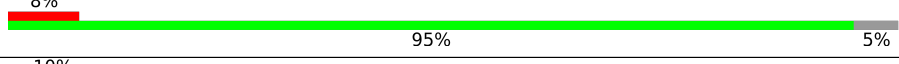
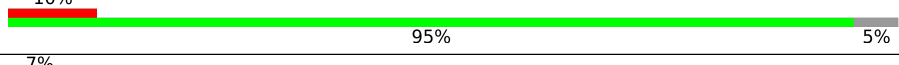
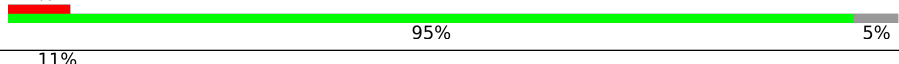
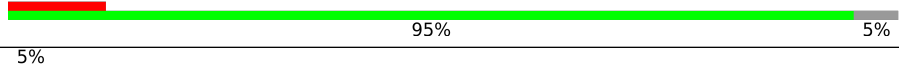
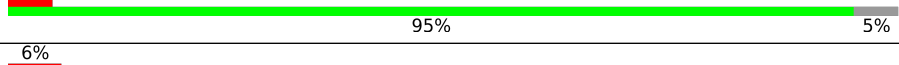
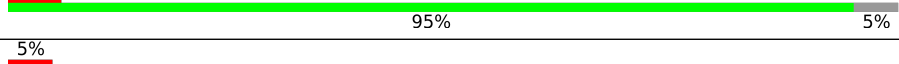
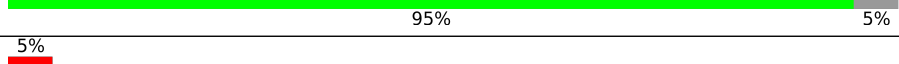
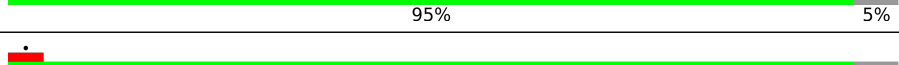
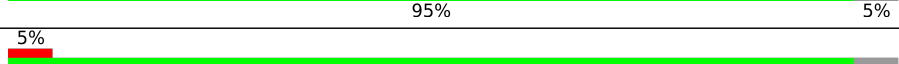
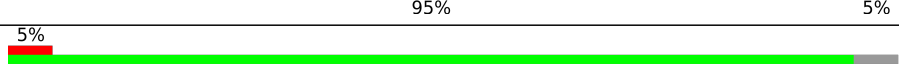
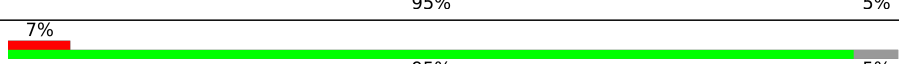
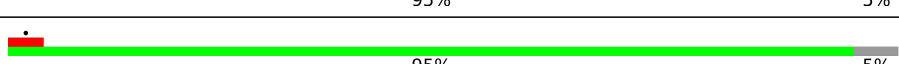
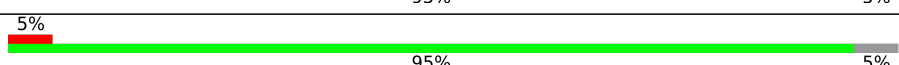
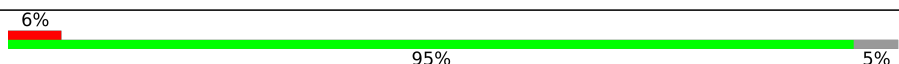
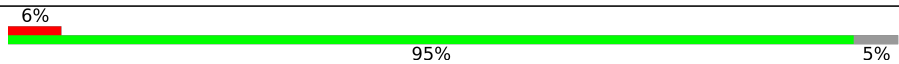
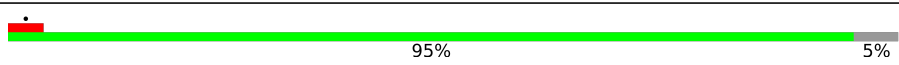
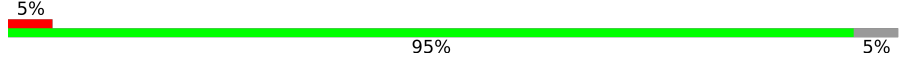
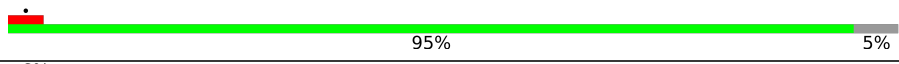
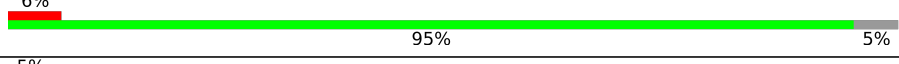
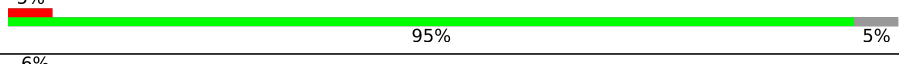
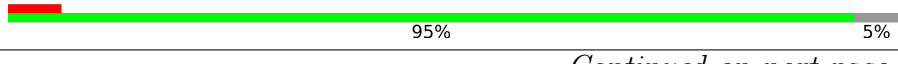

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 2 | DD | 451 |  95% 5% |
| 2 | DF | 451 |  95% 5% |
| 2 | DH | 451 |  95% 5% |
| 2 | DJ | 451 |  95% 5% |
| 2 | DL | 451 |  95% 5% |
| 2 | EB | 451 |  97% 5% |
| 2 | ED | 451 |  95% 5% |
| 2 | EF | 451 |  97% 5% |
| 2 | EH | 451 |  95% 5% |
| 2 | EJ | 451 |  97% 5% |
| 2 | EL | 451 |  95% 5% |
| 2 | FB | 451 |  95% 5% |
| 2 | FD | 451 |  95% 5% |
| 2 | FF | 451 |  95% 5% |
| 2 | FH | 451 |  95% 5% |
| 2 | FJ | 451 |  95% 5% |
| 2 | FL | 451 |  95% 5% |
| 2 | GD | 451 |  95% 5% |
| 2 | GF | 451 |  95% 5% |
| 2 | GH | 451 |  95% 5% |
| 2 | GJ | 451 |  95% 5% |
| 2 | GL | 451 |  95% 5% |
| 2 | HD | 451 |  95% 5% |
| 2 | HF | 451 |  95% 5% |
| 2 | HH | 451 |  95% 5% |

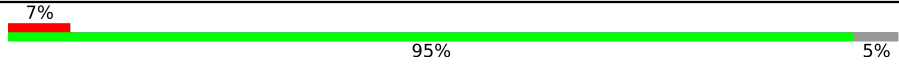
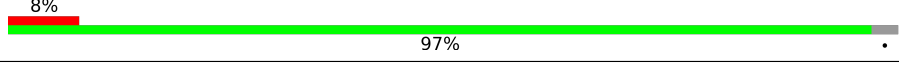
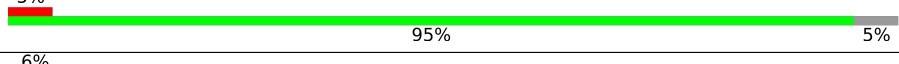
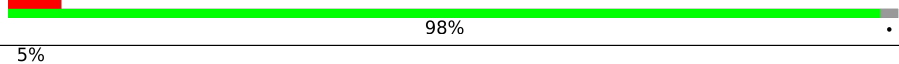
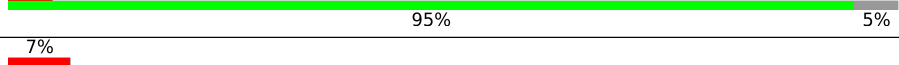
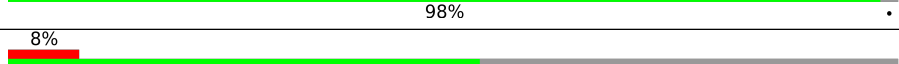
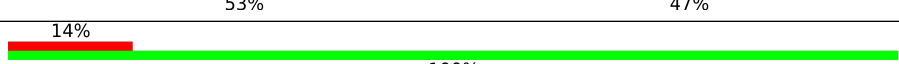
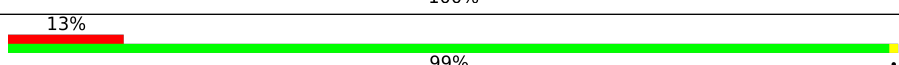
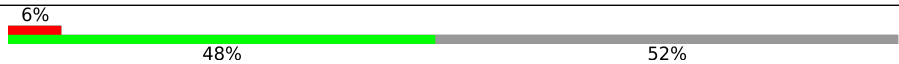
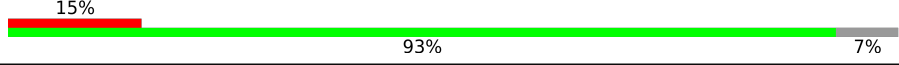
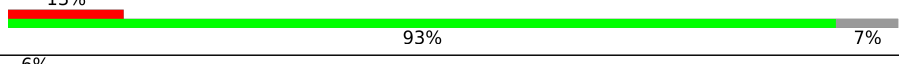
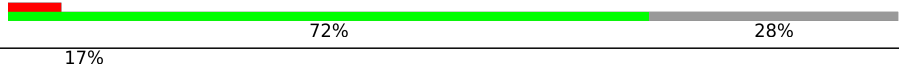
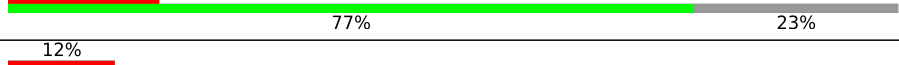

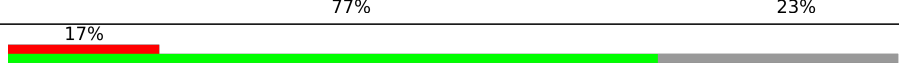





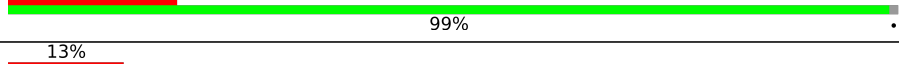
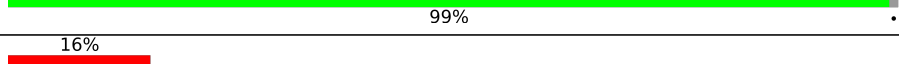
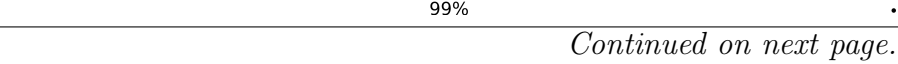


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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 2 | HJ | 451 |  |
| 2 | HL | 451 |  |
| 2 | ID | 451 |  |
| 2 | IF | 451 |  |
| 2 | IH | 451 |  |
| 2 | IJ | 451 |  |
| 2 | IL | 451 |  |
| 2 | JB | 451 |  |
| 2 | JD | 451 |  |
| 2 | JF | 451 |  |
| 2 | JH | 451 |  |
| 2 | JJ | 451 |  |
| 2 | JL | 451 |  |
| 2 | KB | 451 |  |
| 2 | KD | 451 |  |
| 2 | KF | 451 |  |
| 2 | KH | 451 |  |
| 2 | KJ | 451 |  |
| 2 | KL | 451 |  |
| 2 | LB | 451 |  |
| 2 | LD | 451 |  |
| 2 | LF | 451 |  |
| 2 | LH | 451 |  |
| 2 | LJ | 451 |  |
| 2 | LL | 451 |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 2 | MB | 451 |  |
| 2 | MD | 451 |  |
| 2 | MF | 451 |  |
| 2 | MH | 451 |  |
| 2 | MJ | 451 |  |
| 2 | ML | 451 |  |
| 3 | a | 618 |  |
| 3 | b | 618 |  |
| 3 | c | 618 |  |
| 3 | d | 618 |  |
| 4 | e | 201 |  |
| 4 | f | 201 |  |
| 4 | g | 201 |  |
| 5 | h | 758 |  |
| 5 | i | 758 |  |
| 5 | j | 758 |  |
| 6 | k | 528 |  |
| 6 | l | 528 |  |
| 6 | s | 528 |  |
| 7 | m | 421 |  |
| 7 | n | 421 |  |
| 7 | o | 421 |  |
| 8 | p | 89 |  |
| 8 | q | 89 |  |
| 8 | r | 89 |  |

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| Mol | Chain | Length | Quality of chain | |
|-----|-------|--------|------------------|-----|
| 9 | A | 190 | 23% | 98% |
| 9 | B | 190 | 17% | 98% |
| 9 | C | 190 | 28% | 98% |
| 10 | P | 606 | 50% | 71% |
| 10 | Q | 606 | 36% | 71% |
| 10 | R | 606 | 50% | 71% |
| 10 | S | 606 | 32% | 71% |
| 10 | Z | 606 | 15% | 85% |
| 10 | aa | 606 | 34% | 48% |
| 10 | cc | 606 | 15% | 85% |
| 11 | T | 93 | 28% | 68% |
| 11 | U | 93 | 23% | 62% |
| 11 | V | 93 | 37% | 72% |
| 11 | W | 93 | 25% | 68% |
| 12 | D | 2257 | 20% | 67% |
| 12 | E | 2257 | 20% | 67% |
| 12 | bb | 2257 | 8% | 92% |
| 13 | F | 1074 | 27% | 91% |
| 13 | G | 1074 | 31% | 92% |
| 13 | H | 1074 | 27% | 91% |
| 13 | I | 1074 | 31% | 92% |
| 14 | J | 976 | 15% | 68% |
| 14 | K | 976 | 14% | 68% |
| 15 | L | 222 | 32% | 48% |
| 15 | M | 222 | 42% | 48% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 15 | N | 222 | |
| 15 | O | 222 | |
| 15 | X | 222 | |
| 15 | Y | 222 | |
| 16 | A1 | 48 | |
| 17 | A2 | 77 | |
| 17 | A4 | 77 | |
| 18 | A3 | 47 | |

2 Entry composition [i](#)

There are 21 unique types of molecules in this entry. The entry contains 618760 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 Tubulin beta.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| | | | Total | C | N | O | S | | |
| 1 | AA | 431 | 3379 | 2121 | 579 | 649 | 30 | 0 | 0 |
| 1 | AC | 430 | 3370 | 2116 | 578 | 646 | 30 | 0 | 0 |
| 1 | AE | 431 | 3379 | 2121 | 579 | 649 | 30 | 0 | 0 |
| 1 | AG | 431 | 3379 | 2121 | 579 | 649 | 30 | 0 | 0 |
| 1 | AI | 431 | 3379 | 2121 | 579 | 649 | 30 | 0 | 0 |
| 1 | AK | 431 | 3379 | 2121 | 579 | 649 | 30 | 0 | 0 |
| 1 | BA | 432 | 3388 | 2126 | 580 | 652 | 30 | 0 | 0 |
| 1 | BC | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | BE | 432 | 3388 | 2126 | 580 | 652 | 30 | 0 | 0 |
| 1 | BG | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | BI | 432 | 3388 | 2126 | 580 | 652 | 30 | 0 | 0 |
| 1 | BK | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | CC | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | CE | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | CG | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | CI | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | CK | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|----------|----------|---------|---------|-------|
| 1 | DC | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | DE | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | DG | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | DI | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | DK | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | EA | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | EC | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | EE | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | EG | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | EI | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | EK | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | FA | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | FC | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | FE | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | FG | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | FI | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | FK | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | GC | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | GE | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | GG | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |
| 1 | GI | 427 | Total 3354 | C 2107 | N 575 | O 642 | S 30 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| | | | Total | C | N | O | S | | |
| 1 | GK | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | GM | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | HC | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | HE | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | HG | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | HI | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | HK | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | HM | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | IC | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | IE | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | IG | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | II | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | IK | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | IM | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | JC | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | JE | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | JG | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | JI | 426 | 3346 | 2103 | 574 | 639 | 30 | 0 | 0 |
| 1 | JK | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |
| 1 | JM | 426 | 3346 | 2103 | 574 | 639 | 30 | 0 | 0 |
| 1 | KC | 427 | 3354 | 2107 | 575 | 642 | 30 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 1 | KE | 427 | Total | C | N | O | S | 0 | 0 |
| | | | 3354 | 2107 | 575 | 642 | 30 | | |
| 1 | KG | 427 | Total | C | N | O | S | 0 | 0 |
| | | | 3354 | 2107 | 575 | 642 | 30 | | |
| 1 | KI | 427 | Total | C | N | O | S | 0 | 0 |
| | | | 3354 | 2107 | 575 | 642 | 30 | | |
| 1 | KK | 427 | Total | C | N | O | S | 0 | 0 |
| | | | 3354 | 2107 | 575 | 642 | 30 | | |
| 1 | LC | 427 | Total | C | N | O | S | 0 | 0 |
| | | | 3354 | 2107 | 575 | 642 | 30 | | |
| 1 | LE | 427 | Total | C | N | O | S | 0 | 0 |
| | | | 3354 | 2107 | 575 | 642 | 30 | | |
| 1 | LG | 427 | Total | C | N | O | S | 0 | 0 |
| | | | 3354 | 2107 | 575 | 642 | 30 | | |
| 1 | LI | 427 | Total | C | N | O | S | 0 | 0 |
| | | | 3354 | 2107 | 575 | 642 | 30 | | |
| 1 | LK | 427 | Total | C | N | O | S | 0 | 0 |
| | | | 3354 | 2107 | 575 | 642 | 30 | | |
| 1 | MC | 431 | Total | C | N | O | S | 0 | 0 |
| | | | 3379 | 2121 | 579 | 649 | 30 | | |
| 1 | ME | 427 | Total | C | N | O | S | 0 | 0 |
| | | | 3354 | 2107 | 575 | 642 | 30 | | |
| 1 | MG | 431 | Total | C | N | O | S | 0 | 0 |
| | | | 3379 | 2121 | 579 | 649 | 30 | | |
| 1 | MI | 427 | Total | C | N | O | S | 0 | 0 |
| | | | 3354 | 2107 | 575 | 642 | 30 | | |
| 1 | MK | 431 | Total | C | N | O | S | 0 | 0 |
| | | | 3379 | 2121 | 579 | 649 | 30 | | |
| 1 | CA | 427 | Total | C | N | O | S | 0 | 0 |
| | | | 3354 | 2107 | 575 | 642 | 30 | | |

- Molecule 2 is a protein called Tubulin alpha.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 2 | AB | 432 | Total | C | N | O | S | 0 | 0 |
| | | | 3355 | 2124 | 570 | 639 | 22 | | |
| 2 | AD | 432 | Total | C | N | O | S | 0 | 0 |
| | | | 3355 | 2123 | 570 | 640 | 22 | | |
| 2 | AF | 432 | Total | C | N | O | S | 0 | 0 |
| | | | 3355 | 2124 | 570 | 639 | 22 | | |
| 2 | AH | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 2 | AJ | 432 | Total | C | N | O | S | 0 | 0 |
| | | | 3355 | 2124 | 570 | 639 | 22 | | |
| 2 | AL | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | BB | 438 | Total | C | N | O | S | 0 | 0 |
| | | | 3393 | 2146 | 577 | 648 | 22 | | |
| 2 | BD | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | BF | 438 | Total | C | N | O | S | 0 | 0 |
| | | | 3393 | 2146 | 577 | 648 | 22 | | |
| 2 | BH | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | BJ | 438 | Total | C | N | O | S | 0 | 0 |
| | | | 3393 | 2146 | 577 | 648 | 22 | | |
| 2 | BL | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | CB | 429 | Total | C | N | O | S | 0 | 0 |
| | | | 3335 | 2113 | 567 | 633 | 22 | | |
| 2 | CD | 429 | Total | C | N | O | S | 0 | 0 |
| | | | 3335 | 2113 | 567 | 633 | 22 | | |
| 2 | CF | 429 | Total | C | N | O | S | 0 | 0 |
| | | | 3335 | 2113 | 567 | 633 | 22 | | |
| 2 | CH | 429 | Total | C | N | O | S | 0 | 0 |
| | | | 3335 | 2113 | 567 | 633 | 22 | | |
| 2 | CJ | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | DB | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | DD | 429 | Total | C | N | O | S | 0 | 0 |
| | | | 3335 | 2113 | 567 | 633 | 22 | | |
| 2 | DF | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | DH | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | DJ | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | DL | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | EB | 438 | Total | C | N | O | S | 0 | 0 |
| | | | 3393 | 2146 | 577 | 648 | 22 | | |
| 2 | ED | 429 | Total | C | N | O | S | 0 | 0 |
| | | | 3335 | 2113 | 567 | 633 | 22 | | |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|----------|----------|---------|---------|-------|
| | | | Total | C | N | O | S | | |
| 2 | EF | 439 | Total 3399 | C 2149 | N 578 | O 650 | S 22 | 0 | 0 |
| 2 | EH | 429 | Total 3335 | C 2113 | N 567 | O 633 | S 22 | 0 | 0 |
| 2 | EJ | 438 | Total 3393 | C 2146 | N 577 | O 648 | S 22 | 0 | 0 |
| 2 | EL | 429 | Total 3335 | C 2113 | N 567 | O 633 | S 22 | 0 | 0 |
| 2 | FB | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | FD | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | FF | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | FH | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | FJ | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | FL | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | GD | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | GF | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | GH | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | GJ | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | GL | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | HD | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | HF | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | HH | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | HJ | 428 | Total 3326 | C 2108 | N 566 | O 630 | S 22 | 0 | 0 |
| 2 | HL | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | ID | 429 | Total 3335 | C 2113 | N 567 | O 633 | S 22 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|---------------|-----------|----------|----------|---------|---------|-------|
| | | | Total | C | N | O | S | | |
| 2 | IF | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | IH | 429 | Total 3335 | C 2113 | N 567 | O 633 | S 22 | 0 | 0 |
| 2 | IJ | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | IL | 429 | Total 3335 | C 2113 | N 567 | O 633 | S 22 | 0 | 0 |
| 2 | JB | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | JD | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | JF | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | JH | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | JJ | 429 | Total 3335 | C 2113 | N 567 | O 633 | S 22 | 0 | 0 |
| 2 | JL | 429 | Total 3335 | C 2113 | N 567 | O 633 | S 22 | 0 | 0 |
| 2 | KB | 429 | Total 3335 | C 2113 | N 567 | O 633 | S 22 | 0 | 0 |
| 2 | KD | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | KF | 429 | Total 3335 | C 2113 | N 567 | O 633 | S 22 | 0 | 0 |
| 2 | KH | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | KJ | 429 | Total 3335 | C 2113 | N 567 | O 633 | S 22 | 0 | 0 |
| 2 | KL | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | LB | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | LD | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | LF | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | LH | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |
| 2 | LJ | 430 | Total 3341 | C 2116 | N 568 | O 635 | S 22 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 2 | LL | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | MB | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | MD | 439 | Total | C | N | O | S | 0 | 0 |
| | | | 3399 | 2149 | 578 | 650 | 22 | | |
| 2 | MF | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | MH | 440 | Total | C | N | O | S | 0 | 0 |
| | | | 3404 | 2152 | 579 | 651 | 22 | | |
| 2 | MJ | 430 | Total | C | N | O | S | 0 | 0 |
| | | | 3341 | 2116 | 568 | 635 | 22 | | |
| 2 | ML | 440 | Total | C | N | O | S | 0 | 0 |
| | | | 3404 | 2152 | 579 | 651 | 22 | | |

- Molecule 3 is a protein called Cilia- and flagella-associated protein 20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 3 | a | 325 | Total | C | N | O | S | 0 | 0 |
| | | | 2380 | 1491 | 422 | 453 | 14 | | |
| 3 | b | 617 | Total | C | N | O | S | 0 | 0 |
| | | | 4537 | 2823 | 824 | 857 | 33 | | |
| 3 | c | 617 | Total | C | N | O | S | 0 | 0 |
| | | | 4537 | 2823 | 824 | 857 | 33 | | |
| 3 | d | 295 | Total | C | N | O | S | 0 | 0 |
| | | | 2180 | 1345 | 407 | 409 | 19 | | |

- Molecule 4 is a protein called Unknown protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 4 | e | 186 | Total | C | N | O | S | 0 | 0 |
| | | | 1464 | 886 | 289 | 286 | 3 | | |
| 4 | f | 186 | Total | C | N | O | S | 0 | 0 |
| | | | 1464 | 886 | 289 | 286 | 3 | | |
| 4 | g | 145 | Total | C | N | O | S | 0 | 0 |
| | | | 1136 | 690 | 220 | 223 | 3 | | |

- Molecule 5 is a protein called Unknown protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 5 | h | 585 | Total | C | N | O | S | 0 | 0 |
| | | | 4525 | 2788 | 856 | 866 | 15 | | |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 5 | i | 585 | Total | C | N | O | S | 0 | 0 |
| | | | 4525 | 2788 | 856 | 866 | 15 | | |
| 5 | j | 585 | Total | C | N | O | S | 0 | 0 |
| | | | 4525 | 2788 | 856 | 866 | 15 | | |

- Molecule 6 is a protein called Unknown protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 6 | k | 388 | Total | C | N | O | S | 0 | 0 |
| | | | 3017 | 1857 | 582 | 572 | 6 | | |
| 6 | l | 388 | Total | C | N | O | S | 0 | 0 |
| | | | 3017 | 1857 | 582 | 572 | 6 | | |
| 6 | s | 285 | Total | C | N | O | S | 0 | 0 |
| | | | 2208 | 1369 | 420 | 415 | 4 | | |

- Molecule 7 is a protein called FAP65.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 7 | m | 352 | Total | C | N | O | S | 0 | 0 |
| | | | 2737 | 1685 | 532 | 512 | 8 | | |
| 7 | n | 352 | Total | C | N | O | S | 0 | 0 |
| | | | 2737 | 1685 | 532 | 512 | 8 | | |
| 7 | o | 352 | Total | C | N | O | S | 0 | 0 |
| | | | 2737 | 1685 | 532 | 512 | 8 | | |

- Molecule 8 is a protein called FAP70.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 8 | p | 88 | Total | C | N | O | S | 0 | 0 |
| | | | 698 | 432 | 135 | 129 | 2 | | |
| 8 | q | 88 | Total | C | N | O | S | 0 | 0 |
| | | | 698 | 432 | 135 | 129 | 2 | | |
| 8 | r | 88 | Total | C | N | O | S | 0 | 0 |
| | | | 698 | 432 | 135 | 129 | 2 | | |

- Molecule 9 is a protein called FAP147.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 9 | A | 186 | Total | C | N | O | S | 0 | 0 |
| | | | 1530 | 982 | 266 | 275 | 7 | | |
| 9 | B | 186 | Total | C | N | O | S | 0 | 0 |
| | | | 1530 | 982 | 266 | 275 | 7 | | |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 9 | C | 186 | 1530 | 982 | 266 | 275 | 7 | 0 | 0 |

- Molecule 10 is a protein called FAP178.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 10 | P | 433 | 2493 | 1507 | 495 | 486 | 5 | 0 | 0 |
| 10 | Q | 432 | 2488 | 1504 | 494 | 485 | 5 | 0 | 0 |
| 10 | R | 433 | 2493 | 1507 | 495 | 486 | 5 | 0 | 0 |
| 10 | S | 432 | 2488 | 1504 | 494 | 485 | 5 | 0 | 0 |
| 10 | aa | 292 | 1435 | 850 | 292 | 293 | | 0 | 0 |
| 10 | cc | 89 | 758 | 475 | 147 | 131 | 5 | 0 | 0 |
| 10 | Z | 92 | 775 | 486 | 150 | 134 | 5 | 0 | 0 |

- Molecule 11 is a protein called Flagellar WD repeat-containing protein Pf20.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| | | | Total | C | N | O | | |
| 11 | T | 63 | 312 | 186 | 63 | 63 | 0 | 0 |
| 11 | U | 58 | 287 | 171 | 58 | 58 | 0 | 0 |
| 11 | V | 67 | 332 | 198 | 67 | 67 | 0 | 0 |
| 11 | W | 63 | 312 | 186 | 63 | 63 | 0 | 0 |

- Molecule 12 is a protein called Flagellar associated protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 12 | bb | 175 | 1065 | 650 | 211 | 202 | 2 | 0 | 0 |
| 12 | D | 1516 | 7474 | 4442 | 1516 | 1516 | | 0 | 0 |
| 12 | E | 1516 | 7474 | 4442 | 1516 | 1516 | | 0 | 0 |

- Molecule 13 is a protein called FAP196.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 13 | F | 982 | Total | C | N | O | 0 | 0 |
| | | | 4832 | 2868 | 982 | 982 | | |
| 13 | G | 993 | Total | C | N | O | 0 | 0 |
| | | | 4884 | 2898 | 993 | 993 | | |
| 13 | H | 982 | Total | C | N | O | 0 | 0 |
| | | | 4832 | 2868 | 982 | 982 | | |
| 13 | I | 993 | Total | C | N | O | 0 | 0 |
| | | | 4884 | 2898 | 993 | 993 | | |

- Molecule 14 is a protein called FAP213.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 14 | J | 666 | Total | C | N | O | S | 0 | 0 |
| | | | 3874 | 2350 | 768 | 752 | 4 | | |
| 14 | K | 666 | Total | C | N | O | S | 0 | 0 |
| | | | 3874 | 2350 | 768 | 752 | 4 | | |

- Molecule 15 is a protein called FAP225.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15 | O | 107 | Total | C | N | O | S | 0 | 0 |
| | | | 841 | 534 | 154 | 149 | 4 | | |
| 15 | Y | 107 | Total | C | N | O | S | 0 | 0 |
| | | | 841 | 534 | 154 | 149 | 4 | | |
| 15 | L | 107 | Total | C | N | O | S | 0 | 0 |
| | | | 841 | 534 | 154 | 149 | 4 | | |
| 15 | M | 107 | Total | C | N | O | S | 0 | 0 |
| | | | 841 | 534 | 154 | 149 | 4 | | |
| 15 | N | 107 | Total | C | N | O | S | 0 | 0 |
| | | | 841 | 534 | 154 | 149 | 4 | | |
| 15 | X | 107 | Total | C | N | O | S | 0 | 0 |
| | | | 841 | 534 | 154 | 149 | 4 | | |

- Molecule 16 is a protein called FAP239.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 16 | A1 | 48 | Total | C | N | O | 0 | 0 |
| | | | 240 | 144 | 48 | 48 | | |

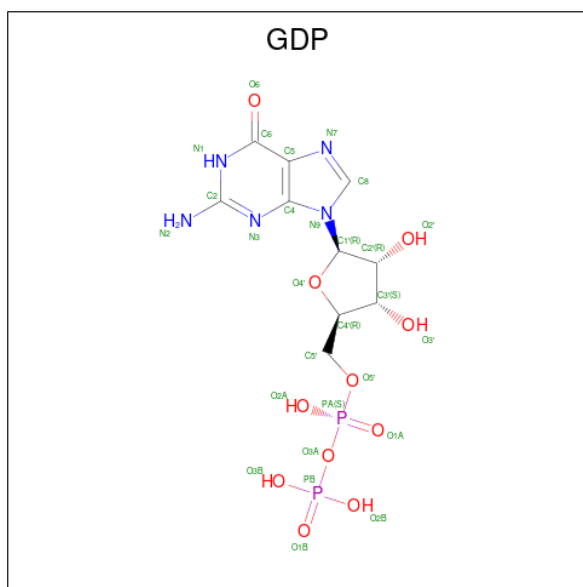
- Molecule 17 is a protein called FAP388.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 17 | A2 | 77 | Total | C | N | O | 0 | 0 |
| | | | 385 | 231 | 77 | 77 | | |
| 17 | A4 | 77 | Total | C | N | O | 0 | 0 |
| | | | 385 | 231 | 77 | 77 | | |

- Molecule 18 is a protein called FAP424.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 18 | A3 | 47 | Total | C | N | O | 0 | 0 |
| | | | 235 | 141 | 47 | 47 | | |

- Molecule 19 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|----|---|---------|
| 19 | AA | 1 | Total | C | N | O | P | 0 |
| | | | 28 | 10 | 5 | 11 | 2 | |
| 19 | AC | 1 | Total | C | N | O | P | 0 |
| | | | 28 | 10 | 5 | 11 | 2 | |
| 19 | AE | 1 | Total | C | N | O | P | 0 |
| | | | 28 | 10 | 5 | 11 | 2 | |
| 19 | AG | 1 | Total | C | N | O | P | 0 |
| | | | 28 | 10 | 5 | 11 | 2 | |
| 19 | AI | 1 | Total | C | N | O | P | 0 |
| | | | 28 | 10 | 5 | 11 | 2 | |
| 19 | AK | 1 | Total | C | N | O | P | 0 |
| | | | 28 | 10 | 5 | 11 | 2 | |

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| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|----|---|---------|
| | | | Total | C | N | O | P | |
| 19 | BA | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | BC | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | BE | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | BG | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | BI | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | BK | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | CC | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | CE | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | CG | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | CI | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | CK | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | DC | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | DE | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | DG | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | DI | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | DK | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | EA | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | EC | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | EE | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | EG | 1 | 28 | 10 | 5 | 11 | 2 | 0 |
| 19 | EI | 1 | 28 | 10 | 5 | 11 | 2 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------------|---------|--------|---------|--------|---------|
| | | | Total | C | N | O | P | |
| 19 | EK | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | FA | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | FC | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | FE | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | FG | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | FI | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | FK | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | GC | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | GE | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | GG | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | GI | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | GK | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | GM | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | HC | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | HE | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | HG | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | HI | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | HK | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | HM | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | IC | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | IE | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |

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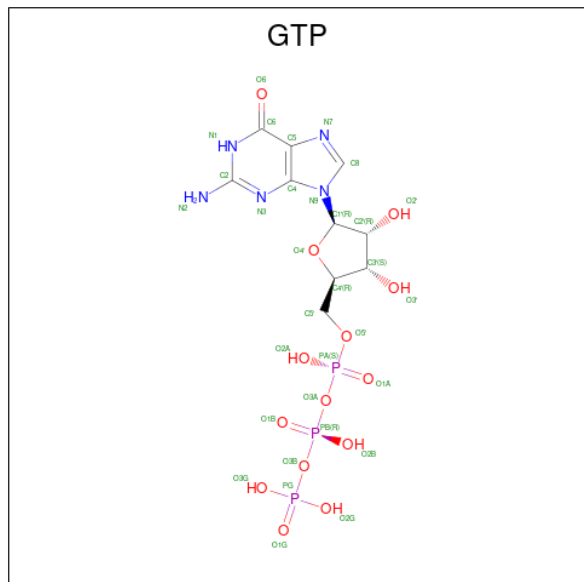
| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------------|---------|--------|---------|--------|---------|
| | | | Total | C | N | O | P | |
| 19 | IG | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | II | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | IK | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | IM | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | JC | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | JE | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | JG | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | JI | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | JK | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | JM | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | KC | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | KE | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | KG | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | KI | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | KK | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | LC | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | LE | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | LG | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | LI | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | LK | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | MC | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------------|---------|--------|---------|--------|---------|
| | | | Total | C | N | O | P | |
| 19 | ME | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | MG | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | MI | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | MK | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |
| 19 | CA | 1 | Total 28 | C 10 | N 5 | O 11 | P 2 | 0 |

- Molecule 20 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------------|---------|--------|---------|--------|---------|
| | | | Total | C | N | O | P | |
| 20 | AB | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | AD | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | AF | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | AH | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | AJ | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | AL | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------------|---------|--------|---------|--------|---------|
| | | | Total | C | N | O | P | |
| 20 | BB | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | BD | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | BF | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | BH | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | BJ | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | BL | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | CB | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | CD | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | CF | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | CH | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | CJ | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | DB | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | DD | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | DF | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | DH | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | DJ | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | DL | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | EB | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | ED | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | EF | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | EH | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------------|---------|--------|---------|--------|---------|
| | | | Total | C | N | O | P | |
| 20 | EJ | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | EL | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | FB | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | FD | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | FF | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | FH | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | FJ | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | FL | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | GD | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | GF | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | GH | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | GJ | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | GL | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | HD | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | HF | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | HI | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | HJ | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | HL | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | ID | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | IF | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | IH | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------------|---------|--------|---------|--------|---------|
| | | | Total | C | N | O | P | |
| 20 | IJ | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | IL | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | JB | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | JD | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | JF | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | JH | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | JJ | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | JL | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | KB | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | KD | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | KF | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | KH | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | KJ | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | KL | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | LB | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | LD | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | LF | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | LH | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | LJ | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | LL | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |
| 20 | MB | 1 | Total 32 | C 10 | N 5 | O 14 | P 3 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|----|---|---------|
| | | | Total | C | N | O | P | |
| 20 | MD | 1 | 32 | 10 | 5 | 14 | 3 | 0 |
| 20 | MF | 1 | 32 | 10 | 5 | 14 | 3 | 0 |
| 20 | MH | 1 | 32 | 10 | 5 | 14 | 3 | 0 |
| 20 | MJ | 1 | 32 | 10 | 5 | 14 | 3 | 0 |
| 20 | ML | 1 | 32 | 10 | 5 | 14 | 3 | 0 |

- Molecule 21 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| | | | Total | Mg | |
| 21 | AB | 1 | 1 | 1 | 0 |
| 21 | AD | 1 | 1 | 1 | 0 |
| 21 | AF | 1 | 1 | 1 | 0 |
| 21 | AH | 1 | 1 | 1 | 0 |
| 21 | AJ | 1 | 1 | 1 | 0 |
| 21 | AL | 1 | 1 | 1 | 0 |
| 21 | BB | 1 | 1 | 1 | 0 |
| 21 | BD | 1 | 1 | 1 | 0 |
| 21 | BF | 1 | 1 | 1 | 0 |
| 21 | BH | 1 | 1 | 1 | 0 |
| 21 | BJ | 1 | 1 | 1 | 0 |
| 21 | BL | 1 | 1 | 1 | 0 |
| 21 | CB | 1 | 1 | 1 | 0 |
| 21 | CD | 1 | 1 | 1 | 0 |

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| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| | | | Total | Mg | |
| 21 | CF | 1 | 1 | 1 | 0 |
| 21 | CH | 1 | 1 | 1 | 0 |
| 21 | CJ | 1 | 1 | 1 | 0 |
| 21 | DB | 1 | 1 | 1 | 0 |
| 21 | DD | 1 | 1 | 1 | 0 |
| 21 | DF | 1 | 1 | 1 | 0 |
| 21 | DH | 1 | 1 | 1 | 0 |
| 21 | DJ | 1 | 1 | 1 | 0 |
| 21 | DL | 1 | 1 | 1 | 0 |
| 21 | EB | 1 | 1 | 1 | 0 |
| 21 | EE | 1 | 1 | 1 | 0 |
| 21 | EF | 1 | 1 | 1 | 0 |
| 21 | EH | 1 | 1 | 1 | 0 |
| 21 | EJ | 1 | 1 | 1 | 0 |
| 21 | EL | 1 | 1 | 1 | 0 |
| 21 | FB | 1 | 1 | 1 | 0 |
| 21 | FD | 1 | 1 | 1 | 0 |
| 21 | FF | 1 | 1 | 1 | 0 |
| 21 | FH | 1 | 1 | 1 | 0 |
| 21 | FJ | 1 | 1 | 1 | 0 |
| 21 | FL | 1 | 1 | 1 | 0 |

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| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| | | | Total | Mg | |
| 21 | GD | 1 | 1 | 1 | 0 |
| 21 | GF | 1 | 1 | 1 | 0 |
| 21 | GH | 1 | 1 | 1 | 0 |
| 21 | GJ | 1 | 1 | 1 | 0 |
| 21 | GL | 1 | 1 | 1 | 0 |
| 21 | HD | 1 | 1 | 1 | 0 |
| 21 | HF | 1 | 1 | 1 | 0 |
| 21 | HH | 1 | 1 | 1 | 0 |
| 21 | HJ | 1 | 1 | 1 | 0 |
| 21 | HL | 1 | 1 | 1 | 0 |
| 21 | ID | 1 | 1 | 1 | 0 |
| 21 | IF | 1 | 1 | 1 | 0 |
| 21 | IH | 1 | 1 | 1 | 0 |
| 21 | IJ | 1 | 1 | 1 | 0 |
| 21 | IL | 1 | 1 | 1 | 0 |
| 21 | JB | 1 | 1 | 1 | 0 |
| 21 | JD | 1 | 1 | 1 | 0 |
| 21 | JF | 1 | 1 | 1 | 0 |
| 21 | JH | 1 | 1 | 1 | 0 |
| 21 | JJ | 1 | 1 | 1 | 0 |
| 21 | JL | 1 | 1 | 1 | 0 |

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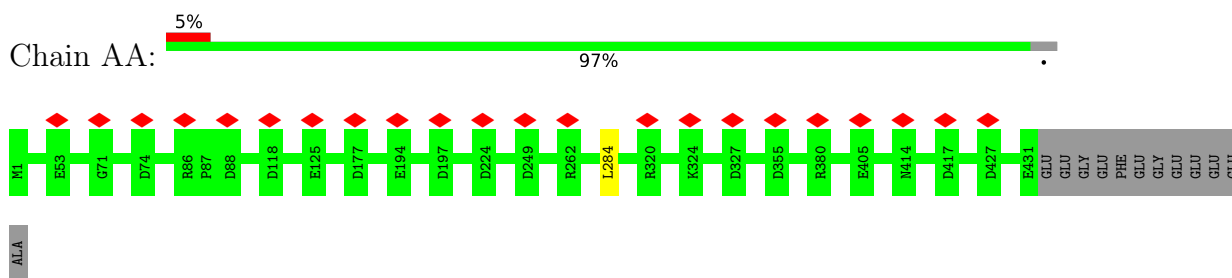
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| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|---------|---------|
| 21 | KB | 1 | Total 1 | Mg 1 | 0 |
| 21 | KD | 1 | Total 1 | Mg 1 | 0 |
| 21 | KF | 1 | Total 1 | Mg 1 | 0 |
| 21 | KI | 1 | Total 1 | Mg 1 | 0 |
| 21 | KJ | 1 | Total 1 | Mg 1 | 0 |
| 21 | KL | 1 | Total 1 | Mg 1 | 0 |
| 21 | LB | 1 | Total 1 | Mg 1 | 0 |
| 21 | LD | 1 | Total 1 | Mg 1 | 0 |
| 21 | LF | 1 | Total 1 | Mg 1 | 0 |
| 21 | LH | 1 | Total 1 | Mg 1 | 0 |
| 21 | LJ | 1 | Total 1 | Mg 1 | 0 |
| 21 | LL | 1 | Total 1 | Mg 1 | 0 |
| 21 | MB | 1 | Total 1 | Mg 1 | 0 |
| 21 | MD | 1 | Total 1 | Mg 1 | 0 |
| 21 | MF | 1 | Total 1 | Mg 1 | 0 |
| 21 | MH | 1 | Total 1 | Mg 1 | 0 |
| 21 | MJ | 1 | Total 1 | Mg 1 | 0 |
| 21 | ML | 1 | Total 1 | Mg 1 | 0 |

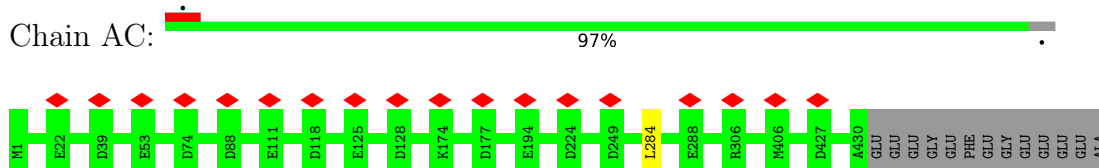
3 Residue-property plots [i](#)

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

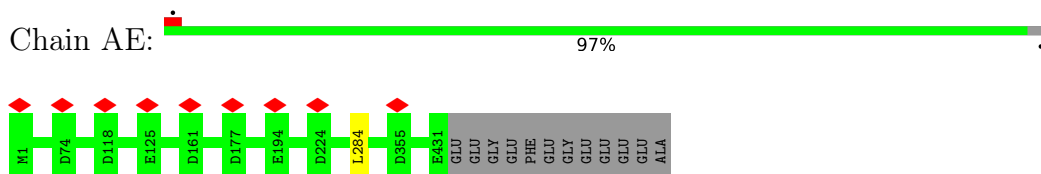
- Molecule 1: Tubulin beta



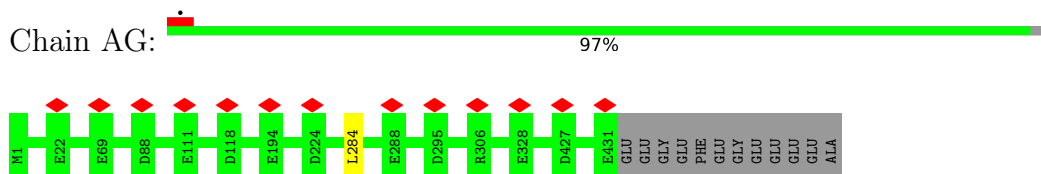
- Molecule 1: Tubulin beta



- Molecule 1: Tubulin beta

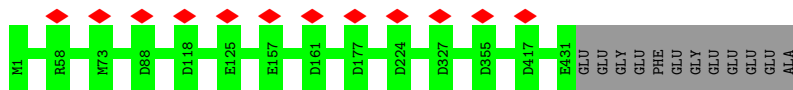


- Molecule 1: Tubulin beta

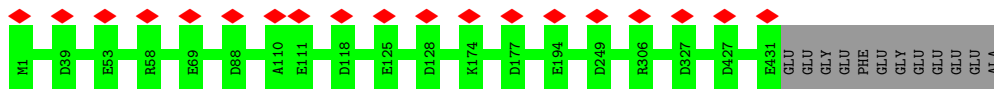


- Molecule 1: Tubulin beta

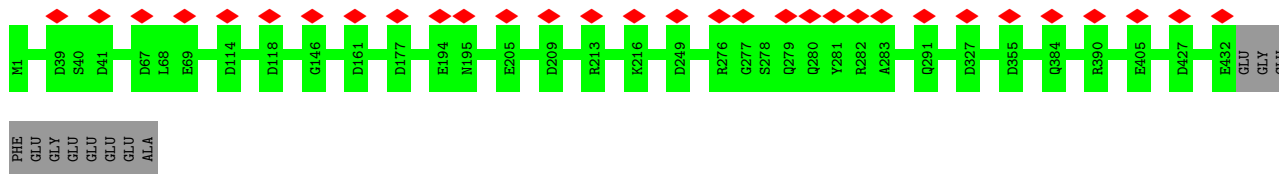




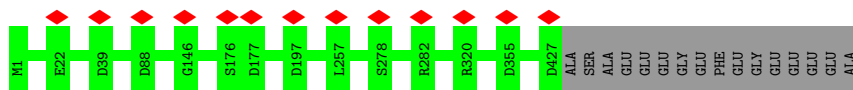
• Molecule 1: Tubulin beta



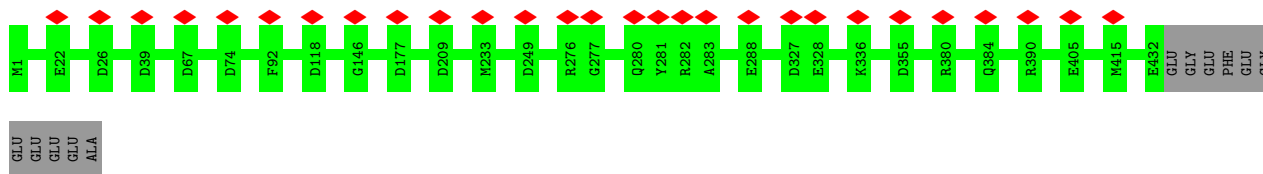
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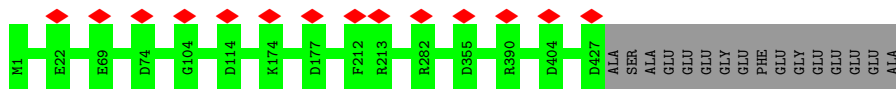
• Molecule 1: Tubulin beta



• Molecule 1: Tubulin beta

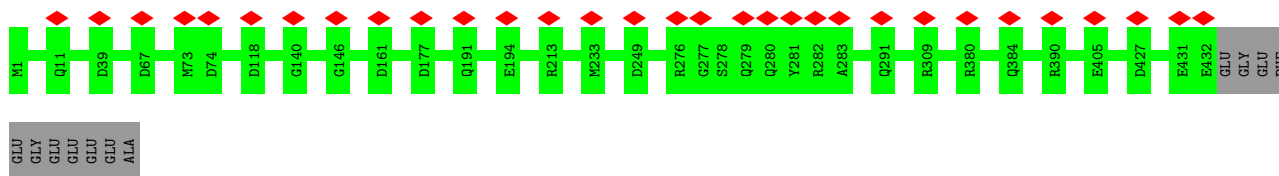


• Molecule 1: Tubulin beta

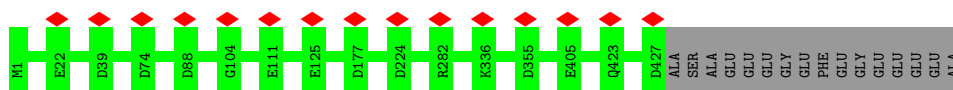


• Molecule 1: Tubulin beta

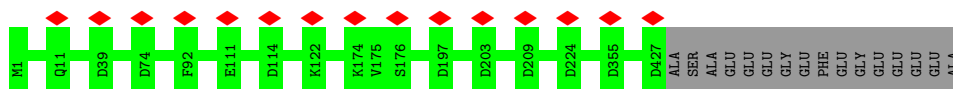




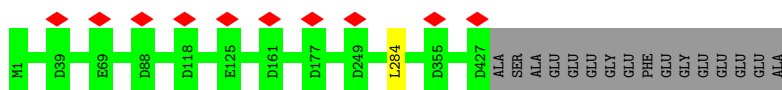
• Molecule 1: Tubulin beta



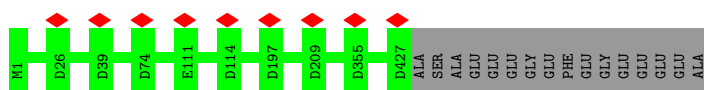
• Molecule 1: Tubulin beta



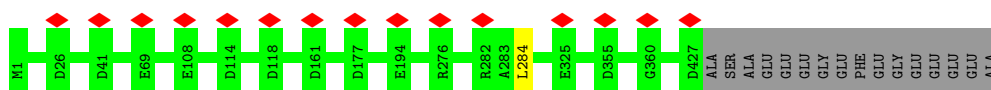
• Molecule 1: Tubulin beta



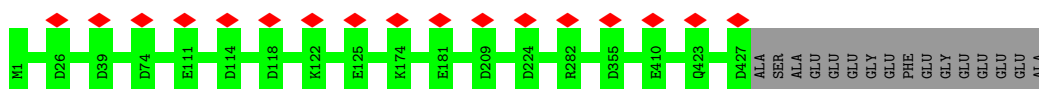
• Molecule 1: Tubulin beta



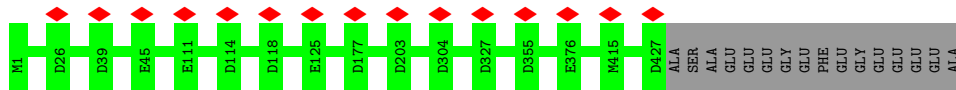
• Molecule 1: Tubulin beta



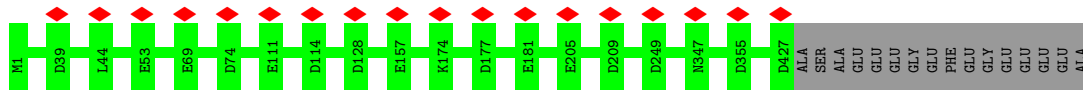
• Molecule 1: Tubulin beta



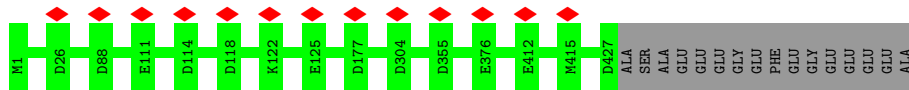
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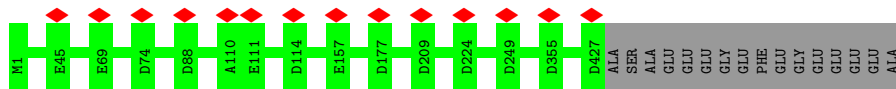
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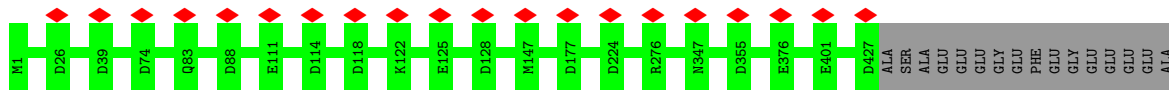
• Molecule 1: Tubulin beta



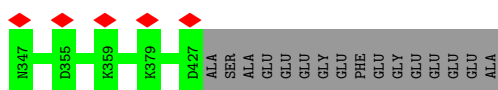
• Molecule 1: Tubulin beta



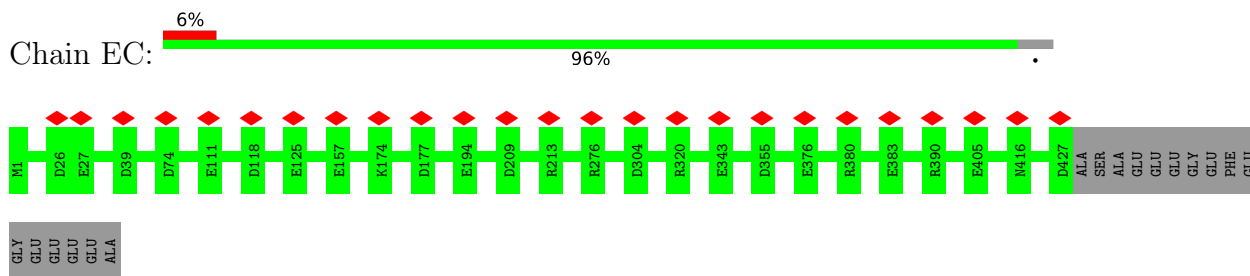
• Molecule 1: Tubulin beta



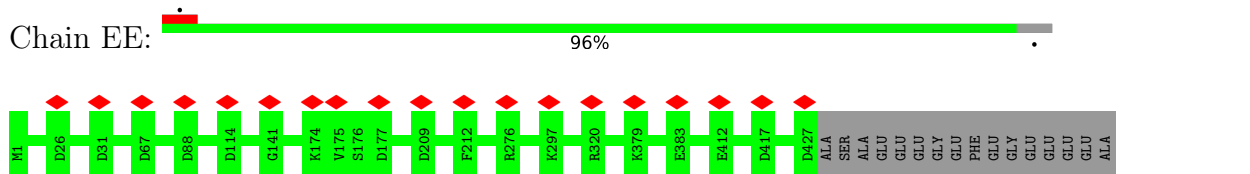
• Molecule 1: Tubulin beta



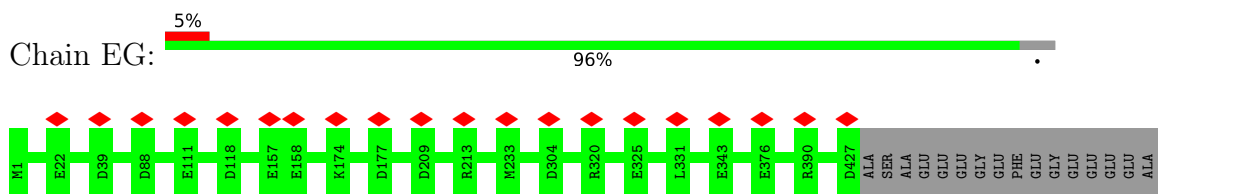
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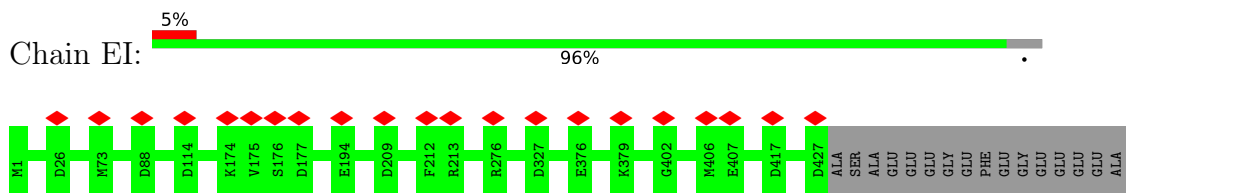
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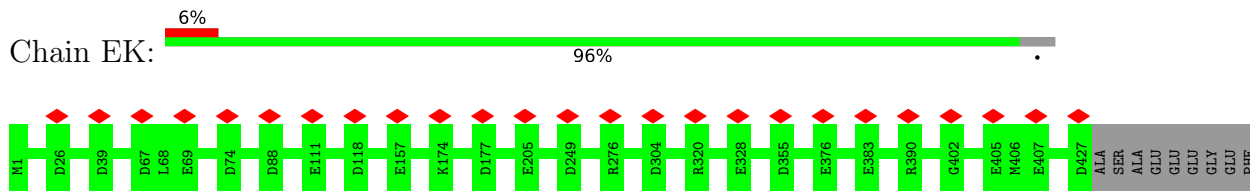
• Molecule 1: Tubulin beta



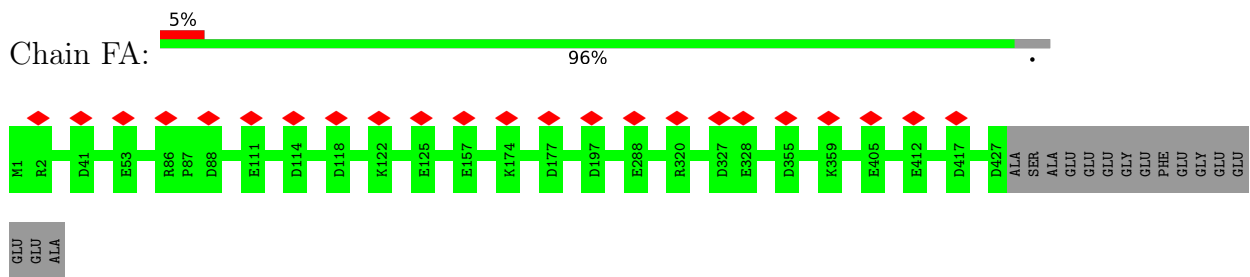
• Molecule 1: Tubulin beta



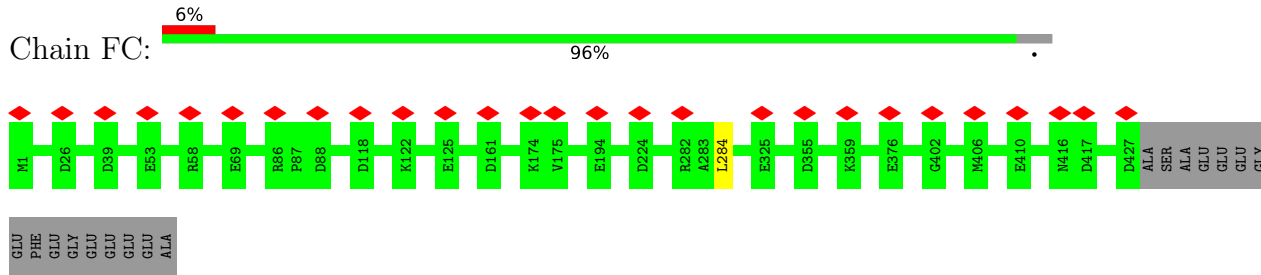
• Molecule 1: Tubulin beta



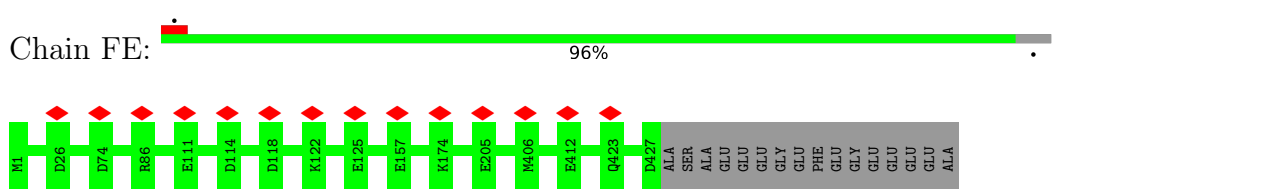
• Molecule 1: Tubulin beta



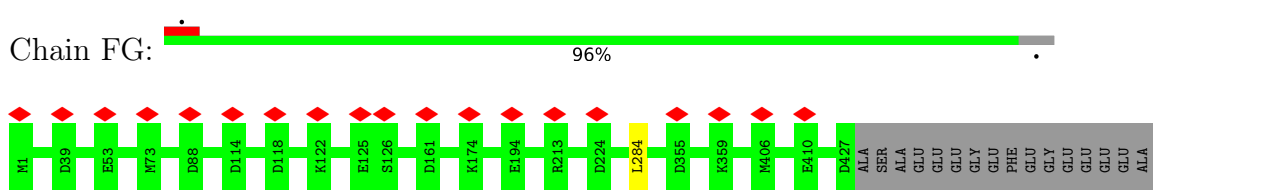
• Molecule 1: Tubulin beta



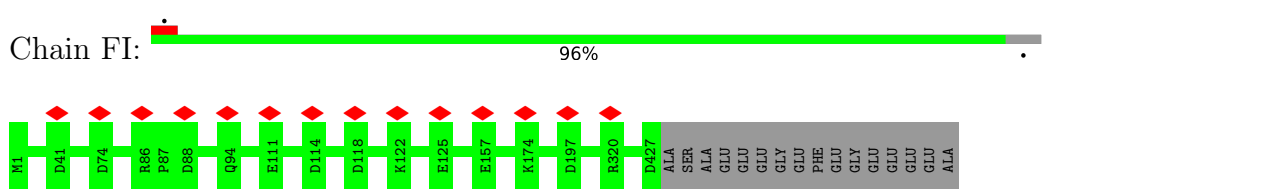
• Molecule 1: Tubulin beta



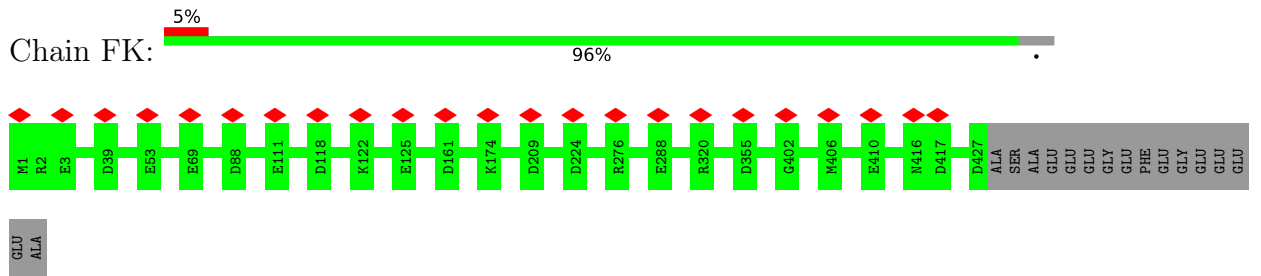
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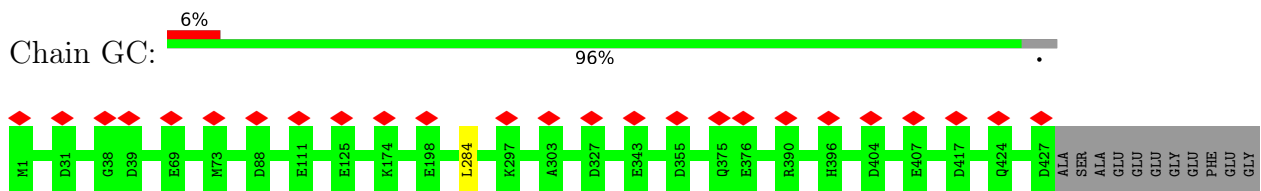
• Molecule 1: Tubulin beta



• Molecule 1: Tubulin beta

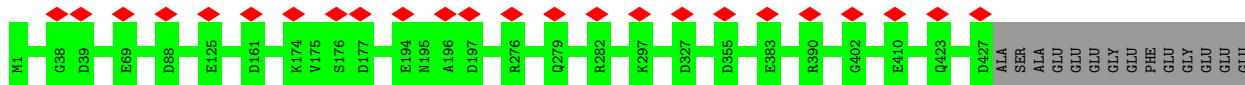


• Molecule 1: Tubulin beta



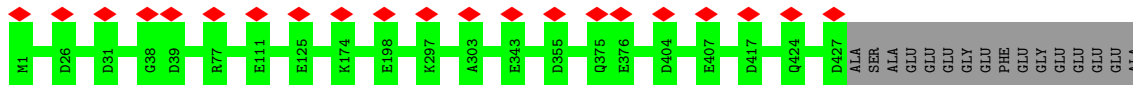
GLU
GLU
GLU
ALA

• Molecule 1: Tubulin beta

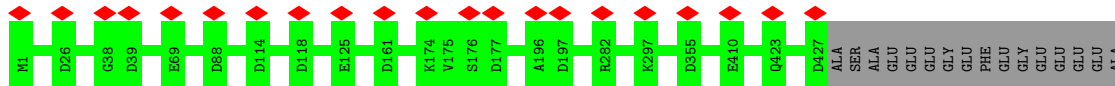


GLU
ALA

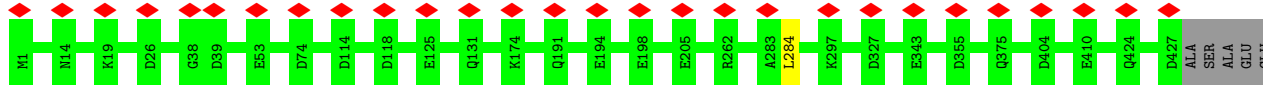
• Molecule 1: Tubulin beta



• Molecule 1: Tubulin beta

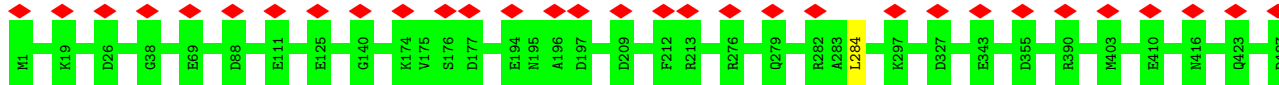


• Molecule 1: Tubulin beta



GLU
GLY
GLU
PHE
GLU
GLU
GLU
GLU
GLU
ALA

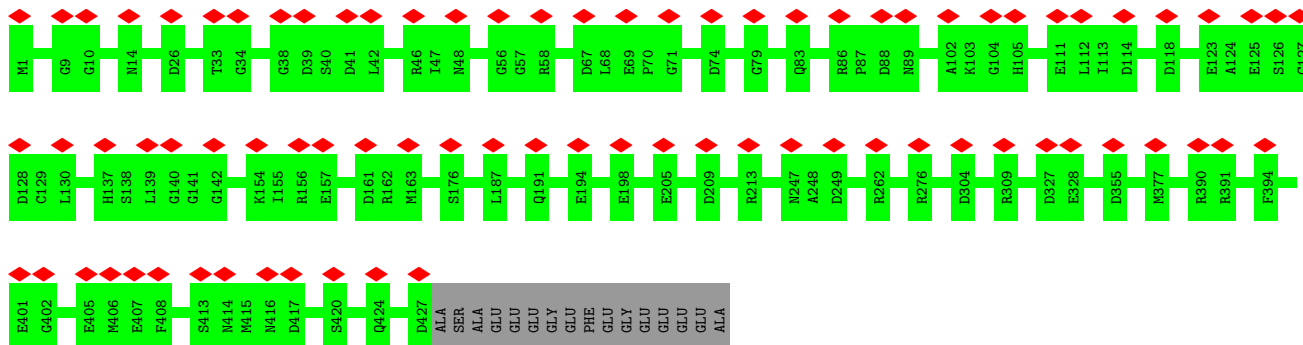
• Molecule 1: Tubulin beta



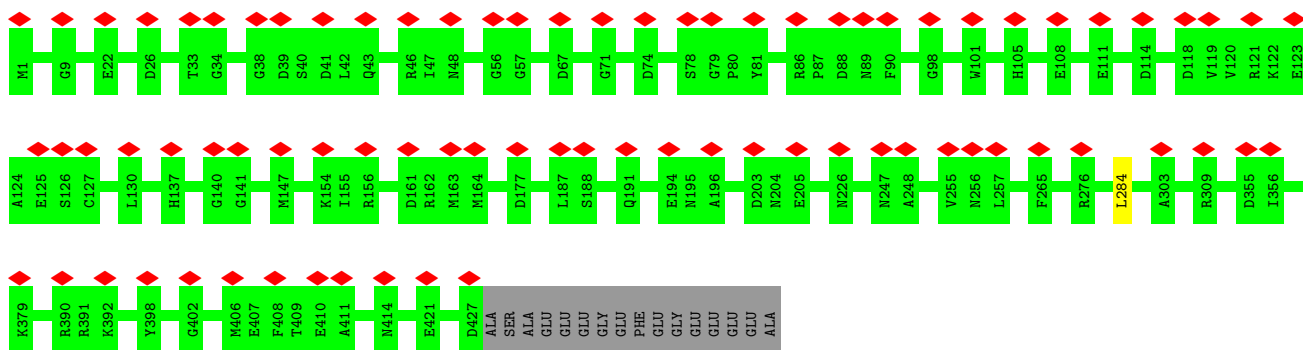
ALA
SER
ALA
GLU
GLU
GLU
GLU
GLU
PHE
GLY
GLU
GLU
GLU
ALA

• Molecule 1: Tubulin beta

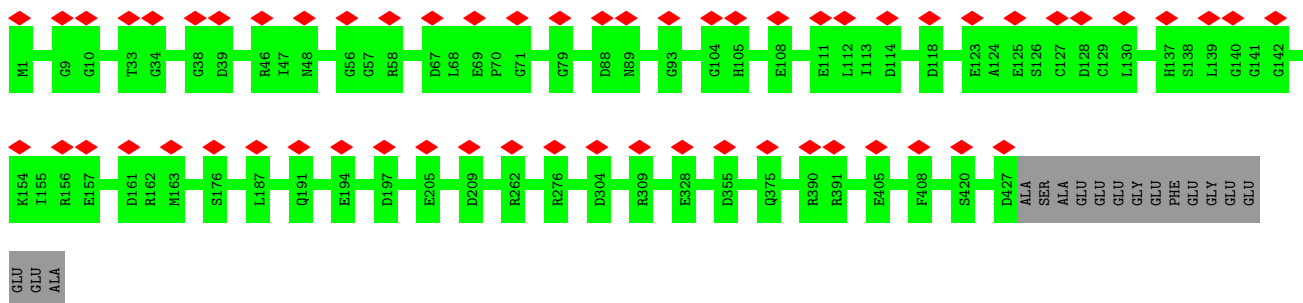




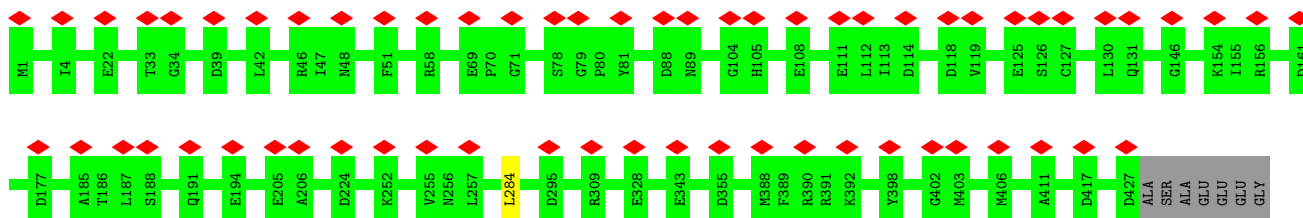
• Molecule 1: Tubulin beta



• Molecule 1: Tubulin beta

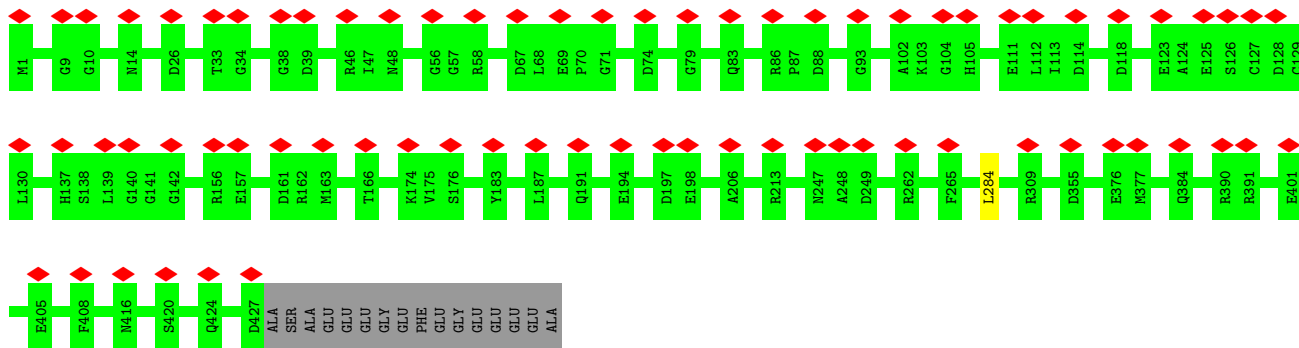


• Molecule 1: Tubulin beta

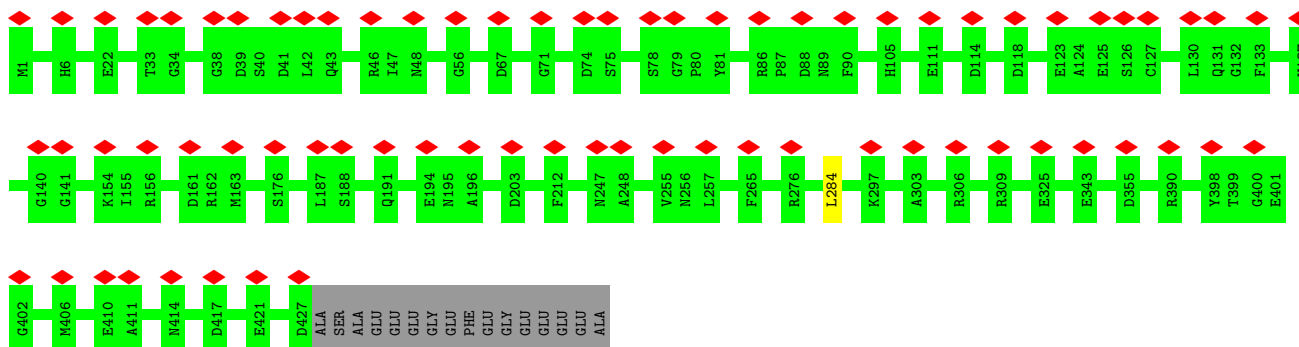


GLU
PHE
GLU
GLY
GLU
GLU
GLU
GLU
ALA

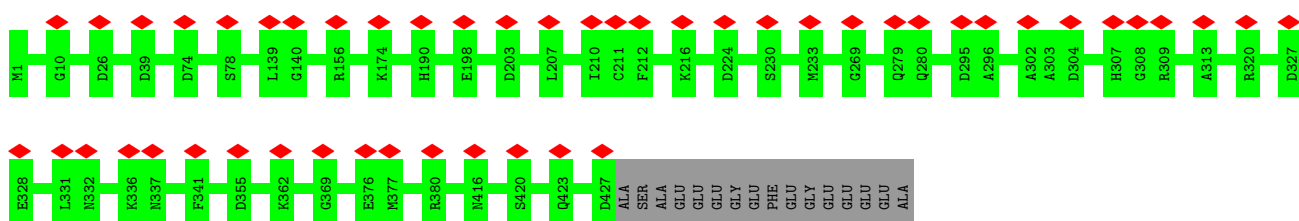
• Molecule 1: Tubulin beta



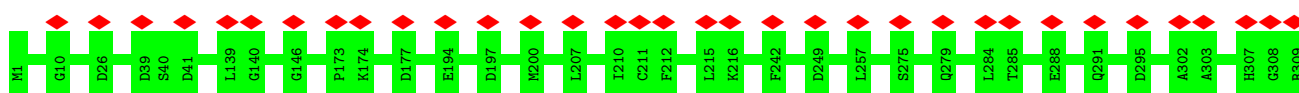
• Molecule 1: Tubulin beta

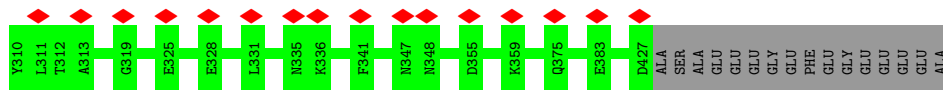


• Molecule 1: Tubulin beta

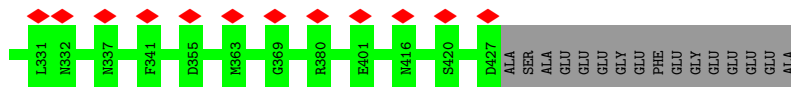
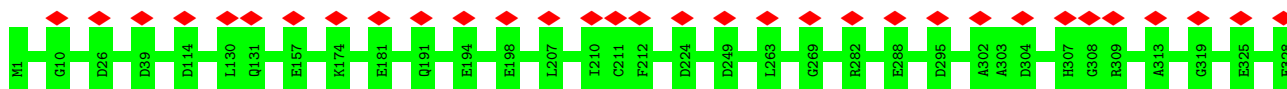


• Molecule 1: Tubulin beta

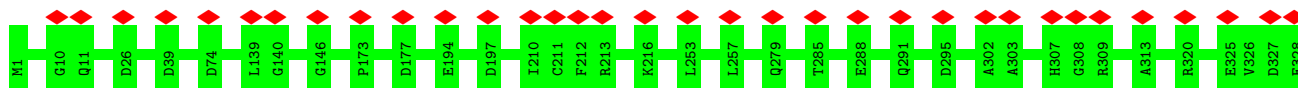




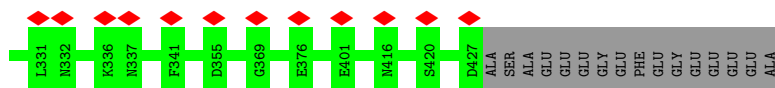
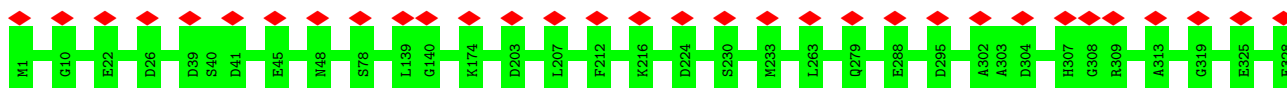
• Molecule 1: Tubulin beta



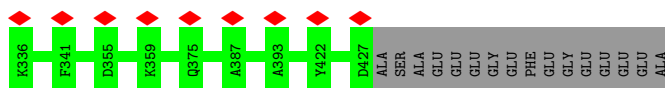
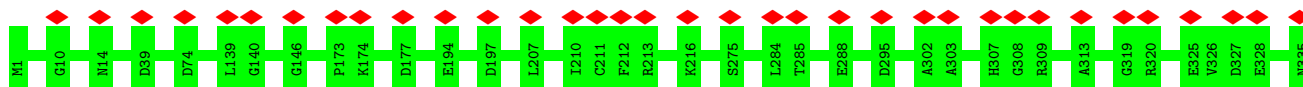
• Molecule 1: Tubulin beta



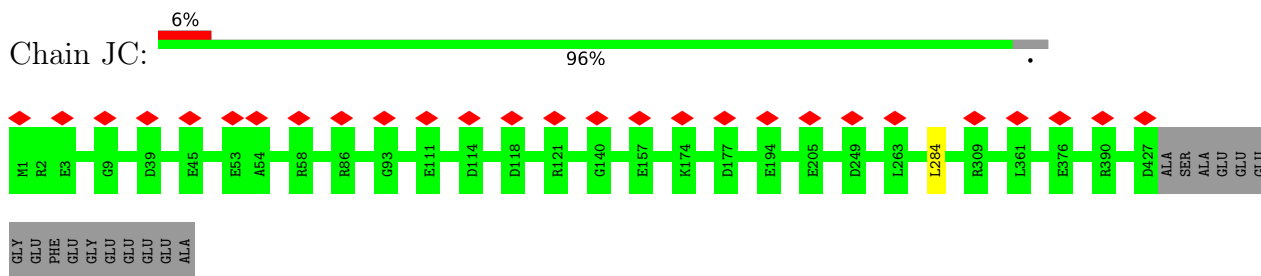
• Molecule 1: Tubulin beta



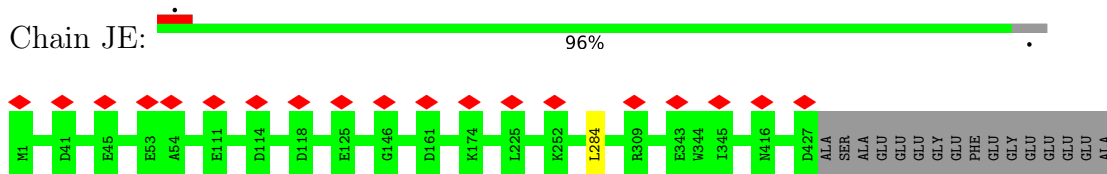
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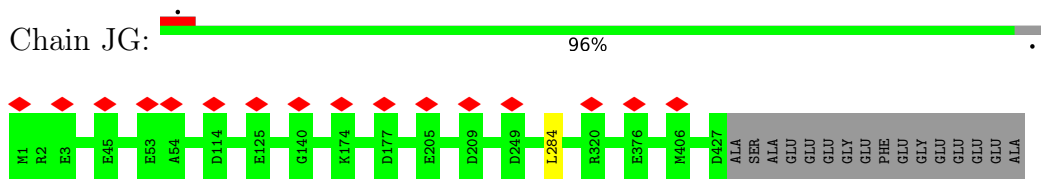
• Molecule 1: Tubulin beta



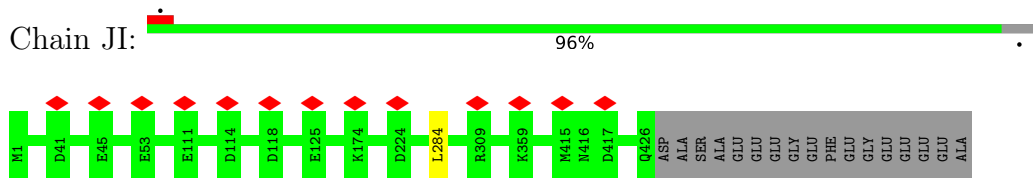
• Molecule 1: Tubulin beta



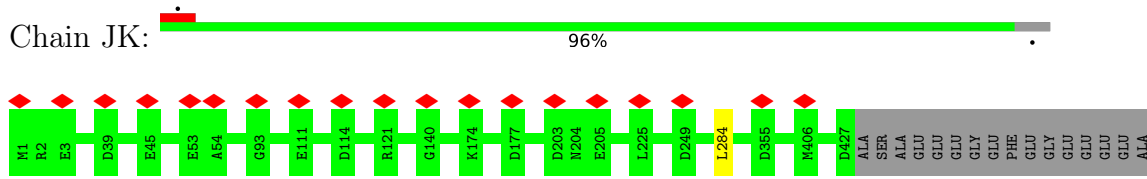
• Molecule 1: Tubulin beta



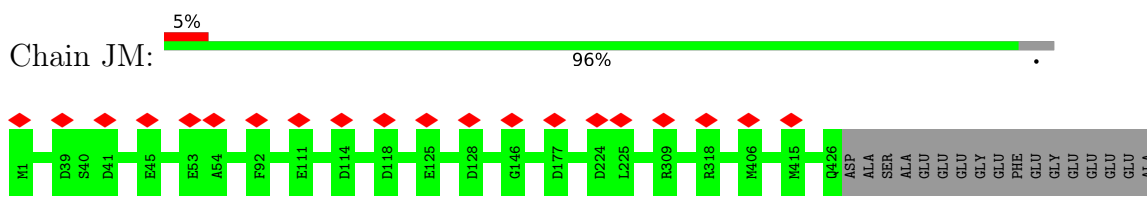
• Molecule 1: Tubulin beta



• Molecule 1: Tubulin beta

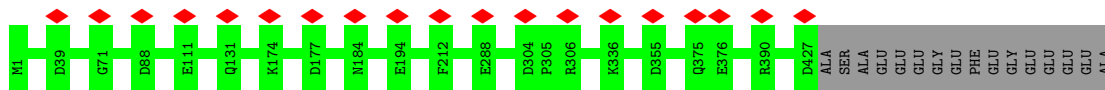


• Molecule 1: Tubulin beta

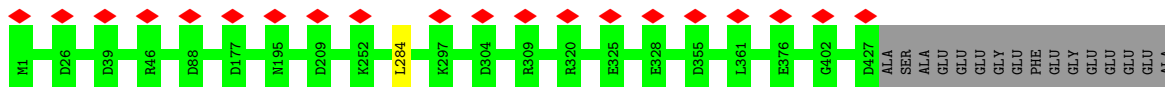


• Molecule 1: Tubulin beta

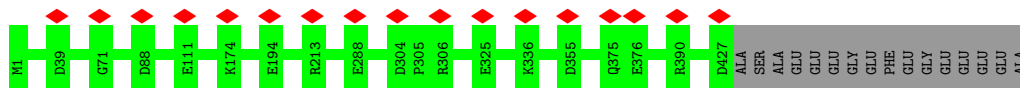




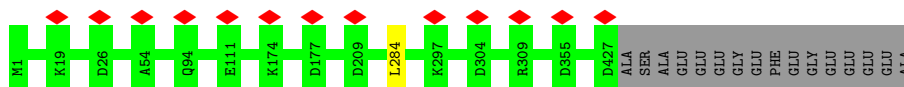
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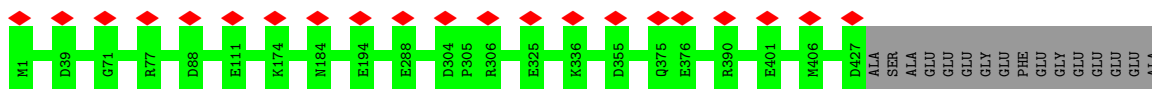
• Molecule 1: Tubulin beta



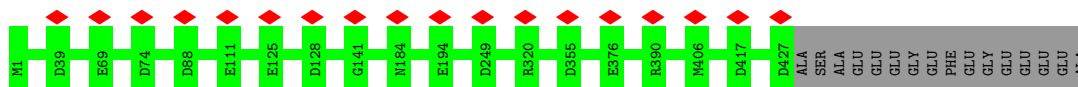
• Molecule 1: Tubulin beta



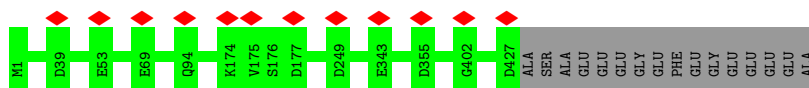
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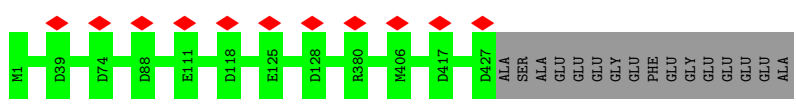
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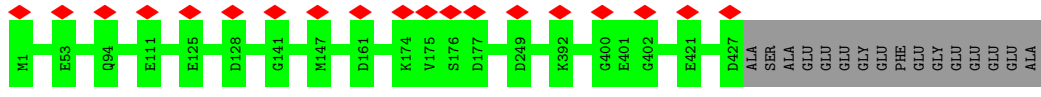
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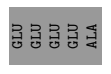
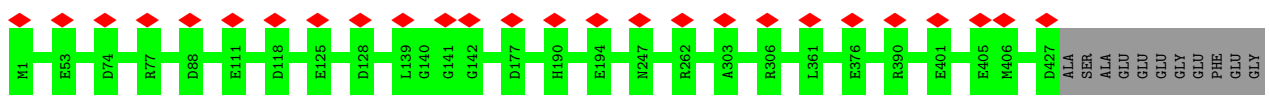
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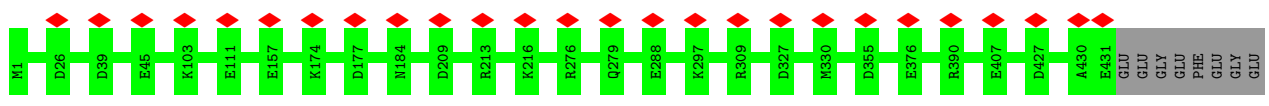
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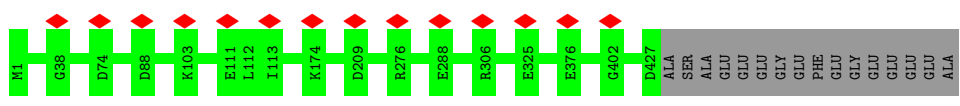
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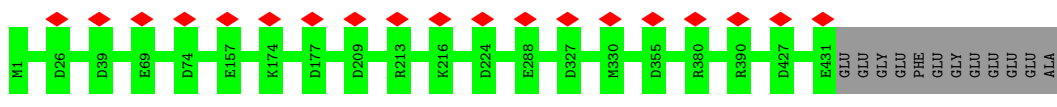
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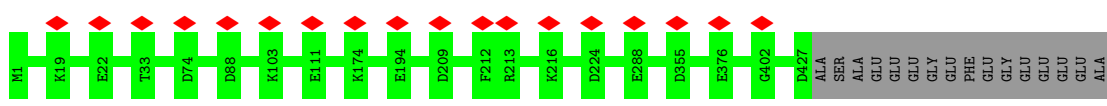
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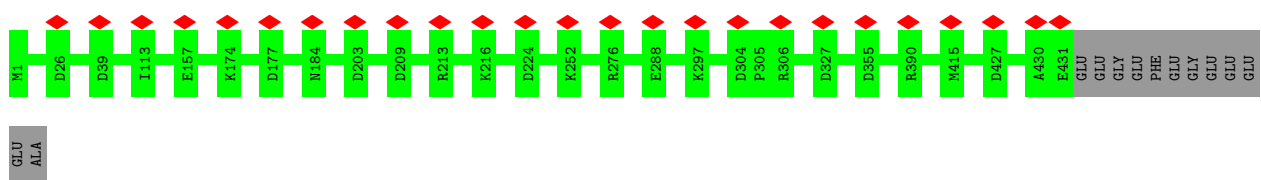
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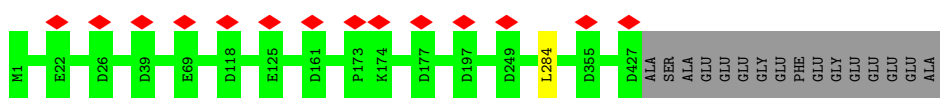
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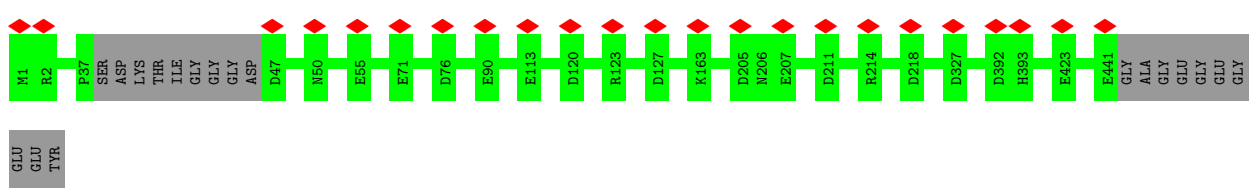
• Molecule 1: Tubulin beta



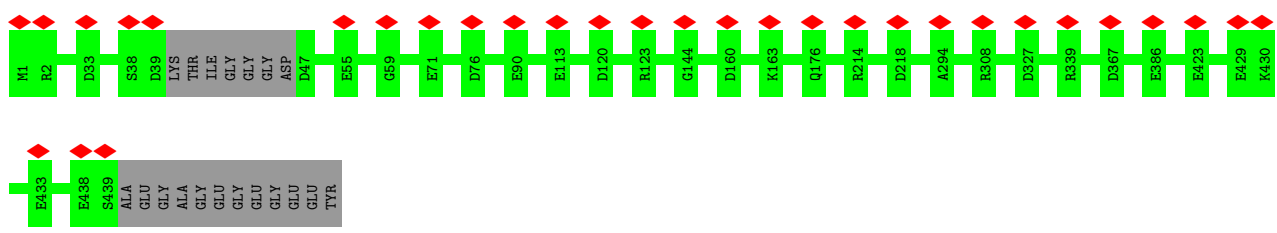
• Molecule 1: Tubulin beta



• Molecule 2: Tubulin alpha

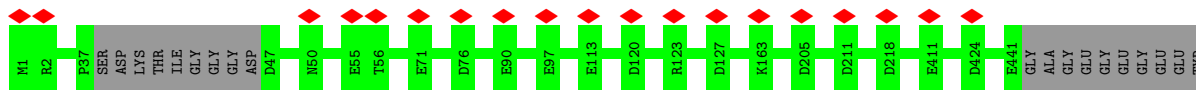


• Molecule 2: Tubulin alpha

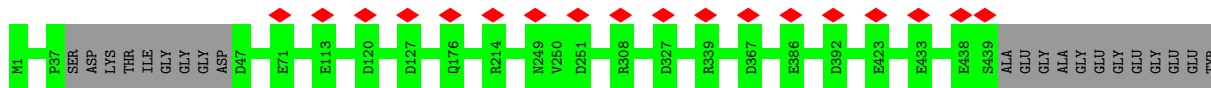


• Molecule 2: Tubulin alpha

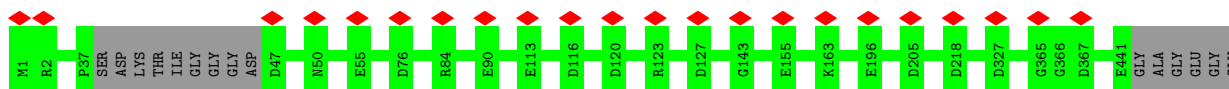




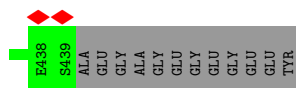
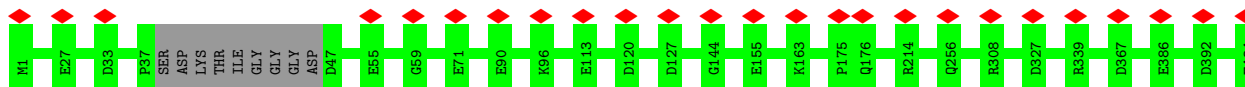
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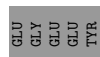
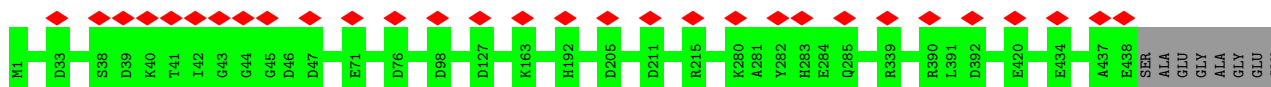
• Molecule 2: Tubulin alpha



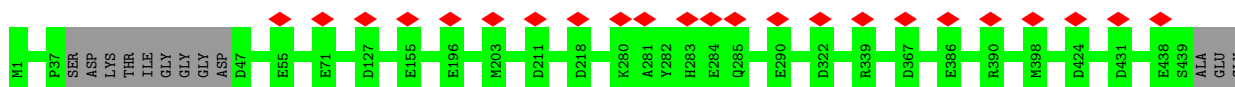
• Molecule 2: Tubulin alpha



• Molecule 2: Tubulin alpha

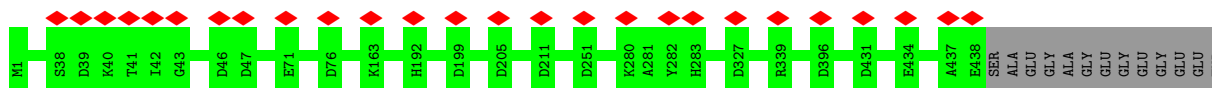


• Molecule 2: Tubulin alpha

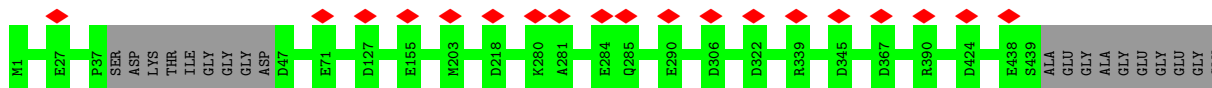


ALA
GLY
GLY
GLY
GLY
GLY
GLY
TYR

• Molecule 2: Tubulin alpha

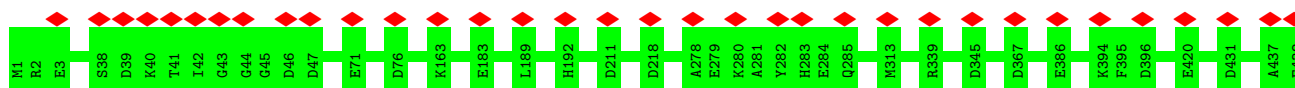


• Molecule 2: Tubulin alpha



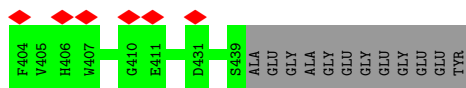
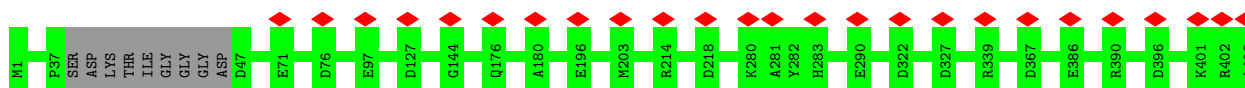
GLU
TYR

• Molecule 2: Tubulin alpha

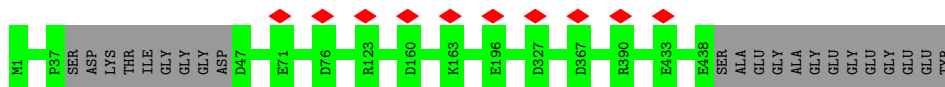


SER
ALA
GLY
GLY
GLY
GLY
GLY
TYR

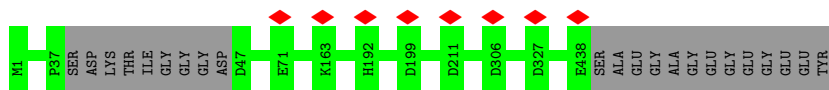
• Molecule 2: Tubulin alpha



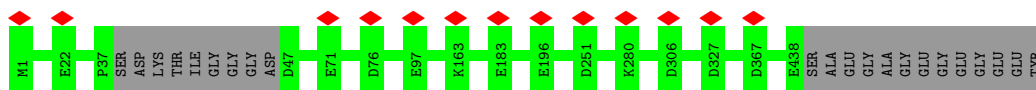
• Molecule 2: Tubulin alpha



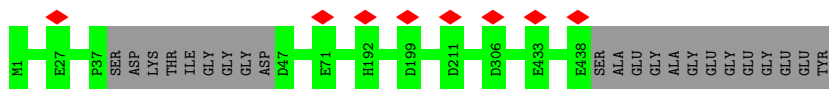
• Molecule 2: Tubulin alpha



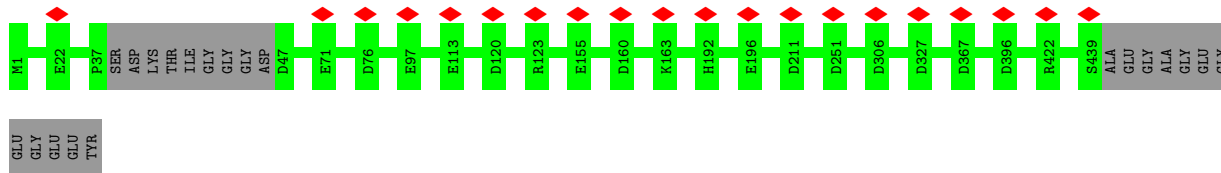
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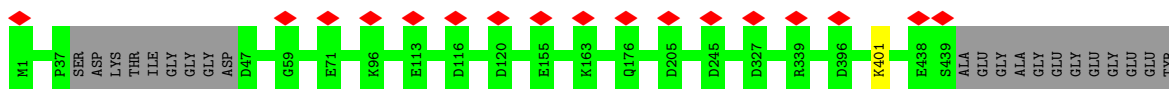
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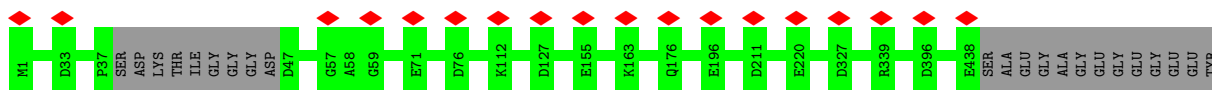
• Molecule 2: Tubulin alpha



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• Molecule 2: Tubulin alpha

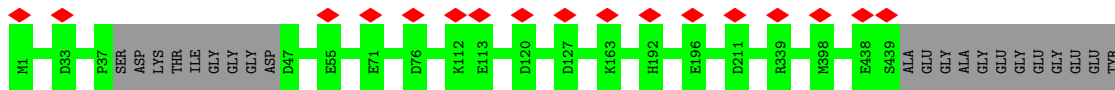


• Molecule 2: Tubulin alpha

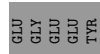
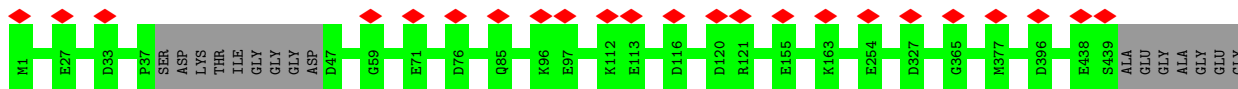




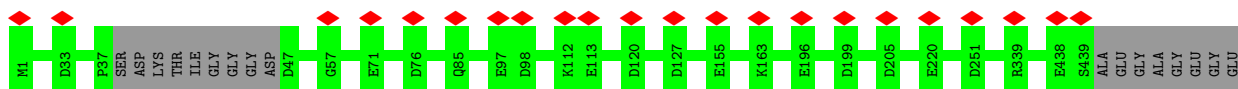
• Molecule 2: Tubulin alpha



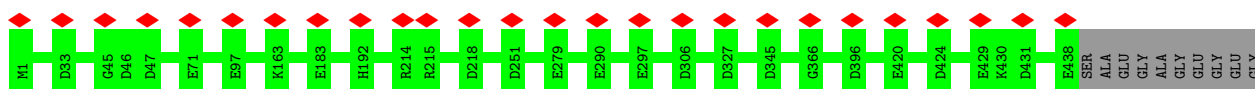
• Molecule 2: Tubulin alpha



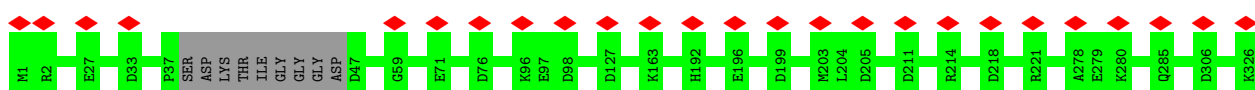
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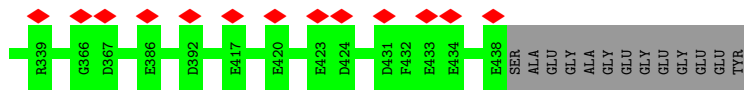


• Molecule 2: Tubulin alpha

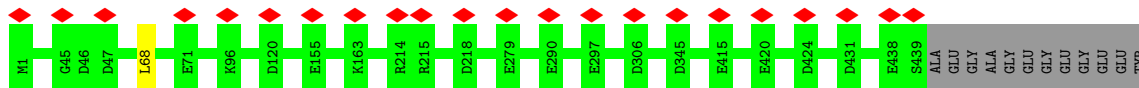


• Molecule 2: Tubulin alpha

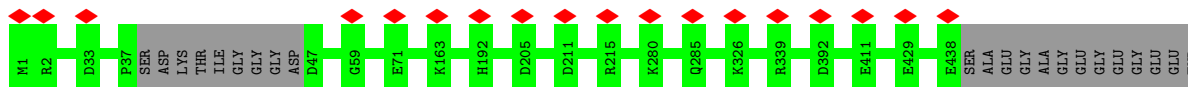




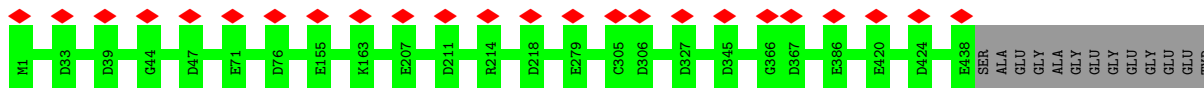
• Molecule 2: Tubulin alpha



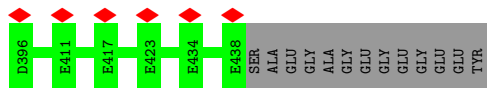
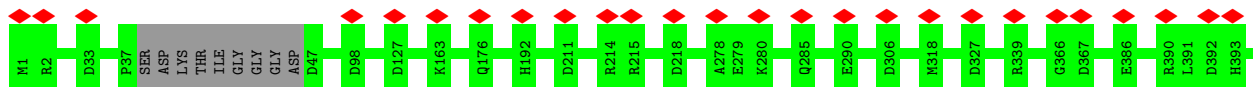
• Molecule 2: Tubulin alpha



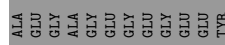
• Molecule 2: Tubulin alpha



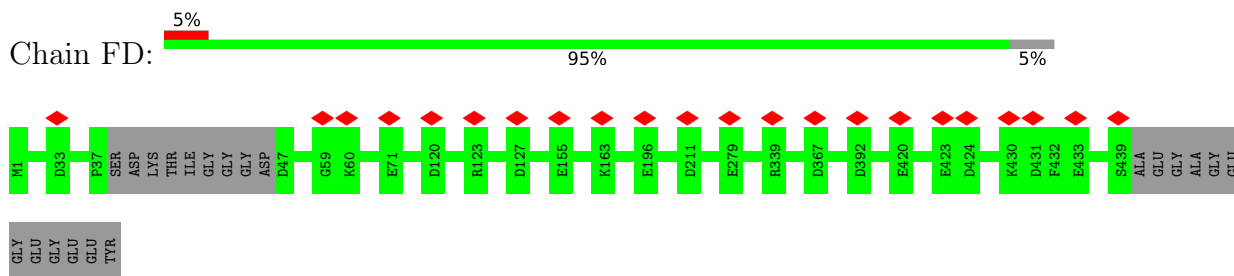
• Molecule 2: Tubulin alpha



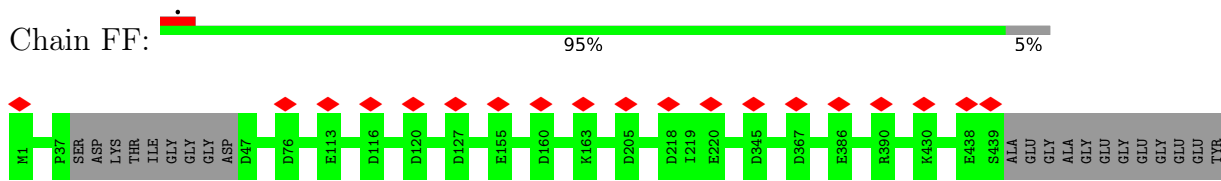
• Molecule 2: Tubulin alpha



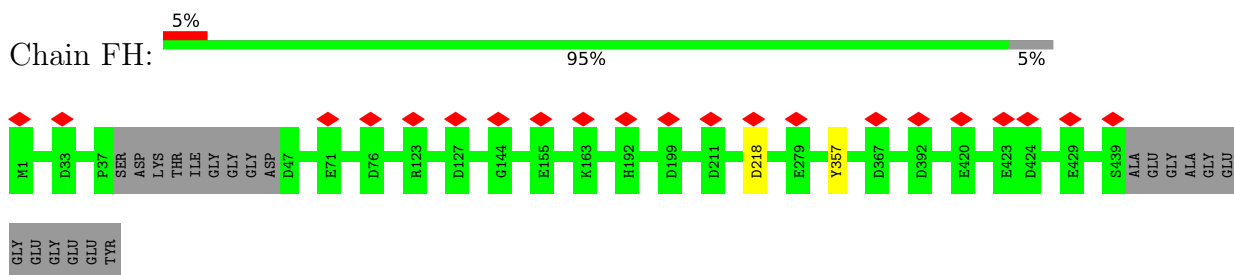
• Molecule 2: Tubulin alpha



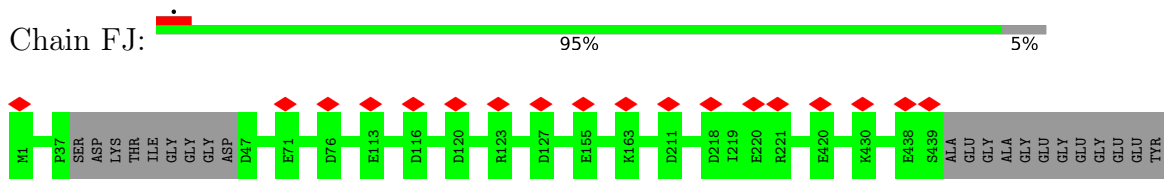
• Molecule 2: Tubulin alpha



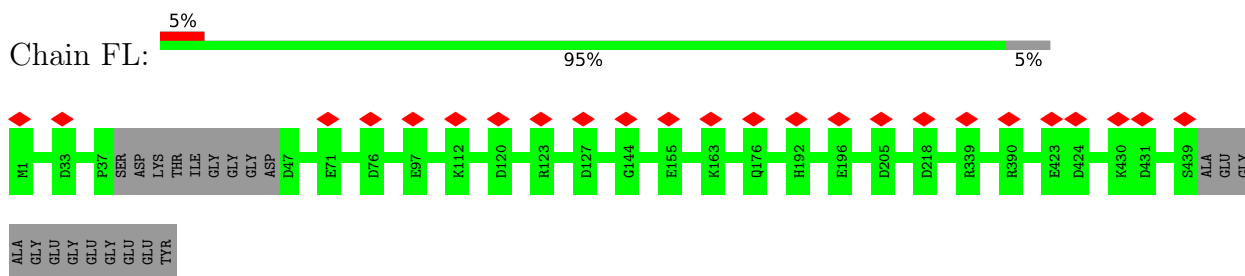
• Molecule 2: Tubulin alpha



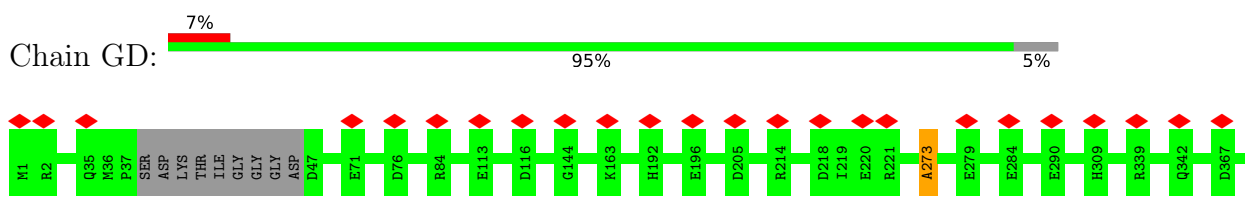
• Molecule 2: Tubulin alpha

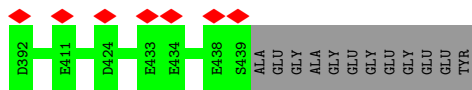


• Molecule 2: Tubulin alpha

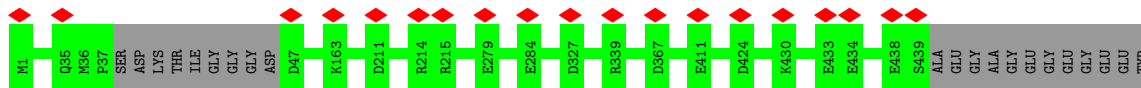


• Molecule 2: Tubulin alpha

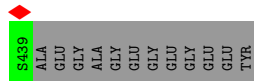




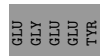
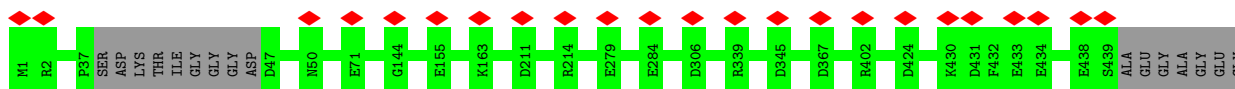
• Molecule 2: Tubulin alpha



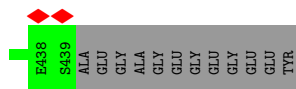
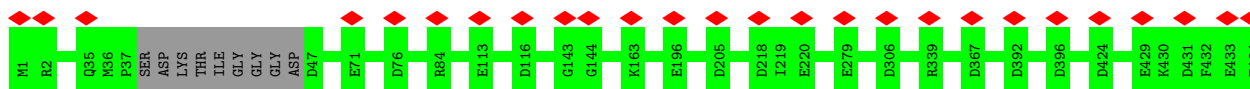
• Molecule 2: Tubulin alpha



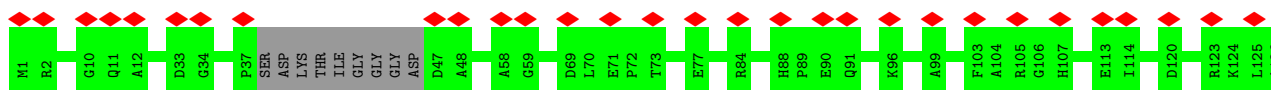
• Molecule 2: Tubulin alpha

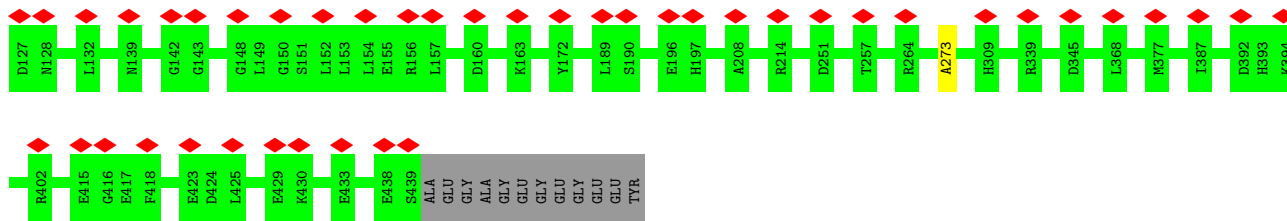


• Molecule 2: Tubulin alpha

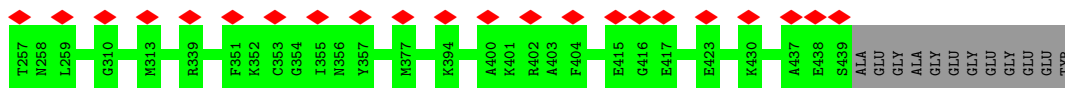
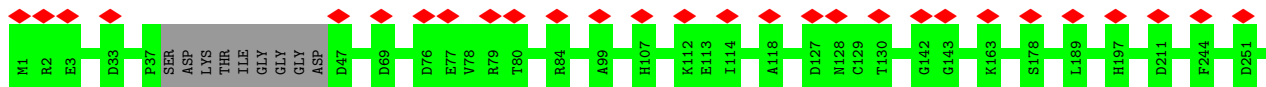


• Molecule 2: Tubulin alpha

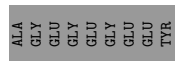
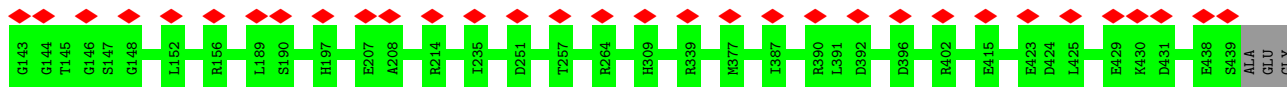
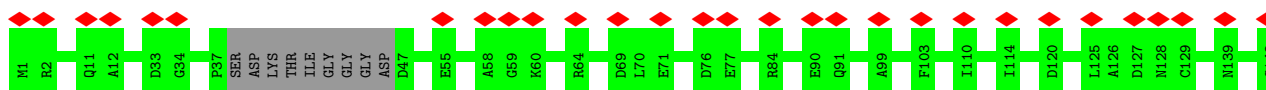




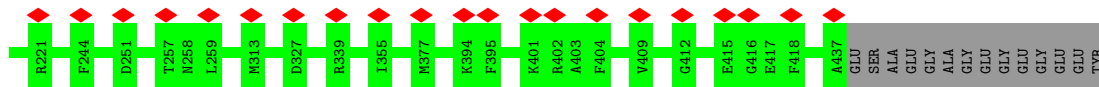
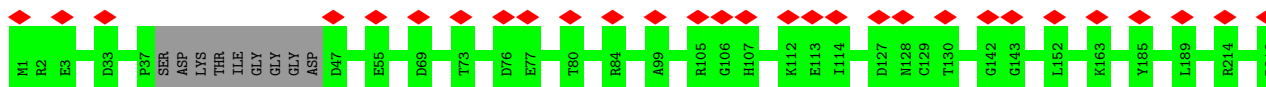
• Molecule 2: Tubulin alpha



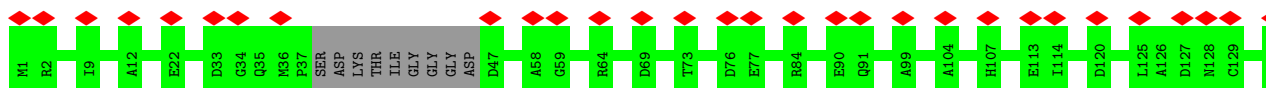
• Molecule 2: Tubulin alpha

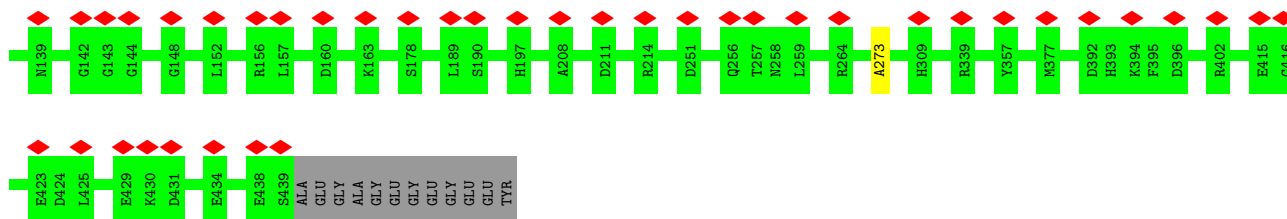


• Molecule 2: Tubulin alpha

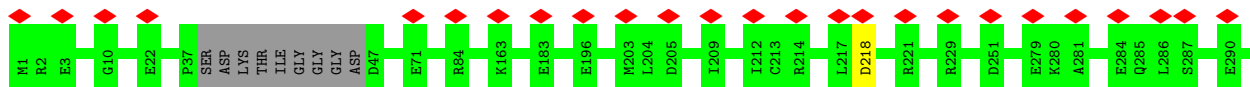


• Molecule 2: Tubulin alpha

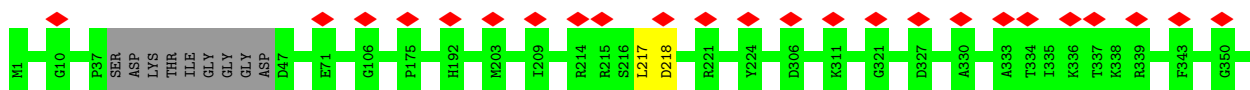




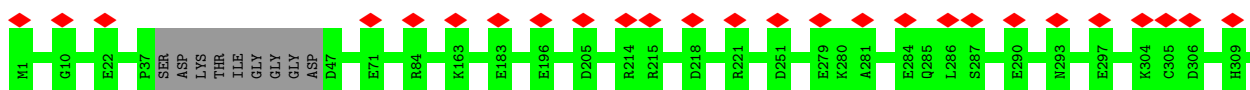
• Molecule 2: Tubulin alpha



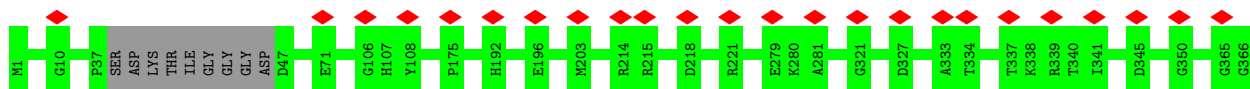
• Molecule 2: Tubulin alpha

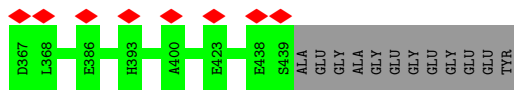


• Molecule 2: Tubulin alpha

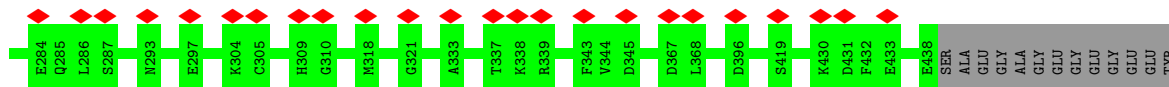


• Molecule 2: Tubulin alpha

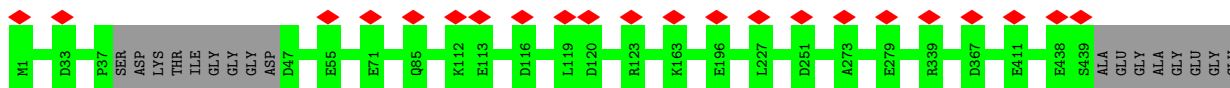




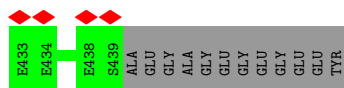
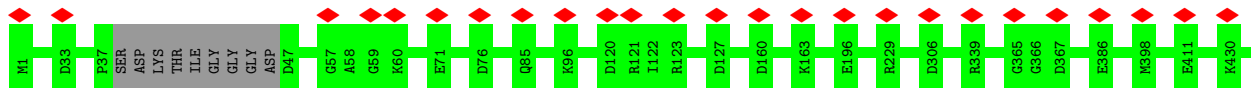
• Molecule 2: Tubulin alpha



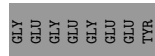
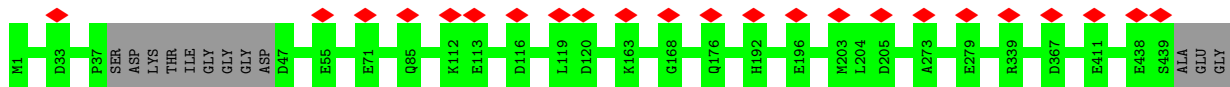
• Molecule 2: Tubulin alpha



• Molecule 2: Tubulin alpha

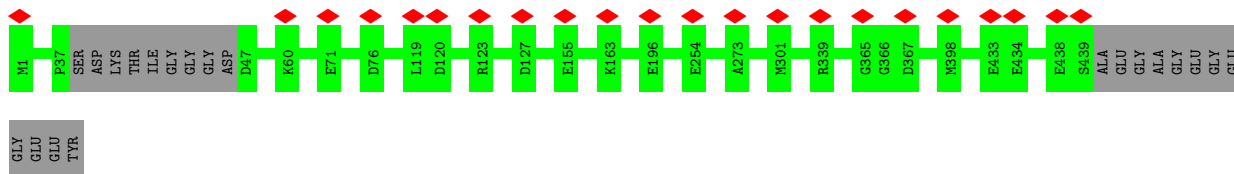


• Molecule 2: Tubulin alpha



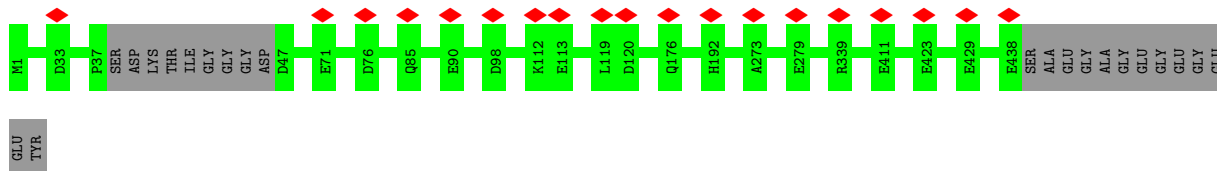
• Molecule 2: Tubulin alpha





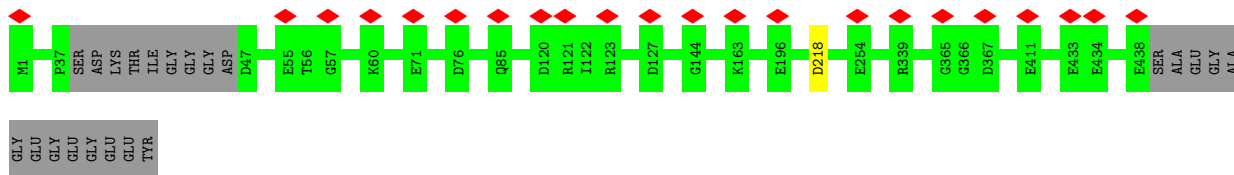
• Molecule 2: Tubulin alpha

Chain JJ:



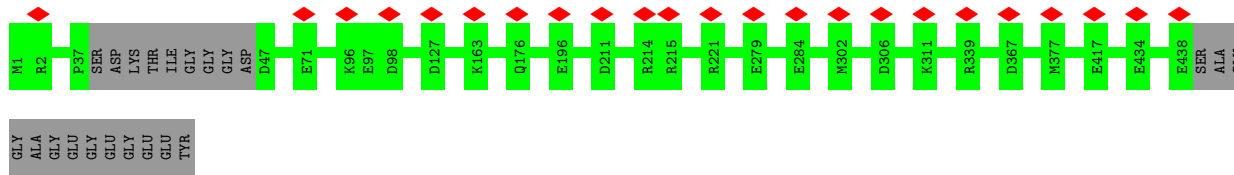
• Molecule 2: Tubulin alpha

Chain JL:



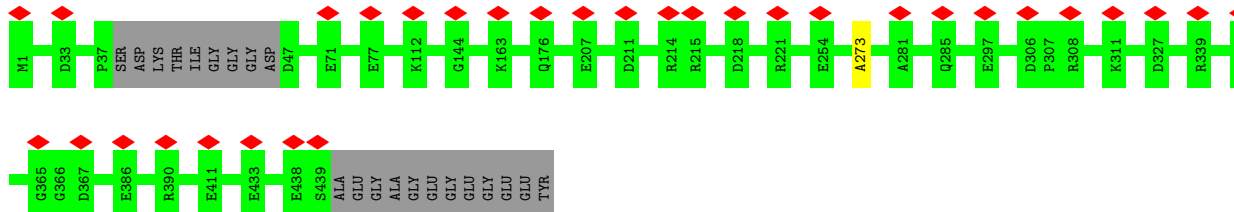
• Molecule 2: Tubulin alpha

Chain KB:



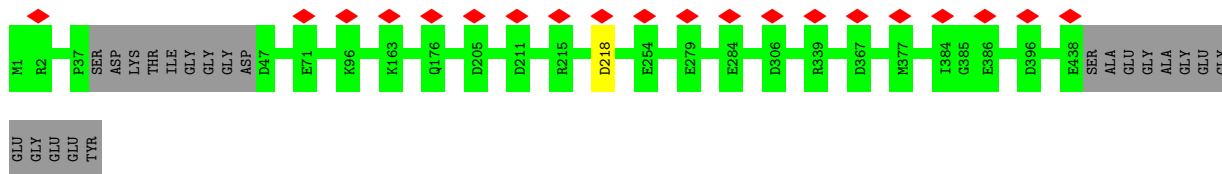
• Molecule 2: Tubulin alpha

Chain KD:

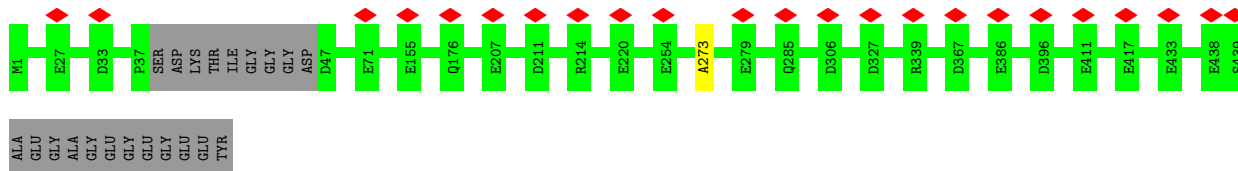


• Molecule 2: Tubulin alpha

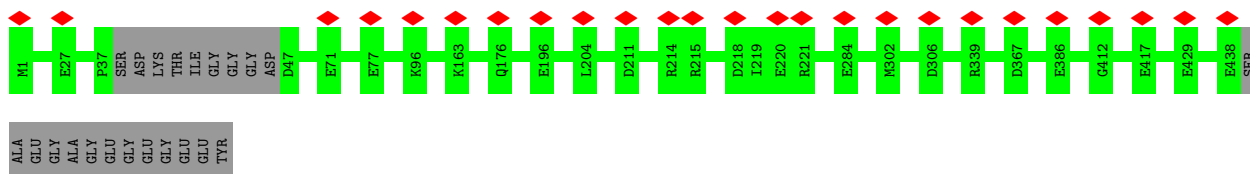
Chain KF:



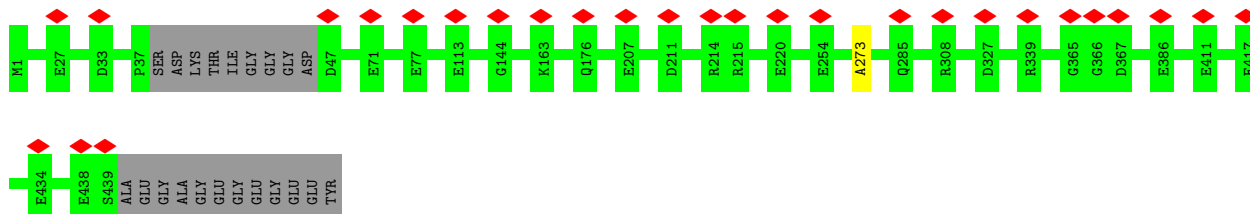
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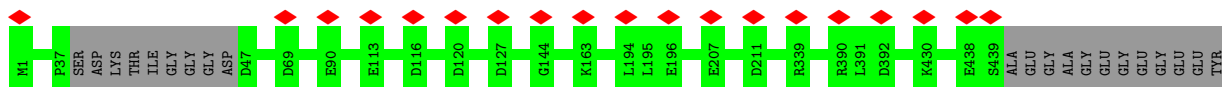
• Molecule 2: Tubulin alpha



• Molecule 2: Tubulin alpha

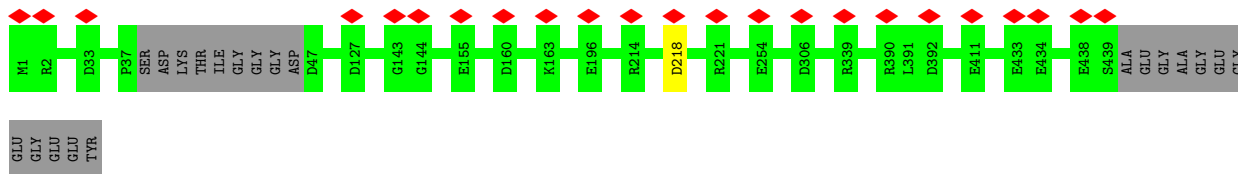


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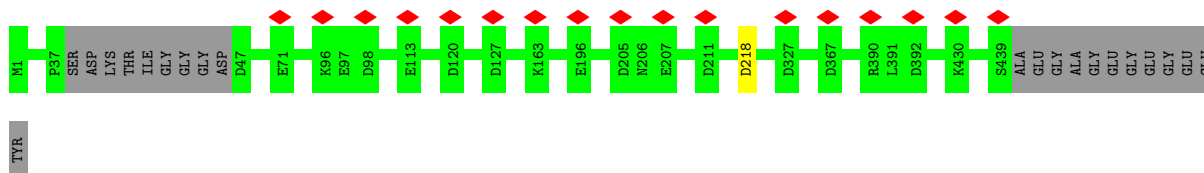


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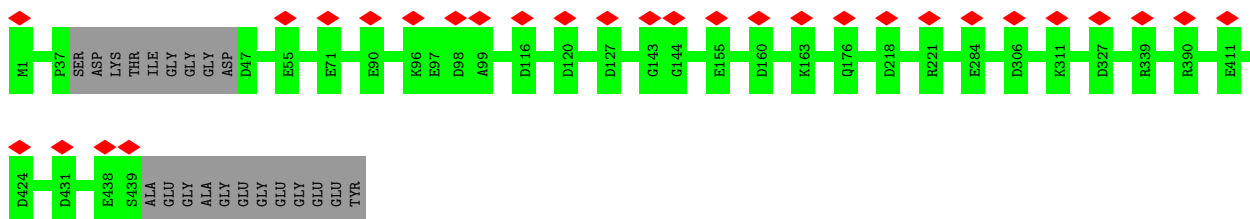




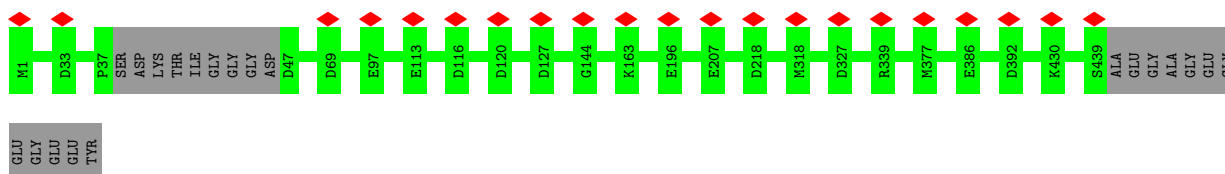
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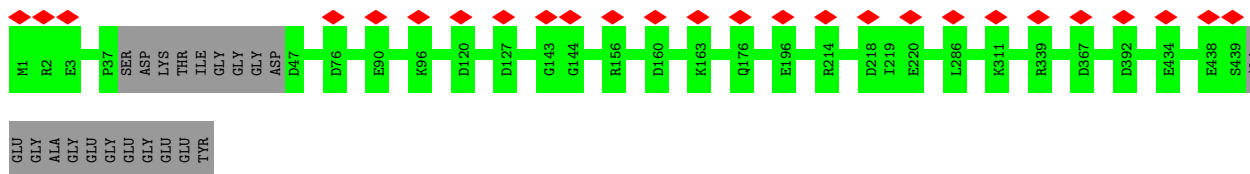
• Molecule 2: Tubulin alpha



• Molecule 2: Tubulin alpha

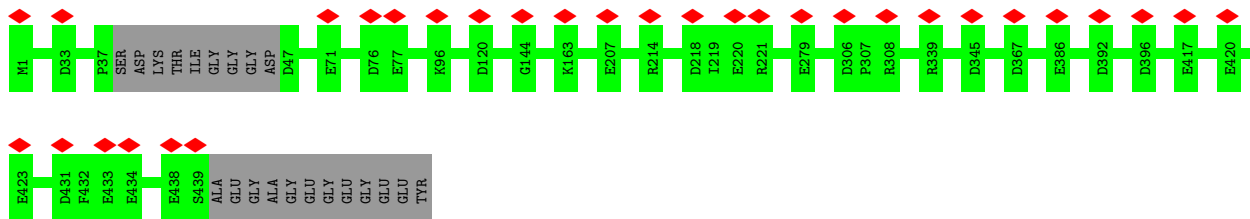


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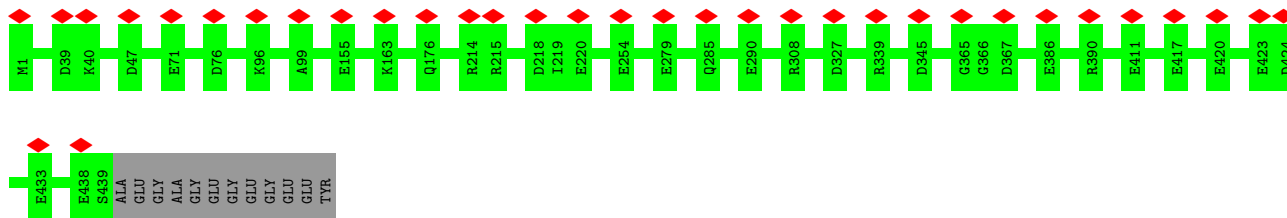


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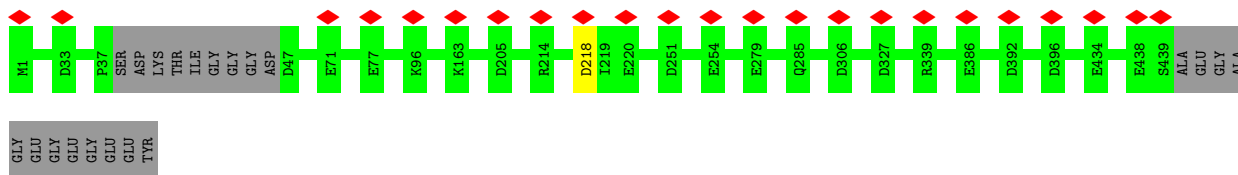




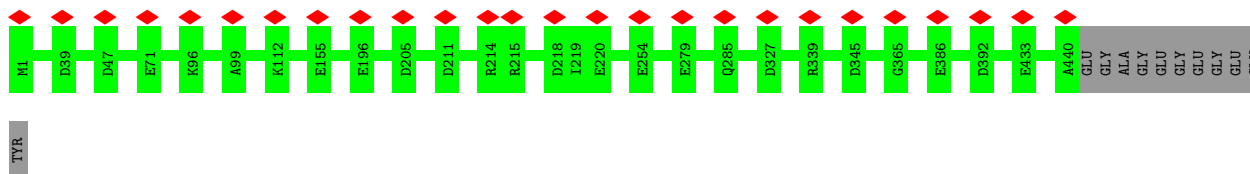
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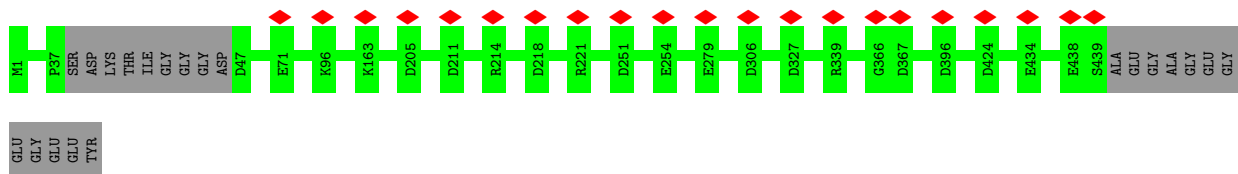
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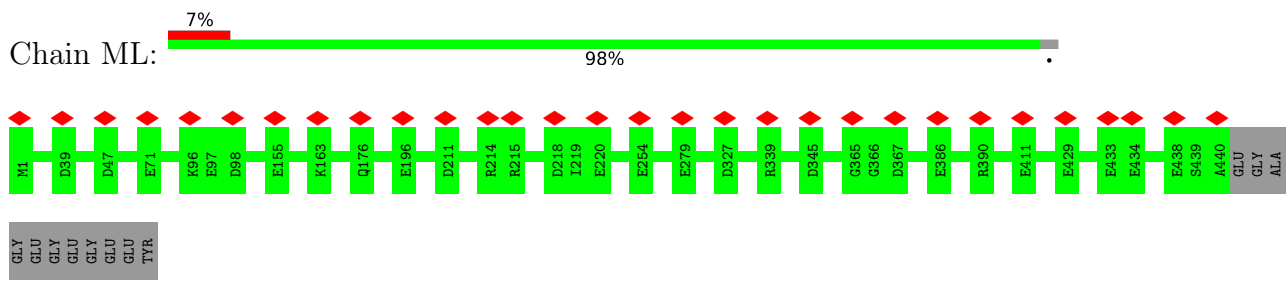
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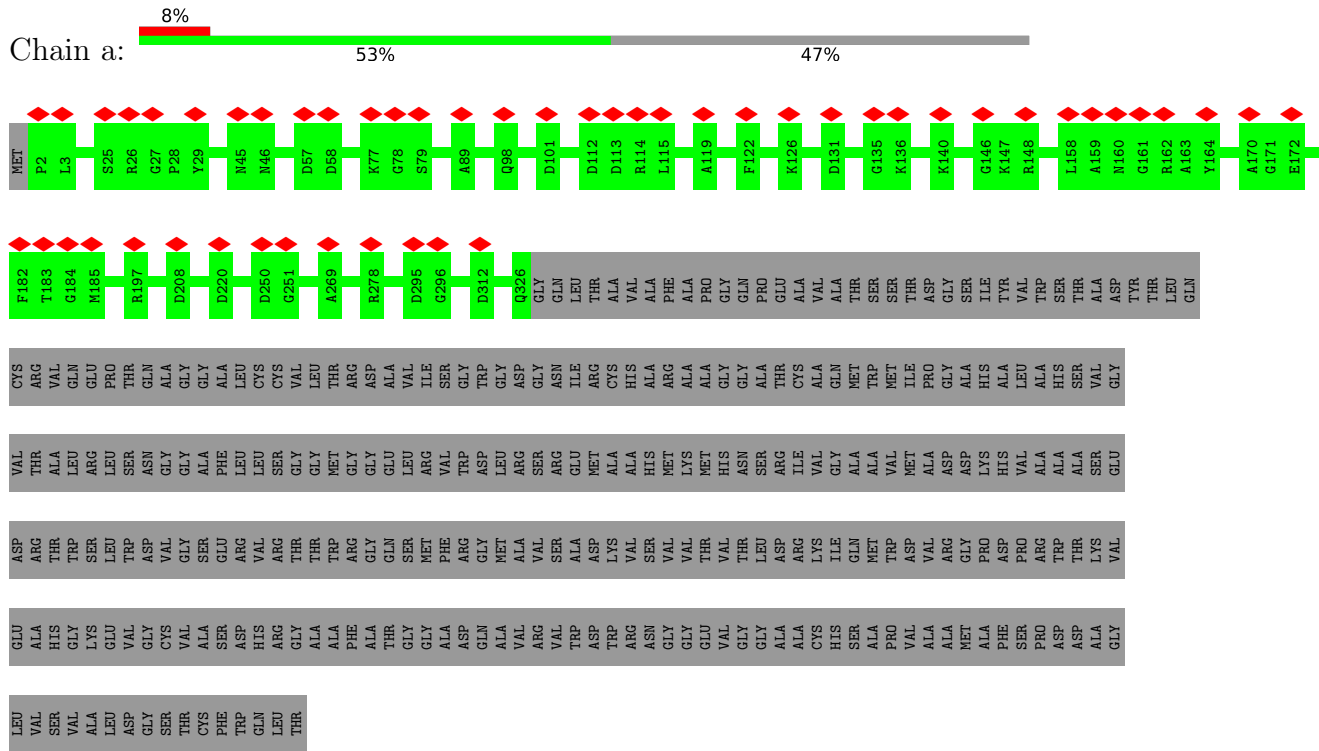
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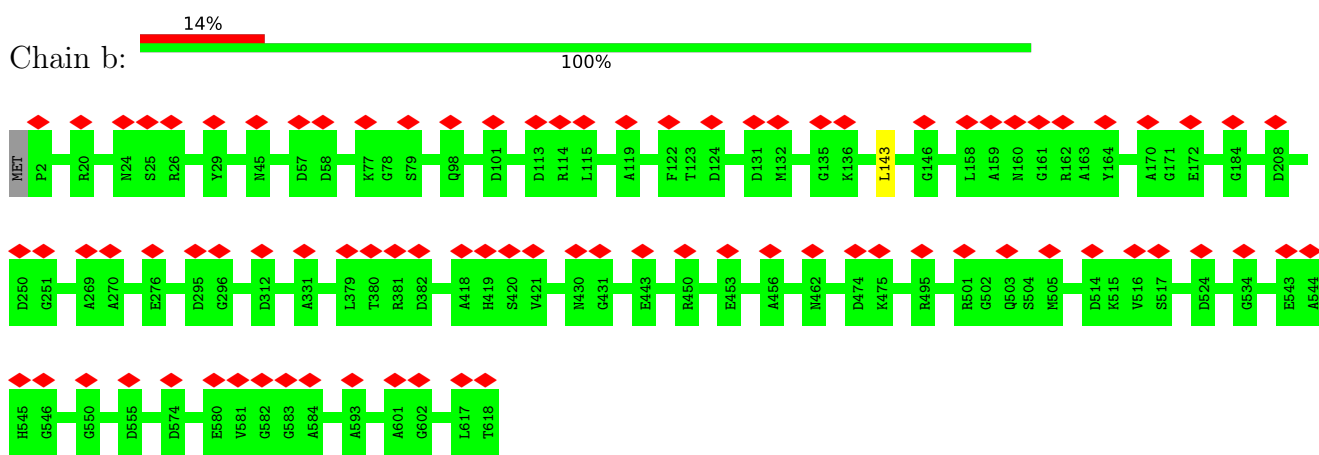
• Molecule 2: Tubulin alpha



• Molecule 3: Cilia- and flagella-associated protein 20

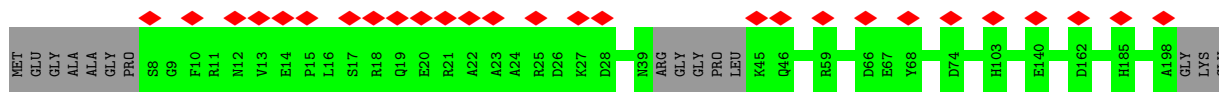


• Molecule 3: Cilia- and flagella-associated protein 20

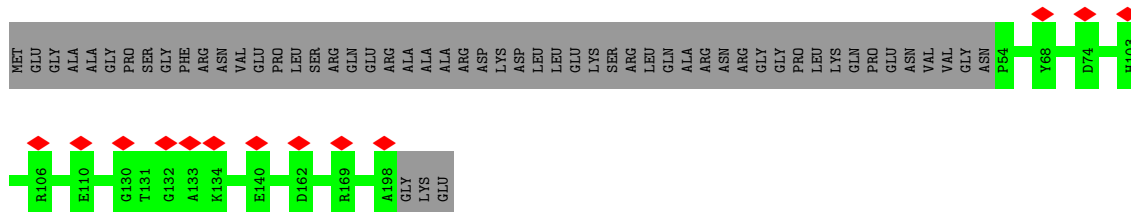


• Molecule 3: Cilia- and flagella-associated protein 20

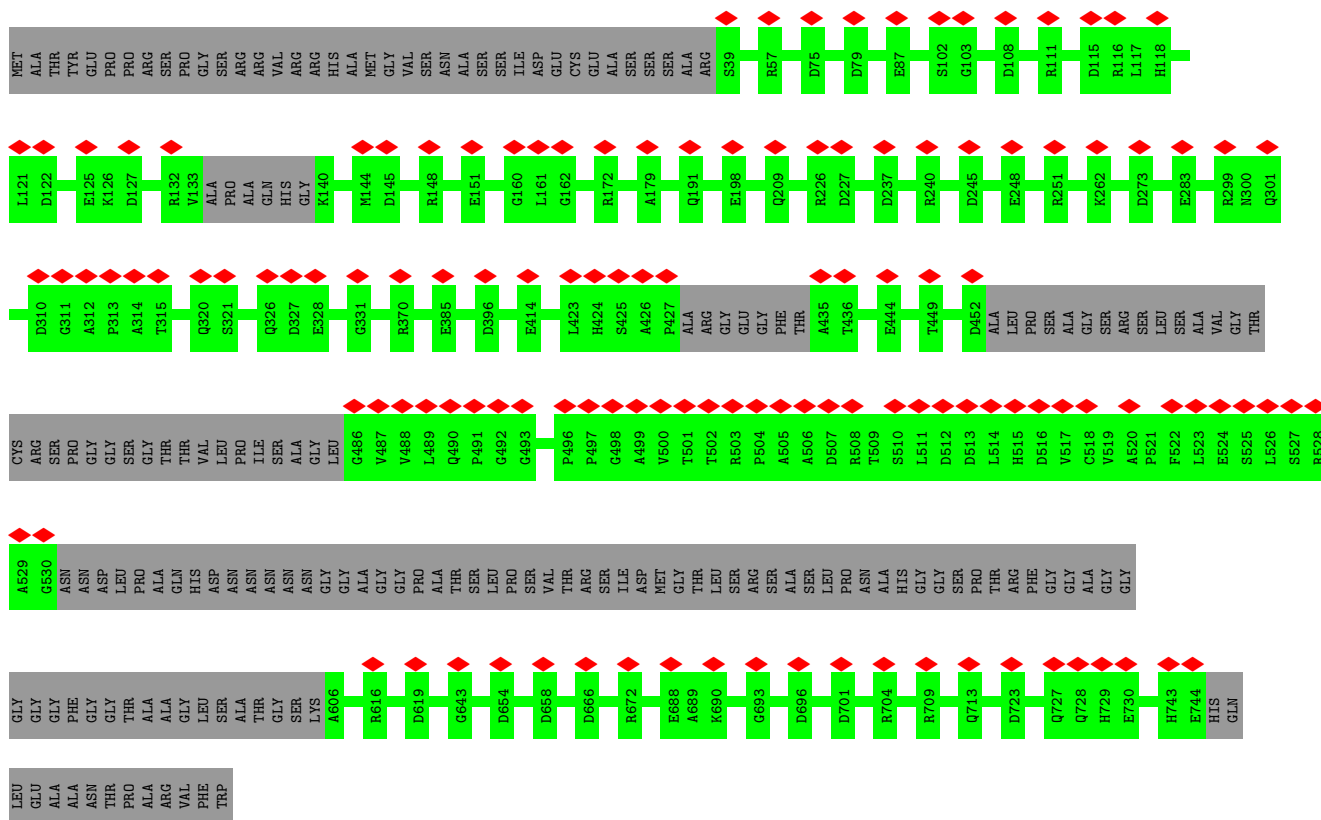
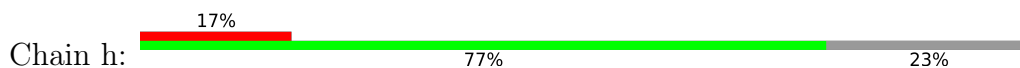




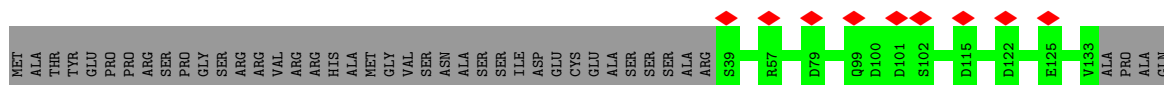
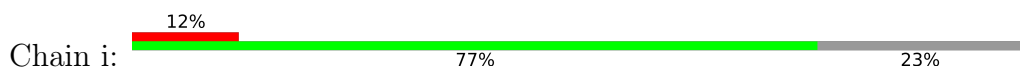
• Molecule 4: Unknown protein

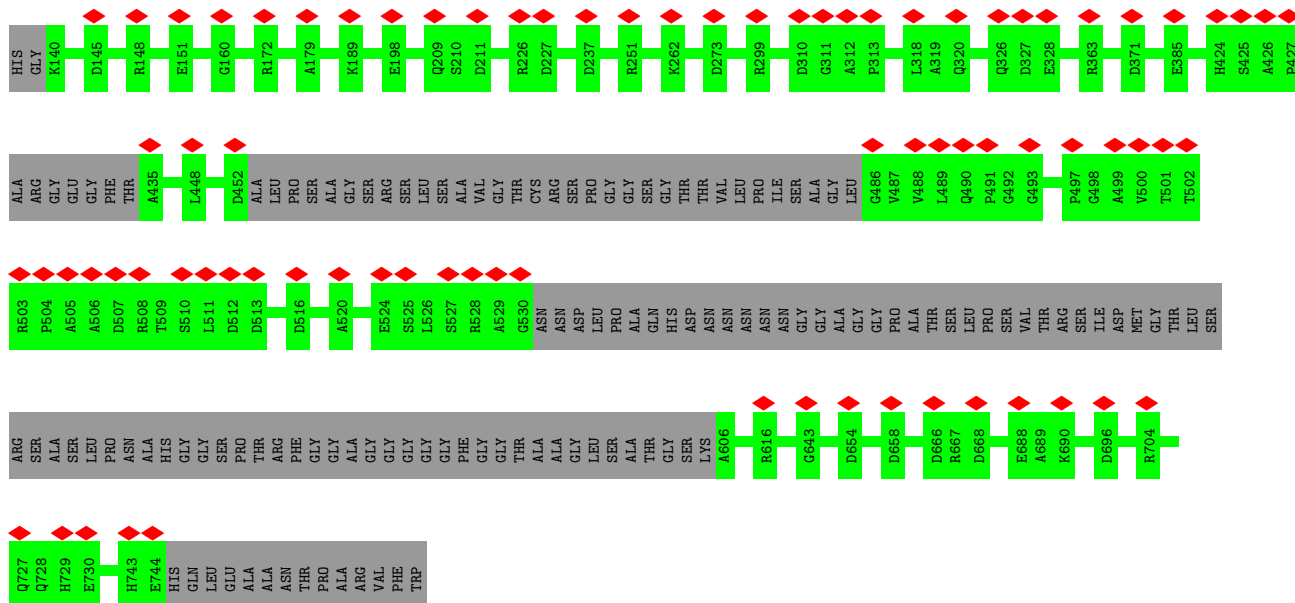


• Molecule 5: Unknown protein

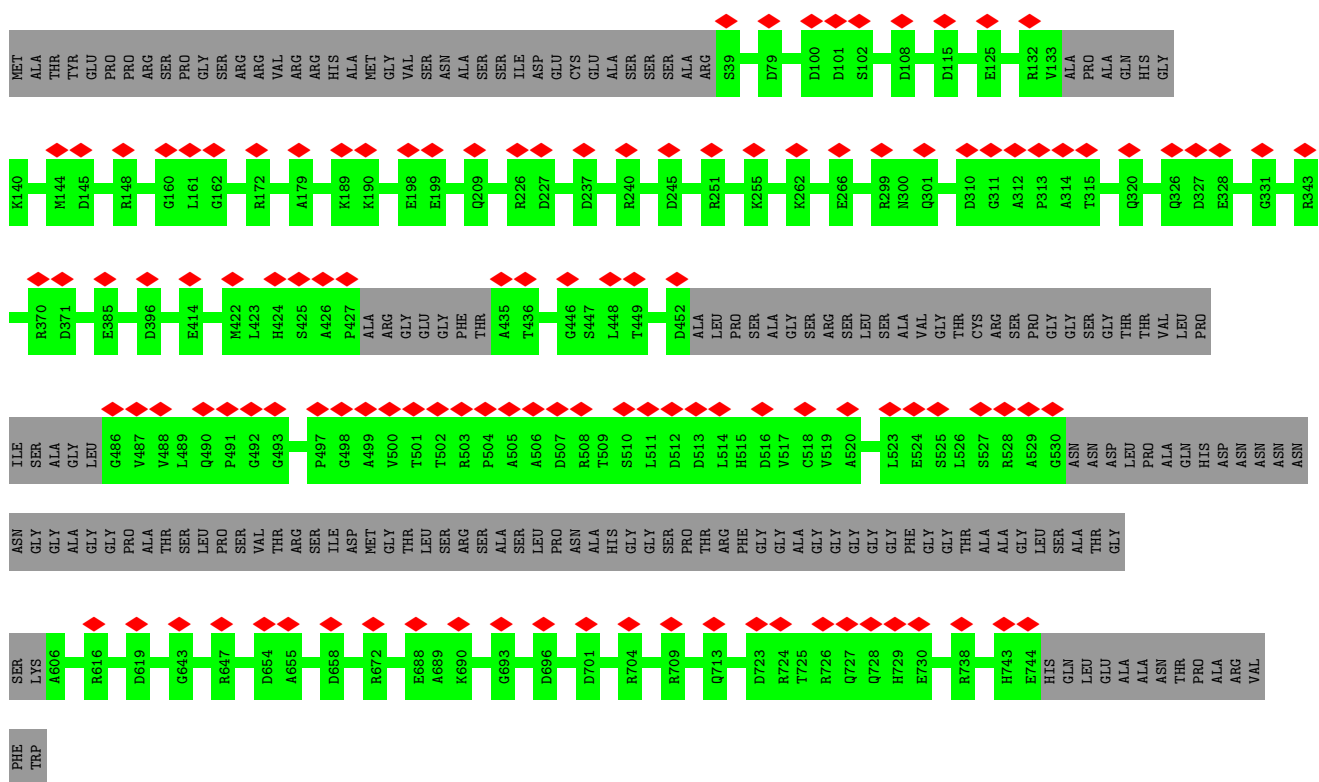
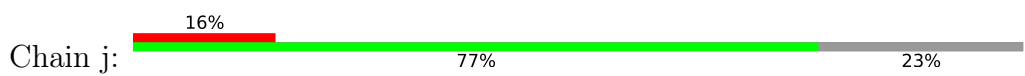


• Molecule 5: Unknown protein

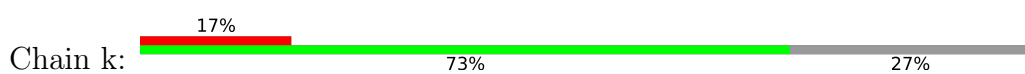


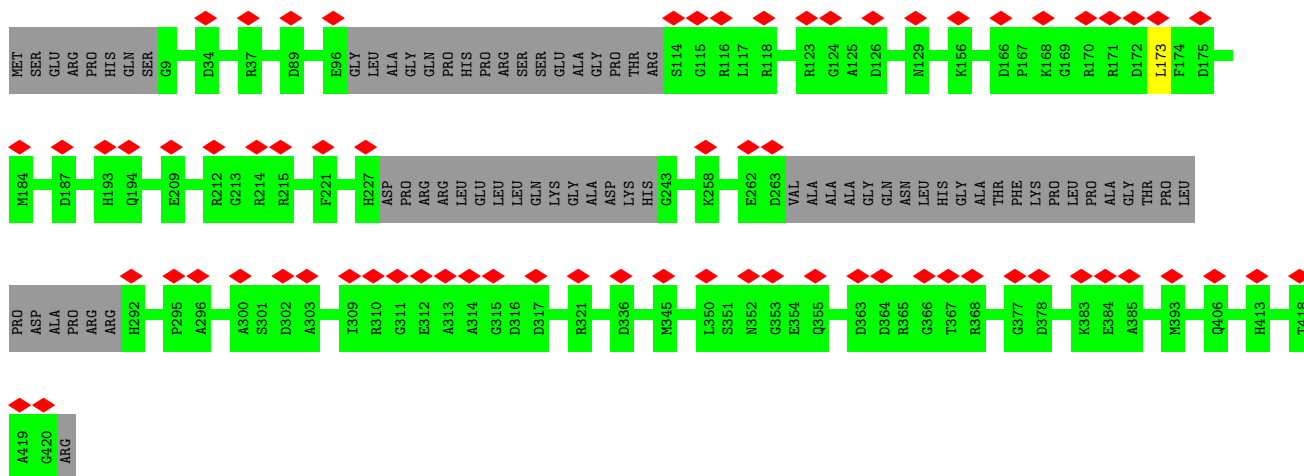


• Molecule 5: Unknown protein

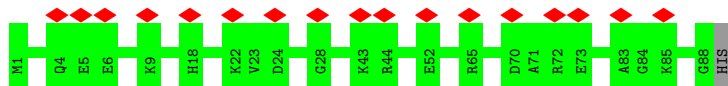


• Molecule 6: Unknown protein

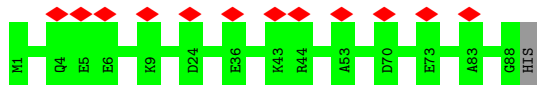




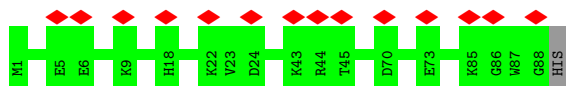
• Molecule 8: FAP70



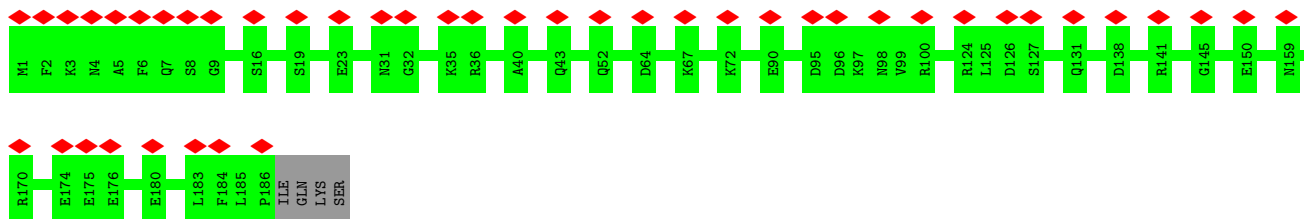
• Molecule 8: FAP70



• Molecule 8: FAP70



• Molecule 9: FAP147

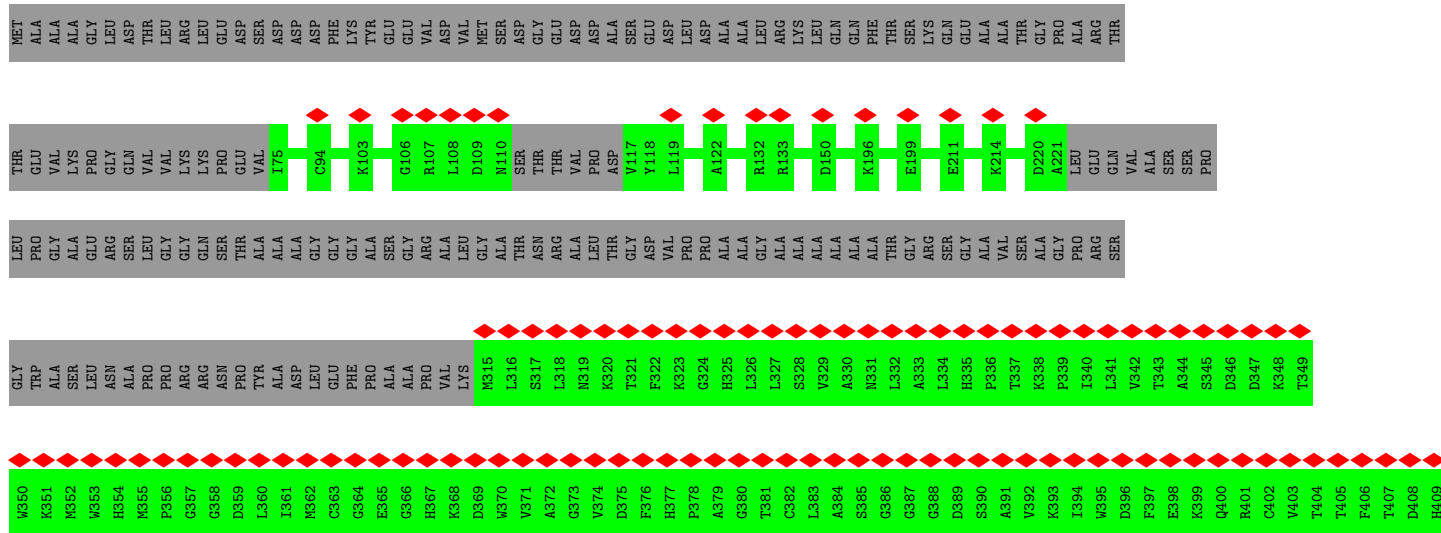
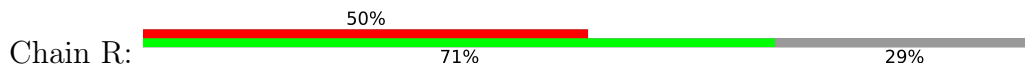


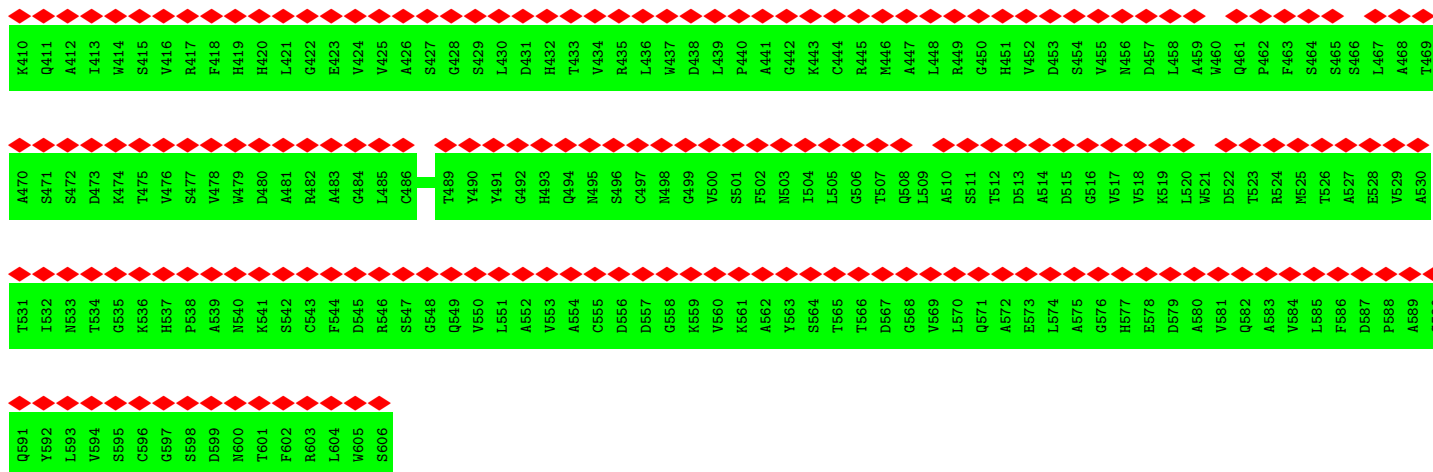
• Molecule 9: FAP147

• Molecule 10: FAP178

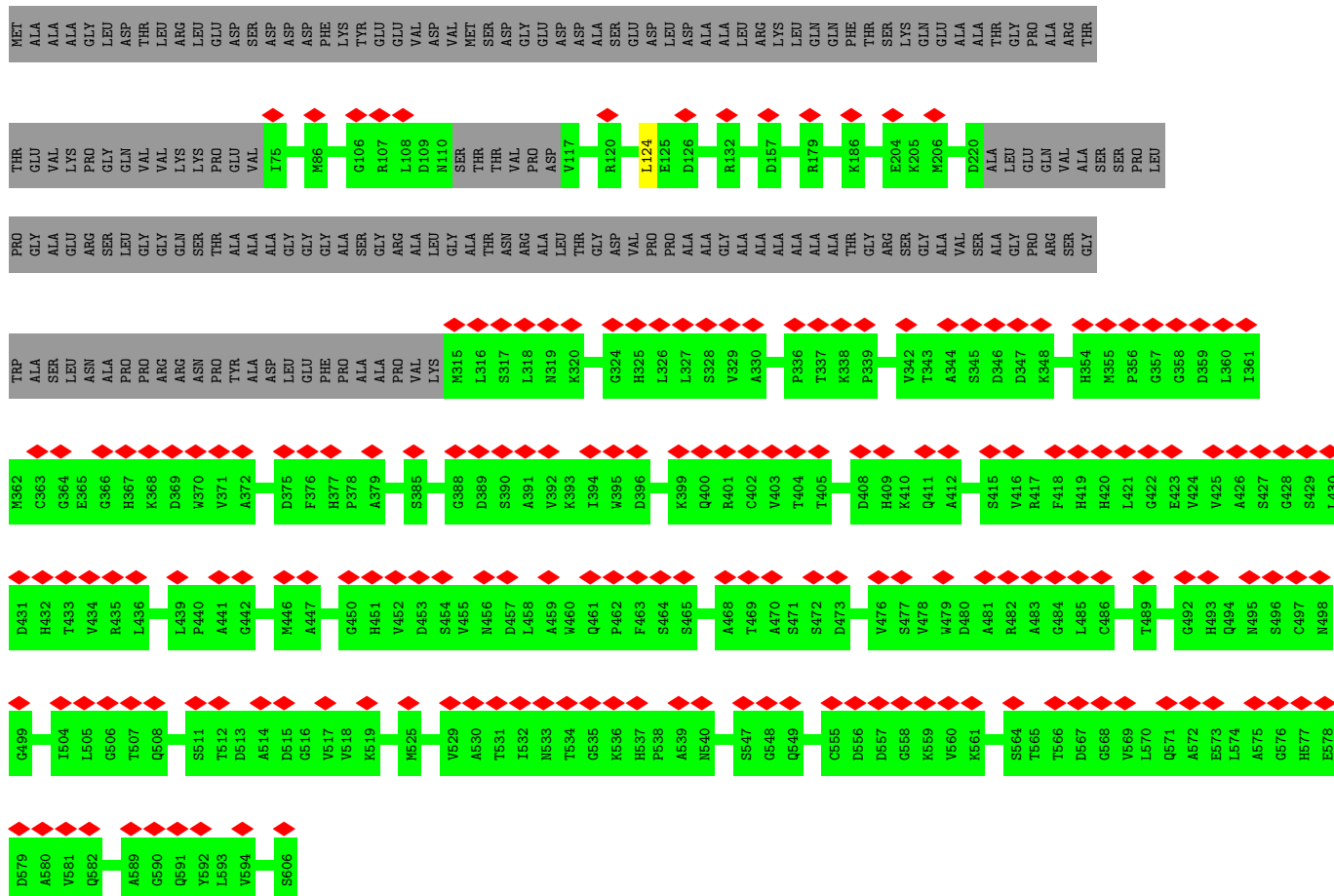


• Molecule 10: FAP178

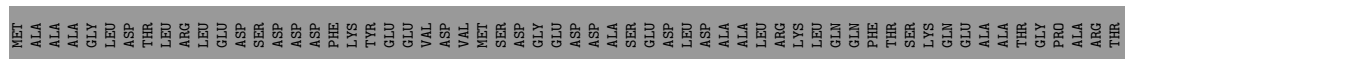


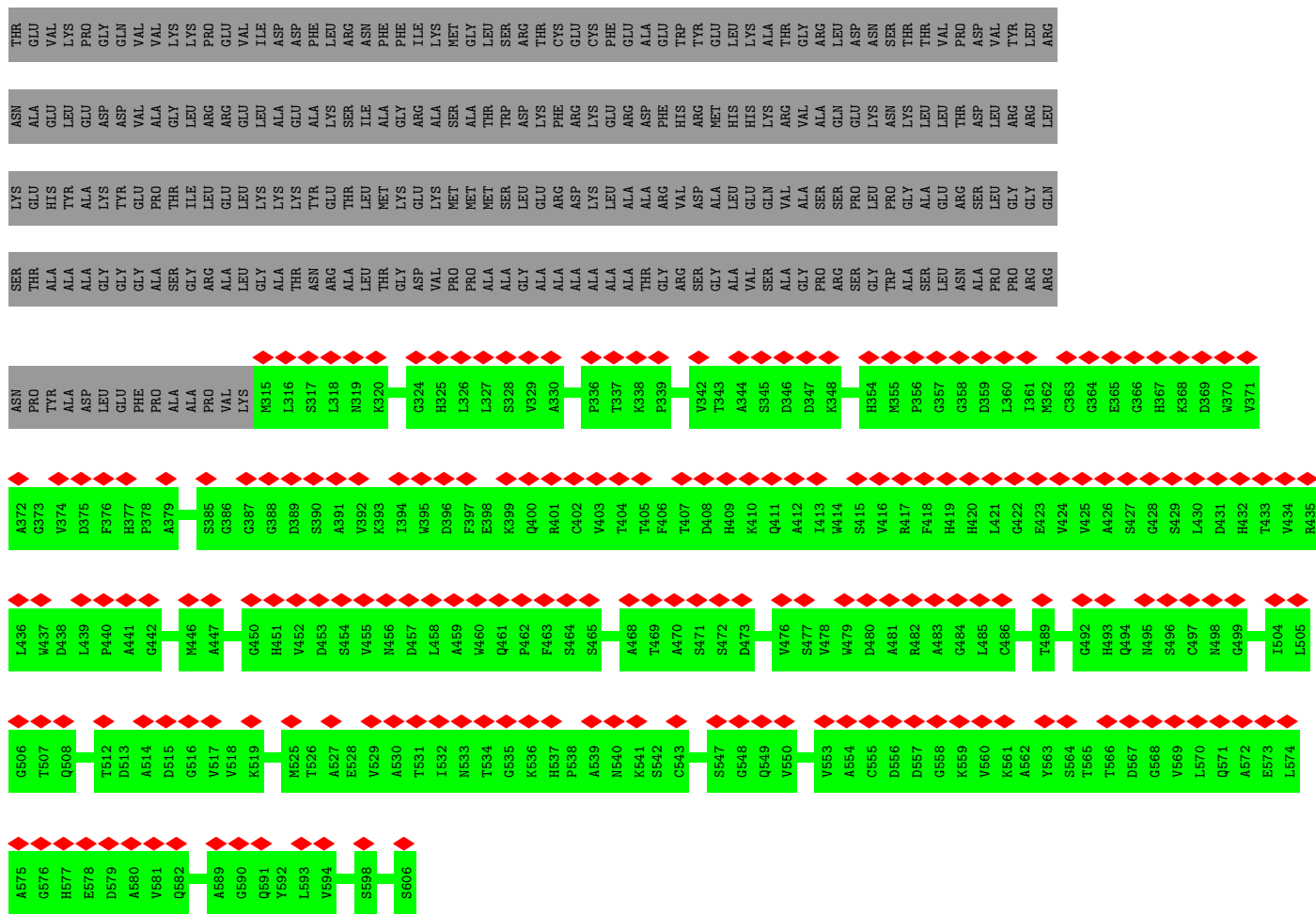


● Molecule 10: FAP178

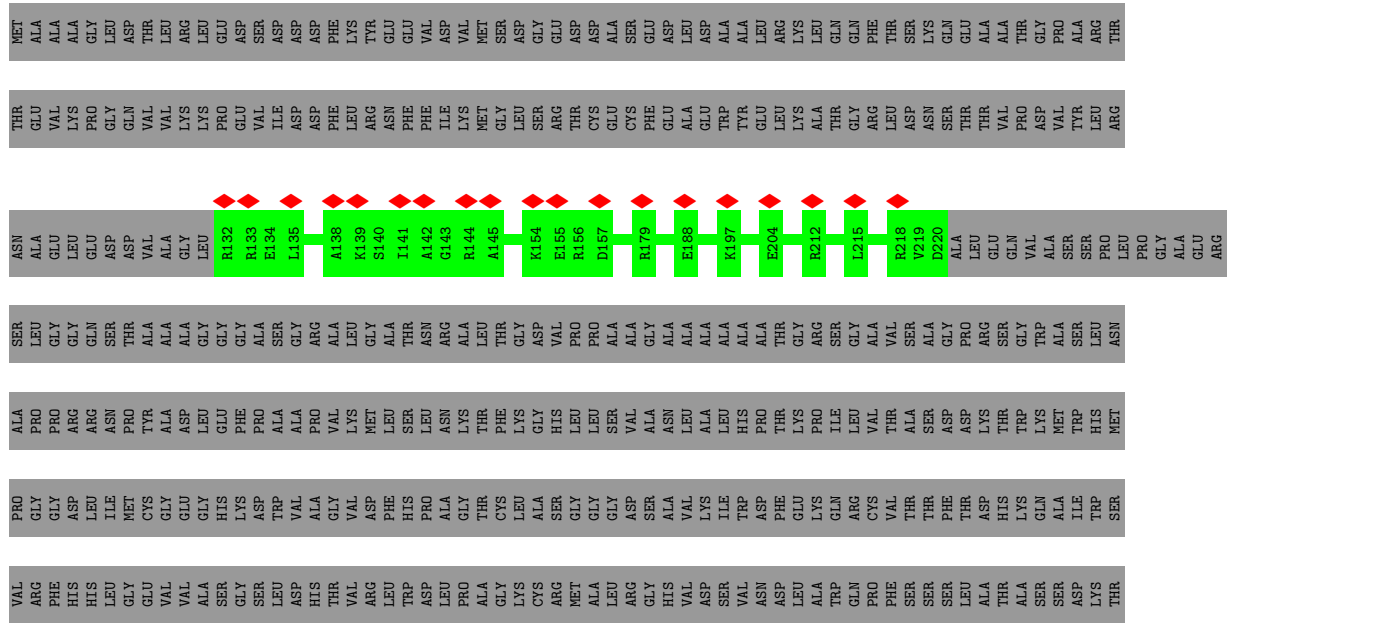


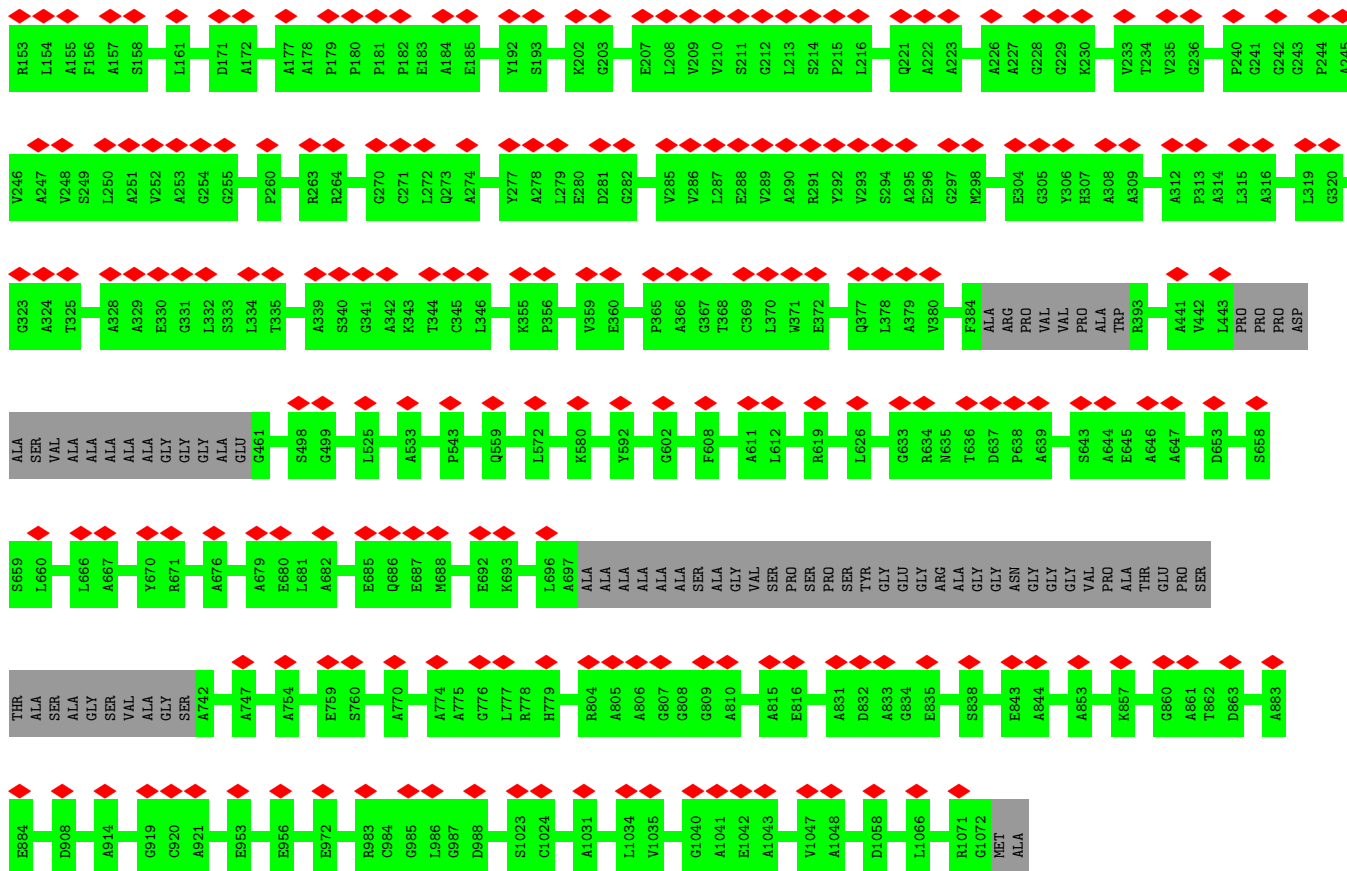
● Molecule 10: FAP178



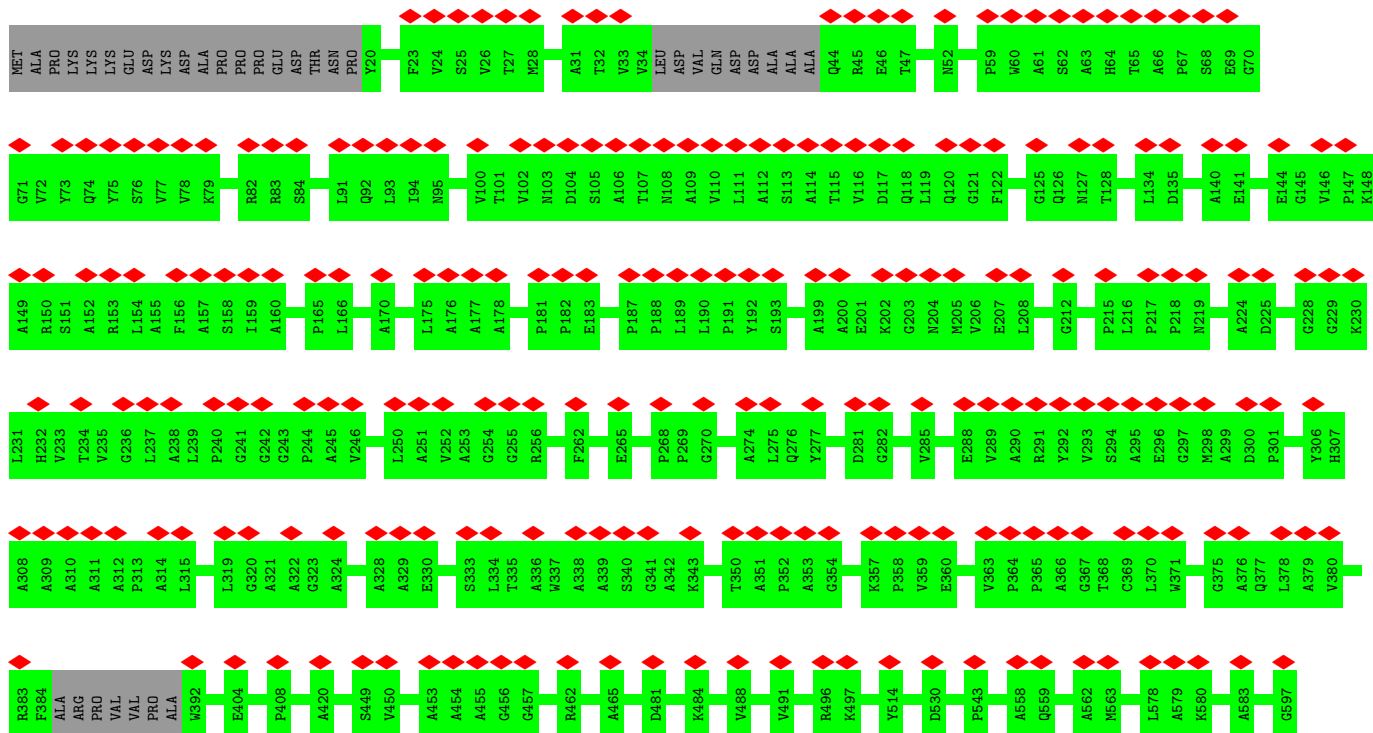
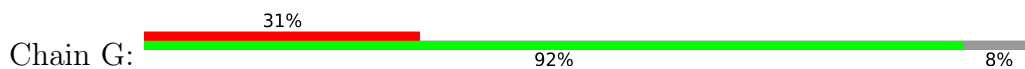


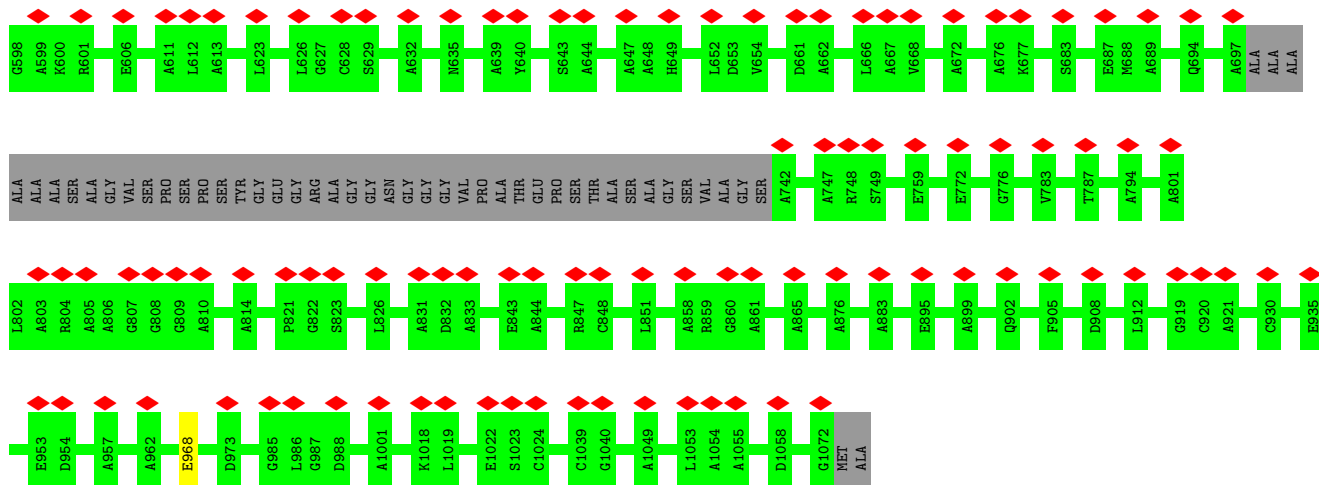
• Molecule 10: FAP178



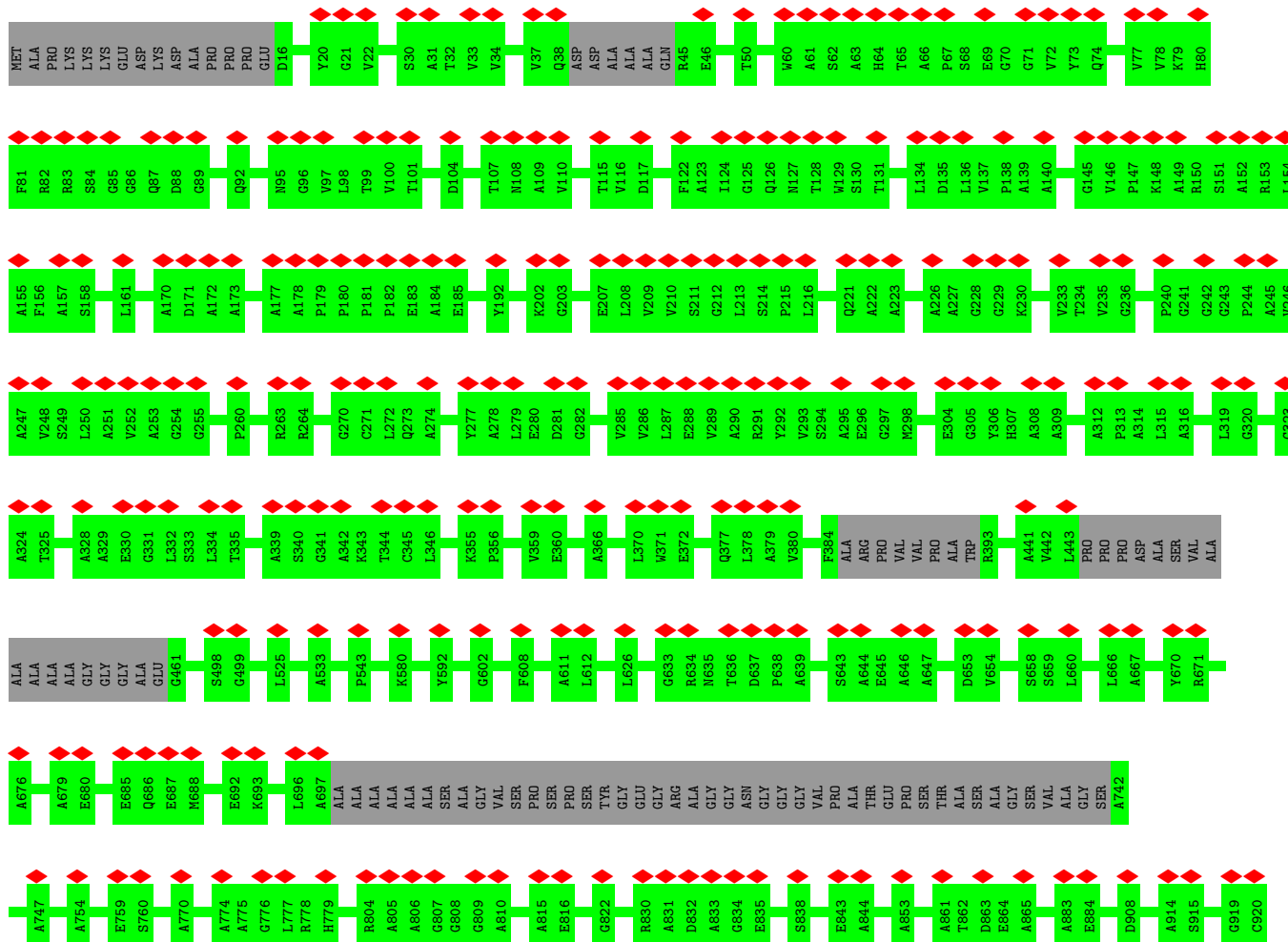
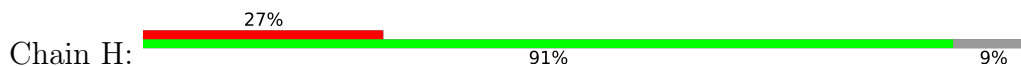


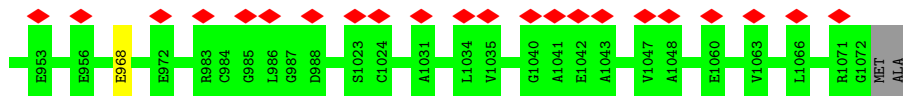
• Molecule 13: FAP196



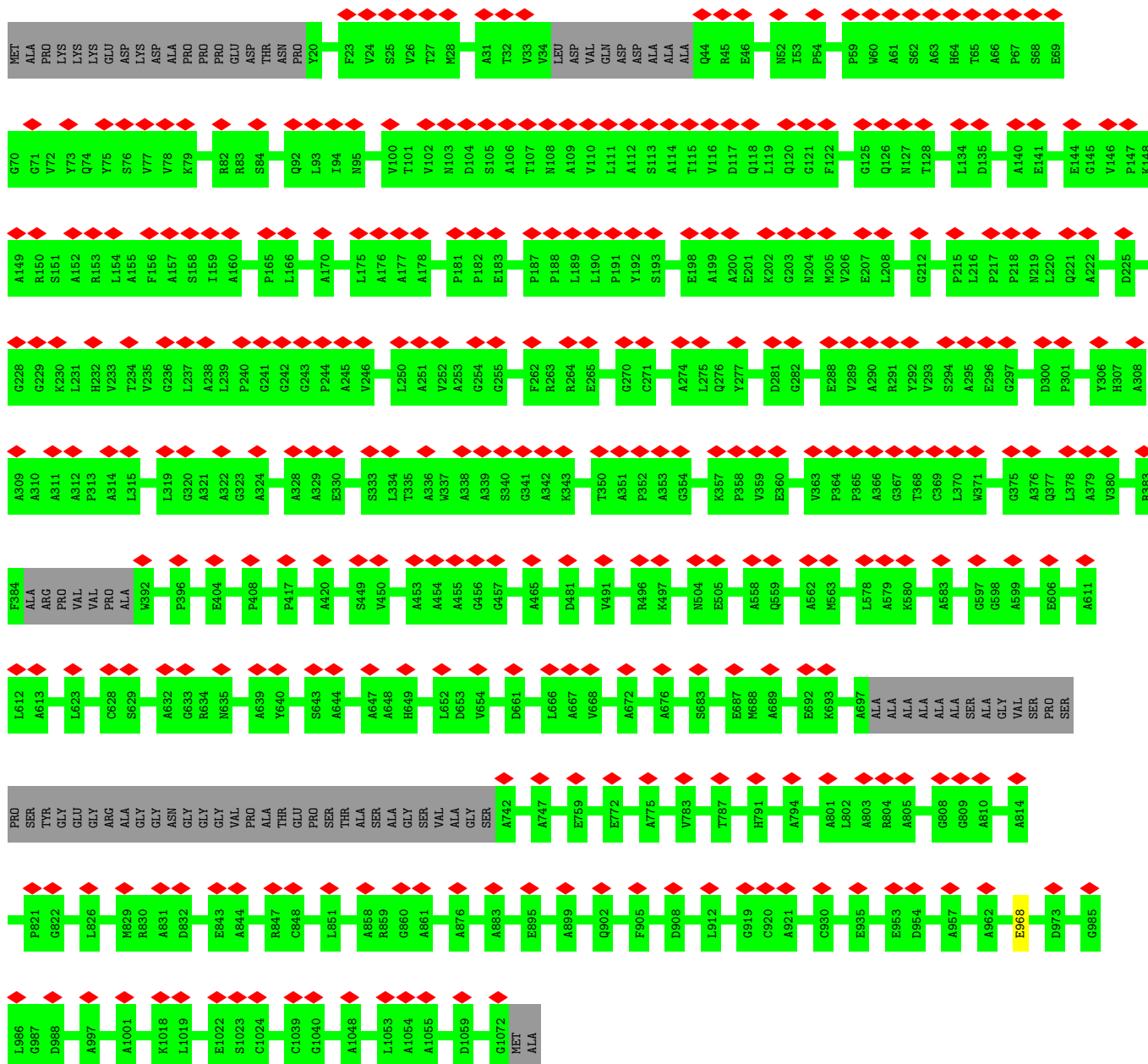
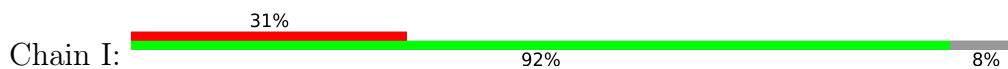


• Molecule 13: FAP196



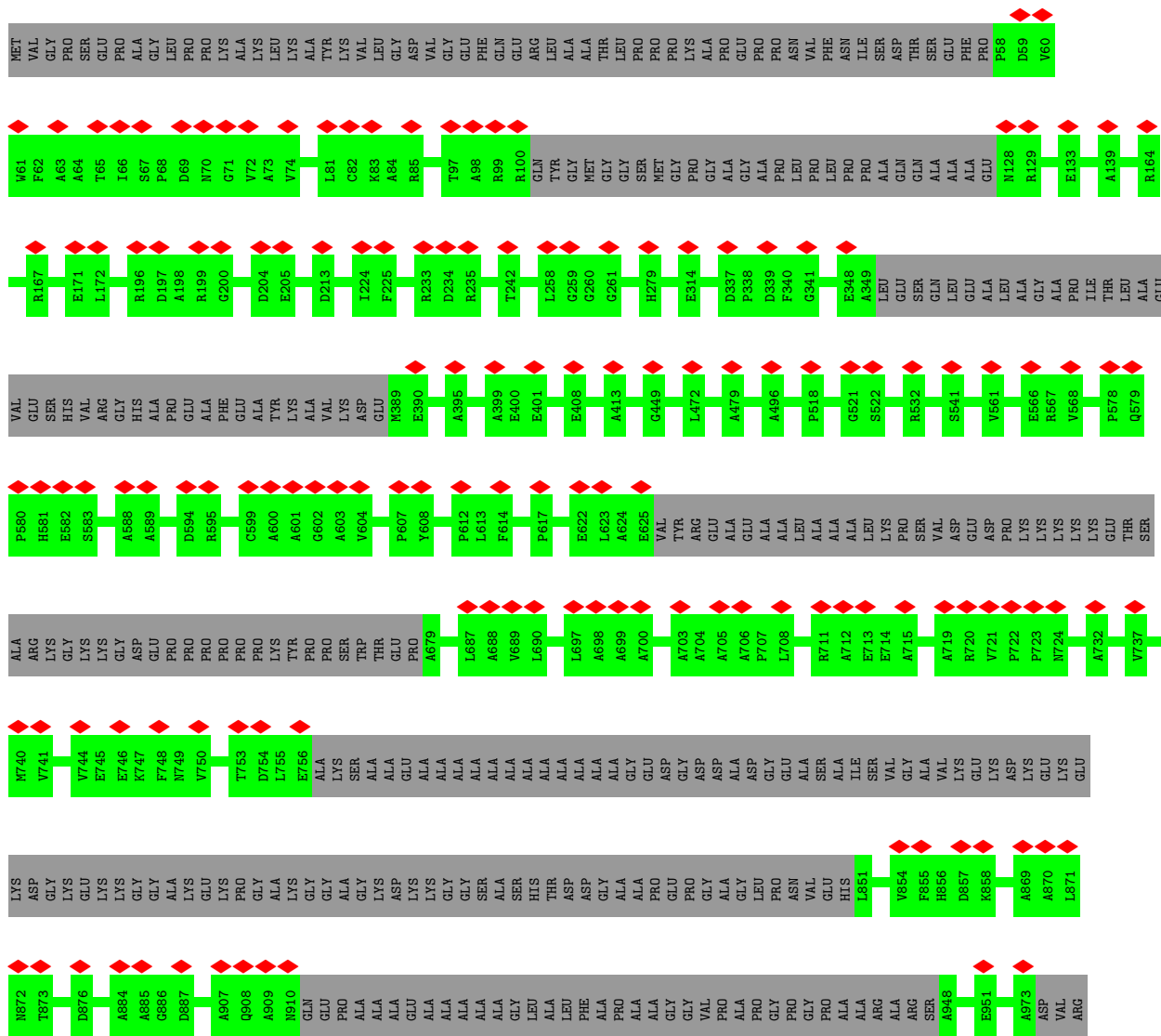


- Molecule 13: FAP196

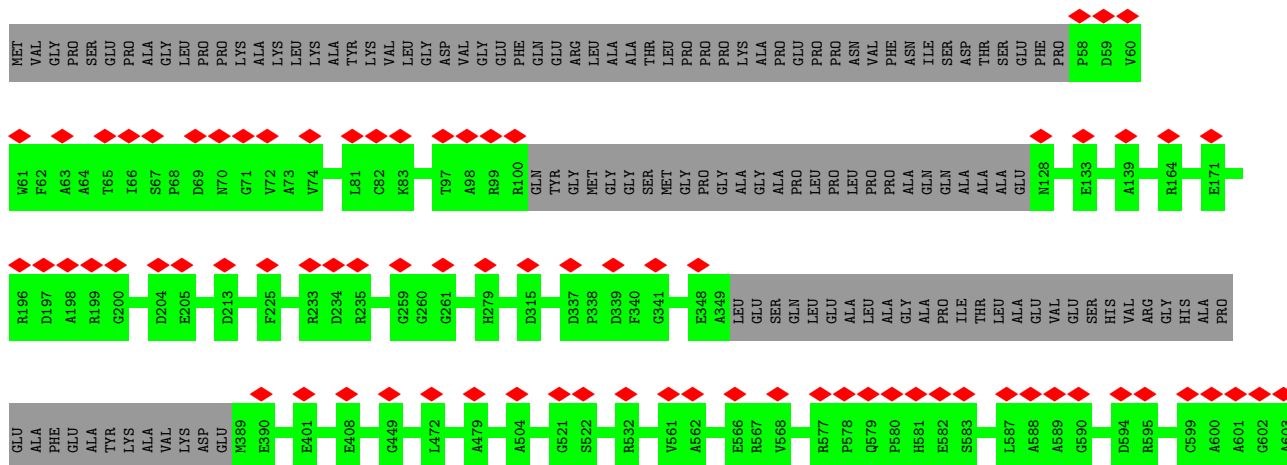


- Molecule 14: FAP213



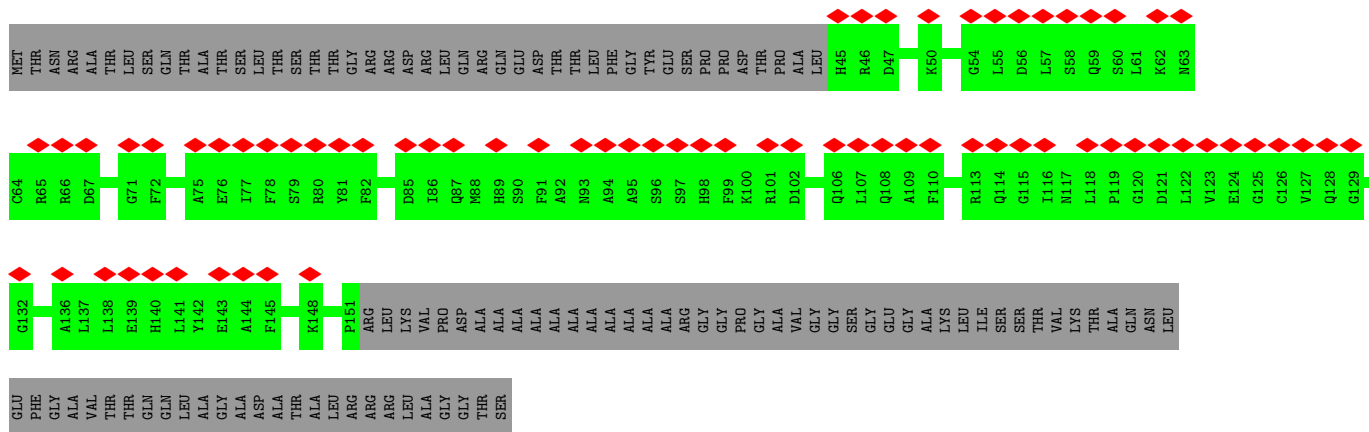


• Molecule 14: FAP213

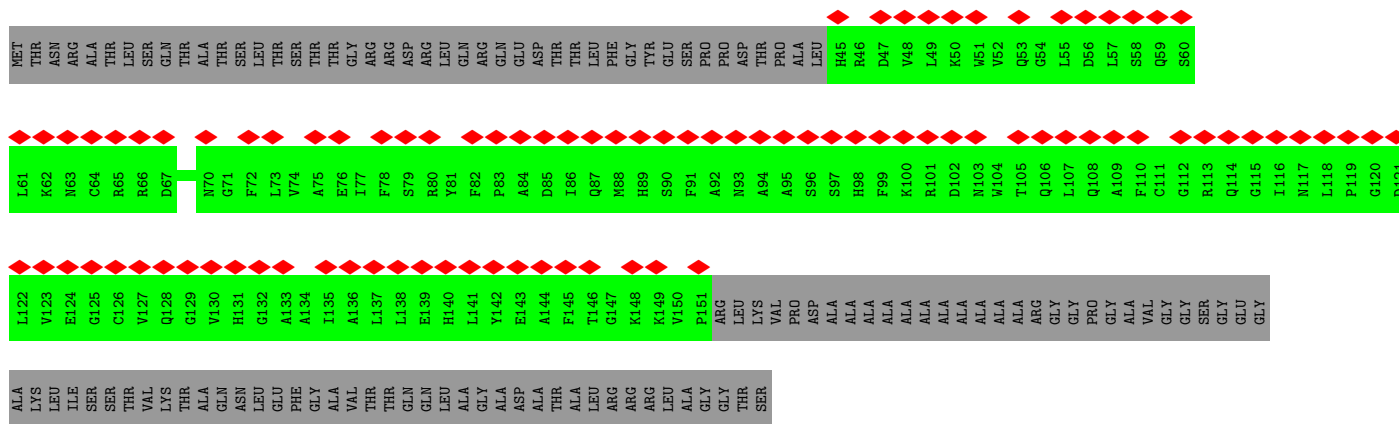
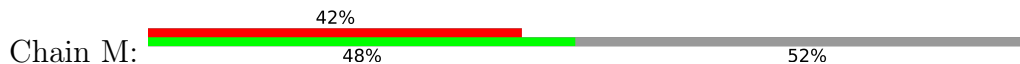


GLY
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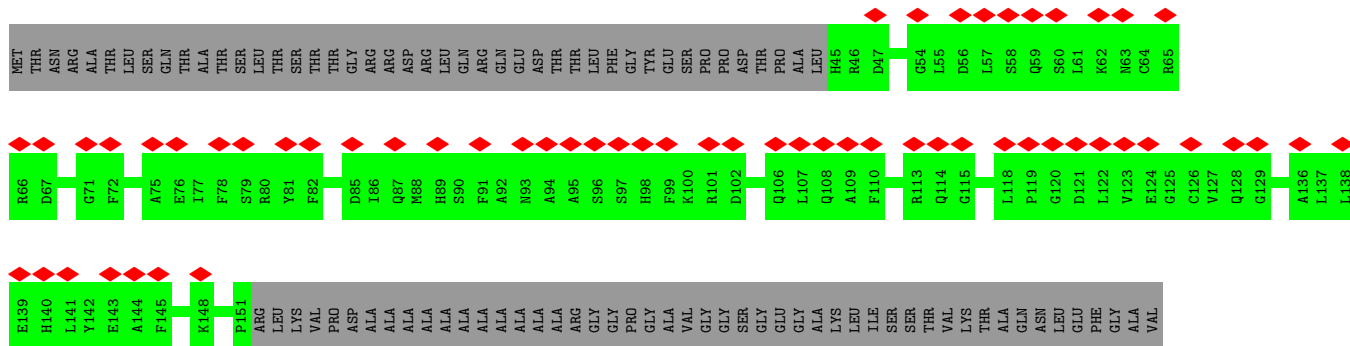
• Molecule 15: FAP225



• Molecule 15: FAP225

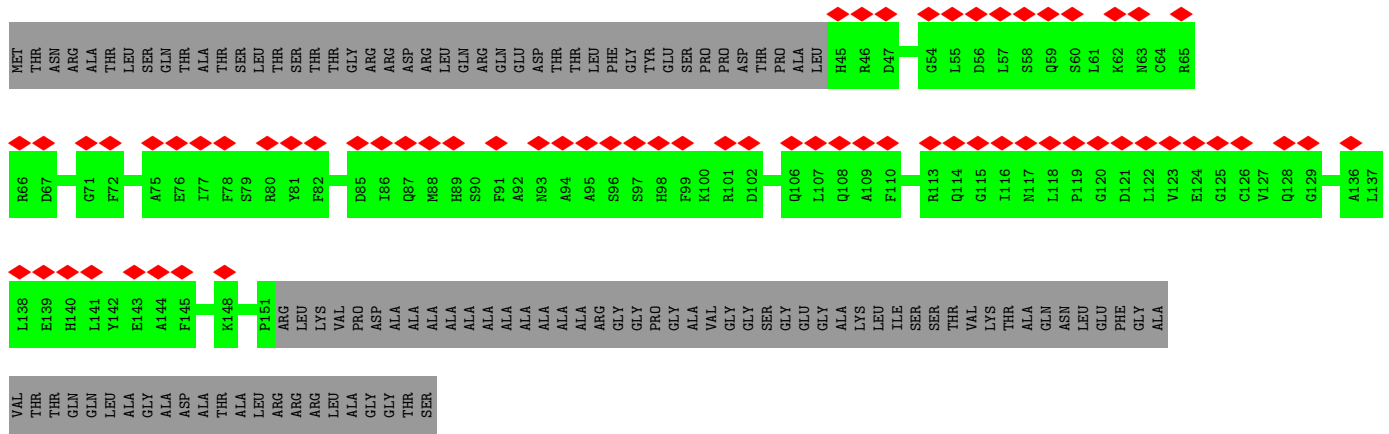


• Molecule 15: FAP225

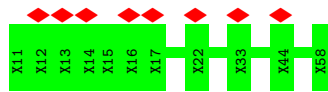


THR THR GLN GLN LEU ALA ALA ASP THR ALA LEU LEU ARG ARG ARG ARG ARG ALA ALA GLY GLY THR SER

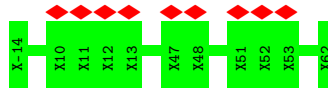
• Molecule 15: FAP225



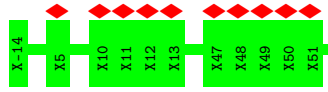
• Molecule 16: FAP239



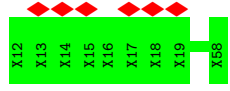
• Molecule 17: FAP388



• Molecule 17: FAP388



• Molecule 18: FAP424



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 104806 | 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 ($e^-/\text{\AA}^2$) | 39.6 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |
| Maximum map value | 1.998 | Depositor |
| Minimum map value | 0.000 | Depositor |
| Average map value | 0.006 | Depositor |
| Map value standard deviation | 0.050 | Depositor |
| Recommended contour level | 0.2 | Depositor |
| Map size (Å) | 711.68, 711.68, 711.68 | wwPDB |
| Map dimensions | 512, 512, 512 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.39, 1.39, 1.39 | Depositor |

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, MG, GDP

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 | AA | 0.27 | 0/3453 | 0.52 | 1/4673 (0.0%) |
| 1 | AC | 0.27 | 0/3444 | 0.53 | 1/4661 (0.0%) |
| 1 | AE | 0.28 | 0/3453 | 0.54 | 1/4673 (0.0%) |
| 1 | AG | 0.29 | 0/3453 | 0.54 | 1/4673 (0.0%) |
| 1 | AI | 0.27 | 0/3453 | 0.52 | 0/4673 |
| 1 | AK | 0.26 | 0/3453 | 0.52 | 0/4673 |
| 1 | BA | 0.27 | 0/3462 | 0.52 | 0/4685 |
| 1 | BC | 0.27 | 0/3428 | 0.53 | 0/4639 |
| 1 | BE | 0.28 | 0/3462 | 0.52 | 0/4685 |
| 1 | BG | 0.28 | 0/3428 | 0.54 | 0/4639 |
| 1 | BI | 0.27 | 0/3462 | 0.51 | 0/4685 |
| 1 | BK | 0.27 | 0/3428 | 0.53 | 0/4639 |
| 1 | CA | 0.26 | 0/3428 | 0.51 | 1/4639 (0.0%) |
| 1 | CC | 0.28 | 0/3428 | 0.52 | 0/4639 |
| 1 | CE | 0.28 | 0/3428 | 0.53 | 1/4639 (0.0%) |
| 1 | CG | 0.28 | 0/3428 | 0.52 | 0/4639 |
| 1 | CI | 0.27 | 0/3428 | 0.53 | 1/4639 (0.0%) |
| 1 | CK | 0.27 | 0/3428 | 0.52 | 0/4639 |
| 1 | DC | 0.27 | 0/3428 | 0.51 | 0/4639 |
| 1 | DE | 0.27 | 0/3428 | 0.51 | 0/4639 |
| 1 | DG | 0.29 | 0/3428 | 0.51 | 0/4639 |
| 1 | DI | 0.28 | 0/3428 | 0.52 | 0/4639 |
| 1 | DK | 0.27 | 0/3428 | 0.52 | 0/4639 |
| 1 | EA | 0.27 | 0/3428 | 0.51 | 0/4639 |
| 1 | EC | 0.27 | 0/3428 | 0.52 | 0/4639 |
| 1 | EE | 0.28 | 0/3428 | 0.52 | 0/4639 |
| 1 | EG | 0.29 | 0/3428 | 0.53 | 0/4639 |
| 1 | EI | 0.27 | 0/3428 | 0.51 | 0/4639 |
| 1 | EK | 0.27 | 0/3428 | 0.52 | 0/4639 |
| 1 | FA | 0.27 | 0/3428 | 0.52 | 0/4639 |
| 1 | FC | 0.26 | 0/3428 | 0.52 | 1/4639 (0.0%) |
| 1 | FE | 0.28 | 0/3428 | 0.54 | 0/4639 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|---------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 1 | FG | 0.27 | 0/3428 | 0.53 | 1/4639 (0.0%) |
| 1 | FI | 0.27 | 0/3428 | 0.52 | 0/4639 |
| 1 | FK | 0.27 | 0/3428 | 0.53 | 0/4639 |
| 1 | GC | 0.27 | 0/3428 | 0.52 | 1/4639 (0.0%) |
| 1 | GE | 0.27 | 0/3428 | 0.52 | 0/4639 |
| 1 | GG | 0.27 | 0/3428 | 0.53 | 0/4639 |
| 1 | GI | 0.28 | 0/3428 | 0.52 | 0/4639 |
| 1 | GK | 0.27 | 0/3428 | 0.52 | 1/4639 (0.0%) |
| 1 | GM | 0.27 | 0/3428 | 0.53 | 1/4639 (0.0%) |
| 1 | HC | 0.26 | 0/3428 | 0.52 | 0/4639 |
| 1 | HE | 0.27 | 0/3428 | 0.53 | 1/4639 (0.0%) |
| 1 | HG | 0.28 | 0/3428 | 0.54 | 0/4639 |
| 1 | HI | 0.26 | 0/3428 | 0.54 | 1/4639 (0.0%) |
| 1 | HK | 0.26 | 0/3428 | 0.53 | 1/4639 (0.0%) |
| 1 | HM | 0.26 | 0/3428 | 0.54 | 1/4639 (0.0%) |
| 1 | IC | 0.26 | 0/3428 | 0.52 | 0/4639 |
| 1 | IE | 0.26 | 0/3428 | 0.53 | 0/4639 |
| 1 | IG | 0.27 | 0/3428 | 0.53 | 0/4639 |
| 1 | II | 0.27 | 0/3428 | 0.54 | 0/4639 |
| 1 | IK | 0.27 | 0/3428 | 0.53 | 0/4639 |
| 1 | IM | 0.27 | 0/3428 | 0.52 | 0/4639 |
| 1 | JC | 0.26 | 0/3428 | 0.52 | 1/4639 (0.0%) |
| 1 | JE | 0.27 | 0/3428 | 0.53 | 1/4639 (0.0%) |
| 1 | JG | 0.27 | 0/3428 | 0.53 | 1/4639 (0.0%) |
| 1 | JI | 0.29 | 0/3420 | 0.55 | 1/4628 (0.0%) |
| 1 | JK | 0.27 | 0/3428 | 0.54 | 1/4639 (0.0%) |
| 1 | JM | 0.26 | 0/3420 | 0.52 | 0/4628 |
| 1 | KC | 0.27 | 0/3428 | 0.52 | 0/4639 |
| 1 | KE | 0.28 | 0/3428 | 0.54 | 1/4639 (0.0%) |
| 1 | KG | 0.28 | 0/3428 | 0.53 | 0/4639 |
| 1 | KI | 0.28 | 0/3428 | 0.55 | 1/4639 (0.0%) |
| 1 | KK | 0.27 | 0/3428 | 0.52 | 0/4639 |
| 1 | LC | 0.27 | 0/3428 | 0.51 | 0/4639 |
| 1 | LE | 0.27 | 0/3428 | 0.53 | 0/4639 |
| 1 | LG | 0.28 | 0/3428 | 0.52 | 0/4639 |
| 1 | LI | 0.28 | 0/3428 | 0.53 | 0/4639 |
| 1 | LK | 0.26 | 0/3428 | 0.52 | 0/4639 |
| 1 | MC | 0.27 | 0/3453 | 0.52 | 0/4673 |
| 1 | ME | 0.28 | 0/3428 | 0.53 | 0/4639 |
| 1 | MG | 0.29 | 0/3453 | 0.52 | 0/4673 |
| 1 | MI | 0.28 | 0/3428 | 0.52 | 0/4639 |
| 1 | MK | 0.28 | 0/3453 | 0.52 | 0/4673 |
| 2 | AB | 0.27 | 0/3426 | 0.53 | 0/4644 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|---------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 2 | AD | 0.26 | 0/3426 | 0.52 | 0/4644 |
| 2 | AF | 0.28 | 0/3426 | 0.53 | 0/4644 |
| 2 | AH | 0.29 | 0/3412 | 0.54 | 0/4625 |
| 2 | AJ | 0.26 | 0/3426 | 0.51 | 0/4644 |
| 2 | AL | 0.26 | 0/3412 | 0.52 | 0/4625 |
| 2 | BB | 0.26 | 0/3465 | 0.53 | 0/4697 |
| 2 | BD | 0.28 | 0/3412 | 0.52 | 0/4625 |
| 2 | BF | 0.28 | 0/3465 | 0.55 | 0/4697 |
| 2 | BH | 0.28 | 0/3412 | 0.53 | 0/4625 |
| 2 | BJ | 0.27 | 0/3465 | 0.53 | 0/4697 |
| 2 | BL | 0.26 | 0/3412 | 0.52 | 0/4625 |
| 2 | CB | 0.28 | 0/3406 | 0.53 | 0/4617 |
| 2 | CD | 0.28 | 0/3406 | 0.53 | 0/4617 |
| 2 | CF | 0.28 | 0/3406 | 0.52 | 0/4617 |
| 2 | CH | 0.28 | 0/3406 | 0.54 | 0/4617 |
| 2 | CJ | 0.27 | 0/3412 | 0.52 | 0/4625 |
| 2 | DB | 0.28 | 0/3412 | 0.54 | 0/4625 |
| 2 | DD | 0.28 | 0/3406 | 0.53 | 0/4617 |
| 2 | DF | 0.28 | 0/3412 | 0.55 | 0/4625 |
| 2 | DH | 0.28 | 0/3412 | 0.52 | 0/4625 |
| 2 | DJ | 0.27 | 0/3412 | 0.52 | 0/4625 |
| 2 | DL | 0.27 | 0/3412 | 0.53 | 0/4625 |
| 2 | EB | 0.27 | 0/3465 | 0.53 | 0/4697 |
| 2 | ED | 0.27 | 0/3406 | 0.53 | 0/4617 |
| 2 | EF | 0.29 | 0/3471 | 0.54 | 1/4705 (0.0%) |
| 2 | EH | 0.28 | 0/3406 | 0.54 | 0/4617 |
| 2 | EJ | 0.27 | 0/3465 | 0.53 | 0/4697 |
| 2 | EL | 0.27 | 0/3406 | 0.52 | 0/4617 |
| 2 | FB | 0.27 | 0/3412 | 0.52 | 0/4625 |
| 2 | FD | 0.26 | 0/3412 | 0.51 | 0/4625 |
| 2 | FF | 0.28 | 0/3412 | 0.53 | 0/4625 |
| 2 | FH | 0.29 | 0/3412 | 0.56 | 2/4625 (0.0%) |
| 2 | FJ | 0.27 | 0/3412 | 0.52 | 0/4625 |
| 2 | FL | 0.26 | 0/3412 | 0.52 | 0/4625 |
| 2 | GD | 0.27 | 0/3412 | 0.54 | 1/4625 (0.0%) |
| 2 | GF | 0.27 | 0/3412 | 0.55 | 0/4625 |
| 2 | GH | 0.28 | 0/3412 | 0.53 | 1/4625 (0.0%) |
| 2 | GJ | 0.28 | 0/3412 | 0.53 | 0/4625 |
| 2 | GL | 0.27 | 0/3412 | 0.53 | 0/4625 |
| 2 | HD | 0.27 | 0/3412 | 0.54 | 0/4625 |
| 2 | HF | 0.27 | 0/3412 | 0.55 | 0/4625 |
| 2 | HH | 0.27 | 0/3412 | 0.53 | 0/4625 |
| 2 | HJ | 0.27 | 0/3397 | 0.54 | 0/4605 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|---------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 2 | HL | 0.26 | 0/3412 | 0.52 | 0/4625 |
| 2 | ID | 0.27 | 0/3406 | 0.54 | 1/4617 (0.0%) |
| 2 | IF | 0.27 | 0/3412 | 0.55 | 2/4625 (0.0%) |
| 2 | IH | 0.27 | 0/3406 | 0.52 | 0/4617 |
| 2 | IJ | 0.27 | 0/3412 | 0.54 | 0/4625 |
| 2 | IL | 0.27 | 0/3406 | 0.54 | 1/4617 (0.0%) |
| 2 | JB | 0.26 | 0/3412 | 0.54 | 0/4625 |
| 2 | JD | 0.27 | 0/3412 | 0.52 | 0/4625 |
| 2 | JF | 0.27 | 0/3412 | 0.55 | 0/4625 |
| 2 | JH | 0.28 | 0/3412 | 0.52 | 0/4625 |
| 2 | JJ | 0.27 | 0/3406 | 0.53 | 0/4617 |
| 2 | JL | 0.27 | 0/3406 | 0.53 | 1/4617 (0.0%) |
| 2 | KB | 0.27 | 0/3406 | 0.52 | 0/4617 |
| 2 | KD | 0.27 | 0/3412 | 0.53 | 0/4625 |
| 2 | KF | 0.28 | 0/3406 | 0.54 | 1/4617 (0.0%) |
| 2 | KH | 0.28 | 0/3412 | 0.54 | 0/4625 |
| 2 | KJ | 0.27 | 0/3406 | 0.53 | 0/4617 |
| 2 | KL | 0.27 | 0/3412 | 0.53 | 0/4625 |
| 2 | LB | 0.26 | 0/3412 | 0.52 | 0/4625 |
| 2 | LD | 0.27 | 0/3412 | 0.53 | 1/4625 (0.0%) |
| 2 | LF | 0.28 | 0/3412 | 0.54 | 1/4625 (0.0%) |
| 2 | LH | 0.27 | 0/3412 | 0.54 | 0/4625 |
| 2 | LJ | 0.27 | 0/3412 | 0.53 | 0/4625 |
| 2 | LL | 0.26 | 0/3412 | 0.51 | 0/4625 |
| 2 | MB | 0.27 | 0/3412 | 0.52 | 0/4625 |
| 2 | MD | 0.27 | 0/3471 | 0.51 | 0/4705 |
| 2 | MF | 0.28 | 0/3412 | 0.53 | 1/4625 (0.0%) |
| 2 | MH | 0.28 | 0/3476 | 0.53 | 0/4712 |
| 2 | MJ | 0.28 | 0/3412 | 0.52 | 0/4625 |
| 2 | ML | 0.27 | 0/3476 | 0.52 | 0/4712 |
| 3 | a | 0.27 | 0/2428 | 0.58 | 0/3300 |
| 3 | b | 0.28 | 0/4634 | 0.61 | 1/6298 (0.0%) |
| 3 | c | 0.28 | 0/4634 | 0.64 | 3/6298 (0.0%) |
| 3 | d | 0.27 | 0/2228 | 0.62 | 0/3026 |
| 4 | e | 0.26 | 0/1484 | 0.57 | 0/1994 |
| 4 | f | 0.27 | 0/1484 | 0.54 | 0/1994 |
| 4 | g | 0.28 | 0/1154 | 0.52 | 0/1553 |
| 5 | h | 0.26 | 0/4608 | 0.56 | 0/6234 |
| 5 | i | 0.27 | 0/4608 | 0.58 | 0/6234 |
| 5 | j | 0.26 | 0/4608 | 0.56 | 0/6234 |
| 6 | k | 0.26 | 0/3072 | 0.58 | 0/4147 |
| 6 | l | 0.27 | 0/3072 | 0.58 | 2/4147 (0.0%) |
| 6 | s | 0.26 | 0/2253 | 0.56 | 0/3048 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|----------|-------------|------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 7 | m | 0.27 | 0/2808 | 0.60 | 1/3798 (0.0%) |
| 7 | n | 0.27 | 0/2808 | 0.63 | 1/3798 (0.0%) |
| 7 | o | 0.26 | 0/2808 | 0.60 | 1/3798 (0.0%) |
| 8 | p | 0.25 | 0/714 | 0.58 | 0/962 |
| 8 | q | 0.26 | 0/714 | 0.58 | 0/962 |
| 8 | r | 0.25 | 0/714 | 0.58 | 0/962 |
| 9 | A | 0.26 | 0/1564 | 0.58 | 0/2113 |
| 9 | B | 0.26 | 0/1564 | 0.57 | 0/2113 |
| 9 | C | 0.26 | 0/1564 | 0.58 | 0/2113 |
| 10 | P | 0.27 | 0/2503 | 0.51 | 0/3420 |
| 10 | Q | 0.26 | 0/2498 | 0.52 | 1/3413 (0.0%) |
| 10 | R | 0.27 | 0/2503 | 0.53 | 0/3420 |
| 10 | S | 0.26 | 0/2498 | 0.53 | 1/3413 (0.0%) |
| 10 | Z | 0.23 | 0/786 | 0.47 | 0/1041 |
| 10 | aa | 0.24 | 0/1434 | 0.47 | 0/1989 |
| 10 | cc | 0.23 | 0/769 | 0.48 | 0/1018 |
| 11 | T | 0.24 | 0/310 | 0.33 | 0/429 |
| 11 | U | 0.24 | 0/285 | 0.30 | 0/394 |
| 11 | V | 0.25 | 0/331 | 0.39 | 0/460 |
| 11 | W | 0.23 | 0/311 | 0.34 | 0/432 |
| 12 | D | 0.26 | 0/7465 | 0.45 | 0/10373 |
| 12 | E | 0.26 | 0/7465 | 0.45 | 0/10373 |
| 12 | bb | 0.27 | 0/1076 | 0.57 | 0/1482 |
| 13 | F | 0.26 | 0/4827 | 0.40 | 0/6703 |
| 13 | G | 0.26 | 0/4880 | 0.40 | 0/6777 |
| 13 | H | 0.26 | 0/4827 | 0.40 | 0/6703 |
| 13 | I | 0.26 | 0/4880 | 0.40 | 0/6777 |
| 14 | J | 0.26 | 0/3904 | 0.49 | 0/5372 |
| 14 | K | 0.26 | 0/3904 | 0.49 | 0/5372 |
| 15 | L | 0.26 | 0/861 | 0.47 | 0/1163 |
| 15 | M | 0.26 | 0/861 | 0.47 | 0/1163 |
| 15 | N | 0.27 | 0/861 | 0.47 | 0/1163 |
| 15 | O | 0.26 | 0/861 | 0.48 | 0/1163 |
| 15 | X | 0.27 | 0/861 | 0.47 | 0/1163 |
| 15 | Y | 0.26 | 0/861 | 0.48 | 0/1163 |
| All | All | 0.27 | 0/625065 | 0.53 | 48/848033 (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 |
|-----|-------|---------------------|---------------------|
| 2 | DB | 0 | 1 |
| 2 | DF | 0 | 1 |
| 2 | GD | 0 | 1 |
| 2 | HD | 0 | 1 |
| 2 | HL | 0 | 1 |
| 2 | KD | 0 | 1 |
| 2 | KH | 0 | 1 |
| 2 | KL | 0 | 1 |
| 3 | c | 0 | 1 |
| 3 | d | 0 | 1 |
| 13 | G | 0 | 1 |
| 13 | H | 0 | 1 |
| 13 | I | 0 | 1 |
| All | All | 0 | 13 |

There are no bond length outliers.

The worst 5 of 48 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|------|-------------|----------|
| 7 | o | 173 | LEU | CA-CB-CG | 6.77 | 130.88 | 115.30 |
| 3 | c | 277 | LEU | CA-CB-CG | 6.68 | 130.68 | 115.30 |
| 7 | m | 173 | LEU | CA-CB-CG | 6.59 | 130.46 | 115.30 |
| 1 | CE | 284 | LEU | CA-CB-CG | 6.44 | 130.10 | 115.30 |
| 1 | AG | 284 | LEU | CA-CB-CG | 6.27 | 129.71 | 115.30 |

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 2 | DB | 401 | LYS | Peptide |
| 2 | DF | 273 | ALA | Peptide |
| 2 | GD | 273 | ALA | Peptide |
| 2 | HD | 273 | ALA | Peptide |
| 2 | HL | 273 | ALA | Peptide |

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 222 ligands modelled in this entry, 74 are monoatomic - leaving 148 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 |
| 20 | GTP | AB | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.64 | 7 (21%) |
| 19 | GDP | DC | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.27 | 4 (13%) |
| 20 | GTP | DB | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.67 | 8 (25%) |
| 20 | GTP | GF | 501 | 21 | 26,34,34 | 1.16 | 2 (7%) | 32,54,54 | 1.74 | 6 (18%) |
| 20 | GTP | LB | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.67 | 7 (21%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 19 | GDP | EE | 502 | - | 24,30,30 | 0.97 | 1 (4%) | 30,47,47 | 1.23 | 3 (10%) |
| 19 | GDP | BA | 501 | - | 24,30,30 | 0.91 | 1 (4%) | 30,47,47 | 1.26 | 4 (13%) |
| 19 | GDP | JI | 501 | - | 24,30,30 | 0.99 | 1 (4%) | 30,47,47 | 1.33 | 4 (13%) |
| 20 | GTP | IL | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.65 | 7 (21%) |
| 20 | GTP | MJ | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.61 | 7 (21%) |
| 19 | GDP | HM | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.26 | 4 (13%) |
| 20 | GTP | EH | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.61 | 7 (21%) |
| 20 | GTP | KD | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.66 | 7 (21%) |
| 20 | GTP | EB | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.63 | 7 (21%) |
| 19 | GDP | CK | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.29 | 4 (13%) |
| 20 | GTP | BL | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.65 | 7 (21%) |
| 20 | GTP | BH | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.68 | 7 (21%) |
| 19 | GDP | HI | 502 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.26 | 4 (13%) |
| 20 | GTP | AF | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.65 | 7 (21%) |
| 20 | GTP | JH | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.58 | 7 (21%) |
| 19 | GDP | BC | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.35 | 4 (13%) |
| 19 | GDP | HK | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.28 | 4 (13%) |
| 20 | GTP | DD | 501 | 21 | 26,34,34 | 1.17 | 1 (3%) | 32,54,54 | 1.63 | 7 (21%) |
| 19 | GDP | II | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.39 | 5 (16%) |
| 20 | GTP | LL | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.61 | 7 (21%) |
| 20 | GTP | ED | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.65 | 7 (21%) |
| 20 | GTP | LD | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.60 | 7 (21%) |
| 20 | GTP | MD | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.78 | 7 (21%) |
| 20 | GTP | CD | 501 | 21 | 26,34,34 | 1.19 | 2 (7%) | 32,54,54 | 1.69 | 7 (21%) |
| 19 | GDP | AK | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.23 | 3 (10%) |
| 19 | GDP | CE | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.26 | 4 (13%) |
| 19 | GDP | EA | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.28 | 4 (13%) |
| 19 | GDP | FC | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.27 | 4 (13%) |
| 19 | GDP | HE | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.25 | 4 (13%) |
| 19 | GDP | CA | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.31 | 4 (13%) |
| 19 | GDP | GM | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.32 | 4 (13%) |
| 19 | GDP | DE | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.38 | 4 (13%) |
| 20 | GTP | GD | 501 | 21 | 26,34,34 | 1.16 | 2 (7%) | 32,54,54 | 1.71 | 7 (21%) |
| 20 | GTP | IH | 501 | 21 | 26,34,34 | 1.19 | 2 (7%) | 32,54,54 | 1.65 | 7 (21%) |
| 20 | GTP | JF | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.66 | 8 (25%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 20 | GTP | IF | 501 | 21 | 26,34,34 | 1.20 | 2 (7%) | 32,54,54 | 1.69 | 7 (21%) |
| 20 | GTP | KB | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.70 | 7 (21%) |
| 20 | GTP | DJ | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.71 | 7 (21%) |
| 19 | GDP | LG | 501 | - | 24,30,30 | 0.93 | 1 (4%) | 30,47,47 | 1.32 | 4 (13%) |
| 20 | GTP | KF | 501 | 21 | 26,34,34 | 1.19 | 2 (7%) | 32,54,54 | 1.68 | 7 (21%) |
| 19 | GDP | JM | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.37 | 4 (13%) |
| 19 | GDP | BK | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.37 | 4 (13%) |
| 19 | GDP | IE | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.30 | 4 (13%) |
| 19 | GDP | DG | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.21 | 4 (13%) |
| 20 | GTP | HL | 501 | 21 | 26,34,34 | 1.15 | 2 (7%) | 32,54,54 | 1.71 | 7 (21%) |
| 19 | GDP | IM | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.31 | 4 (13%) |
| 20 | GTP | HI | 501 | 21 | 26,34,34 | 1.16 | 2 (7%) | 32,54,54 | 1.70 | 6 (18%) |
| 19 | GDP | LI | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.27 | 4 (13%) |
| 20 | GTP | GL | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.65 | 7 (21%) |
| 19 | GDP | GG | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.29 | 4 (13%) |
| 20 | GTP | DF | 501 | 21 | 26,34,34 | 1.20 | 2 (7%) | 32,54,54 | 1.69 | 7 (21%) |
| 19 | GDP | MI | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.33 | 4 (13%) |
| 19 | GDP | FE | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.31 | 4 (13%) |
| 20 | GTP | EL | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.66 | 7 (21%) |
| 19 | GDP | GI | 501 | - | 24,30,30 | 0.99 | 1 (4%) | 30,47,47 | 1.26 | 4 (13%) |
| 20 | GTP | FH | 501 | 21 | 26,34,34 | 1.19 | 2 (7%) | 32,54,54 | 1.68 | 7 (21%) |
| 19 | GDP | GE | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.32 | 4 (13%) |
| 20 | GTP | GJ | 501 | 21 | 26,34,34 | 1.16 | 2 (7%) | 32,54,54 | 1.71 | 7 (21%) |
| 20 | GTP | CB | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.67 | 7 (21%) |
| 20 | GTP | JJ | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.65 | 7 (21%) |
| 19 | GDP | EG | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.26 | 4 (13%) |
| 20 | GTP | BB | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.64 | 7 (21%) |
| 19 | GDP | FA | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.31 | 4 (13%) |
| 20 | GTP | EF | 501 | 21 | 26,34,34 | 1.20 | 2 (7%) | 32,54,54 | 1.60 | 7 (21%) |
| 20 | GTP | AD | 501 | 21 | 26,34,34 | 1.16 | 2 (7%) | 32,54,54 | 1.66 | 7 (21%) |
| 19 | GDP | KC | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.28 | 4 (13%) |
| 19 | GDP | CI | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.29 | 4 (13%) |
| 19 | GDP | KI | 502 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.30 | 4 (13%) |
| 20 | GTP | LF | 501 | 21 | 26,34,34 | 1.19 | 2 (7%) | 32,54,54 | 1.71 | 7 (21%) |
| 19 | GDP | BI | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.25 | 4 (13%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 20 | GTP | ID | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.64 | 7 (21%) |
| 19 | GDP | JC | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.25 | 4 (13%) |
| 19 | GDP | KG | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.30 | 4 (13%) |
| 19 | GDP | EC | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.28 | 4 (13%) |
| 20 | GTP | MB | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.62 | 7 (21%) |
| 20 | GTP | AJ | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.66 | 7 (21%) |
| 20 | GTP | BD | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.68 | 7 (21%) |
| 19 | GDP | AI | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.31 | 4 (13%) |
| 19 | GDP | AE | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.32 | 4 (13%) |
| 19 | GDP | JE | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.27 | 4 (13%) |
| 20 | GTP | CJ | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.68 | 7 (21%) |
| 19 | GDP | AA | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.34 | 4 (13%) |
| 20 | GTP | FF | 501 | 21 | 26,34,34 | 1.19 | 2 (7%) | 32,54,54 | 1.63 | 7 (21%) |
| 19 | GDP | FI | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.28 | 4 (13%) |
| 19 | GDP | MG | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.29 | 4 (13%) |
| 20 | GTP | FJ | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.73 | 7 (21%) |
| 20 | GTP | HJ | 501 | 21 | 26,34,34 | 1.15 | 2 (7%) | 32,54,54 | 1.71 | 6 (18%) |
| 19 | GDP | EK | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.28 | 4 (13%) |
| 19 | GDP | IK | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.25 | 4 (13%) |
| 19 | GDP | ME | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.30 | 4 (13%) |
| 19 | GDP | GK | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.26 | 4 (13%) |
| 19 | GDP | MK | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.31 | 4 (13%) |
| 20 | GTP | FL | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.67 | 7 (21%) |
| 19 | GDP | FG | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.22 | 4 (13%) |
| 19 | GDP | LE | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.24 | 4 (13%) |
| 20 | GTP | MH | 501 | 21 | 26,34,34 | 1.20 | 2 (7%) | 32,54,54 | 1.69 | 7 (21%) |
| 19 | GDP | AC | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.26 | 4 (13%) |
| 20 | GTP | HD | 501 | 21 | 26,34,34 | 1.14 | 2 (7%) | 32,54,54 | 1.68 | 7 (21%) |
| 20 | GTP | DL | 501 | 21 | 26,34,34 | 1.20 | 2 (7%) | 32,54,54 | 1.69 | 7 (21%) |
| 19 | GDP | DK | 501 | - | 24,30,30 | 0.93 | 1 (4%) | 30,47,47 | 1.27 | 4 (13%) |
| 20 | GTP | FB | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.68 | 7 (21%) |
| 20 | GTP | KH | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.67 | 7 (21%) |
| 19 | GDP | GC | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.32 | 4 (13%) |
| 19 | GDP | JK | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.35 | 5 (16%) |
| 20 | GTP | KL | 501 | 21 | 26,34,34 | 1.16 | 2 (7%) | 32,54,54 | 1.62 | 7 (21%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 19 | GDP | EI | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.29 | 4 (13%) |
| 19 | GDP | MC | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.30 | 4 (13%) |
| 19 | GDP | BG | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.31 | 5 (16%) |
| 19 | GDP | FK | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.28 | 4 (13%) |
| 20 | GTP | JL | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.69 | 7 (21%) |
| 20 | GTP | CH | 501 | 21 | 26,34,34 | 1.19 | 2 (7%) | 32,54,54 | 1.71 | 7 (21%) |
| 19 | GDP | CG | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.15 | 4 (13%) |
| 19 | GDP | IG | 501 | - | 24,30,30 | 0.93 | 1 (4%) | 30,47,47 | 1.25 | 4 (13%) |
| 20 | GTP | AH | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.67 | 7 (21%) |
| 20 | GTP | CF | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.64 | 7 (21%) |
| 20 | GTP | IJ | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.65 | 7 (21%) |
| 19 | GDP | KE | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.33 | 4 (13%) |
| 19 | GDP | CC | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.29 | 4 (13%) |
| 20 | GTP | FD | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.66 | 7 (21%) |
| 19 | GDP | LC | 501 | - | 24,30,30 | 0.97 | 1 (4%) | 30,47,47 | 1.30 | 4 (13%) |
| 19 | GDP | HC | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.27 | 4 (13%) |
| 20 | GTP | JD | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.59 | 8 (25%) |
| 19 | GDP | KK | 501 | - | 24,30,30 | 0.94 | 1 (4%) | 30,47,47 | 1.30 | 4 (13%) |
| 20 | GTP | ML | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.73 | 7 (21%) |
| 20 | GTP | LJ | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.69 | 7 (21%) |
| 20 | GTP | HF | 501 | 21 | 26,34,34 | 1.14 | 2 (7%) | 32,54,54 | 1.67 | 7 (21%) |
| 20 | GTP | JB | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.66 | 7 (21%) |
| 19 | GDP | HG | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.29 | 4 (13%) |
| 19 | GDP | LK | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.28 | 4 (13%) |
| 20 | GTP | BF | 501 | 21 | 26,34,34 | 1.19 | 2 (7%) | 32,54,54 | 1.62 | 7 (21%) |
| 20 | GTP | GH | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.71 | 7 (21%) |
| 20 | GTP | BJ | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.69 | 7 (21%) |
| 20 | GTP | AL | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.65 | 7 (21%) |
| 19 | GDP | BE | 501 | - | 24,30,30 | 1.00 | 1 (4%) | 30,47,47 | 1.20 | 4 (13%) |
| 20 | GTP | DH | 501 | 21 | 26,34,34 | 1.23 | 1 (3%) | 32,54,54 | 1.78 | 8 (25%) |
| 19 | GDP | IC | 501 | - | 24,30,30 | 0.96 | 1 (4%) | 30,47,47 | 1.29 | 4 (13%) |
| 20 | GTP | MF | 501 | 21 | 26,34,34 | 1.20 | 2 (7%) | 32,54,54 | 1.70 | 7 (21%) |
| 19 | GDP | DI | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.31 | 4 (13%) |
| 19 | GDP | JG | 501 | - | 24,30,30 | 0.95 | 1 (4%) | 30,47,47 | 1.27 | 5 (16%) |
| 20 | GTP | KJ | 501 | 21 | 26,34,34 | 1.17 | 2 (7%) | 32,54,54 | 1.67 | 7 (21%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 19 | GDP | AG | 501 | - | 24,30,30 | 1.01 | 1 (4%) | 30,47,47 | 1.21 | 4 (13%) |
| 20 | GTP | EJ | 501 | 21 | 26,34,34 | 1.16 | 2 (7%) | 32,54,54 | 1.60 | 7 (21%) |
| 20 | GTP | LH | 501 | 21 | 26,34,34 | 1.18 | 2 (7%) | 32,54,54 | 1.68 | 6 (18%) |

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 |
|-----|------|-------|-----|------|---------|------------|---------|
| 20 | GTP | AB | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 19 | GDP | DC | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 20 | GTP | DB | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 20 | GTP | GF | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 20 | GTP | LB | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |
| 19 | GDP | EE | 502 | - | - | 7/12/32/32 | 0/3/3/3 |
| 19 | GDP | BA | 501 | - | - | 7/12/32/32 | 0/3/3/3 |
| 19 | GDP | JI | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 20 | GTP | IL | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 20 | GTP | MJ | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 19 | GDP | HM | 501 | - | - | 5/12/32/32 | 0/3/3/3 |
| 20 | GTP | EH | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 20 | GTP | KD | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 20 | GTP | EB | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 19 | GDP | CK | 501 | - | - | 6/12/32/32 | 0/3/3/3 |
| 20 | GTP | BL | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 20 | GTP | BH | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 19 | GDP | HI | 502 | - | - | 3/12/32/32 | 0/3/3/3 |
| 20 | GTP | AF | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |
| 20 | GTP | JH | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 19 | GDP | BC | 501 | - | - | 4/12/32/32 | 0/3/3/3 |
| 19 | GDP | HK | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 20 | GTP | DD | 501 | 21 | - | 8/18/38/38 | 0/3/3/3 |
| 19 | GDP | II | 501 | - | - | 7/12/32/32 | 0/3/3/3 |
| 20 | GTP | LL | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 20 | GTP | ED | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|------------|---------|
| 20 | GTP | LD | 501 | 21 | - | 7/18/38/38 | 0/3/3/3 |
| 20 | GTP | MD | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 20 | GTP | CD | 501 | 21 | - | 7/18/38/38 | 0/3/3/3 |
| 19 | GDP | AK | 501 | - | - | 4/12/32/32 | 0/3/3/3 |
| 19 | GDP | CE | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 19 | GDP | EA | 501 | - | - | 6/12/32/32 | 0/3/3/3 |
| 19 | GDP | FC | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 19 | GDP | HE | 501 | - | - | 5/12/32/32 | 0/3/3/3 |
| 19 | GDP | CA | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 19 | GDP | GM | 501 | - | - | 1/12/32/32 | 0/3/3/3 |
| 19 | GDP | DE | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 20 | GTP | GD | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 20 | GTP | IH | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 20 | GTP | JF | 501 | 21 | - | 1/18/38/38 | 0/3/3/3 |
| 20 | GTP | IF | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 20 | GTP | KB | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 20 | GTP | DJ | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 19 | GDP | LG | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 20 | GTP | KF | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 19 | GDP | JM | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 19 | GDP | BK | 501 | - | - | 4/12/32/32 | 0/3/3/3 |
| 19 | GDP | IE | 501 | - | - | 3/12/32/32 | 0/3/3/3 |
| 19 | GDP | DG | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 20 | GTP | HL | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 19 | GDP | IM | 501 | - | - | 4/12/32/32 | 0/3/3/3 |
| 20 | GTP | HI | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |
| 19 | GDP | LI | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 20 | GTP | GL | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 19 | GDP | GG | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 20 | GTP | DF | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 19 | GDP | MI | 501 | - | - | 4/12/32/32 | 0/3/3/3 |
| 19 | GDP | FE | 501 | - | - | 1/12/32/32 | 0/3/3/3 |
| 20 | GTP | EL | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 19 | GDP | GI | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 20 | GTP | FH | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 19 | GDP | GE | 501 | - | - | 2/12/32/32 | 0/3/3/3 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|------------|---------|
| 20 | GTP | GJ | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 20 | GTP | CB | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 20 | GTP | JJ | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 19 | GDP | EG | 501 | - | - | 4/12/32/32 | 0/3/3/3 |
| 20 | GTP | BB | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |
| 19 | GDP | FA | 501 | - | - | 1/12/32/32 | 0/3/3/3 |
| 20 | GTP | EF | 501 | 21 | - | 7/18/38/38 | 0/3/3/3 |
| 20 | GTP | AD | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 19 | GDP | KC | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 19 | GDP | CI | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 19 | GDP | KI | 502 | - | - | 5/12/32/32 | 0/3/3/3 |
| 20 | GTP | LF | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |
| 19 | GDP | BI | 501 | - | - | 3/12/32/32 | 0/3/3/3 |
| 20 | GTP | ID | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |
| 19 | GDP | JC | 501 | - | - | 1/12/32/32 | 0/3/3/3 |
| 19 | GDP | KG | 501 | - | - | 1/12/32/32 | 0/3/3/3 |
| 19 | GDP | EC | 501 | - | - | 1/12/32/32 | 0/3/3/3 |
| 20 | GTP | MB | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 20 | GTP | AJ | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 20 | GTP | BD | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 19 | GDP | AI | 501 | - | - | 1/12/32/32 | 0/3/3/3 |
| 19 | GDP | AE | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 19 | GDP | JE | 501 | - | - | 4/12/32/32 | 0/3/3/3 |
| 20 | GTP | CJ | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 19 | GDP | AA | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 20 | GTP | FF | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 19 | GDP | FI | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 19 | GDP | MG | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 20 | GTP | FJ | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 20 | GTP | HJ | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |
| 19 | GDP | EK | 501 | - | - | 1/12/32/32 | 0/3/3/3 |
| 19 | GDP | IK | 501 | - | - | 3/12/32/32 | 0/3/3/3 |
| 19 | GDP | ME | 501 | - | - | 3/12/32/32 | 0/3/3/3 |
| 19 | GDP | GK | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 19 | GDP | MK | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 20 | GTP | FL | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 19 | GDP | FG | 501 | - | - | 1/12/32/32 | 0/3/3/3 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|------------|---------|
| 19 | GDP | LE | 501 | - | - | 1/12/32/32 | 0/3/3/3 |
| 20 | GTP | MH | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 19 | GDP | AC | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 20 | GTP | HD | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 20 | GTP | DL | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 19 | GDP | DK | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 20 | GTP | FB | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 20 | GTP | KH | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |
| 19 | GDP | GC | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 19 | GDP | JK | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 20 | GTP | KL | 501 | 21 | - | 7/18/38/38 | 0/3/3/3 |
| 19 | GDP | EI | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 19 | GDP | MC | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 19 | GDP | BG | 501 | - | - | 1/12/32/32 | 0/3/3/3 |
| 19 | GDP | FK | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 20 | GTP | JL | 501 | 21 | - | 7/18/38/38 | 0/3/3/3 |
| 20 | GTP | CH | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 19 | GDP | CG | 501 | - | - | 3/12/32/32 | 0/3/3/3 |
| 19 | GDP | IG | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 20 | GTP | AH | 501 | 21 | - | 7/18/38/38 | 0/3/3/3 |
| 20 | GTP | CF | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |
| 20 | GTP | IJ | 501 | 21 | - | 2/18/38/38 | 0/3/3/3 |
| 19 | GDP | KE | 501 | - | - | 7/12/32/32 | 0/3/3/3 |
| 19 | GDP | CC | 501 | - | - | 5/12/32/32 | 0/3/3/3 |
| 20 | GTP | FD | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |
| 19 | GDP | LC | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 19 | GDP | HC | 501 | - | - | 3/12/32/32 | 0/3/3/3 |
| 20 | GTP | JD | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 19 | GDP | KK | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 20 | GTP | ML | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 20 | GTP | LJ | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 20 | GTP | HF | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |
| 20 | GTP | JB | 501 | 21 | - | 7/18/38/38 | 0/3/3/3 |
| 19 | GDP | HG | 501 | - | - | 1/12/32/32 | 0/3/3/3 |
| 19 | GDP | LK | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 20 | GTP | BF | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|------------|---------|
| 20 | GTP | GH | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 20 | GTP | BJ | 501 | 21 | - | 2/18/38/38 | 0/3/3/3 |
| 20 | GTP | AL | 501 | 21 | - | 3/18/38/38 | 0/3/3/3 |
| 19 | GDP | BE | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 20 | GTP | DH | 501 | 21 | - | 7/18/38/38 | 0/3/3/3 |
| 19 | GDP | IC | 501 | - | - | 5/12/32/32 | 0/3/3/3 |
| 20 | GTP | MF | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 19 | GDP | DI | 501 | - | - | 2/12/32/32 | 0/3/3/3 |
| 19 | GDP | JG | 501 | - | - | 5/12/32/32 | 0/3/3/3 |
| 20 | GTP | KJ | 501 | 21 | - | 5/18/38/38 | 0/3/3/3 |
| 19 | GDP | AG | 501 | - | - | 0/12/32/32 | 0/3/3/3 |
| 20 | GTP | EJ | 501 | 21 | - | 6/18/38/38 | 0/3/3/3 |
| 20 | GTP | LH | 501 | 21 | - | 4/18/38/38 | 0/3/3/3 |

The worst 5 of 220 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 20 | DH | 501 | GTP | C5-C6 | -4.39 | 1.38 | 1.47 |
| 20 | IF | 501 | GTP | C5-C6 | -4.32 | 1.38 | 1.47 |
| 20 | AF | 501 | GTP | C5-C6 | -4.30 | 1.38 | 1.47 |
| 20 | FH | 501 | GTP | C5-C6 | -4.29 | 1.38 | 1.47 |
| 20 | EF | 501 | GTP | C5-C6 | -4.27 | 1.38 | 1.47 |

The worst 5 of 816 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|-------|-------------|----------|
| 20 | DH | 501 | GTP | PB-O3B-PG | -4.74 | 116.55 | 132.83 |
| 20 | MD | 501 | GTP | PB-O3B-PG | -4.64 | 116.91 | 132.83 |
| 20 | ML | 501 | GTP | PB-O3B-PG | -4.63 | 116.92 | 132.83 |
| 19 | DE | 501 | GDP | PA-O3A-PB | -4.62 | 116.98 | 132.83 |
| 20 | IH | 501 | GTP | PB-O3B-PG | -4.56 | 117.17 | 132.83 |

There are no chirality outliers.

5 of 507 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|-----------------|
| 19 | BA | 501 | GDP | C5'-O5'-PA-O3A |
| 19 | BA | 501 | GDP | C5'-O5'-PA-O2A |
| 19 | BA | 501 | GDP | O4'-C4'-C5'-O5' |

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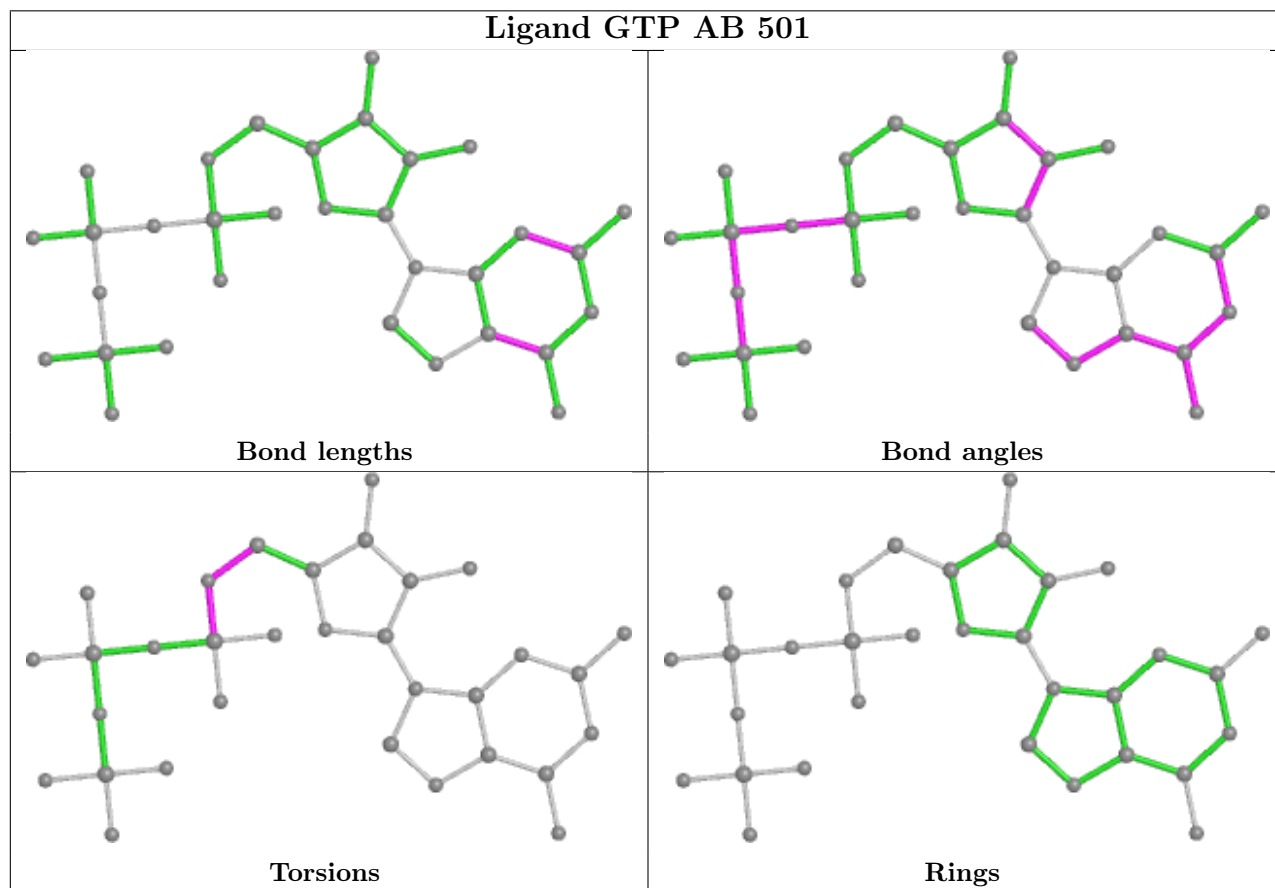
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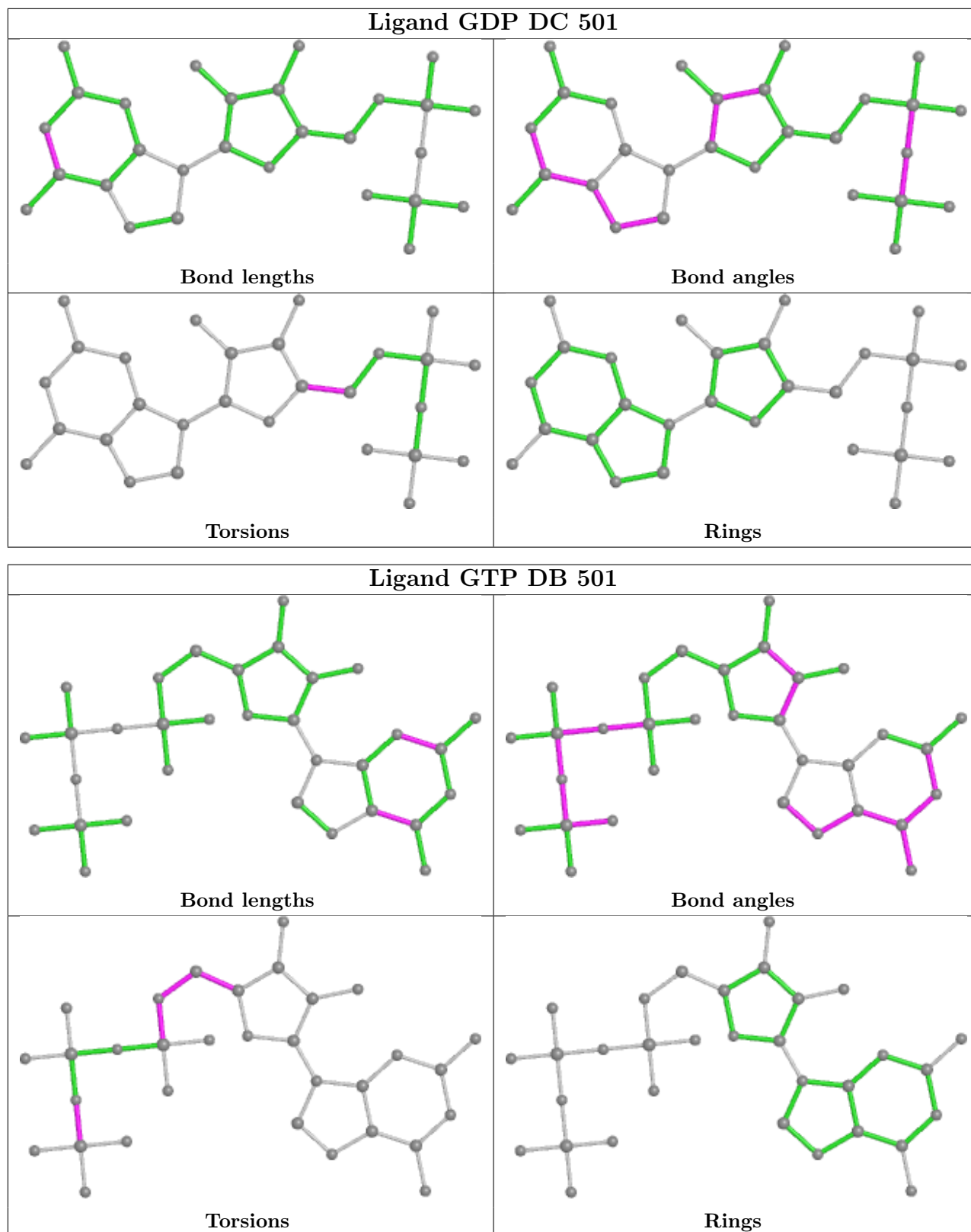
| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|-----------------|
| 19 | BA | 501 | GDP | C3'-C4'-C5'-O5' |
| 19 | BC | 501 | GDP | PA-O3A-PB-O2B |

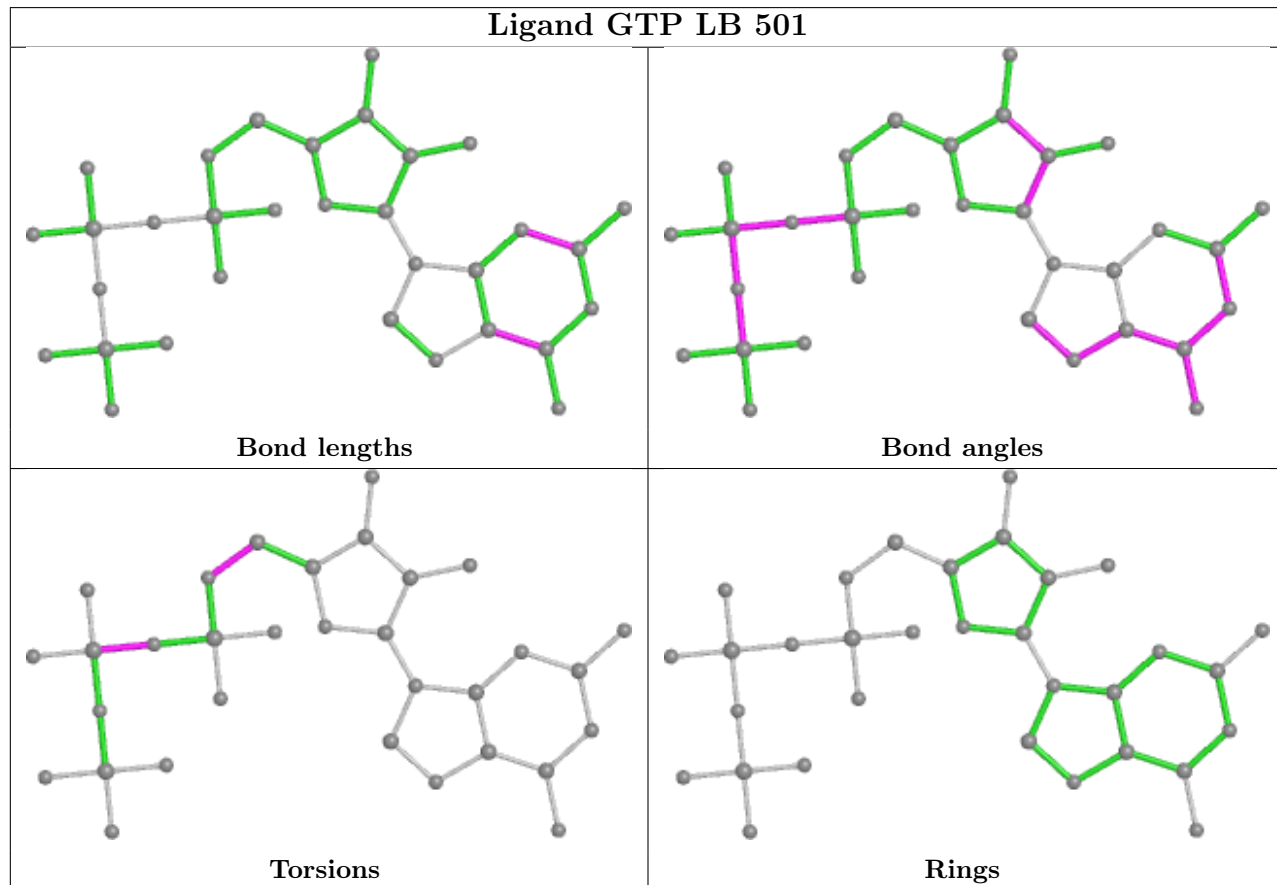
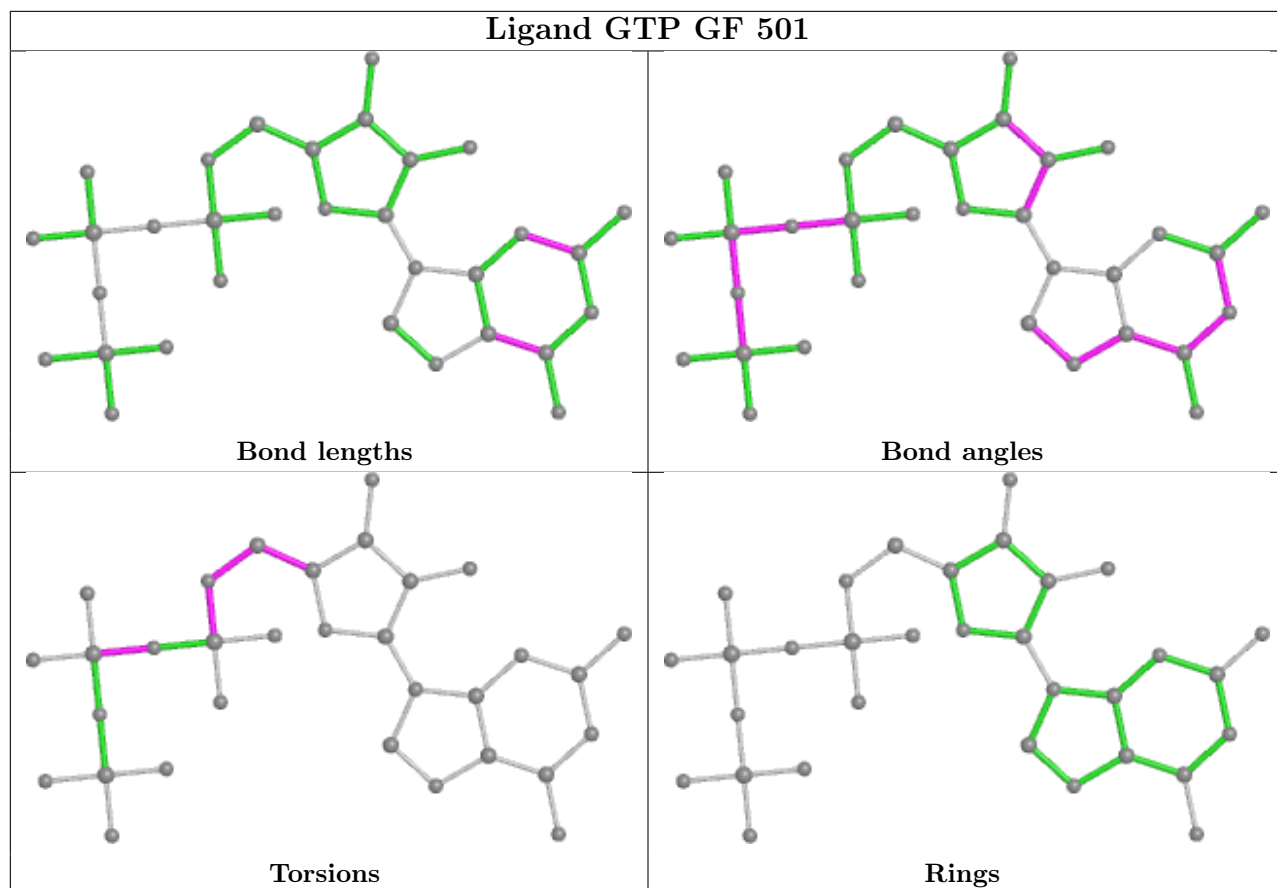
There are no ring outliers.

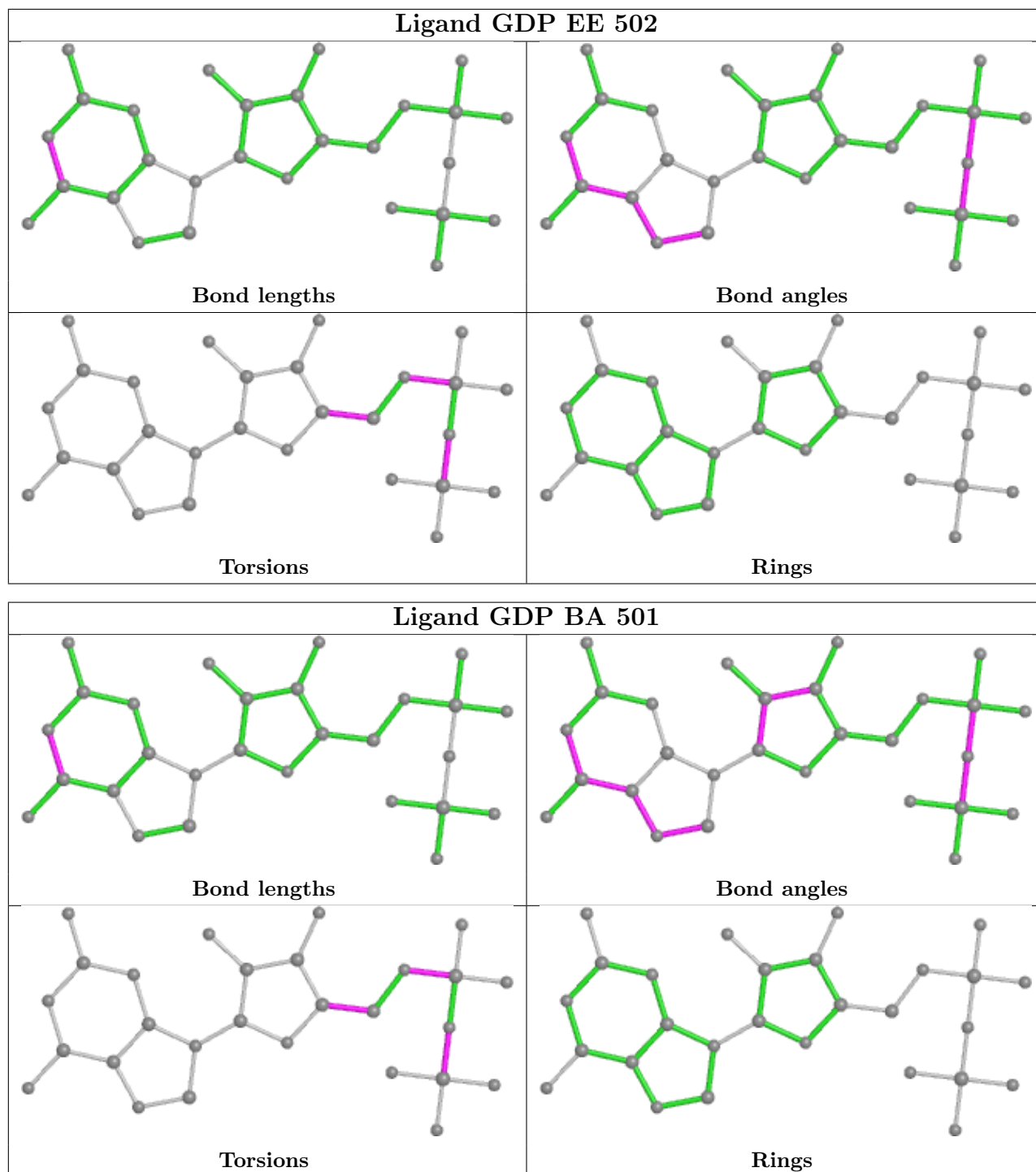
No monomer is involved in short contacts.

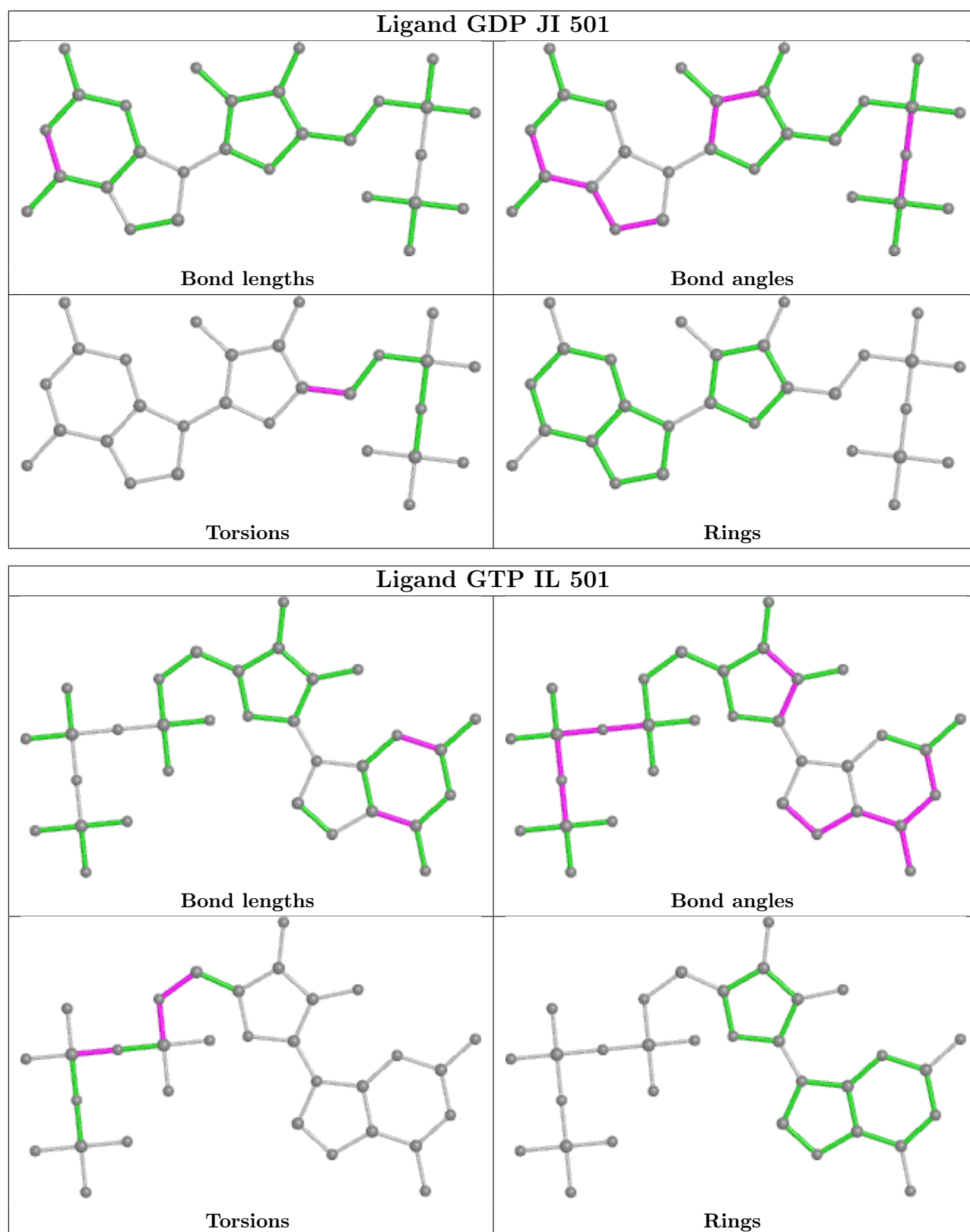
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

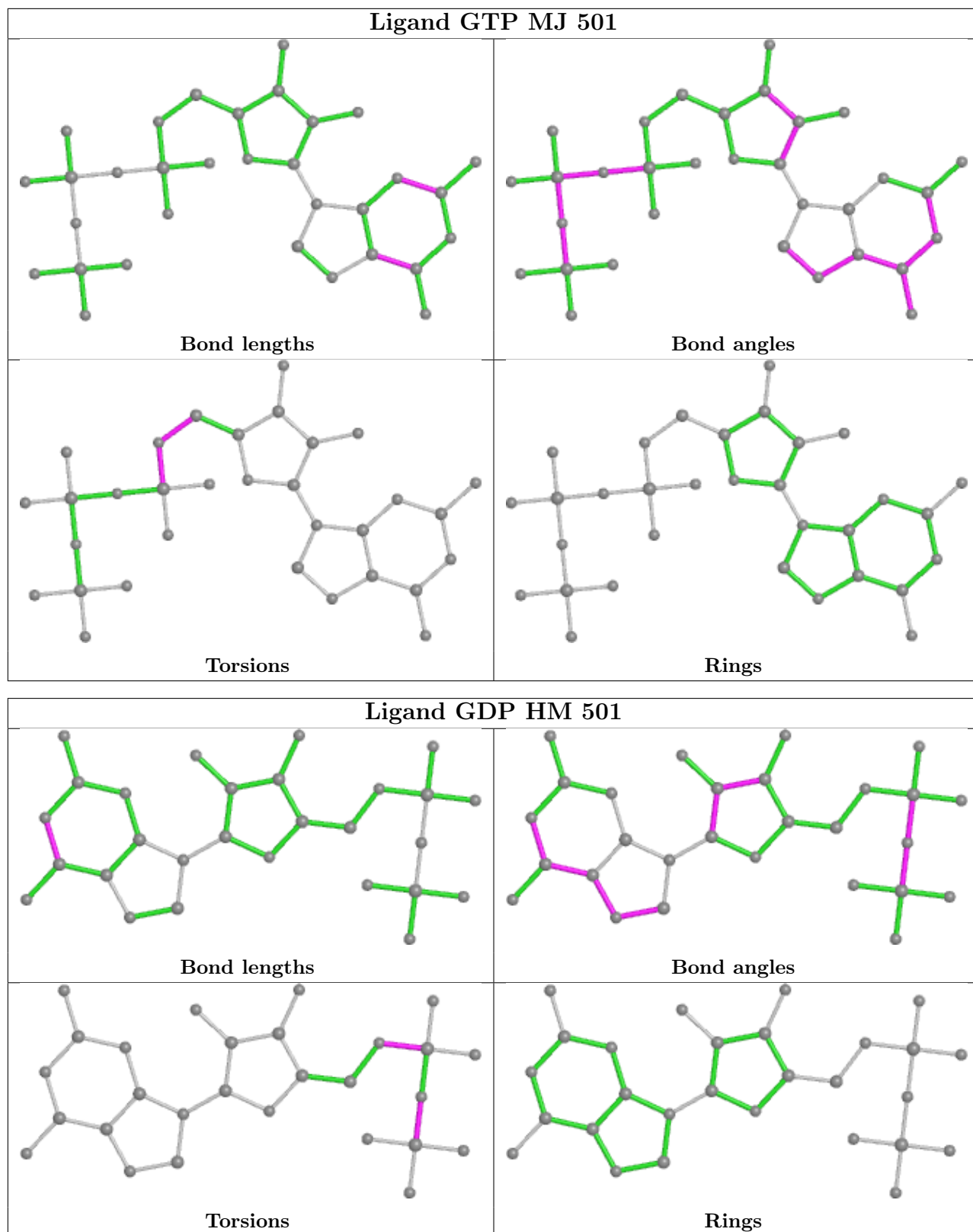


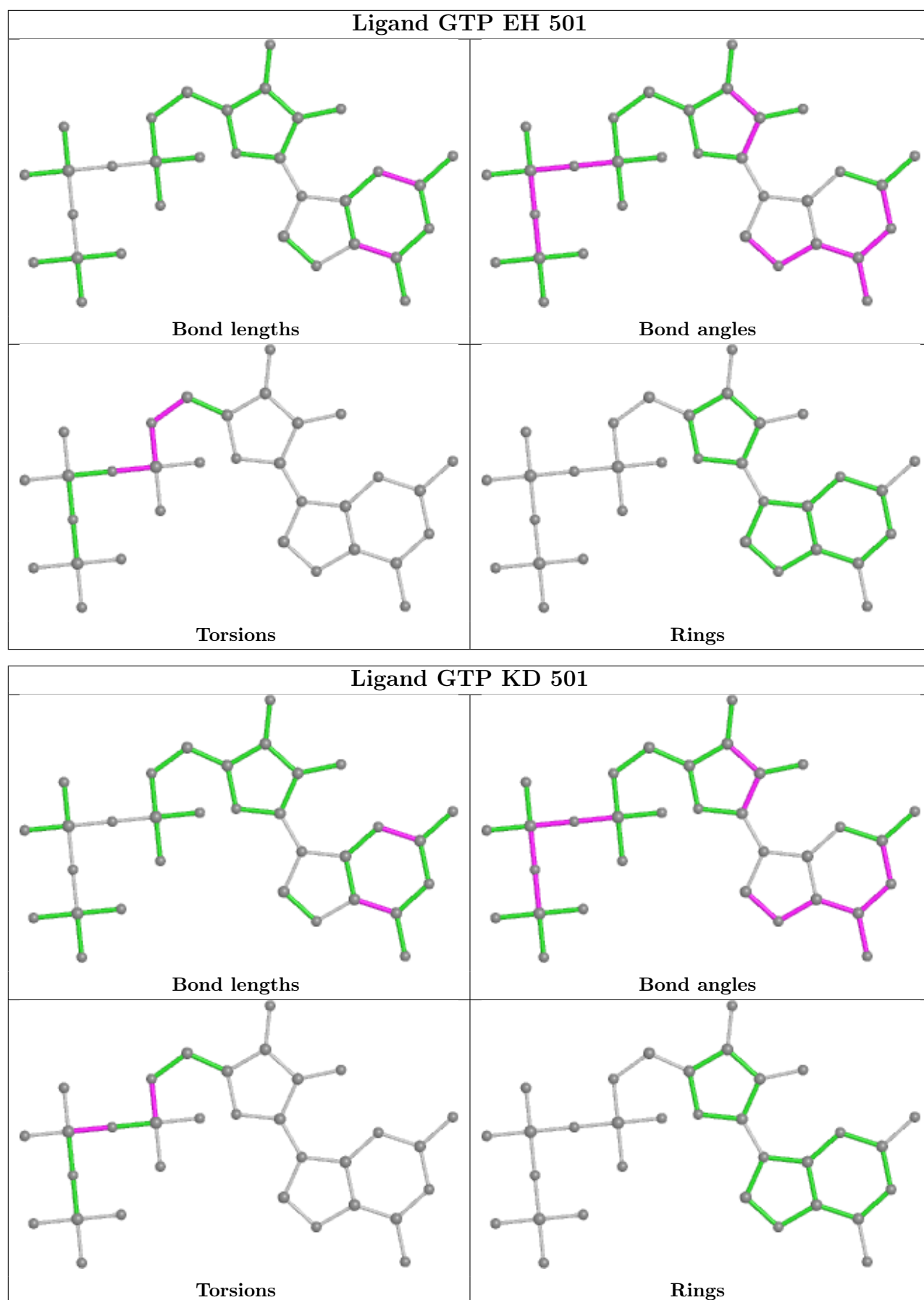


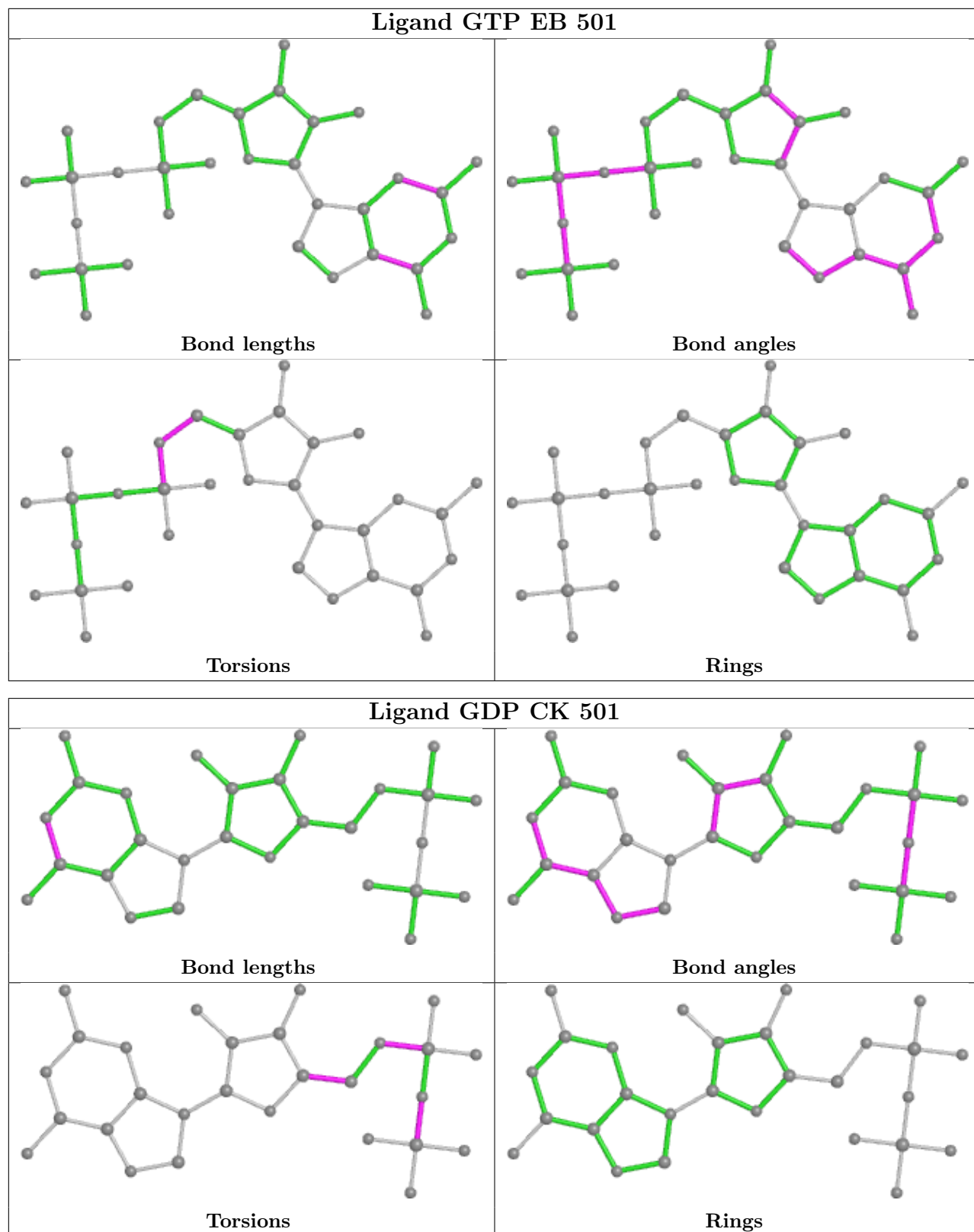


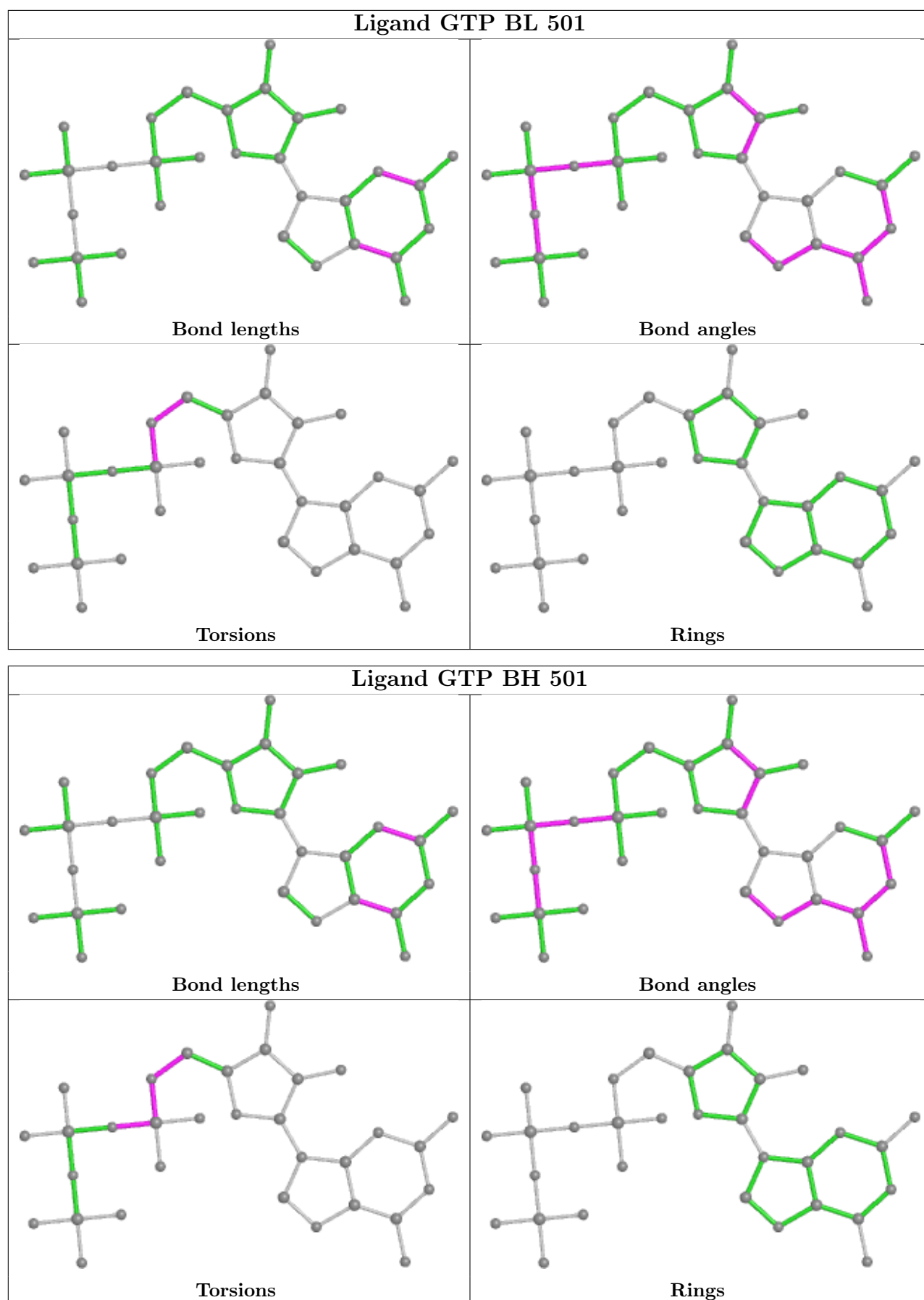


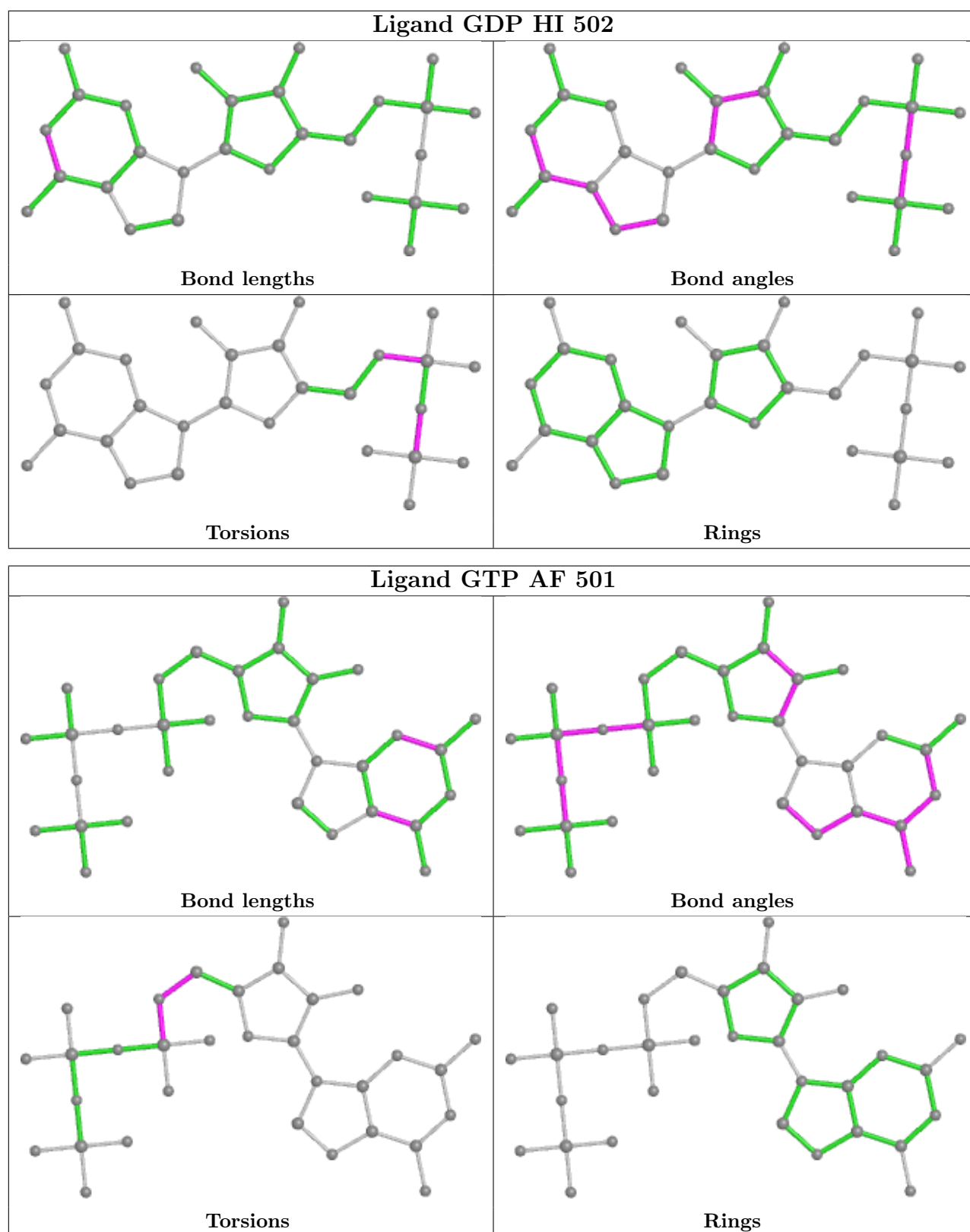


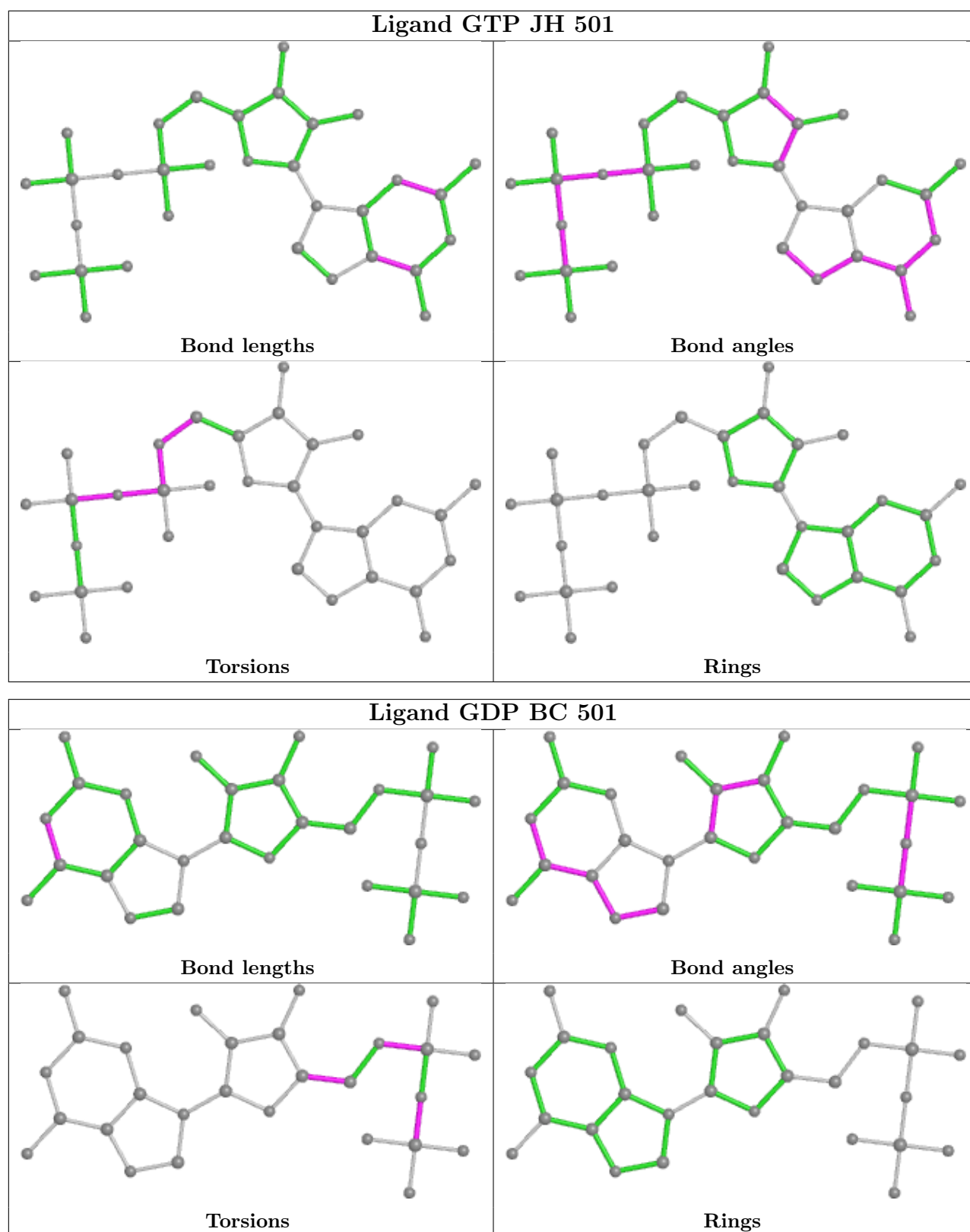


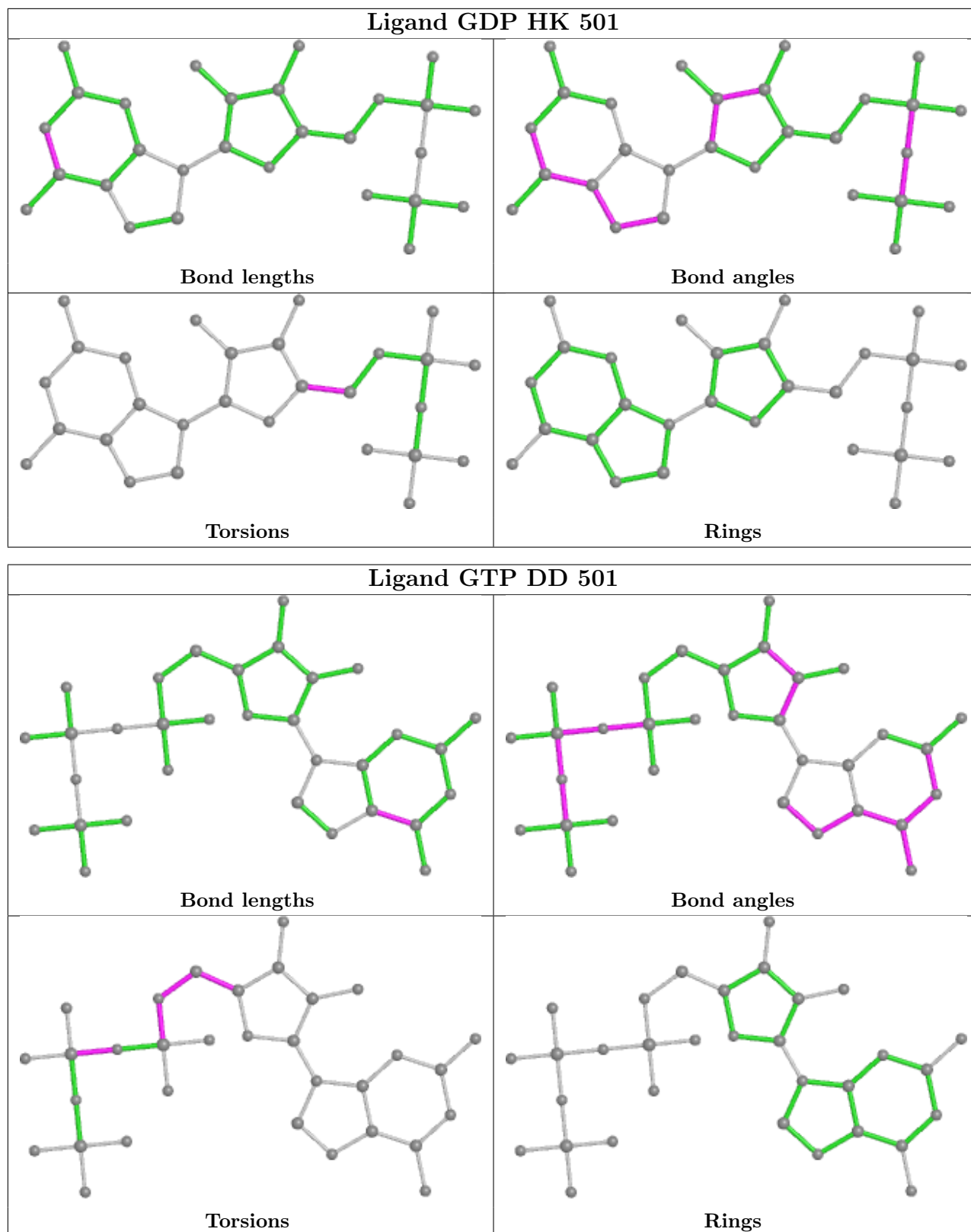


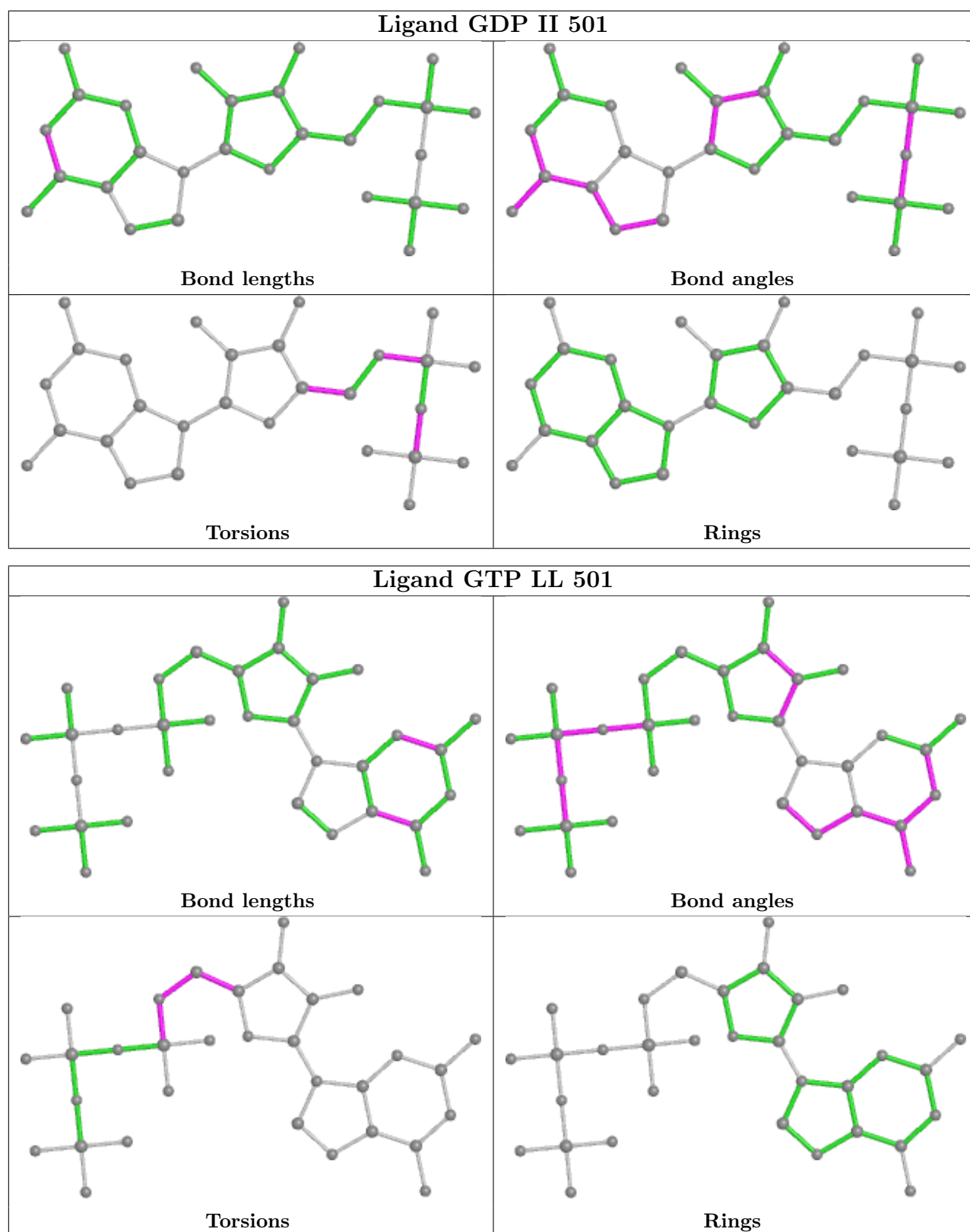


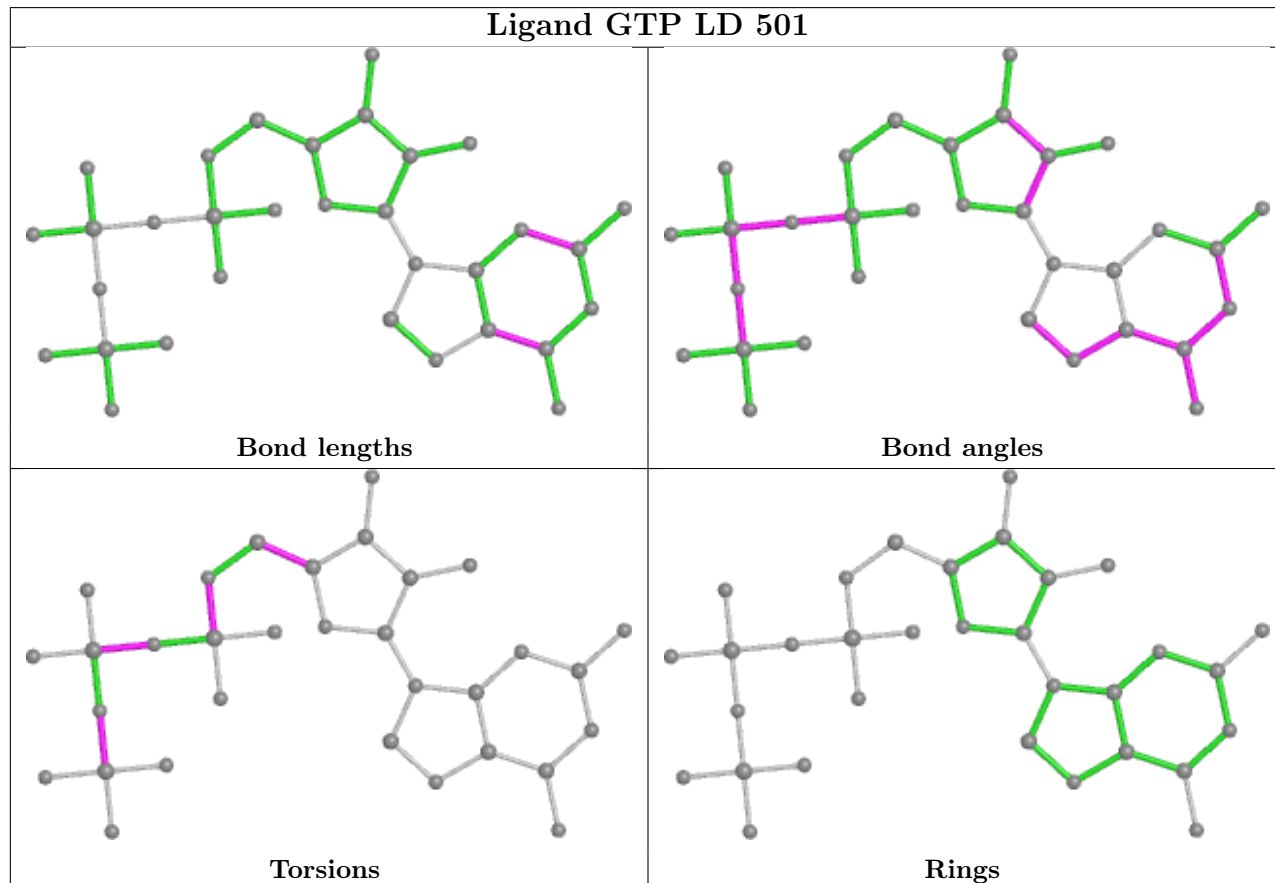
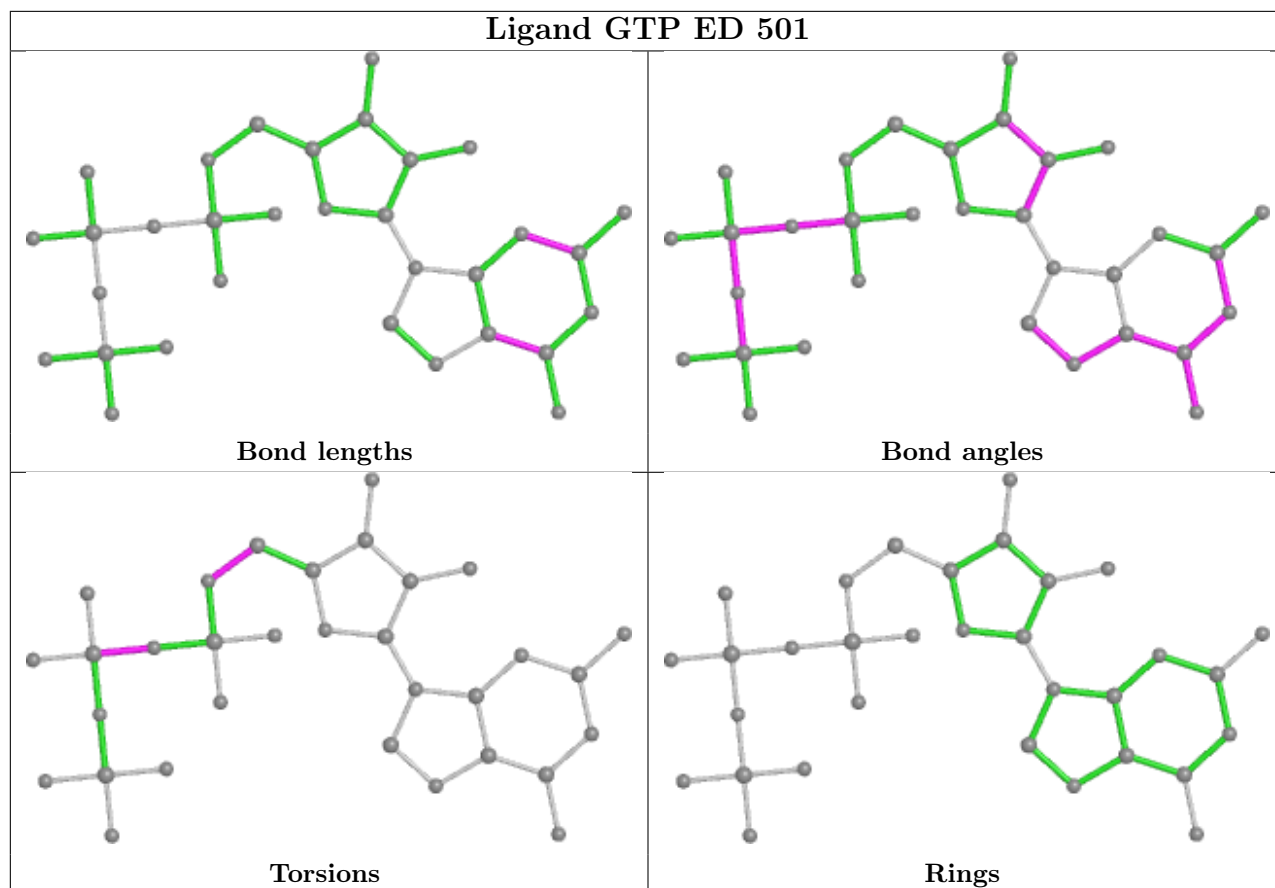


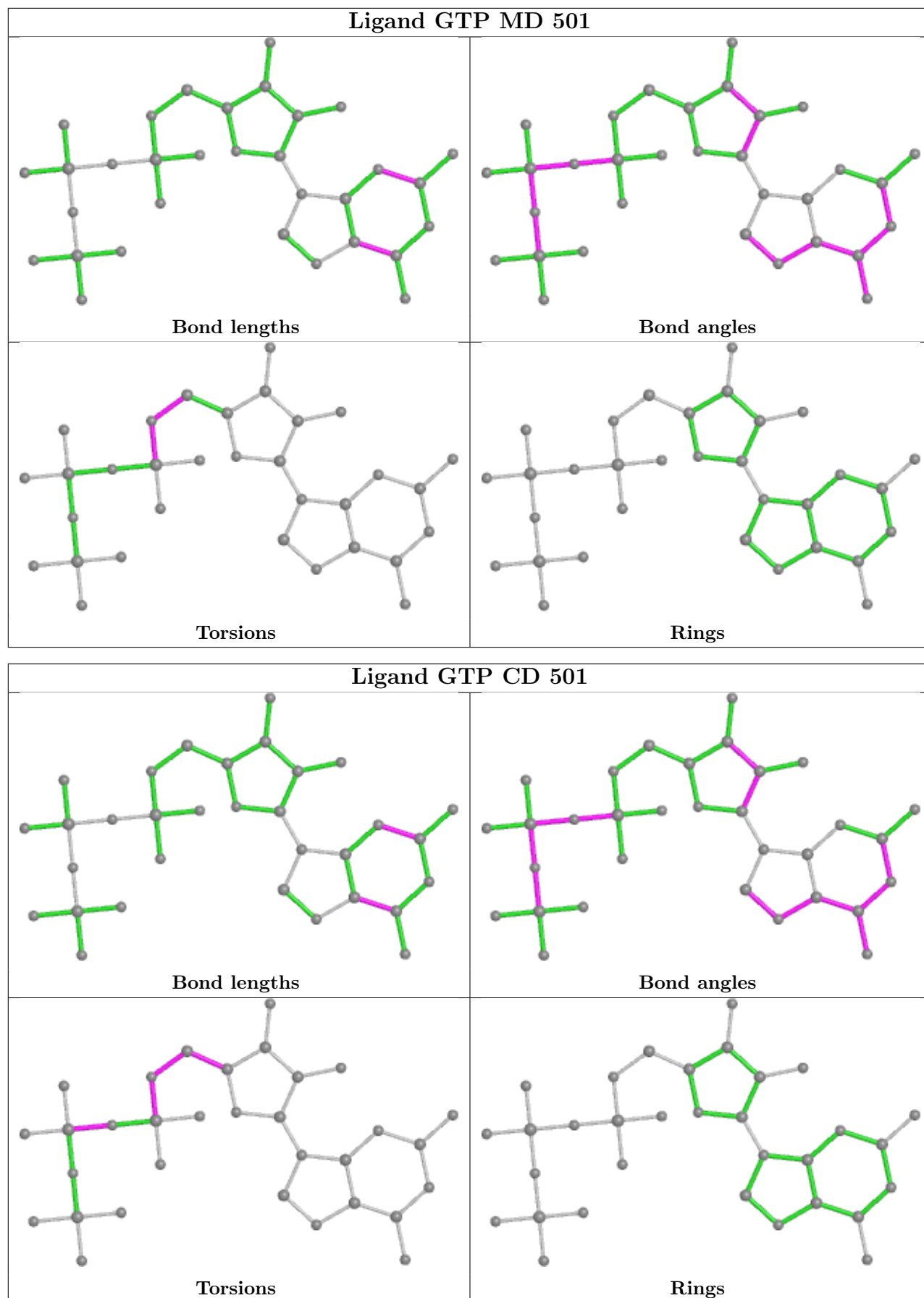


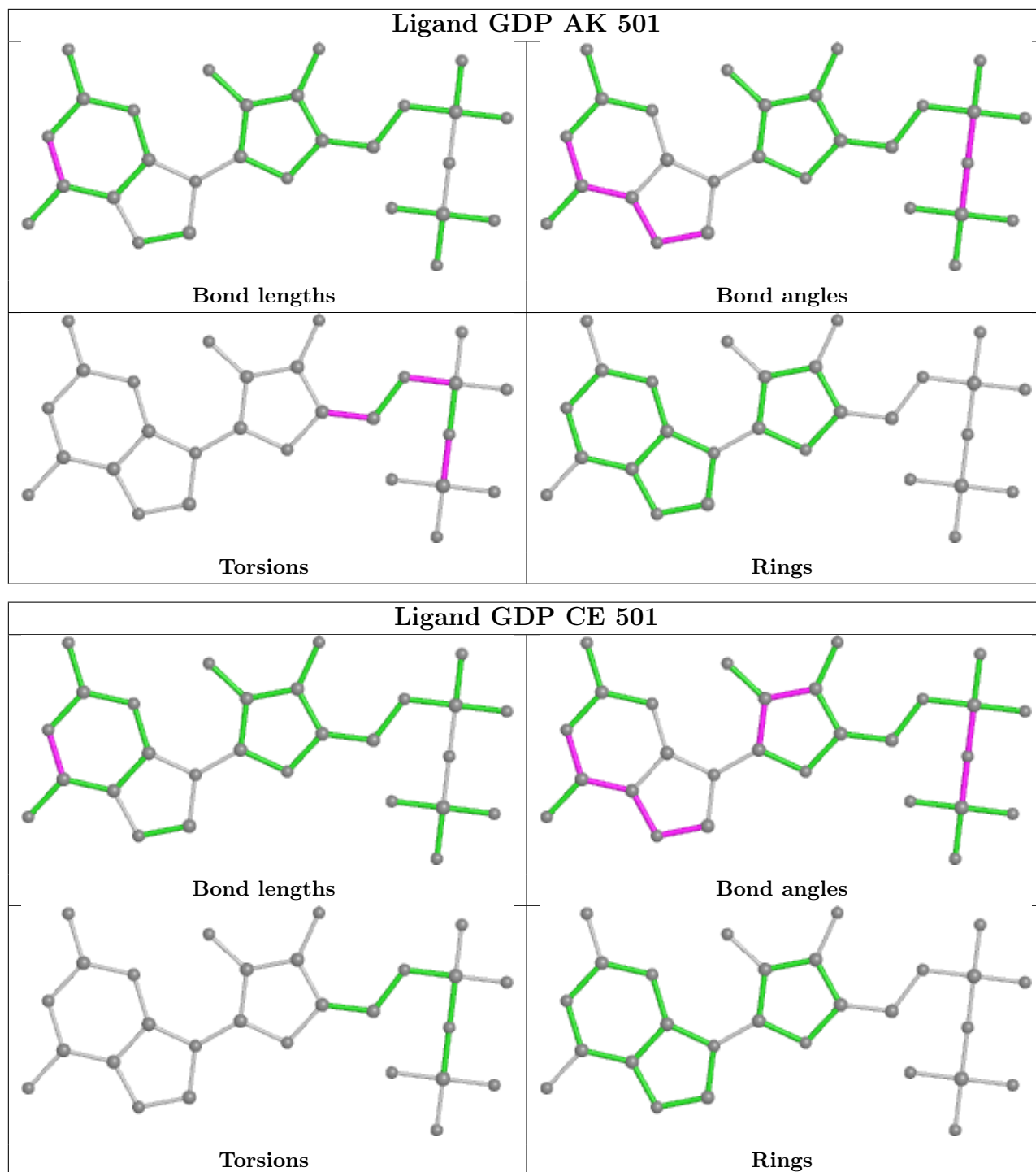


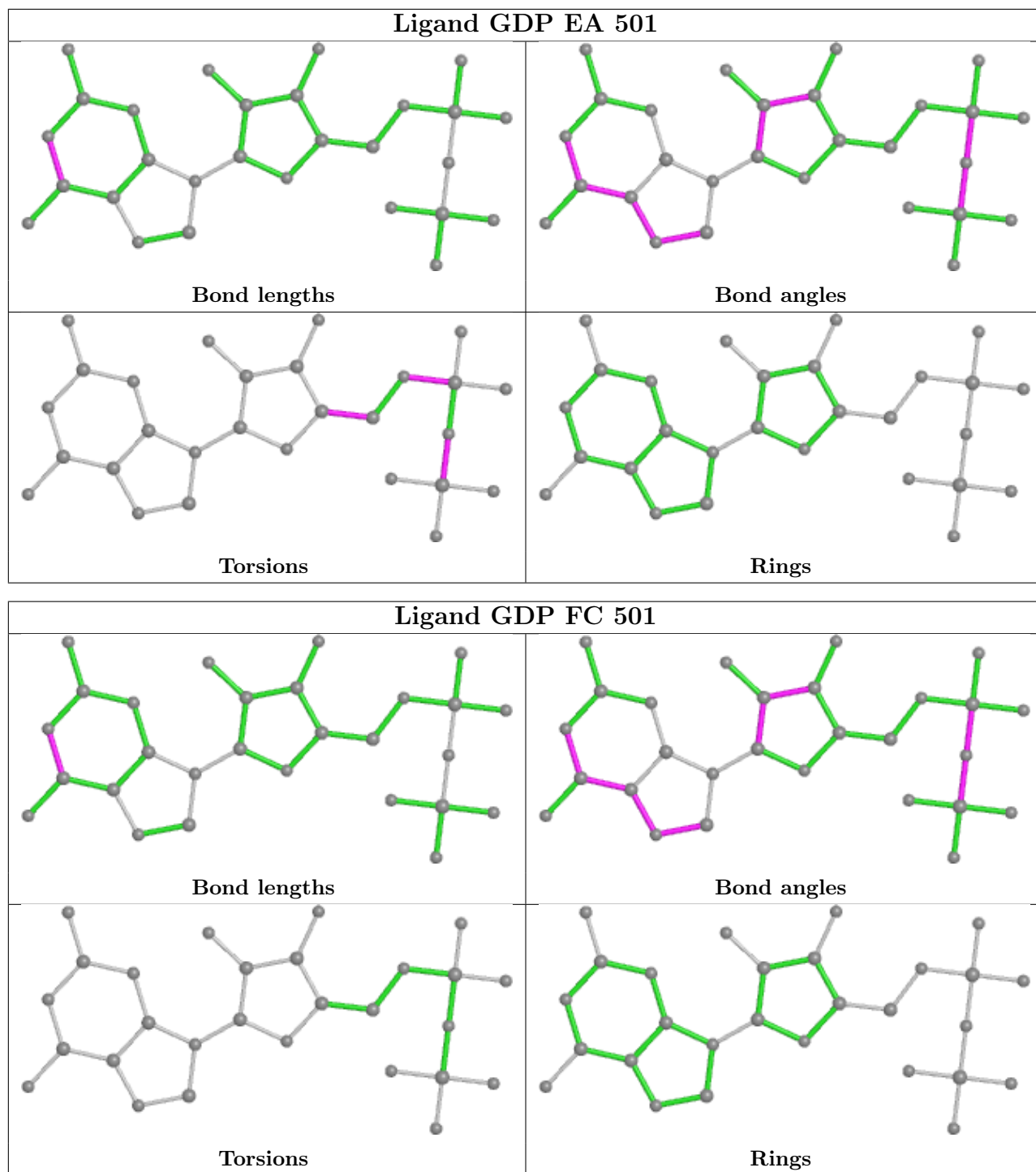


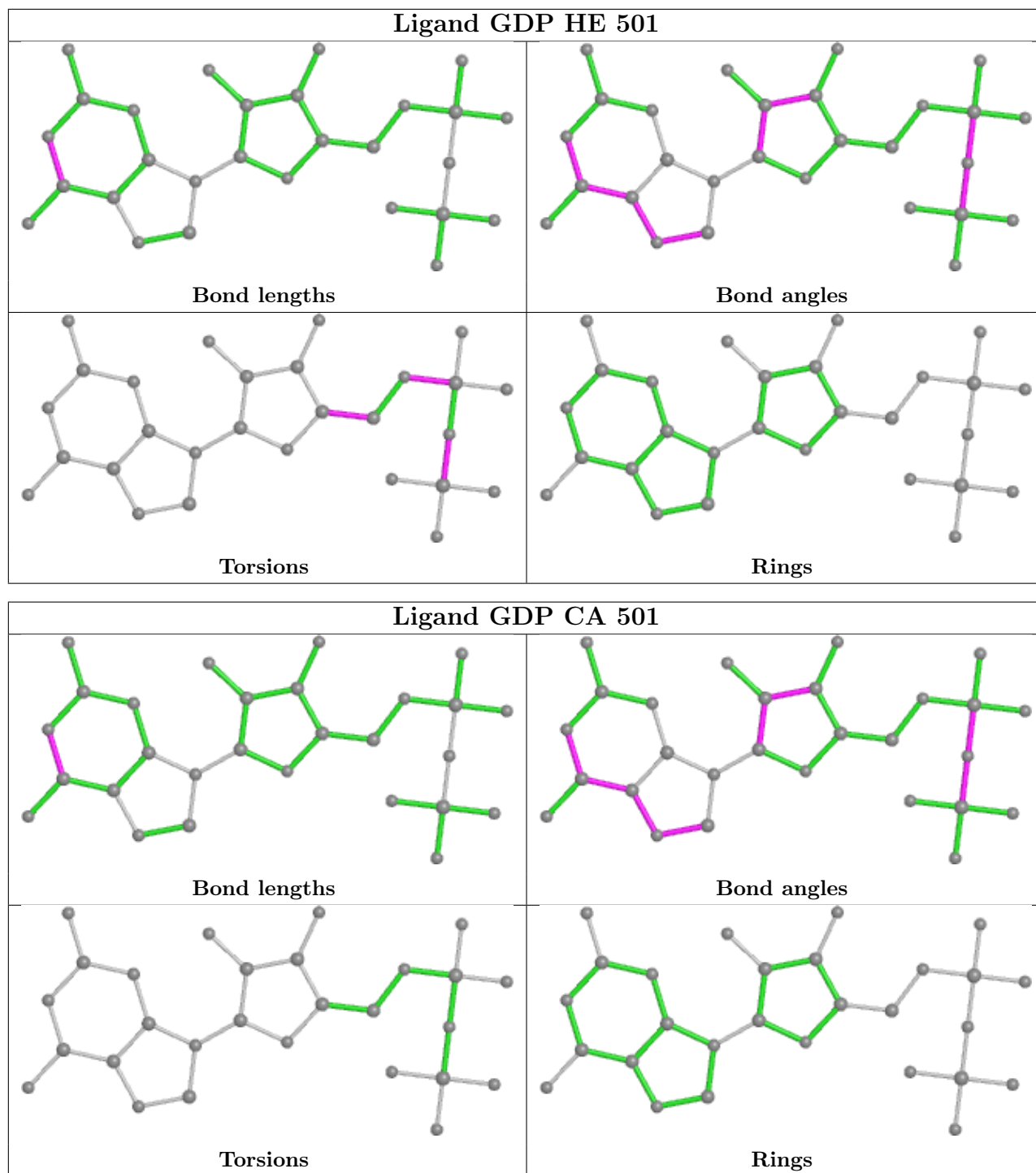


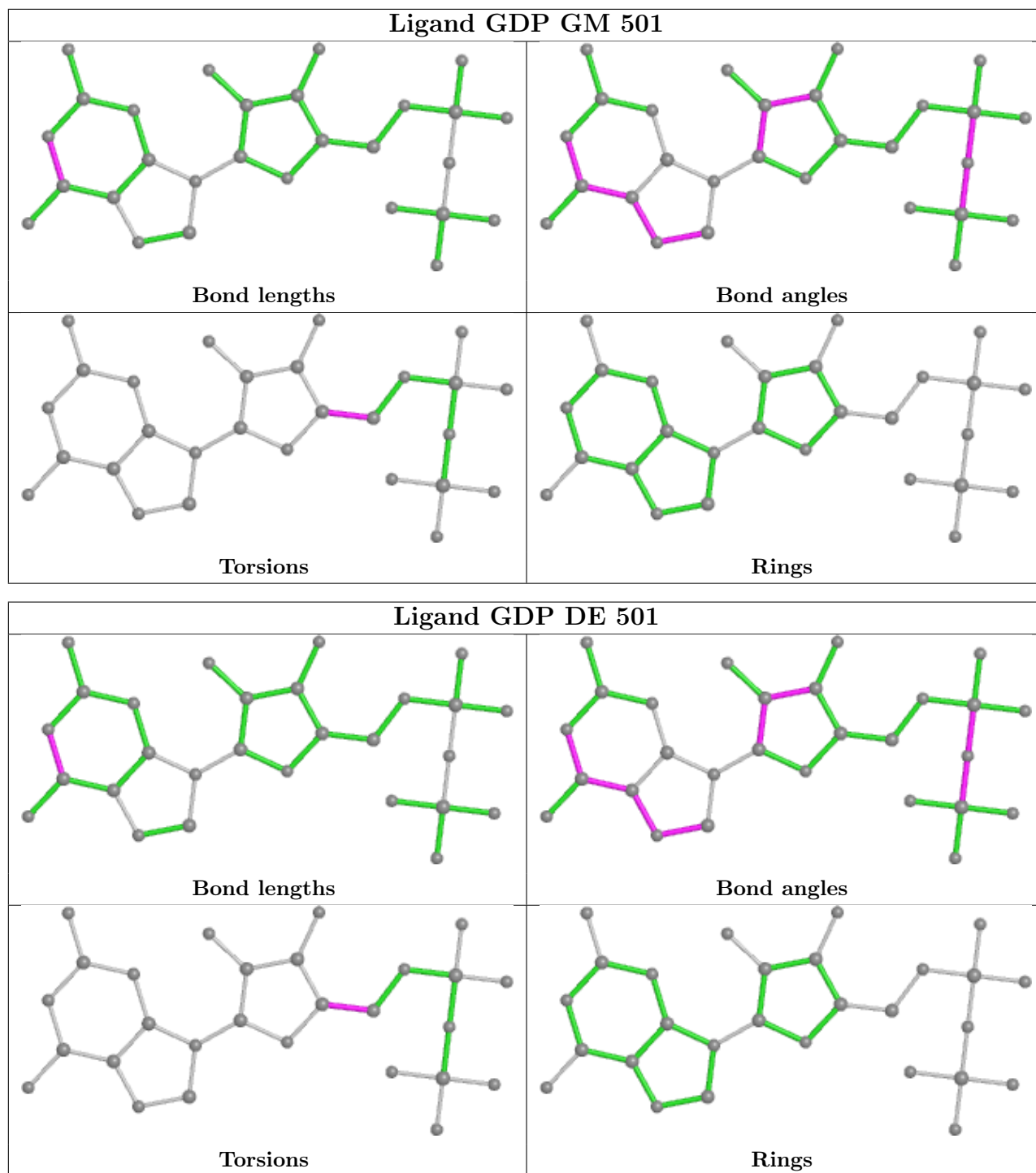


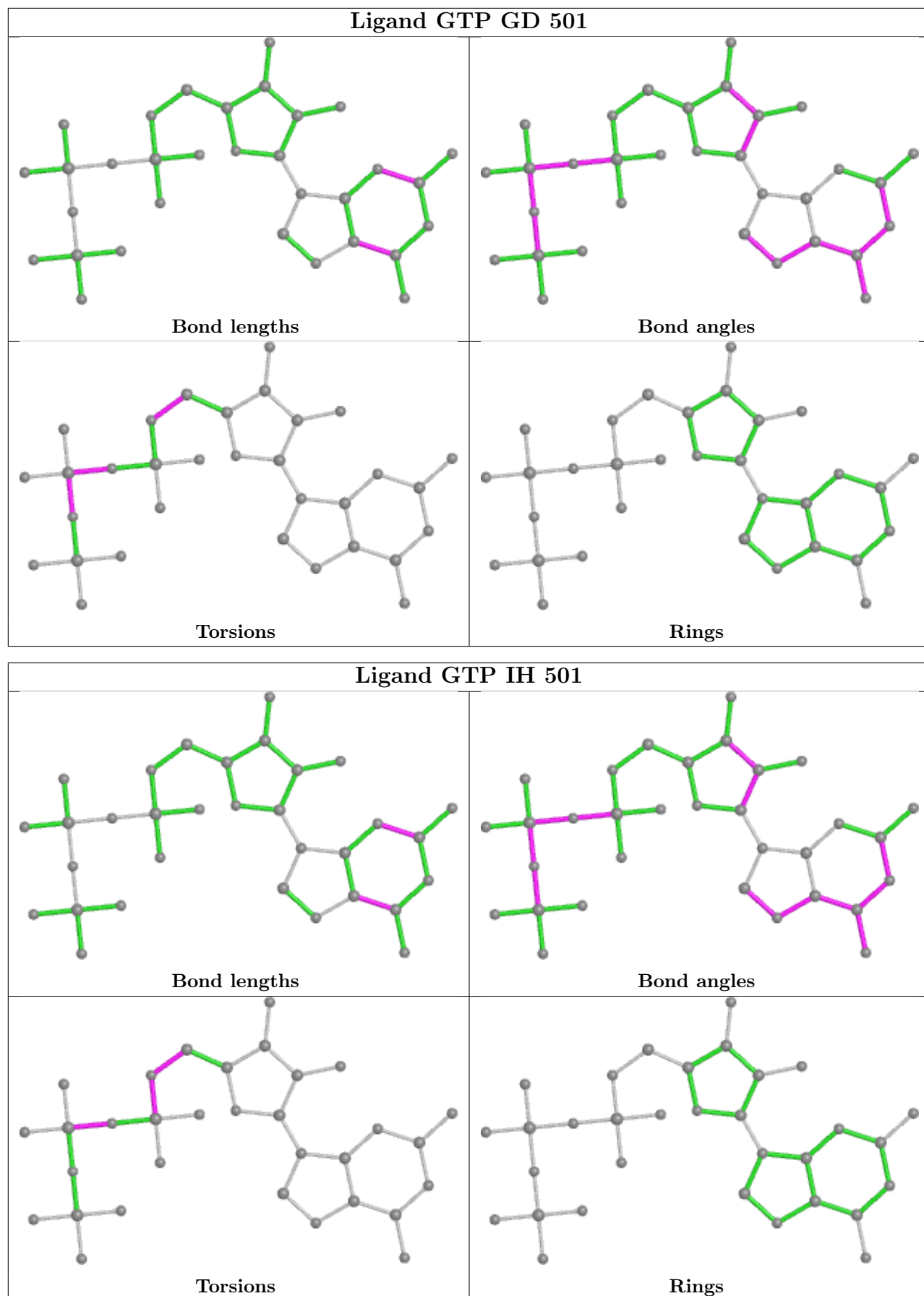


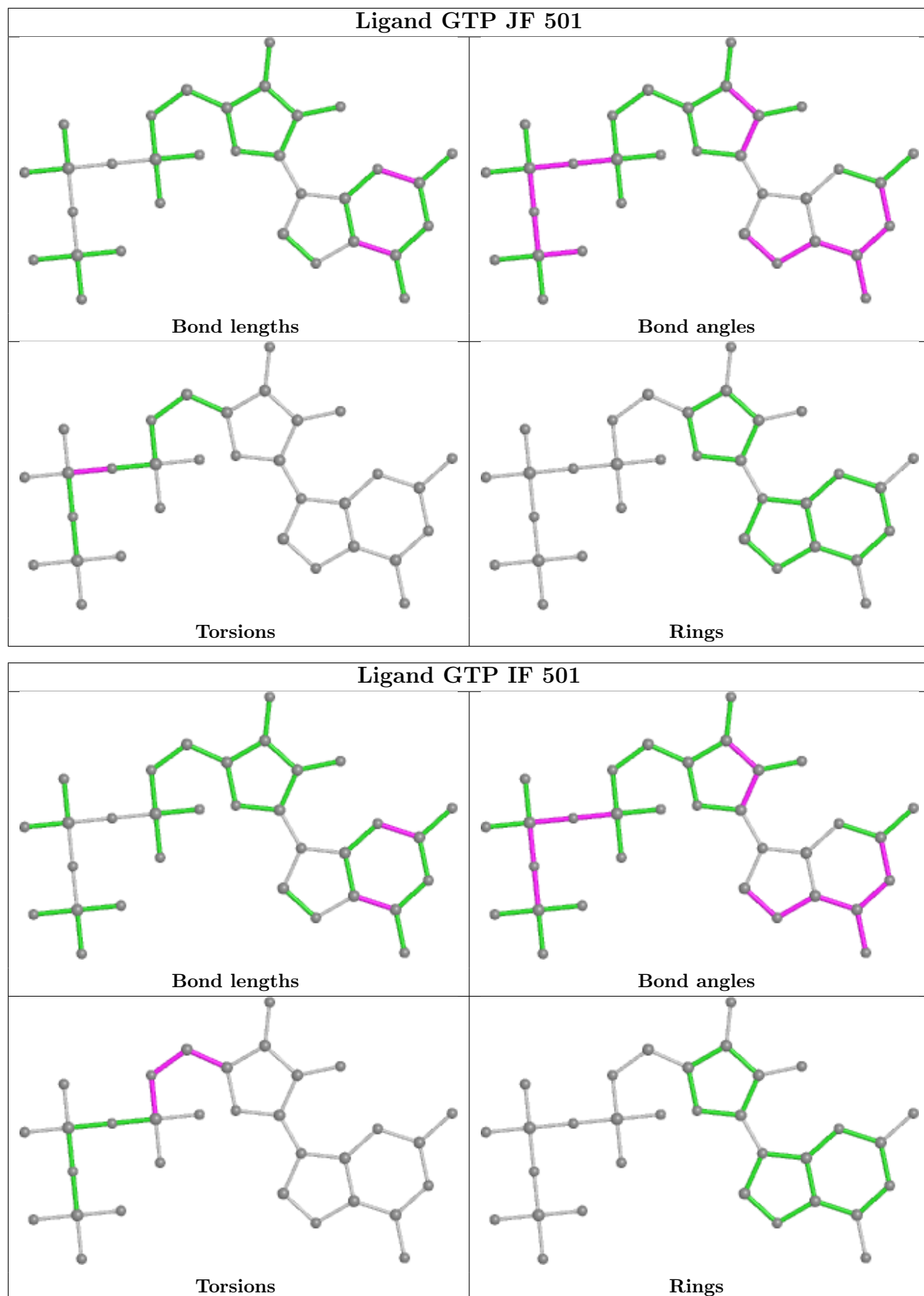


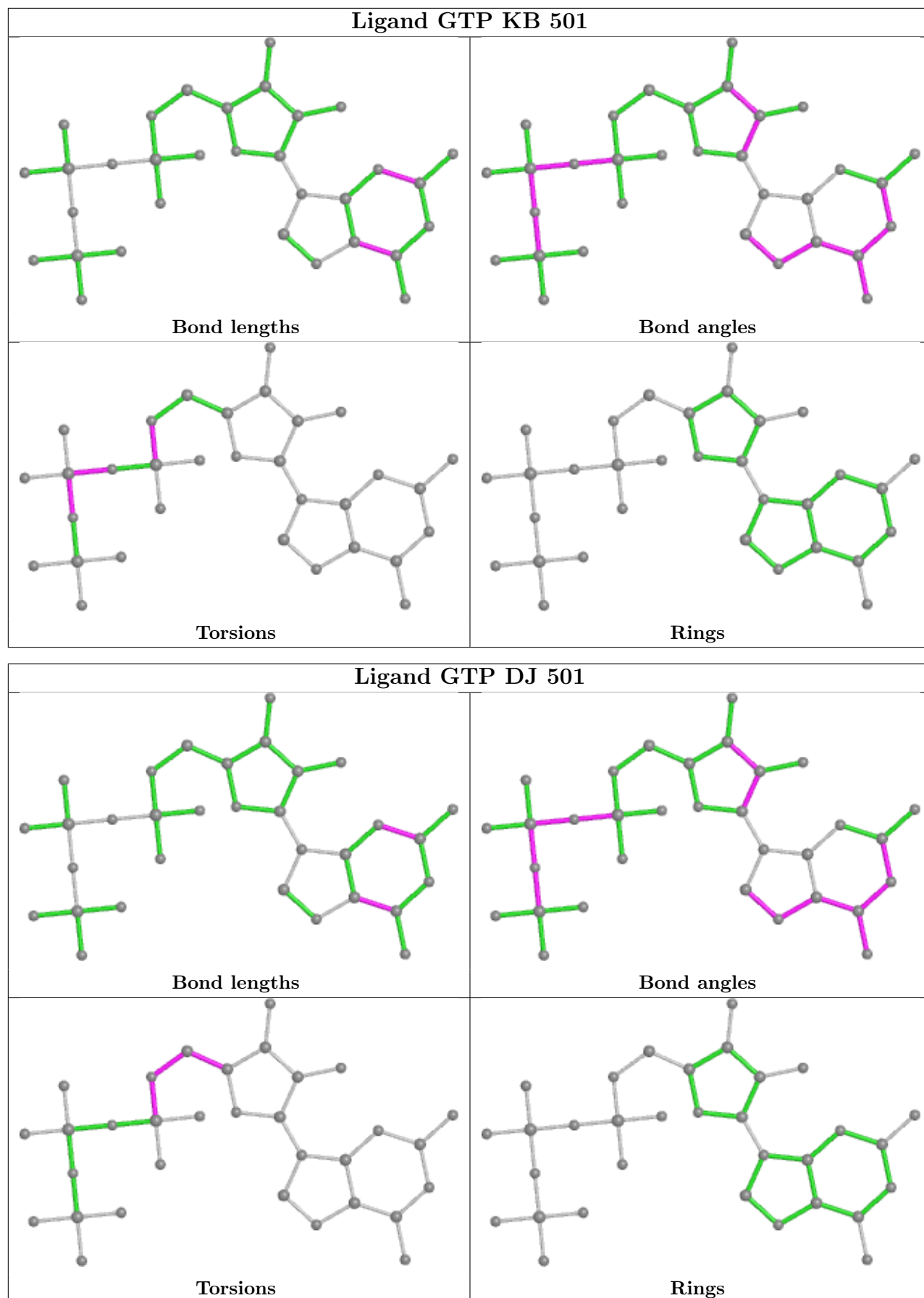


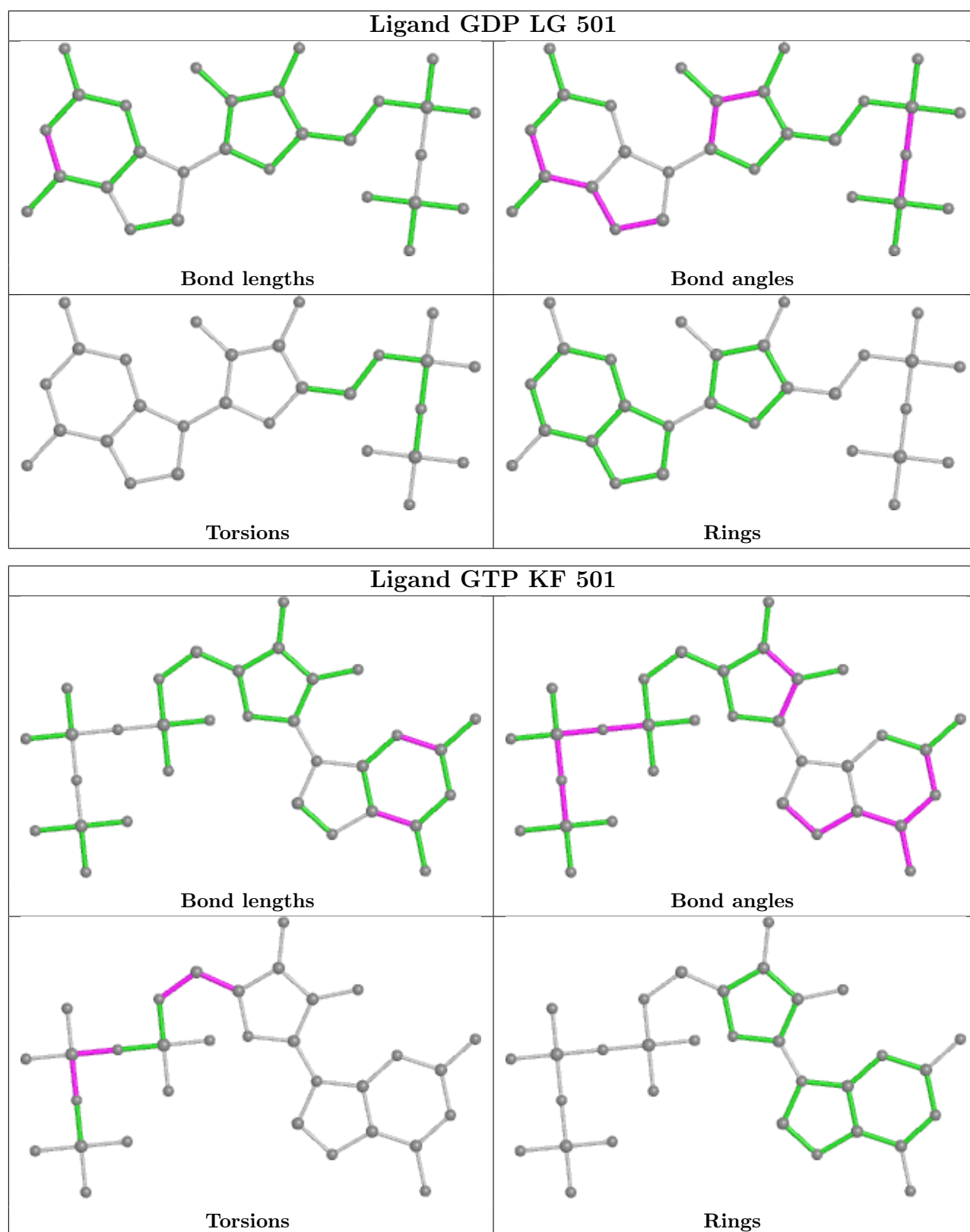


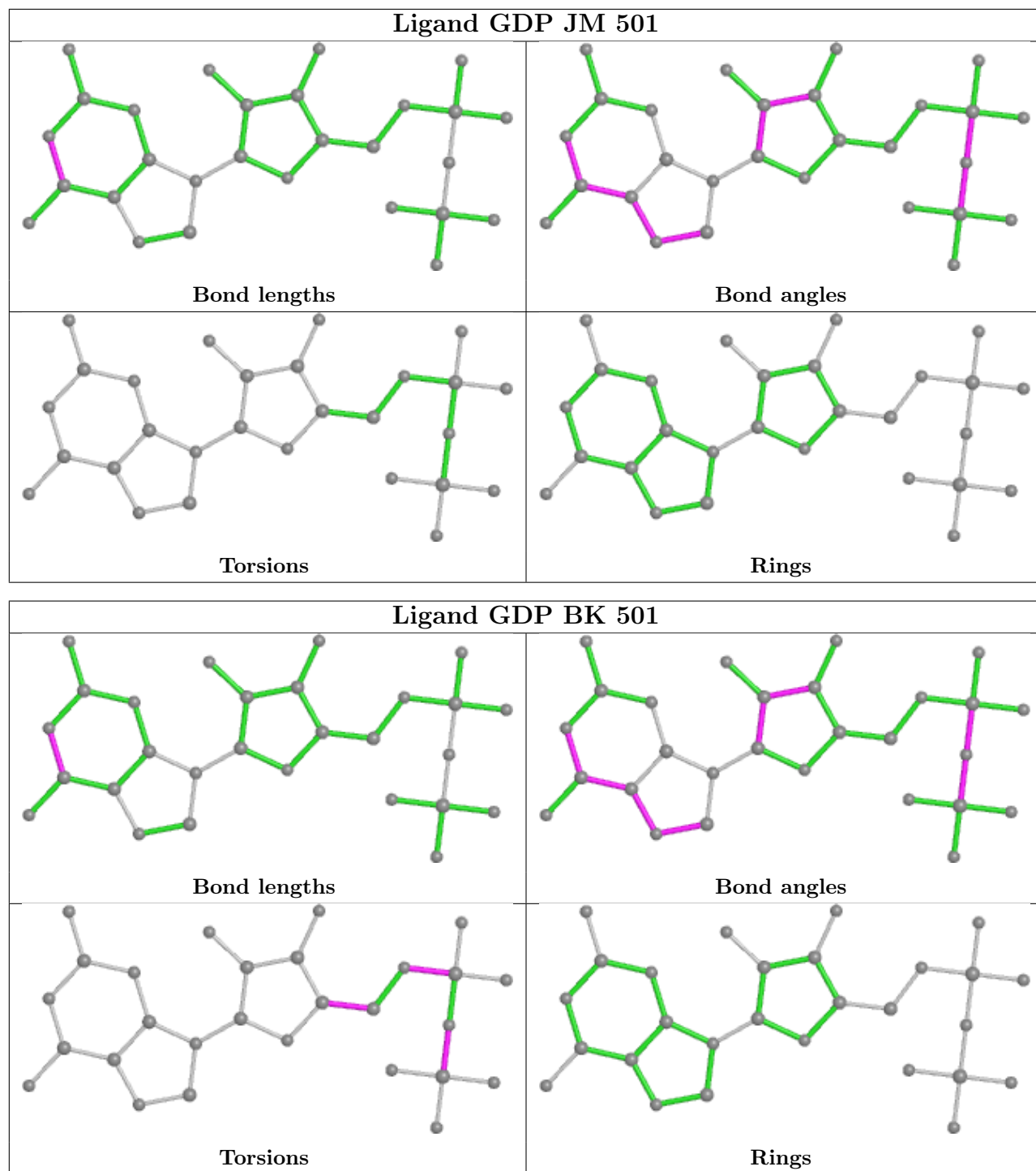


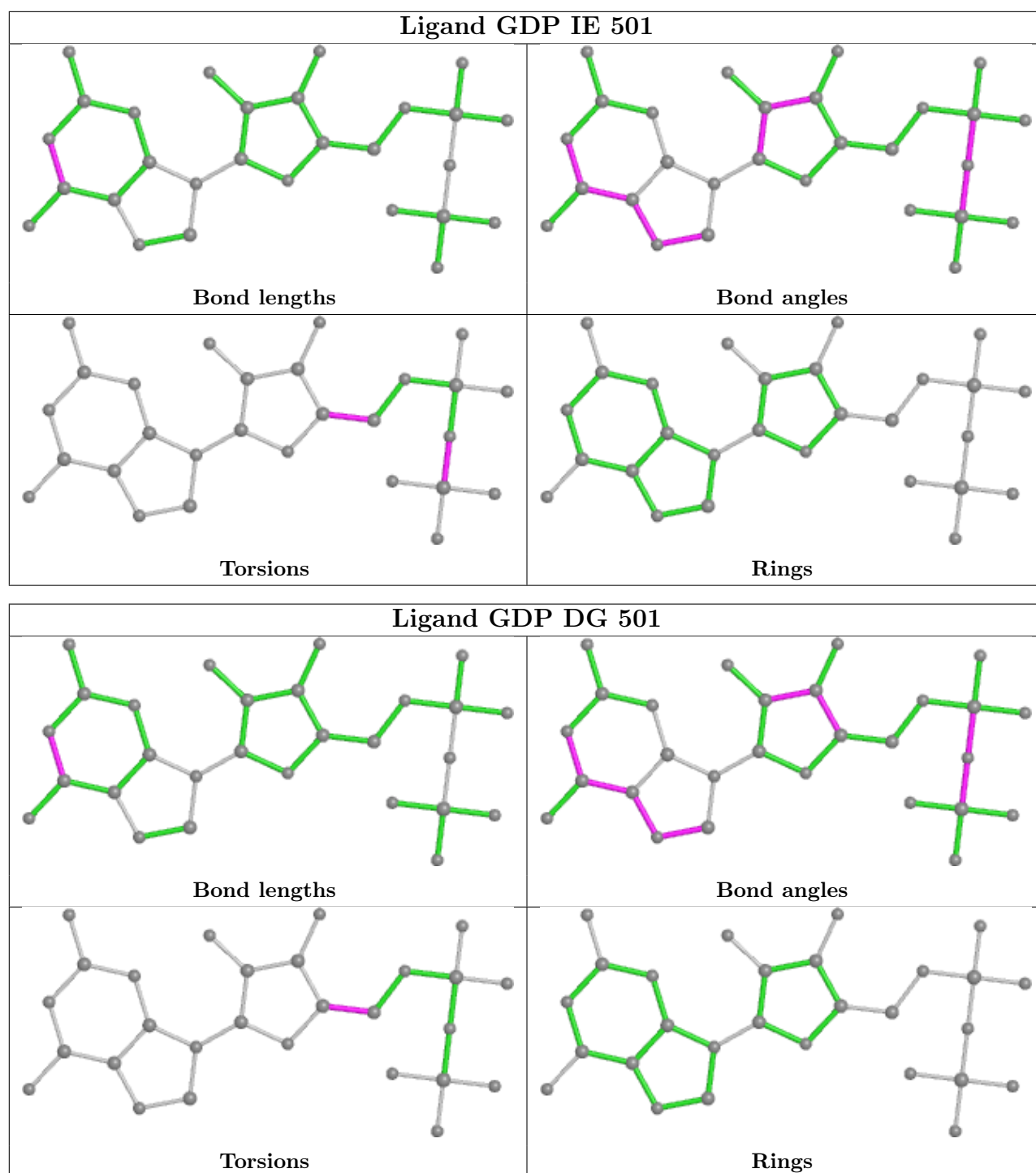


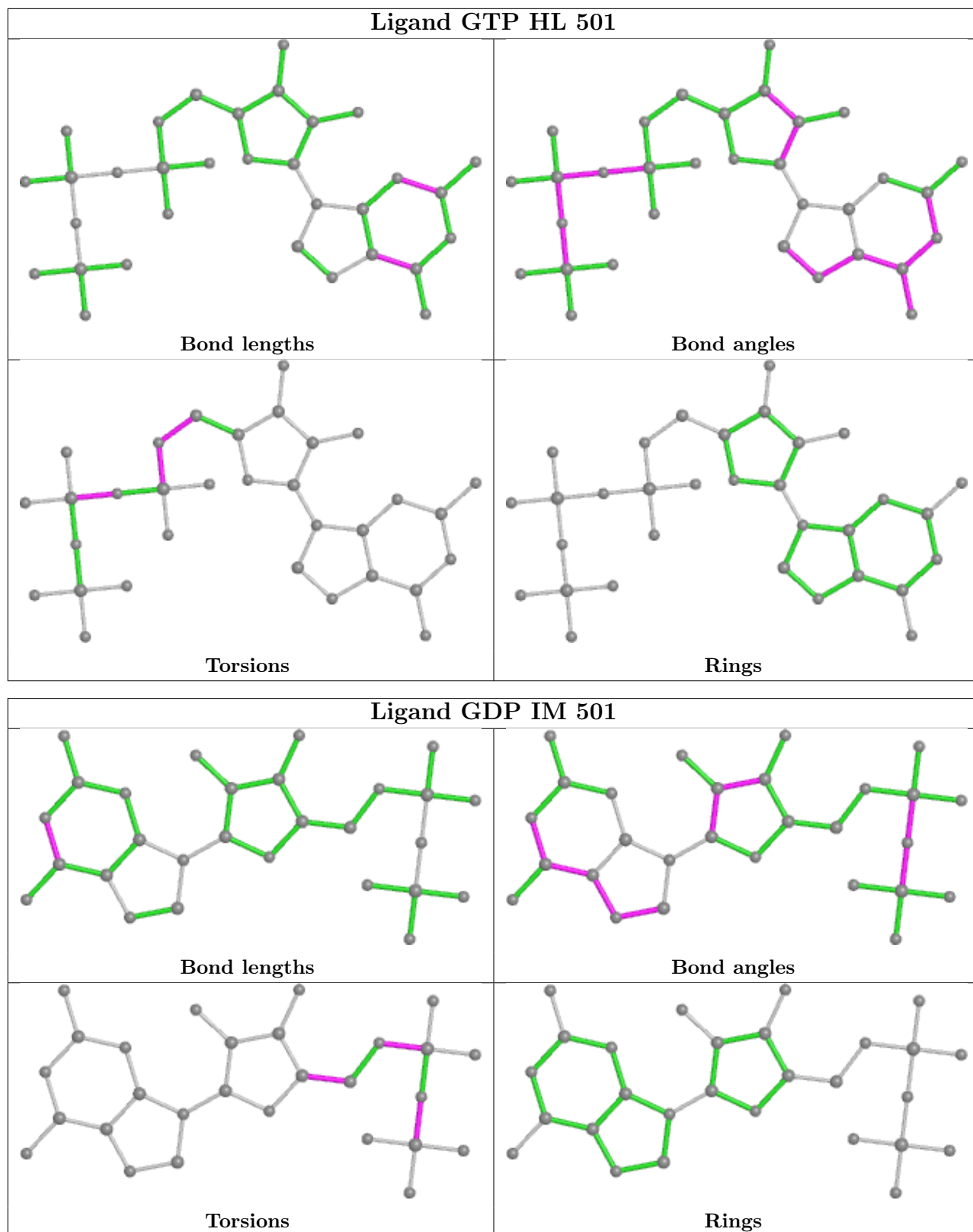


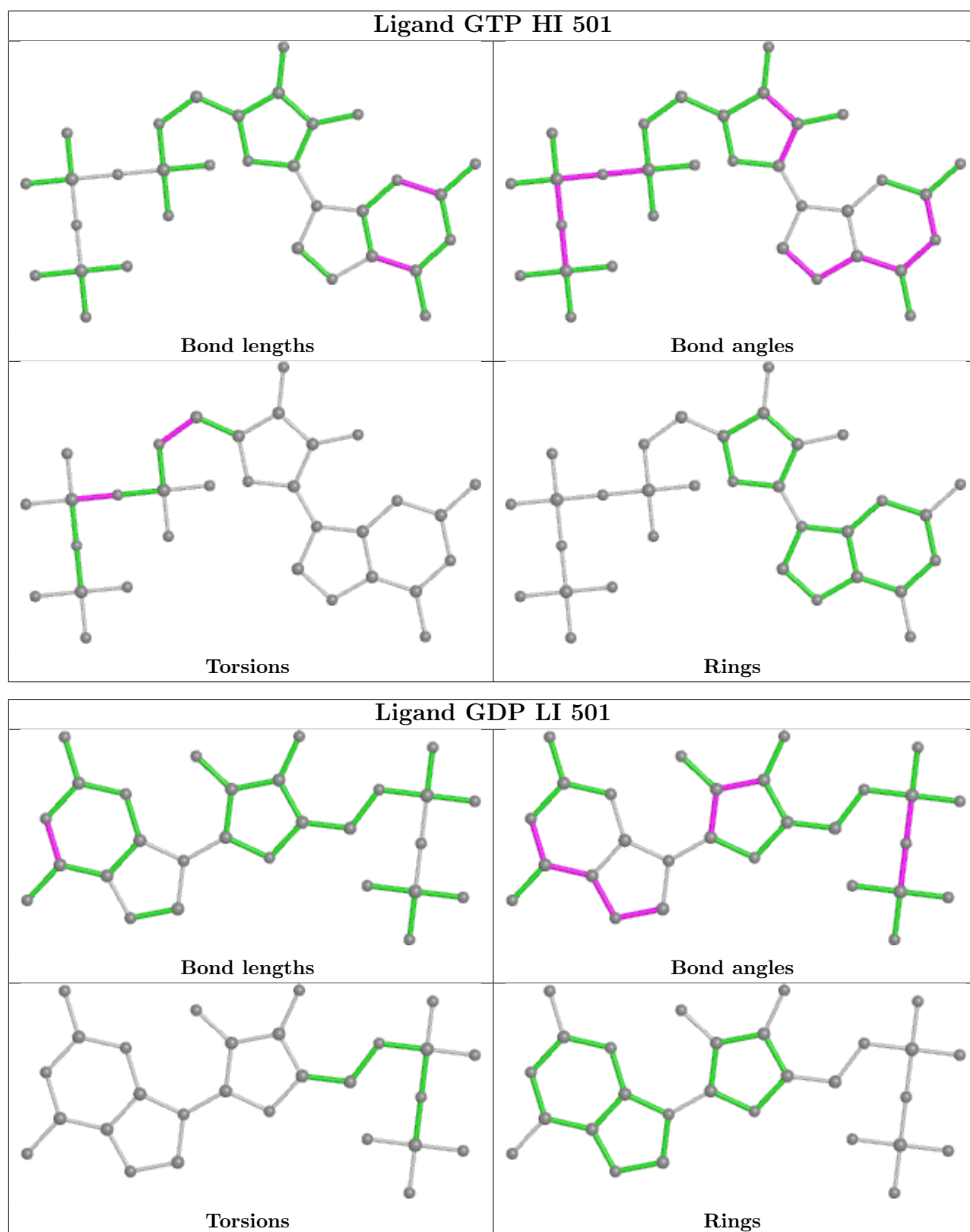


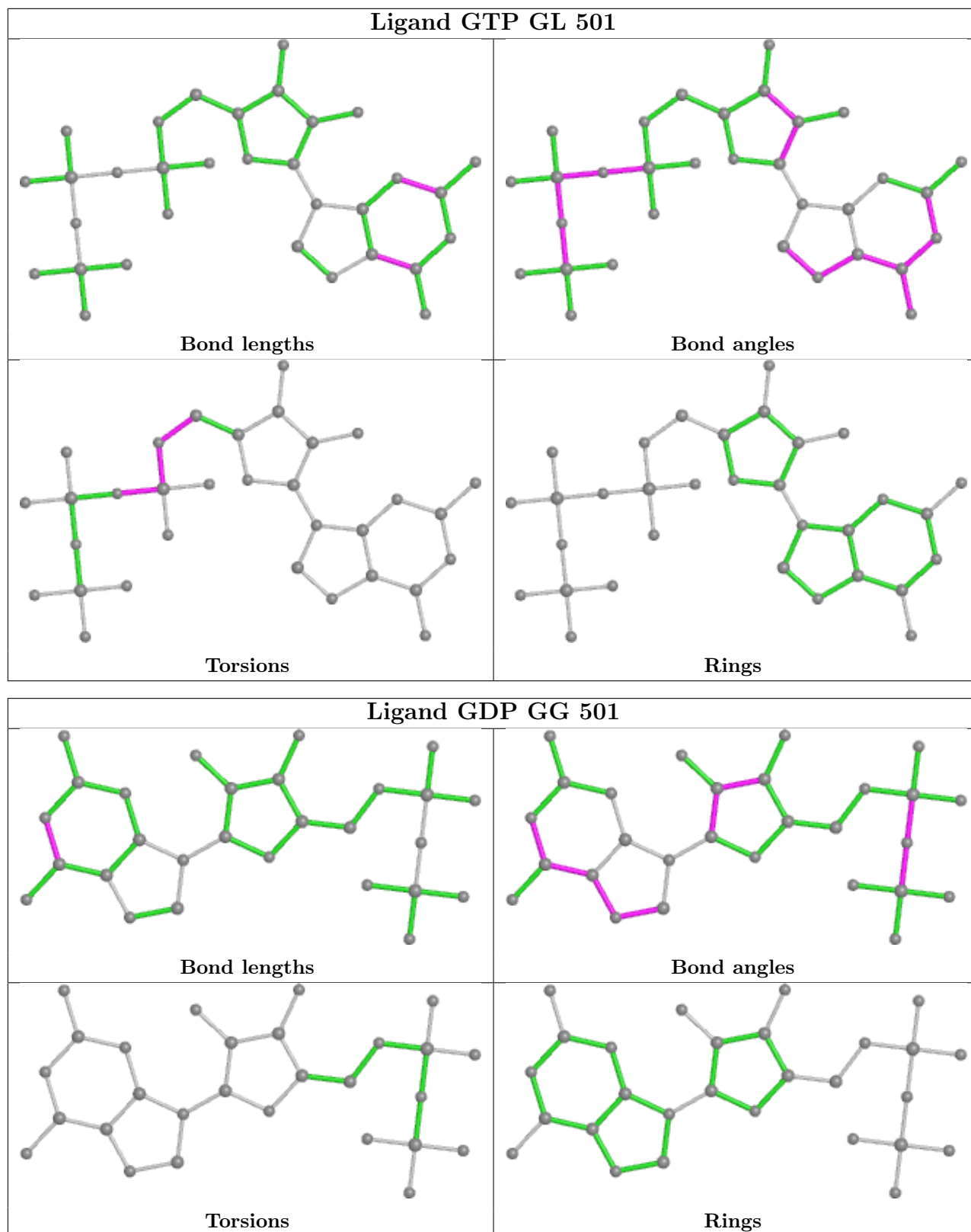


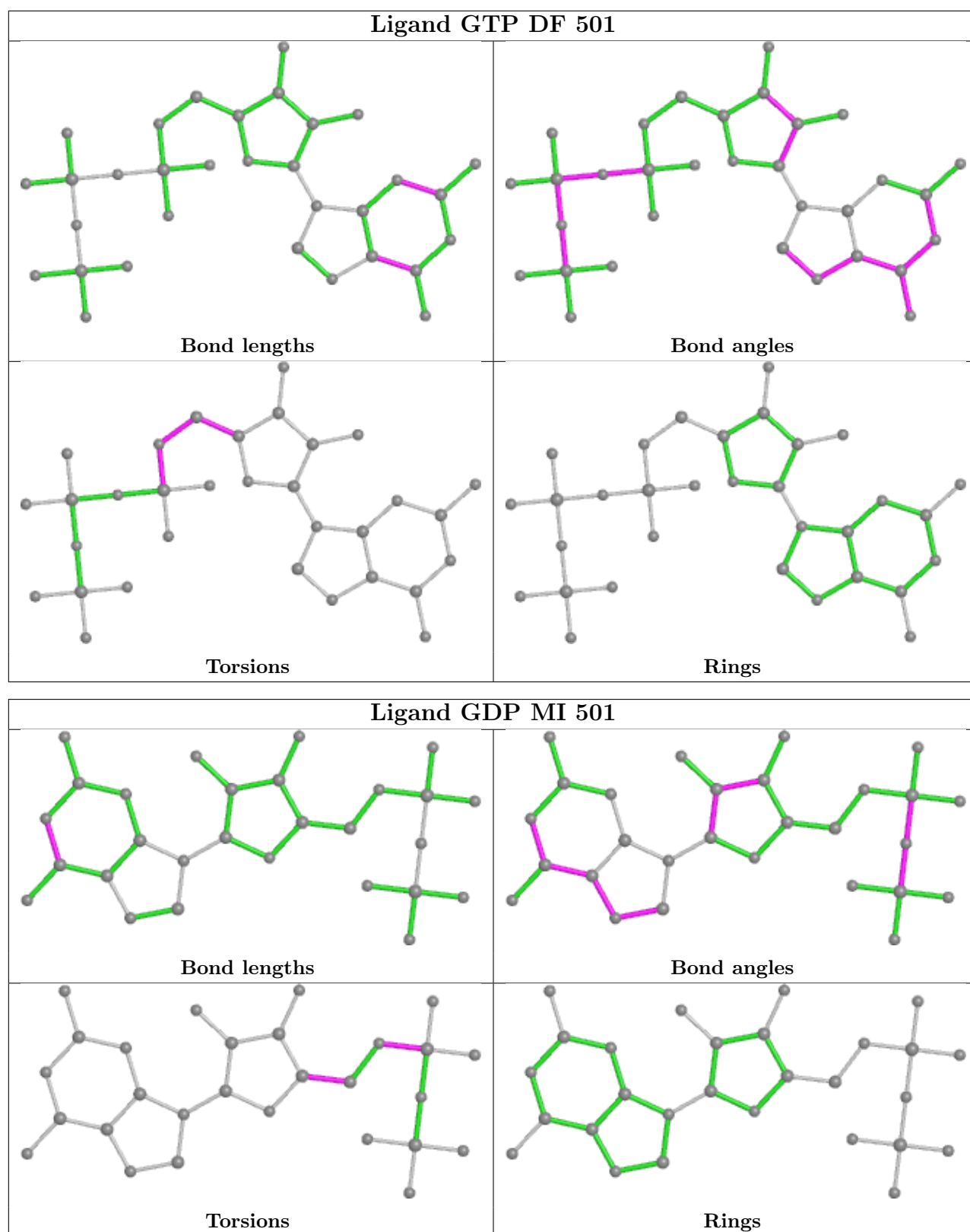


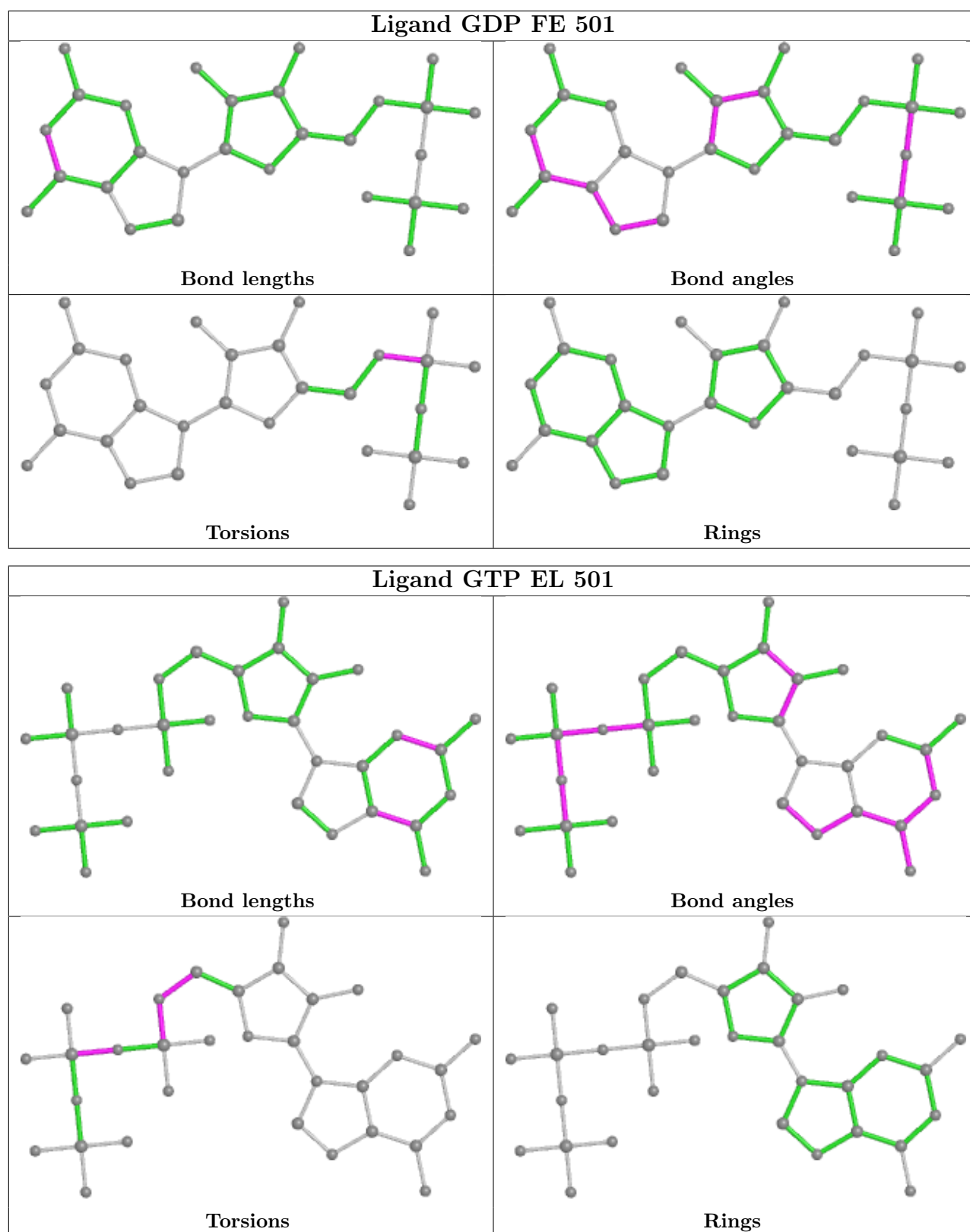


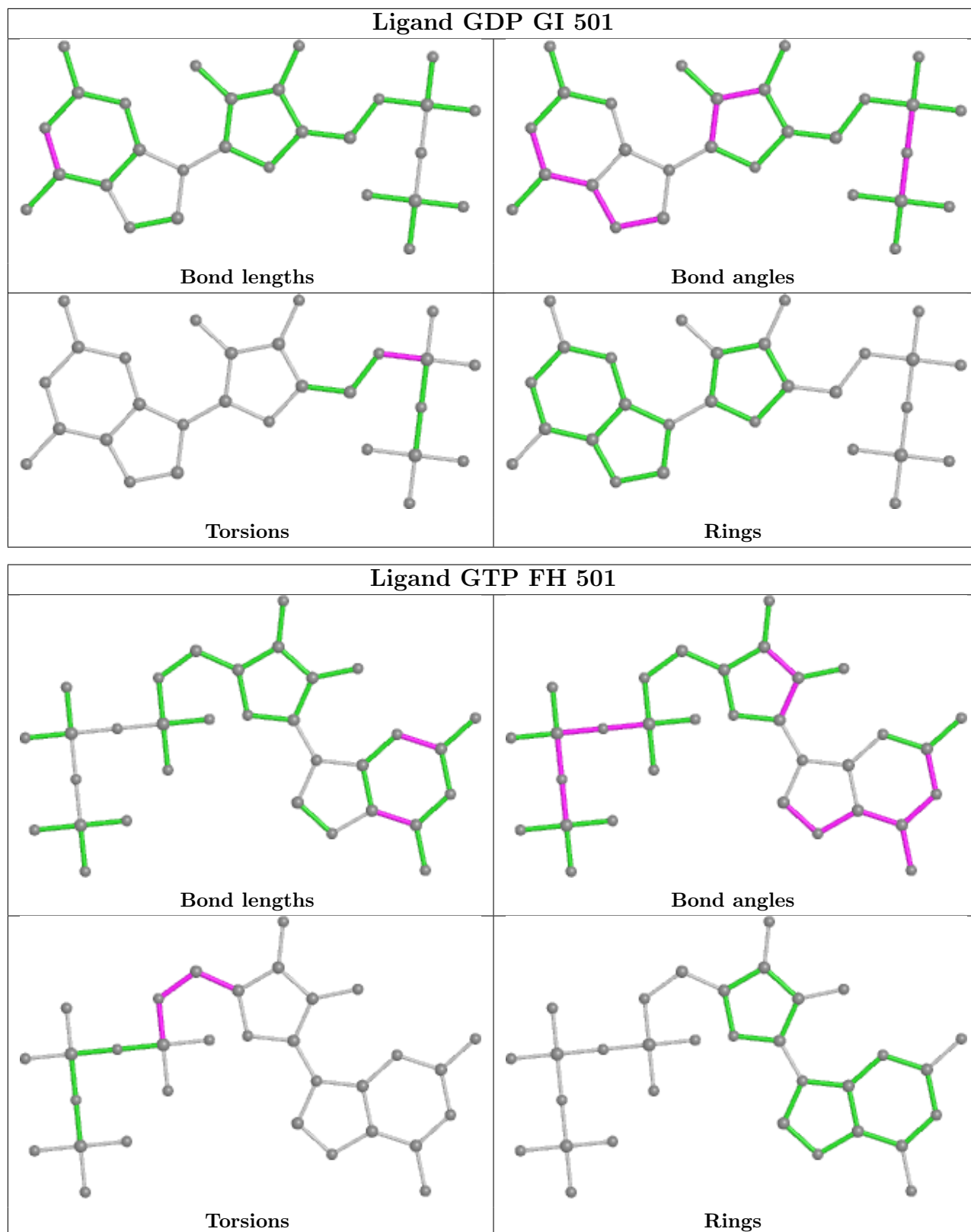


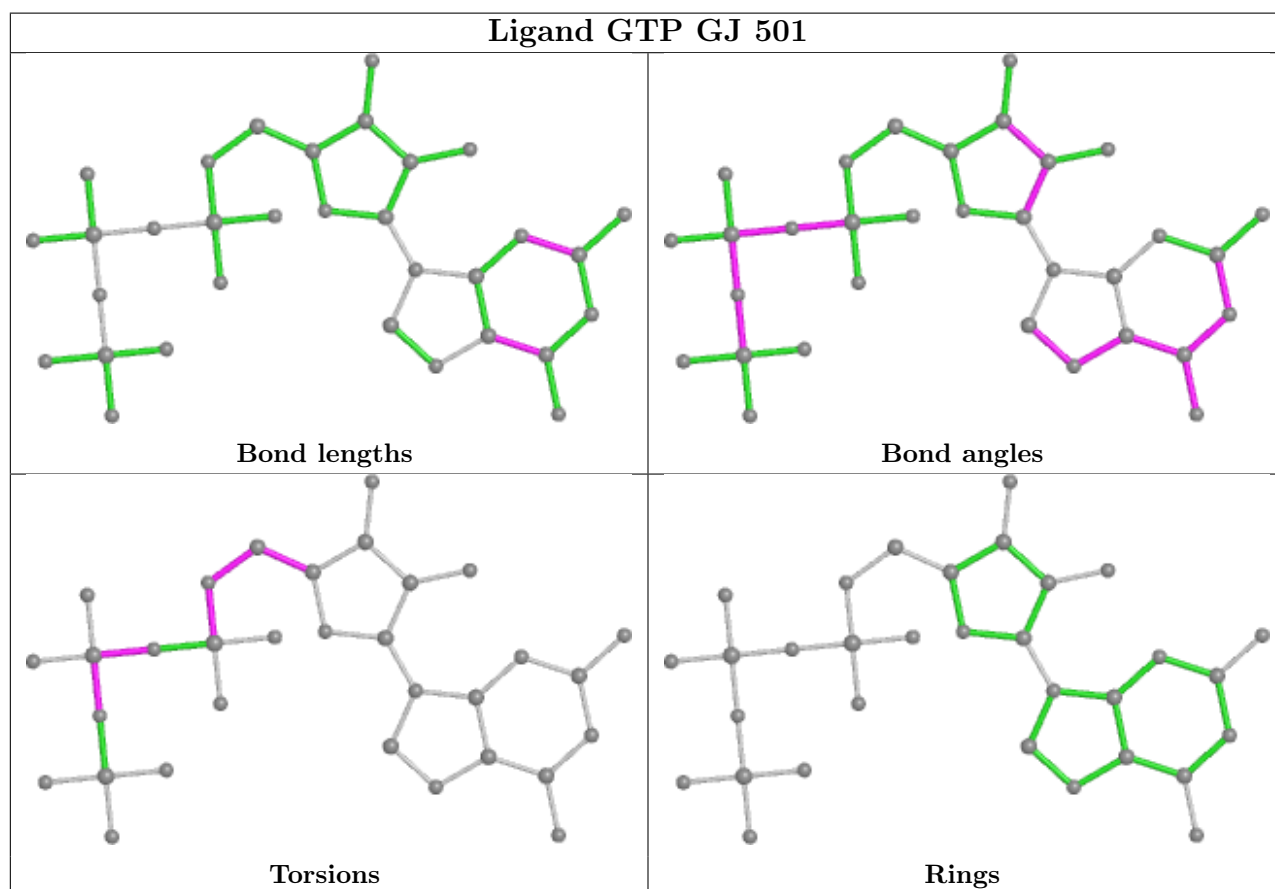
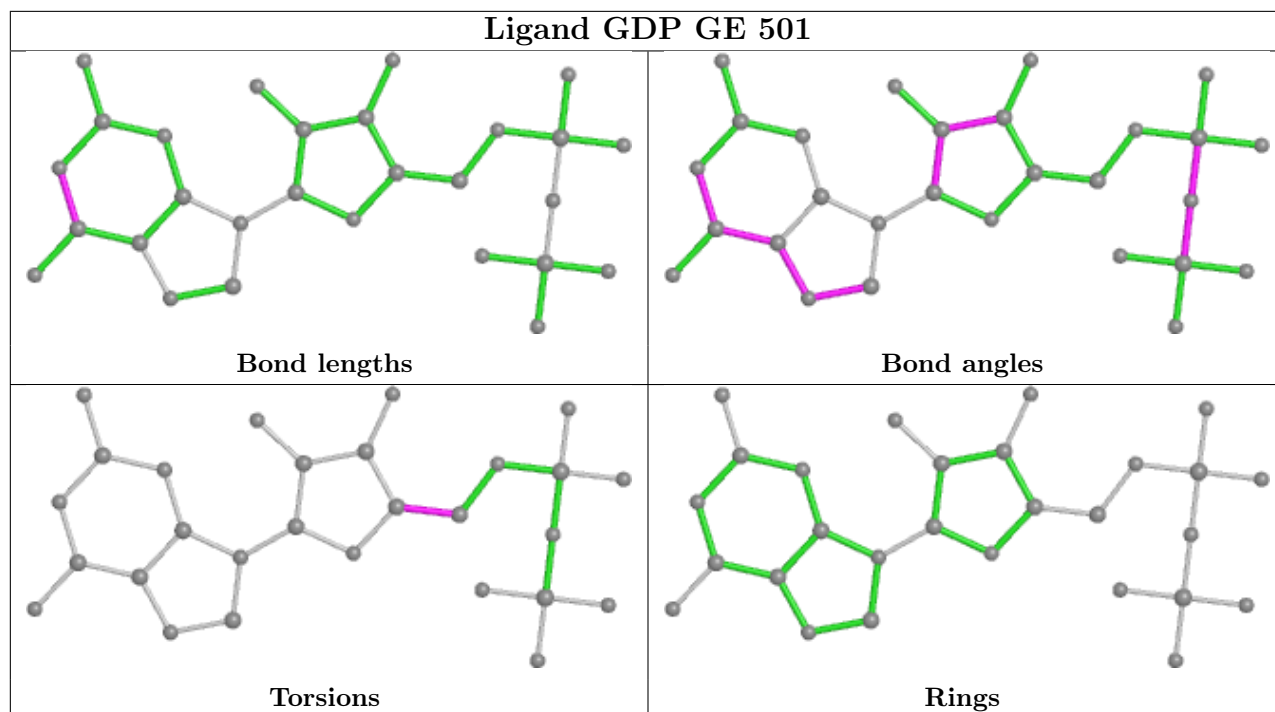


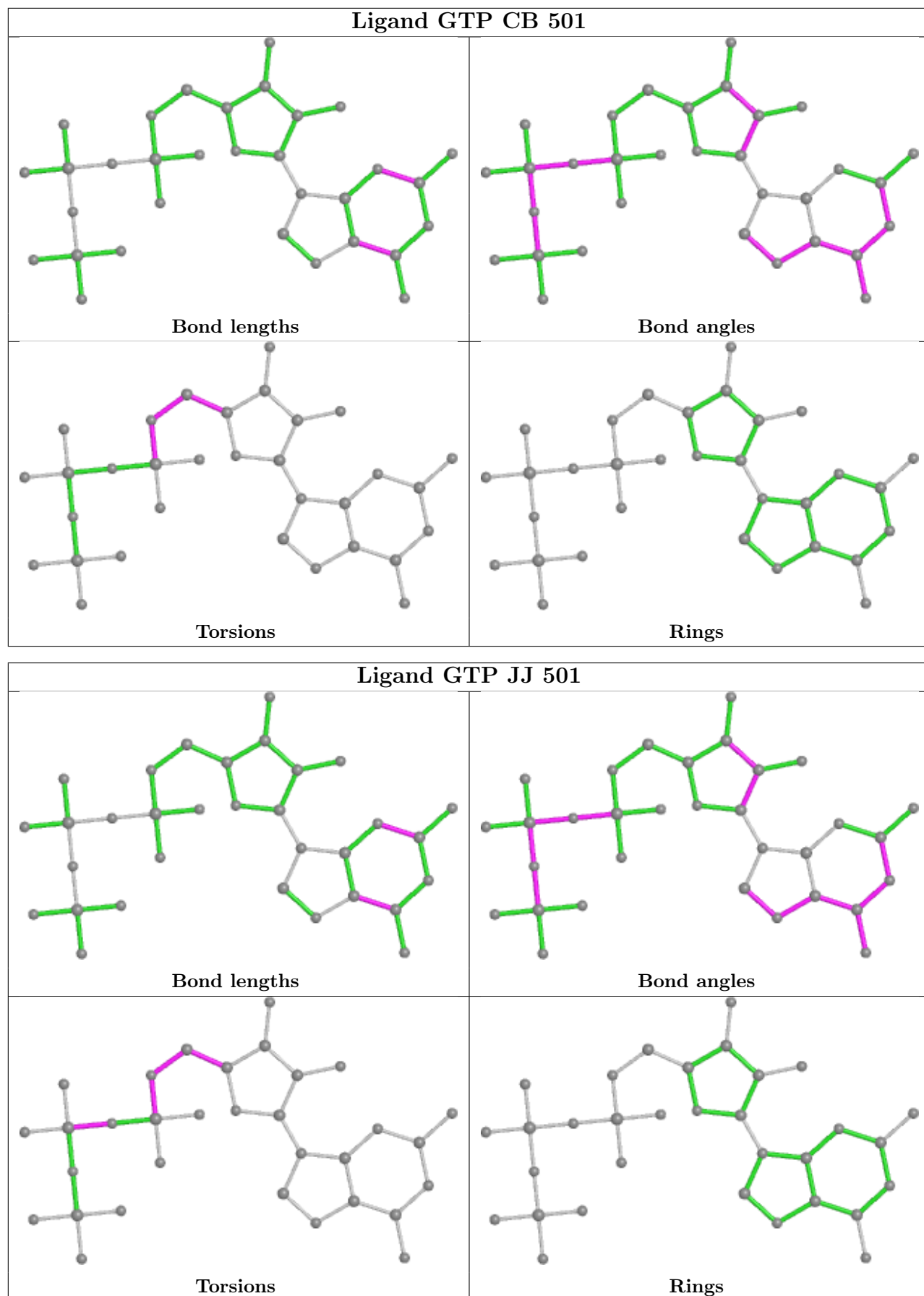


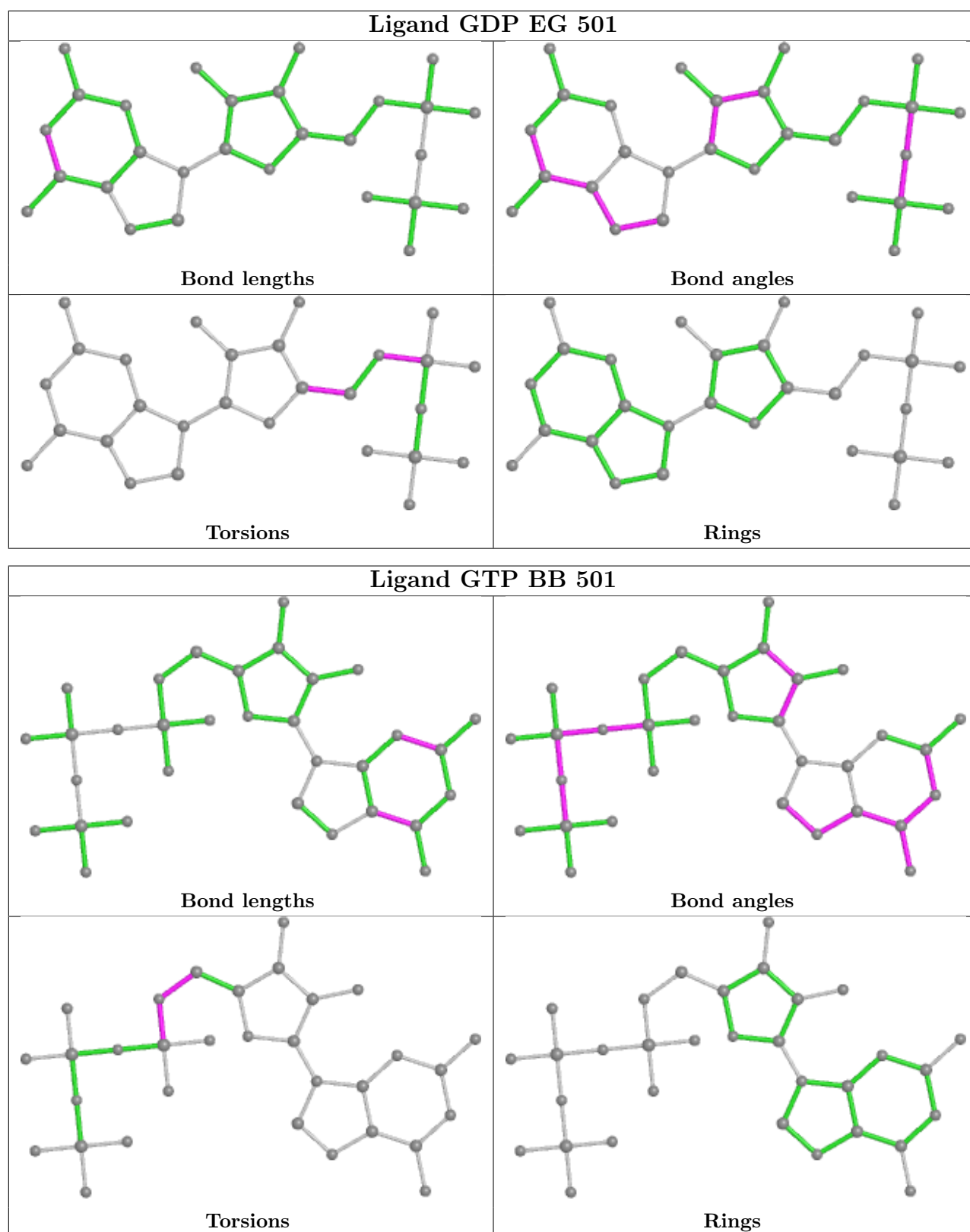


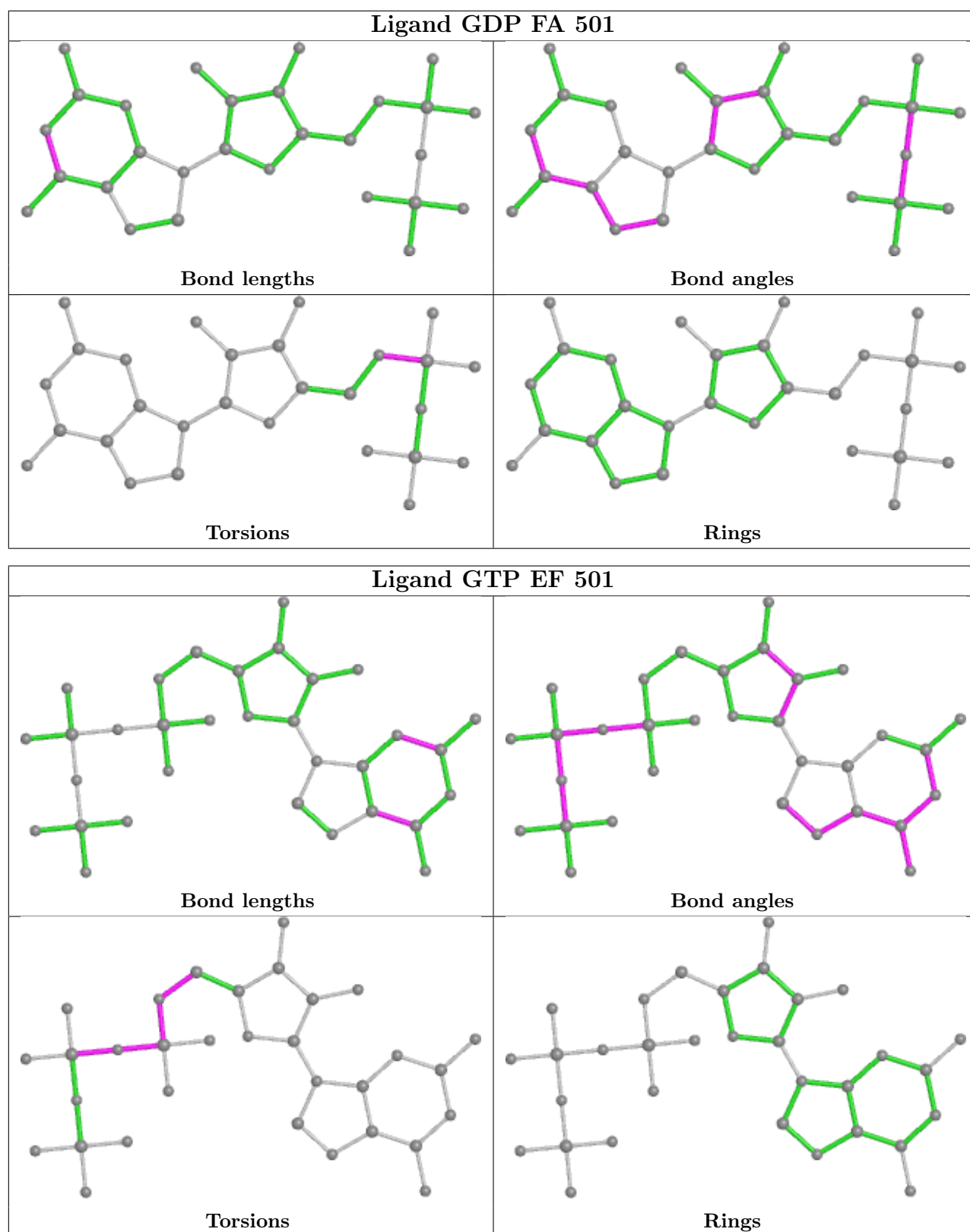


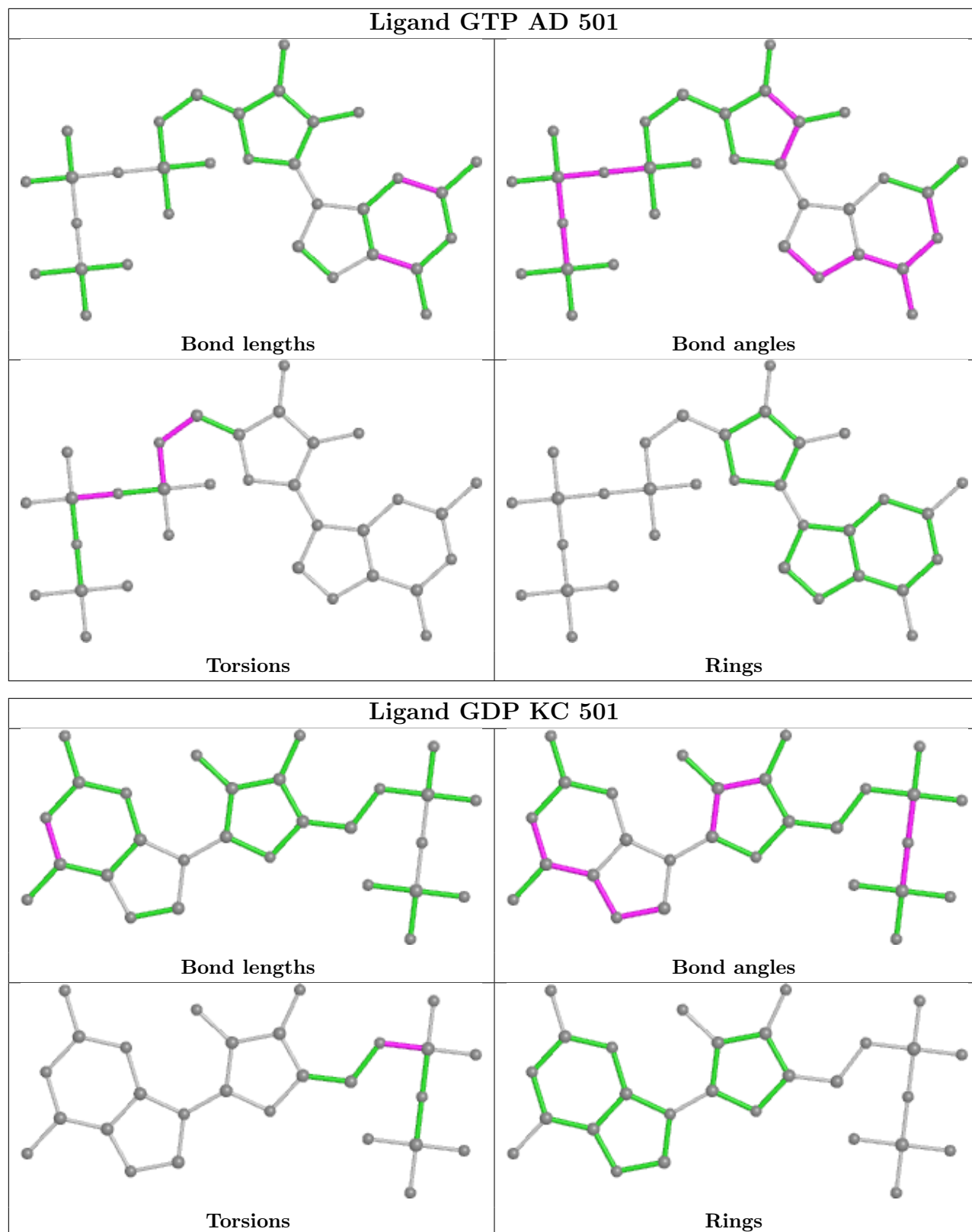


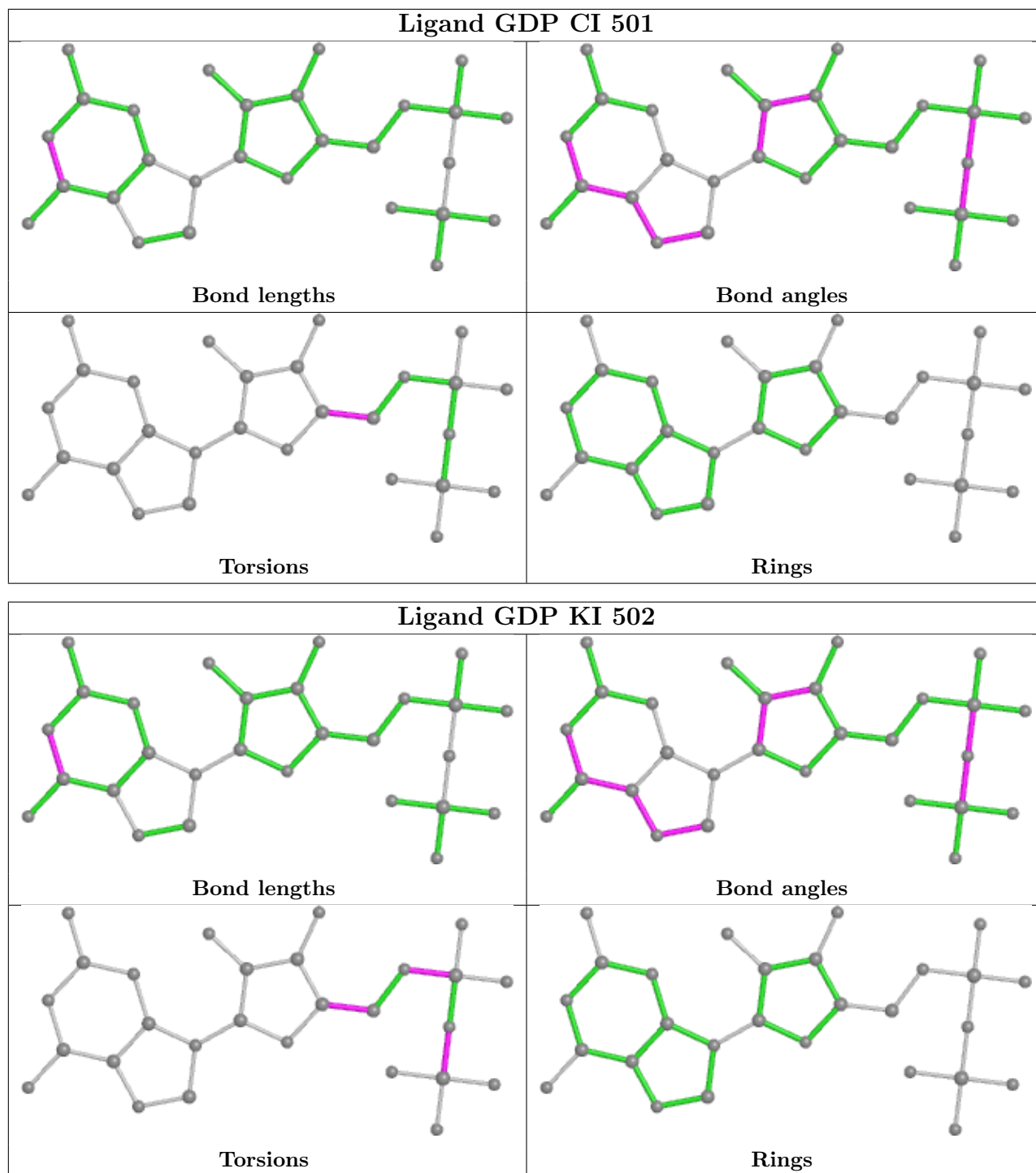


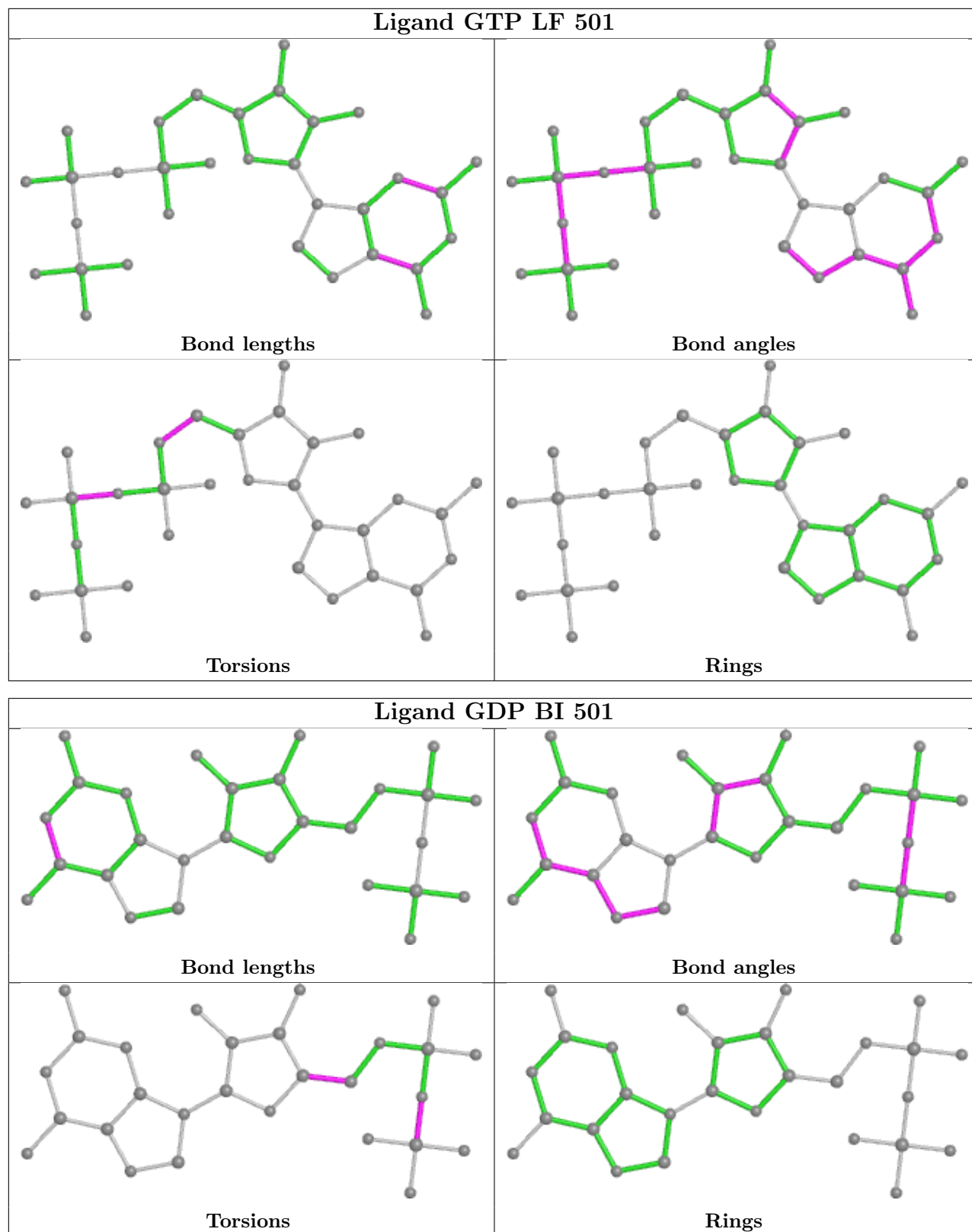


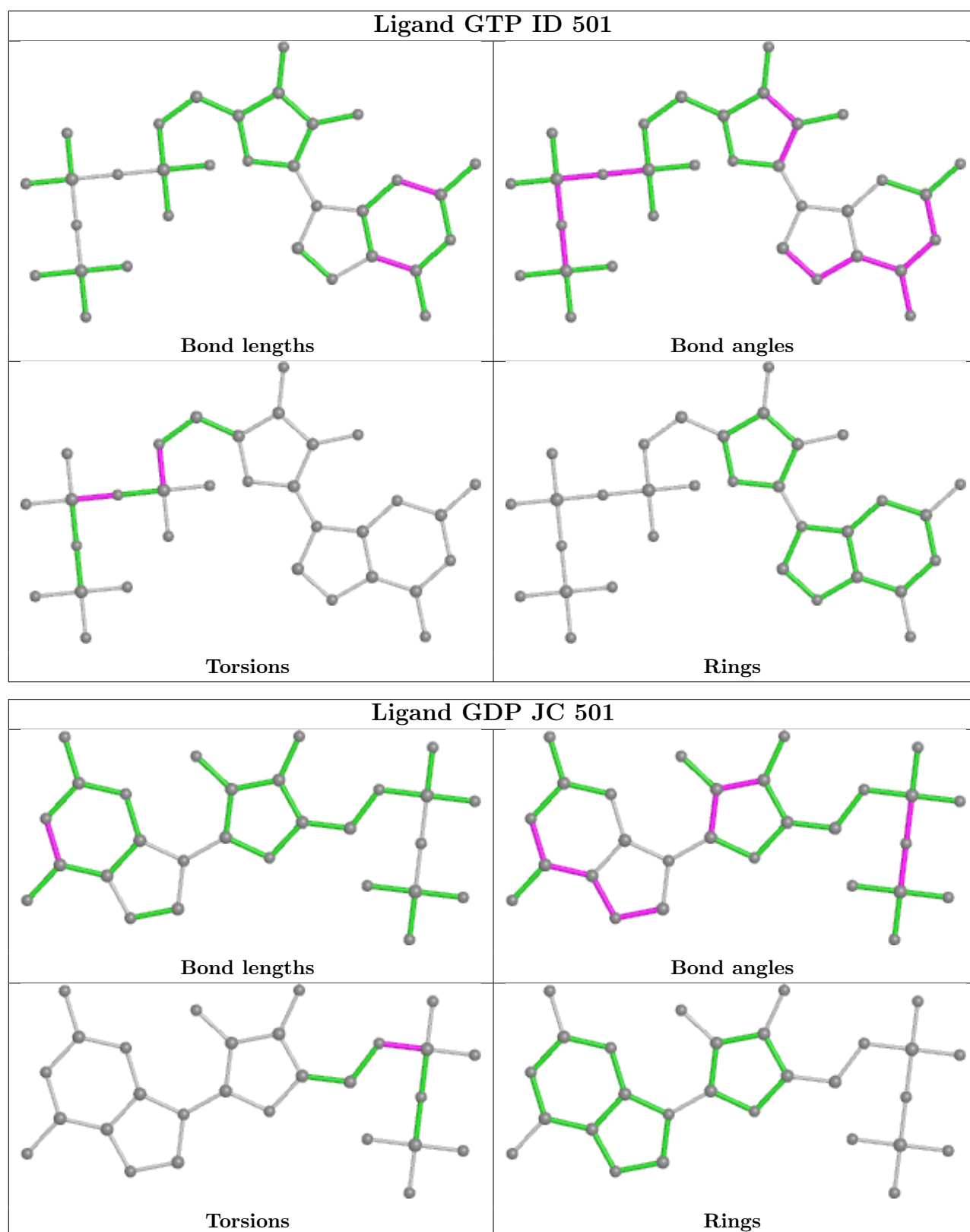


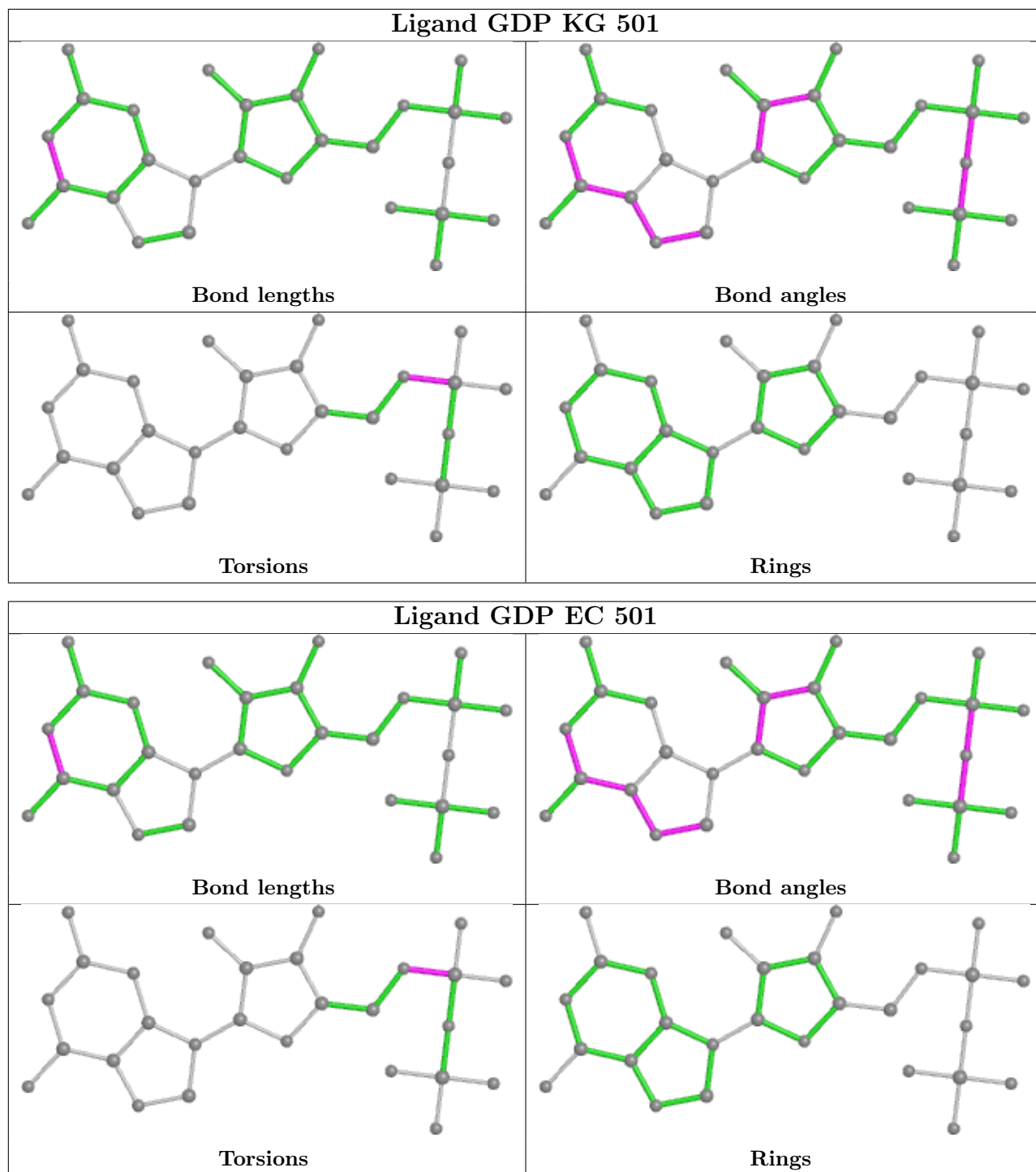


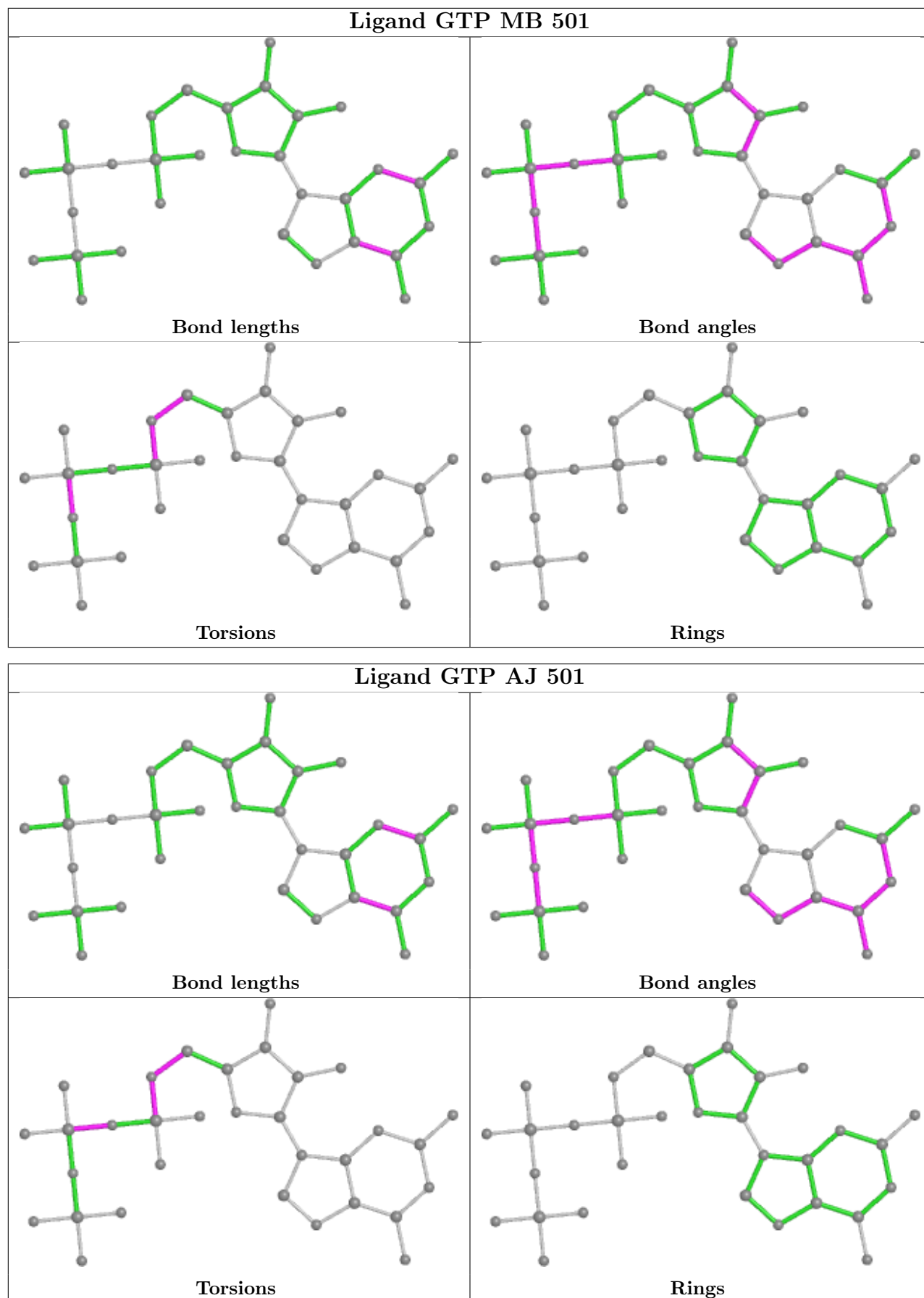


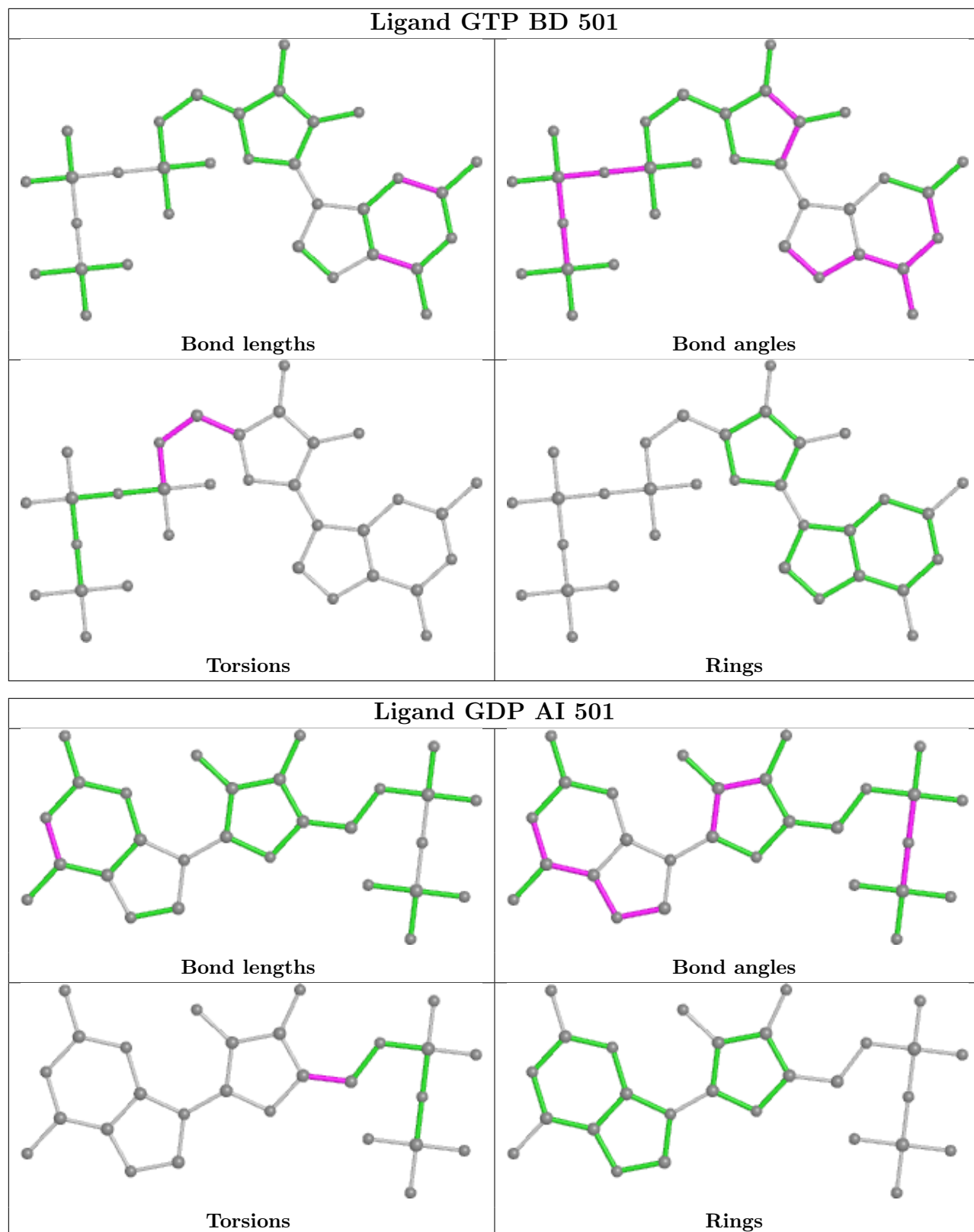


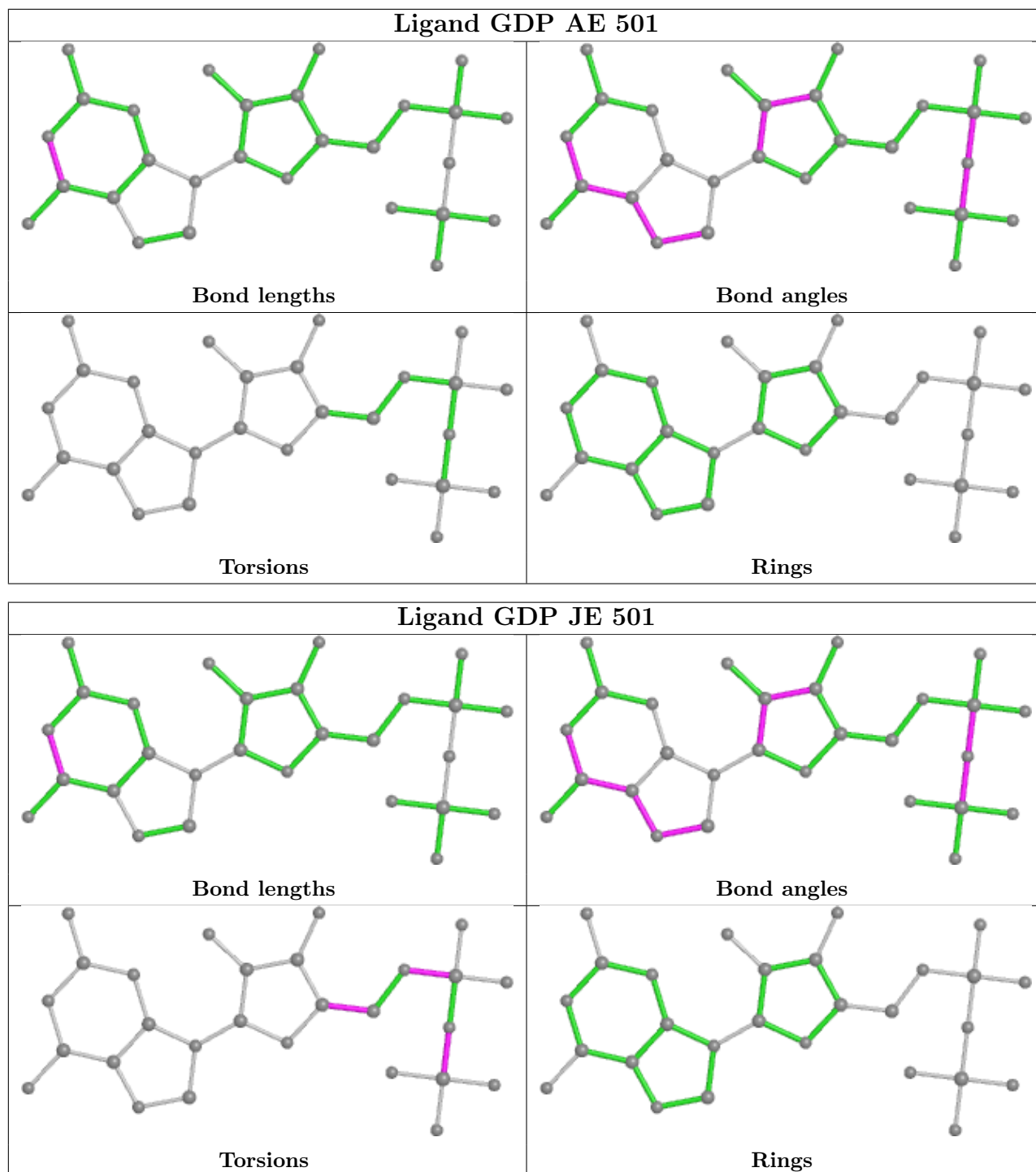


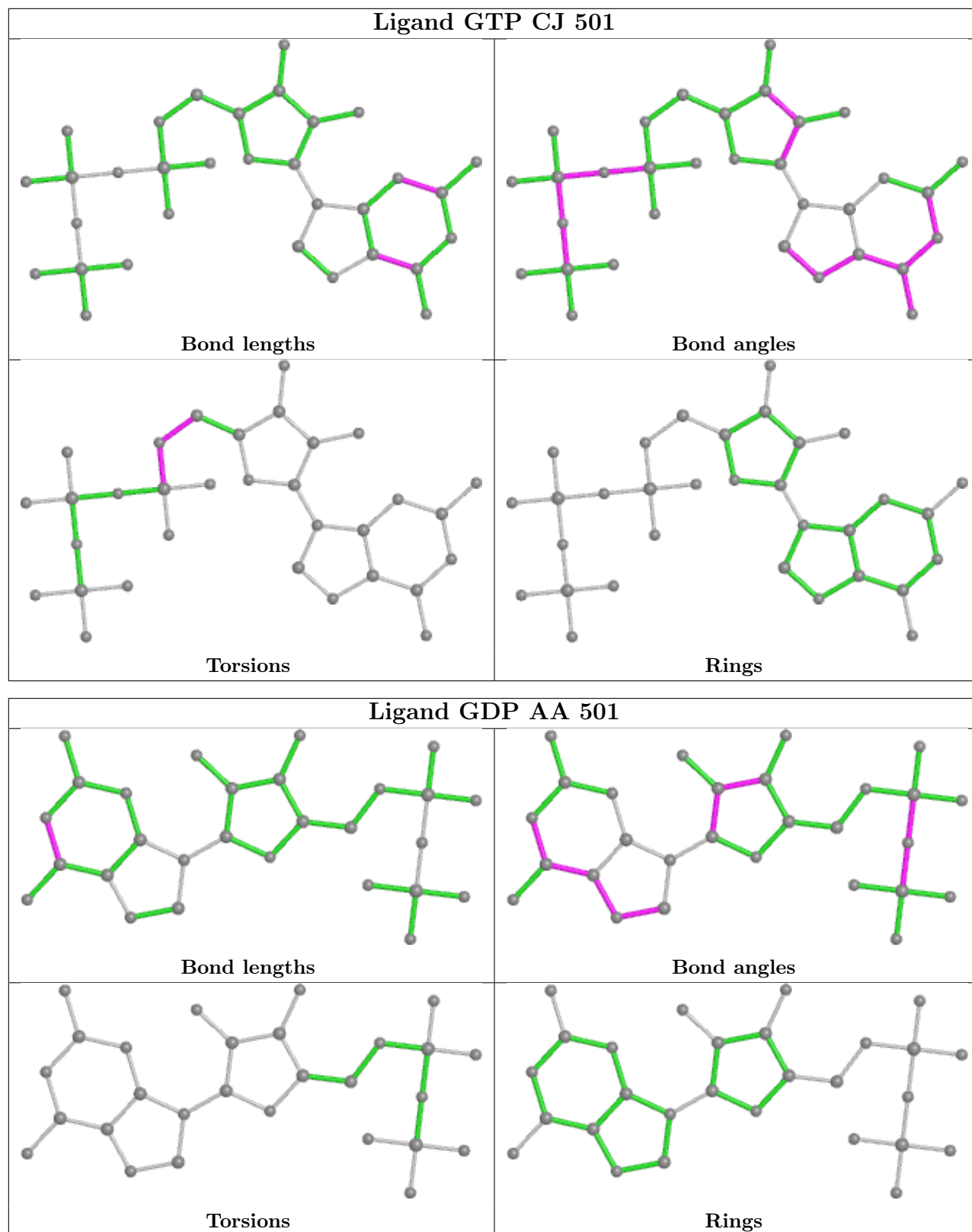


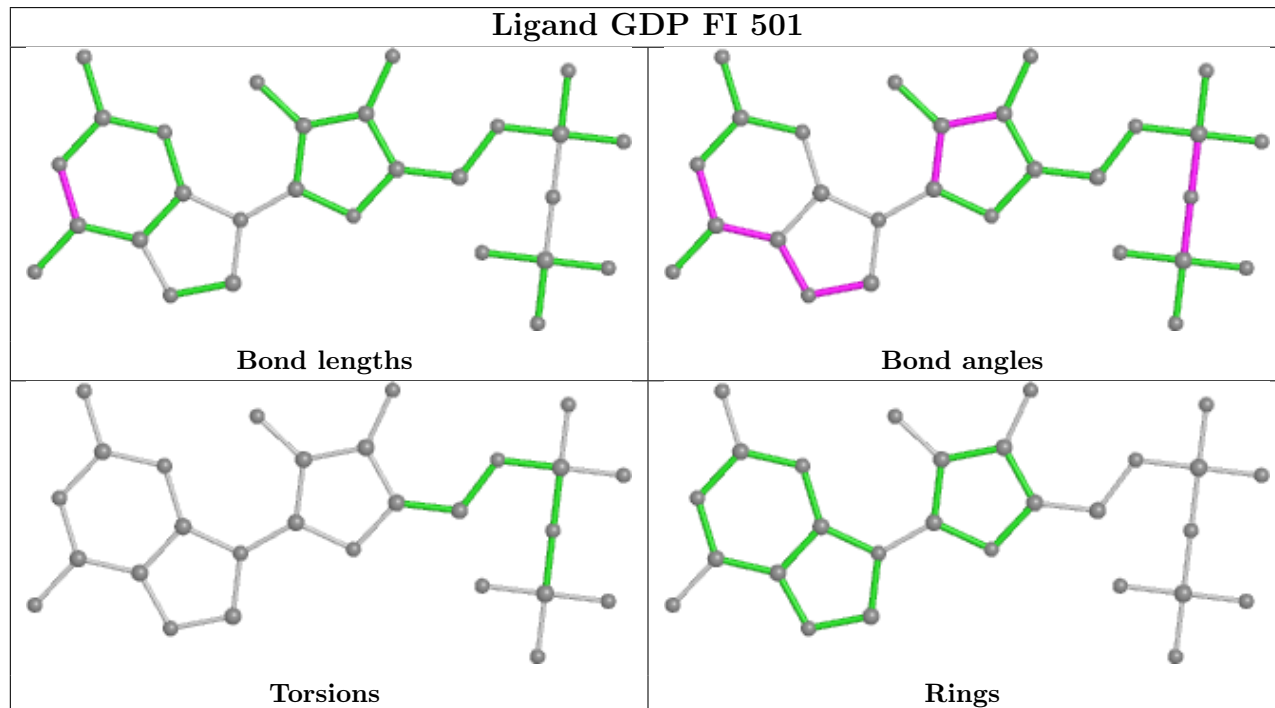
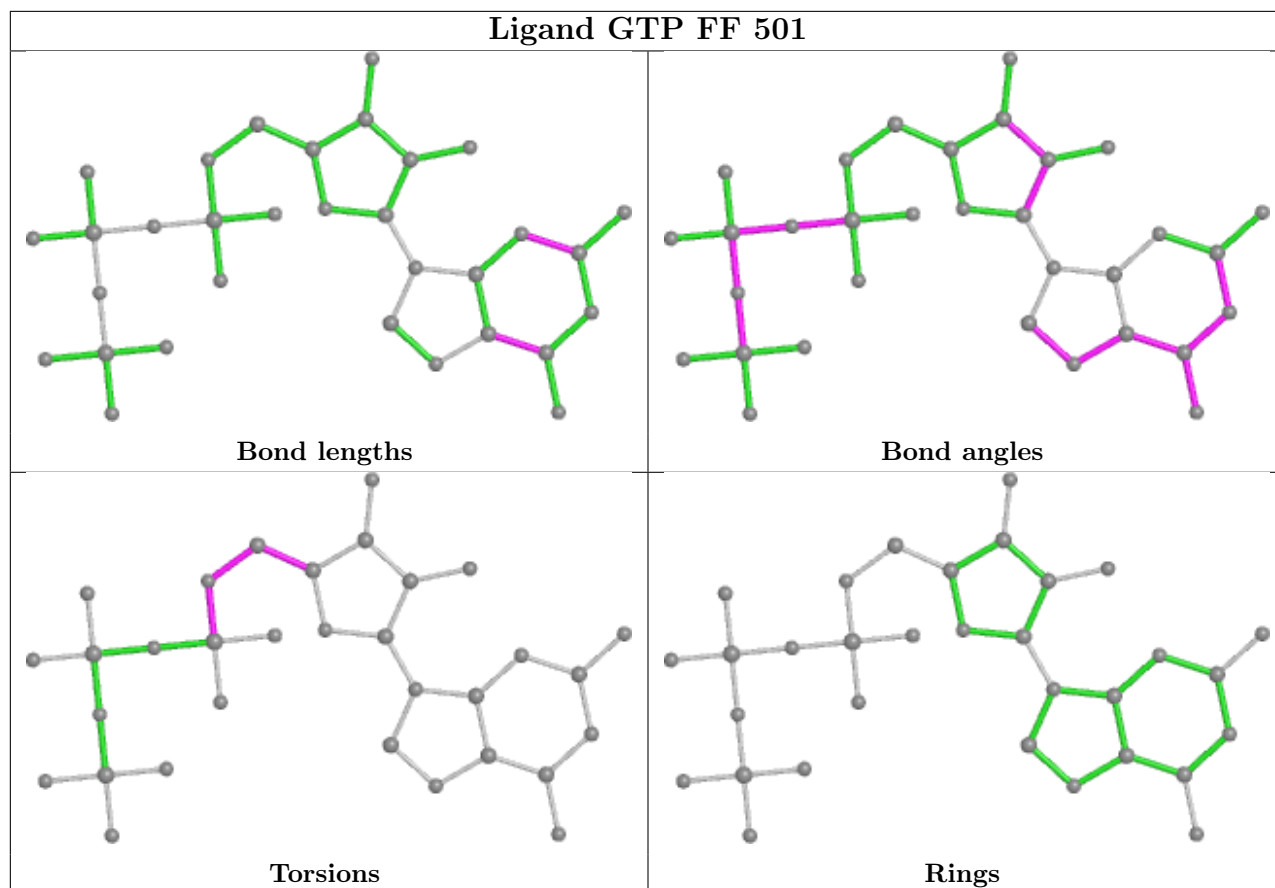


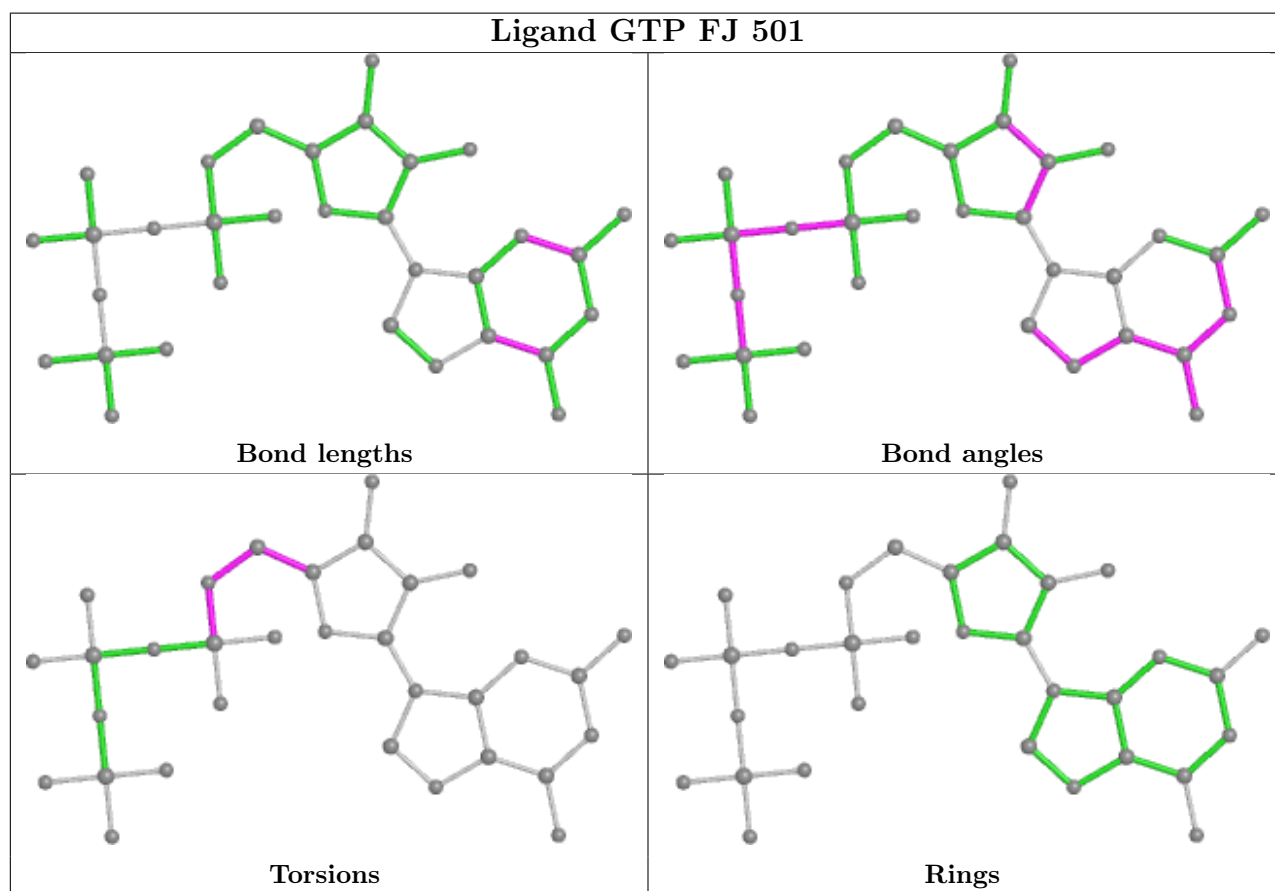
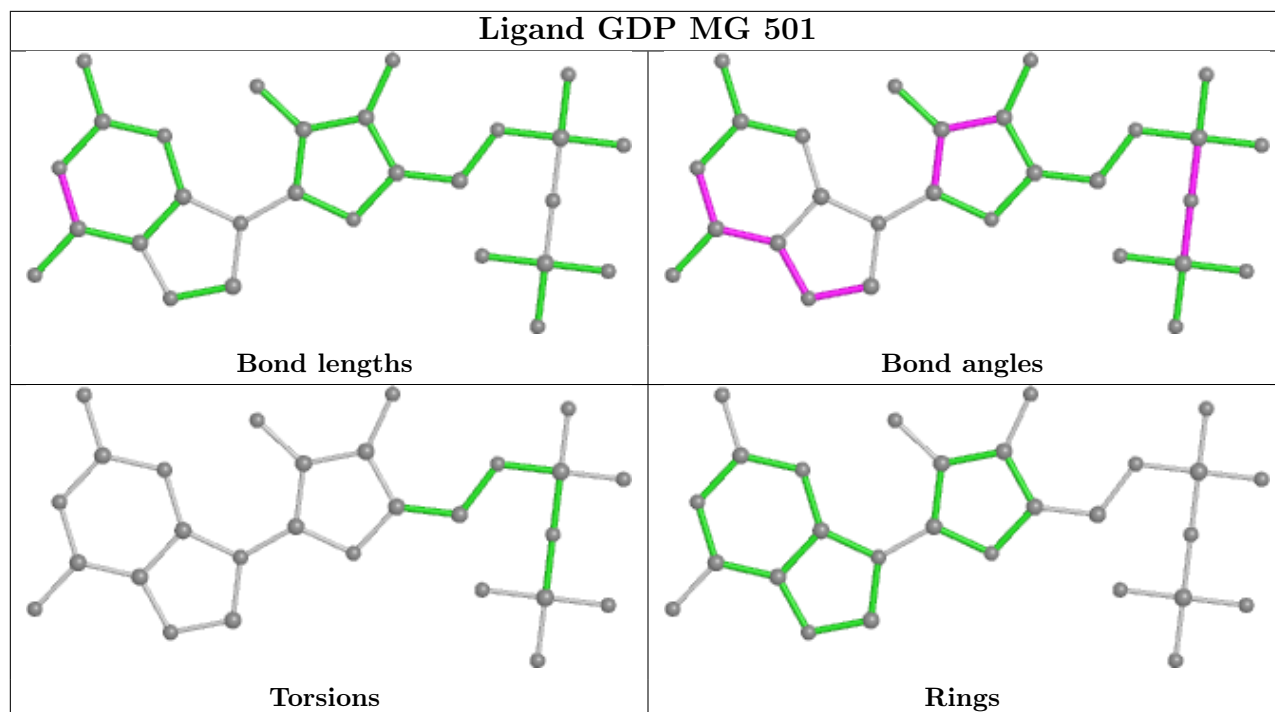


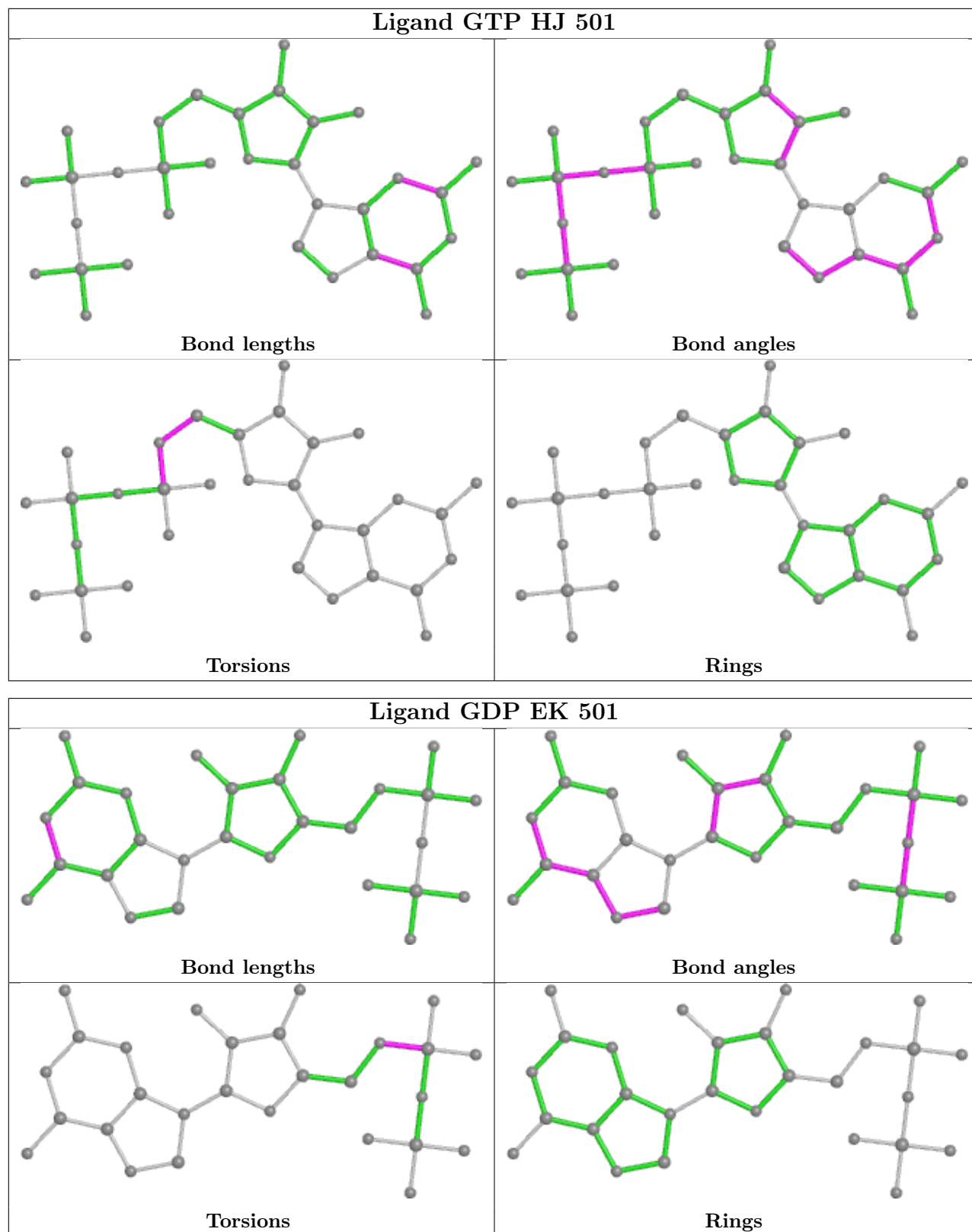


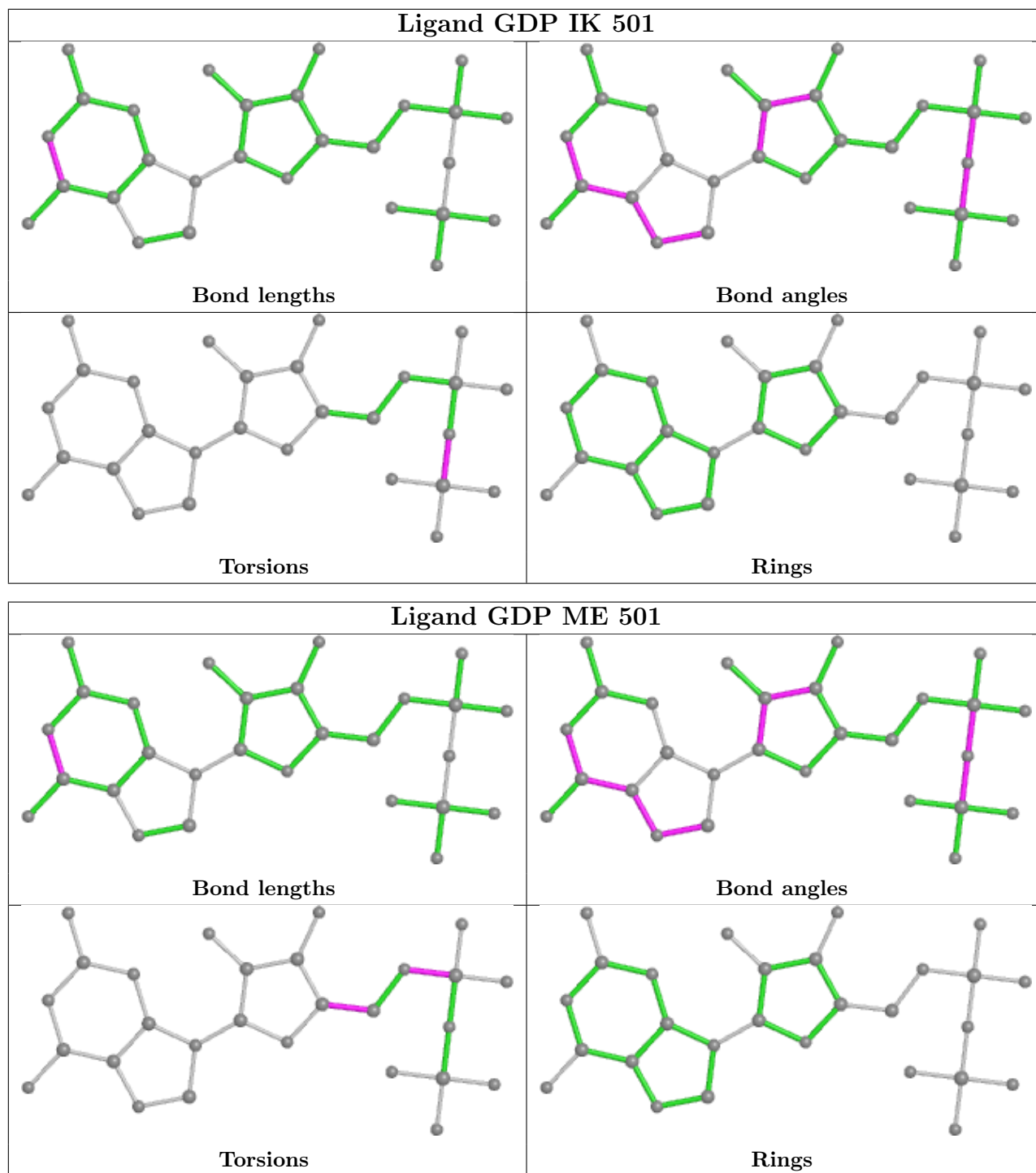


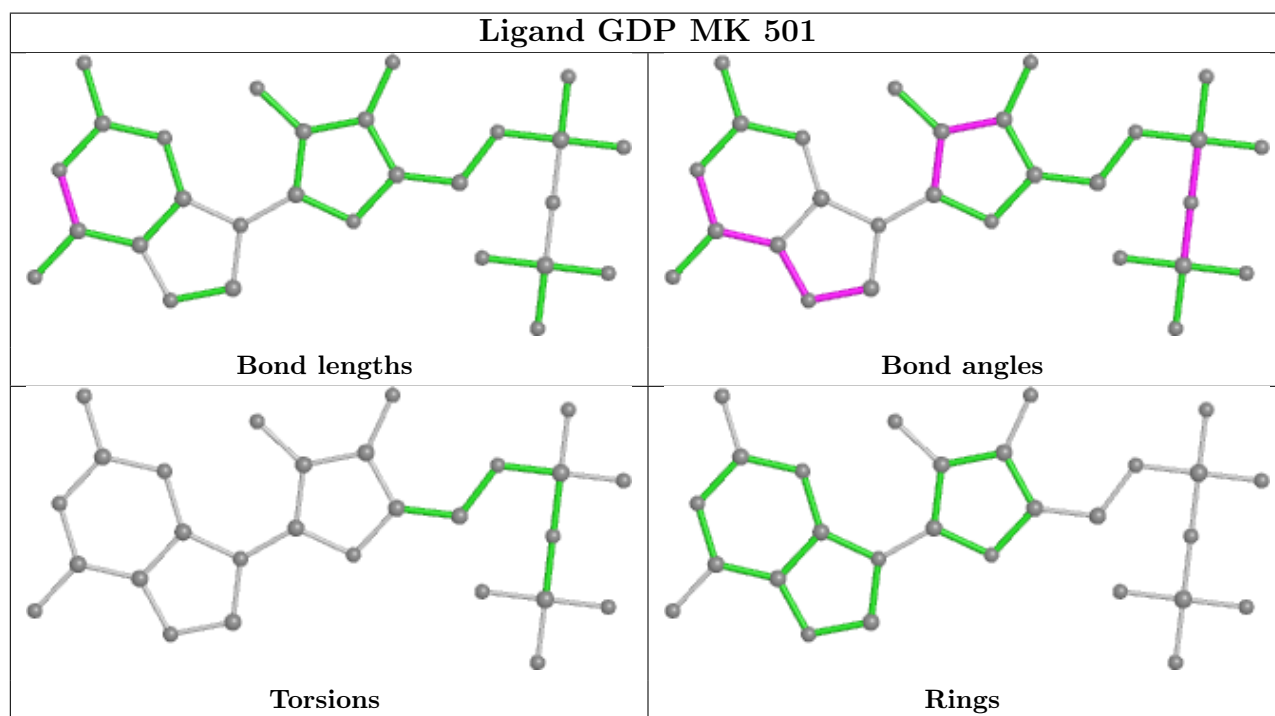
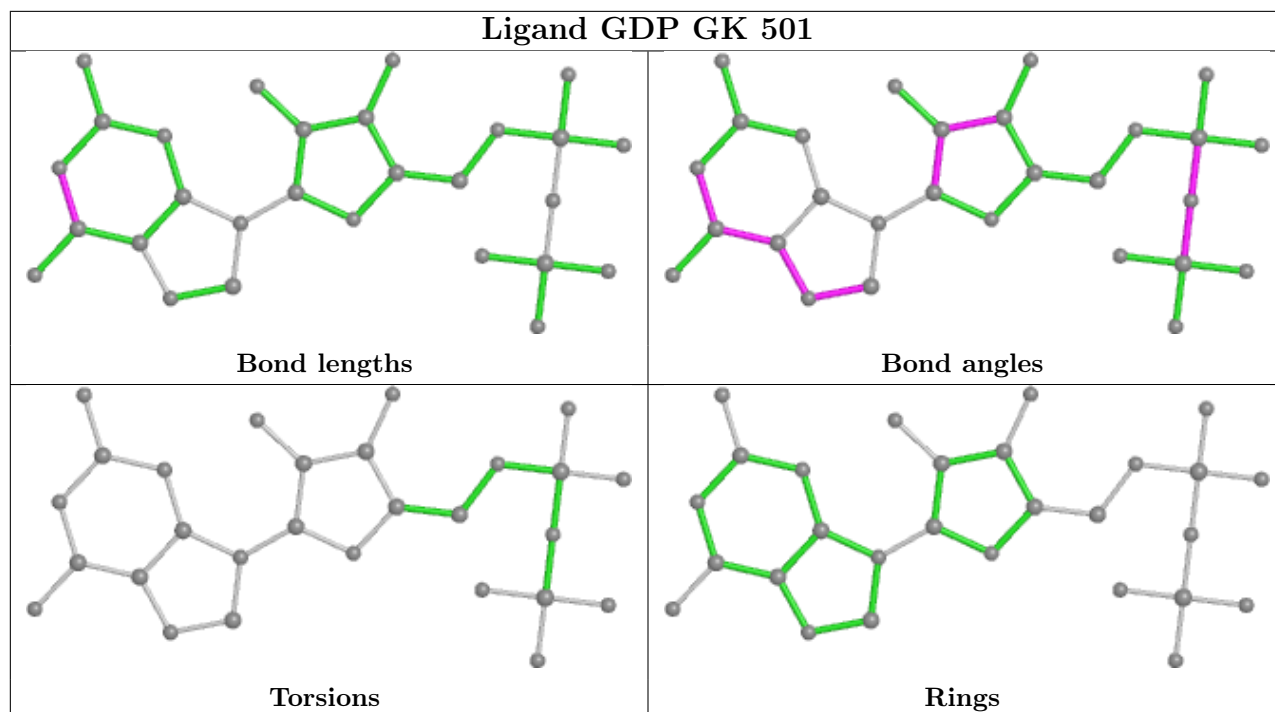


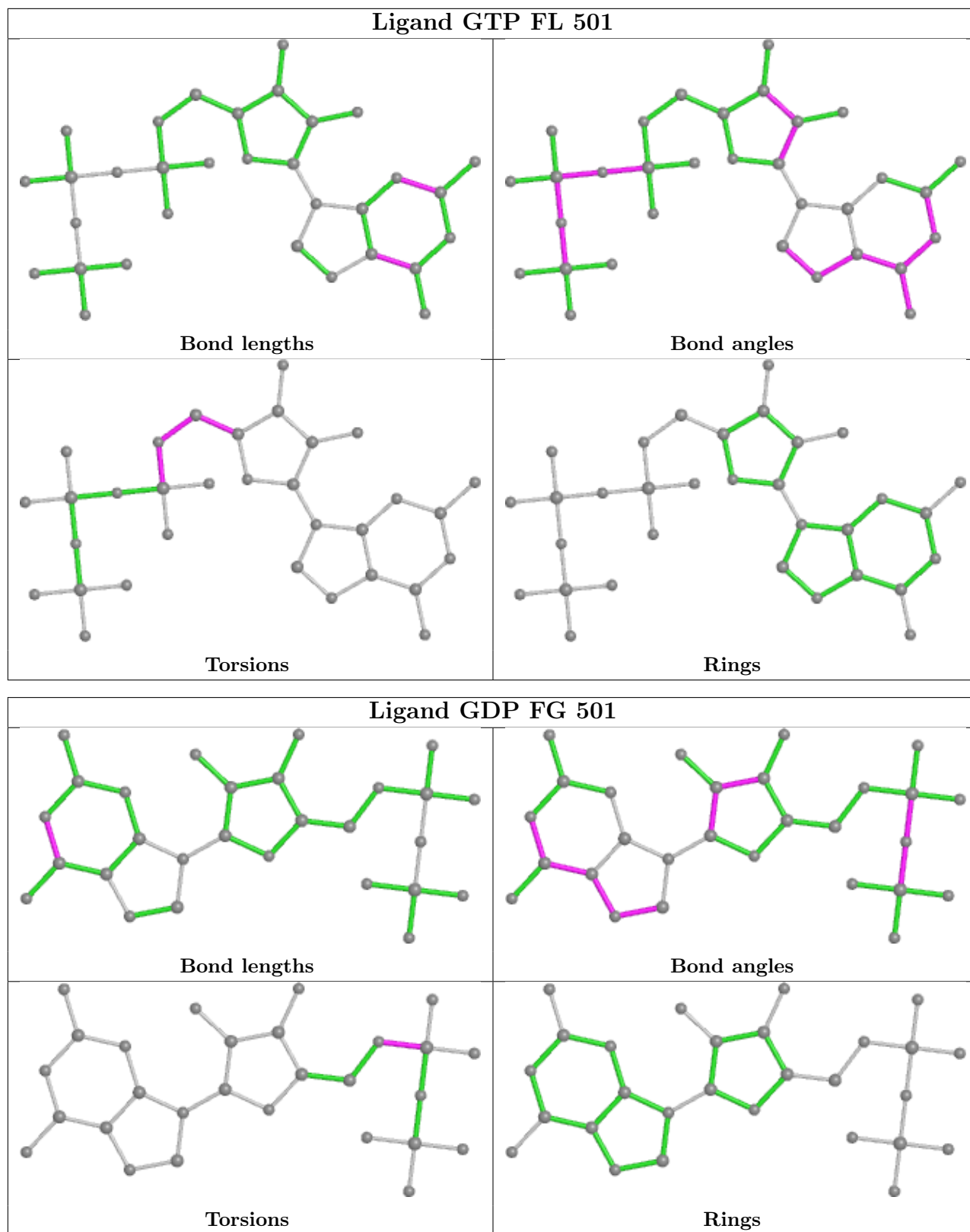


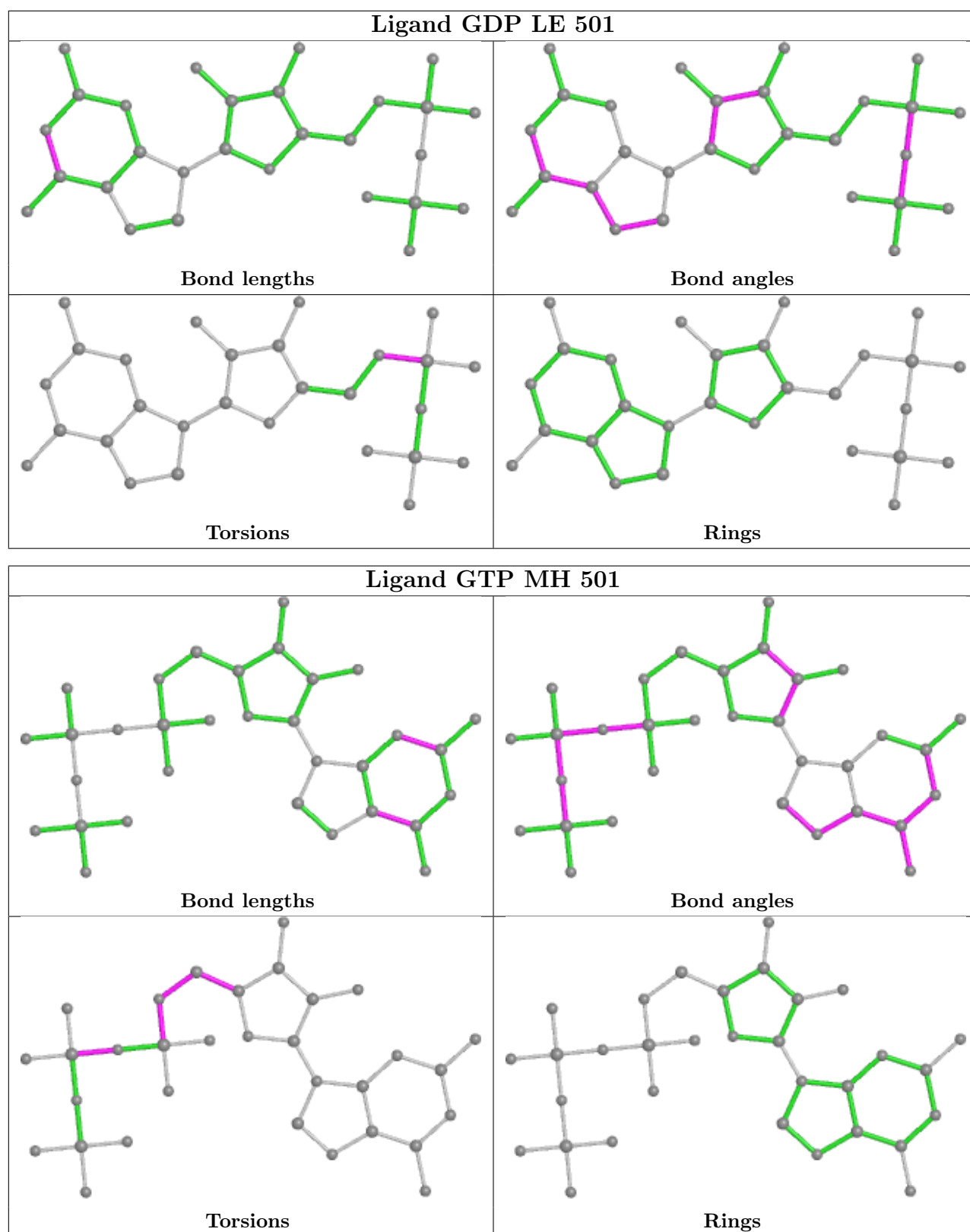


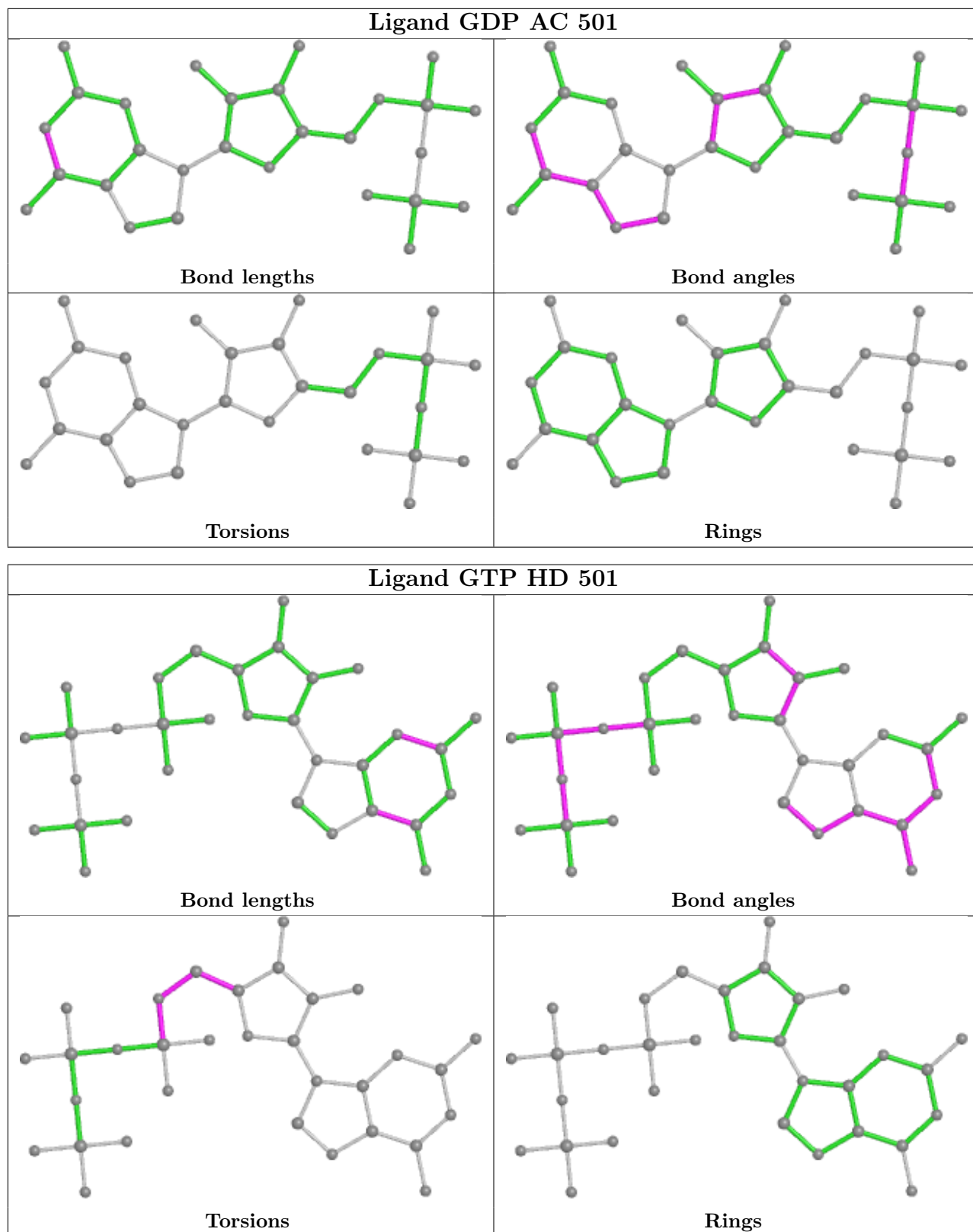


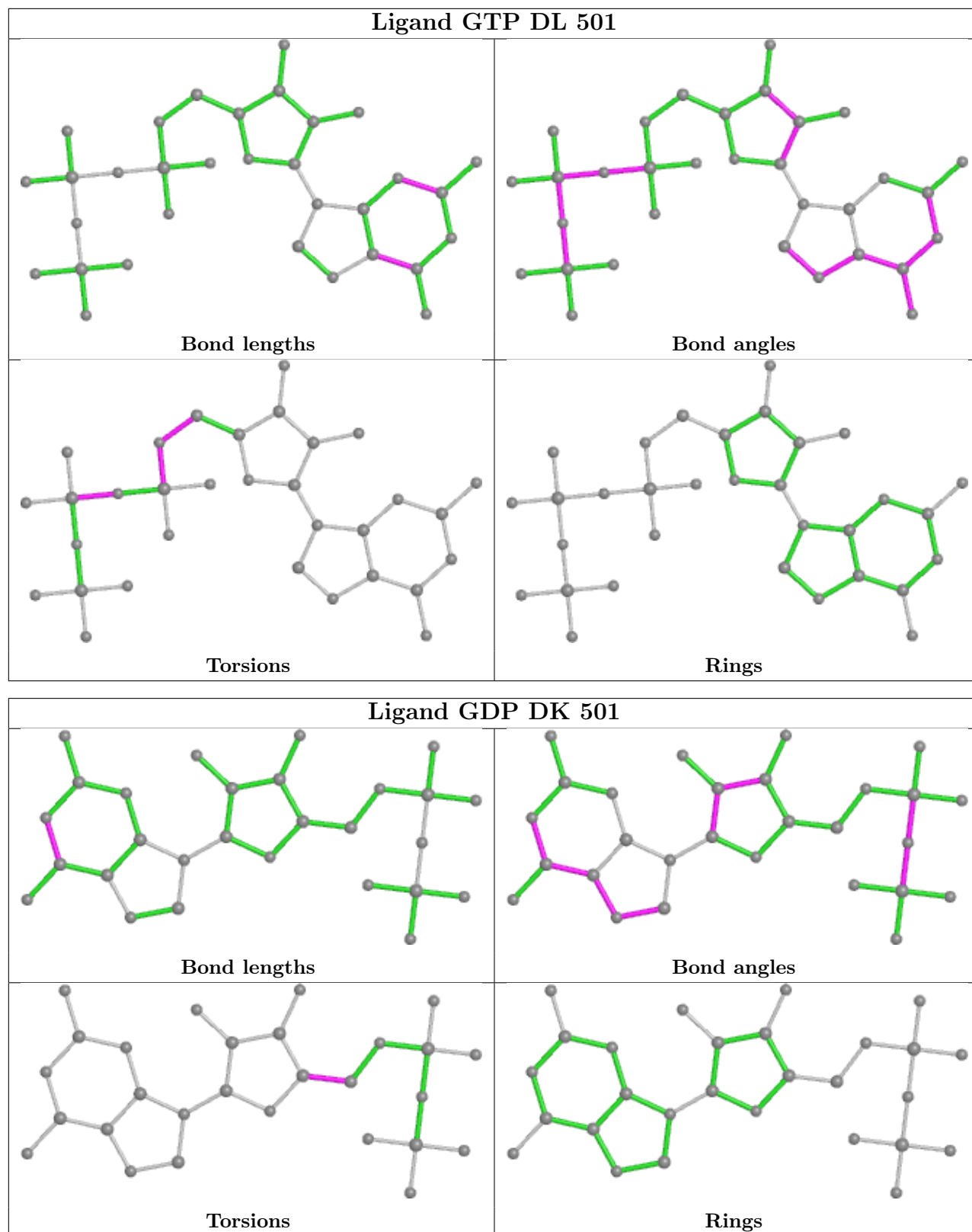


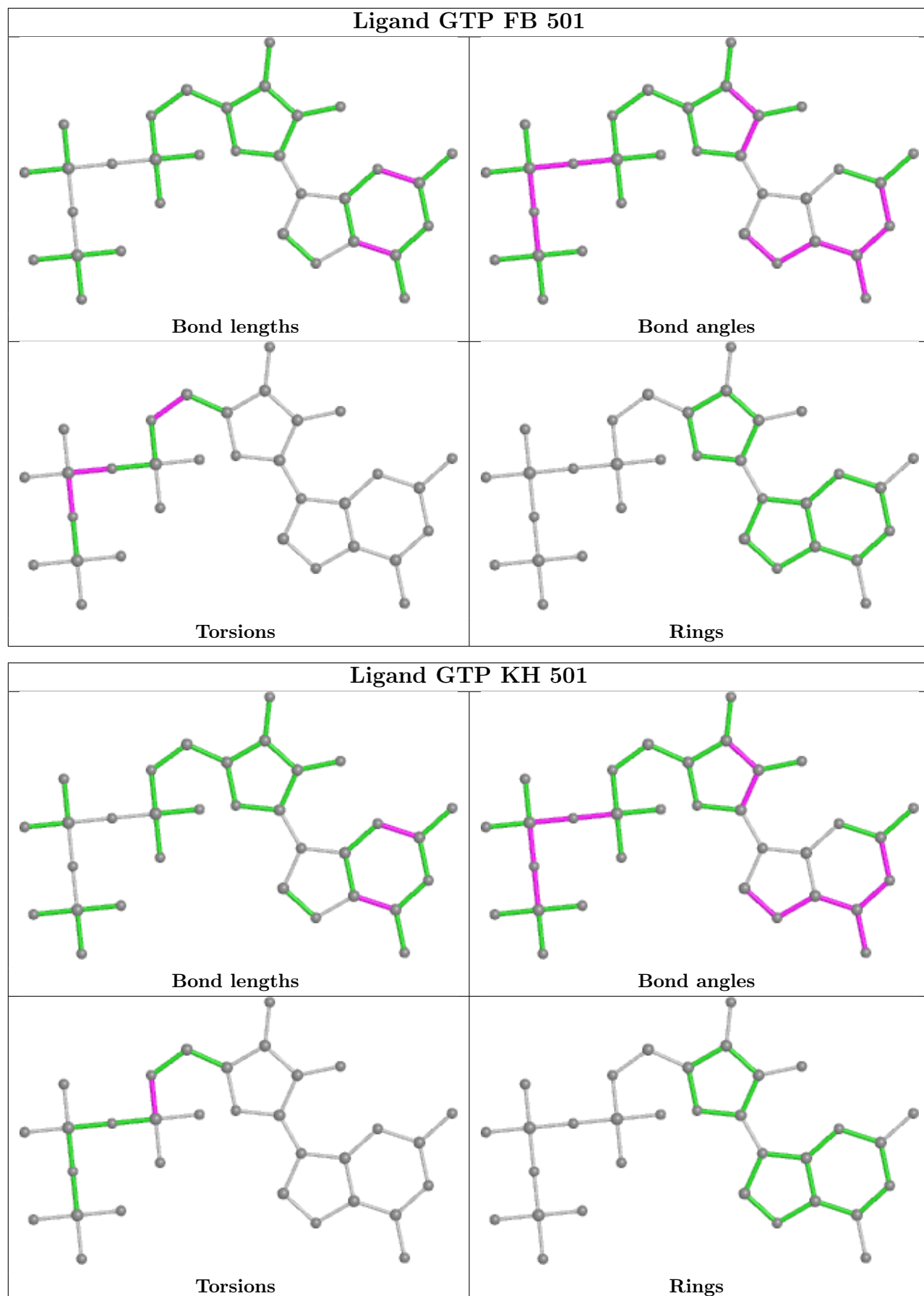


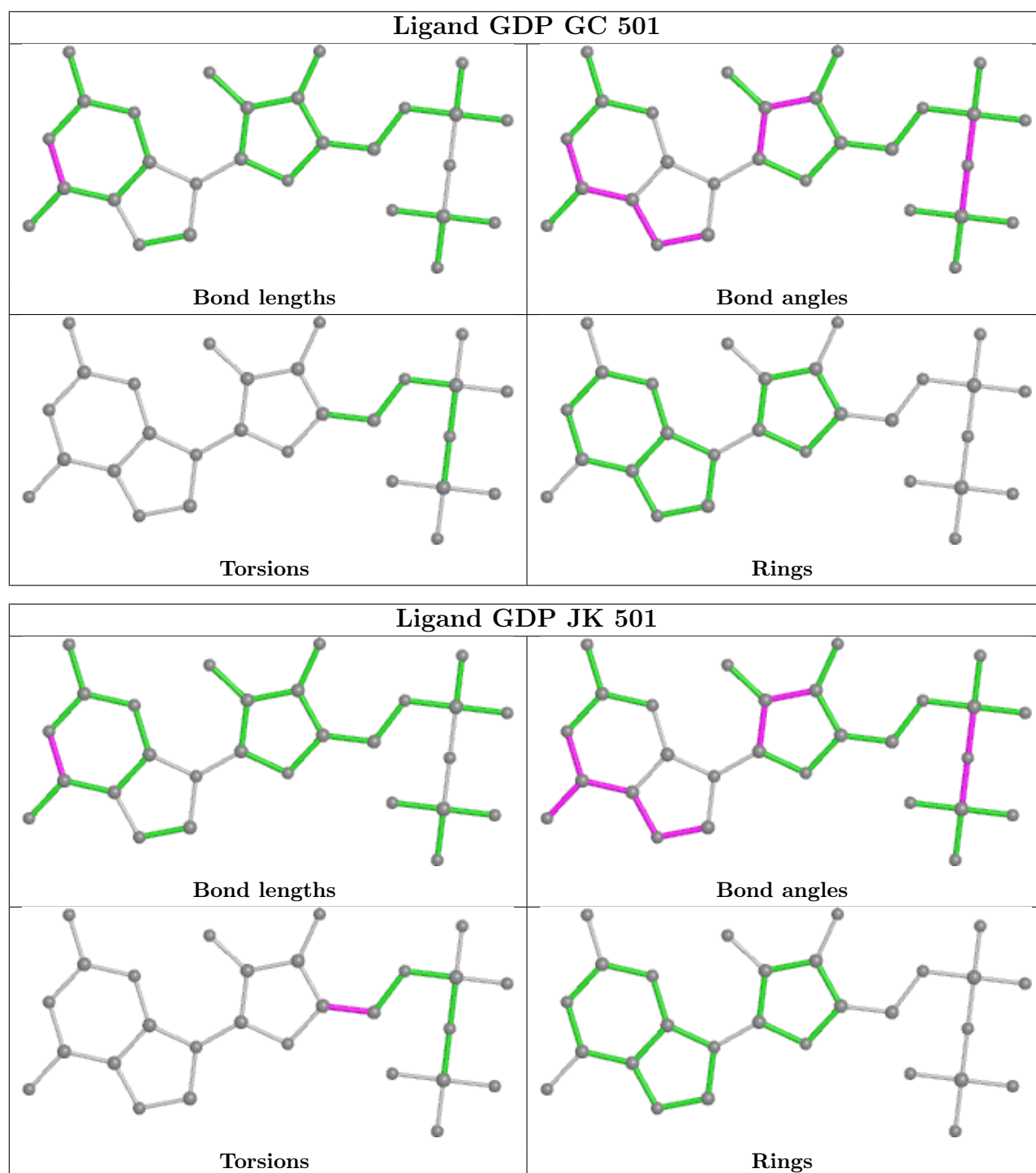


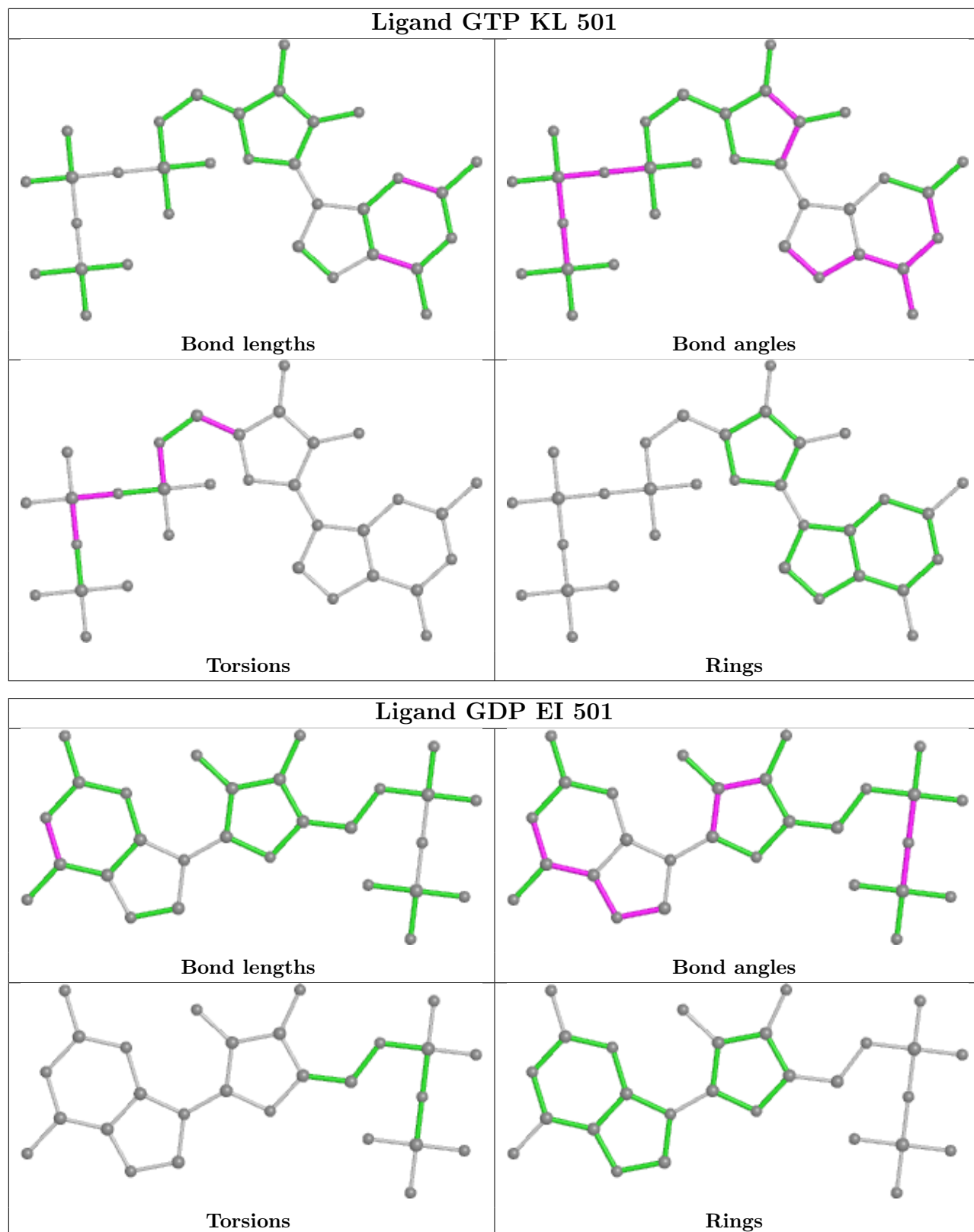


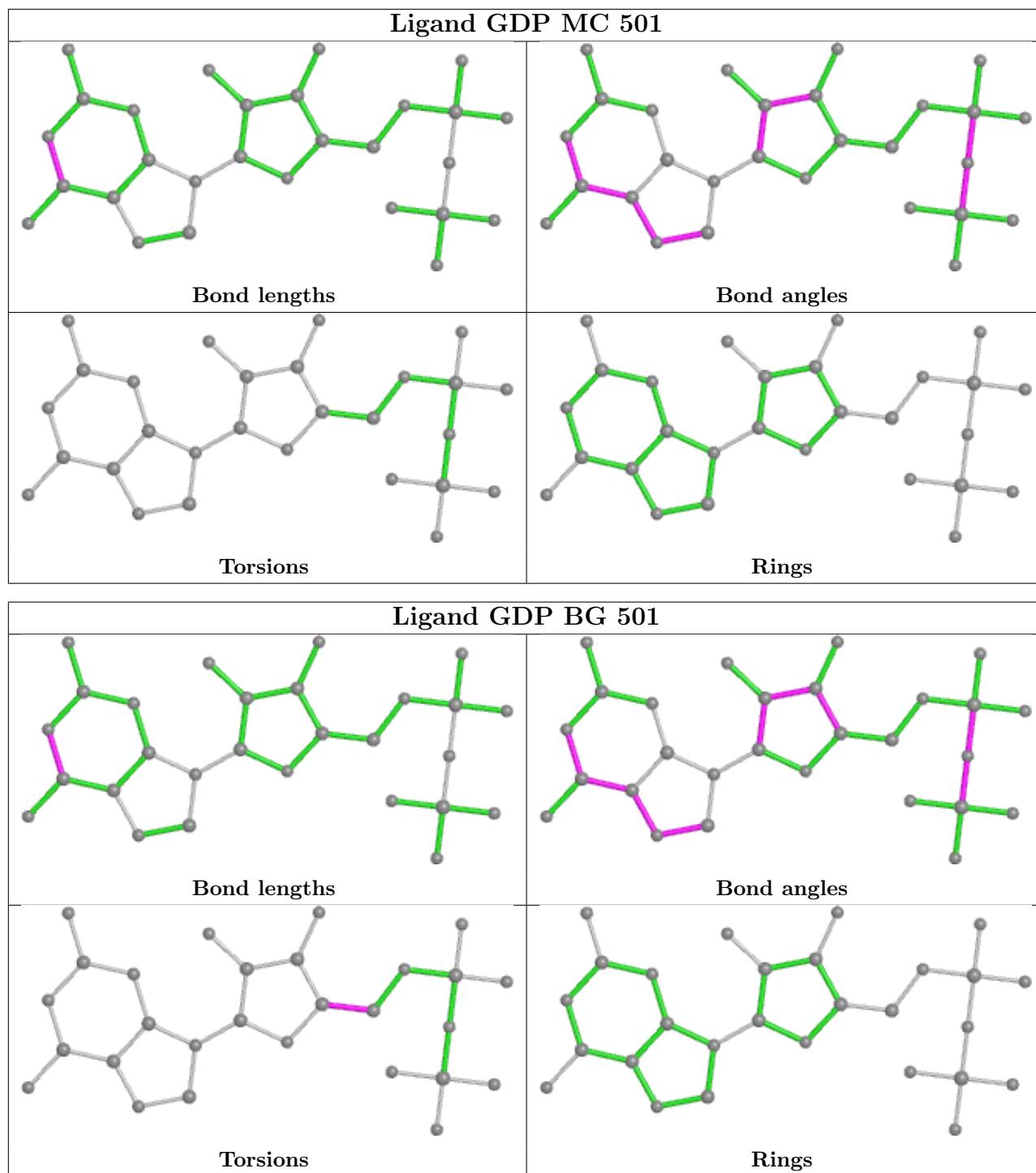


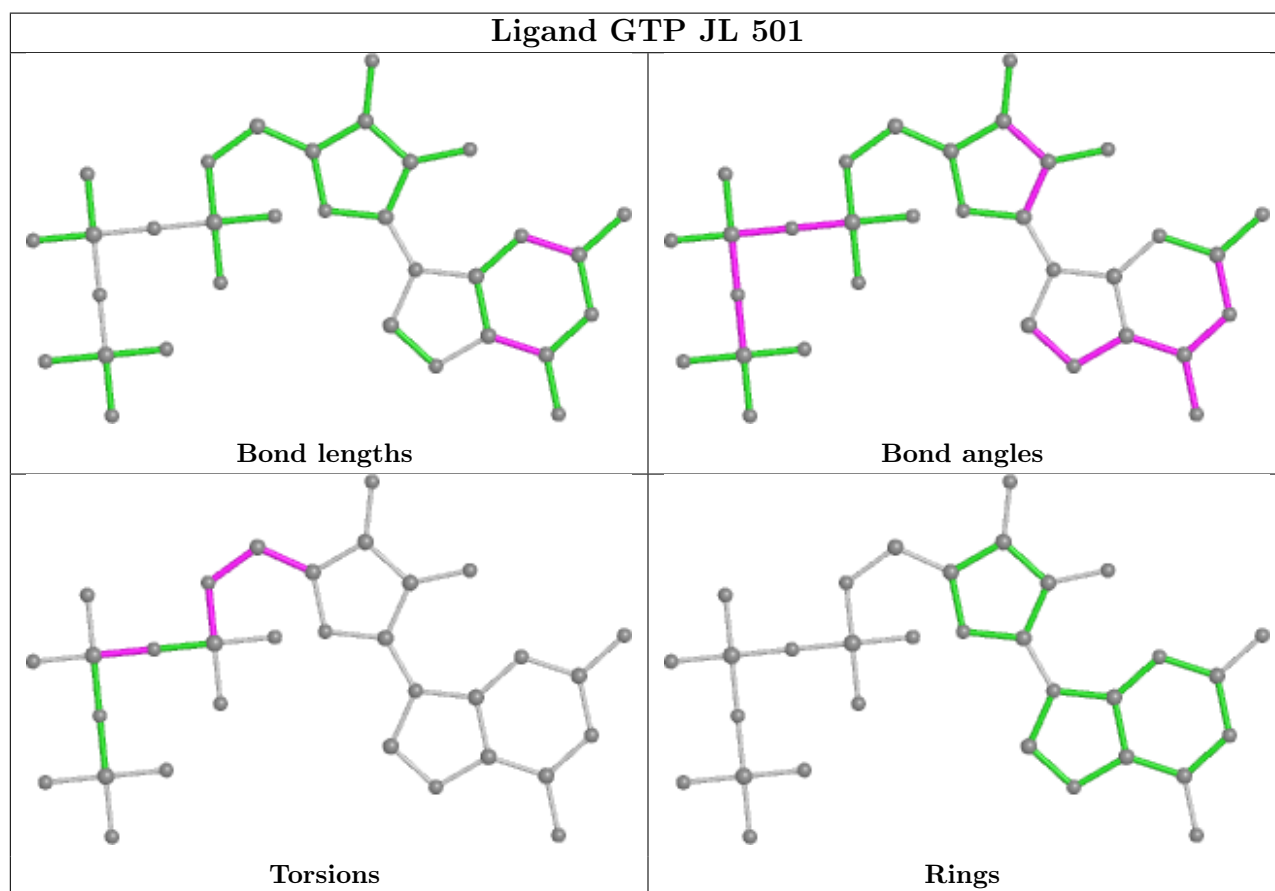
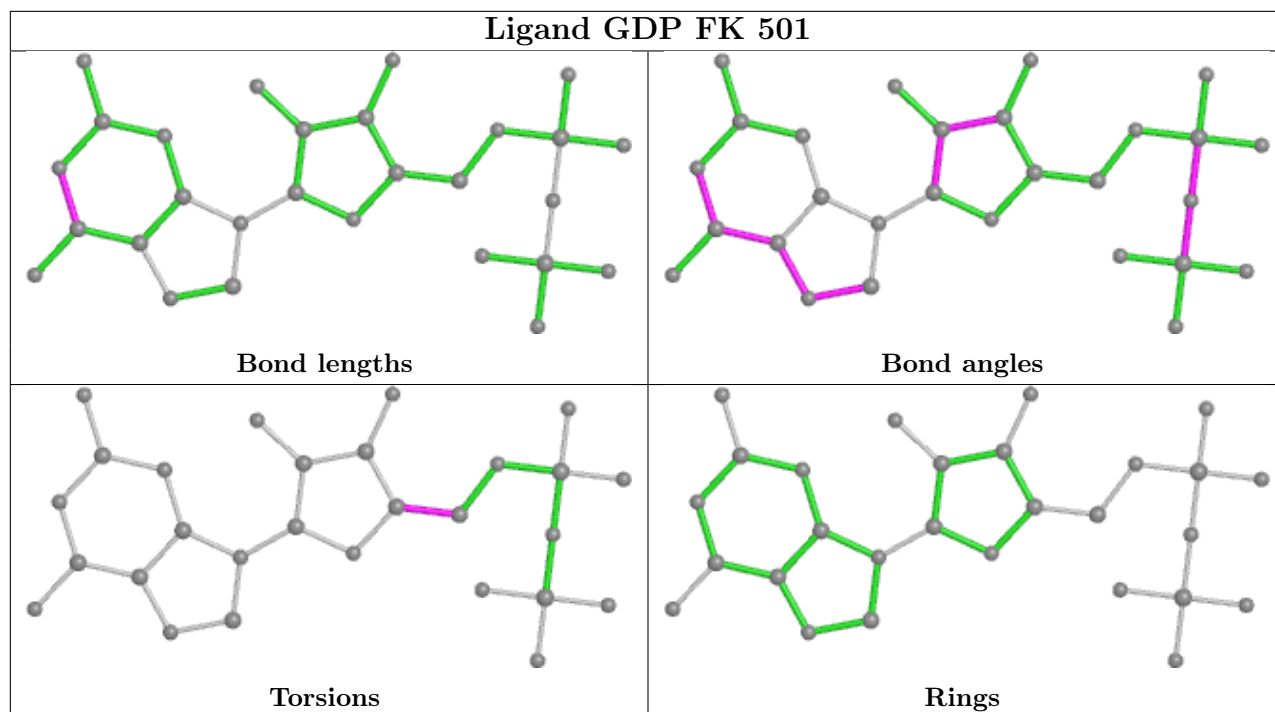


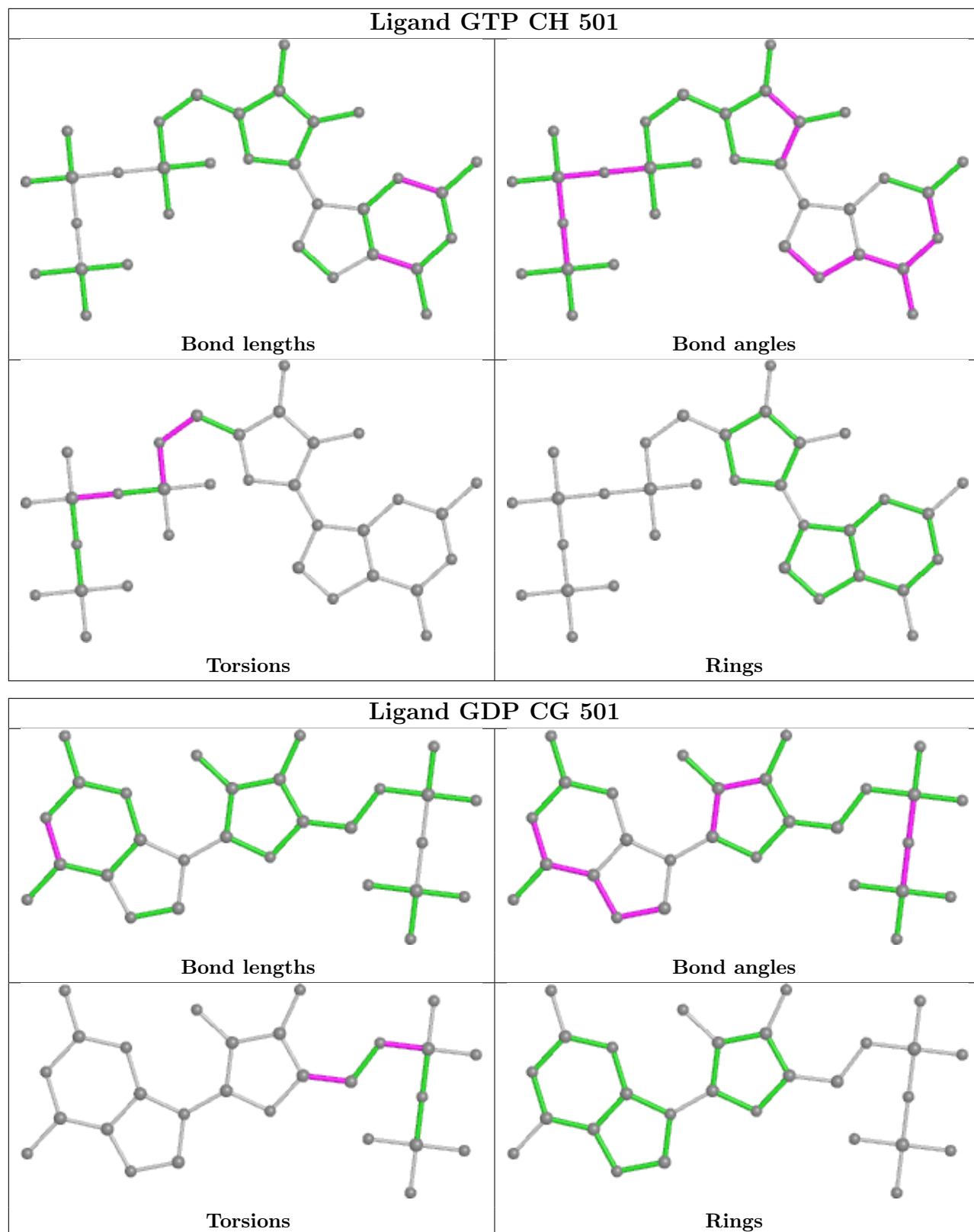


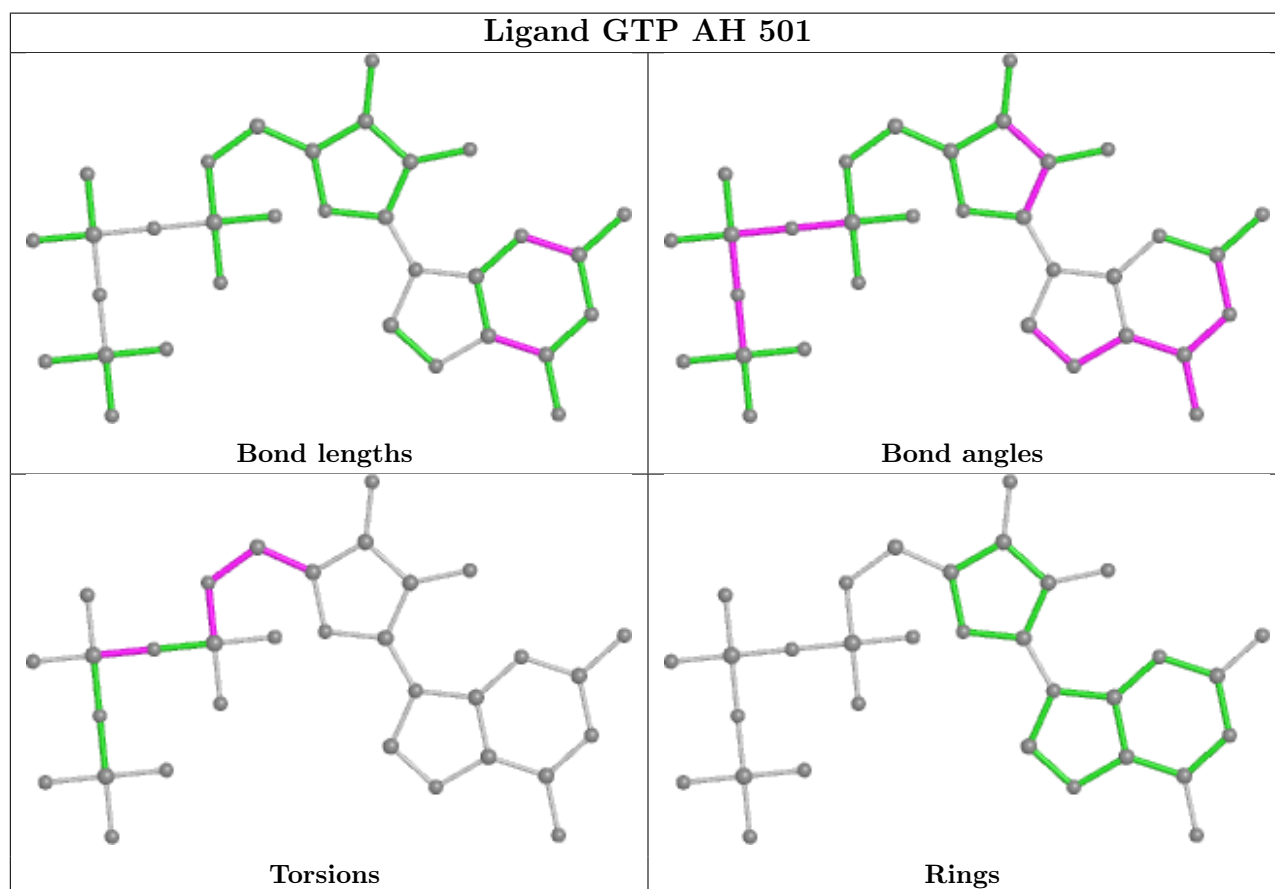
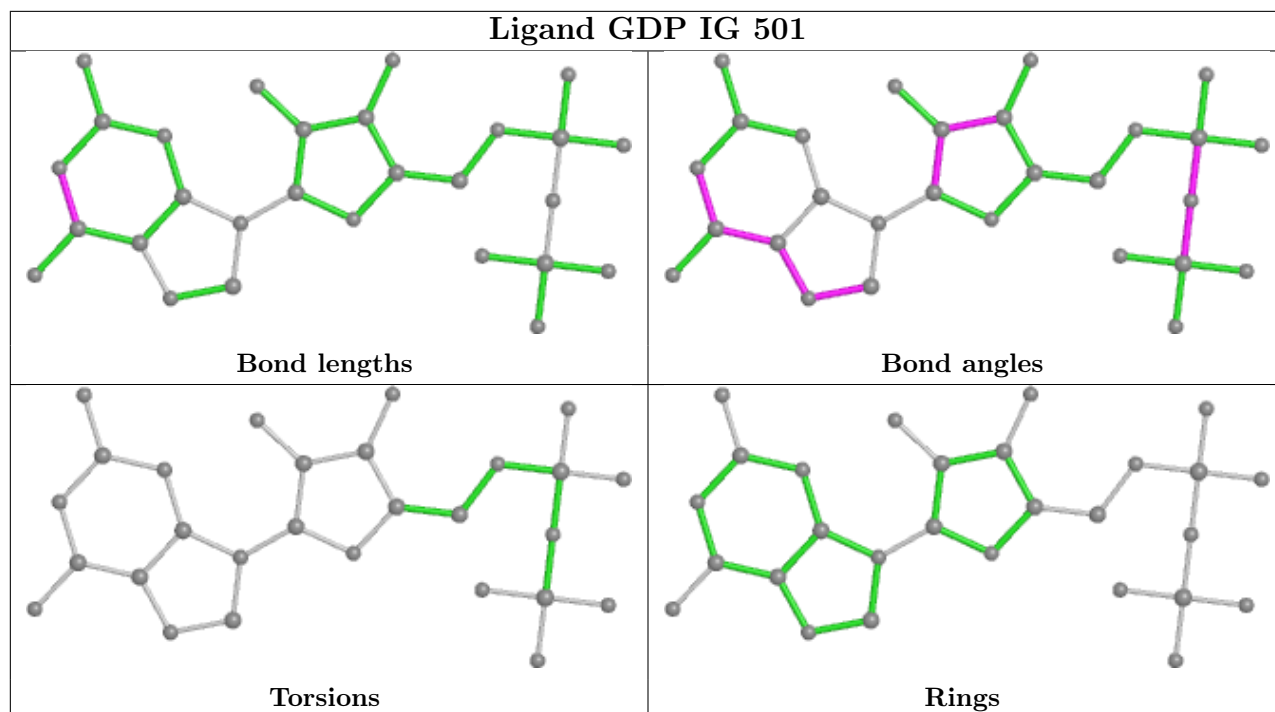


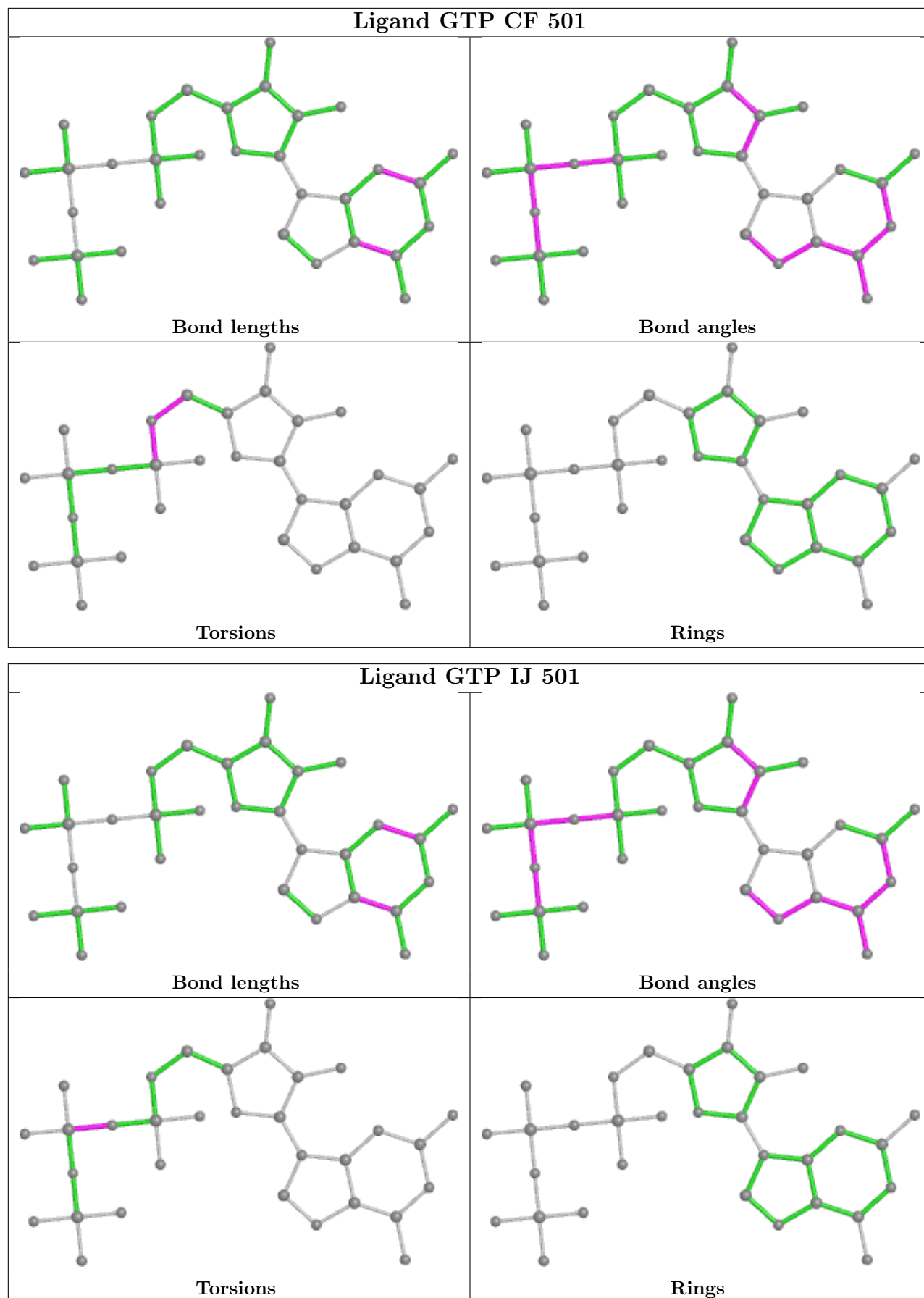


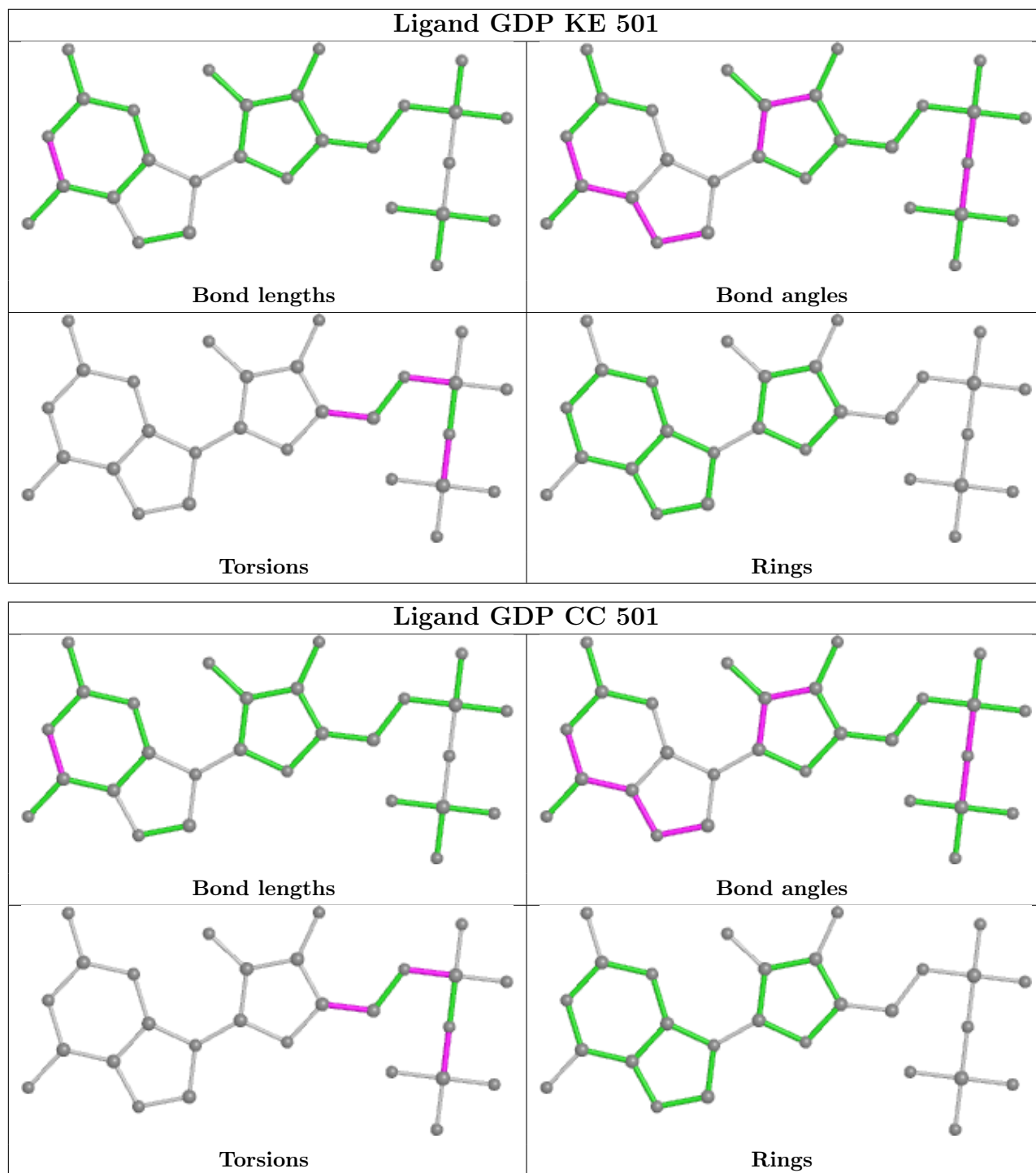


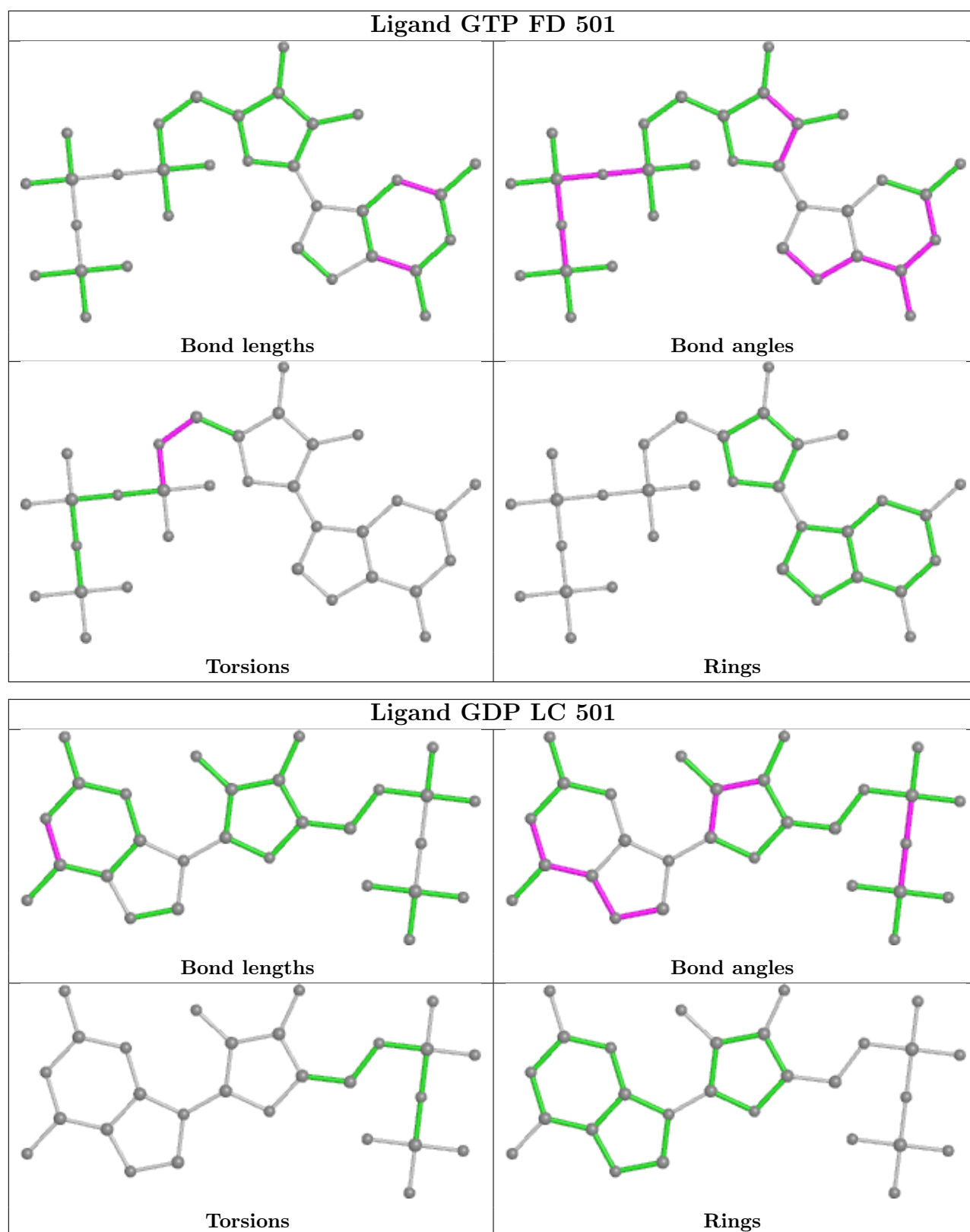


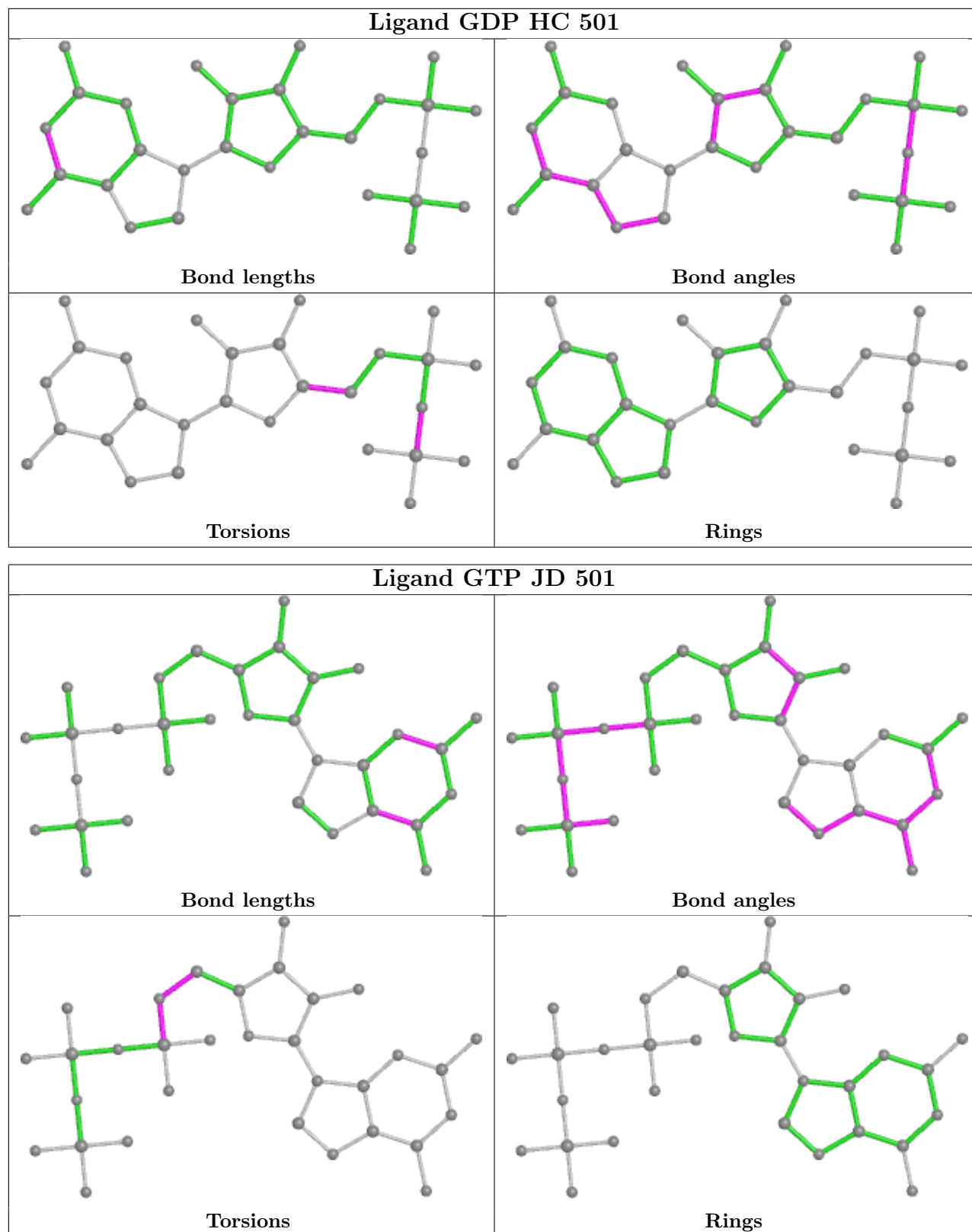


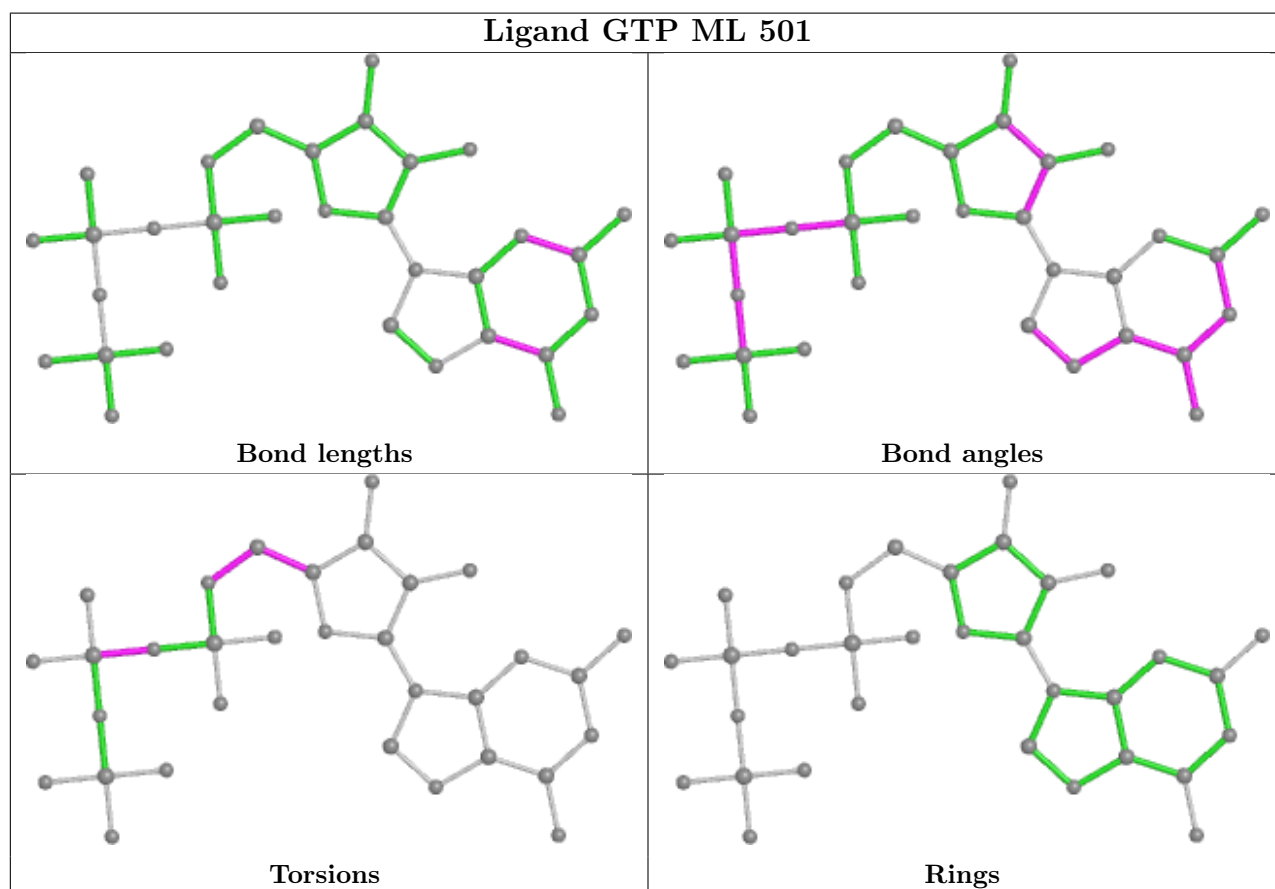
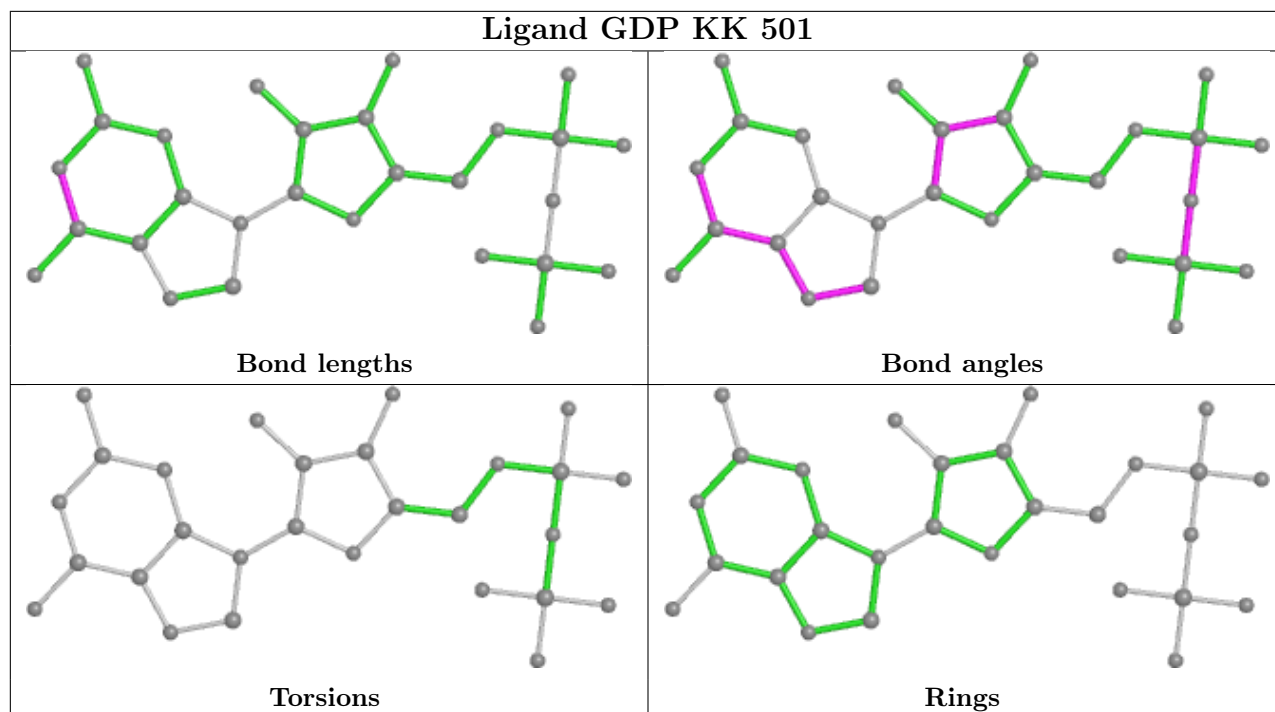


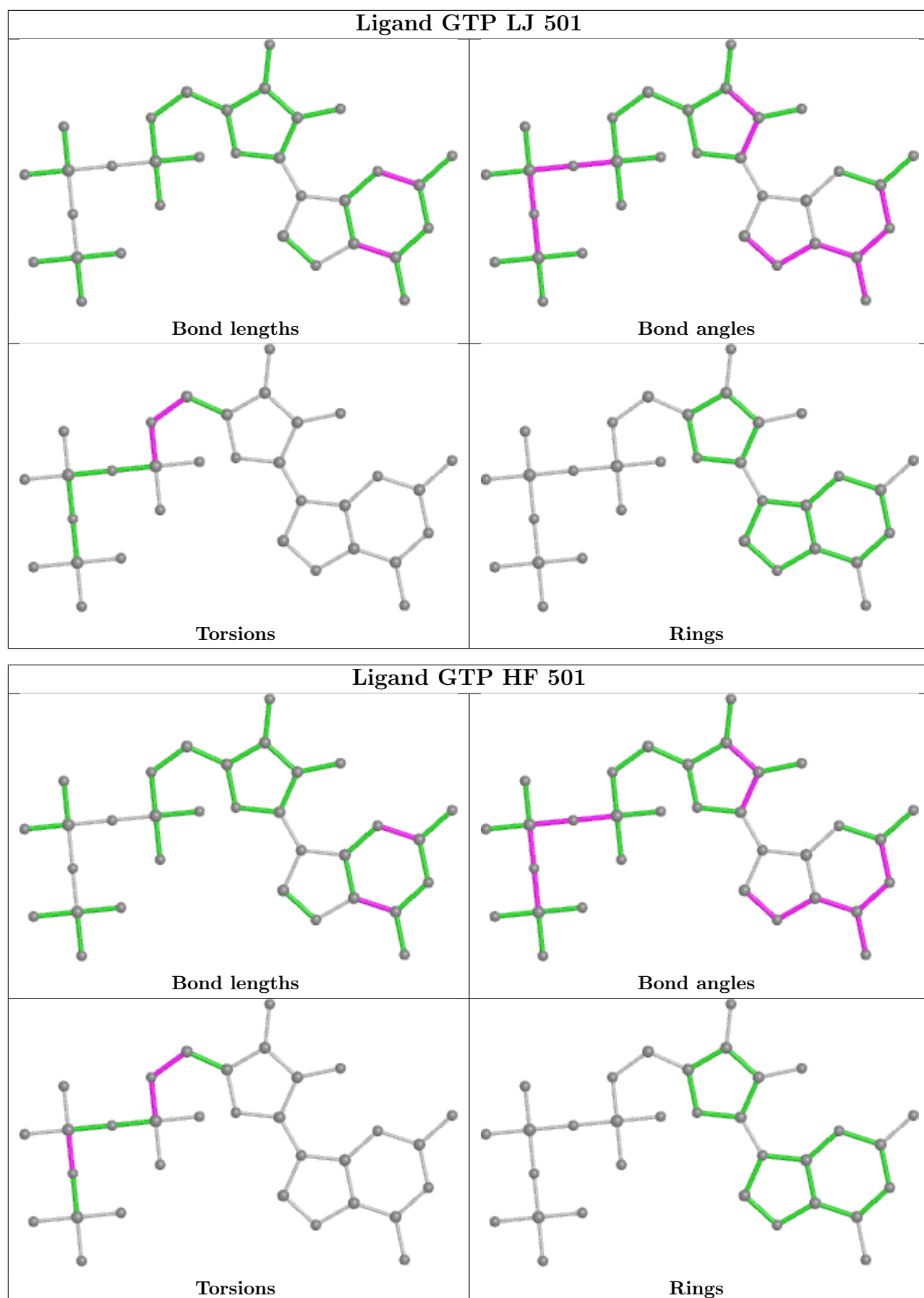


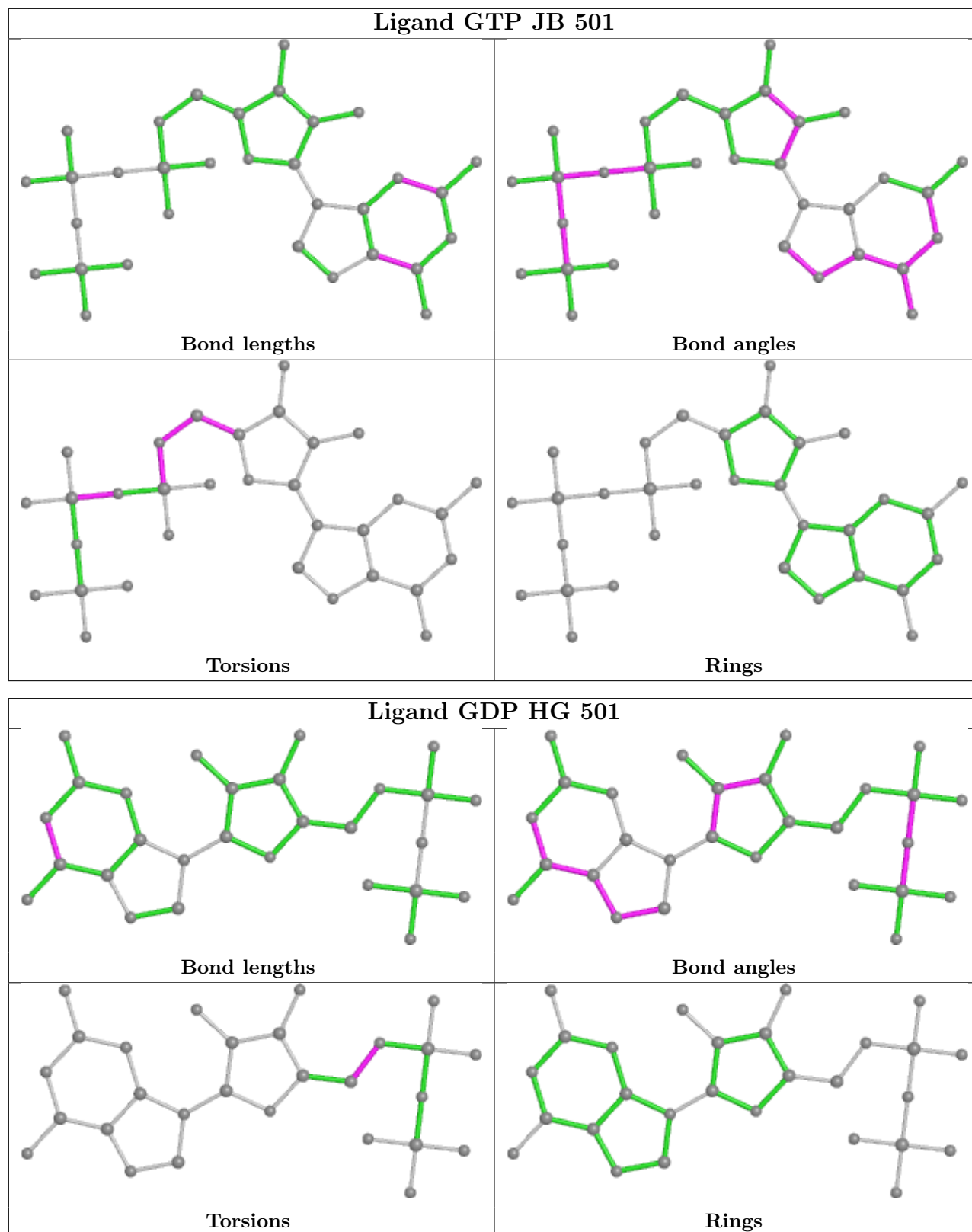


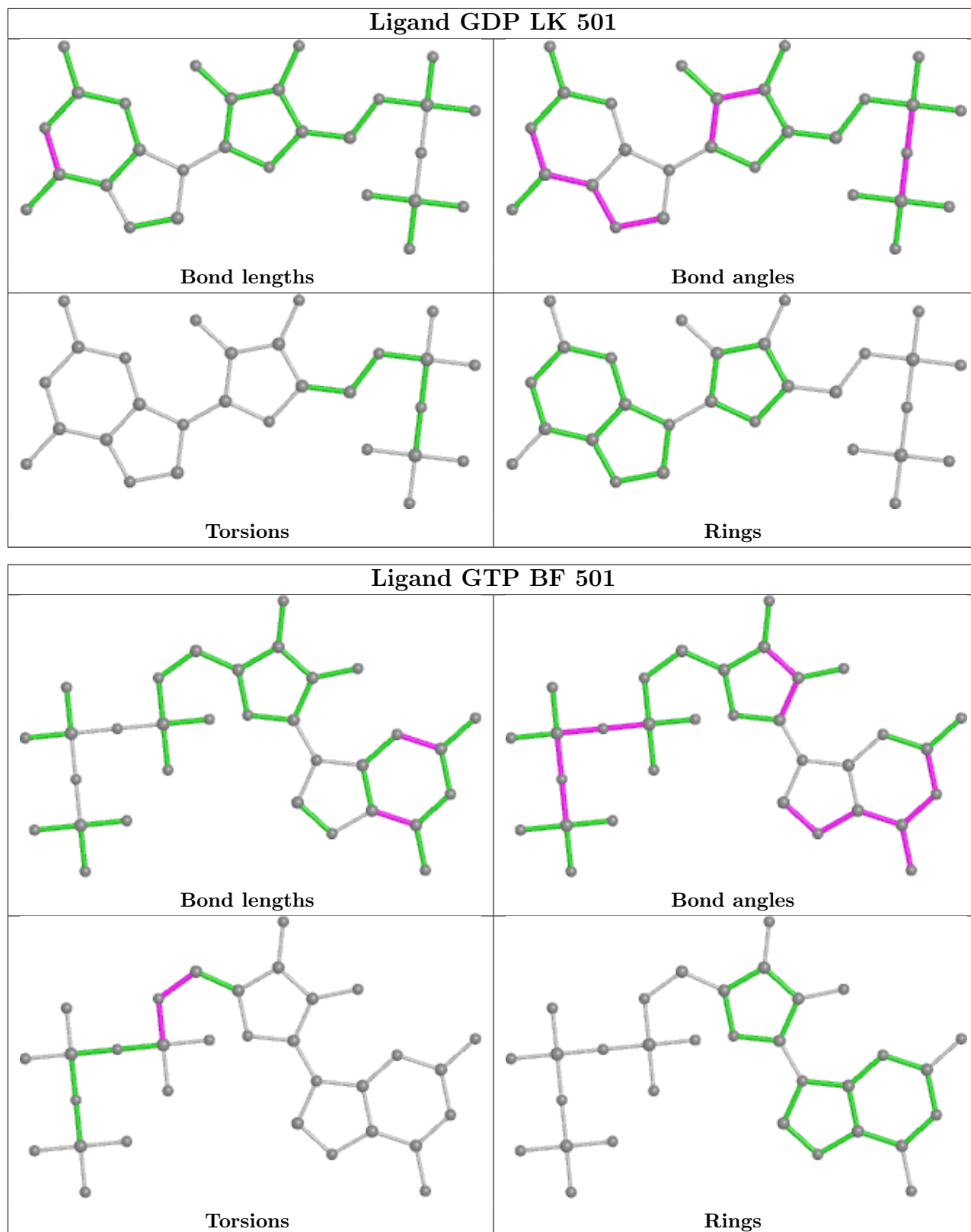


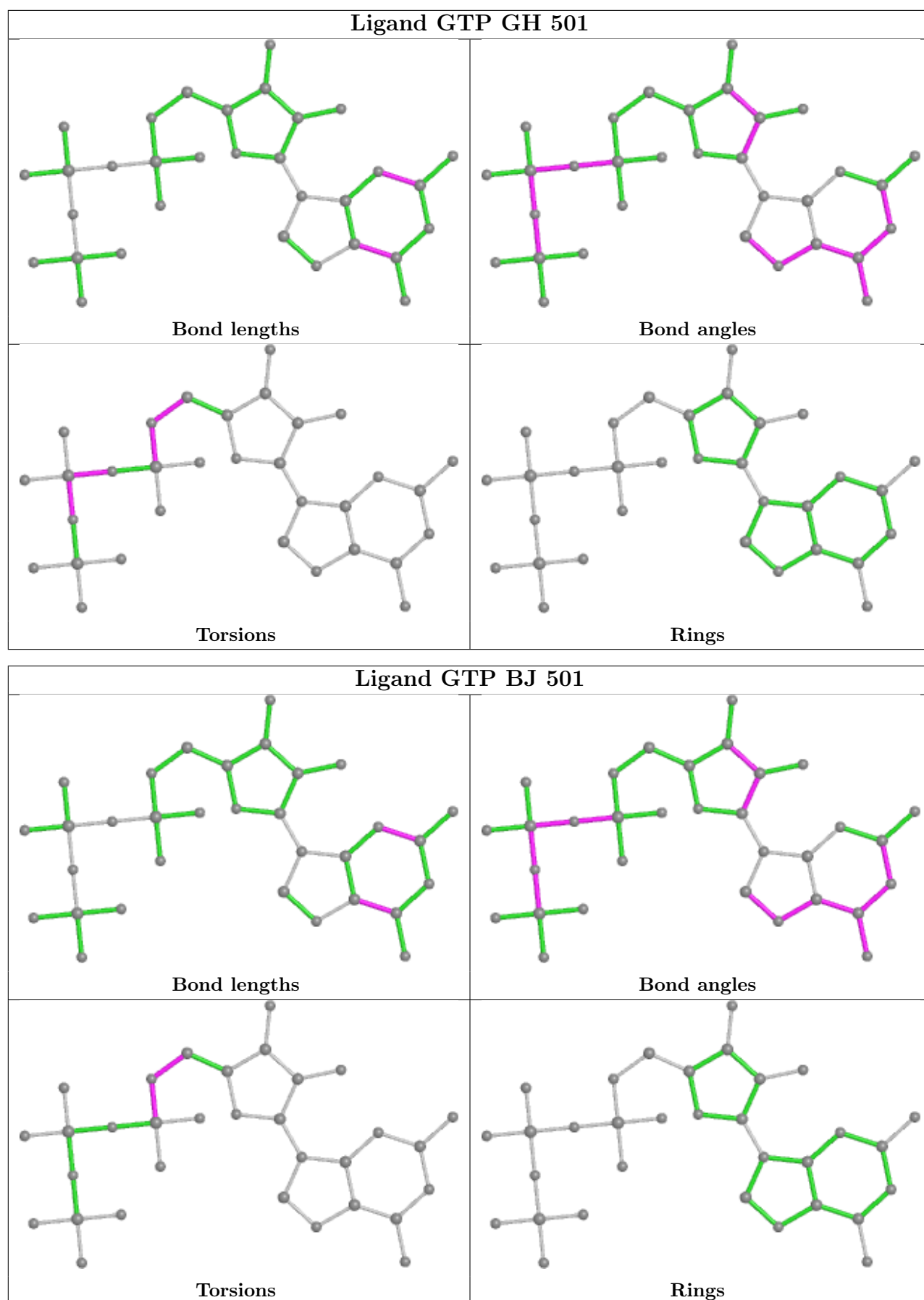


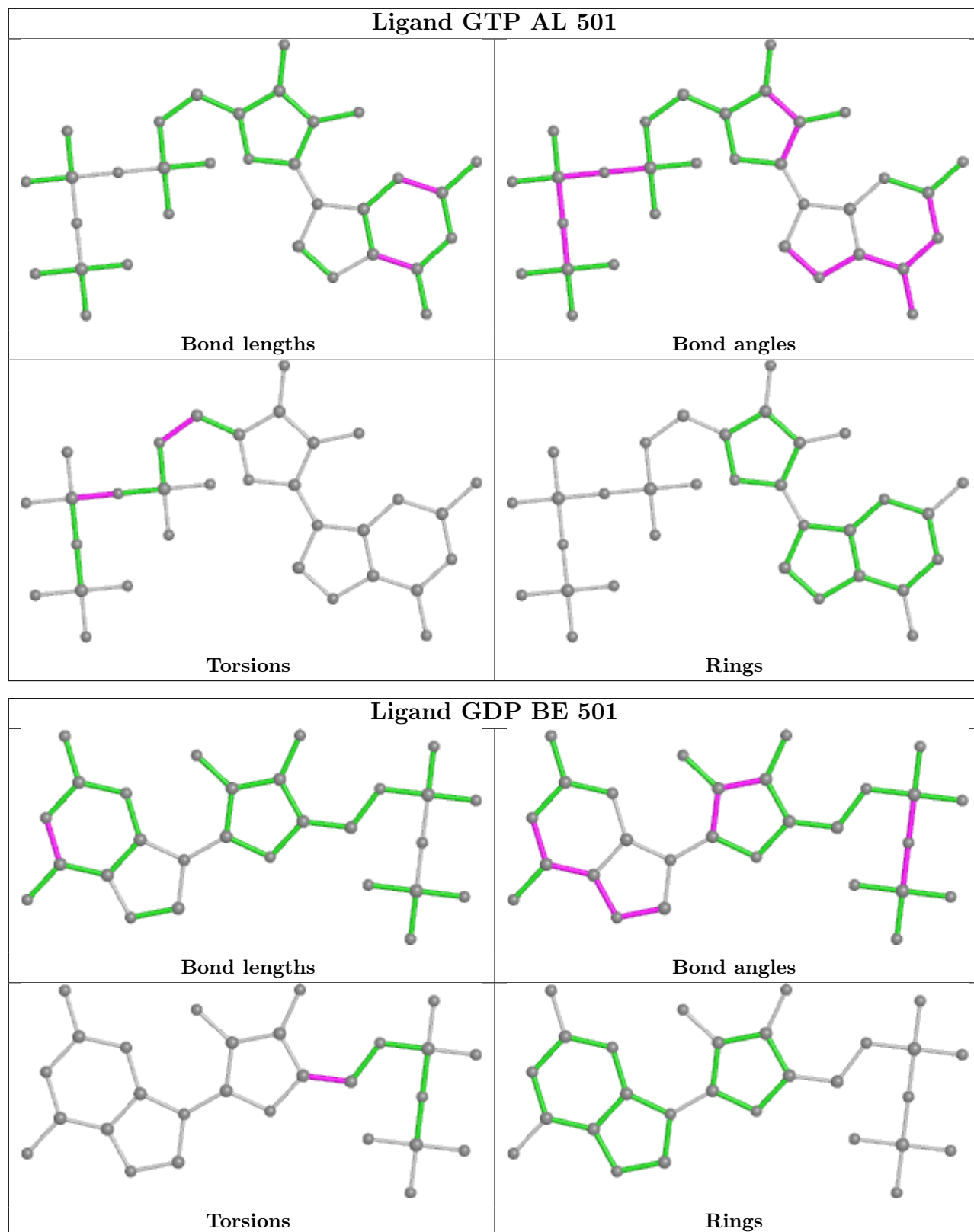


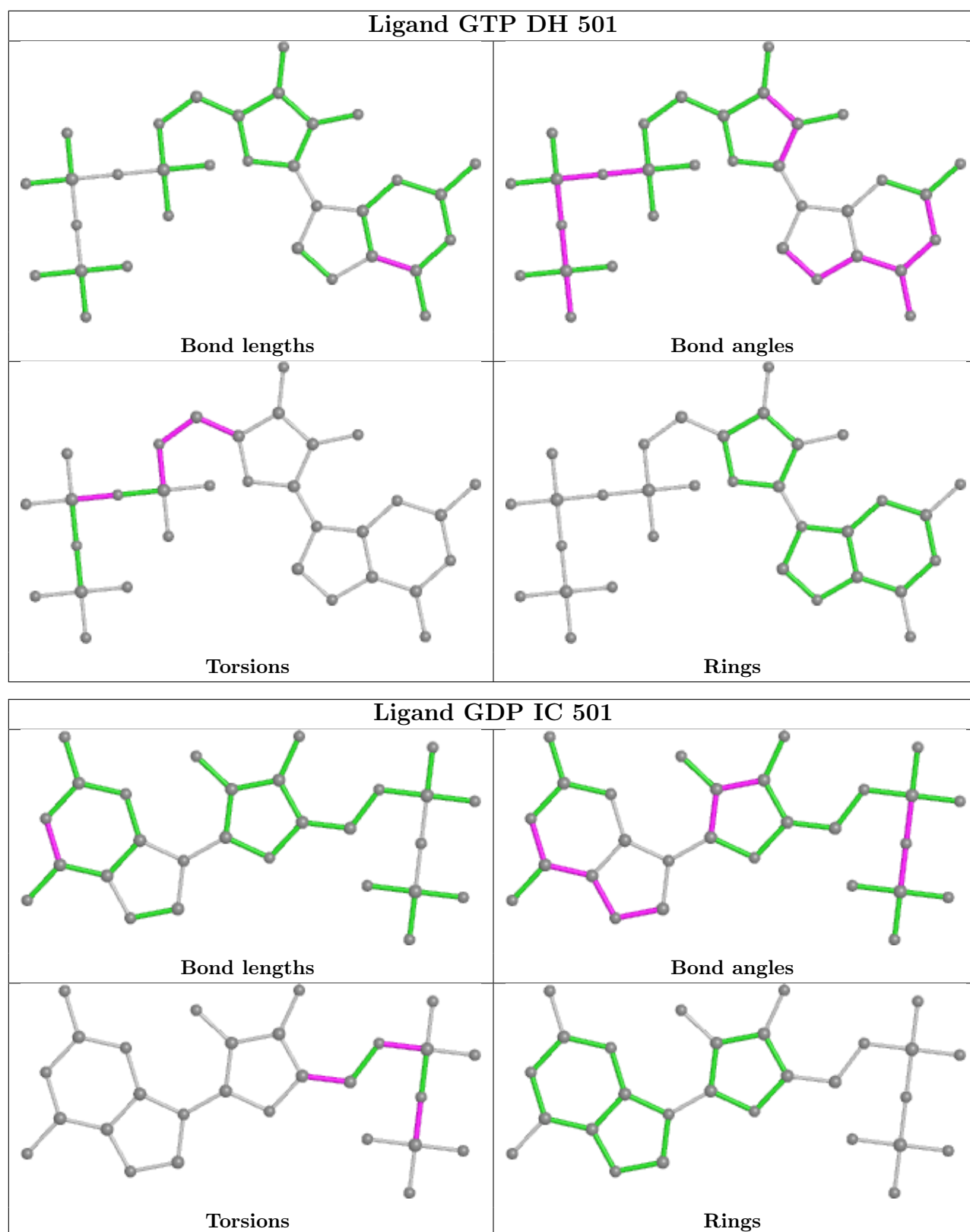


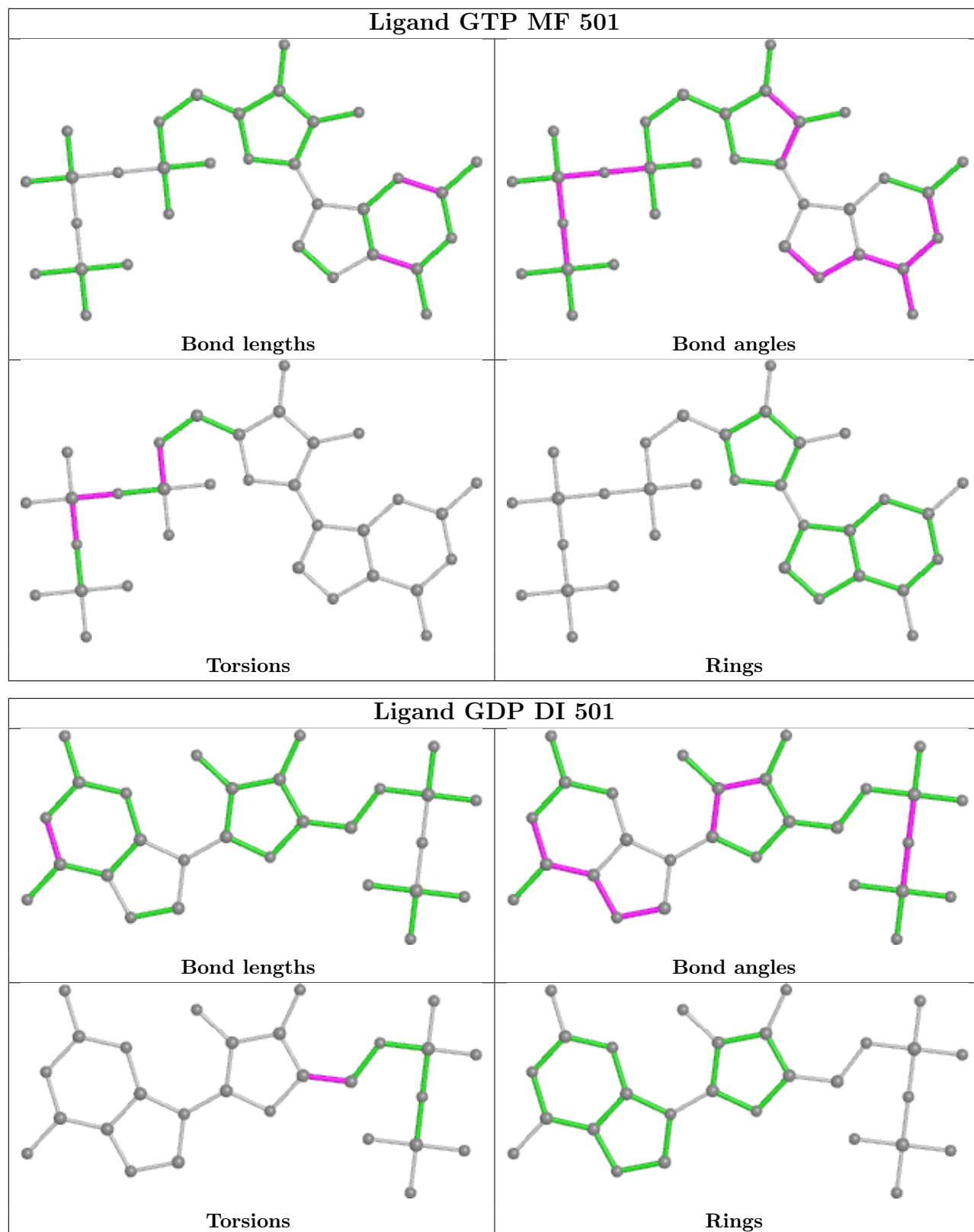


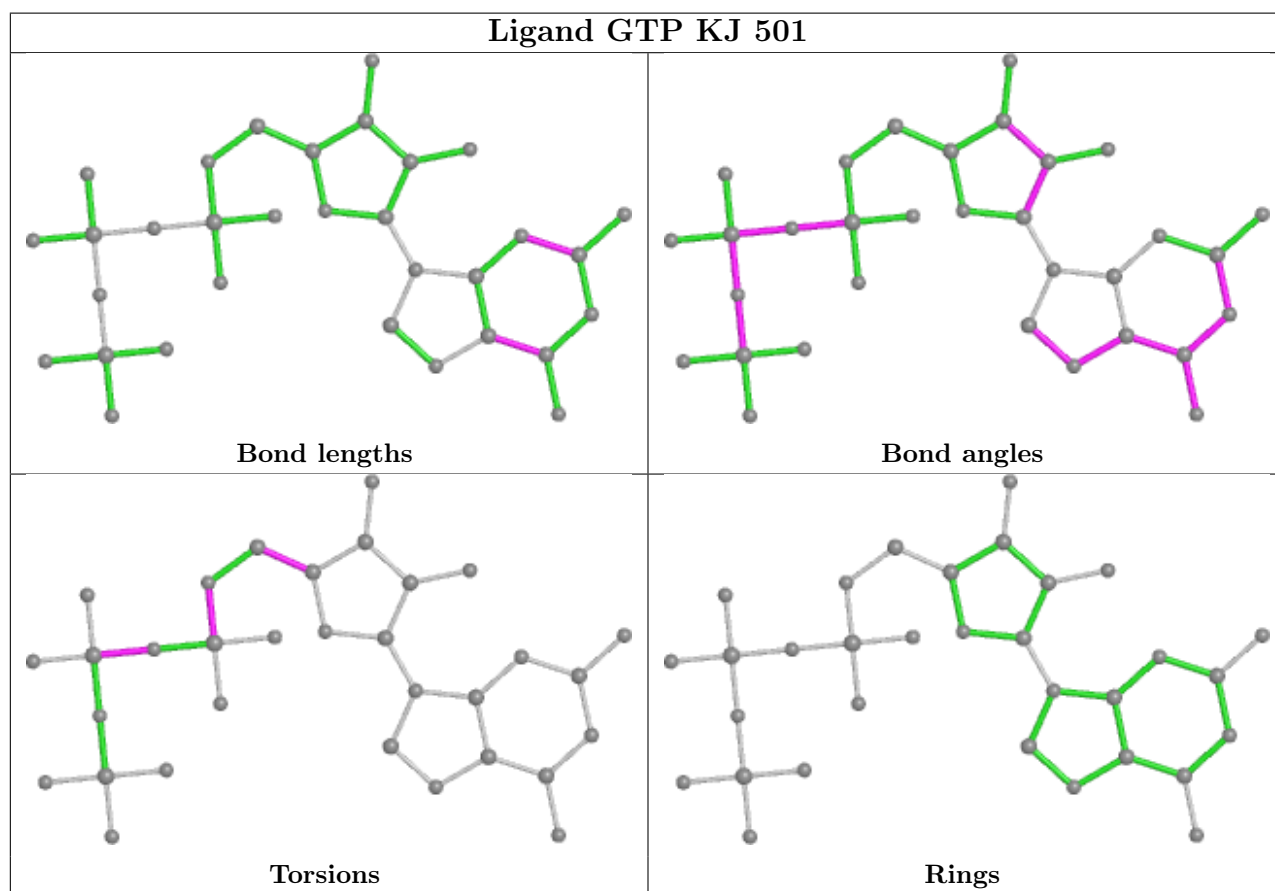
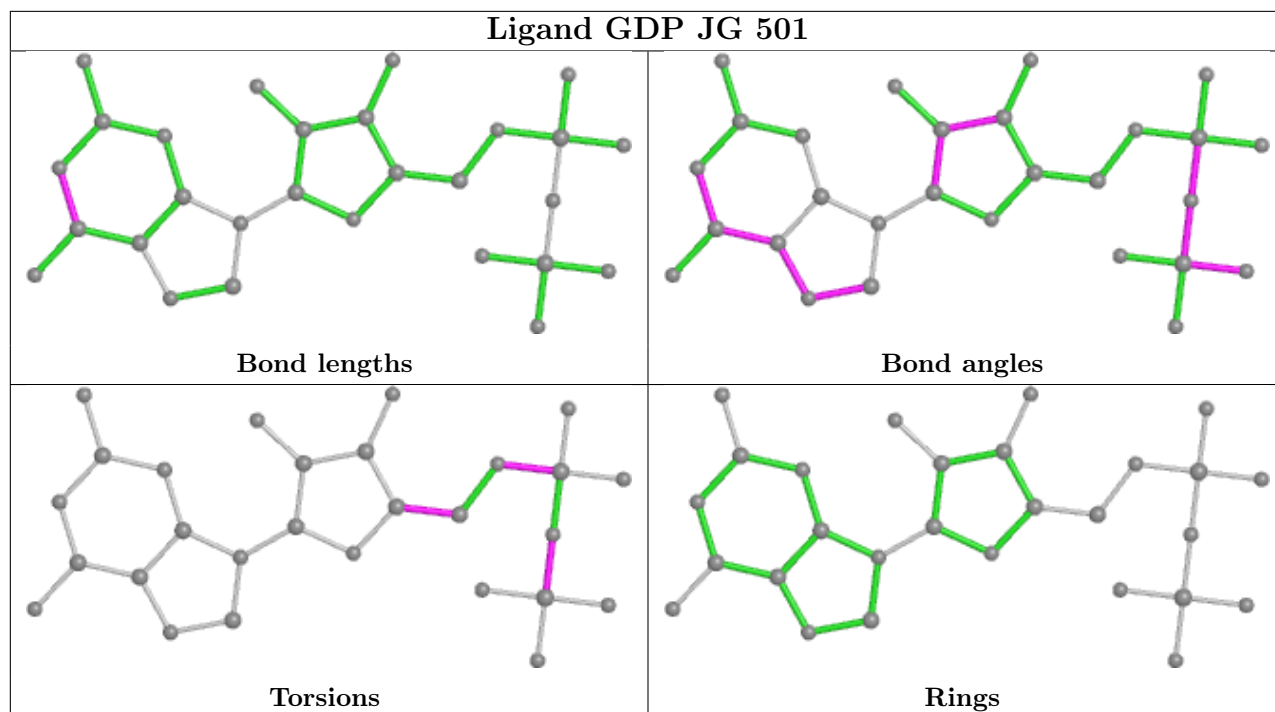


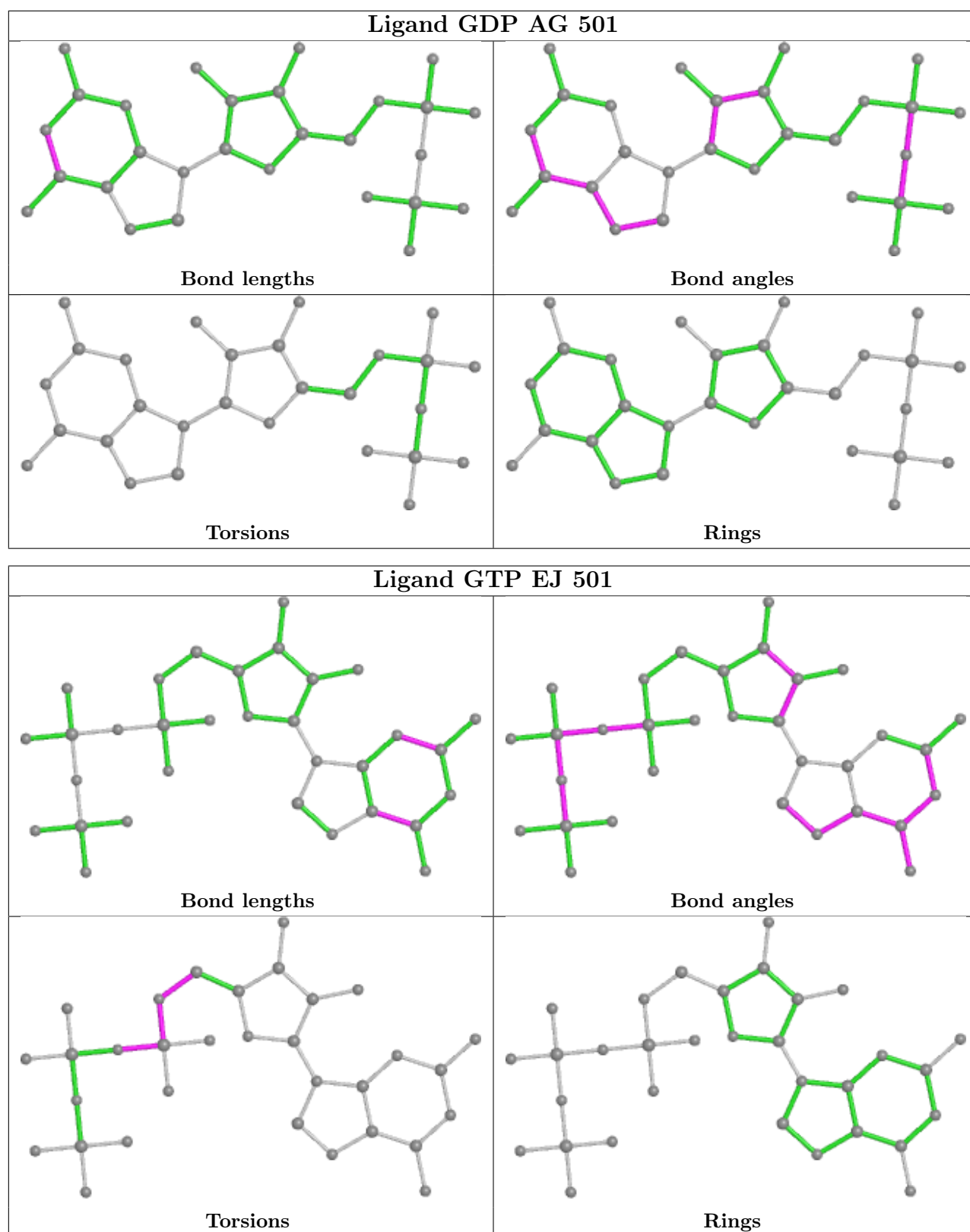


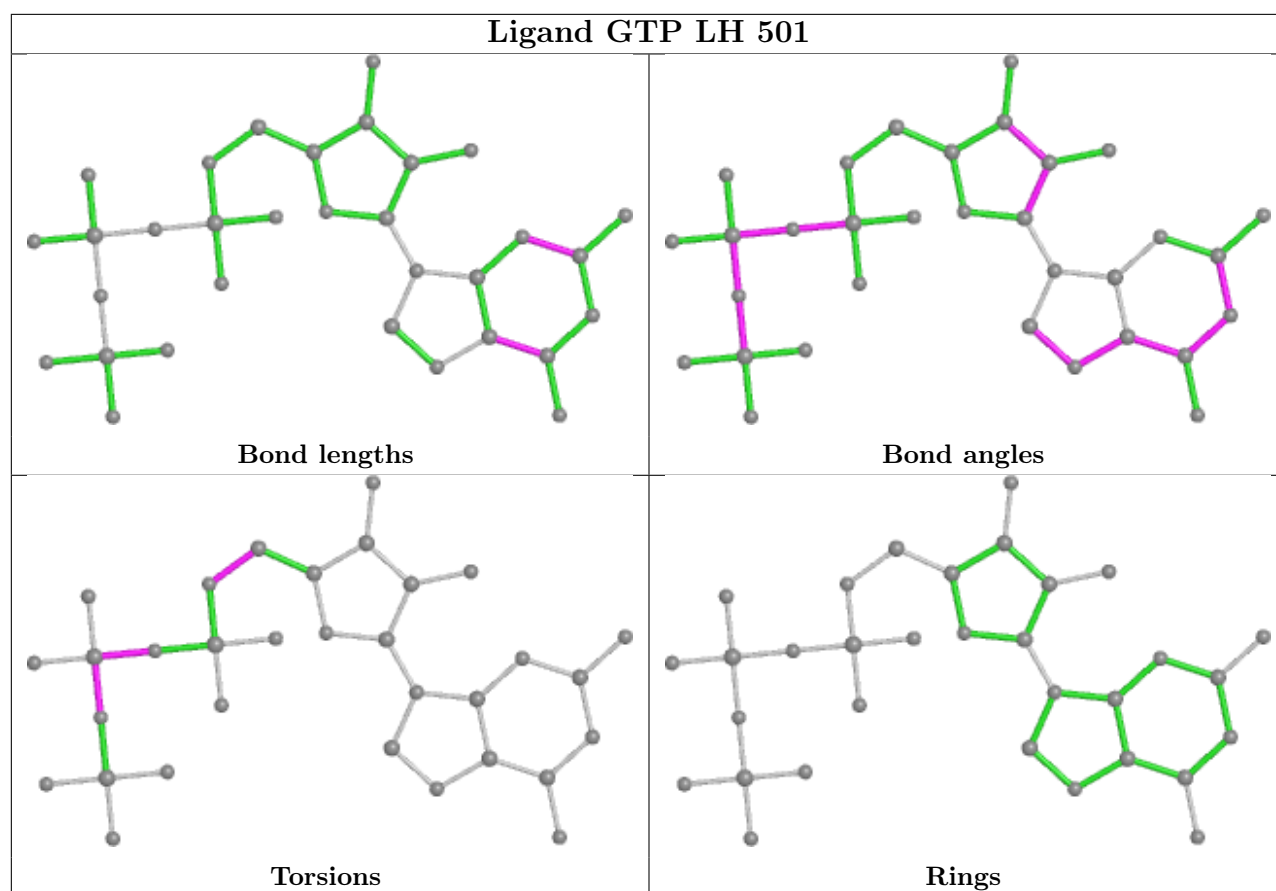












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

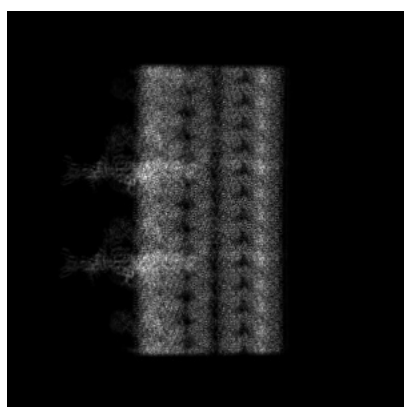
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25361. These allow visual inspection of the internal detail of the map and identification of artifacts.

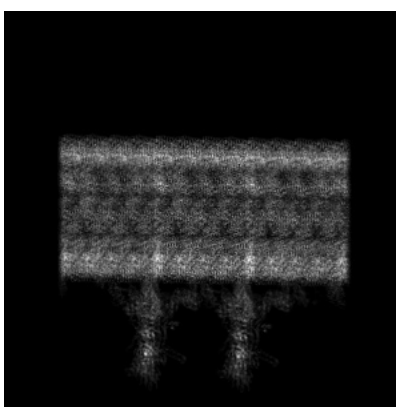
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

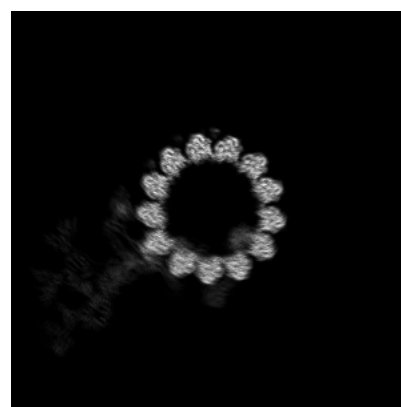
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

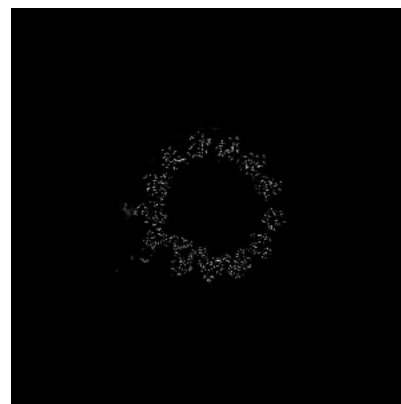
6.2.1 Primary map



X Index: 256



Y Index: 256

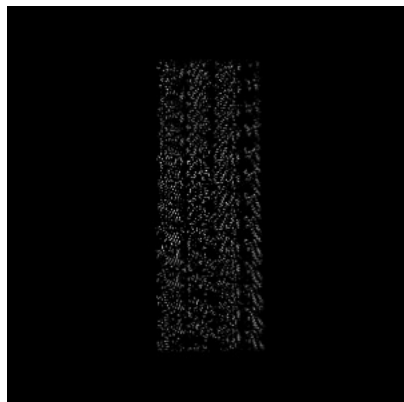


Z Index: 256

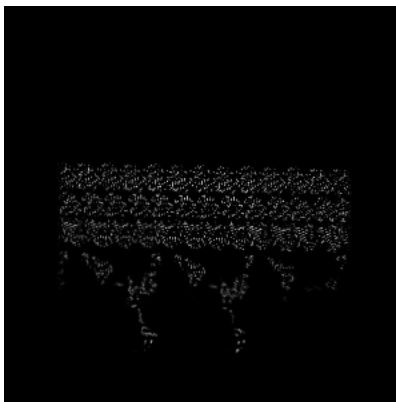
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

6.3.1 Primary map



X Index: 324



Y Index: 187

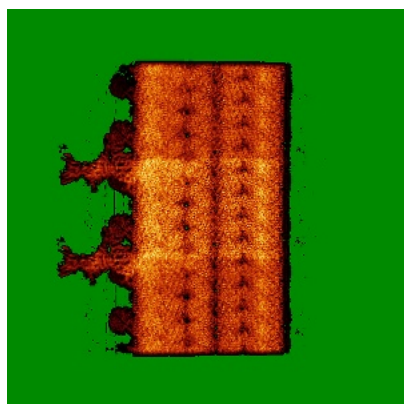


Z Index: 195

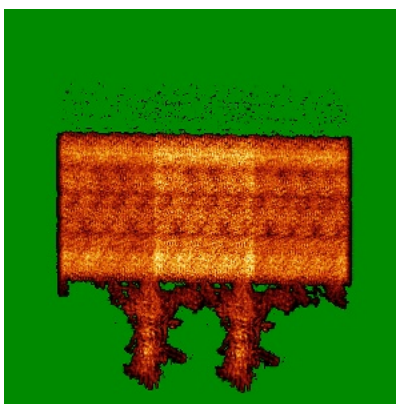
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

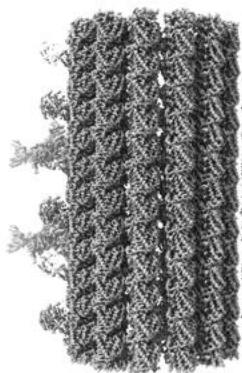


Z

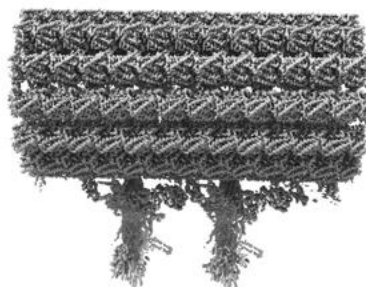
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

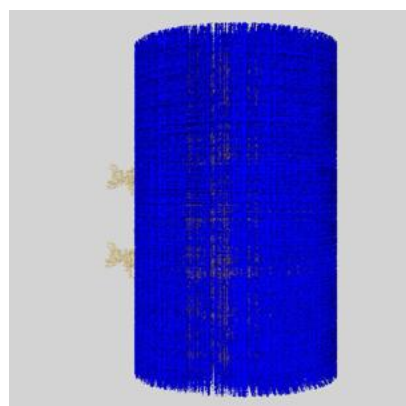
6.6 Mask visualisation [i](#)

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

A mask typically either:

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

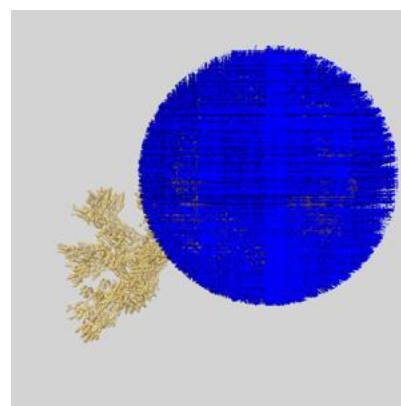
6.6.1 emd_25361_msk_1.map [i](#)



X



Y

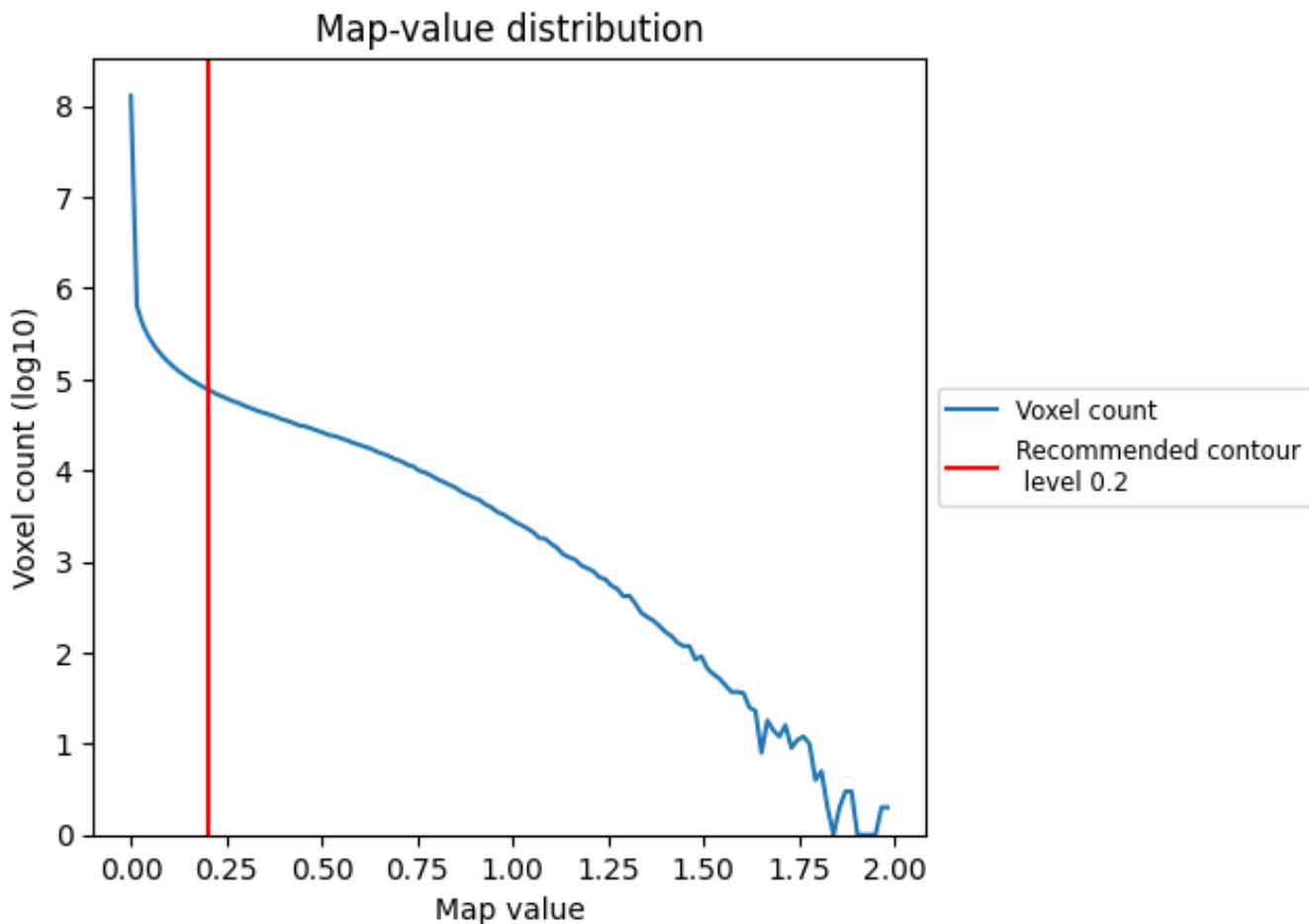


Z

7 Map analysis [i](#)

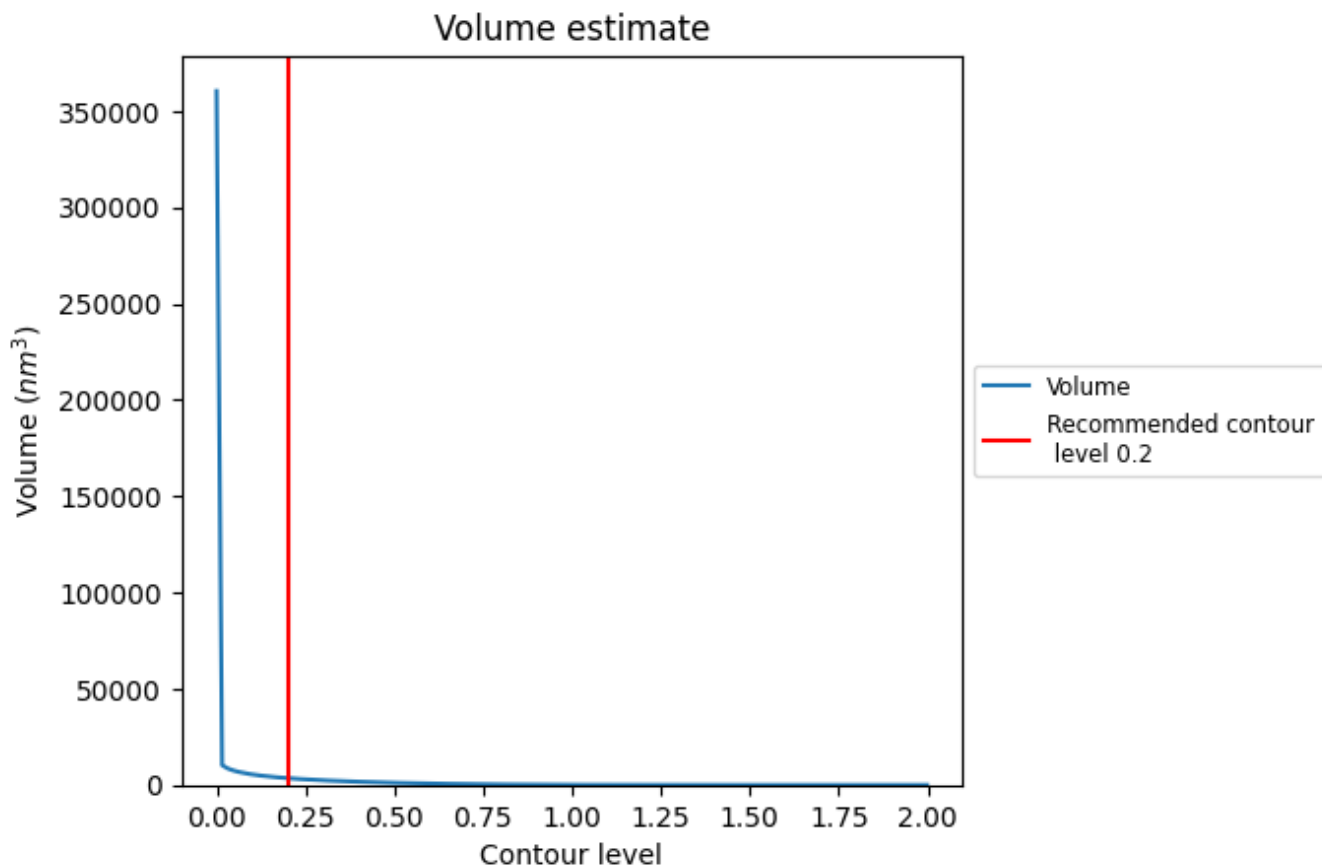
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

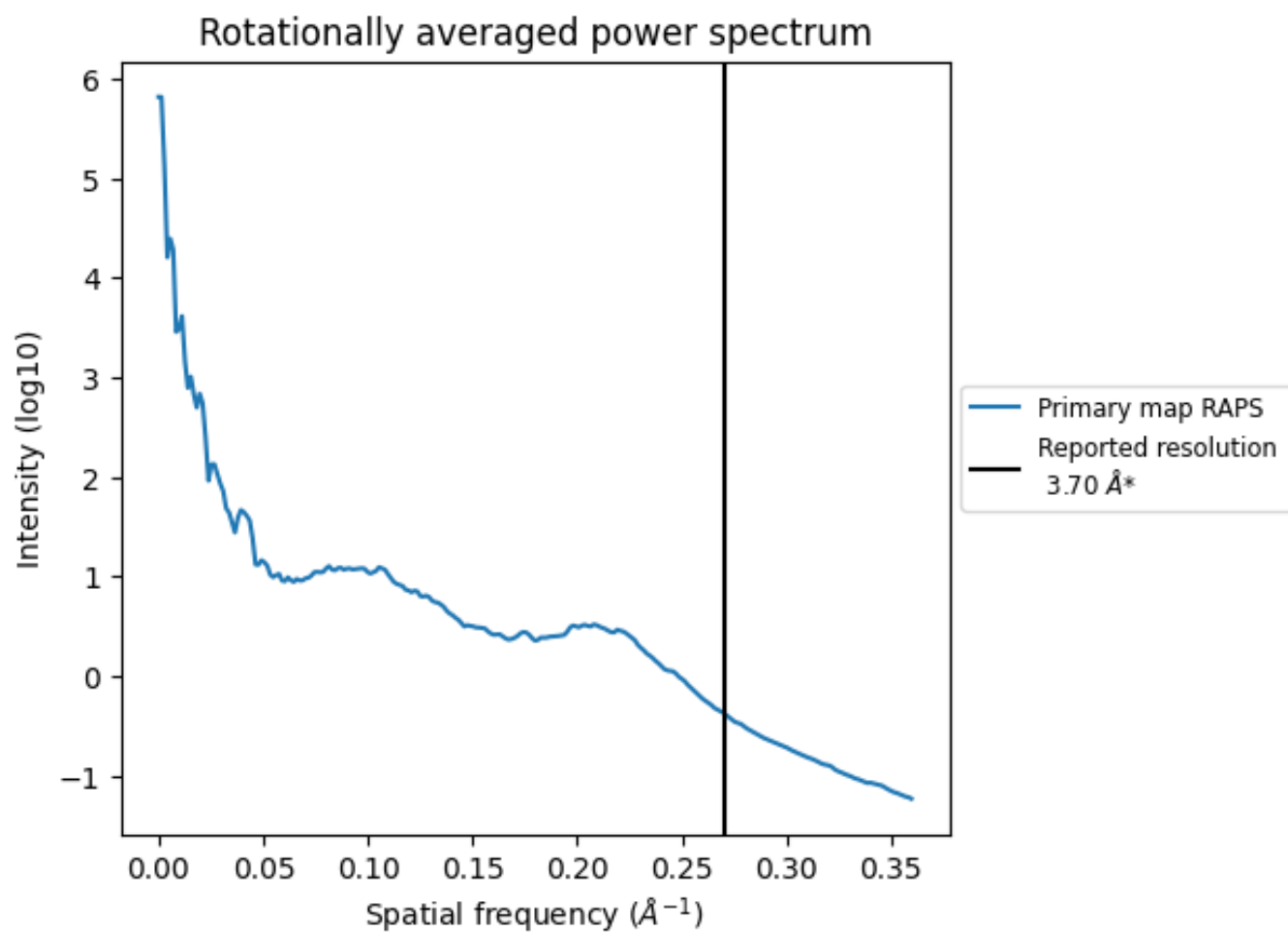
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3525 nm³; this corresponds to an approximate mass of 3184 kDa.

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

7.3 Rotationally averaged power spectrum i

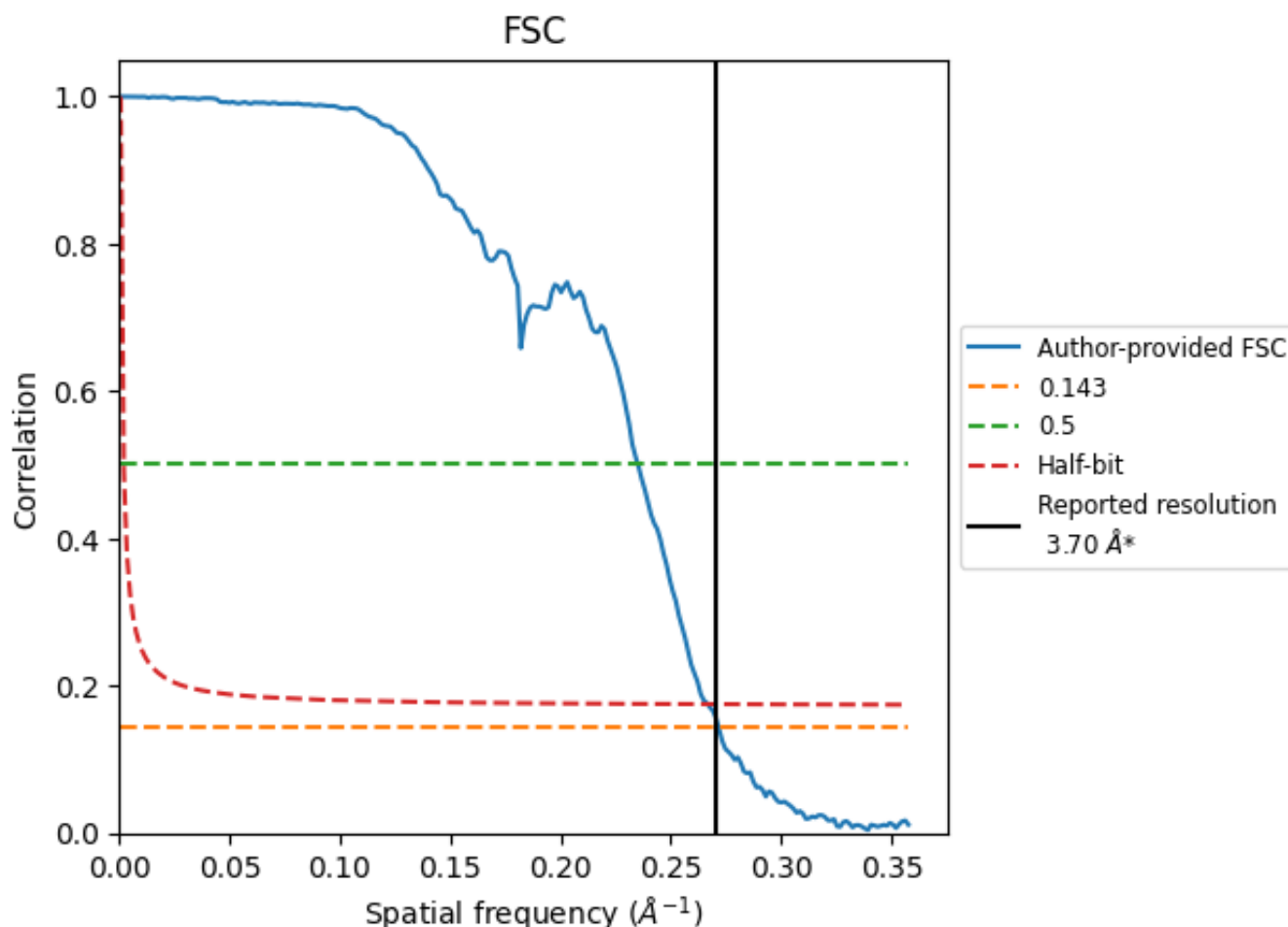


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

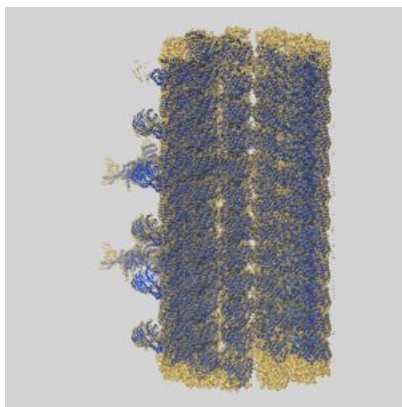
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.70 | - | - |
| Author-provided FSC curve | 3.68 | 4.26 | 3.75 |
| Unmasked-calculated* | - | - | - |

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

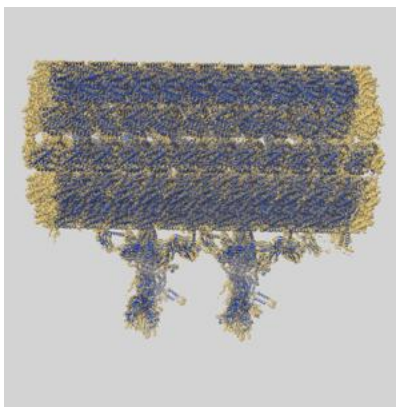
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25361 and PDB model 7SOM. Per-residue inclusion information can be found in section [3](#) on page [34](#).

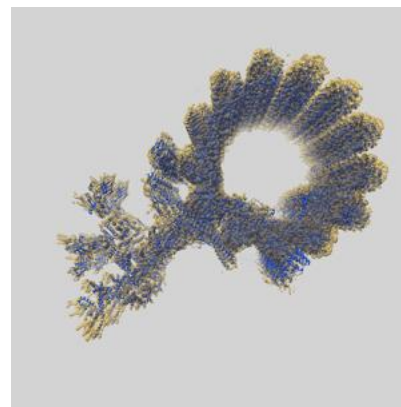
9.1 Map-model overlay [i](#)



X



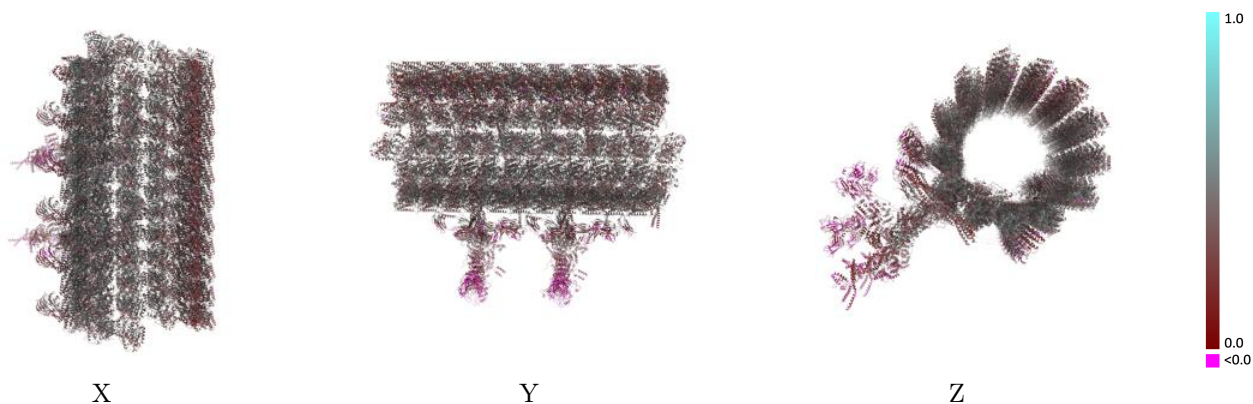
Y



Z

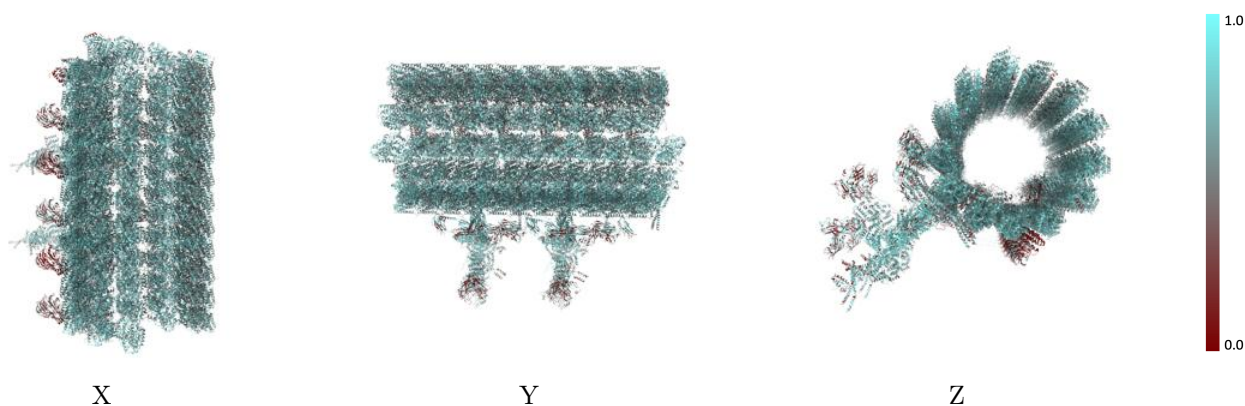
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



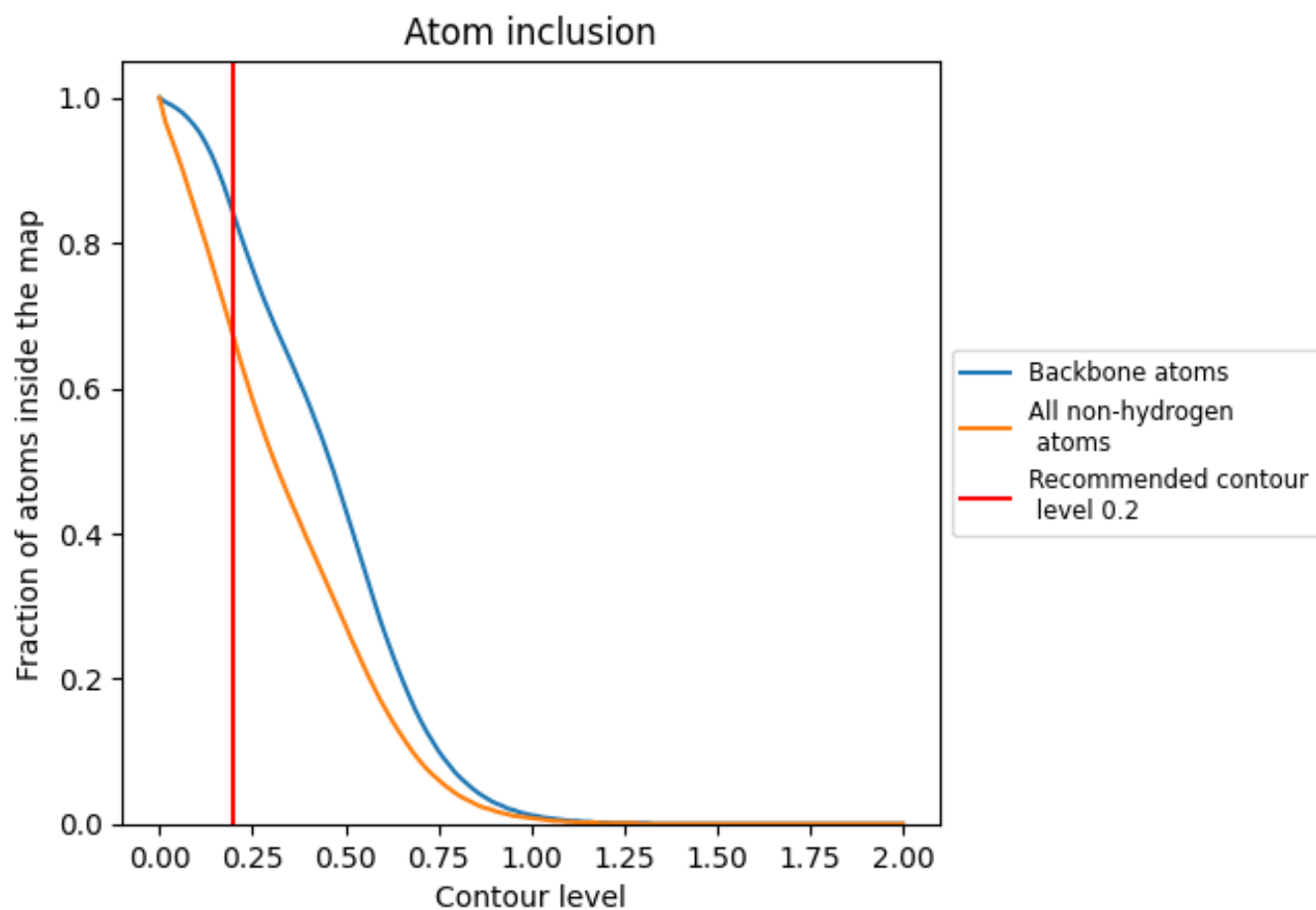
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 67% 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 (0.2) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.6680 |  0.3970 |
| A |  0.5370 |  0.3720 |
| A1 |  0.7080 |  0.3380 |
| A2 |  0.7560 |  0.3430 |
| A3 |  0.6890 |  0.3320 |
| A4 |  0.7560 |  0.3440 |
| AA |  0.7110 |  0.4210 |
| AB |  0.6970 |  0.4310 |
| AC |  0.7070 |  0.4310 |
| AD |  0.6910 |  0.4120 |
| AE |  0.7460 |  0.4430 |
| AF |  0.7100 |  0.4510 |
| AG |  0.7180 |  0.4580 |
| AH |  0.7170 |  0.4440 |
| AI |  0.7320 |  0.4270 |
| AJ |  0.6910 |  0.4220 |
| AK |  0.7080 |  0.4340 |
| AL |  0.7050 |  0.4260 |
| B |  0.5720 |  0.3900 |
| BA |  0.6860 |  0.4220 |
| BB |  0.6850 |  0.4320 |
| BC |  0.7140 |  0.4210 |
| BD |  0.7180 |  0.4200 |
| BE |  0.6910 |  0.4320 |
| BF |  0.6950 |  0.4430 |
| BG |  0.7160 |  0.4420 |
| BH |  0.7270 |  0.4280 |
| BI |  0.6760 |  0.4110 |
| BJ |  0.6800 |  0.4190 |
| BK |  0.7040 |  0.4220 |
| BL |  0.6820 |  0.4060 |
| C |  0.5090 |  0.3720 |
| CA |  0.7170 |  0.4420 |
| CB |  0.7160 |  0.4480 |
| CC |  0.7270 |  0.4430 |























































































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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| CD |  0.7450 |  0.4440 |
| CE |  0.7270 |  0.4590 |
| CF |  0.7240 |  0.4630 |
| CG |  0.7350 |  0.4530 |
| CH |  0.7510 |  0.4430 |
| CI |  0.7100 |  0.4460 |
| CJ |  0.7020 |  0.4420 |
| CK |  0.7170 |  0.4290 |
| D |  0.6240 |  0.3360 |
| DB |  0.7140 |  0.4430 |
| DC |  0.7080 |  0.4470 |
| DD |  0.7130 |  0.4340 |
| DE |  0.7310 |  0.4370 |
| DF |  0.7240 |  0.4520 |
| DG |  0.7150 |  0.4540 |
| DH |  0.7160 |  0.4470 |
| DI |  0.7310 |  0.4380 |
| DJ |  0.7190 |  0.4380 |
| DK |  0.6990 |  0.4350 |
| DL |  0.7060 |  0.4300 |
| E |  0.6190 |  0.3340 |
| EA |  0.6710 |  0.4220 |
| EB |  0.6900 |  0.4320 |
| EC |  0.6740 |  0.4160 |
| ED |  0.6820 |  0.4240 |
| EE |  0.7230 |  0.4390 |
| EF |  0.6990 |  0.4510 |
| EG |  0.6860 |  0.4430 |
| EH |  0.7040 |  0.4480 |
| EI |  0.7140 |  0.4270 |
| EJ |  0.6880 |  0.4320 |
| EK |  0.6810 |  0.4180 |
| EL |  0.6890 |  0.4280 |
| F |  0.6240 |  0.2290 |
| FA |  0.6920 |  0.4160 |
| FB |  0.6900 |  0.4140 |
| FC |  0.6790 |  0.4070 |
| FD |  0.7000 |  0.4140 |
| FE |  0.7140 |  0.4310 |
| FF |  0.7050 |  0.4430 |
| FG |  0.6980 |  0.4370 |
| FH |  0.7180 |  0.4280 |





















































































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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| FI |  0.7100 |  0.4180 |
| FJ |  0.7040 |  0.4260 |
| FK |  0.6930 |  0.4190 |
| FL |  0.6990 |  0.4110 |
| G |  0.5950 |  0.2040 |
| GC |  0.6890 |  0.4070 |
| GD |  0.6850 |  0.4050 |
| GE |  0.6800 |  0.4060 |
| GF |  0.6950 |  0.3960 |
| GG |  0.6920 |  0.4160 |
| GH |  0.6920 |  0.4210 |
| GI |  0.6940 |  0.4220 |
| GJ |  0.6990 |  0.3960 |
| GK |  0.6780 |  0.3990 |
| GL |  0.6900 |  0.4030 |
| GM |  0.6800 |  0.4050 |
| H |  0.6260 |  0.2310 |
| HC |  0.6110 |  0.3320 |
| HD |  0.6100 |  0.3270 |
| HE |  0.5890 |  0.3120 |
| HF |  0.6550 |  0.3230 |
| HG |  0.6290 |  0.3460 |
| HH |  0.6330 |  0.3450 |
| HI |  0.6210 |  0.3420 |
| HJ |  0.6490 |  0.3250 |
| HK |  0.6020 |  0.3200 |
| HL |  0.6070 |  0.3260 |
| HM |  0.6100 |  0.3170 |
| I |  0.5910 |  0.2010 |
| IC |  0.6260 |  0.3490 |
| ID |  0.6470 |  0.3550 |
| IE |  0.6300 |  0.3400 |
| IF |  0.6850 |  0.3480 |
| IG |  0.6490 |  0.3670 |
| IH |  0.6610 |  0.3670 |
| II |  0.6410 |  0.3520 |
| IJ |  0.6810 |  0.3490 |
| IK |  0.6320 |  0.3540 |
| IL |  0.6510 |  0.3560 |
| IM |  0.6360 |  0.3440 |
| J |  0.6390 |  0.3300 |
| JB |  0.6990 |  0.3940 |

















































































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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| JC |  0.6740 |  0.3960 |
| JD |  0.6790 |  0.4000 |
| JE |  0.6950 |  0.4000 |
| JF |  0.7170 |  0.4050 |
| JG |  0.6930 |  0.4140 |
| JH |  0.6980 |  0.4220 |
| JI |  0.7040 |  0.4110 |
| JJ |  0.7100 |  0.3960 |
| JK |  0.6850 |  0.4040 |
| JL |  0.6900 |  0.4050 |
| JM |  0.6900 |  0.4000 |
| K |  0.6510 |  0.3350 |
| KB |  0.6990 |  0.4060 |
| KC |  0.6930 |  0.4190 |
| KD |  0.6820 |  0.4050 |
| KE |  0.6950 |  0.4000 |
| KF |  0.6990 |  0.4190 |
| KG |  0.7010 |  0.4300 |
| KH |  0.6890 |  0.4230 |
| KI |  0.7080 |  0.4110 |
| KJ |  0.6890 |  0.3970 |
| KK |  0.6890 |  0.4110 |
| KL |  0.6820 |  0.4090 |
| L |  0.3190 |  0.2810 |
| LB |  0.7060 |  0.4200 |
| LC |  0.6920 |  0.4230 |
| LD |  0.6880 |  0.4110 |
| LE |  0.7290 |  0.4170 |
| LF |  0.7110 |  0.4440 |
| LG |  0.6980 |  0.4350 |
| LH |  0.6890 |  0.4320 |
| LI |  0.7170 |  0.4200 |
| LJ |  0.6940 |  0.4140 |
| LK |  0.6770 |  0.4070 |
| LL |  0.6930 |  0.4100 |
| M |  0.1770 |  0.2360 |
| MB |  0.6920 |  0.4310 |
| MC |  0.6900 |  0.4310 |
| MD |  0.6950 |  0.4240 |
| ME |  0.7110 |  0.4310 |
| MF |  0.7030 |  0.4480 |
| MG |  0.6980 |  0.4410 |

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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| MH |  0.7010 |  0.4420 |
| MI |  0.7110 |  0.4360 |
| MJ |  0.6990 |  0.4350 |
| MK |  0.6900 |  0.4260 |
| ML |  0.7000 |  0.4310 |
| N |  0.3600 |  0.2880 |
| O |  0.2140 |  0.2400 |
| P |  0.3020 |  0.2320 |
| Q |  0.4590 |  0.3420 |
| R |  0.2880 |  0.2380 |
| S |  0.4960 |  0.3390 |
| T |  0.5320 |  0.1890 |
| U |  0.5680 |  0.2250 |
| V |  0.4640 |  0.1730 |
| W |  0.5580 |  0.2060 |
| X |  0.3150 |  0.2790 |
| Y |  0.1560 |  0.2320 |
| Z |  0.5670 |  0.3170 |
| a |  0.5900 |  0.3810 |
| aa |  0.3150 |  0.3660 |
| b |  0.6280 |  0.3910 |
| bb |  0.5450 |  0.3360 |
| c |  0.6250 |  0.3880 |
| cc |  0.5790 |  0.3280 |
| d |  0.6320 |  0.3820 |
| e |  0.5810 |  0.3700 |
| f |  0.5940 |  0.3940 |
| g |  0.6200 |  0.3830 |
| h |  0.5590 |  0.3980 |
| i |  0.6140 |  0.4150 |
| j |  0.5770 |  0.3990 |
| k |  0.5840 |  0.3510 |
| l |  0.5840 |  0.3420 |
| m |  0.5990 |  0.3980 |
| n |  0.6230 |  0.4130 |
| o |  0.5960 |  0.3970 |
| p |  0.5840 |  0.4030 |
| q |  0.6150 |  0.4130 |
| r |  0.6020 |  0.4180 |
| s |  0.5730 |  0.3570 |