



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 25, 2020 – 06:11 PM BST

PDB ID : 5IY5
Title : Electron transfer complex of cytochrome c and cytochrome c oxidase at 2.0 angstrom resolution
Authors : Shimada, S.; Baba, J.; Aoe, S.; Shimada, A.; Yamashita, E.; Tsukihara, T.
Deposited on : 2016-03-24
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13

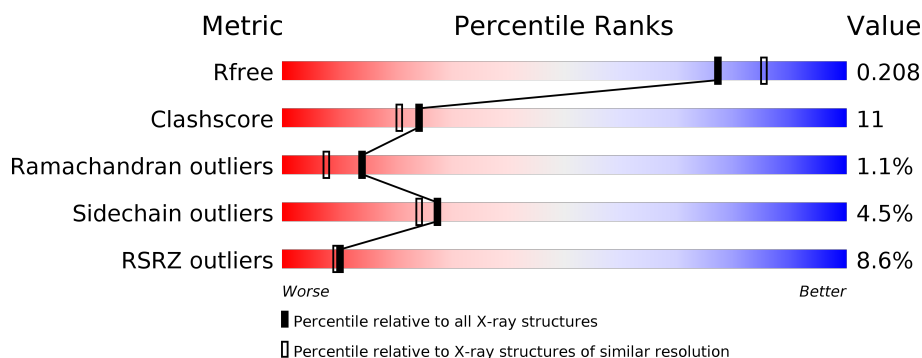
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

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



| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|---|
| R_{free} | 130704 | 8085 (2.00-2.00) |
| Clashscore | 141614 | 9178 (2.00-2.00) |
| Ramachandran outliers | 138981 | 9054 (2.00-2.00) |
| Sidechain outliers | 138945 | 9053 (2.00-2.00) |
| RSRZ outliers | 127900 | 7900 (2.00-2.00) |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower 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 electron density. The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 1 | A | 514 | <div> <div>4%</div> <div>85%</div> <div>14%</div> <div>.</div> </div> |
| 1 | N | 514 | <div> <div>5%</div> <div>88%</div> <div>12%</div> <div>.</div> </div> |
| 2 | B | 227 | <div> <div>%</div> <div>75%</div> <div>22%</div> <div>.</div> </div> |
| 2 | O | 227 | <div> <div>%</div> <div>80%</div> <div>16%</div> <div>.</div> </div> |
| 3 | C | 259 | <div> <div>%</div> <div>86%</div> <div>13%</div> <div>.</div> </div> |
| 3 | P | 259 | <div> <div>2%</div> <div>86%</div> <div>14%</div> <div>.</div> </div> |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 4 | D | 144 | |
| 4 | Q | 144 | |
| 5 | E | 105 | |
| 5 | R | 105 | |
| 6 | F | 98 | |
| 6 | S | 98 | |
| 7 | G | 84 | |
| 7 | T | 84 | |
| 8 | H | 79 | |
| 8 | U | 79 | |
| 9 | I | 73 | |
| 9 | V | 73 | |
| 10 | J | 58 | |
| 10 | W | 58 | |
| 11 | K | 49 | |
| 11 | X | 49 | |
| 12 | L | 46 | |
| 12 | Y | 46 | |
| 13 | M | 43 | |
| 13 | Z | 43 | |
| 14 | 1 | 105 | |
| 14 | 2 | 105 | |

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

| Mol | Type | Chain | Res | Chirality | Geometry | Clashes | Electron density |
|-----|------|-------|-----|-----------|----------|---------|------------------|
| 17 | NA | C | 302 | - | - | - | X |
| 17 | NA | P | 302 | - | - | - | X |
| 18 | HEA | A | 605 | X | - | - | - |
| 18 | HEA | N | 606 | X | - | - | - |
| 24 | CHD | W | 101 | - | - | - | X |
| 26 | CDL | G | 101 | - | - | X | - |
| 26 | CDL | T | 101 | - | - | X | - |
| 27 | UNL | C | 310 | - | - | X | - |
| 27 | UNL | N | 601 | - | - | X | - |
| 27 | UNL | P | 308 | - | - | X | - |
| 27 | UNL | P | 310 | - | - | X | - |
| 28 | PSC | V | 101 | - | - | X | - |
| 29 | ZN | S | 101 | - | - | X | - |
| 9 | SAC | I | 1 | - | X | - | - |
| 9 | SAC | V | 1 | - | - | - | X |

2 Entry composition [i](#)

There are 32 unique types of molecules in this entry. The entry contains 34765 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Cytochrome c oxidase subunit 1.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|---------|-------|
| 1 | A | 514 | Total | C | N | O | S | 0 | 11 | 0 |
| | | | 4084 | 2731 | 628 | 685 | 40 | | | |
| 1 | N | 514 | Total | C | N | O | S | 0 | 8 | 0 |
| | | | 4065 | 2717 | 627 | 683 | 38 | | | |

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

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|---------|-------|
| 2 | B | 227 | Total | C | N | O | S | 0 | 2 | 0 |
| | | | 1836 | 1192 | 283 | 343 | 18 | | | |
| 2 | O | 227 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1824 | 1185 | 281 | 340 | 18 | | | |

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

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|---------|-------|
| 3 | C | 259 | Total | C | N | O | S | 0 | 6 | 0 |
| | | | 2149 | 1437 | 343 | 355 | 14 | | | |
| 3 | P | 259 | Total | C | N | O | S | 0 | 5 | 0 |
| | | | 2143 | 1433 | 342 | 354 | 14 | | | |

- Molecule 4 is a protein called Cytochrome c oxidase subunit 4 isoform 1, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 4 | D | 144 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1195 | 777 | 196 | 218 | 4 | | | |
| 4 | Q | 144 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 1203 | 782 | 199 | 218 | 4 | | | |

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

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 5 | E | 105 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 852 | 544 | 144 | 162 | 2 | | | |
| 5 | R | 105 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 852 | 544 | 144 | 162 | 2 | | | |

- Molecule 6 is a protein called Cytochrome c oxidase subunit 5B, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 6 | F | 98 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 748 | 464 | 134 | 145 | 5 | | | |
| 6 | S | 98 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 748 | 464 | 134 | 145 | 5 | | | |

- Molecule 7 is a protein called Cytochrome c oxidase subunit 6A2, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 7 | G | 84 | Total | C | N | O | P | S | 0 | 0 |
| | | | 675 | 431 | 129 | 113 | 1 | 1 | | |
| 7 | T | 84 | Total | C | N | O | P | S | 0 | 0 |
| | | | 675 | 431 | 129 | 113 | 1 | 1 | | |

- Molecule 8 is a protein called Cytochrome c oxidase subunit 6B1.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 8 | H | 79 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 662 | 417 | 121 | 119 | 5 | | | |
| 8 | U | 79 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 662 | 417 | 121 | 119 | 5 | | | |

- Molecule 9 is a protein called Cytochrome c oxidase subunit 6C.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 9 | I | 73 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 601 | 390 | 107 | 100 | 4 | | | |
| 9 | V | 73 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 601 | 390 | 107 | 100 | 4 | | | |

- Molecule 10 is a protein called Cytochrome c oxidase subunit 7A1, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 10 | J | 58 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 460 | 297 | 78 | 82 | 3 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 10 | W | 58 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 460 | 297 | 78 | 82 | 3 | | | |

- Molecule 11 is a protein called Cytochrome c oxidase subunit 7B, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 11 | K | 49 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 384 | 250 | 65 | 67 | 2 | | | |
| 11 | X | 49 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 384 | 250 | 65 | 67 | 2 | | | |

- Molecule 12 is a protein called Cytochrome c oxidase subunit 7C, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 12 | L | 46 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 380 | 254 | 64 | 60 | 2 | | | |
| 12 | Y | 46 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 380 | 254 | 64 | 60 | 2 | | | |

- Molecule 13 is a protein called Cytochrome c oxidase subunit 8B, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|---------|-------|
| 13 | M | 43 | Total | C | N | O | 0 | 0 | 0 |
| | | | 335 | 223 | 53 | 59 | | | |
| 13 | Z | 43 | Total | C | N | O | 0 | 0 | 0 |
| | | | 335 | 223 | 53 | 59 | | | |

- Molecule 14 is a protein called Cytochrome c.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 14 | 1 | 105 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 826 | 526 | 144 | 152 | 4 | | | |
| 14 | 2 | 105 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 826 | 526 | 144 | 152 | 4 | | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-------------|------------|
| 1 | 0 | ACE | - | acetylation | UNP P00004 |
| 2 | 0 | ACE | - | acetylation | UNP P00004 |

- Molecule 15 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 15 | A | 1 | Total Cu 1 1 | 0 | 0 |
| 15 | N | 1 | Total Cu 1 1 | 0 | 0 |

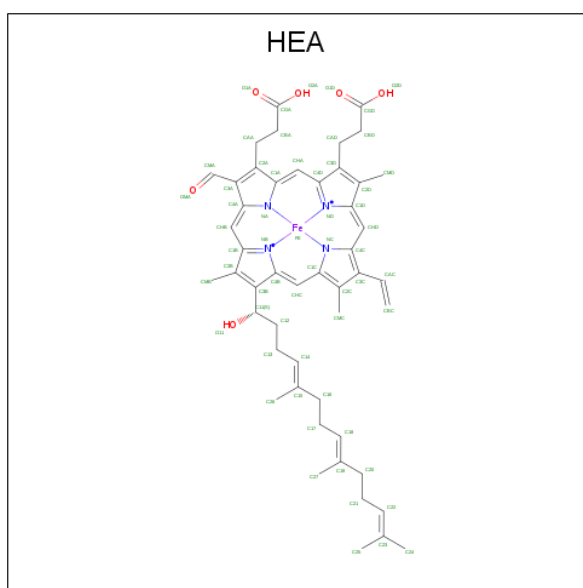
- Molecule 16 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 16 | A | 1 | Total Mg 1 1 | 0 | 0 |
| 16 | N | 1 | Total Mg 1 1 | 0 | 0 |

- Molecule 17 is SODIUM ION (three-letter code: NA) (formula: Na).

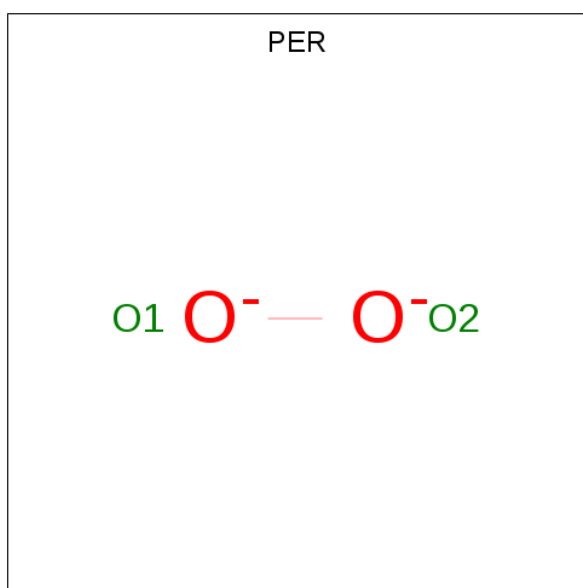
| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 17 | P | 1 | Total Na 1 1 | 0 | 0 |
| 17 | A | 1 | Total Na 1 1 | 0 | 0 |
| 17 | C | 1 | Total Na 1 1 | 0 | 0 |
| 17 | N | 1 | Total Na 1 1 | 0 | 0 |

- Molecule 18 is HEME-A (three-letter code: HEA) (formula: $C_{49}H_{56}FeN_4O_6$).



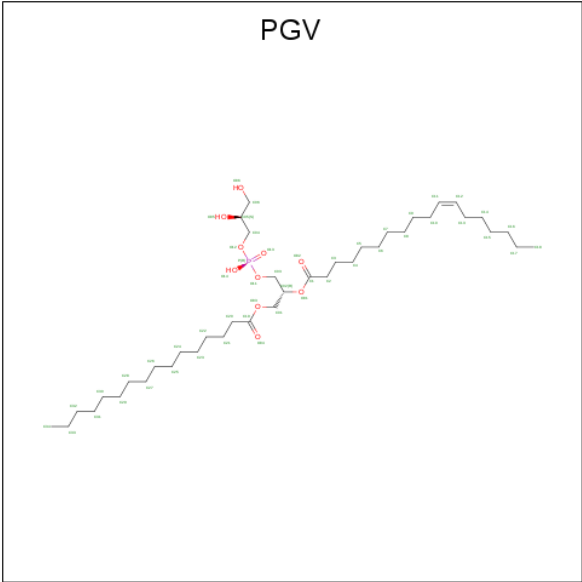
| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|----|---|---|---------|---------|
| 18 | A | 1 | Total | C | Fe | N | O | 0 | 1 |
| | | | 69 | 58 | 1 | 4 | 6 | | |
| 18 | A | 1 | Total | C | Fe | N | O | 0 | 0 |
| | | | 60 | 49 | 1 | 4 | 6 | | |
| 18 | N | 1 | Total | C | Fe | N | O | 0 | 1 |
| | | | 69 | 58 | 1 | 4 | 6 | | |
| 18 | N | 1 | Total | C | Fe | N | O | 0 | 0 |
| | | | 60 | 49 | 1 | 4 | 6 | | |

- Molecule 19 is PEROXIDE ION (three-letter code: PER) (formula: O₂).



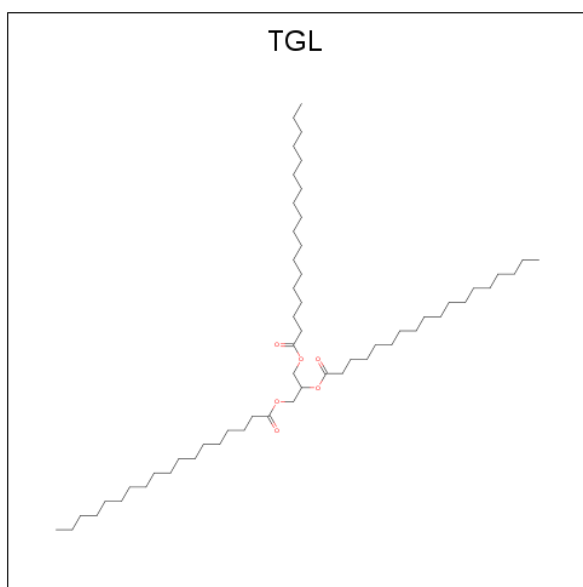
| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---------|---------|
| 19 | A | 1 | Total | O | 0 | 0 |
| | | | 2 | 2 | | |
| 19 | N | 1 | Total | O | 0 | 0 |
| | | | 2 | 2 | | |

- Molecule 20 is (1R)-2-{{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (three-letter code: PGV) (formula: C₄₀H₇₇O₁₀P).



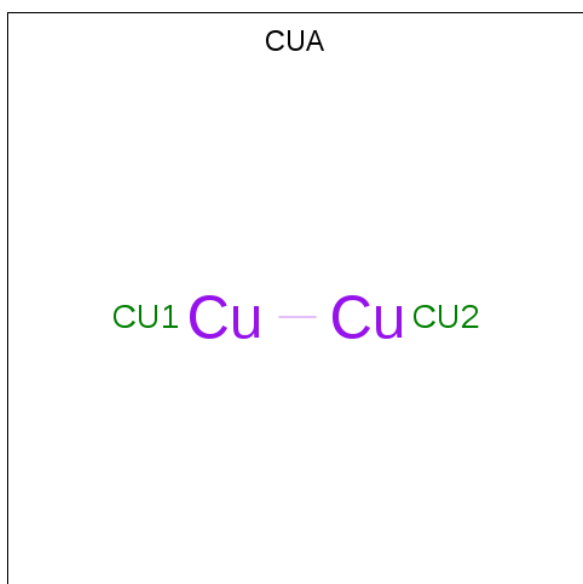
| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|----|---|---------|---------|
| 20 | A | 1 | Total | C | O | P | 0 | 0 |
| | | | 51 | 40 | 10 | 1 | | |
| 20 | A | 1 | Total | C | O | P | 0 | 0 |
| | | | 51 | 40 | 10 | 1 | | |
| 20 | C | 1 | Total | C | O | P | 0 | 0 |
| | | | 51 | 40 | 10 | 1 | | |
| 20 | C | 1 | Total | C | O | P | 0 | 0 |
| | | | 51 | 40 | 10 | 1 | | |
| 20 | N | 1 | Total | C | O | P | 0 | 0 |
| | | | 51 | 40 | 10 | 1 | | |
| 20 | P | 1 | Total | C | O | P | 0 | 0 |
| | | | 51 | 40 | 10 | 1 | | |
| 20 | P | 1 | Total | C | O | P | 0 | 0 |
| | | | 51 | 40 | 10 | 1 | | |

- Molecule 21 is TRISTEAROYLGLYCEROL (three-letter code: TGL) (formula: C₅₇H₁₁₀O₆).



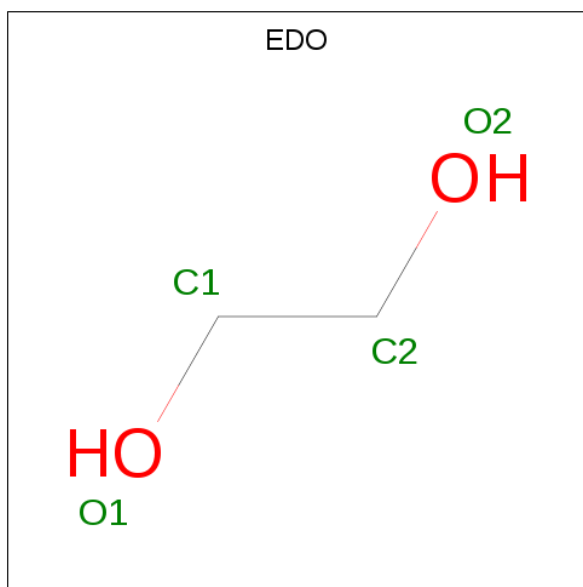
| Mol | Chain | Residues | Atoms | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---|---------|---------|
| 21 | B | 1 | Total | C | O | 0 | 0 |
| | | | 63 | 57 | 6 | | |
| 21 | D | 1 | Total | C | O | 0 | 0 |
| | | | 63 | 57 | 6 | | |
| 21 | L | 1 | Total | C | O | 0 | 0 |
| | | | 63 | 57 | 6 | | |
| 21 | N | 1 | Total | C | O | 0 | 0 |
| | | | 63 | 57 | 6 | | |
| 21 | Q | 1 | Total | C | O | 0 | 0 |
| | | | 63 | 57 | 6 | | |

- Molecule 22 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu₂).



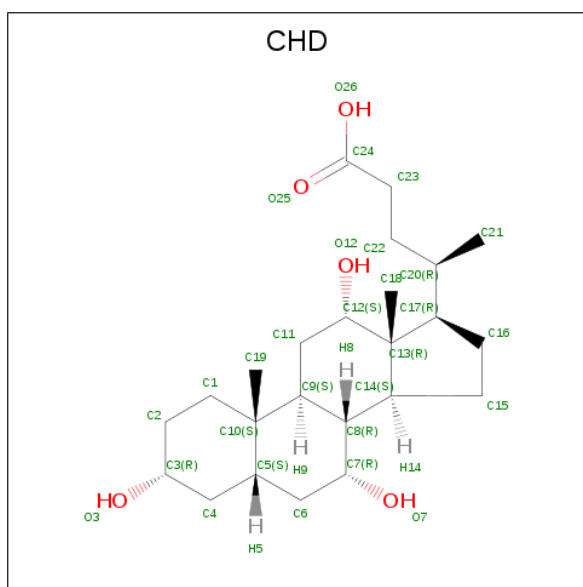
| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 22 | B | 1 | Total Cu 2 2 | 0 | 0 |
| 22 | O | 1 | Total Cu 2 2 | 0 | 0 |

- Molecule 23 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



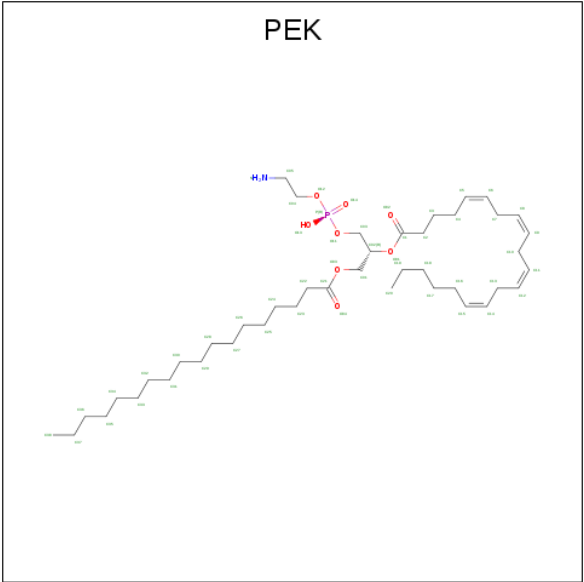
| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|--------------------|---------|---------|
| 23 | B | 1 | Total C O 4 2 2 | 0 | 0 |
| 23 | C | 1 | Total C O 4 2 2 | 0 | 0 |
| 23 | E | 1 | Total C O 4 2 2 | 0 | 0 |
| 23 | F | 1 | Total C O 4 2 2 | 0 | 0 |
| 23 | G | 1 | Total C O 4 2 2 | 0 | 0 |
| 23 | I | 1 | Total C O 4 2 2 | 0 | 0 |
| 23 | N | 1 | Total C O 4 2 2 | 0 | 0 |
| 23 | N | 1 | Total C O 4 2 2 | 0 | 0 |
| 23 | S | 1 | Total C O 4 2 2 | 0 | 0 |

- Molecule 24 is CHOLIC ACID (three-letter code: CHD) (formula: C₂₄H₄₀O₅).



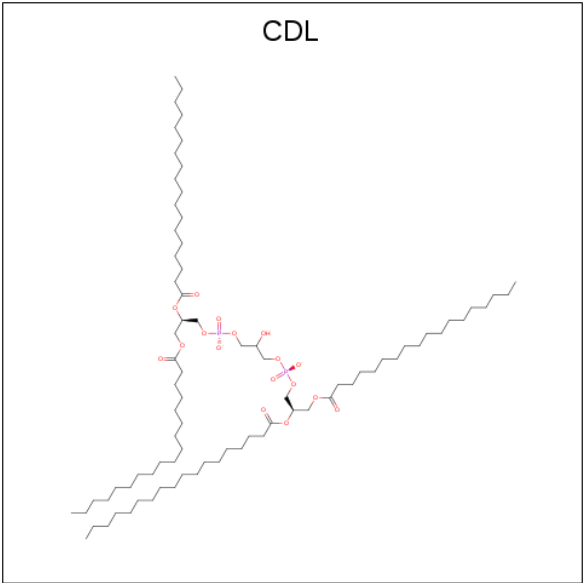
| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|----------------------|---------|---------|
| 24 | C | 1 | Total C O 29 24 5 | 0 | 0 |
| 24 | C | 1 | Total C O 29 24 5 | 0 | 0 |
| 24 | G | 1 | Total C O 29 24 5 | 0 | 0 |
| 24 | J | 1 | Total C O 29 24 5 | 0 | 0 |
| 24 | P | 1 | Total C O 29 24 5 | 0 | 0 |
| 24 | P | 1 | Total C O 29 24 5 | 0 | 0 |
| 24 | T | 1 | Total C O 29 24 5 | 0 | 0 |
| 24 | W | 1 | Total C O 29 24 5 | 0 | 0 |

- Molecule 25 is (1S)-2-[[[(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(STEAROYLOXY)METHYL]ETHYL (5E,8E,11E,14E)-ICOSA-5,8,11,14-TETRAENOATE (three-letter code: PEK) (formula: C₄₃H₇₈NO₈P).



| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---|---|---|---------|---------|
| 25 | C | 1 | Total | C | N | O | P | 0 | 0 |
| | | | 53 | 43 | 1 | 8 | 1 | | |
| 25 | P | 1 | Total | C | N | O | P | 0 | 0 |
| | | | 53 | 43 | 1 | 8 | 1 | | |

- Molecule 26 is CARDIOLIPIN (three-letter code: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).



| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|----|---|---------|---------|
| 26 | C | 1 | Total | C | O | P | 0 | 0 |
| | | | 100 | 81 | 17 | 2 | | |
| 26 | G | 1 | Total | C | O | P | 0 | 0 |
| | | | 100 | 81 | 17 | 2 | | |

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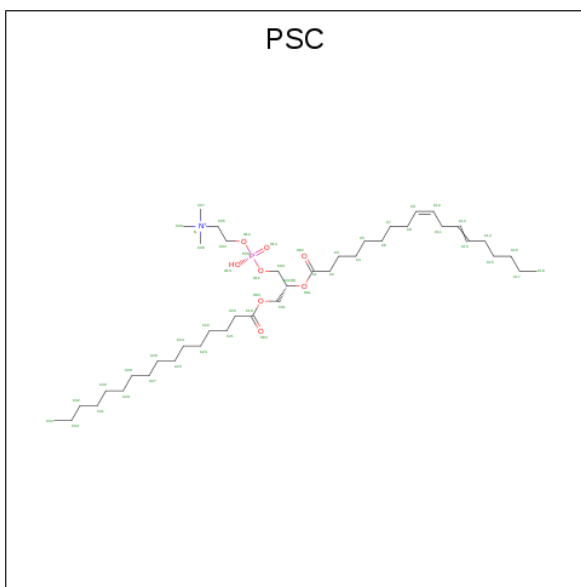
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| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|----|---|---------|---------|
| 26 | P | 1 | Total | C | O | P | 0 | 0 |
| | | | 100 | 81 | 17 | 2 | | |
| 26 | T | 1 | Total | C | O | P | 0 | 0 |
| | | | 100 | 81 | 17 | 2 | | |

- Molecule 27 is UNKNOWN LIGAND (three-letter code: UNL) (formula:).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---------|---------|
| 27 | P | 3 | Total | C | 0 | 0 |
| | | | 43 | 43 | | |
| 27 | J | 1 | Total | C | 0 | 0 |
| | | | 10 | 10 | | |
| 27 | C | 3 | Total | C | 0 | 0 |
| | | | 42 | 42 | | |
| 27 | W | 1 | Total | C | 0 | 0 |
| | | | 9 | 9 | | |
| 27 | T | 1 | Total | C | 0 | 0 |
| | | | 18 | 18 | | |
| 27 | N | 4 | Total | C | 0 | 0 |
| | | | 63 | 63 | | |
| 27 | Y | 1 | Total | C | 0 | 0 |
| | | | 10 | 10 | | |
| 27 | L | 1 | Total | C | 0 | 0 |
| | | | 10 | 10 | | |

- Molecule 28 is (7R,17E,20E)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITOYLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSA-17,20-DIEN-1-AMINIUM 4-OXIDE (three-letter code: PSC) (formula: C₄₂H₈₁NO₈P).

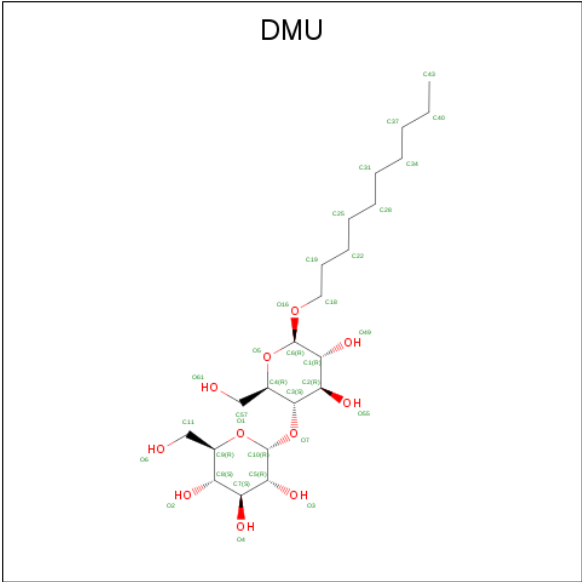


| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---|---|---|---------|---------|
| 28 | E | 1 | Total | C | N | O | P | 0 | 0 |
| | | | 52 | 42 | 1 | 8 | 1 | | |
| 28 | V | 1 | Total | C | N | O | P | 0 | 0 |
| | | | 52 | 42 | 1 | 8 | 1 | | |

- Molecule 29 is ZINC ION (three-letter code: ZN) (formula: Zn).

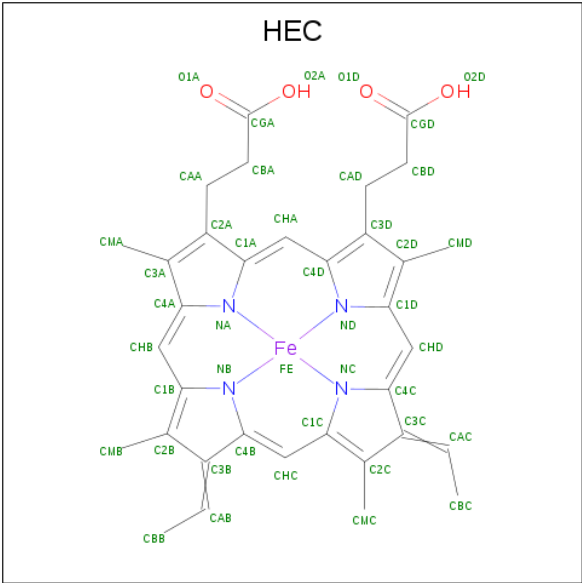
| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---------|---------|
| 29 | S | 1 | Total | Zn | 0 | 0 |
| | | | 1 | 1 | | |
| 29 | F | 1 | Total | Zn | 0 | 0 |
| | | | 1 | 1 | | |

- Molecule 30 is DECYL-BETA-D-MALTOPYRANOSIDE (three-letter code: DMU) (formula: C₂₂H₄₂O₁₁).



| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|----|--|---------|---------|
| 30 | M | 1 | Total | C | O | | 0 | 0 |
| | | | 33 | 22 | 11 | | | |
| 30 | Z | 1 | Total | C | O | | 0 | 0 |
| | | | 33 | 22 | 11 | | | |

- Molecule 31 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|----|---|---|---------|---------|
| 31 | 1 | 1 | Total | C | Fe | N | O | 0 | 0 |
| | | | 43 | 34 | 1 | 4 | 4 | | |
| 31 | 2 | 1 | Total | C | Fe | N | O | 0 | 0 |
| | | | 43 | 34 | 1 | 4 | 4 | | |

- Molecule 32 is water.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|--------------------|---------|---------|
| 32 | A | 252 | Total O 252 252 | 0 | 0 |
| 32 | B | 193 | Total O 193 193 | 0 | 0 |
| 32 | C | 137 | Total O 137 137 | 0 | 0 |
| 32 | D | 122 | Total O 122 122 | 0 | 0 |
| 32 | E | 119 | Total O 119 119 | 0 | 0 |
| 32 | F | 97 | Total O 97 97 | 0 | 0 |
| 32 | G | 60 | Total O 60 60 | 0 | 0 |
| 32 | H | 76 | Total O 76 76 | 0 | 0 |
| 32 | I | 49 | Total O 49 49 | 0 | 0 |
| 32 | J | 30 | Total O 30 30 | 0 | 0 |
| 32 | K | 29 | Total O 29 29 | 0 | 0 |
| 32 | L | 33 | Total O 33 33 | 0 | 0 |
| 32 | M | 26 | Total O 26 26 | 0 | 0 |
| 32 | N | 229 | Total O 229 229 | 0 | 0 |
| 32 | O | 141 | Total O 141 141 | 0 | 0 |
| 32 | P | 110 | Total O 110 110 | 0 | 0 |
| 32 | Q | 99 | Total O 99 99 | 0 | 0 |
| 32 | R | 83 | Total O 83 83 | 0 | 0 |
| 32 | S | 95 | Total O 95 95 | 0 | 0 |
| 32 | T | 41 | Total O 41 41 | 0 | 0 |
| 32 | U | 54 | Total O 54 54 | 0 | 0 |

Continued on next page...

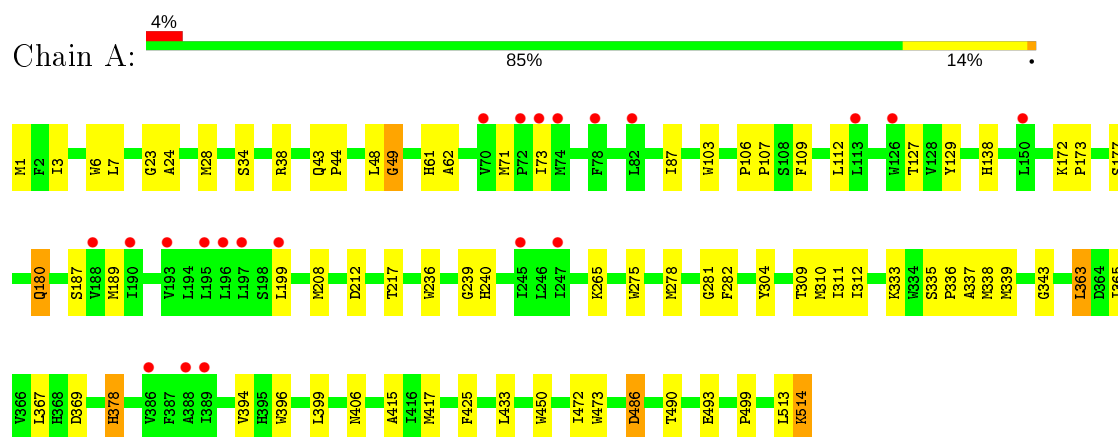
Continued from previous page...

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------------|---------|---------|---------|
| 32 | V | 17 | Total 17 | O 17 | 0 | 0 |
| 32 | W | 10 | Total 10 | O 10 | 0 | 0 |
| 32 | X | 17 | Total 17 | O 17 | 0 | 0 |
| 32 | Y | 21 | Total 21 | O 21 | 0 | 0 |
| 32 | Z | 16 | Total 16 | O 16 | 0 | 0 |
| 32 | 1 | 53 | Total 53 | O 53 | 0 | 0 |
| 32 | 2 | 28 | Total 28 | O 28 | 0 | 0 |

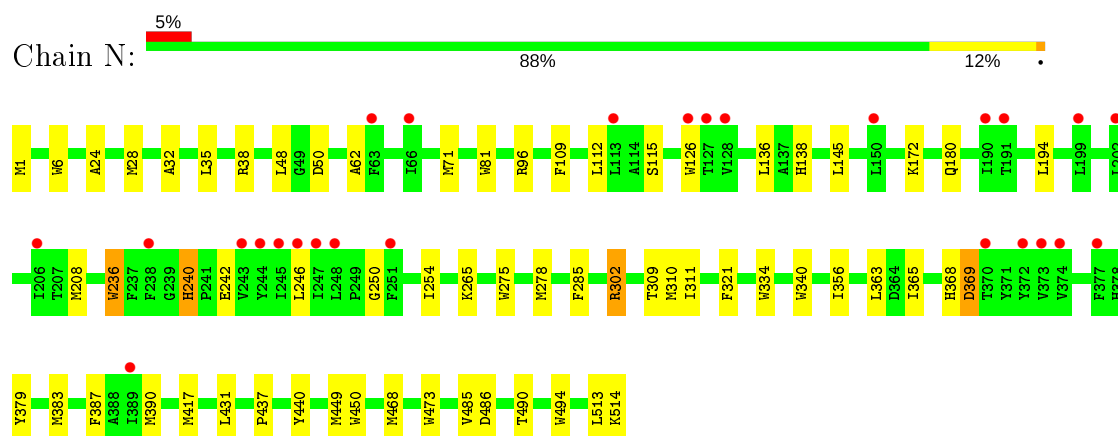
3 Residue-property plots [i](#)

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

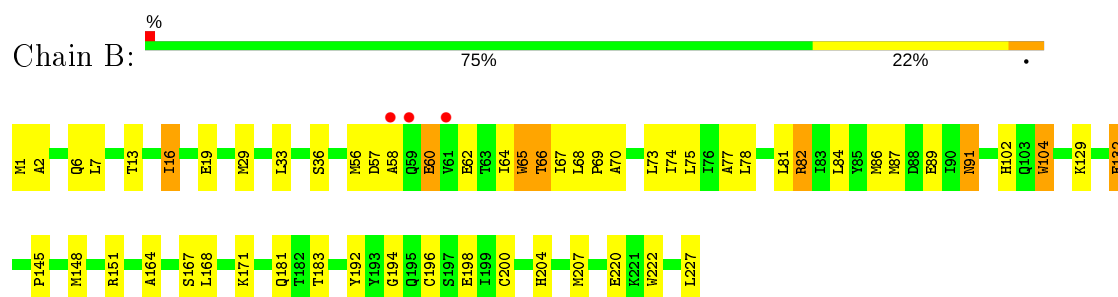
• Molecule 1: Cytochrome c oxidase subunit 1



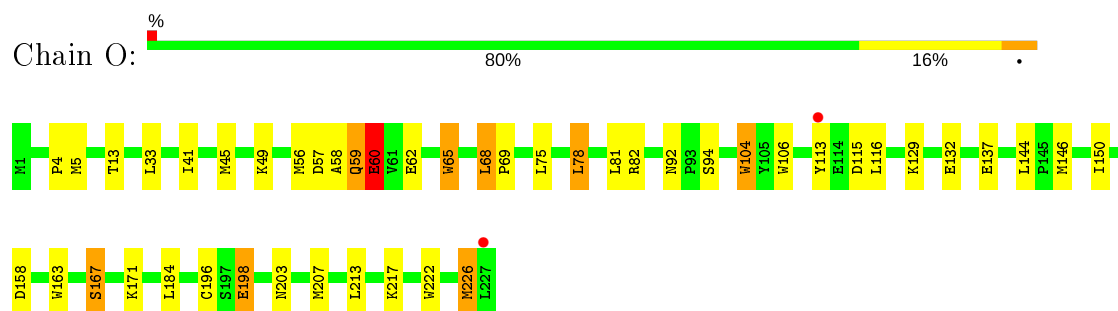
• Molecule 1: Cytochrome c oxidase subunit 1



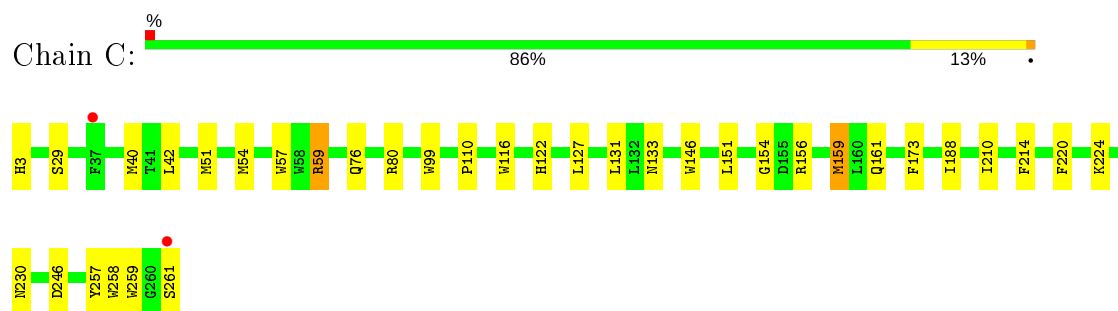
• Molecule 2: Cytochrome c oxidase subunit 2



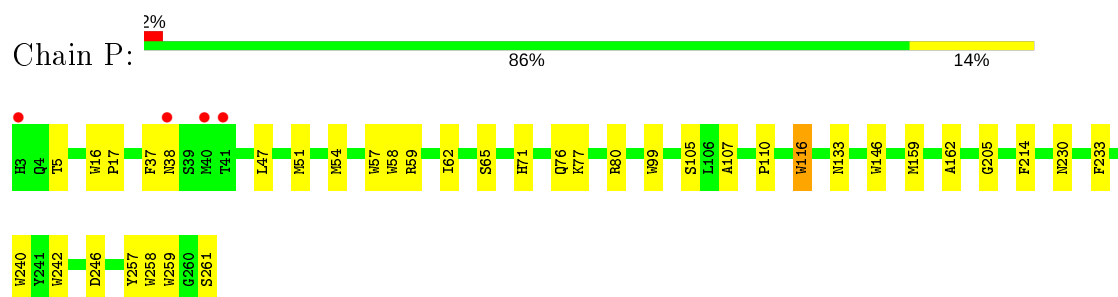
- Molecule 2: Cytochrome c oxidase subunit 2



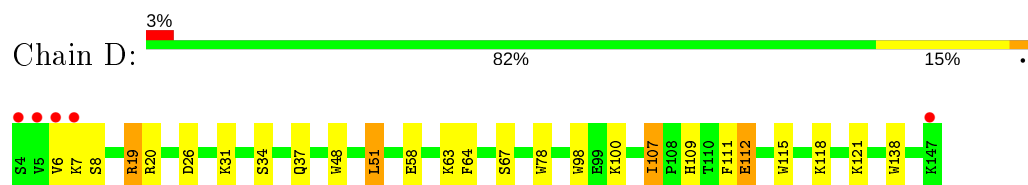
- Molecule 3: Cytochrome c oxidase subunit 3



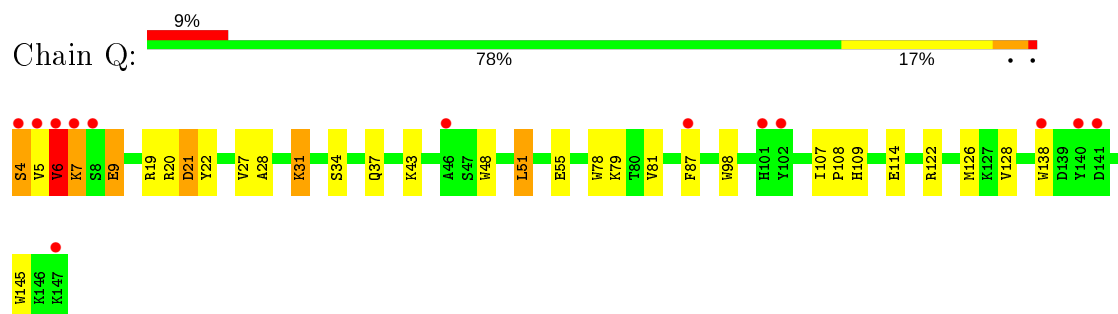
- Molecule 3: Cytochrome c oxidase subunit 3



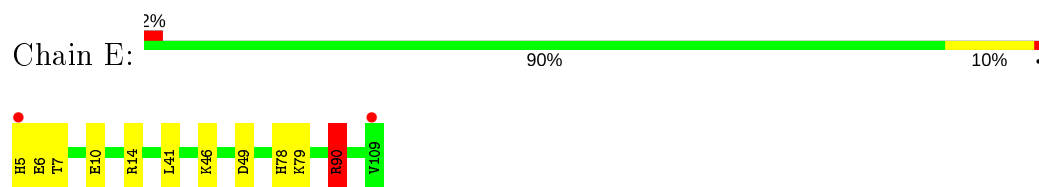
- Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial



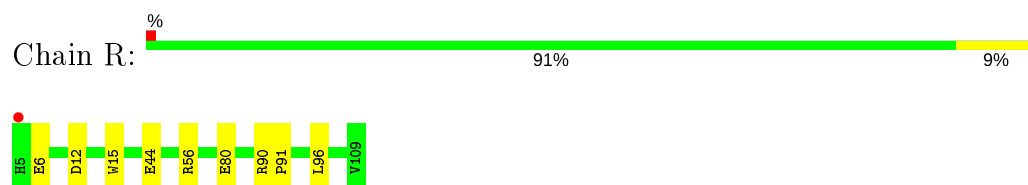
- Molecule 4: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial



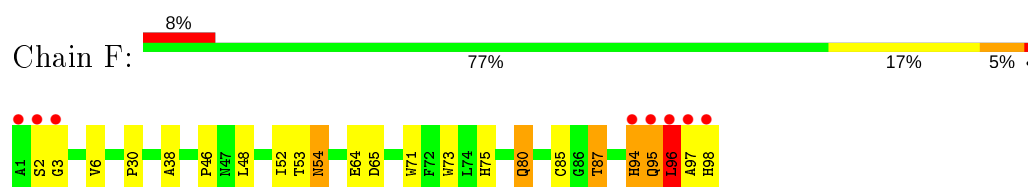
- Molecule 5: Cytochrome c oxidase subunit 5A, mitochondrial



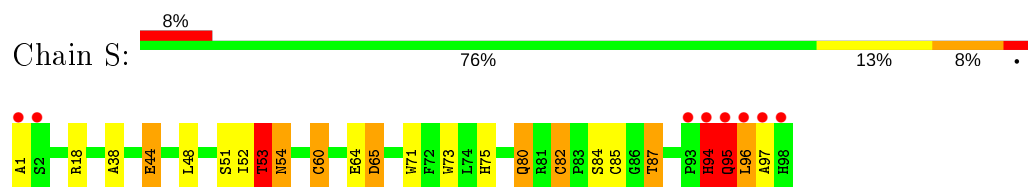
- Molecule 5: Cytochrome c oxidase subunit 5A, mitochondrial



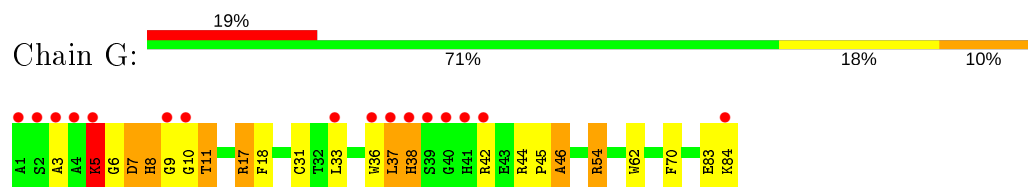
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial



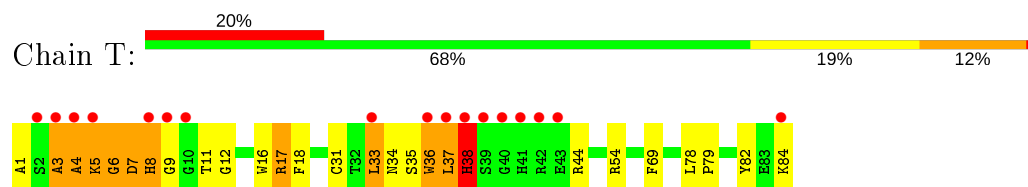
- Molecule 6: Cytochrome c oxidase subunit 5B, mitochondrial



- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial

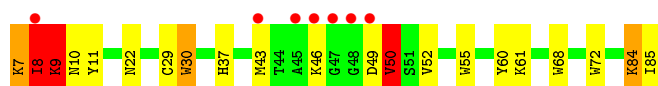


- Molecule 7: Cytochrome c oxidase subunit 6A2, mitochondrial

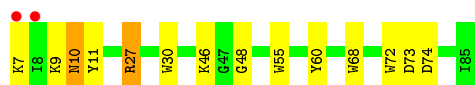
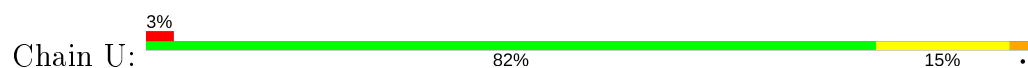


- Molecule 8: Cytochrome c oxidase subunit 6B1

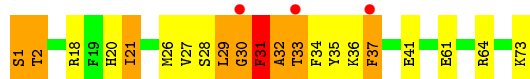




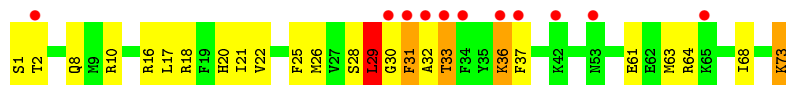
- Molecule 8: Cytochrome c oxidase subunit 6B1



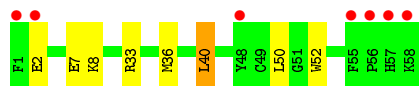
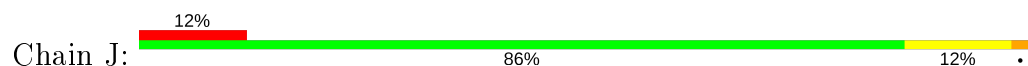
- Molecule 9: Cytochrome c oxidase subunit 6C



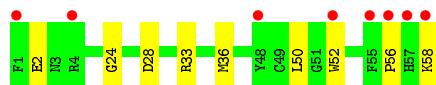
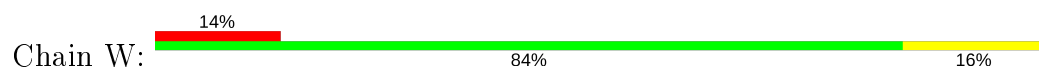
- Molecule 9: Cytochrome c oxidase subunit 6C



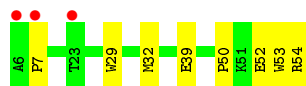
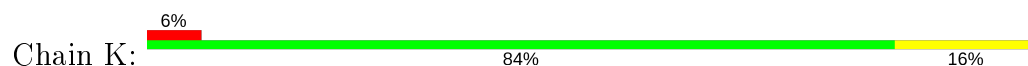
- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial



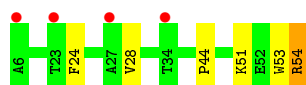
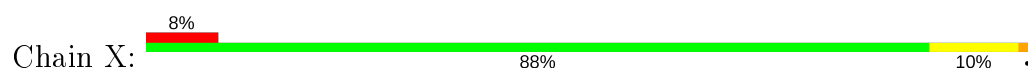
- Molecule 10: Cytochrome c oxidase subunit 7A1, mitochondrial



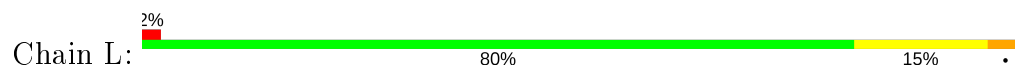
- Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial



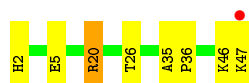
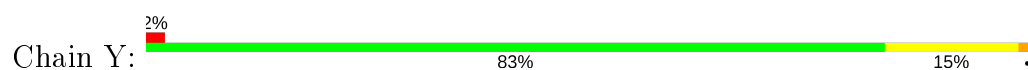
- Molecule 11: Cytochrome c oxidase subunit 7B, mitochondrial



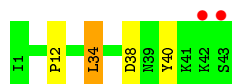
- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial



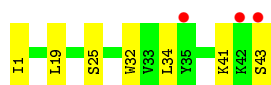
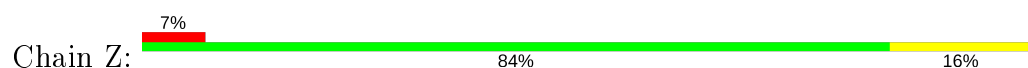
- Molecule 12: Cytochrome c oxidase subunit 7C, mitochondrial



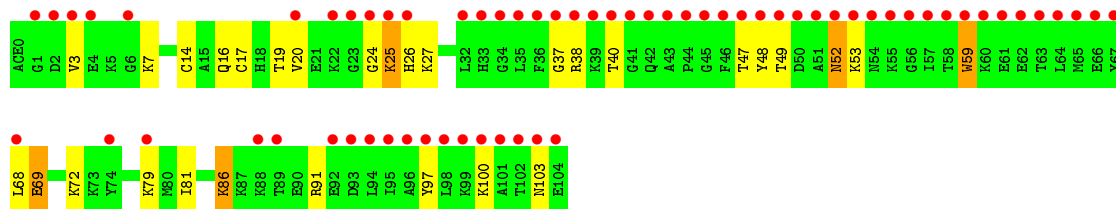
- Molecule 13: Cytochrome c oxidase subunit 8B, mitochondrial



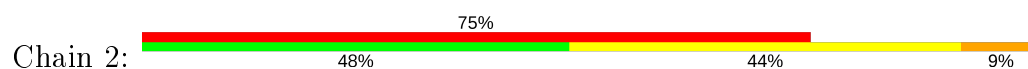
- Molecule 13: Cytochrome c oxidase subunit 8B, mitochondrial

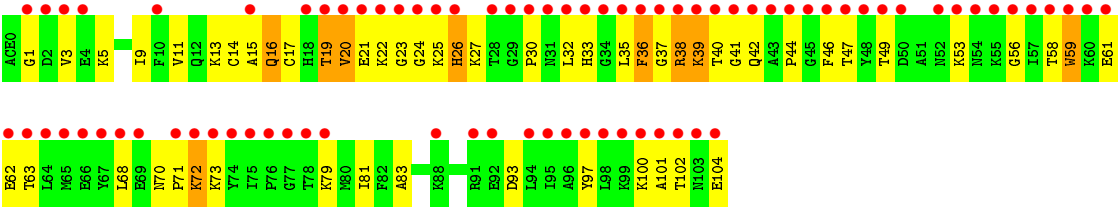


- Molecule 14: Cytochrome c



- Molecule 14: Cytochrome c





4 Data and refinement statistics

| Property | Value | Source |
|---|---|------------------|
| Space group | P 1 21 1 | Depositor |
| Cell constants a, b, c, α , β , γ | 113.29Å 183.87Å 148.93Å 90.00° 102.12° 90.00° | Depositor |
| Resolution (Å) | 40.00 – 2.00 49.35 – 2.00 | Depositor EDS |
| % Data completeness (in resolution range) | 99.4 (40.00-2.00) 99.4 (49.35-2.00) | Depositor EDS |
| R_{merge} | 0.10 | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 1.74 (at 2.00Å) | Xtriage |
| Refinement program | REFMAC 5.8.0048 | Depositor |
| R, R_{free} | 0.167 , 0.207 0.168 , 0.208 | Depositor DCC |
| R_{free} test set | 19990 reflections (5.03%) | wwPDB-VP |
| Wilson B-factor (Å ²) | 33.5 | Xtriage |
| Anisotropy | 0.586 | Xtriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.37 , 72.0 | EDS |
| L-test for twinning ² | $\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| F_o, F_c correlation | 0.97 | EDS |
| Total number of atoms | 34765 | wwPDB-VP |
| Average B, all atoms (Å ²) | 48.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.47% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CDL, ZN, CHD, ACE, PSC, SAC, NA, HEC, MG, PER, EDO, PGV, TPO, CU, DMU, CUA, PEK, FME, UNL, TGL, HEA

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

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-----------------|-------------|-----------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 1 | A | 1.31 | 11/4244 (0.3%) | 1.04 | 9/5793 (0.2%) |
| 1 | N | 1.20 | 9/4214 (0.2%) | 0.94 | 5/5754 (0.1%) |
| 2 | B | 1.26 | 6/1878 (0.3%) | 1.09 | 4/2558 (0.2%) |
| 2 | O | 0.99 | 6/1860 (0.3%) | 0.96 | 1/2534 (0.0%) |
| 3 | C | 1.20 | 5/2247 (0.2%) | 0.87 | 1/3070 (0.0%) |
| 3 | P | 1.15 | 7/2238 (0.3%) | 0.86 | 0/3058 |
| 4 | D | 1.21 | 7/1229 (0.6%) | 1.13 | 8/1658 (0.5%) |
| 4 | Q | 1.09 | 5/1240 (0.4%) | 0.97 | 2/1672 (0.1%) |
| 5 | E | 1.04 | 0/871 | 0.99 | 5/1182 (0.4%) |
| 5 | R | 1.01 | 1/871 (0.1%) | 0.89 | 0/1182 |
| 6 | F | 1.17 | 3/765 (0.4%) | 1.04 | 2/1038 (0.2%) |
| 6 | S | 1.15 | 4/765 (0.5%) | 1.15 | 5/1038 (0.5%) |
| 7 | G | 1.17 | 2/690 (0.3%) | 1.01 | 3/937 (0.3%) |
| 7 | T | 1.20 | 1/690 (0.1%) | 1.09 | 5/937 (0.5%) |
| 8 | H | 1.25 | 7/682 (1.0%) | 1.19 | 4/921 (0.4%) |
| 8 | U | 1.05 | 4/682 (0.6%) | 0.99 | 4/921 (0.4%) |
| 9 | I | 1.09 | 0/605 | 1.09 | 2/802 (0.2%) |
| 9 | V | 0.86 | 0/605 | 0.96 | 1/802 (0.1%) |
| 10 | J | 0.96 | 1/471 (0.2%) | 0.88 | 1/636 (0.2%) |
| 10 | W | 0.87 | 1/471 (0.2%) | 0.86 | 0/636 |
| 11 | K | 1.13 | 1/398 (0.3%) | 0.96 | 0/546 |
| 11 | X | 0.94 | 1/398 (0.3%) | 0.86 | 0/546 |
| 12 | L | 1.15 | 0/393 | 0.90 | 0/526 |
| 12 | Y | 1.05 | 0/393 | 0.95 | 1/526 (0.2%) |
| 13 | M | 1.05 | 0/345 | 1.01 | 1/470 (0.2%) |
| 13 | Z | 1.01 | 1/345 (0.3%) | 1.01 | 2/470 (0.4%) |
| 14 | 1 | 0.73 | 1/840 (0.1%) | 0.78 | 0/1120 |
| 14 | 2 | 0.68 | 1/840 (0.1%) | 0.74 | 0/1120 |
| All | All | 1.14 | 85/31270 (0.3%) | 0.98 | 66/42453 (0.2%) |

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

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1 | A | 0 | 1 |
| 1 | N | 0 | 1 |
| 6 | S | 0 | 2 |
| 8 | H | 0 | 2 |
| 9 | V | 0 | 2 |
| All | All | 0 | 8 |

The worst 5 of 85 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|---------|-------|-------------|----------|
| 3 | P | 116 | TRP | CD2-CE2 | 8.38 | 1.51 | 1.41 |
| 2 | B | 132 | GLU | CD-OE2 | 8.22 | 1.34 | 1.25 |
| 6 | S | 60 | CYS | CB-SG | 8.20 | 1.96 | 1.82 |
| 2 | B | 167 | SER | CB-OG | -8.05 | 1.31 | 1.42 |
| 1 | N | 236 | TRP | CD2-CE2 | 7.79 | 1.50 | 1.41 |

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

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|--------|-------------|----------|
| 4 | D | 20 | ARG | NE-CZ-NH2 | -11.62 | 114.49 | 120.30 |
| 2 | B | 82 | ARG | NE-CZ-NH2 | 11.54 | 126.07 | 120.30 |
| 1 | A | 71 | MET | CG-SD-CE | -11.09 | 82.46 | 100.20 |
| 1 | A | 486 | ASP | CB-CG-OD1 | 10.23 | 127.51 | 118.30 |
| 5 | E | 90 | ARG | NE-CZ-NH1 | 9.99 | 125.29 | 120.30 |

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|-----------|
| 1 | A | 240 | HIS | Sidechain |
| 8 | H | 8 | ILE | Peptide |
| 8 | H | 9 | LYS | Peptide |
| 1 | N | 240 | HIS | Sidechain |
| 6 | S | 94 | HIS | Peptide |

5.2 Too-close contacts ⓘ

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 4084 | 0 | 4069 | 63 | 0 |
| 1 | N | 4065 | 0 | 4046 | 44 | 0 |
| 2 | B | 1836 | 0 | 1843 | 43 | 0 |
| 2 | O | 1824 | 0 | 1833 | 40 | 0 |
| 3 | C | 2149 | 0 | 2075 | 24 | 0 |
| 3 | P | 2143 | 0 | 2067 | 29 | 0 |
| 4 | D | 1195 | 0 | 1183 | 16 | 0 |
| 4 | Q | 1203 | 0 | 1196 | 30 | 0 |
| 5 | E | 852 | 0 | 845 | 8 | 0 |
| 5 | R | 852 | 0 | 845 | 5 | 0 |
| 6 | F | 748 | 0 | 728 | 25 | 0 |
| 6 | S | 748 | 0 | 729 | 25 | 0 |
| 7 | G | 675 | 0 | 643 | 20 | 0 |
| 7 | T | 675 | 0 | 644 | 26 | 0 |
| 8 | H | 662 | 0 | 623 | 36 | 0 |
| 8 | U | 662 | 0 | 623 | 7 | 0 |
| 9 | I | 601 | 0 | 613 | 39 | 0 |
| 9 | V | 601 | 0 | 613 | 19 | 0 |
| 10 | J | 460 | 0 | 459 | 7 | 0 |
| 10 | W | 460 | 0 | 459 | 12 | 0 |
| 11 | K | 384 | 0 | 366 | 5 | 0 |
| 11 | X | 384 | 0 | 366 | 8 | 0 |
| 12 | L | 380 | 0 | 380 | 12 | 0 |
| 12 | Y | 380 | 0 | 380 | 6 | 0 |
| 13 | M | 335 | 0 | 352 | 1 | 0 |
| 13 | Z | 335 | 0 | 352 | 4 | 0 |
| 14 | 1 | 826 | 0 | 849 | 25 | 0 |
| 14 | 2 | 826 | 0 | 848 | 40 | 0 |
| 15 | A | 1 | 0 | 0 | 0 | 0 |
| 15 | N | 1 | 0 | 0 | 0 | 0 |
| 16 | A | 1 | 0 | 0 | 0 | 0 |
| 16 | N | 1 | 0 | 0 | 0 | 0 |
| 17 | A | 1 | 0 | 0 | 0 | 0 |
| 17 | C | 1 | 0 | 0 | 0 | 0 |
| 17 | N | 1 | 0 | 0 | 0 | 0 |
| 17 | P | 1 | 0 | 0 | 0 | 0 |
| 18 | A | 129 | 0 | 88 | 9 | 0 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 18 | N | 129 | 0 | 88 | 10 | 0 |
| 19 | A | 2 | 0 | 0 | 0 | 0 |
| 19 | N | 2 | 0 | 0 | 1 | 0 |
| 20 | A | 102 | 0 | 152 | 9 | 0 |
| 20 | C | 102 | 0 | 152 | 14 | 0 |
| 20 | N | 51 | 0 | 76 | 1 | 0 |
| 20 | P | 102 | 0 | 152 | 10 | 0 |
| 21 | B | 63 | 0 | 110 | 6 | 0 |
| 21 | D | 63 | 0 | 110 | 12 | 0 |
| 21 | L | 63 | 0 | 110 | 20 | 0 |
| 21 | N | 63 | 0 | 110 | 2 | 0 |
| 21 | Q | 63 | 0 | 110 | 10 | 0 |
| 22 | B | 2 | 0 | 0 | 0 | 0 |
| 22 | O | 2 | 0 | 0 | 0 | 0 |
| 23 | B | 4 | 0 | 6 | 0 | 0 |
| 23 | C | 4 | 0 | 6 | 0 | 0 |
| 23 | E | 4 | 0 | 6 | 1 | 0 |
| 23 | F | 4 | 0 | 6 | 0 | 0 |
| 23 | G | 4 | 0 | 6 | 0 | 0 |
| 23 | I | 4 | 0 | 6 | 0 | 0 |
| 23 | N | 8 | 0 | 12 | 0 | 0 |
| 23 | S | 4 | 0 | 6 | 0 | 0 |
| 24 | C | 58 | 0 | 78 | 4 | 0 |
| 24 | G | 29 | 0 | 39 | 0 | 0 |
| 24 | J | 29 | 0 | 38 | 5 | 0 |
| 24 | P | 58 | 0 | 78 | 2 | 0 |
| 24 | T | 29 | 0 | 39 | 1 | 0 |
| 24 | W | 29 | 0 | 37 | 5 | 0 |
| 25 | C | 53 | 0 | 77 | 7 | 0 |
| 25 | P | 53 | 0 | 77 | 3 | 0 |
| 26 | C | 100 | 0 | 156 | 15 | 0 |
| 26 | G | 100 | 0 | 156 | 23 | 0 |
| 26 | P | 100 | 0 | 156 | 12 | 0 |
| 26 | T | 100 | 0 | 156 | 24 | 0 |
| 27 | C | 42 | 0 | 0 | 4 | 0 |
| 27 | J | 10 | 0 | 0 | 1 | 0 |
| 27 | L | 10 | 0 | 0 | 1 | 0 |
| 27 | N | 63 | 0 | 0 | 2 | 0 |
| 27 | P | 43 | 0 | 0 | 6 | 0 |
| 27 | T | 18 | 0 | 0 | 1 | 0 |
| 27 | W | 9 | 0 | 0 | 1 | 0 |
| 27 | Y | 10 | 0 | 0 | 1 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 28 | E | 52 | 0 | 80 | 19 | 0 |
| 28 | V | 52 | 0 | 80 | 21 | 0 |
| 29 | F | 1 | 0 | 0 | 0 | 0 |
| 29 | S | 1 | 0 | 0 | 2 | 0 |
| 30 | M | 33 | 0 | 42 | 1 | 0 |
| 30 | Z | 33 | 0 | 42 | 1 | 0 |
| 31 | 1 | 43 | 0 | 31 | 4 | 0 |
| 31 | 2 | 43 | 0 | 30 | 4 | 0 |
| 32 | 1 | 53 | 0 | 0 | 6 | 0 |
| 32 | 2 | 28 | 0 | 0 | 7 | 0 |
| 32 | A | 252 | 0 | 0 | 19 | 0 |
| 32 | B | 193 | 0 | 0 | 6 | 0 |
| 32 | C | 137 | 0 | 0 | 7 | 0 |
| 32 | D | 122 | 0 | 0 | 7 | 0 |
| 32 | E | 119 | 0 | 0 | 6 | 0 |
| 32 | F | 97 | 0 | 0 | 2 | 2 |
| 32 | G | 60 | 0 | 0 | 11 | 0 |
| 32 | H | 76 | 0 | 0 | 7 | 0 |
| 32 | I | 49 | 0 | 0 | 5 | 0 |
| 32 | J | 30 | 0 | 0 | 3 | 0 |
| 32 | K | 29 | 0 | 0 | 1 | 0 |
| 32 | L | 33 | 0 | 0 | 1 | 0 |
| 32 | M | 26 | 0 | 0 | 2 | 0 |
| 32 | N | 229 | 0 | 0 | 6 | 0 |
| 32 | O | 141 | 0 | 0 | 3 | 0 |
| 32 | P | 110 | 0 | 0 | 9 | 0 |
| 32 | Q | 99 | 0 | 0 | 7 | 0 |
| 32 | R | 83 | 0 | 0 | 1 | 0 |
| 32 | S | 95 | 0 | 0 | 5 | 0 |
| 32 | T | 41 | 0 | 0 | 3 | 0 |
| 32 | U | 54 | 0 | 0 | 4 | 2 |
| 32 | V | 17 | 0 | 0 | 2 | 0 |
| 32 | W | 10 | 0 | 0 | 0 | 0 |
| 32 | X | 17 | 0 | 0 | 3 | 0 |
| 32 | Y | 21 | 0 | 0 | 0 | 0 |
| 32 | Z | 16 | 0 | 0 | 0 | 0 |
| All | All | 34765 | 0 | 32733 | 716 | 2 |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 716 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|-------------------|--------------------------|-------------------|
| 27:C:310:UNL:C4 | 27:C:310:UNL:C6 | 1.76 | 1.36 |
| 32:A:927:HOH:O | 26:T:101:CDL:H412 | 1.17 | 1.28 |
| 5:E:79:LYS:HE3 | 32:E:387:HOH:O | 1.31 | 1.24 |
| 27:W:102:UNL:C5 | 27:W:102:UNL:C4 | 2.17 | 1.23 |
| 1:A:486:ASP:OD2 | 4:D:19:ARG:HD2 | 1.32 | 1.21 |

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|----------------|-----------------------|--------------------------|-------------------|
| 32:F:266:HOH:O | 32:U:148:HOH:O[1_455] | 2.11 | 0.09 |
| 32:F:276:HOH:O | 32:U:141:HOH:O[1_455] | 2.14 | 0.06 |

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|----------------|-----------|---------|----------|-------------|-----|
| 1 | A | 524/514 (102%) | 510 (97%) | 14 (3%) | 0 | 100 | 100 |
| 1 | N | 520/514 (101%) | 504 (97%) | 16 (3%) | 0 | 100 | 100 |
| 2 | B | 227/227 (100%) | 217 (96%) | 9 (4%) | 1 (0%) | 34 | 30 |
| 2 | O | 225/227 (99%) | 216 (96%) | 8 (4%) | 1 (0%) | 34 | 30 |
| 3 | C | 263/259 (102%) | 259 (98%) | 4 (2%) | 0 | 100 | 100 |
| 3 | P | 262/259 (101%) | 256 (98%) | 5 (2%) | 1 (0%) | 34 | 30 |
| 4 | D | 142/144 (99%) | 135 (95%) | 7 (5%) | 0 | 100 | 100 |
| 4 | Q | 143/144 (99%) | 136 (95%) | 5 (4%) | 2 (1%) | 11 | 5 |
| 5 | E | 103/105 (98%) | 102 (99%) | 1 (1%) | 0 | 100 | 100 |
| 5 | R | 103/105 (98%) | 102 (99%) | 1 (1%) | 0 | 100 | 100 |
| 6 | F | 96/98 (98%) | 90 (94%) | 4 (4%) | 2 (2%) | 7 | 2 |
| 6 | S | 96/98 (98%) | 90 (94%) | 3 (3%) | 3 (3%) | 4 | 1 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 7 | G | 81/84 (96%) | 65 (80%) | 10 (12%) | 6 (7%) | 1 | 0 |
| 7 | T | 81/84 (96%) | 64 (79%) | 10 (12%) | 7 (9%) | 1 | 0 |
| 8 | H | 77/79 (98%) | 70 (91%) | 4 (5%) | 3 (4%) | 3 | 1 |
| 8 | U | 77/79 (98%) | 73 (95%) | 3 (4%) | 1 (1%) | 12 | 6 |
| 9 | I | 71/73 (97%) | 67 (94%) | 1 (1%) | 3 (4%) | 3 | 1 |
| 9 | V | 71/73 (97%) | 65 (92%) | 4 (6%) | 2 (3%) | 5 | 1 |
| 10 | J | 56/58 (97%) | 56 (100%) | 0 | 0 | 100 | 100 |
| 10 | W | 56/58 (97%) | 55 (98%) | 0 | 1 (2%) | 8 | 3 |
| 11 | K | 47/49 (96%) | 47 (100%) | 0 | 0 | 100 | 100 |
| 11 | X | 47/49 (96%) | 44 (94%) | 3 (6%) | 0 | 100 | 100 |
| 12 | L | 44/46 (96%) | 42 (96%) | 2 (4%) | 0 | 100 | 100 |
| 12 | Y | 44/46 (96%) | 42 (96%) | 2 (4%) | 0 | 100 | 100 |
| 13 | M | 41/43 (95%) | 38 (93%) | 3 (7%) | 0 | 100 | 100 |
| 13 | Z | 41/43 (95%) | 41 (100%) | 0 | 0 | 100 | 100 |
| 14 | 1 | 103/105 (98%) | 90 (87%) | 11 (11%) | 2 (2%) | 8 | 3 |
| 14 | 2 | 103/105 (98%) | 81 (79%) | 15 (15%) | 7 (7%) | 1 | 0 |
| All | All | 3744/3768 (99%) | 3557 (95%) | 145 (4%) | 42 (1%) | 14 | 8 |

5 of 42 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 6 | F | 2 | SER |
| 6 | F | 96 | LEU |
| 7 | G | 3 | ALA |
| 7 | G | 7 | ASP |
| 7 | G | 8 | HIS |

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|------------------|------------|----------|-------------|----|
| 1 | A | 437/426 (103%) | 429 (98%) | 8 (2%) | 59 | 63 |
| 1 | N | 433/426 (102%) | 425 (98%) | 8 (2%) | 59 | 63 |
| 2 | B | 212/210 (101%) | 204 (96%) | 8 (4%) | 33 | 31 |
| 2 | O | 210/210 (100%) | 196 (93%) | 14 (7%) | 16 | 11 |
| 3 | C | 230/224 (103%) | 225 (98%) | 5 (2%) | 52 | 55 |
| 3 | P | 229/224 (102%) | 225 (98%) | 4 (2%) | 60 | 65 |
| 4 | D | 128/128 (100%) | 123 (96%) | 5 (4%) | 32 | 30 |
| 4 | Q | 129/128 (101%) | 123 (95%) | 6 (5%) | 26 | 22 |
| 5 | E | 92/92 (100%) | 90 (98%) | 2 (2%) | 52 | 55 |
| 5 | R | 92/92 (100%) | 90 (98%) | 2 (2%) | 52 | 55 |
| 6 | F | 81/81 (100%) | 77 (95%) | 4 (5%) | 25 | 21 |
| 6 | S | 81/81 (100%) | 75 (93%) | 6 (7%) | 13 | 9 |
| 7 | G | 67/67 (100%) | 60 (90%) | 7 (10%) | 7 | 4 |
| 7 | T | 67/67 (100%) | 60 (90%) | 7 (10%) | 7 | 4 |
| 8 | H | 71/71 (100%) | 63 (89%) | 8 (11%) | 6 | 3 |
| 8 | U | 71/71 (100%) | 69 (97%) | 2 (3%) | 43 | 44 |
| 9 | I | 57/57 (100%) | 50 (88%) | 7 (12%) | 4 | 2 |
| 9 | V | 57/57 (100%) | 51 (90%) | 6 (10%) | 7 | 4 |
| 10 | J | 49/49 (100%) | 48 (98%) | 1 (2%) | 55 | 58 |
| 10 | W | 49/49 (100%) | 47 (96%) | 2 (4%) | 30 | 28 |
| 11 | K | 39/39 (100%) | 37 (95%) | 2 (5%) | 24 | 19 |
| 11 | X | 39/39 (100%) | 38 (97%) | 1 (3%) | 46 | 48 |
| 12 | L | 39/39 (100%) | 36 (92%) | 3 (8%) | 13 | 8 |
| 12 | Y | 39/39 (100%) | 36 (92%) | 3 (8%) | 13 | 8 |
| 13 | M | 37/37 (100%) | 34 (92%) | 3 (8%) | 11 | 7 |
| 13 | Z | 37/37 (100%) | 35 (95%) | 2 (5%) | 22 | 18 |
| 14 | 1 | 86/86 (100%) | 78 (91%) | 8 (9%) | 9 | 5 |
| 14 | 2 | 86/86 (100%) | 75 (87%) | 11 (13%) | 4 | 2 |
| All | All | 3244/3212 (101%) | 3099 (96%) | 145 (4%) | 27 | 24 |

5 of 145 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | N | 109 | PHE |
| 2 | O | 167 | SER |
| 14 | 2 | 14 | CYS |
| 1 | N | 138 | HIS |
| 2 | O | 65 | TRP |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | N | 4 | ASN |
| 1 | N | 512 | ASN |
| 9 | V | 20 | HIS |
| 1 | N | 80 | ASN |
| 1 | N | 178 | GLN |

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 1 | FME | N | 1 | 1 | 8,9,10 | 0.82 | 0 | 7,9,11 | 6.36 | 5 (71%) |
| 7 | TPO | T | 11 | 7 | 8,10,11 | 2.15 | 2 (25%) | 10,14,16 | 1.27 | 1 (10%) |
| 7 | TPO | G | 11 | 7 | 8,10,11 | 1.80 | 2 (25%) | 10,14,16 | 1.05 | 0 |
| 1 | FME | A | 1 | 1 | 8,9,10 | 1.47 | 1 (12%) | 7,9,11 | 5.60 | 5 (71%) |
| 9 | SAC | I | 1 | 9 | 7,8,9 | 2.23 | 2 (28%) | 8,9,11 | 2.36 | 3 (37%) |
| 2 | FME | O | 1 | 2 | 8,9,10 | 0.83 | 0 | 7,9,11 | 0.96 | 0 |
| 9 | SAC | V | 1 | 9 | 7,8,9 | 2.50 | 2 (28%) | 8,9,11 | 1.76 | 3 (37%) |
| 2 | FME | B | 1 | 2 | 8,9,10 | 2.62 | 3 (37%) | 7,9,11 | 8.29 | 5 (71%) |

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 |
|-----|------|-------|-----|------|---------|-----------|-------|
| 1 | FME | N | 1 | 1 | - | 4/7/9/11 | - |
| 7 | TPO | T | 11 | 7 | - | 6/9/11/13 | - |
| 7 | TPO | G | 11 | 7 | - | 4/9/11/13 | - |
| 1 | FME | A | 1 | 1 | - | 4/7/9/11 | - |
| 9 | SAC | I | 1 | 9 | - | 6/7/8/10 | - |
| 2 | FME | O | 1 | 2 | - | 0/7/9/11 | - |
| 9 | SAC | V | 1 | 9 | - | 2/7/8/10 | - |
| 2 | FME | B | 1 | 2 | - | 1/7/9/11 | - |

The worst 5 of 12 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|---------|-------|-------------|----------|
| 2 | B | 1 | FME | CA-N | 5.44 | 1.54 | 1.46 |
| 9 | V | 1 | SAC | OAC-C1A | 4.88 | 1.34 | 1.23 |
| 9 | I | 1 | SAC | OAC-C1A | 4.72 | 1.33 | 1.23 |
| 9 | V | 1 | SAC | CA-N | 4.17 | 1.52 | 1.46 |
| 2 | B | 1 | FME | O1-CN | -3.92 | 1.10 | 1.22 |

The worst 5 of 22 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|--------|-------------|----------|
| 2 | B | 1 | FME | CA-N-CN | -20.68 | 91.02 | 122.82 |
| 1 | N | 1 | FME | CA-N-CN | -15.59 | 98.84 | 122.82 |
| 1 | A | 1 | FME | CA-N-CN | -13.93 | 101.39 | 122.82 |
| 2 | B | 1 | FME | O1-CN-N | 5.84 | 140.65 | 125.27 |
| 9 | I | 1 | SAC | CA-N-C1A | 4.65 | 131.72 | 123.15 |

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|-------------|
| 1 | N | 1 | FME | O1-CN-N-CA |
| 1 | N | 1 | FME | N-CA-CB-CG |
| 7 | T | 11 | TPO | N-CA-CB-CG2 |
| 7 | T | 11 | TPO | N-CA-CB-OG1 |
| 7 | T | 11 | TPO | C-CA-CB-CG2 |

There are no ring outliers.

2 monomers are involved in 3 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 7 | G | 11 | TPO | 2 | 0 |
| 9 | I | 1 | SAC | 1 | 0 |

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 76 ligands modelled in this entry, 15 are unknown and 10 are monoatomic - leaving 51 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 | $\# Z > 2$ |
| 18 | HEA | N | 606 | 1,19 | 44,67,67 | 1.31 | 5 (11%) | 37,103,103 | 1.89 | 8 (21%) |
| 22 | CUA | B | 302 | 2 | 0,1,1 | 0.00 | - | - | | |
| 24 | CHD | G | 102 | - | 29,32,32 | 1.16 | 2 (6%) | 48,51,51 | 2.05 | 13 (27%) |
| 26 | CDL | C | 306 | - | 99,99,99 | 1.39 | 12 (12%) | 105,111,111 | 1.41 | 10 (9%) |
| 20 | PGV | N | 612 | - | 50,50,50 | 0.85 | 1 (2%) | 53,56,56 | 1.21 | 4 (7%) |
| 21 | TGL | D | 201 | - | 62,62,62 | 1.39 | 6 (9%) | 65,65,65 | 1.51 | 8 (12%) |
| 20 | PGV | P | 304 | - | 50,50,50 | 0.82 | 2 (4%) | 53,56,56 | 1.17 | 6 (11%) |
| 20 | PGV | A | 607 | - | 50,50,50 | 1.12 | 2 (4%) | 53,56,56 | 1.05 | 5 (9%) |
| 24 | CHD | P | 301 | - | 29,32,32 | 1.08 | 2 (6%) | 48,51,51 | 1.92 | 13 (27%) |
| 28 | PSC | V | 101 | - | 51,51,51 | 1.21 | 3 (5%) | 57,59,59 | 1.31 | 5 (8%) |
| 21 | TGL | B | 301 | - | 62,62,62 | 1.45 | 8 (12%) | 65,65,65 | 1.87 | 13 (20%) |
| 18 | HEA | N | 605[A] | - | 44,67,67 | 1.01 | 2 (4%) | 37,103,103 | 2.12 | 14 (37%) |
| 26 | CDL | G | 101 | - | 99,99,99 | 1.44 | 12 (12%) | 105,111,111 | 1.35 | 13 (12%) |
| 18 | HEA | N | 605[B] | - | 44,67,67 | 1.00 | 2 (4%) | 37,103,103 | 2.15 | 16 (43%) |
| 20 | PGV | C | 304 | - | 50,50,50 | 0.80 | 2 (4%) | 53,56,56 | 1.33 | 7 (13%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|--------|-------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 24 | CHD | C | 307 | - | 29,32,32 | 0.90 | 1 (3%) | 48,51,51 | 3.61 | 26 (54%) |
| 24 | CHD | T | 103 | - | 29,32,32 | 1.10 | 2 (6%) | 48,51,51 | 2.05 | 18 (37%) |
| 23 | EDO | N | 614 | - | 3,3,3 | 0.41 | 0 | 2,2,2 | 0.47 | 0 |
| 20 | PGV | A | 608 | - | 50,50,50 | 1.06 | 4 (8%) | 53,56,56 | 1.28 | 6 (11%) |
| 25 | PEK | P | 303 | - | 52,52,52 | 0.99 | 3 (5%) | 55,57,57 | 0.96 | 2 (3%) |
| 24 | CHD | P | 307 | - | 29,32,32 | 0.58 | 0 | 48,51,51 | 2.48 | 19 (39%) |
| 23 | EDO | C | 311 | - | 3,3,3 | 0.61 | 0 | 2,2,2 | 0.29 | 0 |
| 23 | EDO | I | 101 | - | 3,3,3 | 0.63 | 0 | 2,2,2 | 0.28 | 0 |
| 23 | EDO | N | 613 | - | 3,3,3 | 0.57 | 0 | 2,2,2 | 0.37 | 0 |
| 28 | PSC | E | 201 | - | 51,51,51 | 1.32 | 3 (5%) | 57,59,59 | 1.51 | 9 (15%) |
| 23 | EDO | S | 102 | - | 3,3,3 | 0.64 | 0 | 2,2,2 | 0.79 | 0 |
| 30 | DMU | Z | 101 | - | 34,34,34 | 0.75 | 1 (2%) | 45,45,45 | 1.07 | 5 (11%) |
| 23 | EDO | G | 103 | - | 3,3,3 | 0.84 | 0 | 2,2,2 | 0.68 | 0 |
| 20 | PGV | P | 305 | - | 50,50,50 | 1.29 | 2 (4%) | 53,56,56 | 1.39 | 6 (11%) |
| 23 | EDO | B | 303 | - | 3,3,3 | 0.78 | 0 | 2,2,2 | 0.48 | 0 |
| 26 | CDL | P | 306 | - | 99,99,99 | 1.41 | 12 (12%) | 105,111,111 | 1.22 | 10 (9%) |
| 24 | CHD | J | 101 | - | 29,32,32 | 0.85 | 1 (3%) | 48,51,51 | 2.19 | 16 (33%) |
| 18 | HEA | A | 604[B] | - | 44,67,67 | 1.08 | 2 (4%) | 37,103,103 | 2.05 | 10 (27%) |
| 21 | TGL | N | 608 | - | 62,62,62 | 1.48 | 8 (12%) | 65,65,65 | 2.09 | 14 (21%) |
| 19 | PER | N | 607 | 18,15 | 0,1,1 | 0.00 | - | - | | |
| 19 | PER | A | 606 | 18,15 | 0,1,1 | 0.00 | - | - | | |
| 18 | HEA | A | 604[A] | - | 44,67,67 | 1.09 | 3 (6%) | 37,103,103 | 2.14 | 10 (27%) |
| 23 | EDO | E | 202 | - | 3,3,3 | 0.50 | 0 | 2,2,2 | 0.73 | 0 |
| 21 | TGL | Q | 201 | - | 62,62,62 | 1.40 | 6 (9%) | 65,65,65 | 1.29 | 9 (13%) |
| 25 | PEK | C | 303 | - | 52,52,52 | 0.96 | 2 (3%) | 55,57,57 | 1.20 | 5 (9%) |
| 26 | CDL | T | 101 | - | 99,99,99 | 1.43 | 12 (12%) | 105,111,111 | 1.48 | 15 (14%) |
| 24 | CHD | W | 101 | - | 29,32,32 | 0.87 | 2 (6%) | 48,51,51 | 3.20 | 22 (45%) |
| 20 | PGV | C | 305 | - | 50,50,50 | 1.40 | 3 (6%) | 53,56,56 | 1.42 | 7 (13%) |
| 24 | CHD | C | 301 | - | 29,32,32 | 1.32 | 4 (13%) | 48,51,51 | 1.82 | 12 (25%) |
| 23 | EDO | F | 102 | - | 3,3,3 | 0.45 | 0 | 2,2,2 | 0.54 | 0 |
| 30 | DMU | M | 101 | - | 34,34,34 | 0.74 | 0 | 45,45,45 | 1.77 | 9 (20%) |
| 31 | HEC | 2 | 201 | 14 | 26,50,50 | 1.53 | 4 (15%) | 18,82,82 | 0.95 | 1 (5%) |
| 31 | HEC | 1 | 201 | 14 | 26,50,50 | 1.35 | 3 (11%) | 18,82,82 | 1.95 | 6 (33%) |
| 21 | TGL | L | 101 | - | 62,62,62 | 1.56 | 6 (9%) | 65,65,65 | 1.58 | 14 (21%) |
| 18 | HEA | A | 605 | 1,19 | 44,67,67 | 1.15 | 4 (9%) | 37,103,103 | 1.88 | 8 (21%) |
| 22 | CUA | O | 301 | 2 | 0,1,1 | 0.00 | - | - | | |

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 |
|-----|------|-------|--------|------|----------|----------------|---------|
| 18 | HEA | N | 606 | 1,19 | 2/2/7/16 | 1/24/76/76 | - |
| 24 | CHD | C | 301 | - | - | 0/7/74/74 | 0/4/4/4 |
| 24 | CHD | G | 102 | - | - | 1/7/74/74 | 0/4/4/4 |
| 26 | CDL | C | 306 | - | - | 62/110/110/110 | - |
| 20 | PGV | N | 612 | - | - | 9/55/55/55 | - |
| 21 | TGL | D | 201 | - | - | 38/65/65/65 | - |
| 20 | PGV | P | 304 | - | - | 12/55/55/55 | - |
| 20 | PGV | A | 607 | - | - | 30/55/55/55 | - |
| 24 | CHD | P | 301 | - | - | 0/7/74/74 | 0/4/4/4 |
| 28 | PSC | V | 101 | - | - | 35/55/55/55 | - |
| 21 | TGL | B | 301 | - | - | 33/65/65/65 | - |
| 18 | HEA | N | 605[A] | - | - | 1/24/76/76 | - |
| 26 | CDL | G | 101 | - | - | 58/110/110/110 | - |
| 18 | HEA | N | 605[B] | - | - | 3/24/76/76 | - |
| 20 | PGV | C | 304 | - | - | 19/55/55/55 | - |
| 24 | CHD | C | 307 | - | - | 6/7/74/74 | 0/4/4/4 |
| 24 | CHD | T | 103 | - | - | 0/7/74/74 | 0/4/4/4 |
| 23 | EDO | N | 614 | - | - | 1/1/1/1 | - |
| 20 | PGV | A | 608 | - | - | 12/55/55/55 | - |
| 25 | PEK | P | 303 | - | - | 20/56/56/56 | - |
| 24 | CHD | P | 307 | - | - | 3/7/74/74 | 1/4/4/4 |
| 23 | EDO | C | 311 | - | - | 1/1/1/1 | - |
| 23 | EDO | I | 101 | - | - | 0/1/1/1 | - |
| 23 | EDO | N | 613 | - | - | 0/1/1/1 | - |
| 28 | PSC | E | 201 | - | - | 36/55/55/55 | - |
| 23 | EDO | S | 102 | - | - | 0/1/1/1 | - |
| 30 | DMU | Z | 101 | - | - | 4/19/59/59 | 0/2/2/2 |
| 23 | EDO | G | 103 | - | - | 0/1/1/1 | - |
| 20 | PGV | P | 305 | - | - | 31/55/55/55 | - |
| 26 | CDL | P | 306 | - | - | 67/110/110/110 | - |
| 24 | CHD | J | 101 | - | - | 5/7/74/74 | 0/4/4/4 |
| 18 | HEA | A | 604[B] | - | - | 2/24/76/76 | - |
| 21 | TGL | N | 608 | - | - | 34/65/65/65 | - |
| 18 | HEA | A | 604[A] | - | - | 1/24/76/76 | - |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|----------|----------------|---------|
| 23 | EDO | E | 202 | - | - | 1/1/1/1 | - |
| 21 | TGL | Q | 201 | - | - | 35/65/65/65 | - |
| 25 | PEK | C | 303 | - | - | 20/56/56/56 | - |
| 26 | CDL | T | 101 | - | - | 61/110/110/110 | - |
| 24 | CHD | W | 101 | - | - | 6/7/74/74 | 0/4/4/4 |
| 20 | PGV | C | 305 | - | - | 30/55/55/55 | - |
| 23 | EDO | B | 303 | - | - | 1/1/1/1 | - |
| 23 | EDO | F | 102 | - | - | 0/1/1/1 | - |
| 30 | DMU | M | 101 | - | - | 6/19/59/59 | 0/2/2/2 |
| 31 | HEC | 2 | 201 | 14 | - | 3/6/54/54 | - |
| 31 | HEC | 1 | 201 | 14 | - | 0/6/54/54 | - |
| 21 | TGL | L | 101 | - | - | 46/65/65/65 | - |
| 18 | HEA | A | 605 | 1,19 | 2/2/7/16 | 1/24/76/76 | - |

The worst 5 of 149 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|---------|------|-------------|----------|
| 21 | L | 101 | TGL | OG2-CB1 | 7.00 | 1.54 | 1.34 |
| 20 | C | 305 | PGV | O01-C1 | 5.88 | 1.50 | 1.34 |
| 21 | L | 101 | TGL | OG3-CC1 | 5.77 | 1.50 | 1.33 |
| 28 | E | 201 | PSC | O01-C1 | 5.63 | 1.50 | 1.34 |
| 28 | V | 101 | PSC | O01-C1 | 5.60 | 1.50 | 1.34 |

The worst 5 of 394 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-------------|-------|-------------|----------|
| 24 | C | 307 | CHD | C10-C9-C8 | 10.37 | 122.96 | 111.82 |
| 24 | W | 101 | CHD | C17-C13-C12 | 9.83 | 126.64 | 117.67 |
| 24 | C | 307 | CHD | C6-C5-C4 | -7.51 | 102.55 | 111.19 |
| 24 | W | 101 | CHD | C13-C17-C20 | 7.48 | 128.43 | 119.50 |
| 24 | C | 307 | CHD | C4-C5-C10 | 7.22 | 120.33 | 112.66 |

All (4) chirality outliers are listed below:

| Mol | Chain | Res | Type | Atom |
|-----|-------|-----|------|------|
| 18 | N | 606 | HEA | ND |
| 18 | N | 606 | HEA | NB |
| 18 | A | 605 | HEA | ND |
| 18 | A | 605 | HEA | NB |

5 of 735 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|-----------------|
| 26 | C | 306 | CDL | CA2-C1-CB2-OB2 |
| 26 | C | 306 | CDL | CA3-OA5-PA1-OA3 |
| 26 | C | 306 | CDL | CA3-OA5-PA1-OA4 |
| 26 | C | 306 | CDL | OA7-CA5-OA6-CA4 |
| 26 | C | 306 | CDL | CB3-OB5-PB2-OB2 |

All (1) ring outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|--------------------|
| 24 | P | 307 | CHD | C1-C10-C2-C3-C4-C5 |

38 monomers are involved in 249 short contacts:

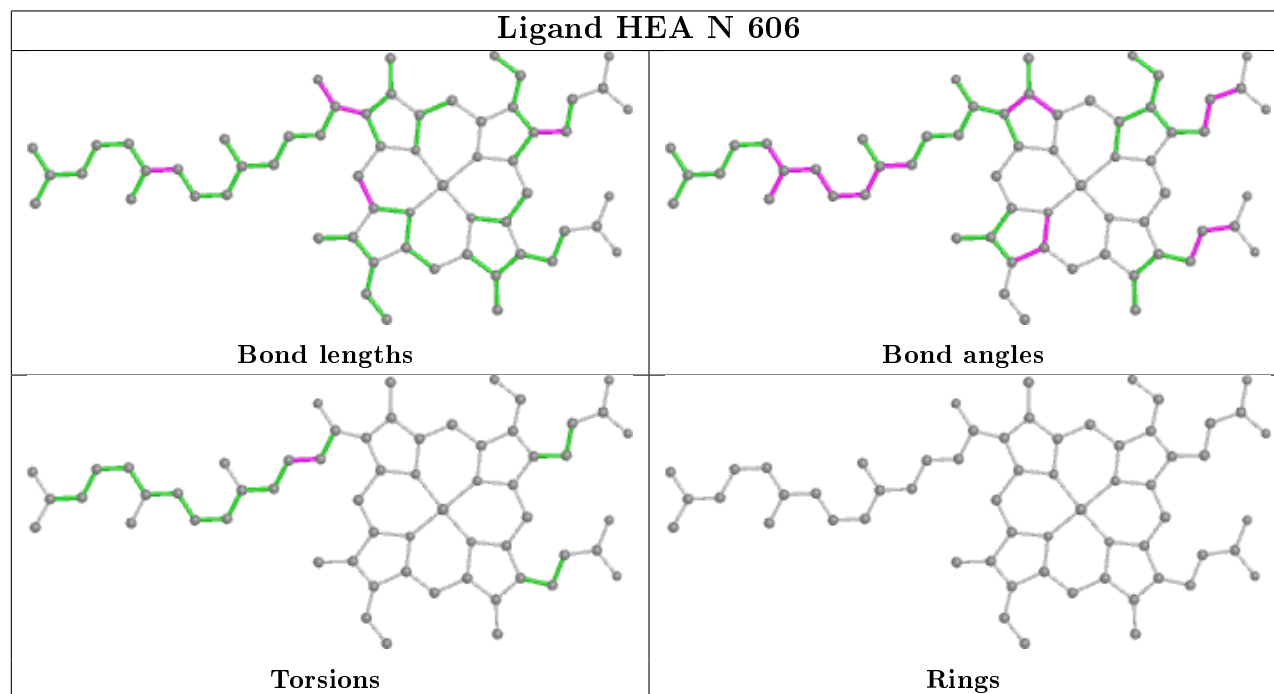
| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|--------|------|---------|--------------|
| 18 | N | 606 | HEA | 3 | 0 |
| 26 | C | 306 | CDL | 15 | 0 |
| 20 | N | 612 | PGV | 1 | 0 |
| 21 | D | 201 | TGL | 12 | 0 |
| 20 | P | 304 | PGV | 6 | 0 |
| 20 | A | 607 | PGV | 5 | 0 |
| 24 | P | 301 | CHD | 1 | 0 |
| 28 | V | 101 | PSC | 21 | 0 |
| 21 | B | 301 | TGL | 6 | 0 |
| 18 | N | 605[A] | HEA | 1 | 0 |
| 26 | G | 101 | CDL | 23 | 0 |
| 18 | N | 605[B] | HEA | 6 | 0 |
| 20 | C | 304 | PGV | 5 | 0 |
| 24 | C | 307 | CHD | 3 | 0 |
| 24 | T | 103 | CHD | 1 | 0 |
| 20 | A | 608 | PGV | 4 | 0 |
| 25 | P | 303 | PEK | 3 | 0 |
| 24 | P | 307 | CHD | 1 | 0 |
| 28 | E | 201 | PSC | 19 | 0 |
| 30 | Z | 101 | DMU | 1 | 0 |
| 20 | P | 305 | PGV | 4 | 0 |
| 26 | P | 306 | CDL | 12 | 0 |
| 24 | J | 101 | CHD | 5 | 0 |
| 18 | A | 604[B] | HEA | 6 | 0 |
| 21 | N | 608 | TGL | 2 | 0 |
| 19 | N | 607 | PER | 1 | 0 |
| 23 | E | 202 | EDO | 1 | 0 |
| 21 | Q | 201 | TGL | 10 | 0 |

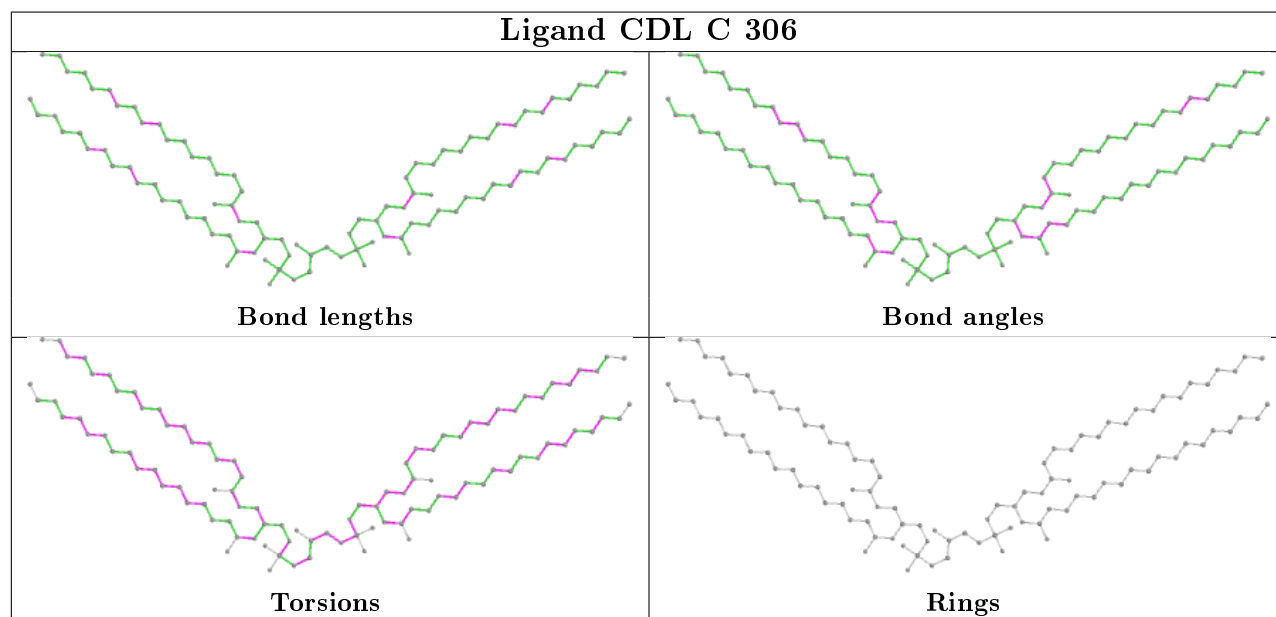
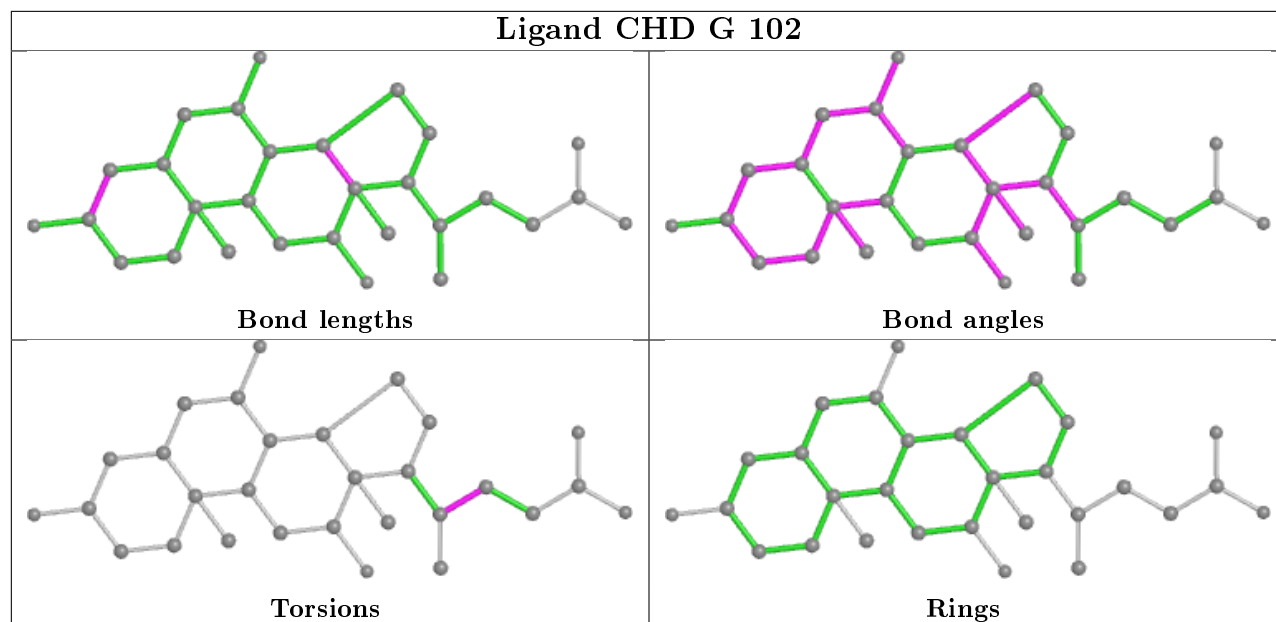
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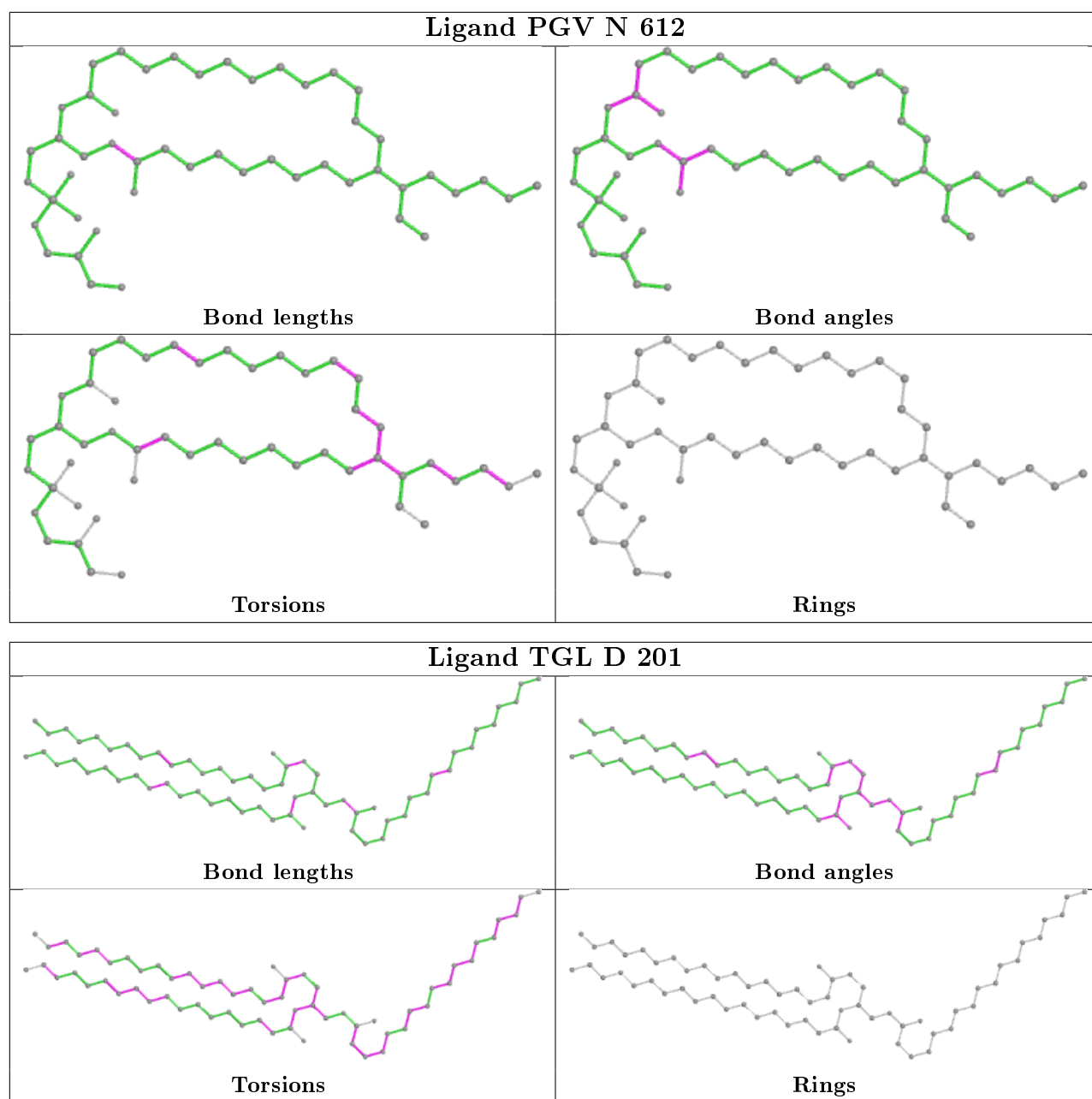
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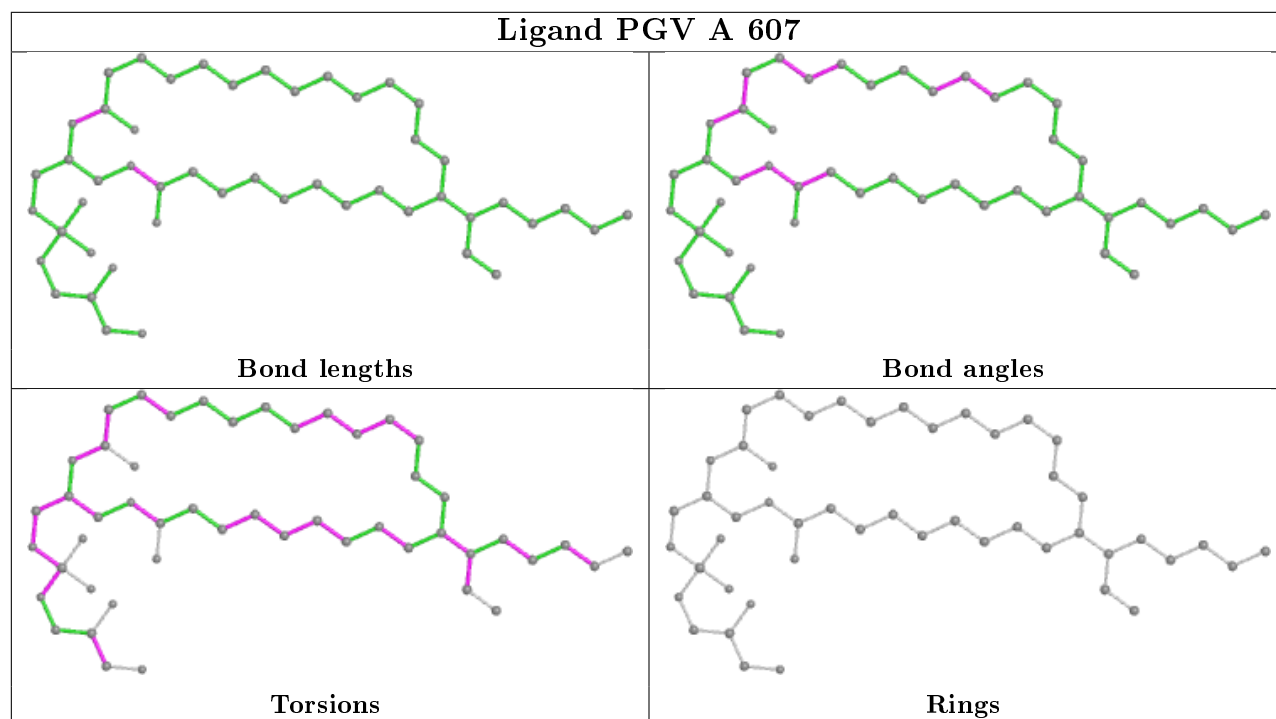
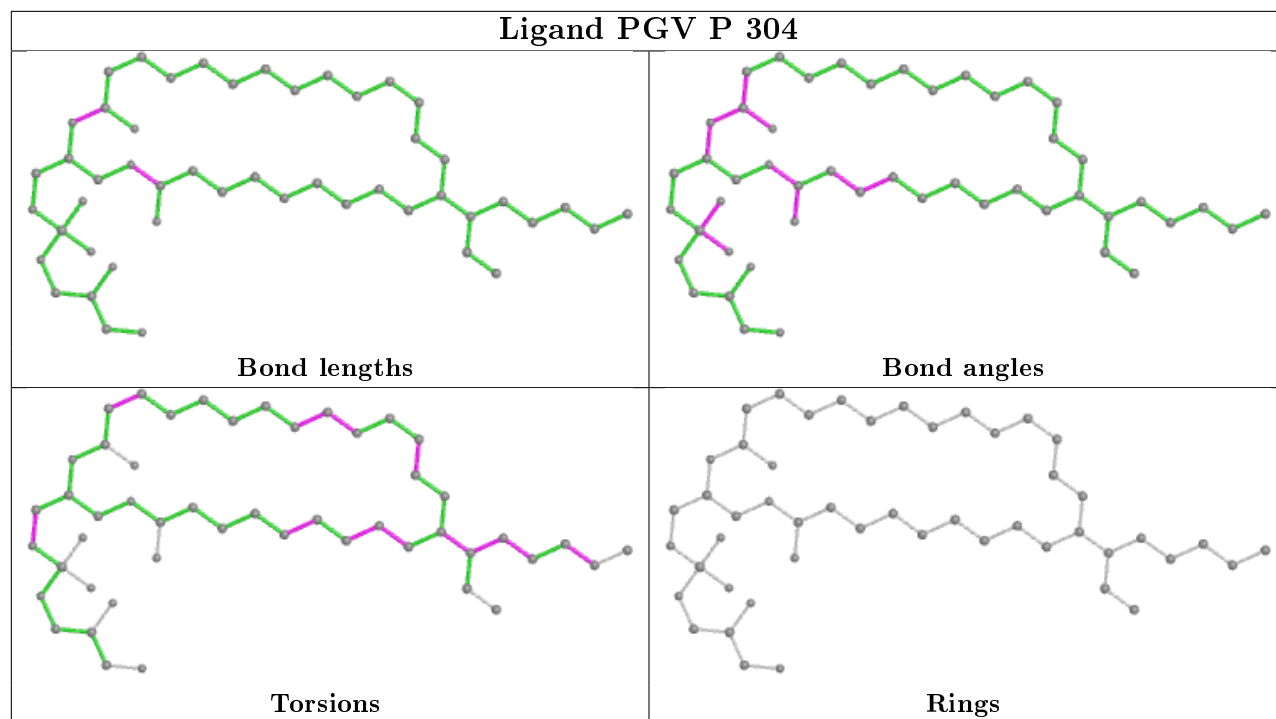
| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 25 | C | 303 | PEK | 7 | 0 |
| 26 | T | 101 | CDL | 24 | 0 |
| 24 | W | 101 | CHD | 5 | 0 |
| 20 | C | 305 | PGV | 9 | 0 |
| 24 | C | 301 | CHD | 1 | 0 |
| 30 | M | 101 | DMU | 1 | 0 |
| 31 | 2 | 201 | HEC | 4 | 0 |
| 31 | 1 | 201 | HEC | 4 | 0 |
| 21 | L | 101 | TGL | 20 | 0 |
| 18 | A | 605 | HEA | 3 | 0 |

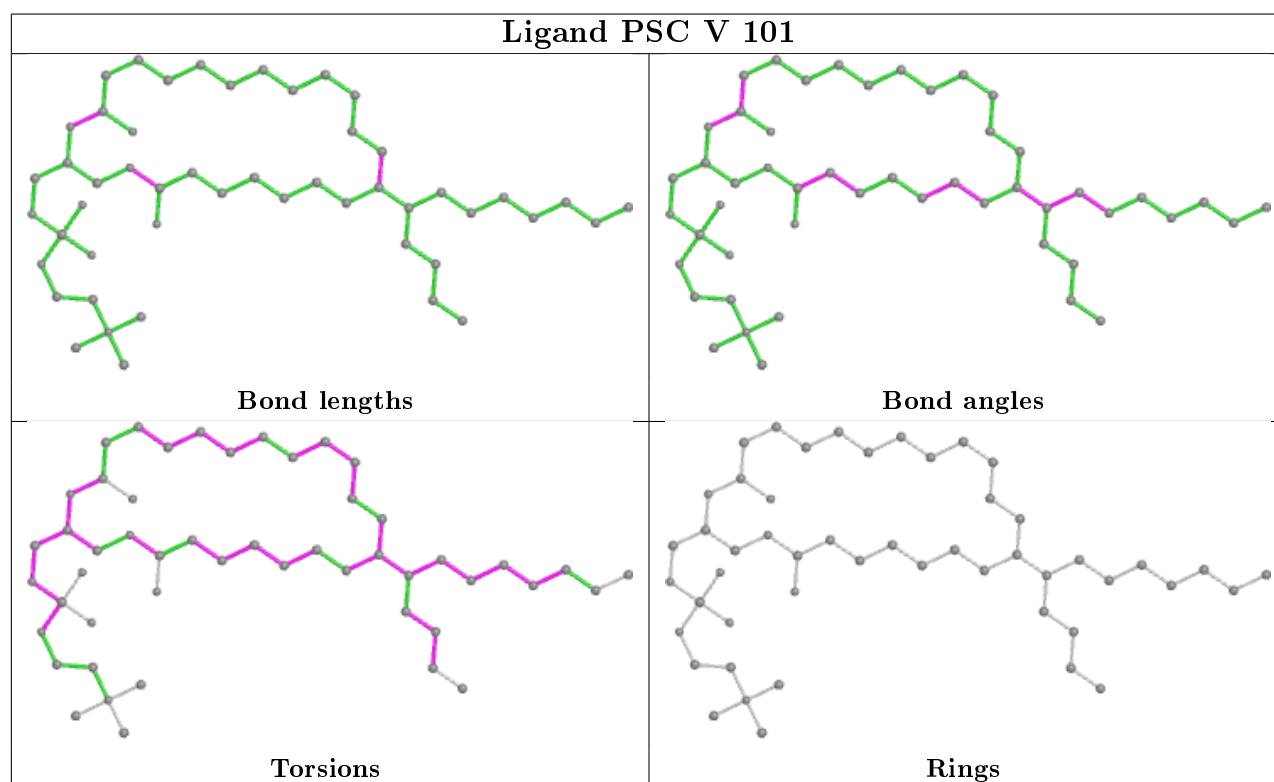
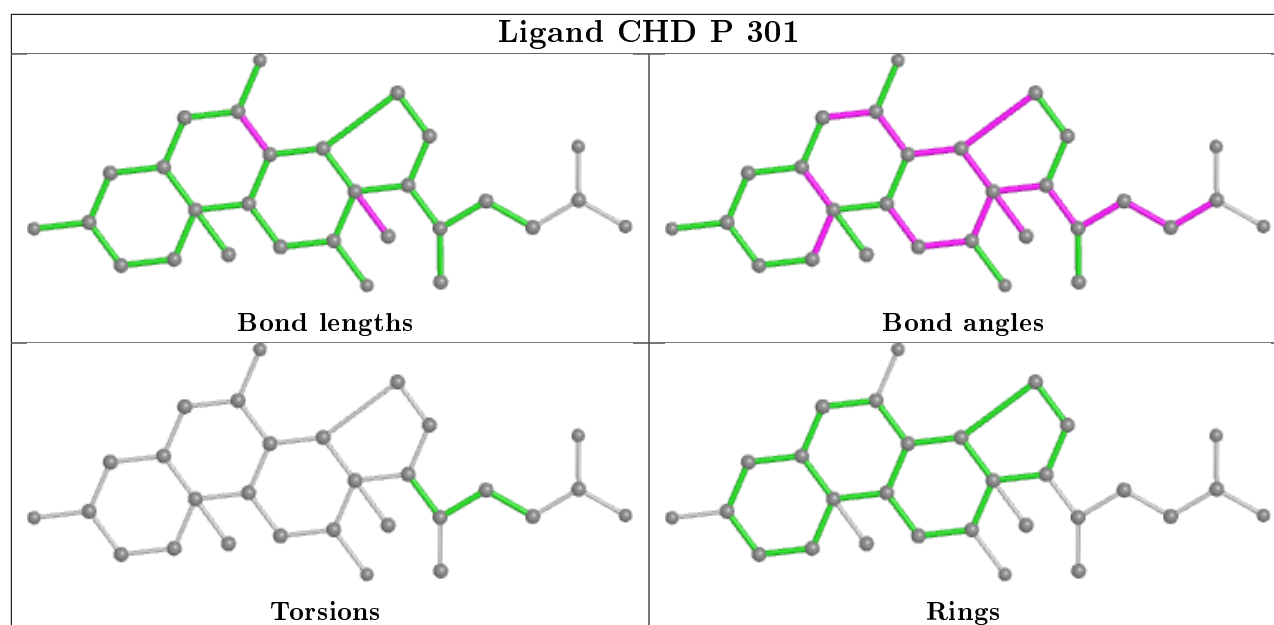
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

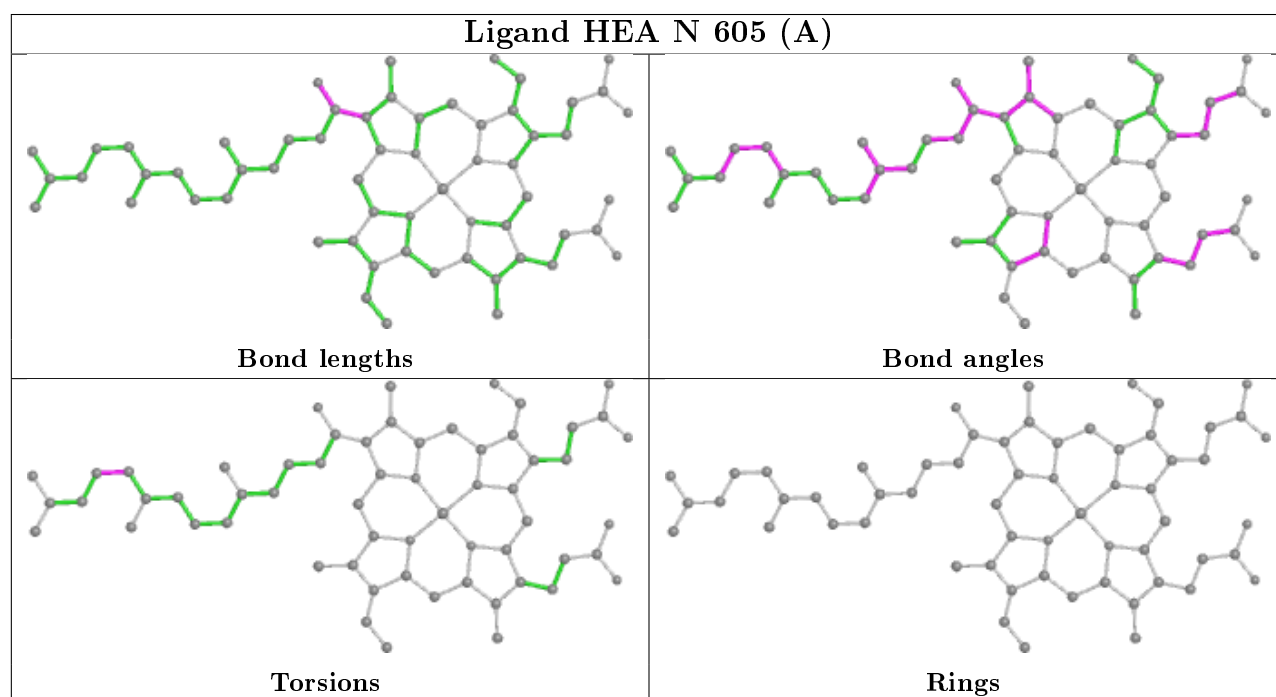
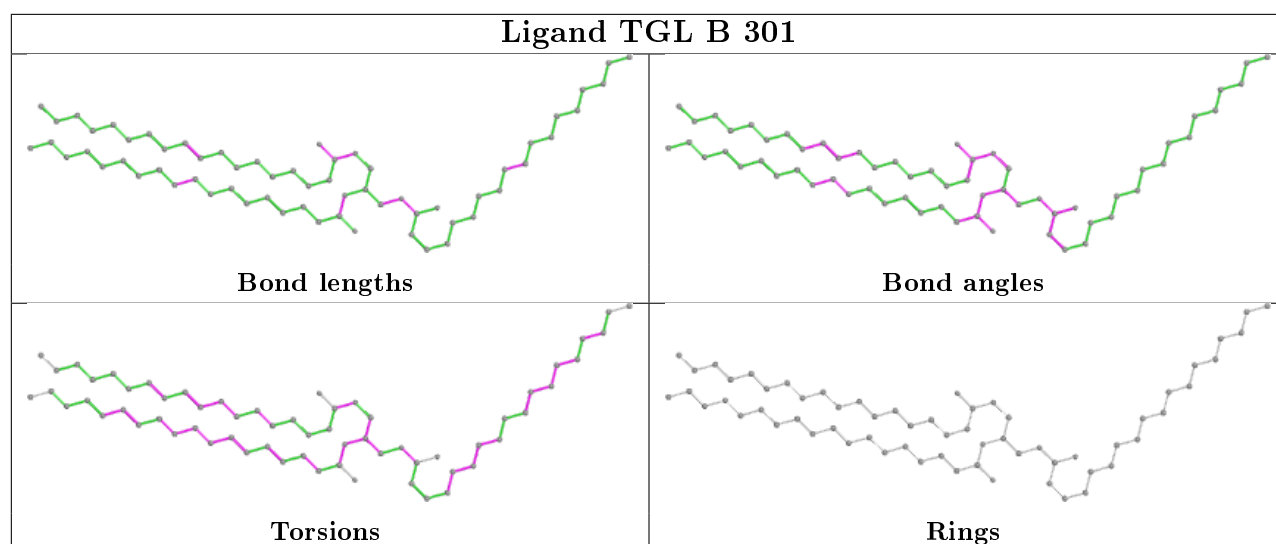


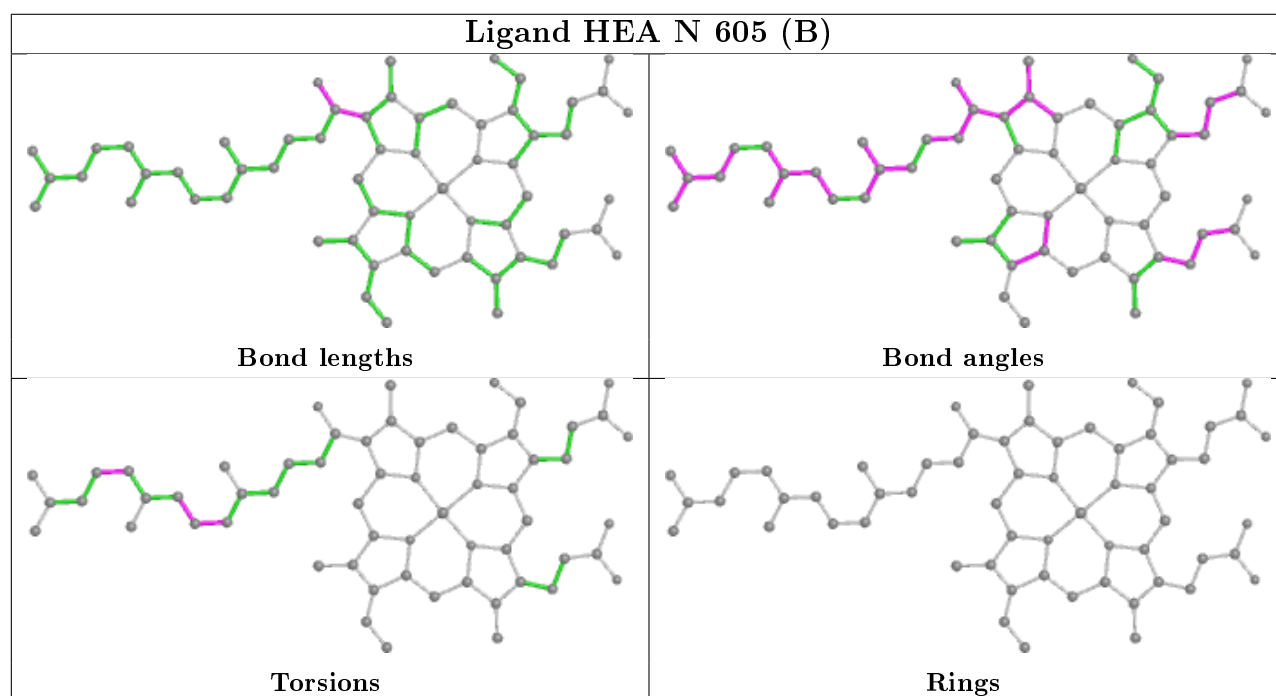
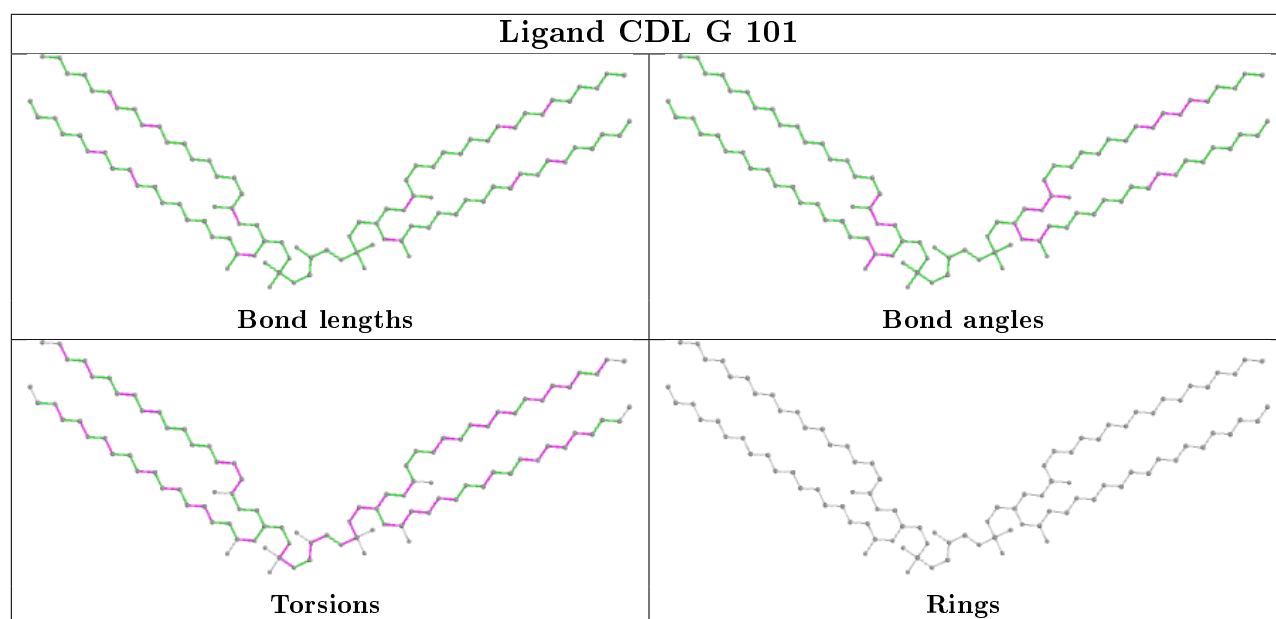


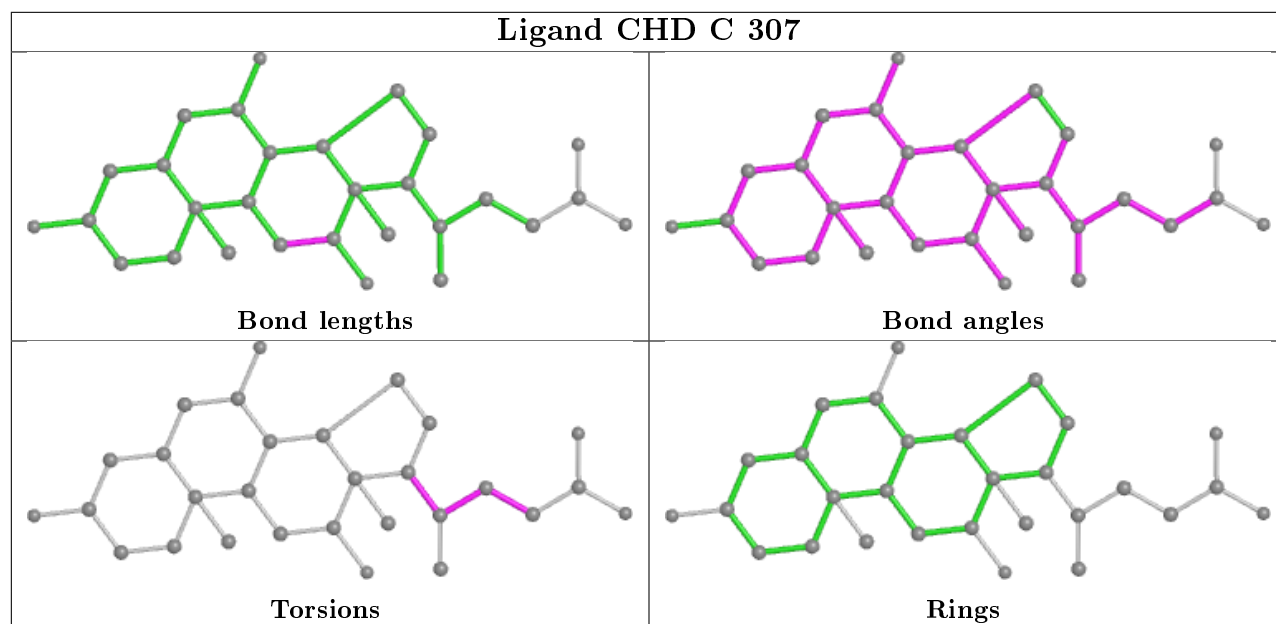
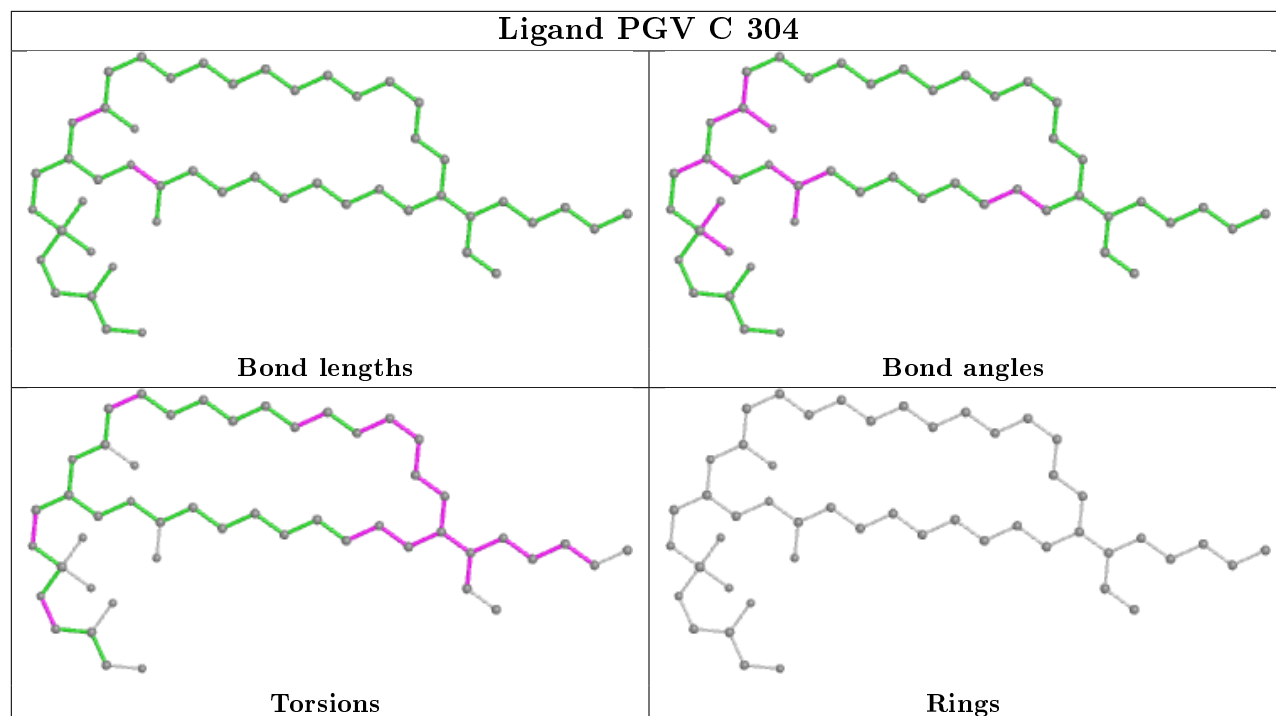


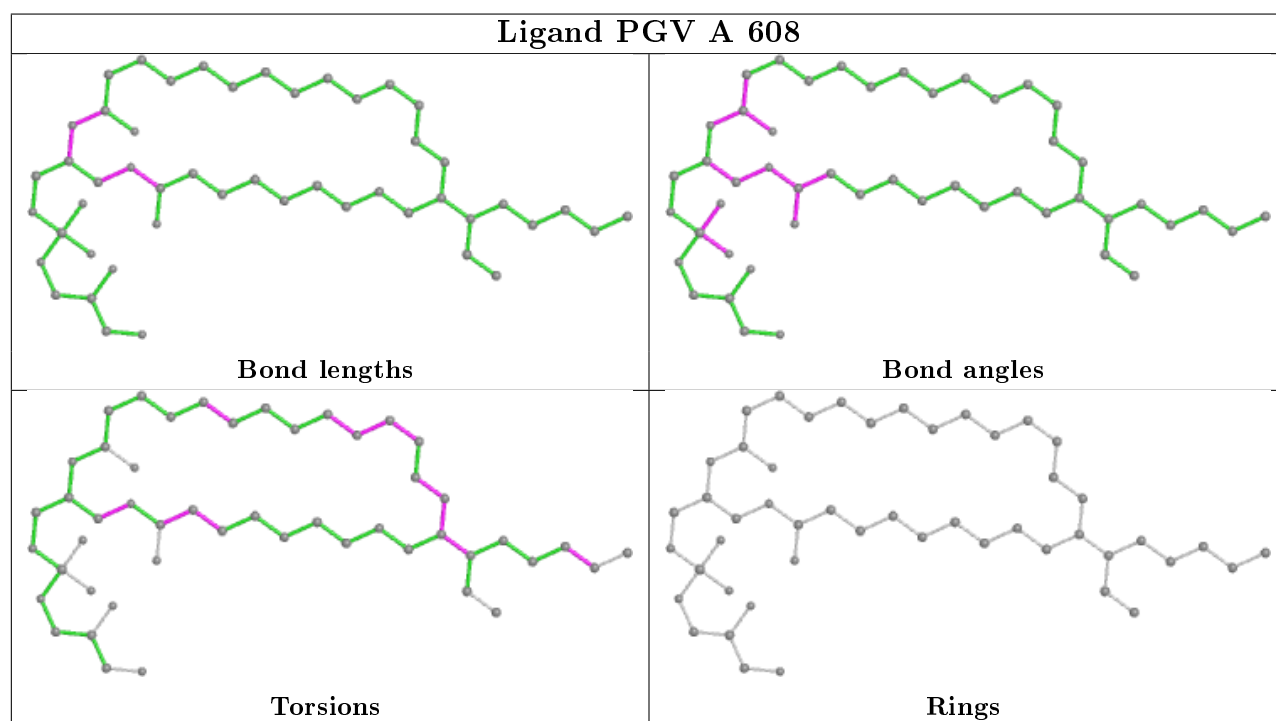
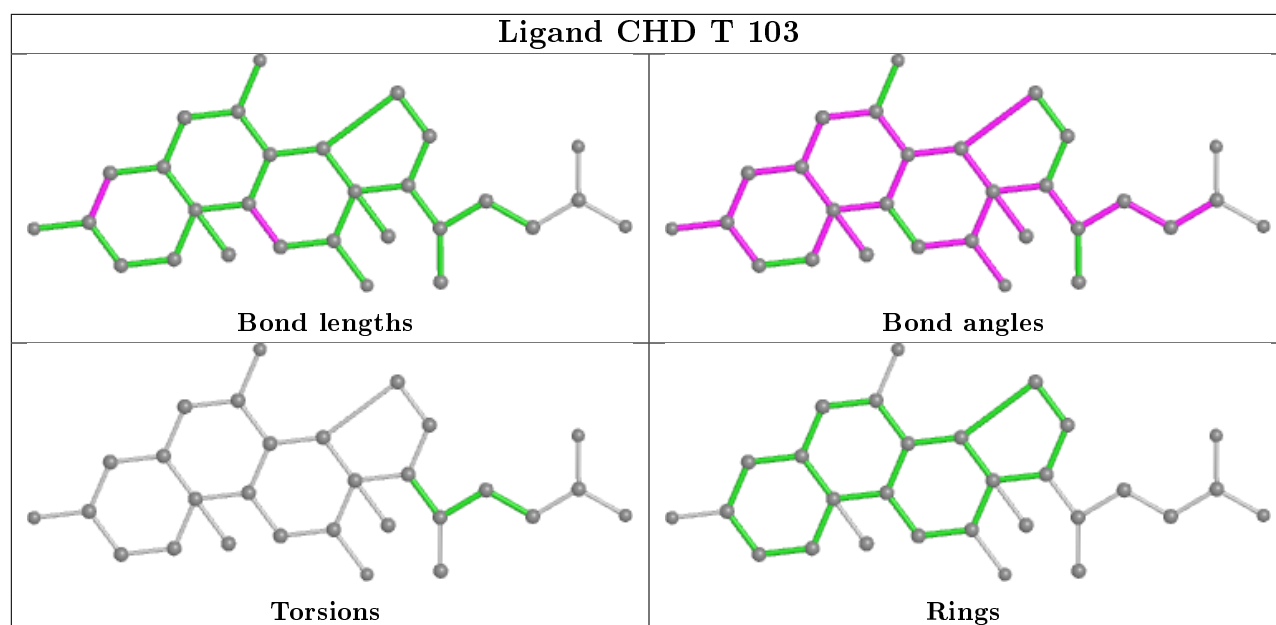




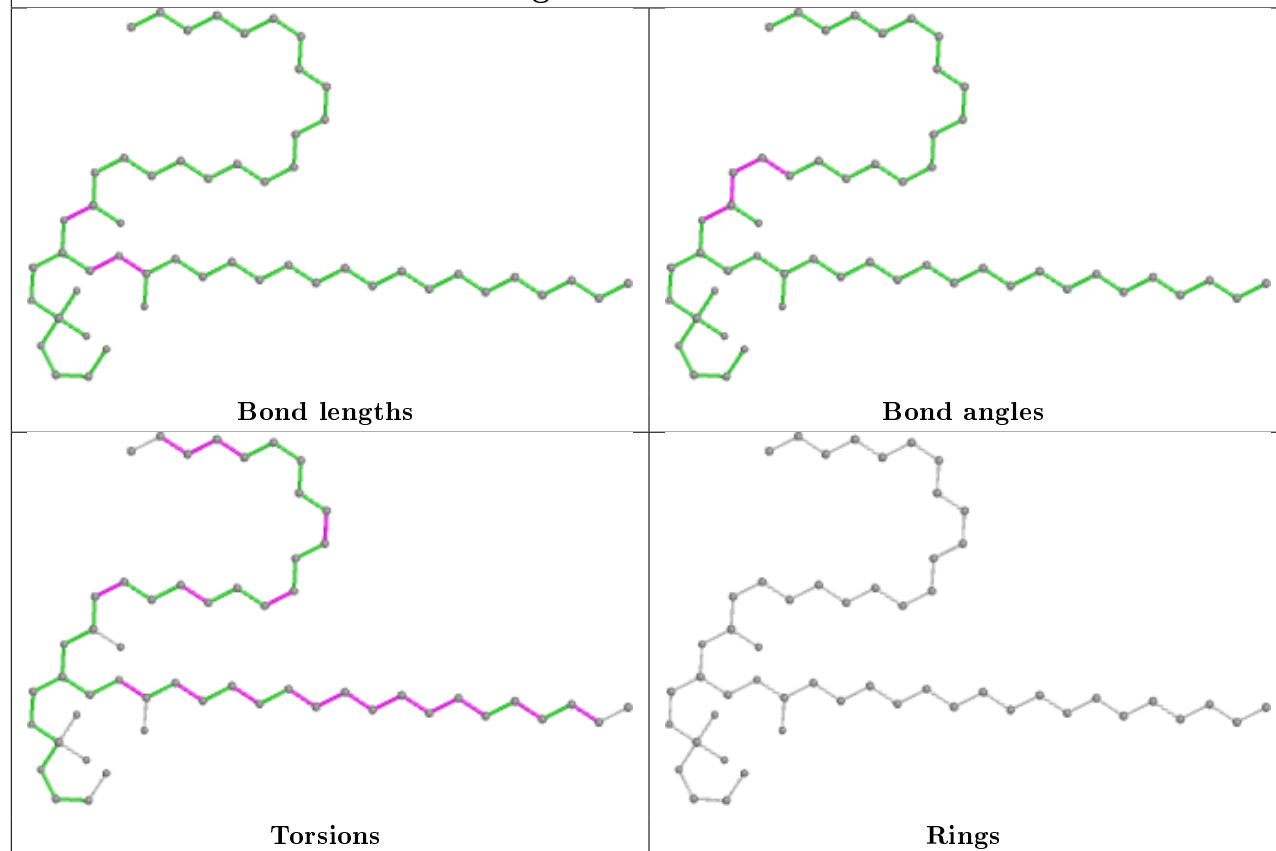




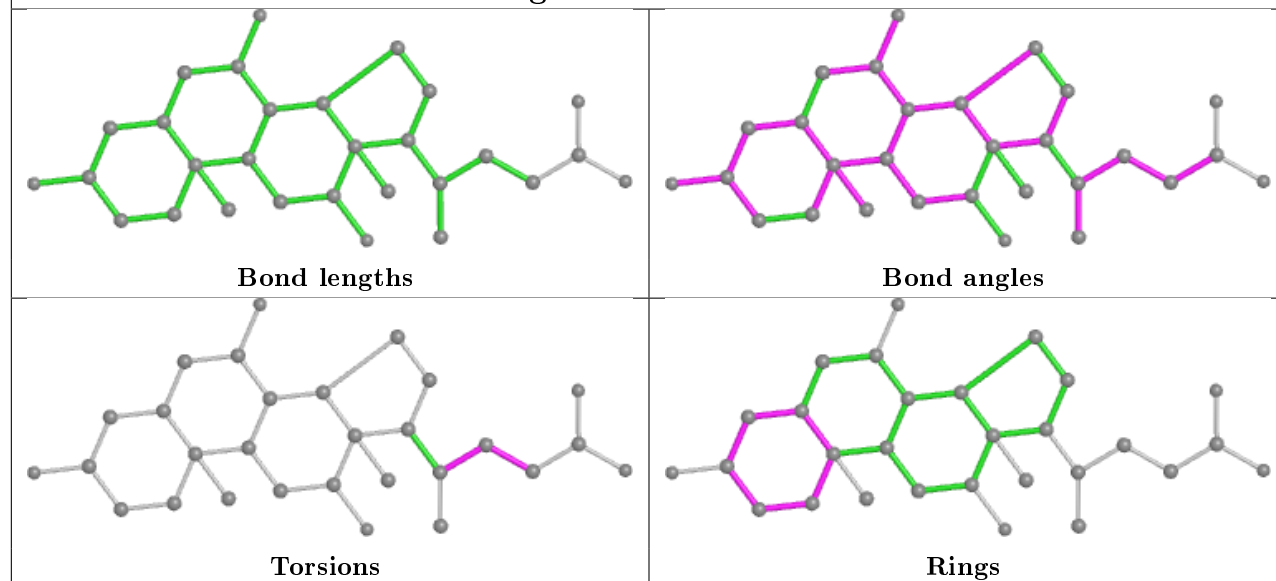




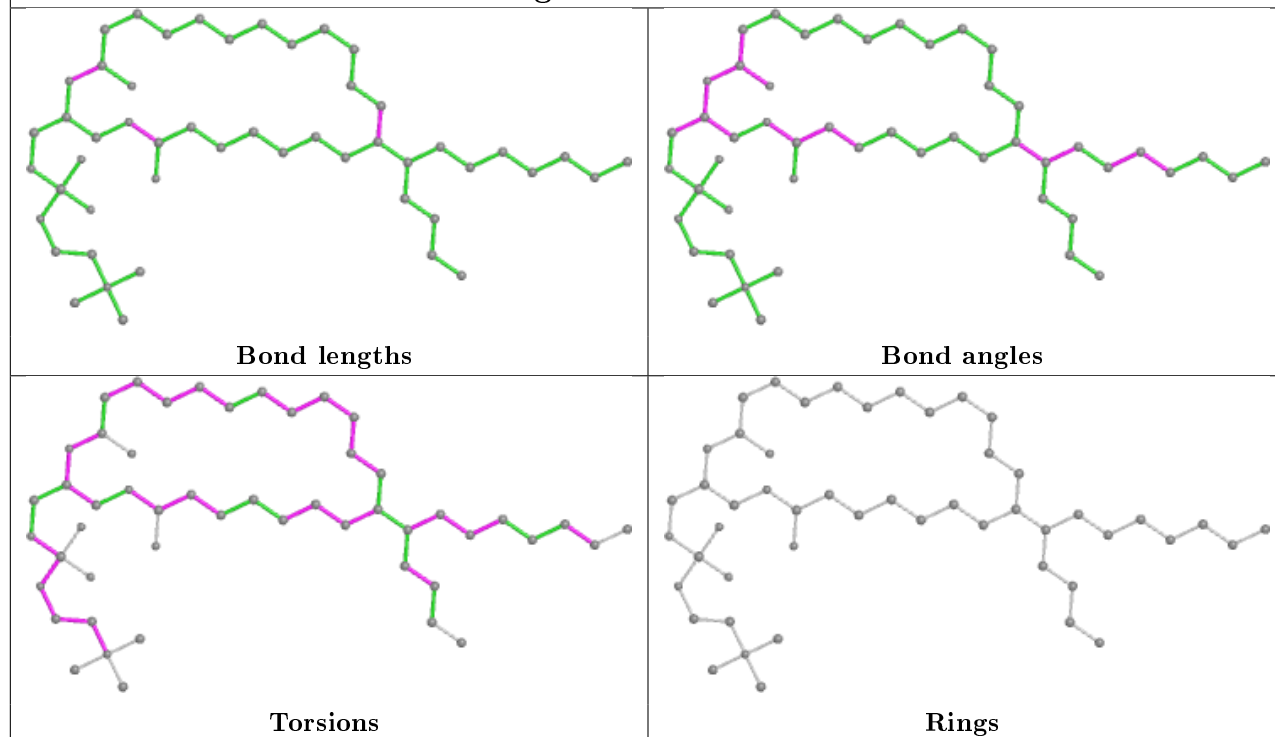
Ligand PEK P 303



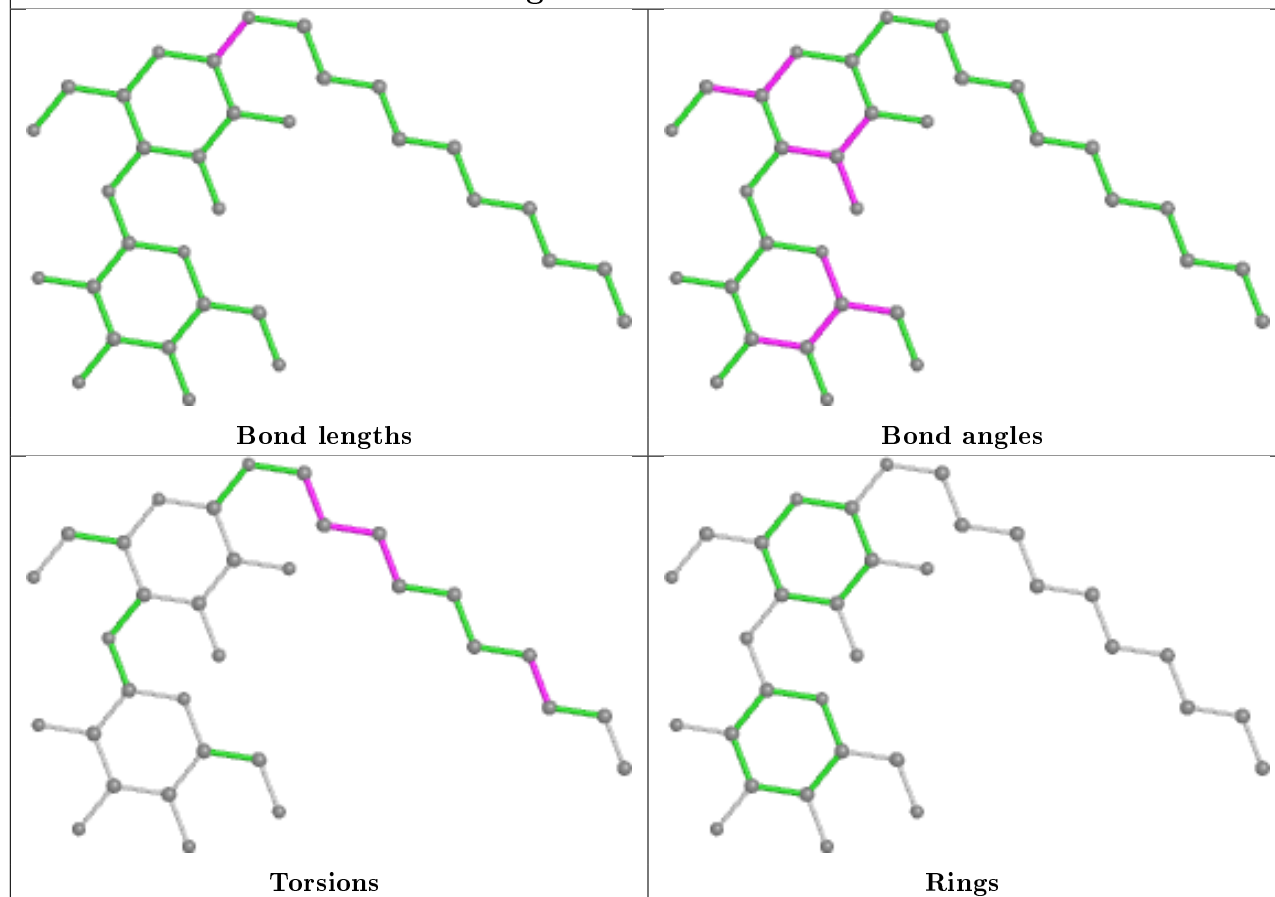
Ligand CHD P 307

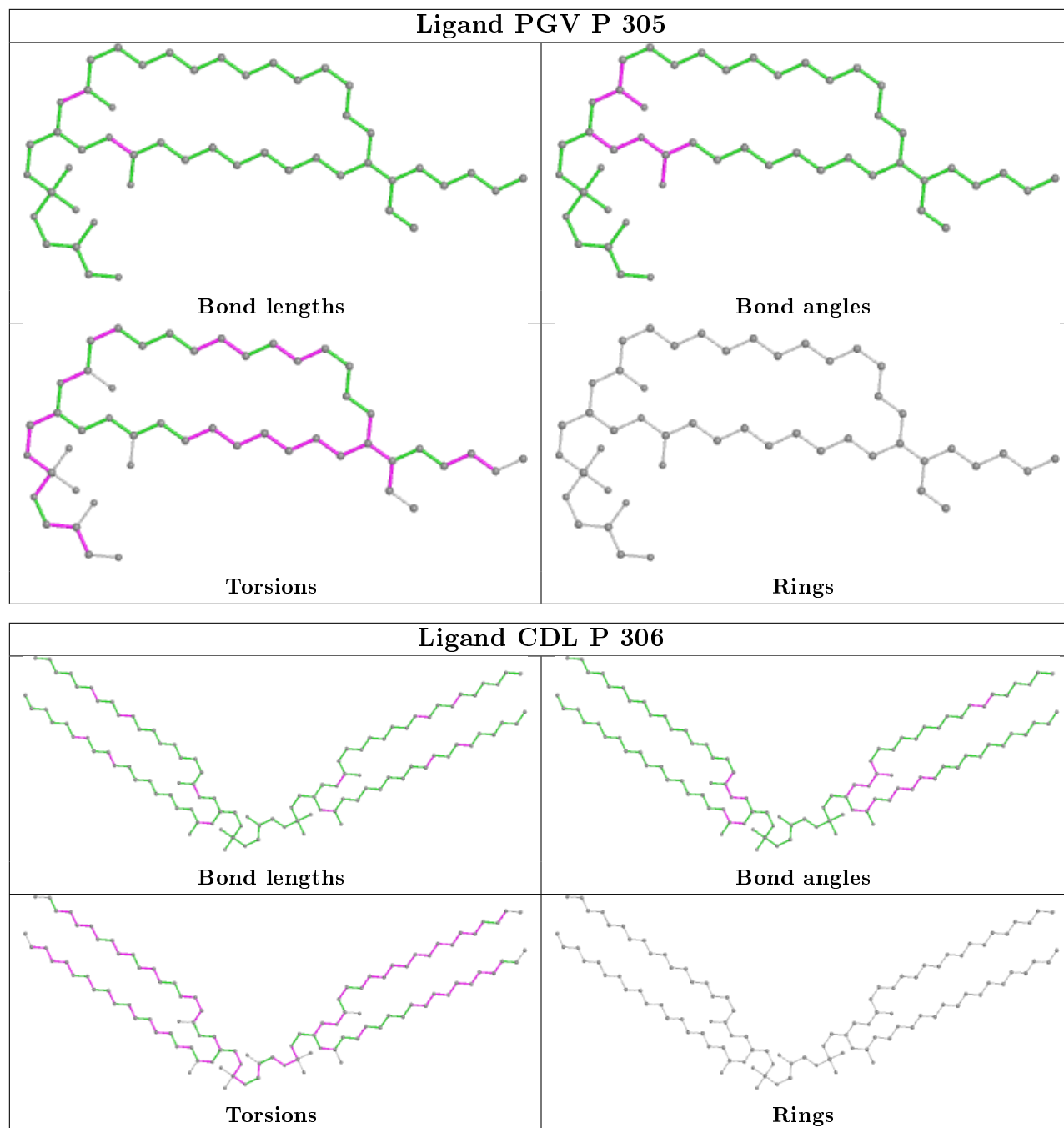


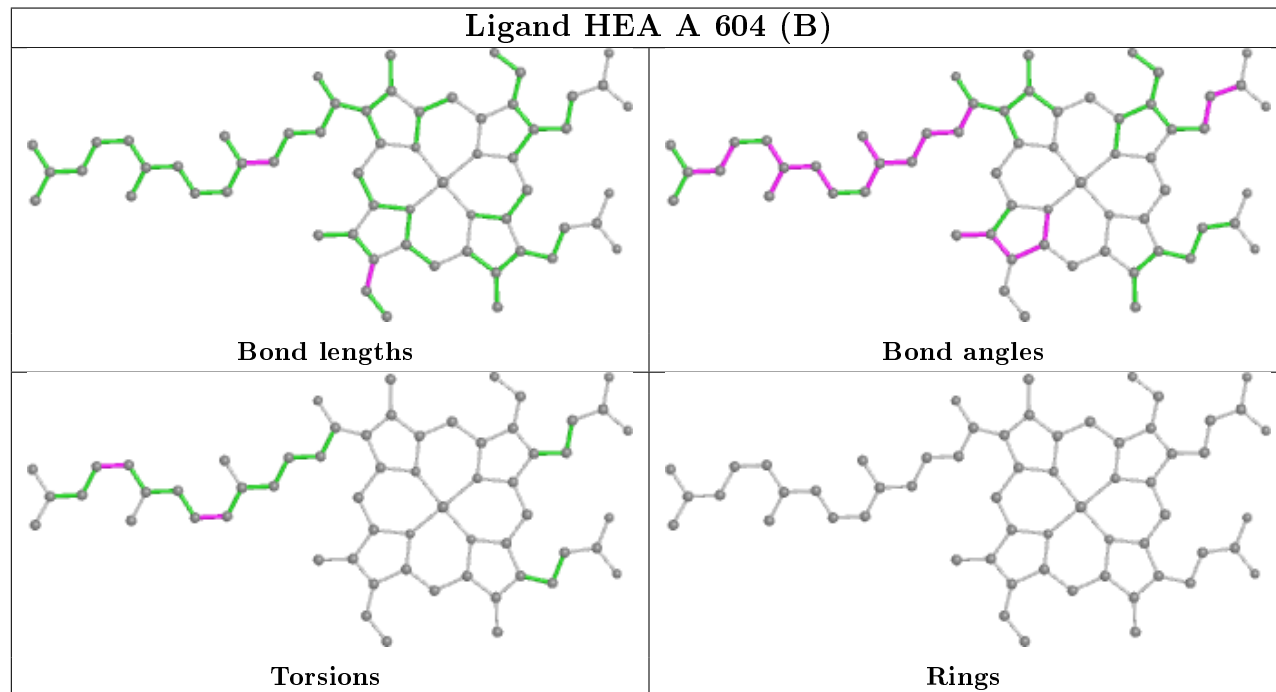
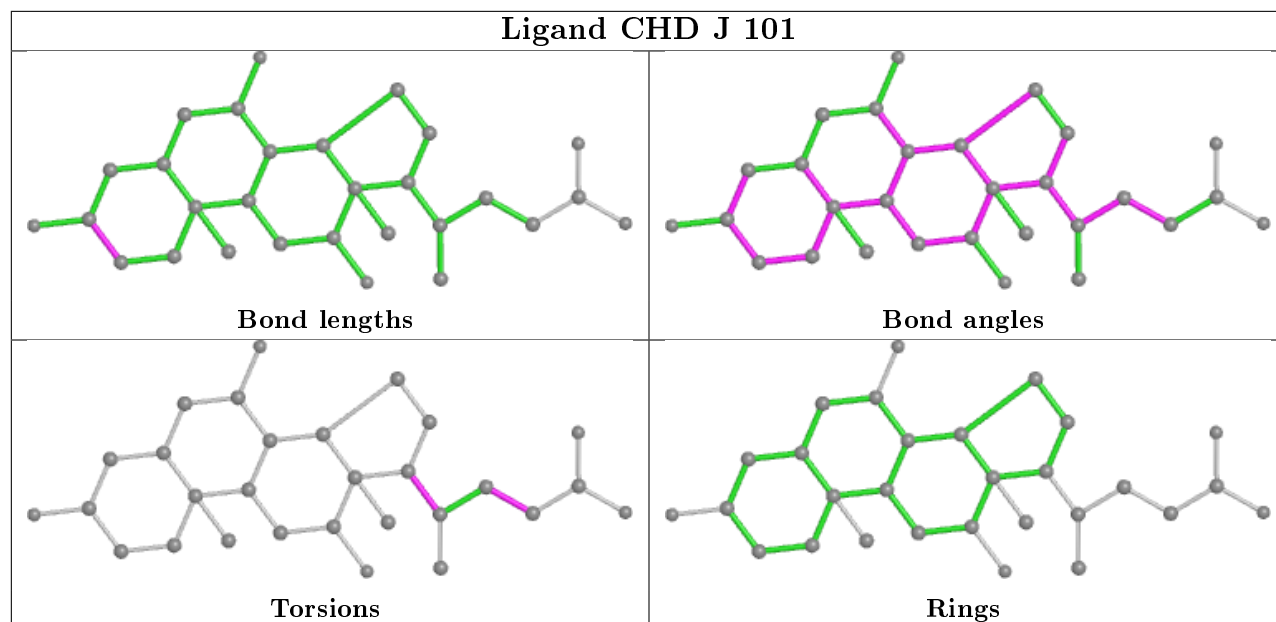
Ligand PSC E 201

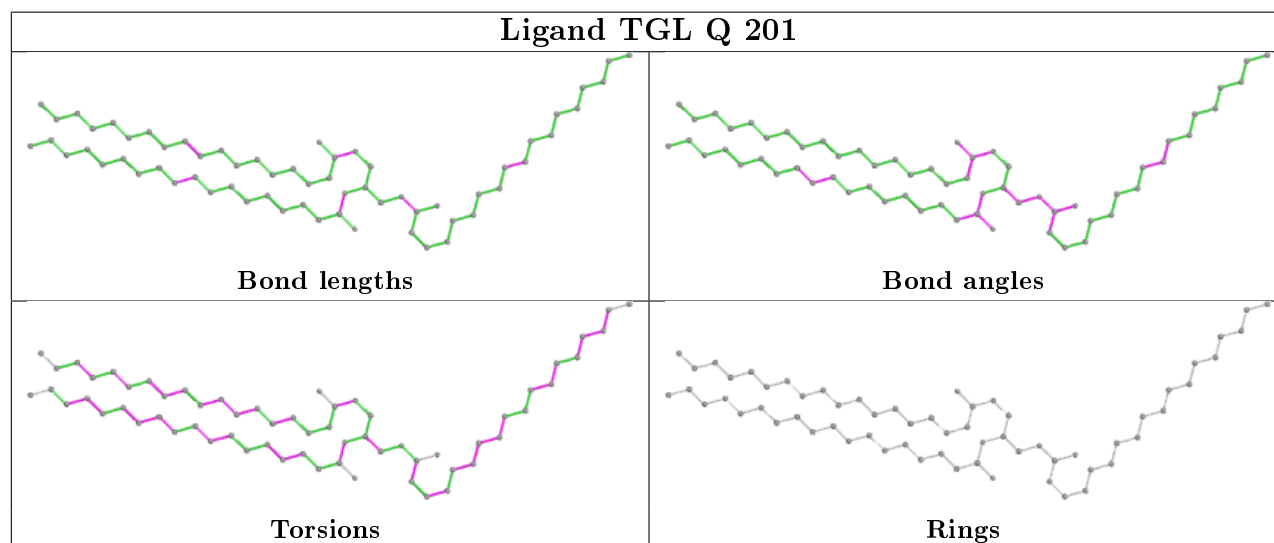
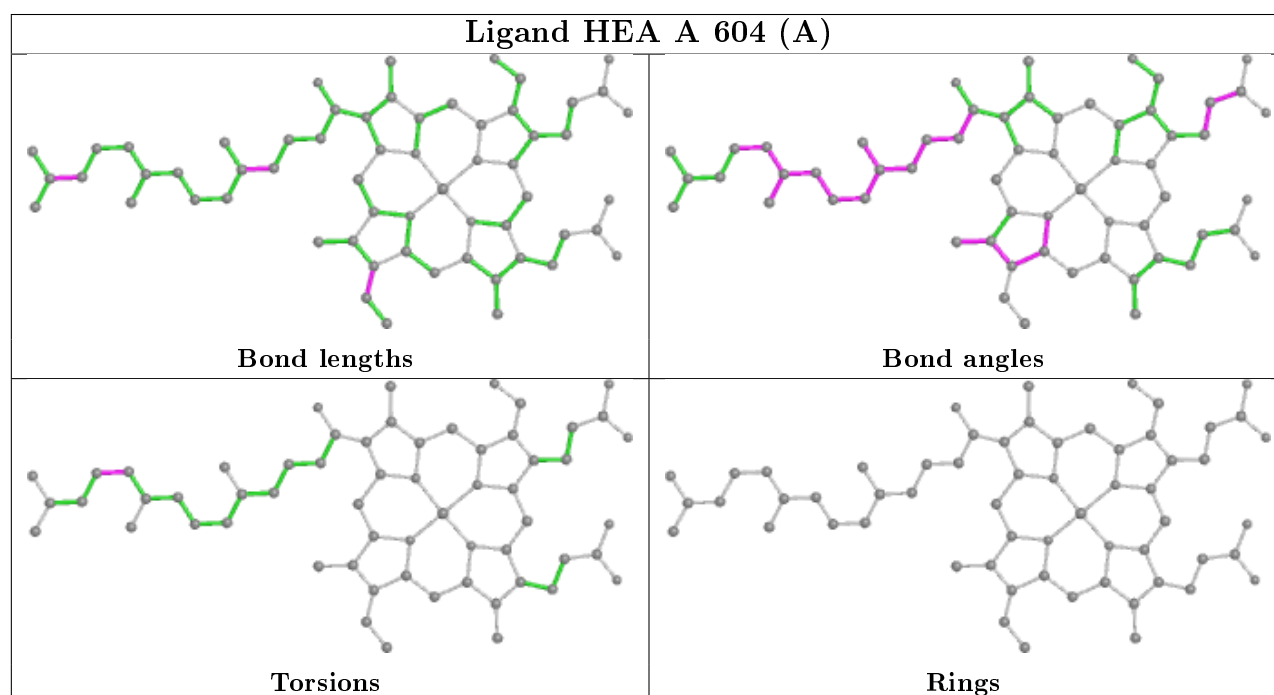
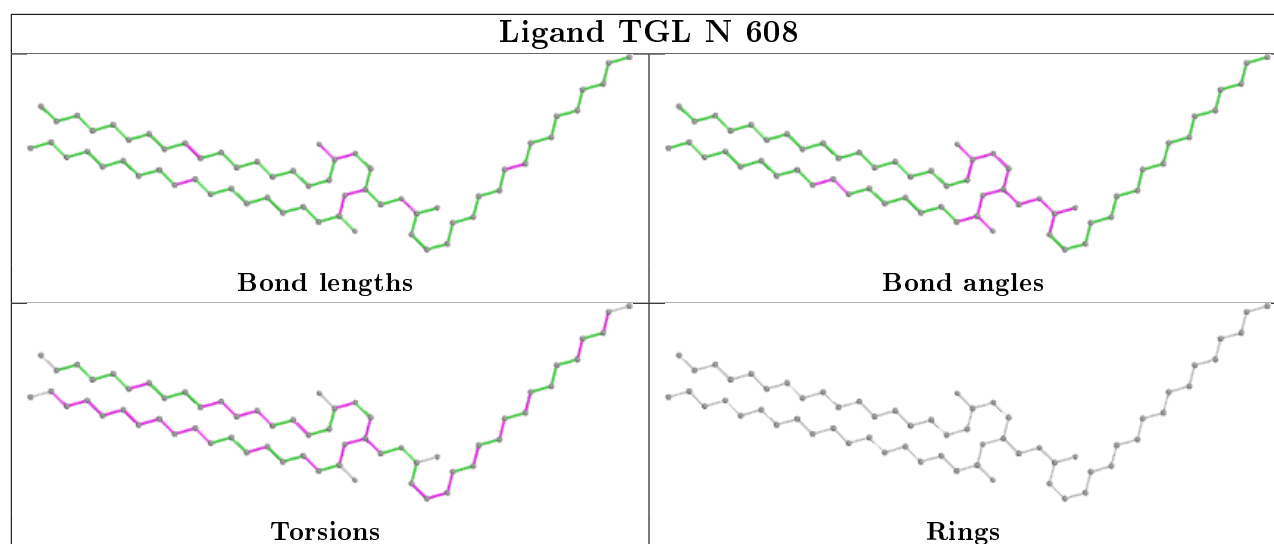


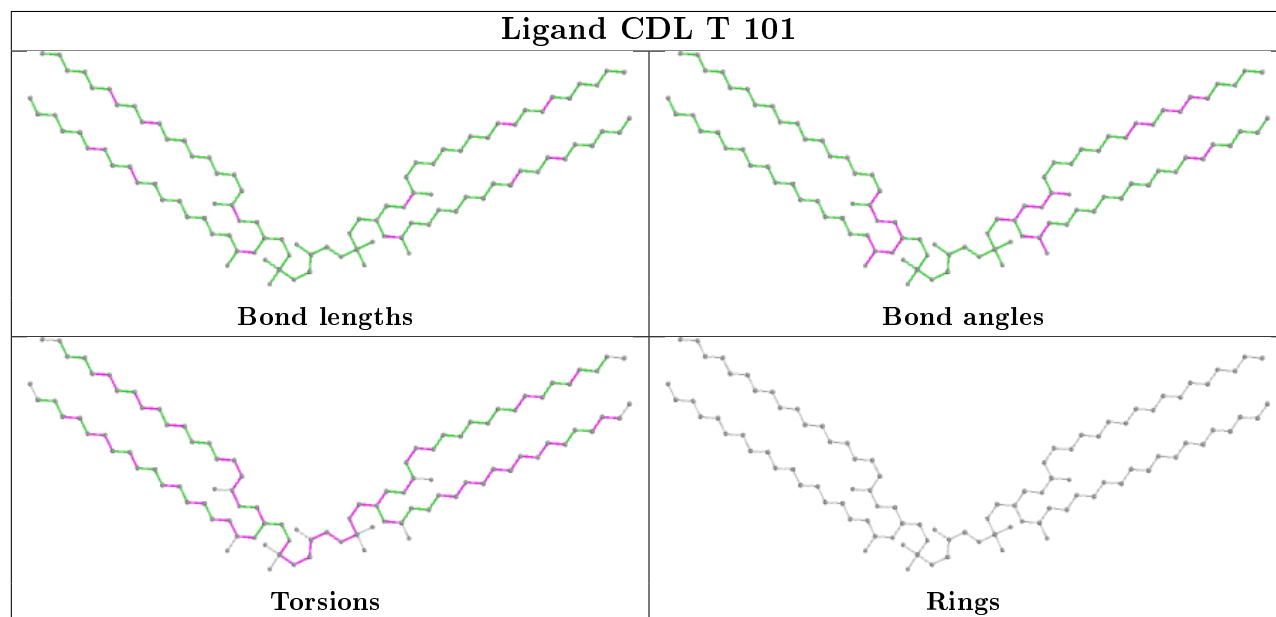
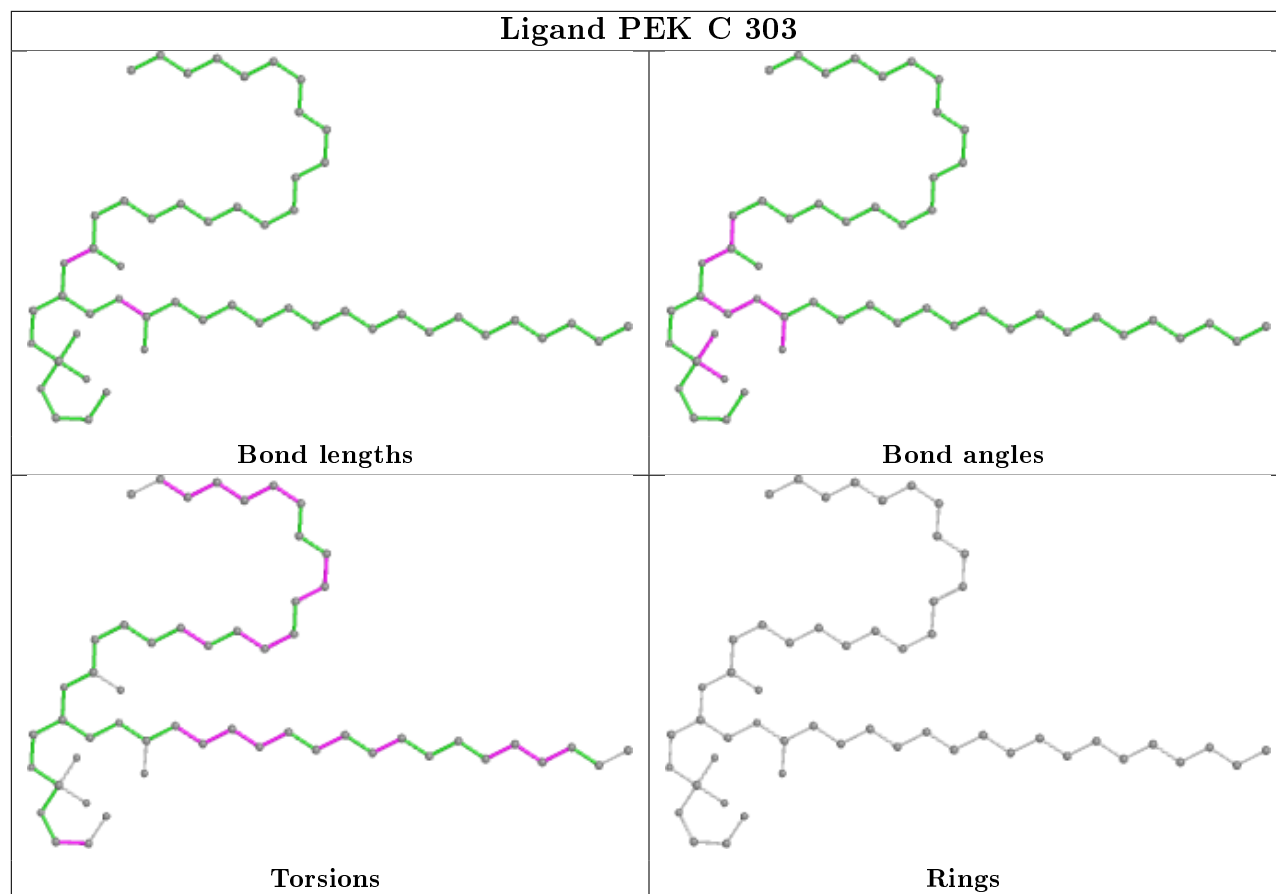
Ligand DMU Z 101



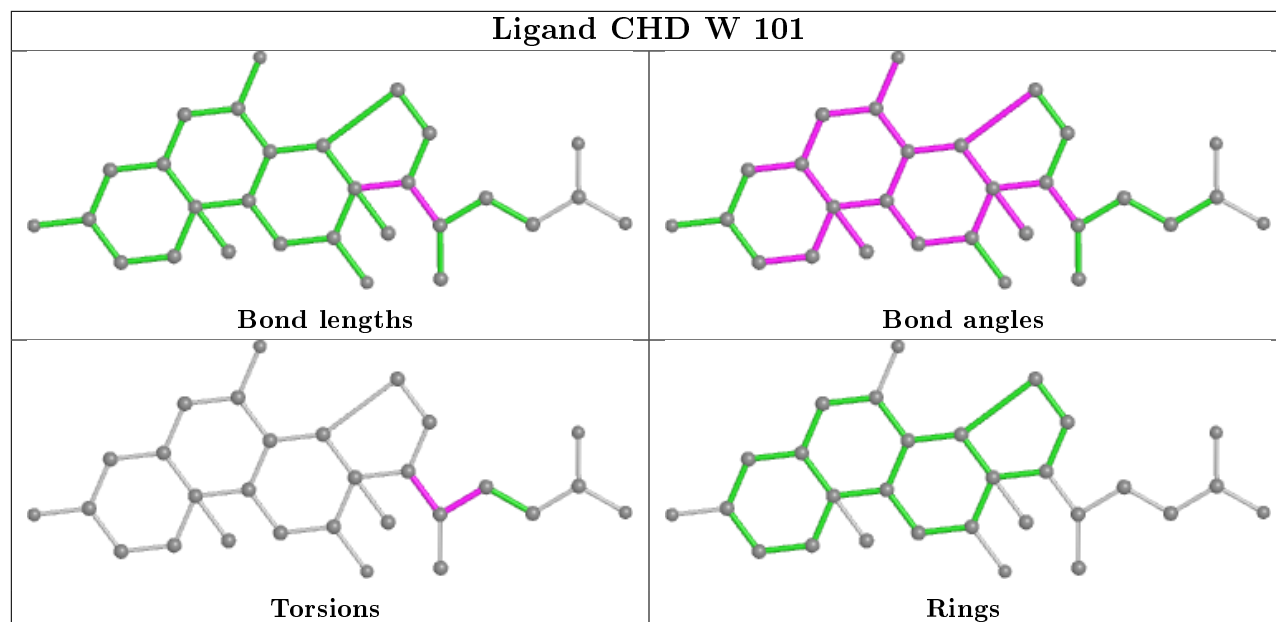




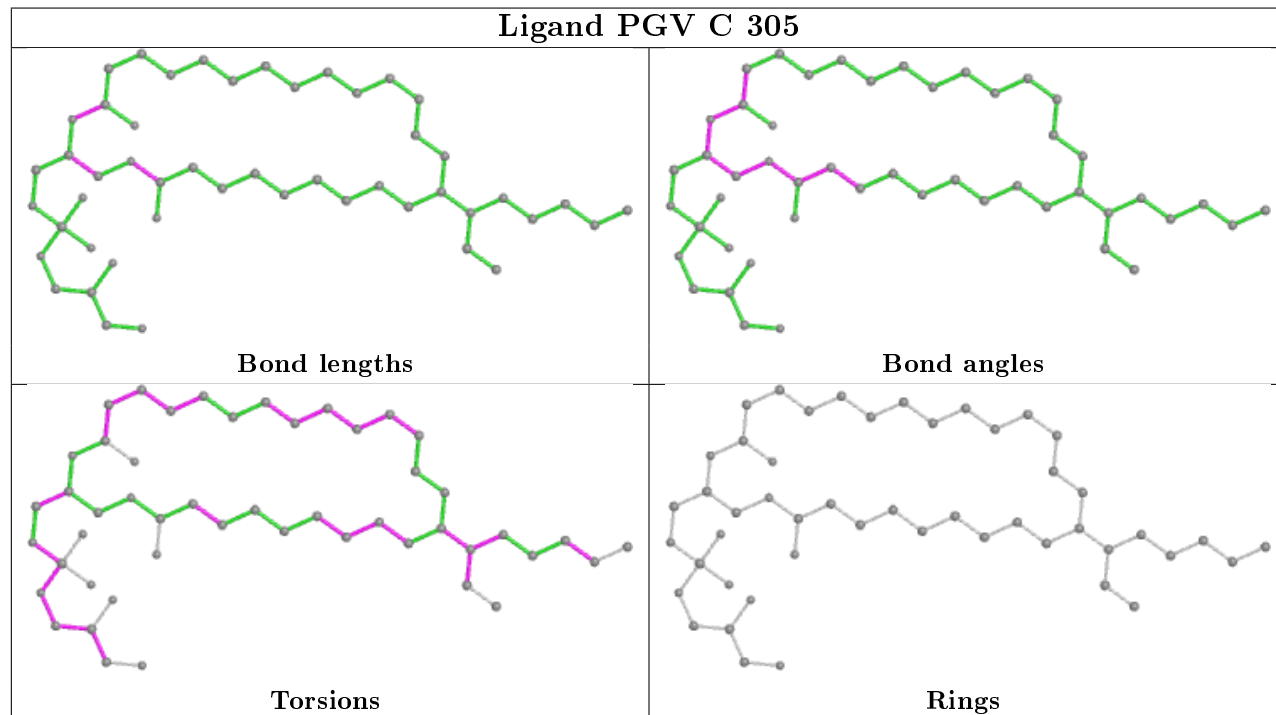


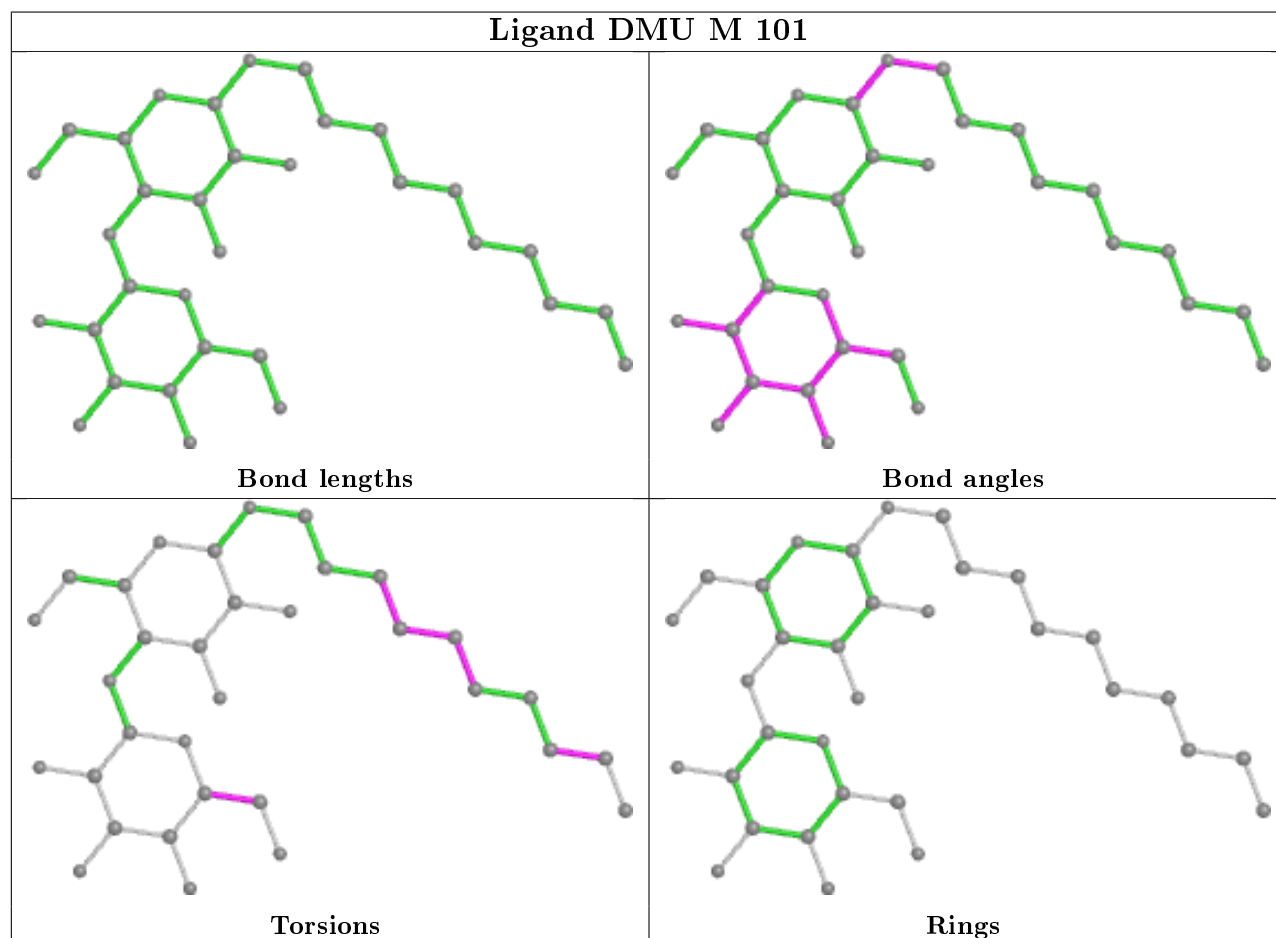
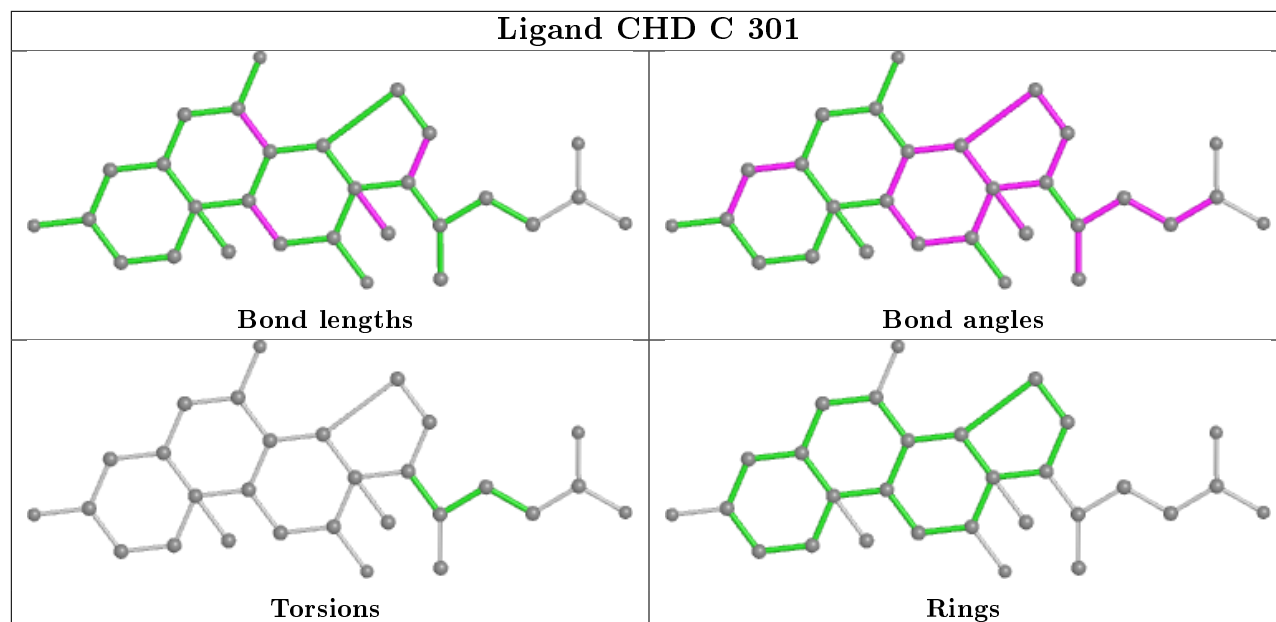


Ligand CHD W 101

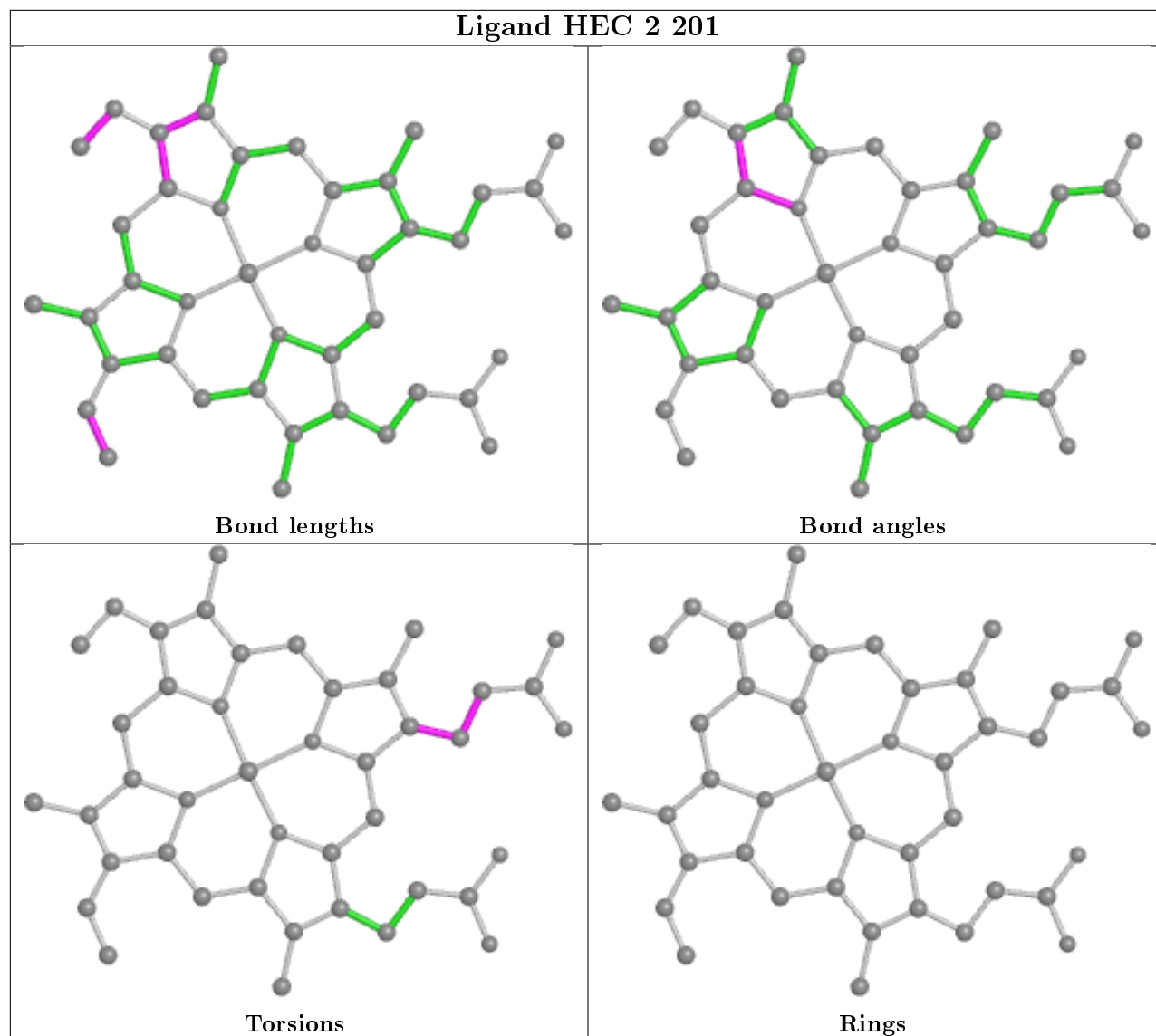


Ligand PGV C 305

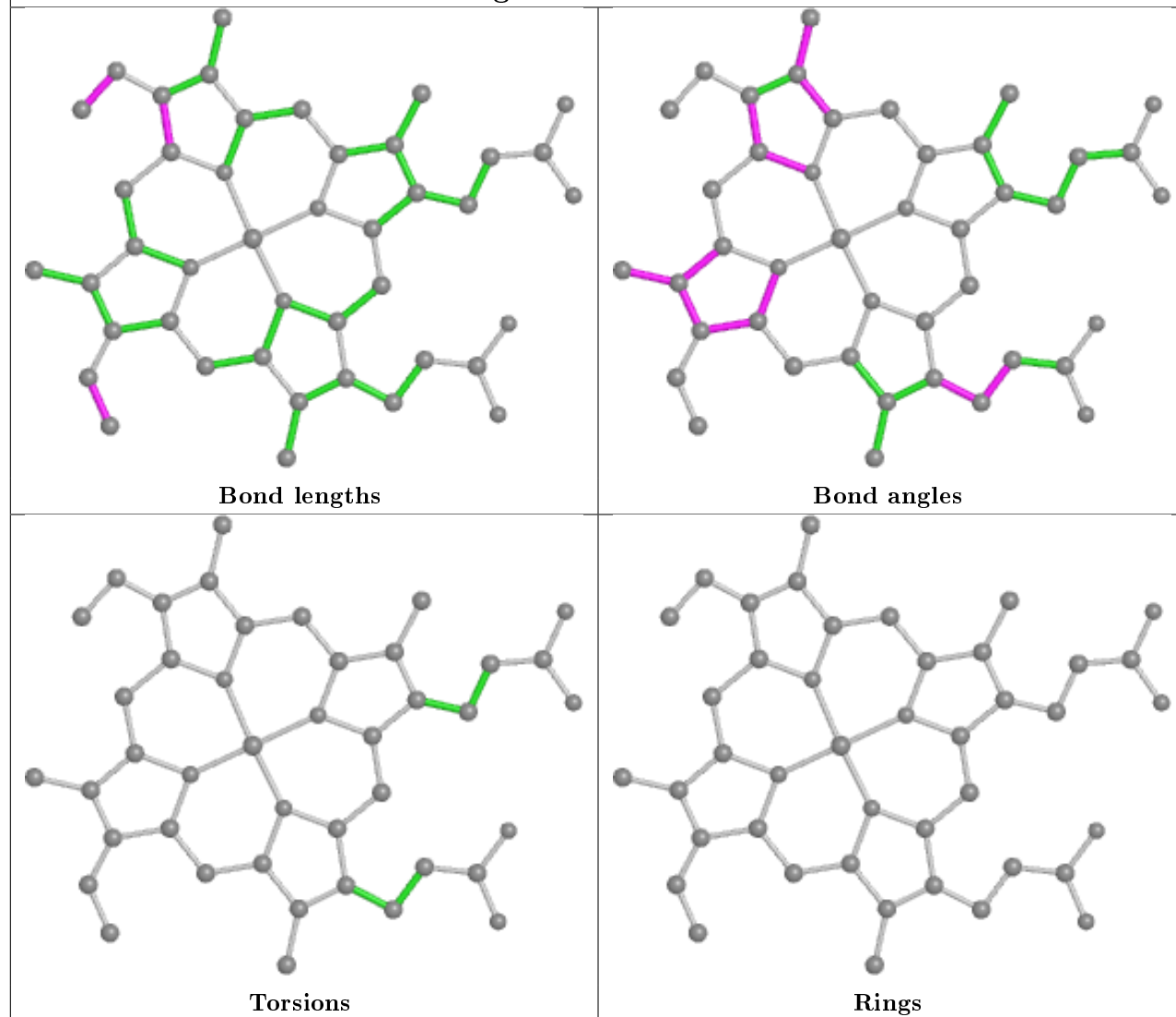




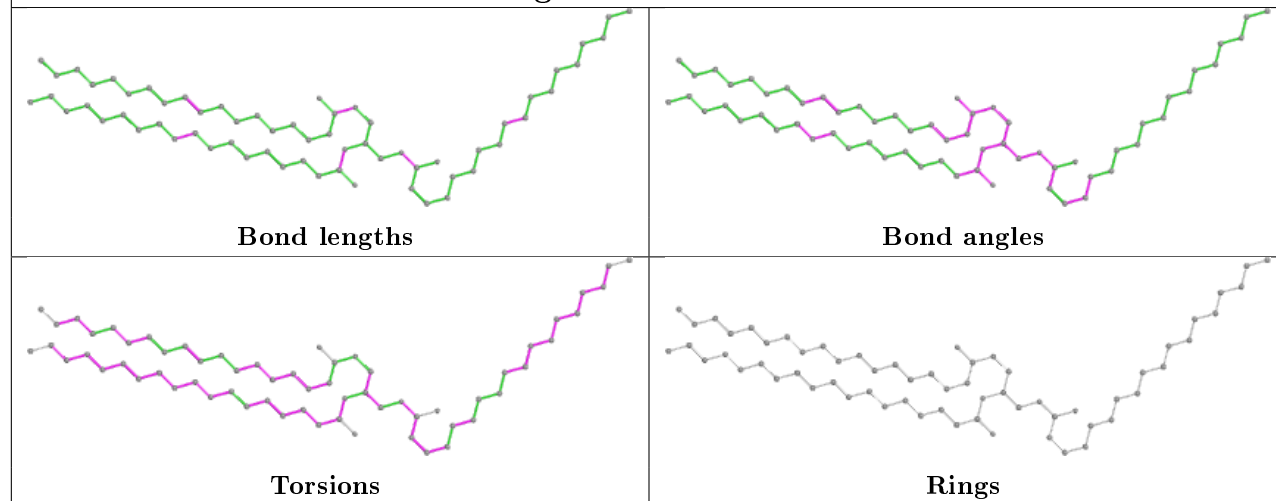
Ligand HEC 2 201

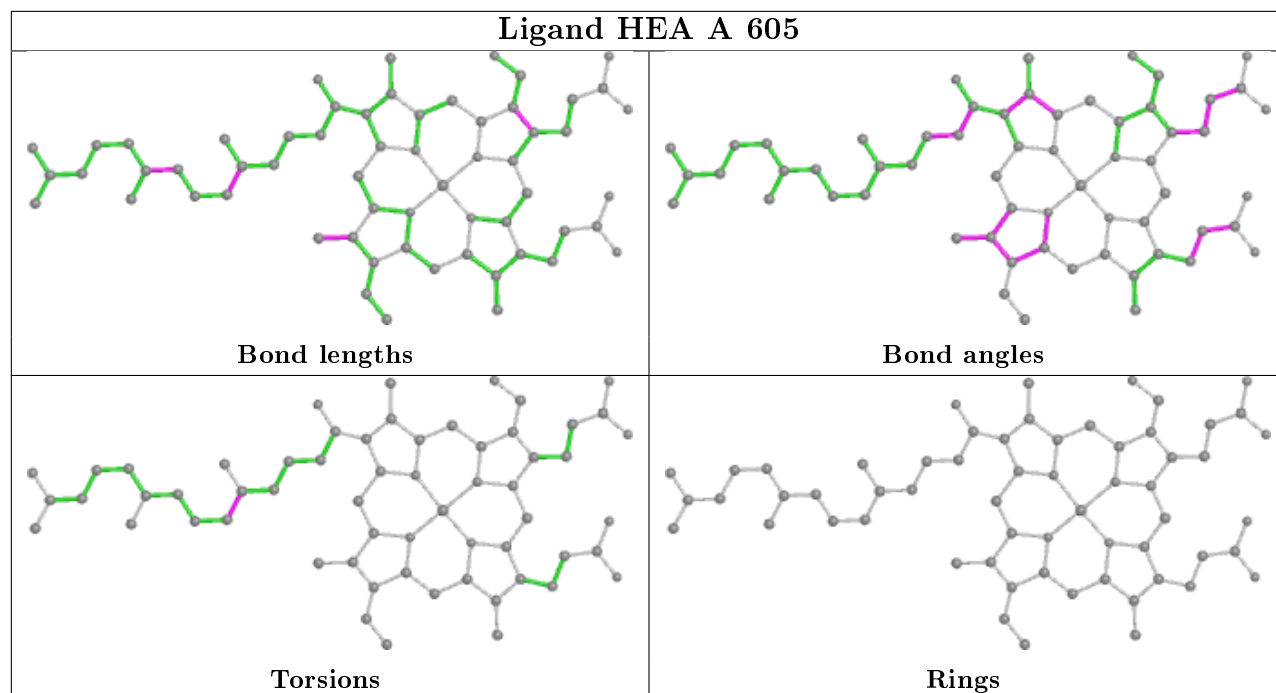


Ligand HEC 1 201



Ligand TGL L 101





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 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 |
|-----|-------|----------------|--------|---------------|-----------------------|-------|
| 1 | A | 513/514 (99%) | 0.21 | 21 (4%) 37 36 | 22, 30, 39, 74 | 0 |
| 1 | N | 513/514 (99%) | 0.23 | 26 (5%) 28 27 | 27, 36, 48, 71 | 0 |
| 2 | B | 226/227 (99%) | -0.34 | 3 (1%) 77 76 | 26, 35, 59, 109 | 0 |
| 2 | O | 226/227 (99%) | -0.15 | 2 (0%) 84 83 | 34, 49, 78, 98 | 0 |
| 3 | C | 259/259 (100%) | -0.54 | 2 (0%) 86 85 | 26, 35, 48, 83 | 0 |
| 3 | P | 259/259 (100%) | -0.55 | 4 (1%) 73 72 | 28, 38, 52, 87 | 0 |
| 4 | D | 144/144 (100%) | -0.53 | 5 (3%) 44 43 | 30, 38, 63, 144 | 0 |
| 4 | Q | 144/144 (100%) | 0.16 | 13 (9%) 9 8 | 32, 50, 81, 139 | 0 |
| 5 | E | 105/105 (100%) | -0.42 | 2 (1%) 66 65 | 30, 38, 62, 134 | 0 |
| 5 | R | 105/105 (100%) | -0.61 | 1 (0%) 82 81 | 33, 41, 62, 123 | 0 |
| 6 | F | 98/98 (100%) | -0.05 | 8 (8%) 11 11 | 30, 40, 95, 141 | 0 |
| 6 | S | 98/98 (100%) | 0.25 | 8 (8%) 11 11 | 32, 45, 106, 141 | 0 |
| 7 | G | 83/84 (98%) | 0.56 | 16 (19%) 1 0 | 34, 44, 116, 138 | 0 |
| 7 | T | 83/84 (98%) | 0.80 | 17 (20%) 1 0 | 31, 47, 111, 136 | 0 |
| 8 | H | 79/79 (100%) | -0.11 | 7 (8%) 9 8 | 33, 43, 90, 106 | 0 |
| 8 | U | 79/79 (100%) | -0.18 | 2 (2%) 57 56 | 38, 49, 69, 137 | 0 |
| 9 | I | 72/73 (98%) | -0.15 | 3 (4%) 36 35 | 33, 46, 66, 79 | 0 |
| 9 | V | 72/73 (98%) | 0.99 | 11 (15%) 2 1 | 36, 63, 85, 111 | 0 |
| 10 | J | 58/58 (100%) | 0.36 | 7 (12%) 4 3 | 36, 46, 75, 135 | 0 |
| 10 | W | 58/58 (100%) | 0.72 | 8 (13%) 2 2 | 39, 53, 84, 144 | 0 |
| 11 | K | 49/49 (100%) | -0.15 | 3 (6%) 21 20 | 35, 42, 58, 70 | 0 |
| 11 | X | 49/49 (100%) | 0.61 | 4 (8%) 11 11 | 47, 58, 77, 78 | 0 |
| 12 | L | 46/46 (100%) | -0.53 | 1 (2%) 62 60 | 30, 38, 59, 104 | 0 |
| 12 | Y | 46/46 (100%) | -0.50 | 1 (2%) 62 60 | 36, 46, 69, 111 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 |
|-----|-------|-----------------|--------|---------------|-----------------------|-------|
| 13 | M | 43/43 (100%) | -0.20 | 2 (4%) 31 30 | 32, 40, 79, 127 | 0 |
| 13 | Z | 43/43 (100%) | -0.05 | 3 (6%) 16 15 | 36, 50, 81, 108 | 0 |
| 14 | 1 | 104/105 (99%) | 2.81 | 65 (62%) 0 0 | 45, 90, 118, 125 | 0 |
| 14 | 2 | 104/105 (99%) | 4.61 | 79 (75%) 0 0 | 67, 115, 139, 147 | 0 |
| All | All | 3758/3768 (99%) | 0.17 | 324 (8%) 10 9 | 22, 40, 98, 147 | 0 |

The worst 5 of 324 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 4 | Q | 5 | VAL | 13.5 |
| 4 | Q | 7 | LYS | 13.3 |
| 6 | S | 1 | ALA | 13.3 |
| 10 | W | 57 | HIS | 12.5 |
| 14 | 2 | 57 | ILE | 12.1 |

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å ²) | Q<0.9 |
|-----|------|-------|-----|-------|------|------|----------------------------|-------|
| 9 | SAC | V | 1 | 9/10 | 0.31 | 0.92 | 131,137,150,153 | 0 |
| 7 | TPO | T | 11 | 11/12 | 0.45 | 0.35 | 85,109,117,125 | 0 |
| 7 | TPO | G | 11 | 11/12 | 0.50 | 0.33 | 81,97,160,160 | 0 |
| 9 | SAC | I | 1 | 9/10 | 0.75 | 0.39 | 98,106,110,119 | 0 |
| 1 | FME | A | 1 | 10/11 | 0.95 | 0.13 | 40,52,71,88 | 0 |
| 1 | FME | N | 1 | 10/11 | 0.96 | 0.17 | 43,61,73,95 | 0 |
| 2 | FME | O | 1 | 10/11 | 0.98 | 0.14 | 49,56,65,78 | 0 |
| 2 | FME | B | 1 | 10/11 | 0.98 | 0.10 | 30,35,39,51 | 0 |

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å ²) | Q<0.9 |
|-----|------|-------|-----|---------|------|------|----------------------------|-------|
| 17 | NA | P | 302 | 1/1 | 0.55 | 0.51 | 57,57,57,57 | 0 |
| 17 | NA | C | 302 | 1/1 | 0.59 | 0.57 | 59,59,59,59 | 0 |
| 26 | CDL | G | 101 | 100/100 | 0.66 | 0.30 | 58,103,158,163 | 0 |
| 27 | UNL | P | 309 | 16/- | 0.68 | 0.17 | 70,79,89,95 | 0 |
| 24 | CHD | W | 101 | 29/29 | 0.70 | 0.43 | 73,114,126,130 | 0 |
| 26 | CDL | T | 101 | 100/100 | 0.73 | 0.25 | 61,95,153,161 | 0 |
| 27 | UNL | J | 102 | 10/- | 0.73 | 0.29 | 61,65,77,92 | 0 |
| 20 | PGV | P | 305 | 51/51 | 0.73 | 0.24 | 54,86,135,150 | 0 |
| 21 | TGL | Q | 201 | 63/63 | 0.74 | 0.21 | 52,82,104,109 | 0 |
| 20 | PGV | C | 305 | 51/51 | 0.74 | 0.24 | 55,80,122,138 | 0 |
| 21 | TGL | D | 201 | 63/63 | 0.76 | 0.22 | 47,70,101,105 | 0 |
| 28 | PSC | E | 201 | 52/52 | 0.76 | 0.26 | 50,79,162,163 | 0 |
| 27 | UNL | N | 601 | 17/- | 0.76 | 0.18 | 52,60,83,85 | 0 |
| 27 | UNL | T | 102 | 18/- | 0.76 | 0.18 | 47,66,85,92 | 0 |
| 30 | DMU | Z | 101 | 33/33 | 0.76 | 0.30 | 55,76,107,113 | 0 |
| 27 | UNL | N | 609 | 16/- | 0.77 | 0.32 | 54,59,79,85 | 0 |
| 27 | UNL | C | 309 | 17/- | 0.77 | 0.16 | 60,71,87,90 | 0 |
| 20 | PGV | A | 607 | 51/51 | 0.77 | 0.30 | 44,84,151,159 | 0 |
| 27 | UNL | W | 102 | 9/- | 0.78 | 0.24 | 59,62,79,82 | 0 |
| 21 | TGL | L | 101 | 63/63 | 0.78 | 0.26 | 45,70,98,107 | 0 |
| 27 | UNL | Y | 101 | 10/- | 0.78 | 0.40 | 69,76,86,94 | 0 |
| 27 | UNL | C | 310 | 7/- | 0.79 | 0.34 | 41,64,76,83 | 0 |
| 26 | CDL | P | 306 | 100/100 | 0.79 | 0.27 | 49,97,149,159 | 0 |
| 27 | UNL | L | 102 | 10/- | 0.80 | 0.27 | 61,75,82,86 | 0 |
| 28 | PSC | V | 101 | 52/52 | 0.82 | 0.23 | 49,77,145,166 | 0 |
| 24 | CHD | C | 307 | 29/29 | 0.82 | 0.26 | 73,85,93,99 | 0 |
| 26 | CDL | C | 306 | 100/100 | 0.83 | 0.23 | 51,86,124,152 | 0 |
| 21 | TGL | N | 608 | 63/63 | 0.83 | 0.19 | 51,73,104,115 | 0 |
| 23 | EDO | I | 101 | 4/4 | 0.83 | 0.14 | 55,59,63,72 | 0 |
| 24 | CHD | J | 101 | 29/29 | 0.84 | 0.32 | 61,75,106,109 | 0 |
| 27 | UNL | N | 611 | 12/- | 0.84 | 0.16 | 48,56,68,69 | 0 |
| 23 | EDO | E | 202 | 4/4 | 0.85 | 0.33 | 57,61,68,79 | 0 |
| 27 | UNL | C | 308 | 18/- | 0.85 | 0.20 | 55,66,77,81 | 0 |
| 27 | UNL | P | 310 | 7/- | 0.85 | 0.27 | 53,60,76,88 | 0 |
| 27 | UNL | N | 610 | 18/- | 0.85 | 0.19 | 51,59,69,70 | 0 |
| 27 | UNL | P | 308 | 20/- | 0.86 | 0.20 | 58,64,72,73 | 0 |
| 24 | CHD | P | 307 | 29/29 | 0.89 | 0.29 | 71,80,88,95 | 0 |

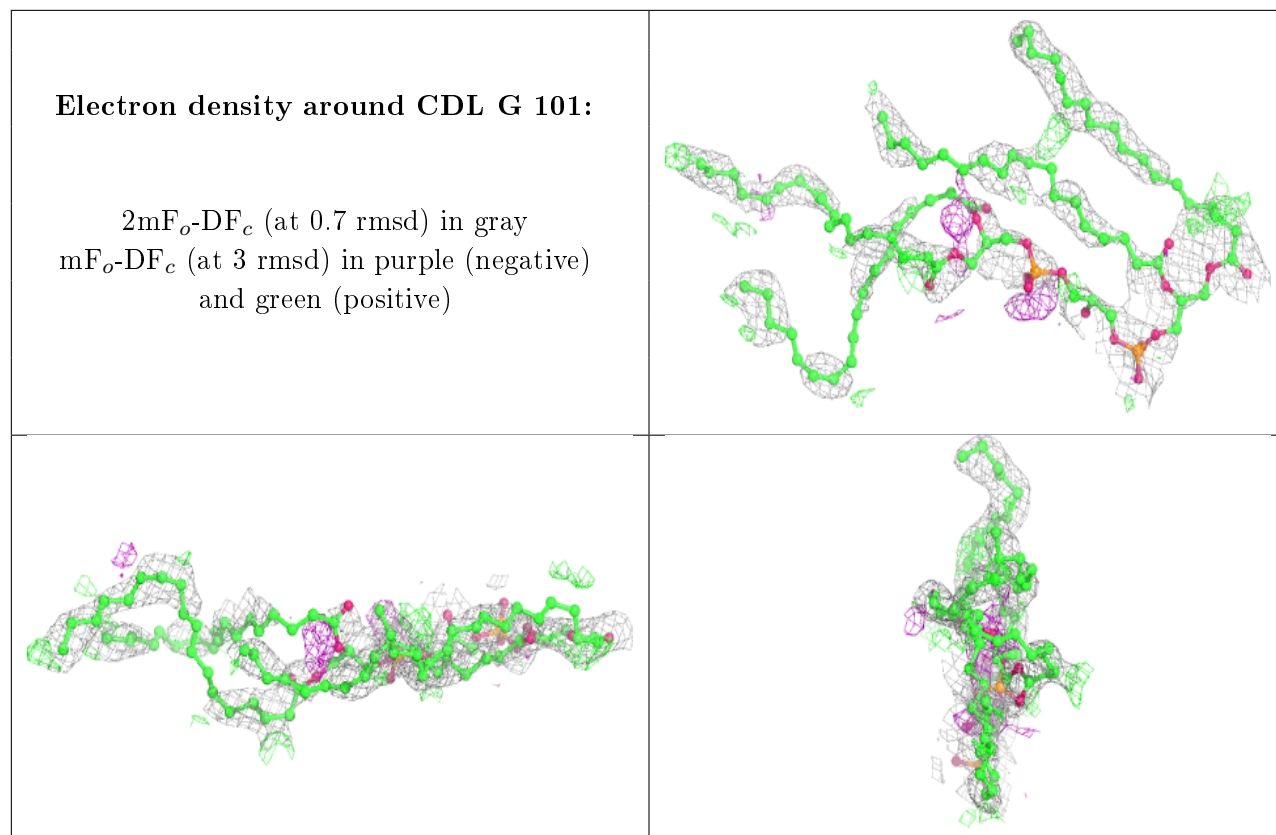
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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å ²) | Q<0.9 |
|-----|------|-------|--------|-------|------|------|----------------------------|-------|
| 21 | TGL | B | 301 | 63/63 | 0.90 | 0.18 | 33,68,103,114 | 0 |
| 24 | CHD | P | 301 | 29/29 | 0.91 | 0.12 | 40,45,52,55 | 0 |
| 30 | DMU | M | 101 | 33/33 | 0.92 | 0.14 | 40,46,62,65 | 0 |
| 25 | PEK | C | 303 | 53/53 | 0.93 | 0.16 | 34,48,88,97 | 0 |
| 23 | EDO | N | 614 | 4/4 | 0.93 | 0.16 | 56,59,63,85 | 0 |
| 31 | HEC | 2 | 201 | 43/43 | 0.94 | 0.26 | 79,101,135,149 | 0 |
| 31 | HEC | 1 | 201 | 43/43 | 0.95 | 0.19 | 57,81,94,99 | 0 |
| 25 | PEK | P | 303 | 53/53 | 0.95 | 0.13 | 39,53,94,101 | 0 |
| 16 | MG | A | 602 | 1/1 | 0.95 | 0.21 | 36,36,36,36 | 0 |
| 20 | PGV | P | 304 | 51/51 | 0.95 | 0.13 | 30,46,73,76 | 0 |
| 16 | MG | N | 603 | 1/1 | 0.96 | 0.25 | 42,42,42,42 | 0 |
| 24 | CHD | T | 103 | 29/29 | 0.96 | 0.08 | 30,36,42,53 | 0 |
| 24 | CHD | C | 301 | 29/29 | 0.96 | 0.08 | 34,40,48,53 | 0 |
| 24 | CHD | G | 102 | 29/29 | 0.96 | 0.08 | 35,38,43,52 | 0 |
| 20 | PGV | C | 304 | 51/51 | 0.96 | 0.12 | 31,38,95,103 | 0 |
| 23 | EDO | F | 102 | 4/4 | 0.97 | 0.14 | 45,47,49,49 | 0 |
| 20 | PGV | N | 612 | 51/51 | 0.97 | 0.15 | 33,43,70,80 | 0 |
| 20 | PGV | A | 608 | 51/51 | 0.97 | 0.15 | 29,41,68,74 | 0 |
| 23 | EDO | C | 311 | 4/4 | 0.97 | 0.08 | 48,51,51,52 | 0 |
| 23 | EDO | G | 103 | 4/4 | 0.97 | 0.09 | 37,39,49,51 | 0 |
| 23 | EDO | S | 102 | 4/4 | 0.97 | 0.08 | 44,45,46,53 | 0 |
| 17 | NA | N | 604 | 1/1 | 0.97 | 0.09 | 45,45,45,45 | 0 |
| 19 | PER | N | 607 | 2/2 | 0.98 | 0.10 | 36,36,36,48 | 0 |
| 23 | EDO | B | 303 | 4/4 | 0.98 | 0.13 | 30,31,33,36 | 0 |
| 18 | HEA | N | 605[B] | 60/60 | 0.98 | 0.18 | 32,38,44,47 | 9 |
| 23 | EDO | N | 613 | 4/4 | 0.98 | 0.16 | 38,38,39,41 | 0 |
| 18 | HEA | N | 605[A] | 60/60 | 0.98 | 0.18 | 32,38,47,50 | 9 |
| 18 | HEA | A | 604[A] | 60/60 | 0.99 | 0.15 | 23,28,38,40 | 9 |
| 18 | HEA | A | 604[B] | 60/60 | 0.99 | 0.15 | 23,28,35,40 | 9 |
| 18 | HEA | N | 606 | 60/60 | 0.99 | 0.19 | 27,33,41,47 | 0 |
| 18 | HEA | A | 605 | 60/60 | 0.99 | 0.14 | 22,26,33,39 | 0 |
| 29 | ZN | S | 101 | 1/1 | 0.99 | 0.05 | 37,37,37,37 | 0 |
| 19 | PER | A | 606 | 2/2 | 0.99 | 0.10 | 40,40,40,54 | 0 |
| 22 | CUA | O | 301 | 2/2 | 0.99 | 0.09 | 42,42,42,43 | 0 |
| 15 | CU | N | 602 | 1/1 | 1.00 | 0.14 | 35,35,35,35 | 0 |
| 29 | ZN | F | 101 | 1/1 | 1.00 | 0.10 | 36,36,36,36 | 0 |
| 22 | CUA | B | 302 | 2/2 | 1.00 | 0.11 | 27,27,27,29 | 0 |
| 15 | CU | A | 601 | 1/1 | 1.00 | 0.13 | 29,29,29,29 | 0 |
| 17 | NA | A | 603 | 1/1 | 1.00 | 0.05 | 31,31,31,31 | 0 |

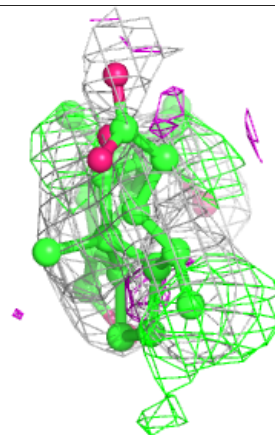
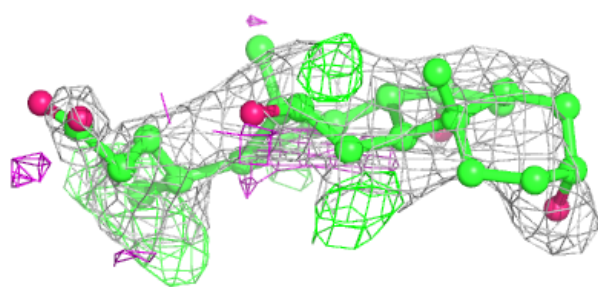
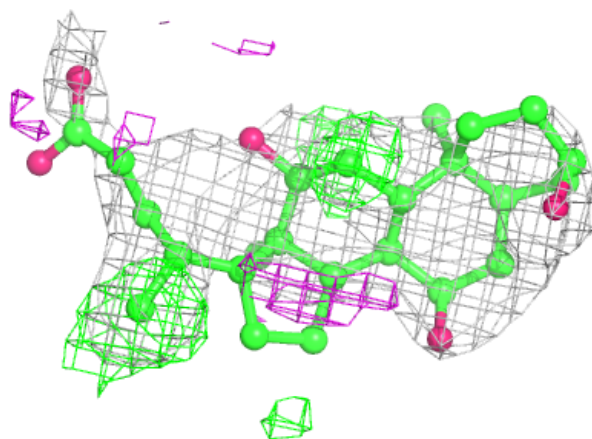
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different

orientation to approximate a three-dimensional view.

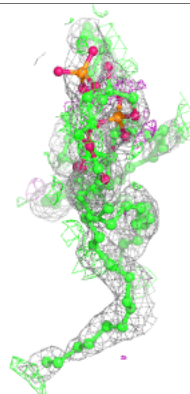
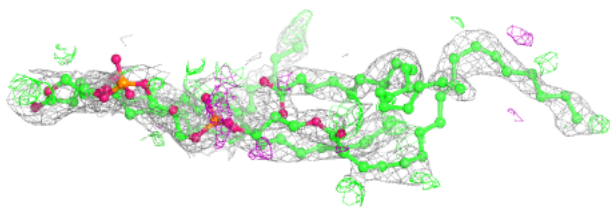
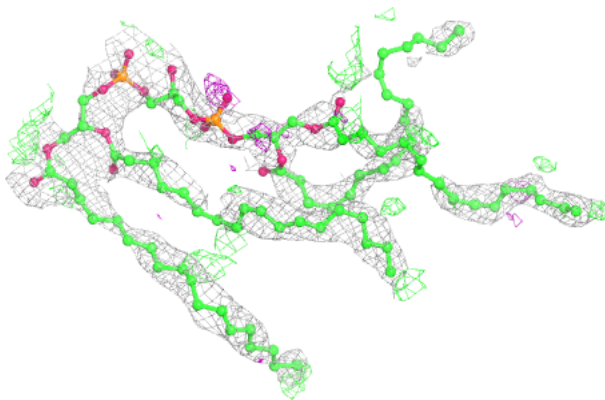


Electron density around CHD W 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

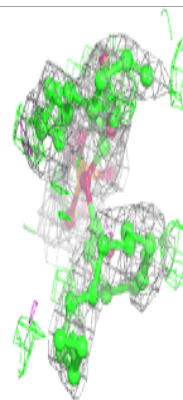
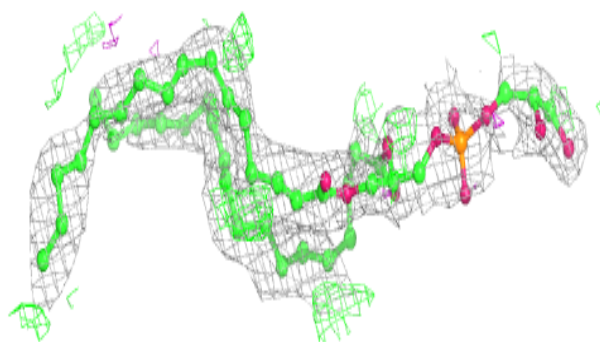
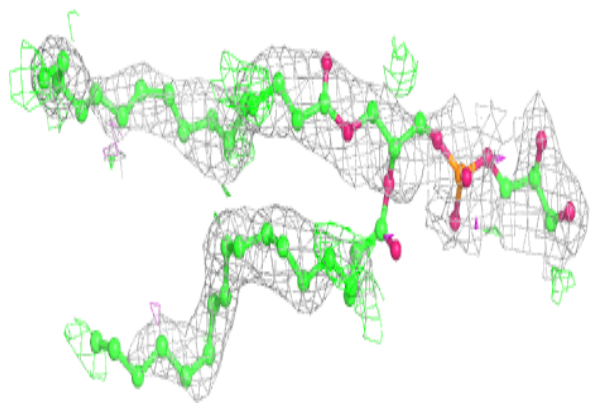
**Electron density around CDL T 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

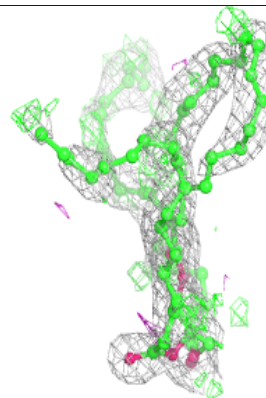
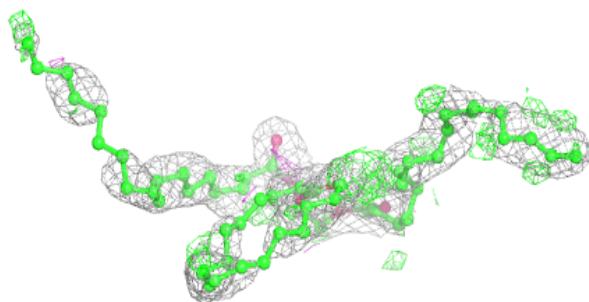
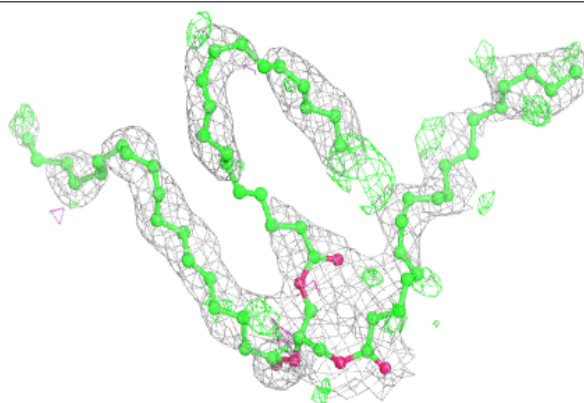


Electron density around PGV P 305:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

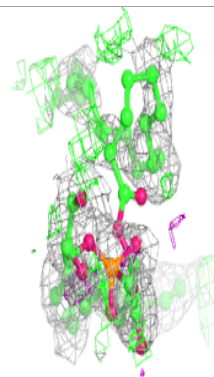
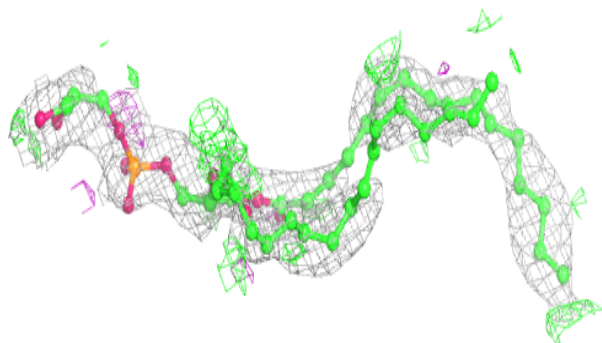
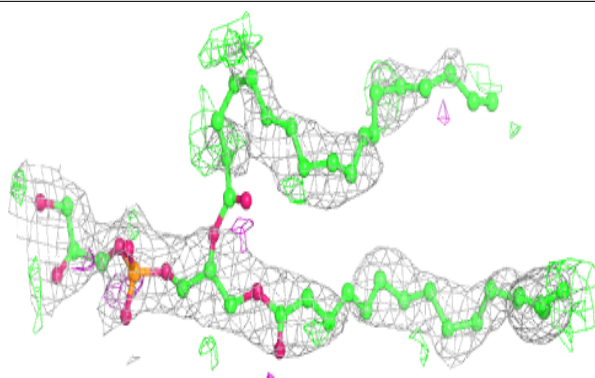
**Electron density around TGL Q 201:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

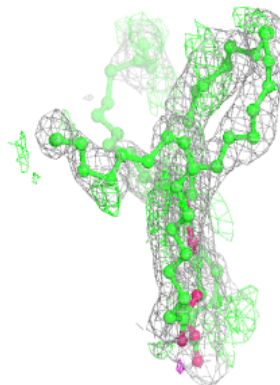
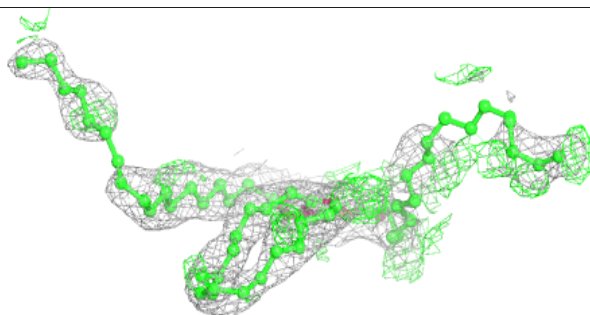
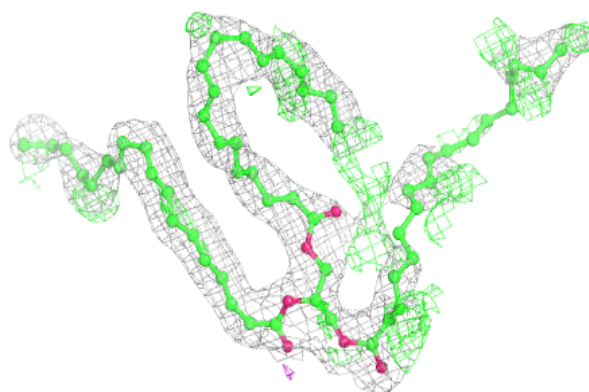


Electron density around PGV C 305:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

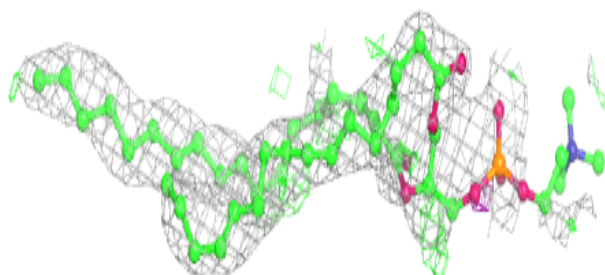
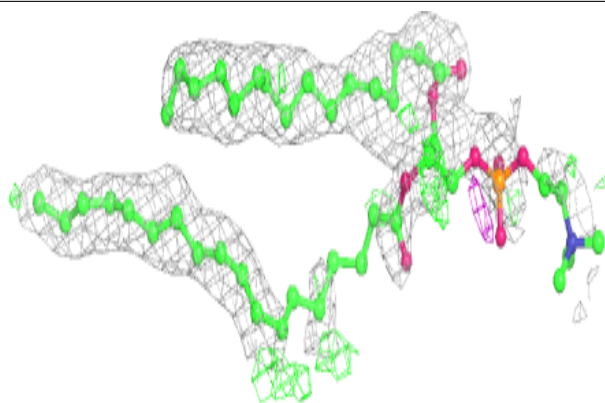
**Electron density around TGL D 201:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

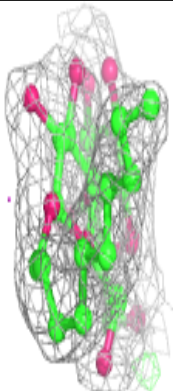
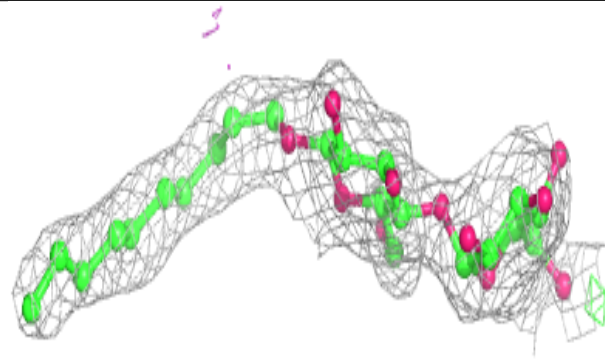
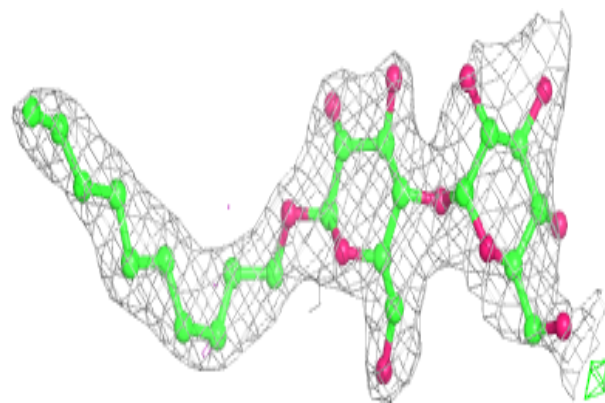


Electron density around PSC E 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

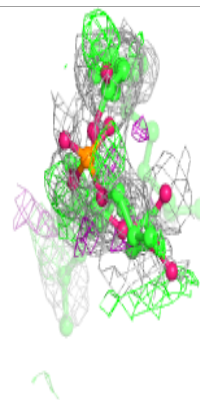
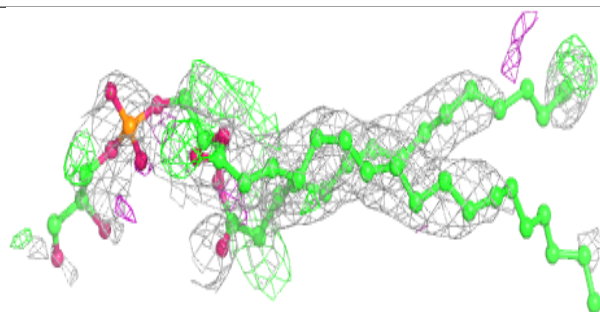
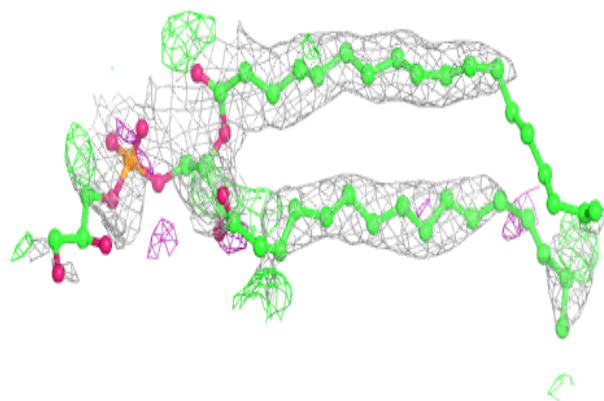
**Electron density around DMU Z 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



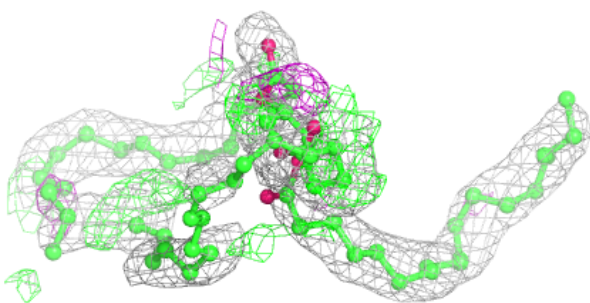
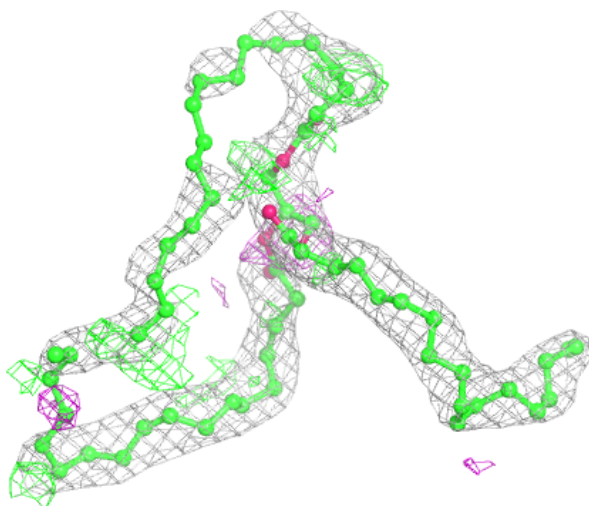
Electron density around PGV A 607:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



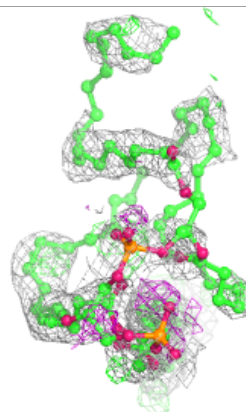
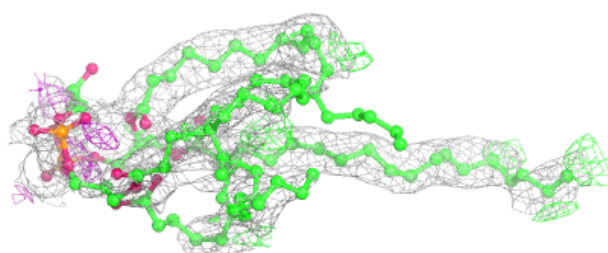
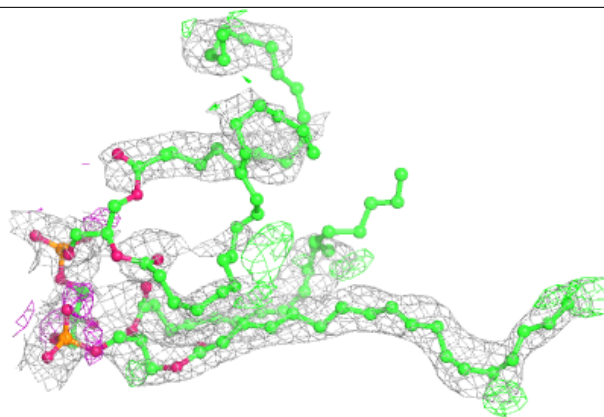
Electron density around TGL L 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

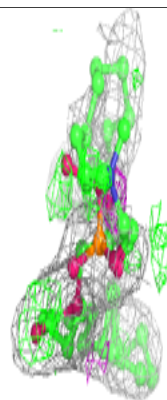
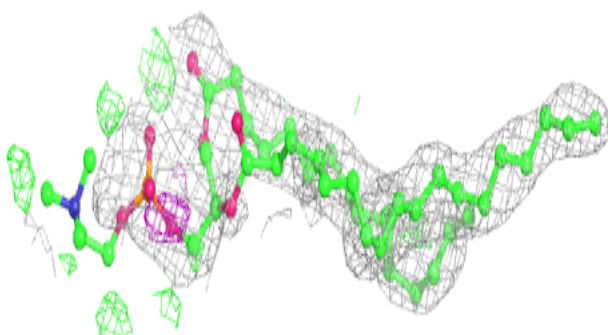
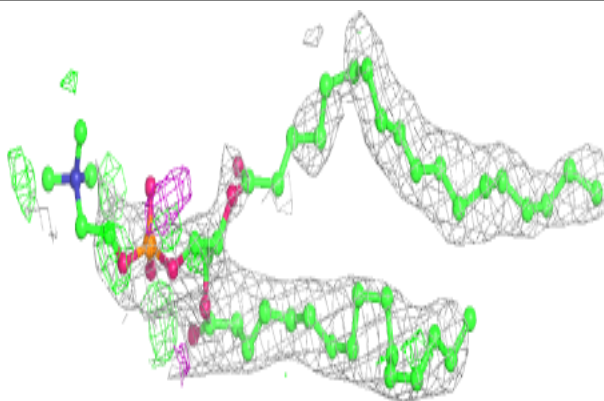


Electron density around CDL P 306:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

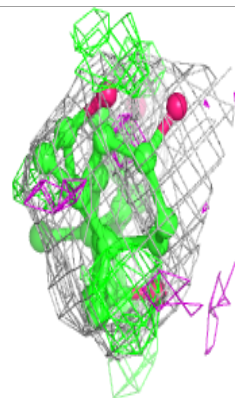
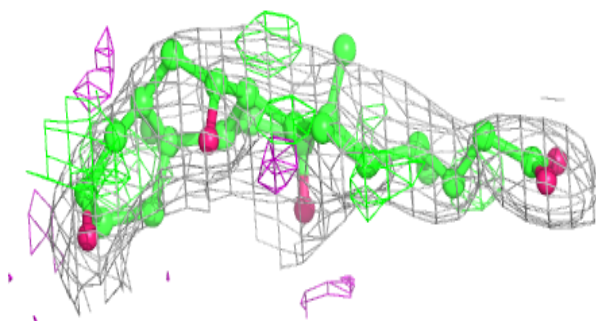
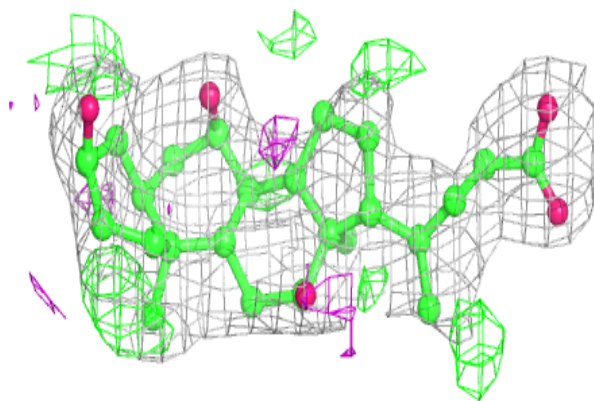
**Electron density around PSC V 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

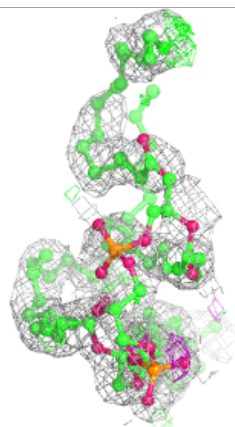
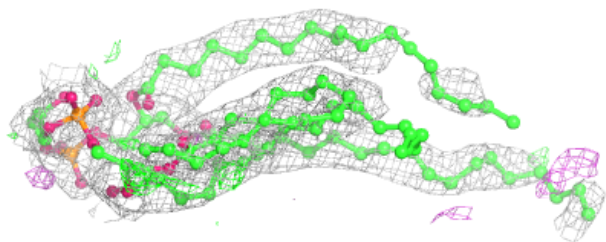
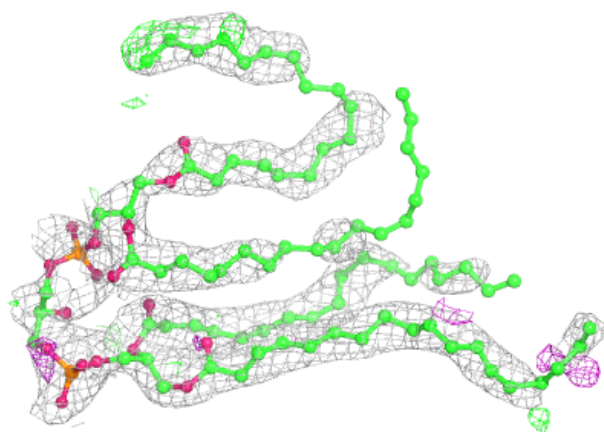


Electron density around CHD C 307:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

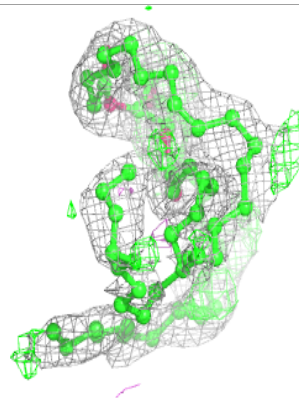
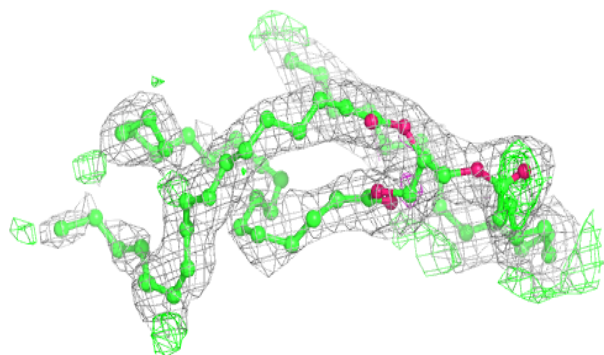
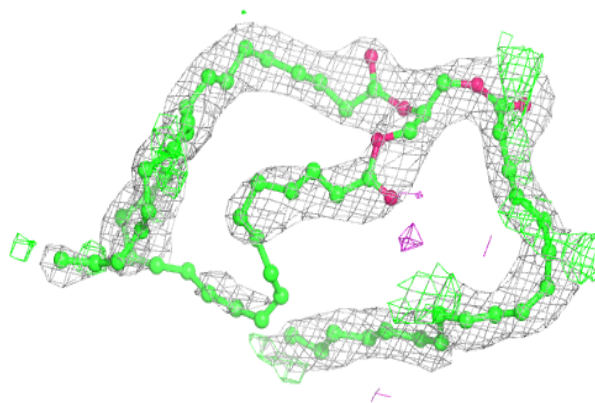
**Electron density around CDL C 306:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

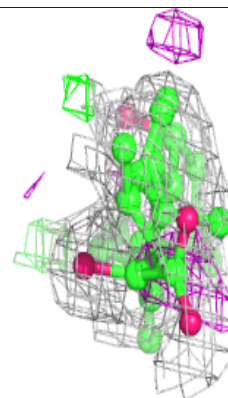
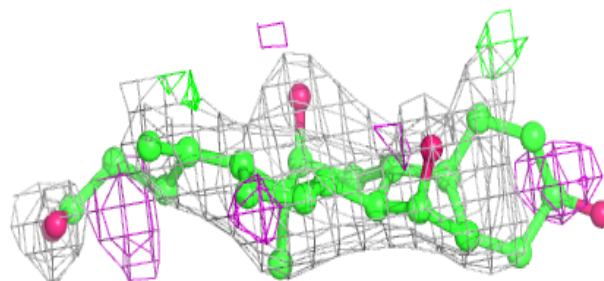
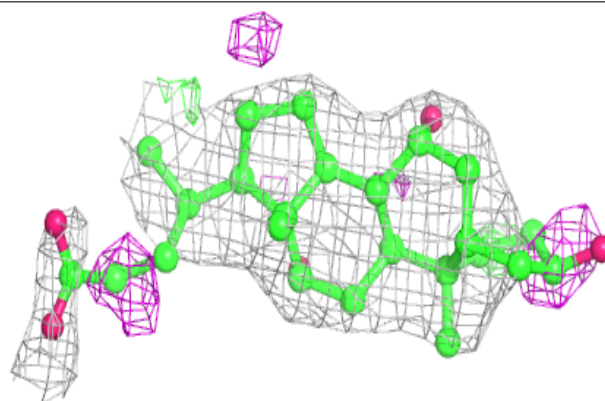


Electron density around TGL N 608:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

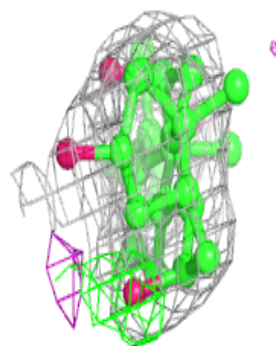
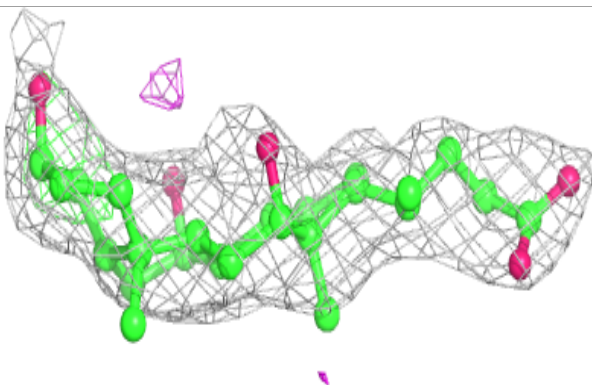
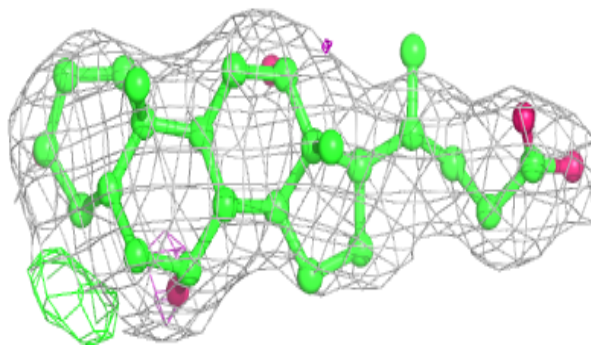
**Electron density around CHD J 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



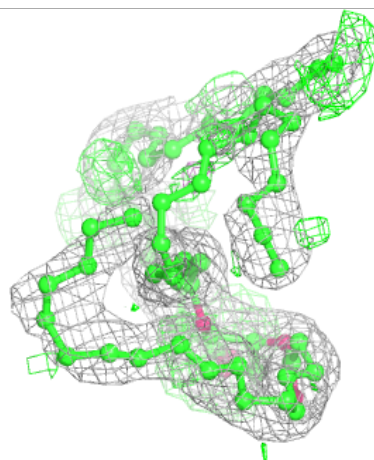
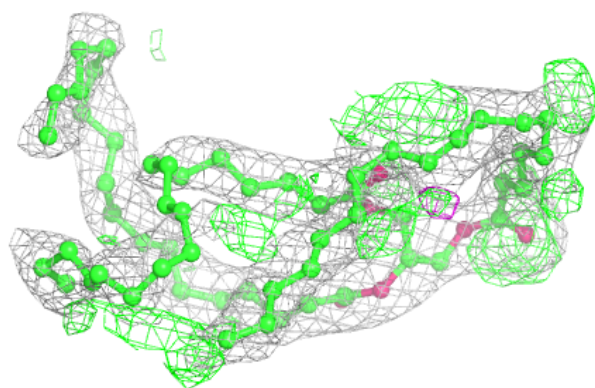
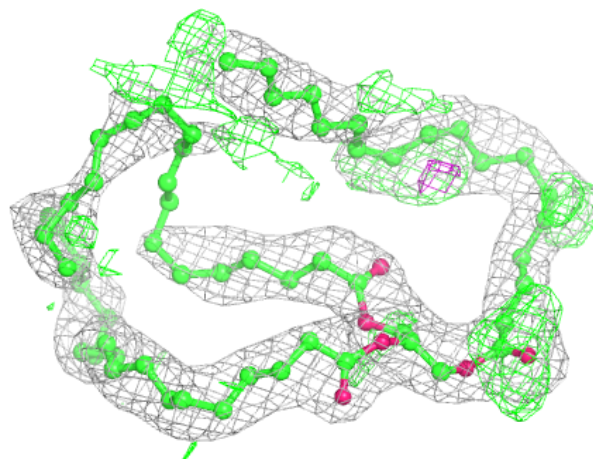
Electron density around CHD P 307:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



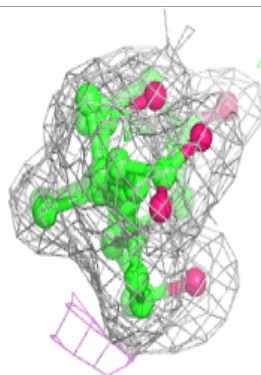
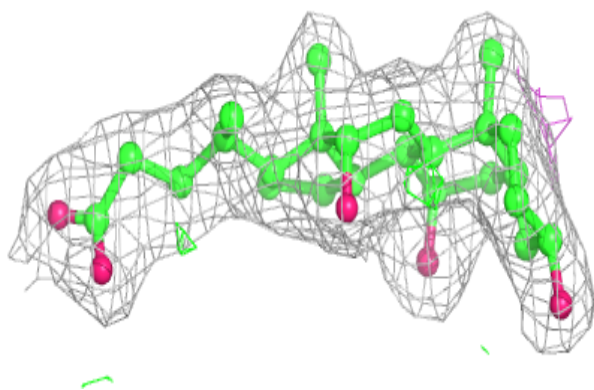
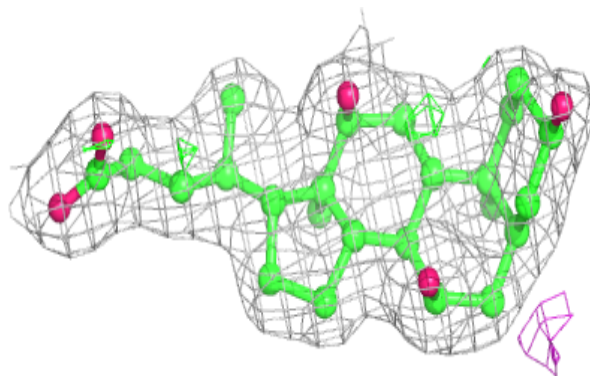
Electron density around TGL B 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

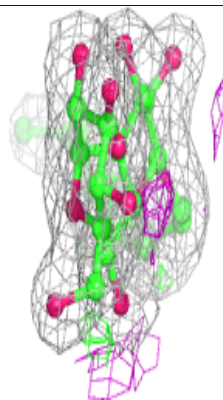
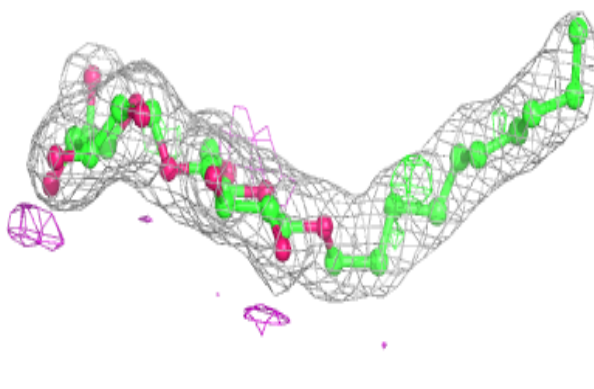
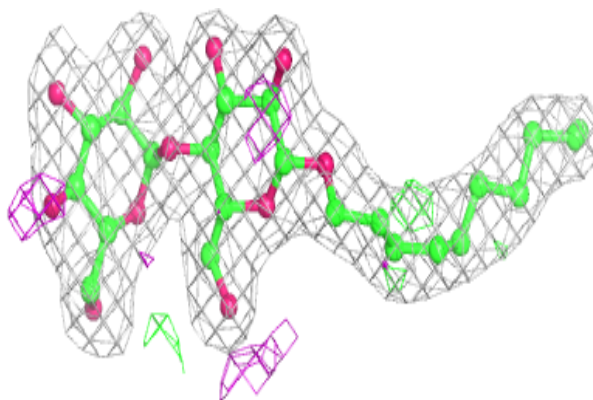


Electron density around CHD P 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

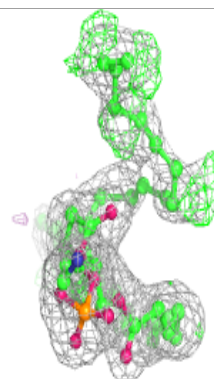
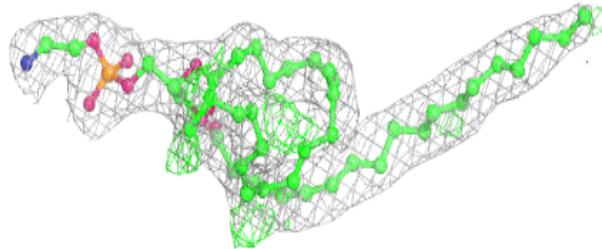
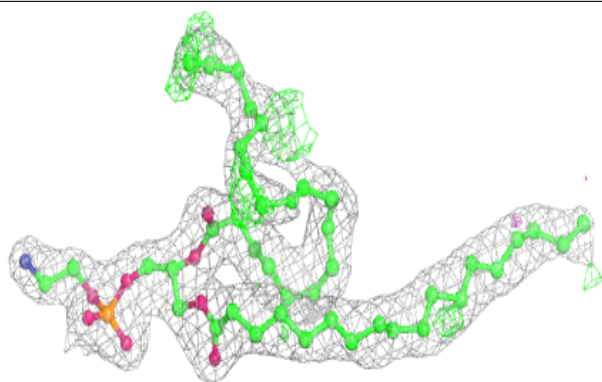
**Electron density around DMU M 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



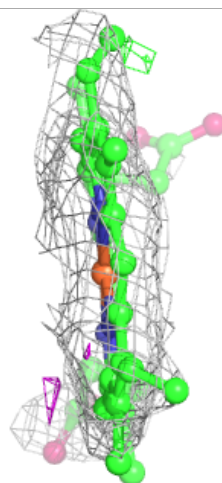
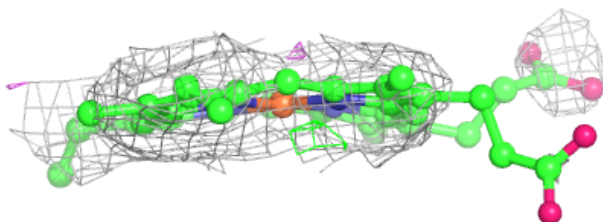
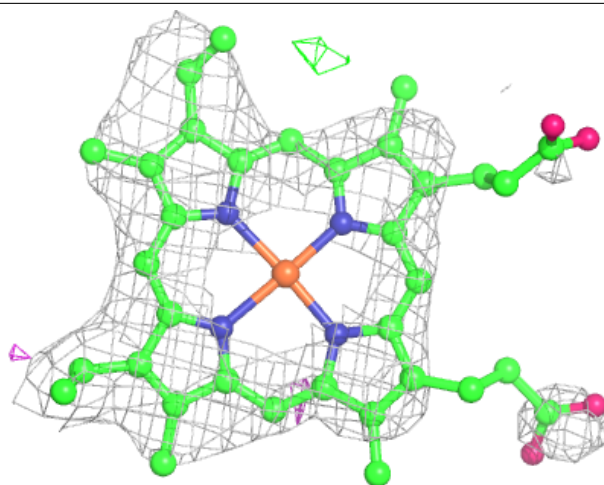
Electron density around PEK C 303:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



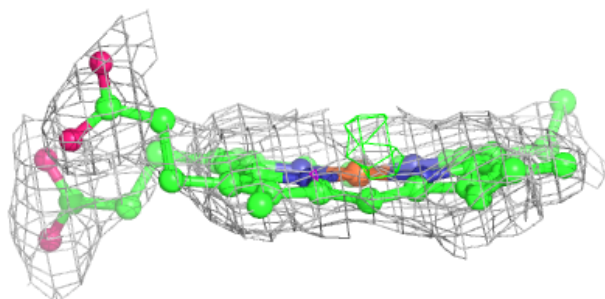
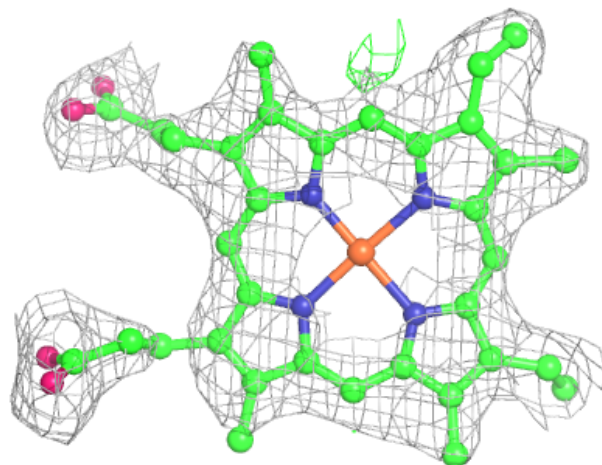
Electron density around HEC 2 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



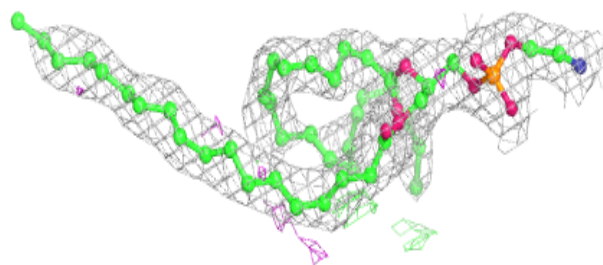
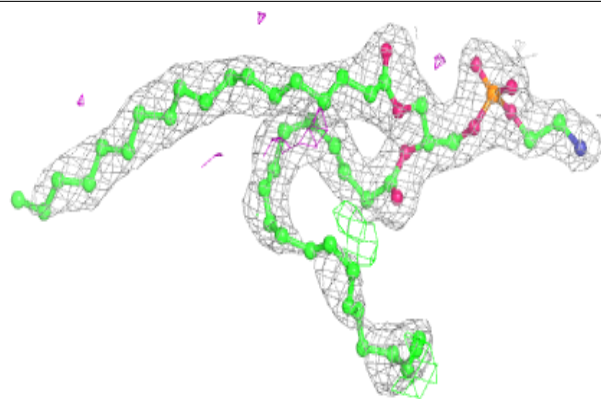
Electron density around HEC 1 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

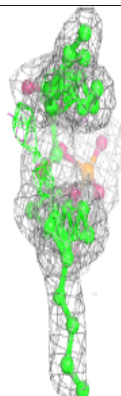
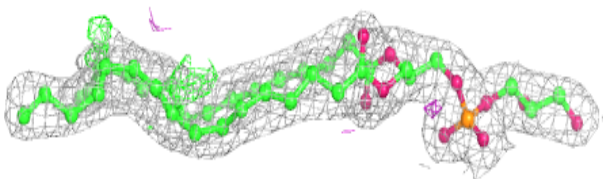
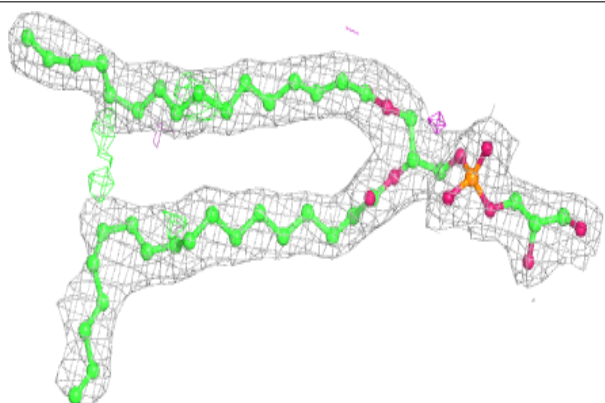


Electron density around PEK P 303:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

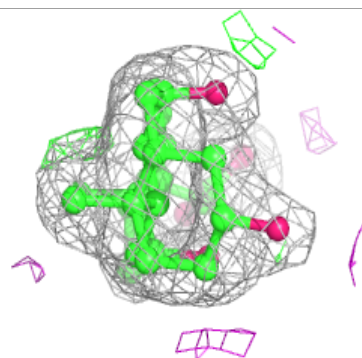
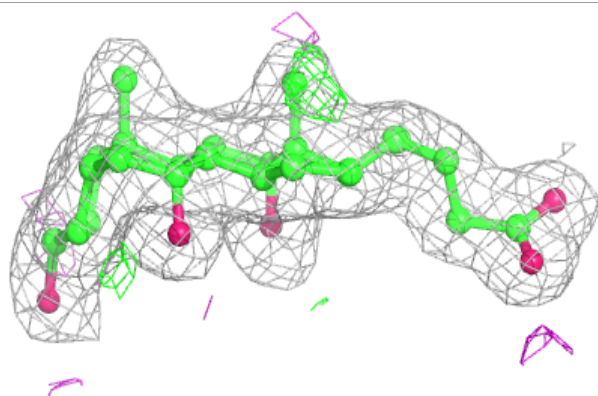
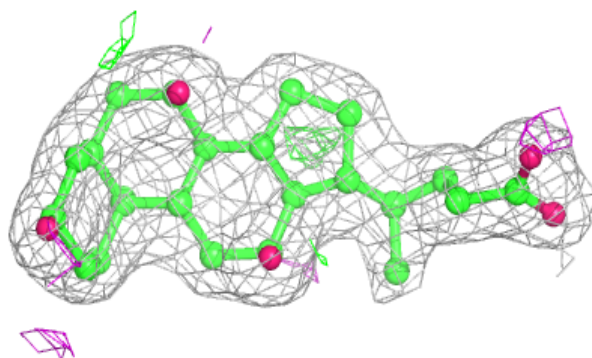
**Electron density around PGV P 304:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

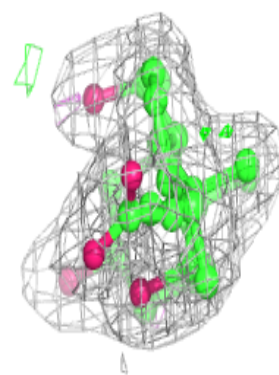
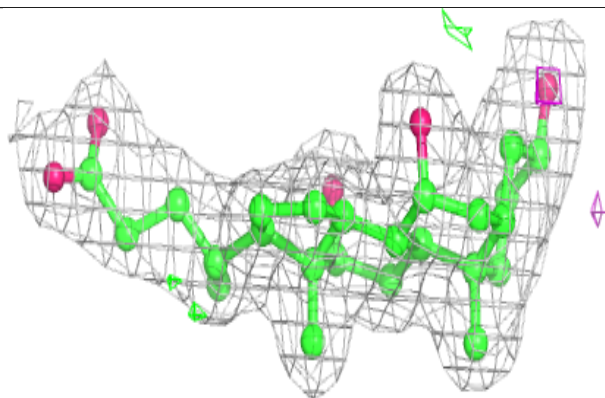
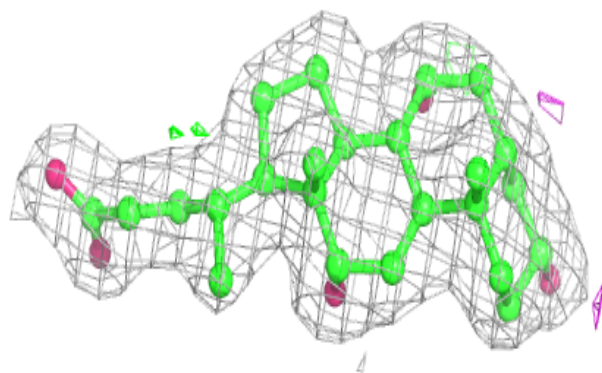


Electron density around CHD T 103:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

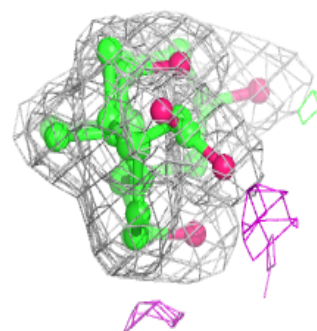
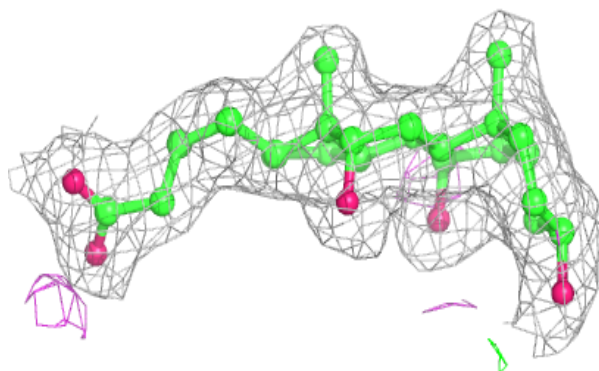
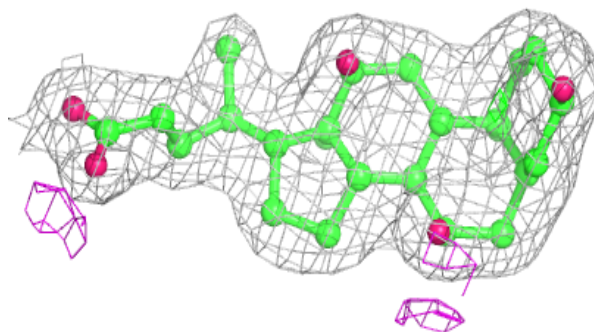
**Electron density around CHD C 301:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

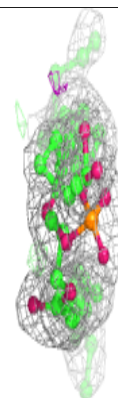
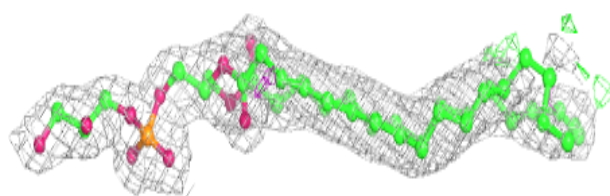
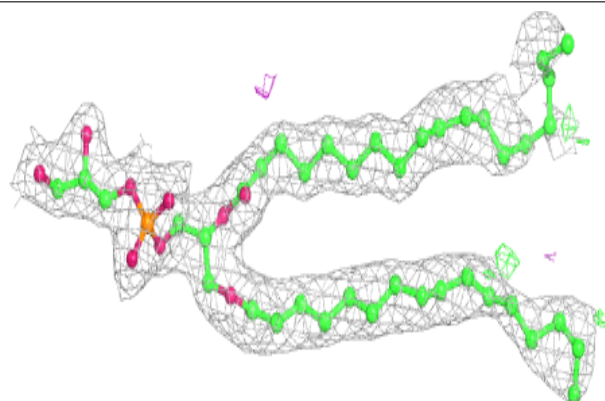


Electron density around CHD G 102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

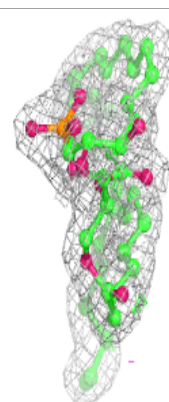
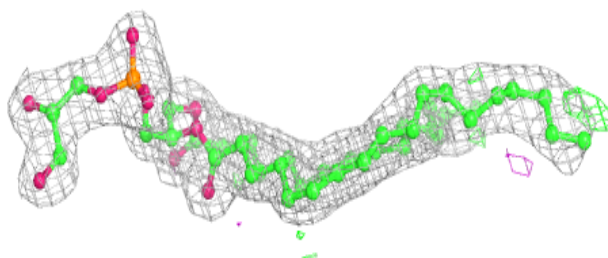
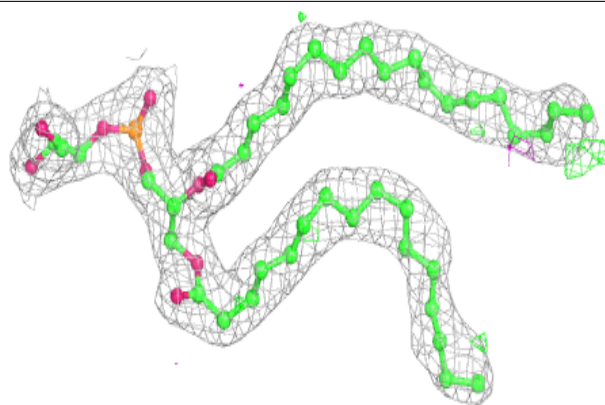
**Electron density around PGV C 304:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

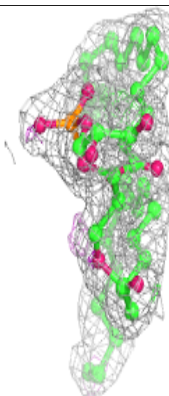
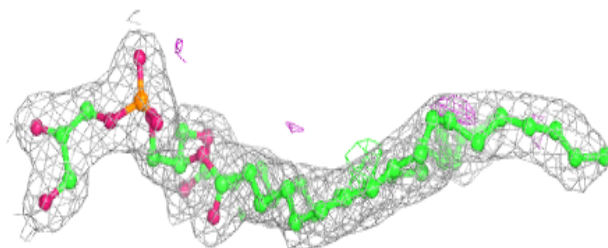
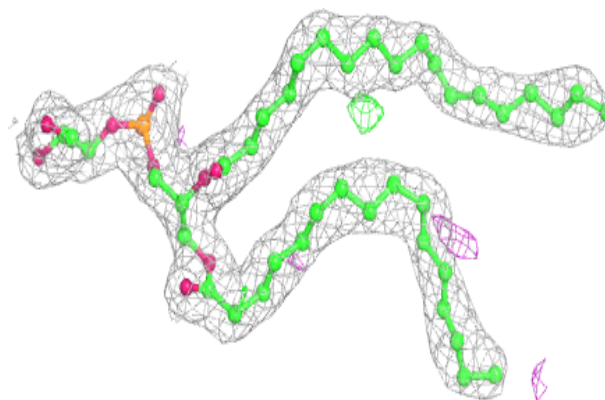


Electron density around PGV N 612:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

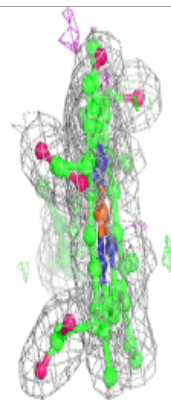
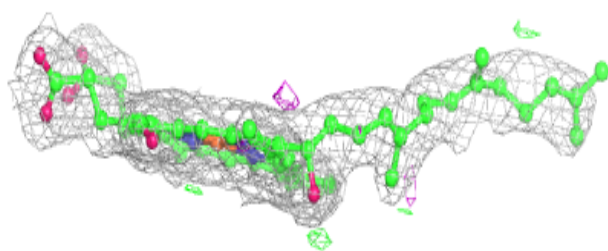
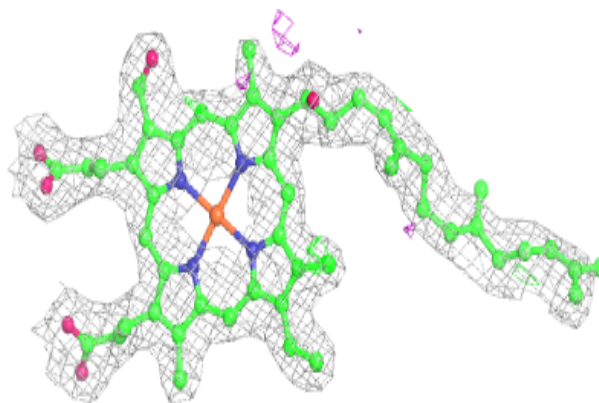
**Electron density around PGV A 608:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

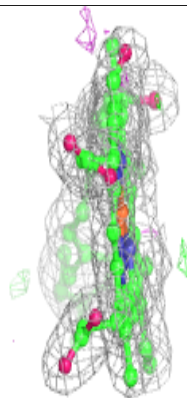
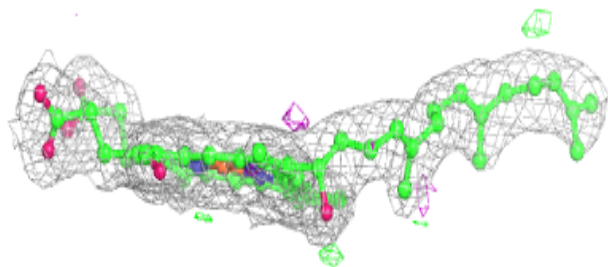
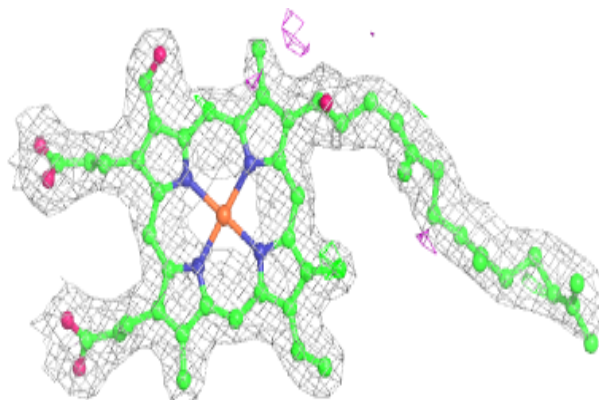


Electron density around HEA N 605 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

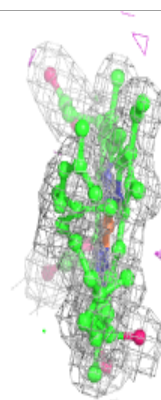
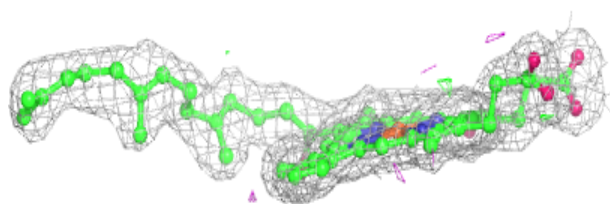
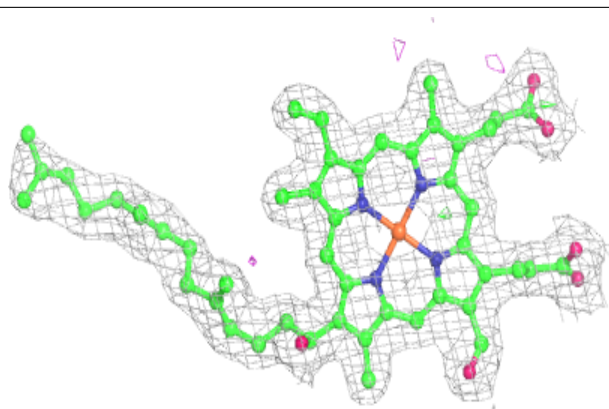
**Electron density around HEA N 605 (A):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

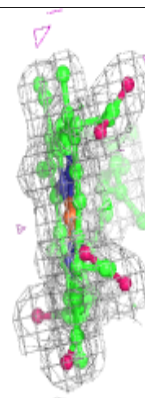
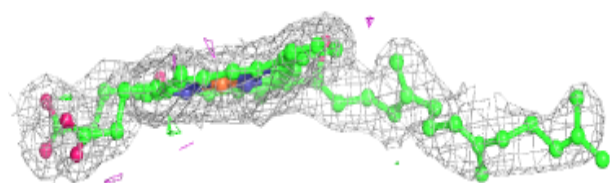
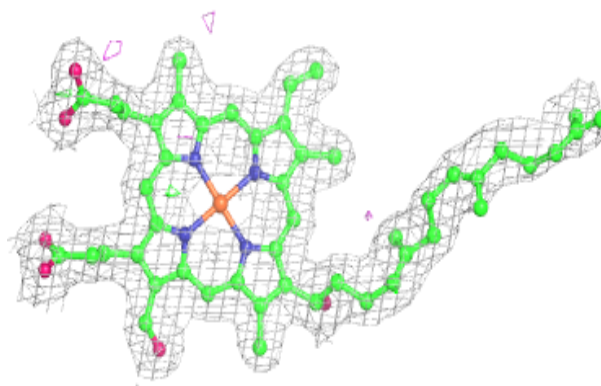


Electron density around HEA A 604 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

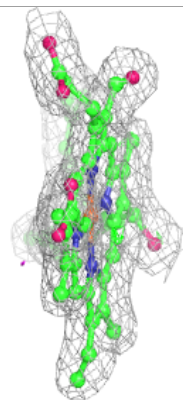
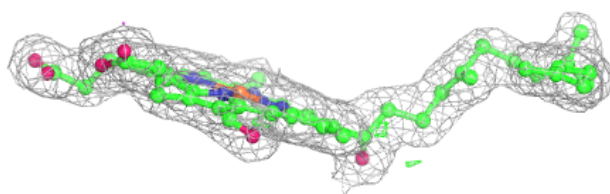
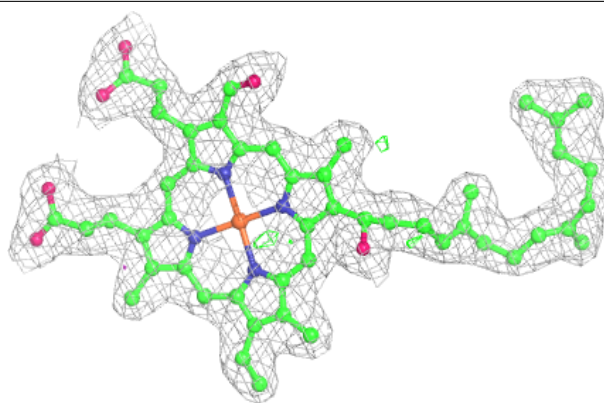
**Electron density around HEA A 604 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

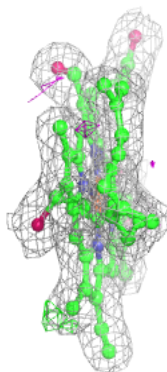
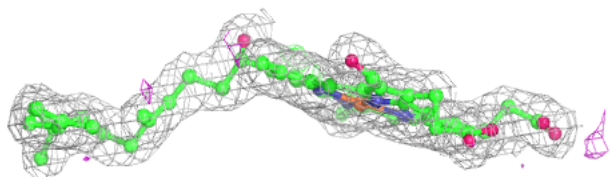
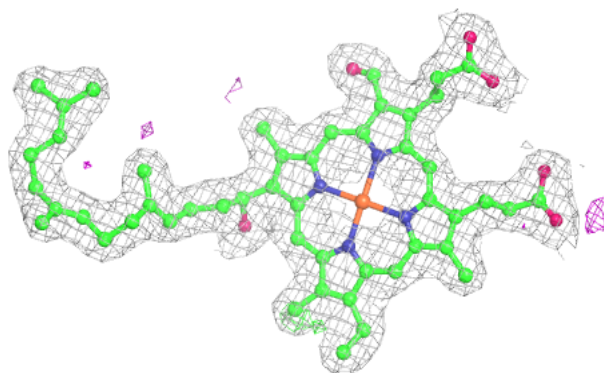


Electron density around HEA N 606:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around HEA A 605:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.