# Full wwPDB X-ray Structure Validation Report (i)

Nov 21, 2022 – 10:42 AM EST

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|---|---|---|
| PDB ID | : | 5WDU |
| Title | : | HIV-1 Env BG505 SOSIP.664 H72C-H564C trimer in complex with bNAbs PGT122 Fab, 35O22 Fab and NIH45-46 scFv |
| Authors | : | Julien, J.-P.; Torrents de la Pena, A.; Sanders, R.W.; Wilson, I.A. |
| Deposited on | : | 2017-07-06 |
| Resolution | : | 7.00 Å(reported) |

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

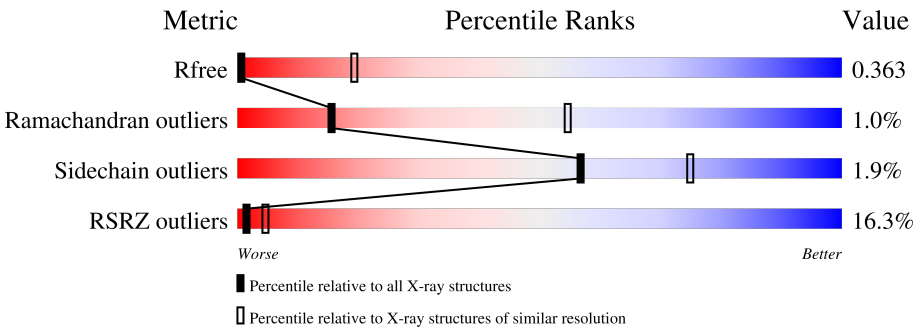
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.31.2 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.31.2 |

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*X-RAY DIFFRACTION*

The reported resolution of this entry is 7.00 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 | 1004 (10.00-3.90) |
| Ramachandran outliers | 138981 | 1002 (10.00-3.90) |
| Sidechain outliers | 138945 | 1002 (10.00-3.86) |
| RSRZ outliers | 127900 | 1004 (9.50-3.80) |

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 of 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 <=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 | F | 471 | 6% 92% • 5% |
| 1 | G | 471 | 3% 92% • 5% |
| 1 | Q | 471 | 5% 92% • 5% |
| 2 | D | 250 | 16% 86% • 11% |
| 2 | O | 250 | 14% 86% • 11% |
| 2 | W | 250 | 16% 86% • 11% |
| 3 | A | 147 | 2% 82% • 14% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 3 | J | 147 | 3% 82% 14% |
| 3 | R | 147 | 3% 82% 14% |
| 4 | B | 210 | 29% 97% |
| 4 | K | 210 | 32% 97% |
| 4 | S | 210 | 28% 99% |
| 5 | C | 232 | 30% 95% |
| 5 | L | 232 | 31% 96% |
| 5 | T | 232 | 41% 97% |
| 6 | H | 242 | 6% 100% |
| 6 | M | 242 | 28% 100% |
| 6 | U | 242 | 18% 99% |
| 7 | I | 213 | 2% 96% |
| 7 | N | 213 | 24% 99% |
| 7 | V | 213 | 11% 99% |
| 8 | E | 5 | 100% |
| 8 | X | 5 | 20% 80% |
| 8 | c | 5 | 60% 40% |
| 8 | e | 5 | 100% |
| 8 | g | 5 | 20% 80% |
| 8 | l | 5 | 60% 40% |
| 8 | n | 5 | 100% |
| 8 | p | 5 | 20% 80% |
| 8 | u | 5 | 60% 40% |
| 9 | P | 3 | 33% 67% |
| 9 | f | 3 | 33% 67% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 9 | o | 3 | 33% 67% |
| 10 | Y | 4 | 75% 25% |
| 10 | h | 4 | 50% 50% |
| 10 | q | 4 | 75% 25% |
| 11 | Z | 7 | 100% |
| 11 | i | 7 | 14% 86% |
| 11 | r | 7 | 100% |
| 12 | a | 6 | 100% |
| 12 | j | 6 | 17% 83% |
| 12 | s | 6 | 17% 83% |
| 13 | b | 2 | 100% |
| 13 | k | 2 | 100% |
| 13 | t | 2 | 100% |
| 14 | d | 8 | 12% 88% |
| 14 | m | 8 | 12% 88% |
| 14 | v | 8 | 12% 88% |

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 |
|---|---|---|---|---|---|---|---|
| 10 | NAG | Y | 1 | - | - | - | X |
| 10 | MAN | Y | 4 | - | - | - | X |
| 10 | NAG | h | 2 | - | - | - | X |
| 10 | BMA | h | 3 | - | - | - | X |
| 10 | MAN | h | 4 | - | - | - | X |
| 11 | NAG | Z | 2 | - | - | - | X |
| 11 | BMA | Z | 3 | - | - | - | X |
| 11 | MAN | Z | 5 | - | - | - | X |
| 11 | MAN | Z | 6 | - | - | - | X |
| 11 | MAN | Z | 7 | - | - | - | X |

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| Mol | Type | Chain | Res | Chirality | Geometry | Clashes | Electron density |
|---|---|---|---|---|---|---|---|
| 11 | NAG | i | 2 | - | - | - | X |
| 11 | BMA | i | 3 | - | - | - | X |
| 11 | MAN | i | 5 | - | - | - | X |
| 11 | MAN | i | 7 | - | - | - | X |
| 11 | NAG | r | 2 | - | - | - | X |
| 11 | BMA | r | 3 | - | - | - | X |
| 11 | MAN | r | 5 | - | - | - | X |
| 11 | MAN | r | 7 | - | - | - | X |
| 12 | MAN | a | 5 | - | - | - | X |
| 12 | MAN | j | 5 | - | - | - | X |
| 12 | MAN | j | 6 | - | - | - | X |
| 12 | MAN | s | 4 | - | - | - | X |
| 12 | MAN | s | 5 | - | - | - | X |
| 14 | NAG | d | 1 | - | - | - | X |
| 14 | MAN | d | 7 | - | - | - | X |
| 14 | MAN | d | 8 | - | - | - | X |
| 14 | NAG | m | 2 | - | - | - | X |
| 14 | MAN | m | 6 | - | - | - | X |
| 14 | MAN | m | 8 | - | - | - | X |
| 14 | MAN | v | 8 | - | - | - | X |
| 15 | NAG | A | 702 | - | - | - | X |
| 15 | NAG | A | 703 | - | - | - | X |
| 15 | NAG | F | 606 | - | - | - | X |
| 15 | NAG | F | 615 | - | - | - | X |
| 15 | NAG | F | 633 | - | - | - | X |
| 15 | NAG | F | 649 | - | - | - | X |
| 15 | NAG | F | 651 | - | - | - | X |
| 15 | NAG | F | 652 | - | - | - | X |
| 15 | NAG | G | 615 | - | - | - | X |
| 15 | NAG | G | 649 | - | - | - | X |
| 15 | NAG | G | 651 | - | - | - | X |
| 15 | NAG | G | 652 | - | - | - | X |
| 15 | NAG | G | 653 | - | - | - | X |
| 15 | NAG | J | 701 | - | - | - | X |
| 15 | NAG | J | 702 | - | - | - | X |
| 15 | NAG | J | 703 | - | - | - | X |
| 15 | NAG | Q | 615 | - | - | - | X |
| 15 | NAG | Q | 633 | - | - | - | X |
| 15 | NAG | Q | 649 | - | - | - | X |
| 15 | NAG | Q | 651 | - | - | - | X |
| 15 | NAG | Q | 652 | - | - | - | X |
| 15 | NAG | Q | 653 | - | - | - | X |

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| Mol | Type | Chain | Res | Chirality | Geometry | Clashes | Electron density |
|---|---|---|---|---|---|---|---|
| 15 | NAG | R | 701 | - | - | - | X |
| 15 | NAG | R | 702 | - | - | - | X |
| 15 | NAG | R | 703 | - | - | - | X |
| 2 | PCA | D | 1 | - | - | - | X |
| 2 | PCA | W | 1 | - | - | - | X |
| 8 | MAN | E | 4 | - | - | - | X |
| 8 | MAN | X | 4 | - | - | - | X |
| 8 | MAN | c | 4 | - | - | - | X |
| 8 | MAN | c | 5 | - | - | - | X |
| 8 | NAG | e | 2 | - | - | - | X |
| 8 | BMA | e | 3 | - | - | - | X |
| 8 | MAN | e | 4 | - | - | - | X |
| 8 | MAN | e | 5 | - | - | - | X |
| 8 | MAN | g | 4 | - | - | - | X |
| 8 | MAN | g | 5 | - | - | - | X |
| 8 | NAG | l | 1 | - | - | - | X |
| 8 | MAN | l | 5 | - | - | - | X |
| 8 | NAG | n | 2 | - | - | - | X |
| 8 | BMA | n | 3 | - | - | - | X |
| 8 | MAN | n | 4 | - | - | - | X |
| 8 | MAN | n | 5 | - | - | - | X |
| 8 | BMA | p | 3 | - | - | - | X |
| 8 | MAN | p | 4 | - | - | - | X |
| 8 | MAN | p | 5 | - | - | - | X |
| 9 | NAG | P | 2 | - | - | - | X |
| 9 | BMA | P | 3 | - | - | - | X |
| 9 | NAG | f | 1 | - | - | - | X |
| 9 | NAG | f | 2 | - | - | - | X |
| 9 | NAG | o | 1 | - | - | - | X |
| 9 | NAG | o | 2 | - | - | - | X |
| 9 | BMA | o | 3 | - | - | - | X |

# 2 Entry composition (i)

There are 15 unique types of molecules in this entry. The entry contains 41285 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 Envelope glycoprotein gp160.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 1 | G | 449 | 3535 | 2218 | 624 | 664 | 29 | 0 | 0 | 0 |
| 1 | F | 449 | 3535 | 2218 | 624 | 664 | 29 | 0 | 0 | 0 |
| 1 | Q | 449 | 3535 | 2218 | 624 | 664 | 29 | 0 | 0 | 0 |

There are 21 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| G | 72 | CYS | HIS | conflict | UNP Q2N0S6 |
| G | 332 | ASN | THR | conflict | UNP Q2N0S6 |
| G | 460 | ALA | SER | conflict | UNP Q2N0S6 |
| G | 461 | ASN | THR | conflict | UNP Q2N0S6 |
| G | 463 | THR | SER | conflict | UNP Q2N0S6 |
| G | 464 | SER | THR | conflict | UNP Q2N0S6 |
| G | 501 | CYS | ALA | conflict | UNP Q2N0S6 |
| F | 72 | CYS | HIS | conflict | UNP Q2N0S6 |
| F | 332 | ASN | THR | conflict | UNP Q2N0S6 |
| F | 460 | ALA | SER | conflict | UNP Q2N0S6 |
| F | 461 | ASN | THR | conflict | UNP Q2N0S6 |
| F | 463 | THR | SER | conflict | UNP Q2N0S6 |
| F | 464 | SER | THR | conflict | UNP Q2N0S6 |
| F | 501 | CYS | ALA | conflict | UNP Q2N0S6 |
| Q | 72 | CYS | HIS | conflict | UNP Q2N0S6 |
| Q | 332 | ASN | THR | conflict | UNP Q2N0S6 |
| Q | 460 | ALA | SER | conflict | UNP Q2N0S6 |
| Q | 461 | ASN | THR | conflict | UNP Q2N0S6 |
| Q | 463 | THR | SER | conflict | UNP Q2N0S6 |
| Q | 464 | SER | THR | conflict | UNP Q2N0S6 |
| Q | 501 | CYS | ALA | conflict | UNP Q2N0S6 |

- Molecule 2 is a protein called bnAb NIH45-46 scFv.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 2 | D | 223 | 1761 | 1107 | 316 | 328 | 10 | 0 | 0 | 0 |
| 2 | O | 222 | 1753 | 1102 | 315 | 326 | 10 | 0 | 0 | 0 |
| 2 | W | 223 | 1761 | 1107 | 316 | 328 | 10 | 0 | 0 | 0 |

- Molecule 3 is a protein called Envelope glycoprotein gp160.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 3 | A | 126 | 1001 | 633 | 172 | 190 | 6 | 0 | 0 | 0 |
| 3 | J | 126 | 1001 | 633 | 172 | 190 | 6 | 0 | 0 | 0 |
| 3 | R | 126 | 1001 | 633 | 172 | 190 | 6 | 0 | 0 | 0 |

There are 3 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| A | 605 | CYS | THR | conflict | UNP Q2N0S8 |
| J | 605 | CYS | THR | conflict | UNP Q2N0S8 |
| R | 605 | CYS | THR | conflict | UNP Q2N0S8 |

- Molecule 4 is a protein called bnAb PGT122 Fab light chain.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 4 | B | 210 | 1589 | 998 | 267 | 320 | 4 | 0 | 0 | 0 |
| 4 | K | 210 | 1589 | 998 | 267 | 320 | 4 | 0 | 0 | 0 |
| 4 | S | 210 | 1589 | 998 | 267 | 320 | 4 | 0 | 0 | 0 |

- Molecule 5 is a protein called bnAb PGT122 Fab heavy chain.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 5 | C | 228 | 1742 | 1109 | 295 | 333 | 5 | 0 | 0 | 0 |
| 5 | L | 228 | 1742 | 1109 | 295 | 333 | 5 | 0 | 0 | 0 |
| 5 | T | 228 | 1742 | 1109 | 295 | 333 | 5 | 0 | 0 | 0 |

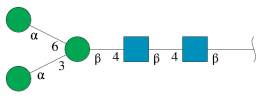
- Molecule 6 is a protein called bnAb 35O22 Fab heavy chain.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 6 | H | 242 | 1832 | 1165 | 306 | 353 | 8 | 0 | 0 | 0 |
| 6 | M | 242 | 1832 | 1165 | 306 | 353 | 8 | 0 | 0 | 0 |
| 6 | U | 242 | 1832 | 1165 | 306 | 353 | 8 | 0 | 0 | 0 |

- Molecule 7 is a protein called bnAb 35O22 Fab light chain.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | | |
| 7 | I | 207 | 1574 | 989 | 258 | 319 | 8 | 0 | 0 | 0 |
| 7 | N | 213 | 1615 | 1012 | 267 | 328 | 8 | 0 | 0 | 0 |
| 7 | V | 213 | 1615 | 1012 | 267 | 328 | 8 | 0 | 0 | 0 |

- Molecule 8 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.




| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | | |
| 8 | E | 5 | 61 | 34 | 2 | 25 | 0 | 0 | 0 |
| 8 | X | 5 | 61 | 34 | 2 | 25 | 0 | 0 | 0 |
| 8 | c | 5 | 61 | 34 | 2 | 25 | 0 | 0 | 0 |
| 8 | e | 5 | 61 | 34 | 2 | 25 | 0 | 0 | 0 |
| 8 | g | 5 | 61 | 34 | 2 | 25 | 0 | 0 | 0 |
| 8 | l | 5 | 61 | 34 | 2 | 25 | 0 | 0 | 0 |
| 8 | n | 5 | 61 | 34 | 2 | 25 | 0 | 0 | 0 |

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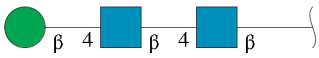
| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | | |
| 8 | p | 5 | 61 | 34 | 2 | 25 | 0 | 0 | 0 |
| 8 | u | 5 | 61 | 34 | 2 | 25 | 0 | 0 | 0 |

- Molecule 9 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

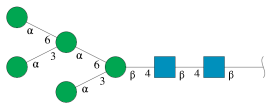



| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | | |
| 9 | P | 3 | 39 | 22 | 2 | 15 | 0 | 0 | 0 |
| 9 | f | 3 | 39 | 22 | 2 | 15 | 0 | 0 | 0 |
| 9 | o | 3 | 39 | 22 | 2 | 15 | 0 | 0 | 0 |

- Molecule 10 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

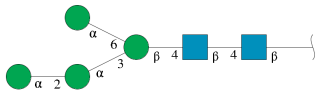
| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | | |
| 10 | Y | 4 | 50 | 28 | 2 | 20 | 0 | 0 | 0 |
| 10 | h | 4 | 50 | 28 | 2 | 20 | 0 | 0 | 0 |
| 10 | q | 4 | 50 | 28 | 2 | 20 | 0 | 0 | 0 |

- Molecule 11 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | | |
| 11 | Z | 7 | 83 | 46 | 2 | 35 | 0 | 0 | 0 |
| 11 | i | 7 | 83 | 46 | 2 | 35 | 0 | 0 | 0 |
| 11 | r | 7 | 83 | 46 | 2 | 35 | 0 | 0 | 0 |

- Molecule 12 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

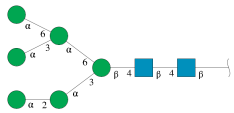


| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | | |
| 12 | a | 6 | 72 | 40 | 2 | 30 | 0 | 0 | 0 |
| 12 | j | 6 | 72 | 40 | 2 | 30 | 0 | 0 | 0 |
| 12 | s | 6 | 72 | 40 | 2 | 30 | 0 | 0 | 0 |

- Molecule 13 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

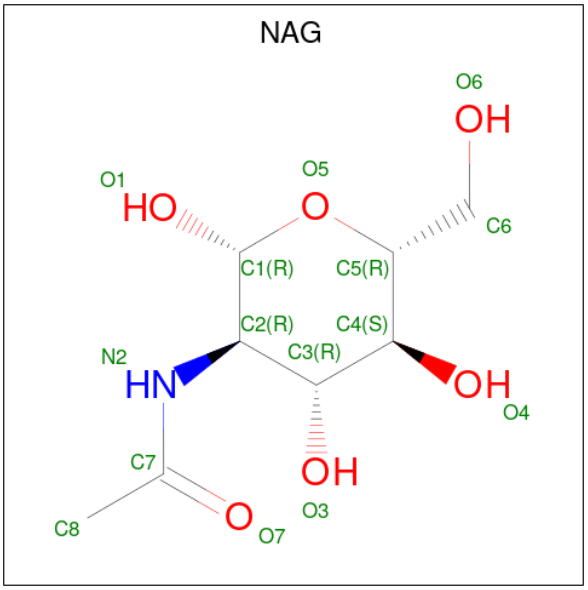
| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | | |
| 13 | b | 2 | 28 | 16 | 2 | 10 | 0 | 0 | 0 |
| 13 | k | 2 | 28 | 16 | 2 | 10 | 0 | 0 | 0 |
| 13 | t | 2 | 28 | 16 | 2 | 10 | 0 | 0 | 0 |

- Molecule 14 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | | |
| 14 | d | 8 | 94 | 52 | 2 | 40 | 0 | 0 | 0 |
| 14 | m | 8 | 94 | 52 | 2 | 40 | 0 | 0 | 0 |
| 14 | v | 8 | 94 | 52 | 2 | 40 | 0 | 0 | 0 |

- Molecule 15 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).




| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 15 | G | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| 15 | G | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| 15 | G | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| 15 | G | 1 | 14 | 8 | 1 | 5 | 0 | 0 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 15 | G | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | G | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | G | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | G | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | F | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | F | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | F | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | F | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | F | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | F | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | F | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | F | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | Q | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | Q | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | Q | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | Q | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | Q | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | Q | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | Q | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | Q | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | A | 1 | 14 | 8 | 1 | 5 | 0 | 0 |

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*Continued from previous page...*

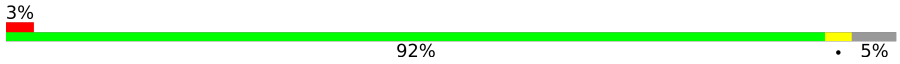
| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 15 | A | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | A | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | J | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | J | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | J | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | R | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | R | 1 | 14 | 8 | 1 | 5 | 0 | 0 |
| | | | Total | C | N | O | | |
| 15 | R | 1 | 14 | 8 | 1 | 5 | 0 | 0 |

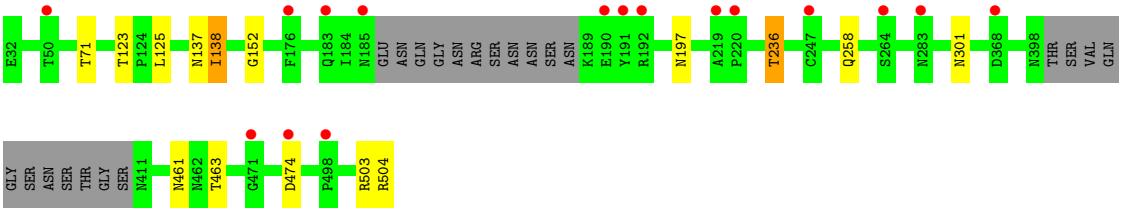
# 3 Residue-property plots (i)

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: Envelope glycoprotein gp160

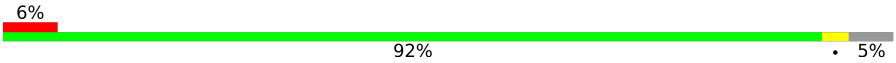
Chain G:

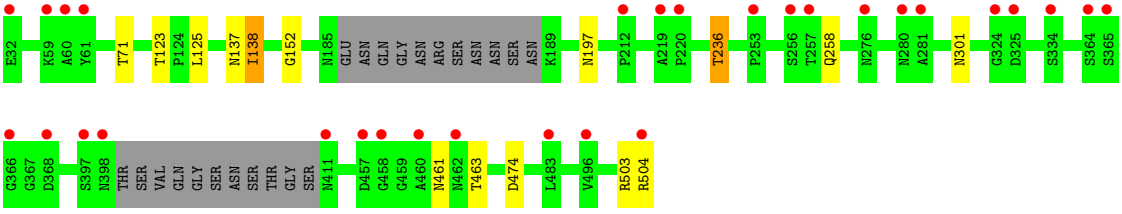



• Molecule 1: Envelope glycoprotein gp160

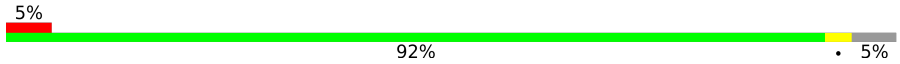
Chain F:

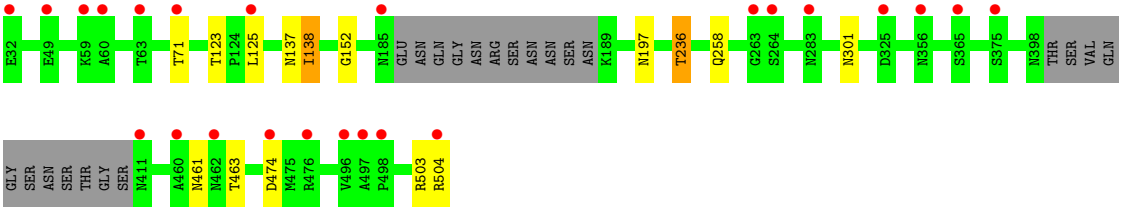



• Molecule 1: Envelope glycoprotein gp160

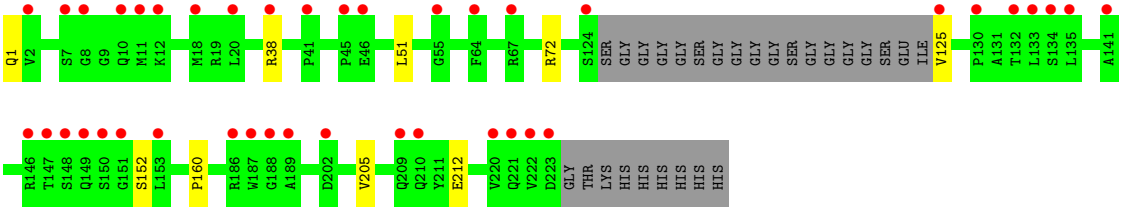
Chain Q:



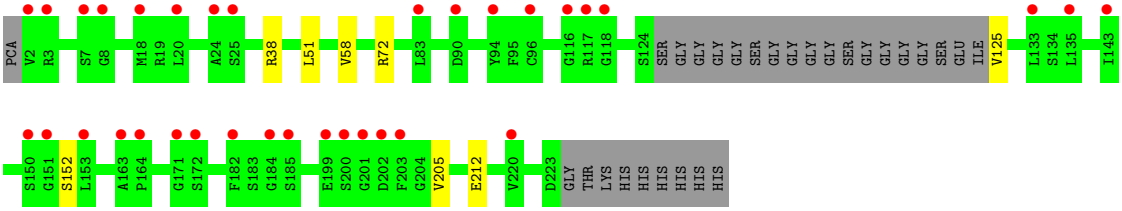

• Molecule 2: bnAb NIH45-46 scFv

Chain D:



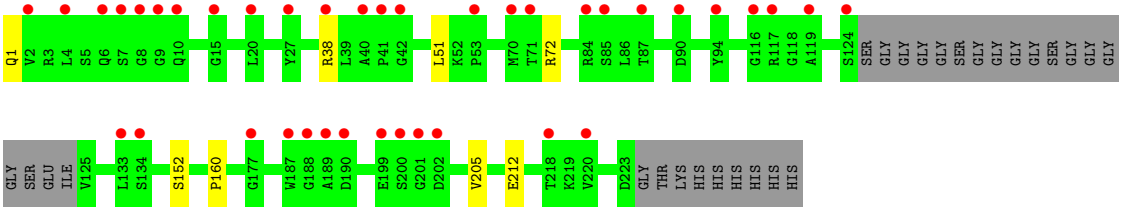

- Molecule 2: bnAb NIH45-46 scFv

Chain O:



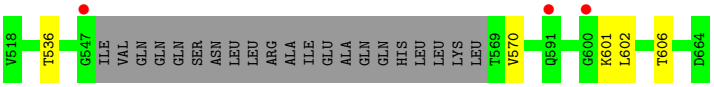

- Molecule 2: bnAb NIH45-46 scFv

Chain W:



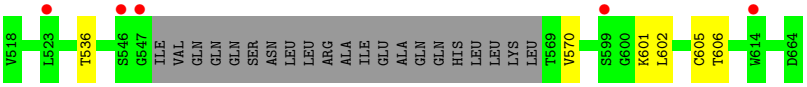

- Molecule 3: Envelope glycoprotein gp160

Chain A:



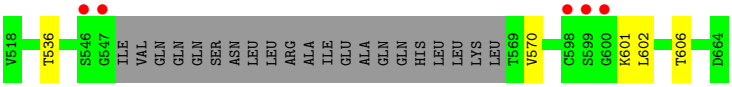

- Molecule 3: Envelope glycoprotein gp160

Chain J:



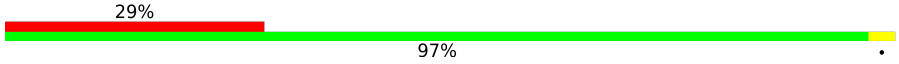

- Molecule 3: Envelope glycoprotein gp160

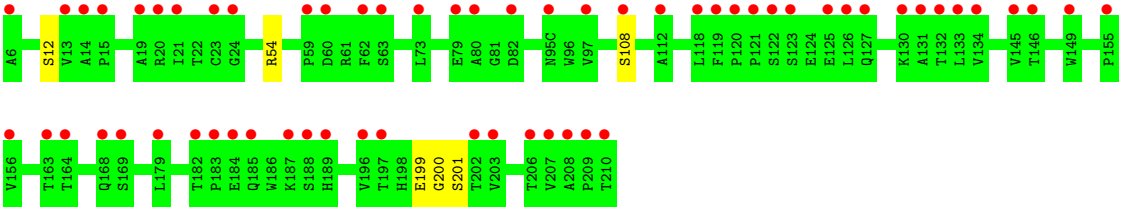
Chain R:



• Molecule 4: bnAb PGT122 Fab light chain

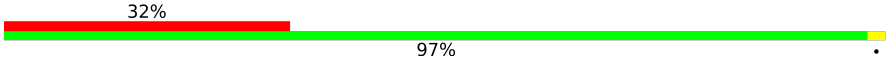
Chain B:

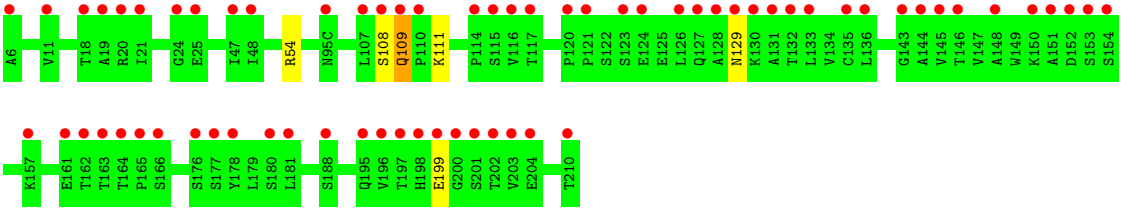



• Molecule 4: bnAb PGT122 Fab light chain

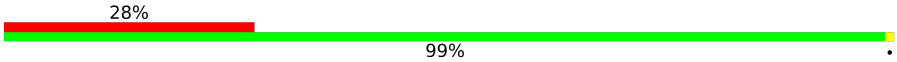
Chain K:

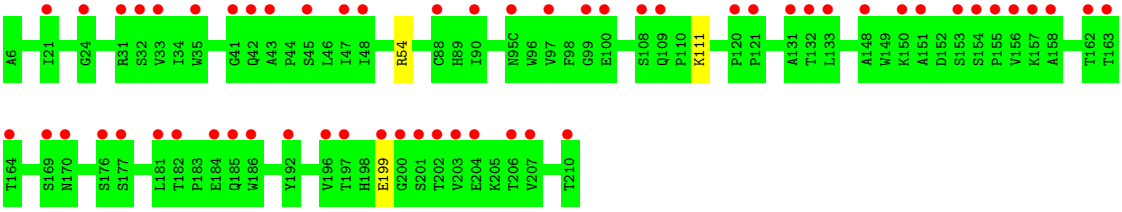



• Molecule 4: bnAb PGT122 Fab light chain

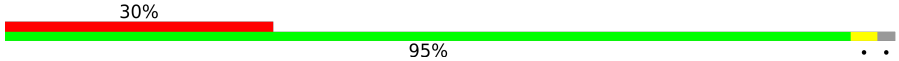
Chain S:

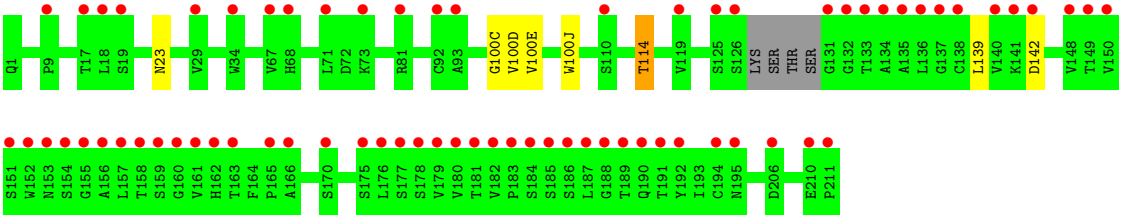



• Molecule 5: bnAb PGT122 Fab heavy chain

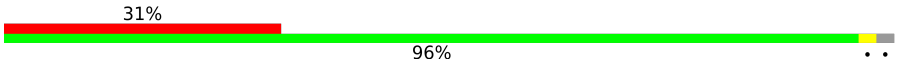
Chain C:

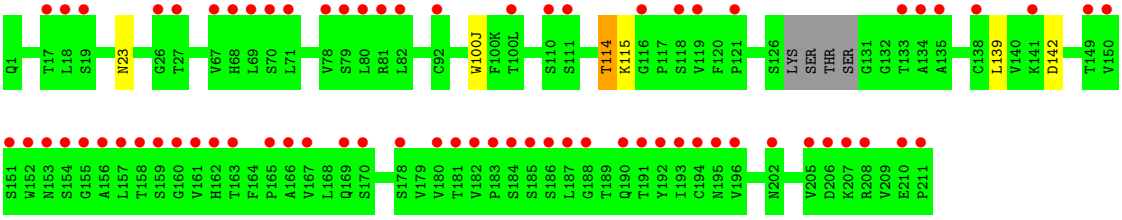



• Molecule 5: bnAb PGT122 Fab heavy chain

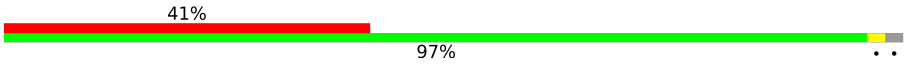
Chain L:

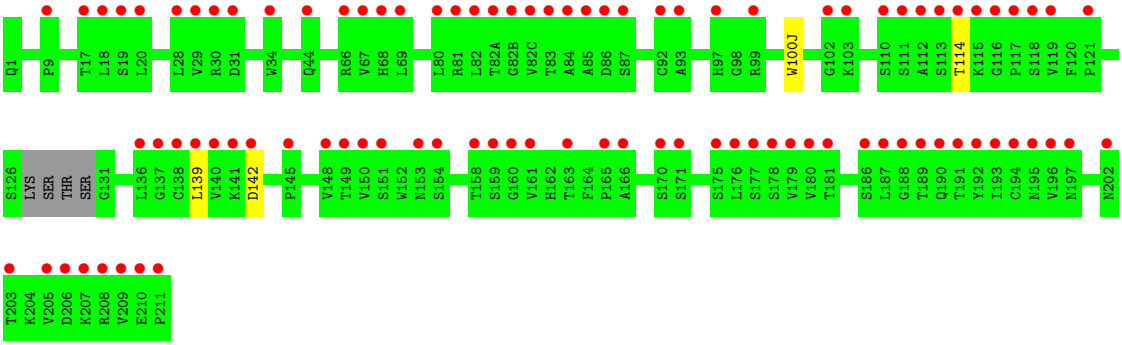





- Molecule 5: bnAb PGT122 Fab heavy chain

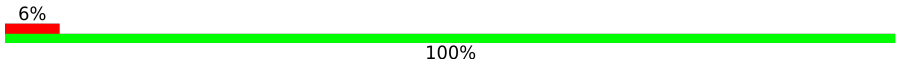
Chain T:

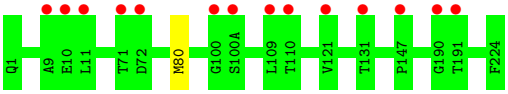



- Molecule 6: bnAb 35O22 Fab heavy chain

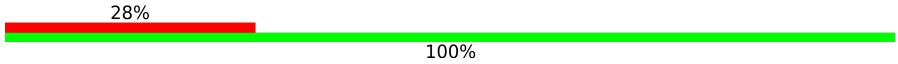
Chain H:

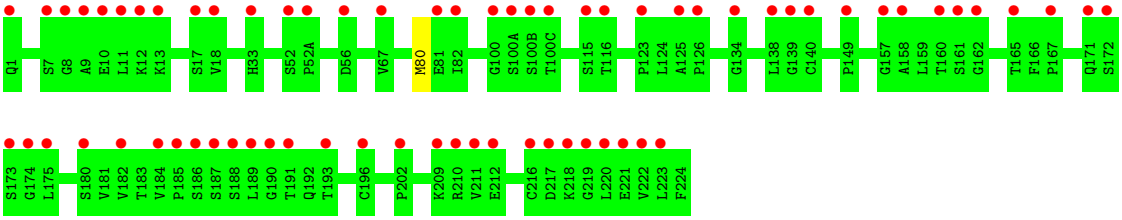



- Molecule 6: bnAb 35O22 Fab heavy chain

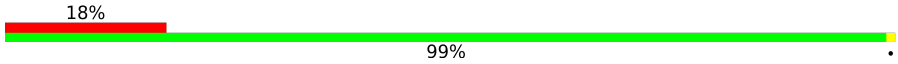
Chain M:

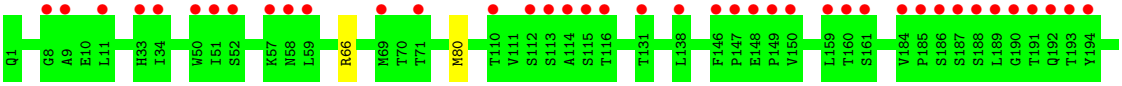



- Molecule 6: bnAb 35O22 Fab heavy chain

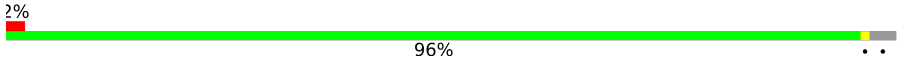
Chain U:

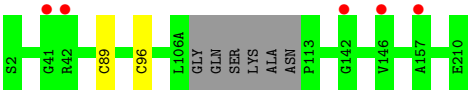


• Molecule 7: bnAb 35O22 Fab light chain

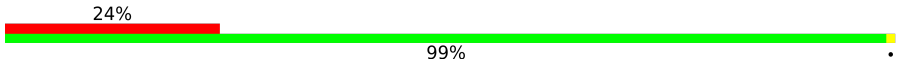
Chain I:

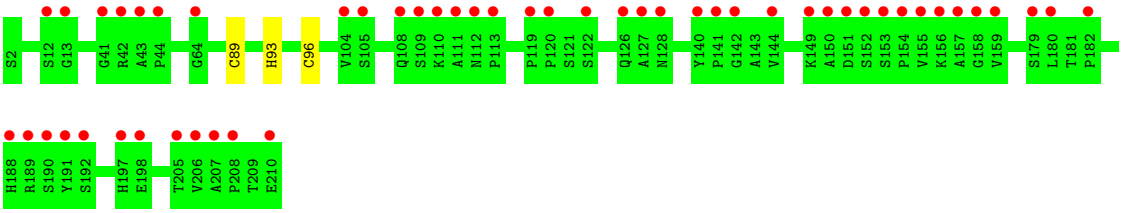



• Molecule 7: bnAb 35O22 Fab light chain

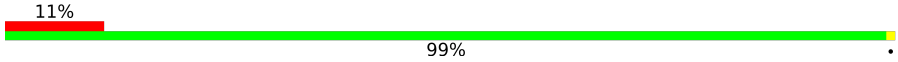
Chain N:

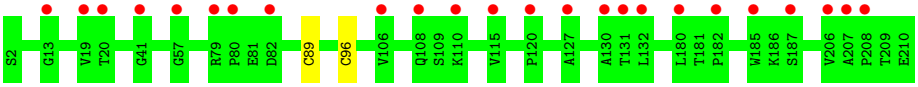



• Molecule 7: bnAb 35O22 Fab light chain

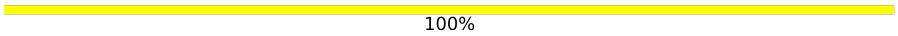
Chain V:



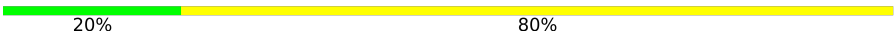

• Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:



• Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

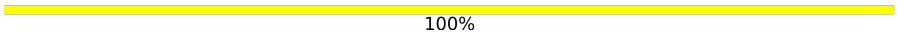
Chain X:



• Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain c:


• Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain e: 

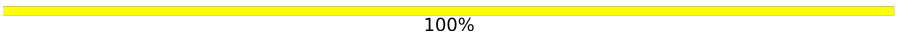
• Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain g:


• Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain l:


• Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain n: 

• Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain p:


• Molecule 8: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyra

nose

Chain u:


• Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:


• Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain f:


• Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain o:


• Molecule 10: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:


• Molecule 10: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain h:


• Molecule 10: alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain q:


• Molecule 11: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z: 100%

• Molecule 11: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain i: 14% 86%

• Molecule 11: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain r: 100%

• Molecule 12: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a: 100%

• Molecule 12: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain j: 17% 83%

• Molecule 12: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain s: 17% 83%

NAG1 NAG2 BMA3 MAN4 MAN5 MAN6

• Molecule 13: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain b: 100%

NAG1 NAG2

• Molecule 13: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain k: 100%

NAG1 NAG2

• Molecule 13: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain t: 100%

NAG1 NAG2

• Molecule 14: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d: 12% 88%

NAG1 NAG2 BMA3 MAN4 MAN5 MAN6 MAN7 MAN8

• Molecule 14: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain m: 12% 88%

NAG1 NAG2 BMA3 MAN4 MAN5 MAN6 MAN7 MAN8

• Molecule 14: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(

1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain v:

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | C 1 2 1 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 361.81Å 215.85Å 176.61Å<br>90.00° 114.03° 90.00° | Depositor |
| Resolution (Å) | 39.71 – 7.00<br>39.71 – 7.00 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 99.9 (39.71-7.00)<br>99.9 (39.71-7.00) | Depositor<br>EDS |
| $R_{merge}$ | (Not available) | Depositor |
| $R_{sym}$ | 0.20 | Depositor |
| $< I/\sigma(I) >$ [1] | 1.94 (at 7.33Å) | Xtriage |
| Refinement program | PHENIX (1.13_2998: ???) | Depositor |
| R, $R_{free}$ | 0.301 , 0.363<br>0.301 , 0.363 | Depositor<br>DCC |
| $R_{free}$ test set | 978 reflections (5.00%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 277.9 | Xtriage |
| Anisotropy | 0.587 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.24 , 387.0 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.32$, $< L^2 > = 0.16$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| $F_o$,$F_c$ correlation | 0.77 | EDS |
| Total number of atoms | 41285 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 458.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

# 5 Model quality (i)

## 5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, PCA, MAN, BMA

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 | F | 0.27 | 0/3608 | 0.51 | 0/4898 |
| 1 | G | 0.28 | 0/3608 | 0.52 | 0/4898 |
| 1 | Q | 0.27 | 0/3608 | 0.51 | 0/4898 |
| 2 | D | 0.25 | 0/1800 | 0.46 | 0/2439 |
| 2 | O | 0.25 | 0/1799 | 0.45 | 0/2436 |
| 2 | W | 0.25 | 0/1800 | 0.46 | 0/2439 |
| 3 | A | 0.25 | 0/1019 | 0.45 | 0/1382 |
| 3 | J | 0.25 | 0/1019 | 0.47 | 1/1382 (0.1%) |
| 3 | R | 0.26 | 0/1019 | 0.45 | 0/1382 |
| 4 | B | 0.29 | 0/1632 | 0.55 | 1/2236 (0.0%) |
| 4 | K | 0.26 | 0/1632 | 0.52 | 1/2236 (0.0%) |
| 4 | S | 0.26 | 0/1632 | 0.48 | 0/2236 |
| 5 | C | 0.33 | 0/1789 | 0.59 | 1/2443 (0.0%) |
| 5 | L | 0.26 | 0/1789 | 0.49 | 0/2443 |
| 5 | T | 0.26 | 0/1789 | 0.47 | 0/2443 |
| 6 | H | 0.26 | 0/1880 | 0.48 | 0/2560 |
| 6 | M | 0.25 | 0/1880 | 0.48 | 0/2560 |
| 6 | U | 0.25 | 0/1880 | 0.48 | 0/2560 |
| 7 | I | 0.26 | 0/1617 | 0.49 | 1/2211 (0.0%) |
| 7 | N | 0.25 | 0/1659 | 0.48 | 1/2269 (0.0%) |
| 7 | V | 0.25 | 0/1659 | 0.47 | 1/2269 (0.0%) |
| All | All | 0.27 | 0/40118 | 0.49 | 7/54620 (0.0%) |

There are no bond length outliers.

All (7) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 7 | V | 89 | CYS | CA-CB-SG | -6.07 | 103.08 | 114.00 |
| 7 | I | 89 | CYS | CA-CB-SG | -6.02 | 103.16 | 114.00 |
| 7 | N | 89 | CYS | CA-CB-SG | -5.79 | 103.57 | 114.00 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 3 | J | 605 | CYS | CA-CB-SG | -5.37 | 104.33 | 114.00 |
| 4 | K | 109 | GLN | CB-CA-C | -5.29 | 99.82 | 110.40 |
| 4 | B | 12 | SER | N-CA-CB | 5.24 | 118.36 | 110.50 |
| 5 | C | 114 | THR | CA-CB-CG2 | -5.16 | 105.18 | 112.40 |

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts (i)

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

## 5.3 Torsion angles (i)

### 5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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 | F | 443/471 (94%) | 392 (88%) | 43 (10%) | 8 (2%) | 8 | 40 |
| 1 | G | 443/471 (94%) | 392 (88%) | 43 (10%) | 8 (2%) | 8 | 40 |
| 1 | Q | 443/471 (94%) | 391 (88%) | 44 (10%) | 8 (2%) | 8 | 40 |
| 2 | D | 219/250 (88%) | 209 (95%) | 8 (4%) | 2 (1%) | 17 | 57 |
| 2 | O | 218/250 (87%) | 208 (95%) | 9 (4%) | 1 (0%) | 29 | 69 |
| 2 | W | 219/250 (88%) | 209 (95%) | 8 (4%) | 2 (1%) | 17 | 57 |
| 3 | A | 122/147 (83%) | 107 (88%) | 13 (11%) | 2 (2%) | 9 | 44 |
| 3 | J | 122/147 (83%) | 107 (88%) | 13 (11%) | 2 (2%) | 9 | 44 |
| 3 | R | 122/147 (83%) | 107 (88%) | 13 (11%) | 2 (2%) | 9 | 44 |
| 4 | B | 208/210 (99%) | 193 (93%) | 13 (6%) | 2 (1%) | 15 | 54 |
| 4 | K | 208/210 (99%) | 193 (93%) | 13 (6%) | 2 (1%) | 15 | 54 |
| 4 | S | 208/210 (99%) | 192 (92%) | 15 (7%) | 1 (0%) | 29 | 69 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 5 | C | 224/232 (97%) | 210 (94%) | 10 (4%) | 4 (2%) | 8 | 40 |
| 5 | L | 224/232 (97%) | 210 (94%) | 11 (5%) | 3 (1%) | 12 | 48 |
| 5 | T | 224/232 (97%) | 210 (94%) | 13 (6%) | 1 (0%) | 34 | 72 |
| 6 | H | 240/242 (99%) | 227 (95%) | 13 (5%) | 0 | 100 | 100 |
| 6 | M | 240/242 (99%) | 228 (95%) | 12 (5%) | 0 | 100 | 100 |
| 6 | U | 240/242 (99%) | 228 (95%) | 11 (5%) | 1 (0%) | 34 | 72 |
| 7 | I | 203/213 (95%) | 188 (93%) | 15 (7%) | 0 | 100 | 100 |
| 7 | N | 211/213 (99%) | 195 (92%) | 16 (8%) | 0 | 100 | 100 |
| 7 | V | 211/213 (99%) | 196 (93%) | 15 (7%) | 0 | 100 | 100 |
| All | All | 4992/5295 (94%) | 4592 (92%) | 351 (7%) | 49 (1%) | 15 | 54 |

All (49) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | G | 138 | ILE |
| 1 | G | 197 | ASN |
| 1 | F | 138 | ILE |
| 1 | F | 197 | ASN |
| 1 | Q | 138 | ILE |
| 1 | Q | 197 | ASN |
| 5 | C | 100(D) | VAL |
| 5 | L | 114 | THR |
| 1 | G | 71 | THR |
| 1 | G | 236 | THR |
| 1 | F | 71 | THR |
| 1 | F | 236 | THR |
| 1 | Q | 71 | THR |
| 1 | Q | 236 | THR |
| 5 | C | 100(C) | GLY |
| 5 | C | 100(E) | VAL |
| 5 | L | 115 | LYS |
| 1 | G | 152 | GLY |
| 1 | G | 301 | ASN |
| 1 | G | 461 | ASN |
| 2 | D | 152 | SER |
| 1 | F | 152 | GLY |
| 1 | F | 301 | ASN |
| 1 | F | 461 | ASN |
| 2 | O | 152 | SER |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | Q | 152 | GLY |
| 1 | Q | 301 | ASN |
| 1 | Q | 461 | ASN |
| 2 | W | 152 | SER |
| 3 | A | 602 | LEU |
| 4 | B | 199 | GLU |
| 3 | J | 602 | LEU |
| 3 | R | 602 | LEU |
| 4 | S | 199 | GLU |
| 1 | G | 258 | GLN |
| 1 | F | 258 | GLN |
| 1 | Q | 258 | GLN |
| 3 | A | 601 | LYS |
| 3 | J | 601 | LYS |
| 4 | K | 108 | SER |
| 4 | K | 199 | GLU |
| 5 | L | 142 | ASP |
| 3 | R | 601 | LYS |
| 5 | T | 142 | ASP |
| 5 | C | 142 | ASP |
| 6 | U | 66 | ARG |
| 4 | B | 200 | GLY |
| 2 | D | 160 | PRO |
| 2 | W | 160 | PRO |

### 5.3.2 Protein sidechains (i)

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 | F | 400/419 (96%) | 391 (98%) | 9 (2%) | 50 | 70 |
| 1 | G | 400/419 (96%) | 391 (98%) | 9 (2%) | 50 | 70 |
| 1 | Q | 400/419 (96%) | 391 (98%) | 9 (2%) | 50 | 70 |
| 2 | D | 184/198 (93%) | 178 (97%) | 6 (3%) | 38 | 61 |
| 2 | O | 184/198 (93%) | 177 (96%) | 7 (4%) | 33 | 57 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 2 | W | 184/198 (93%) | 179 (97%) | 5 (3%) | 44 | 65 |
| 3 | A | 108/127 (85%) | 105 (97%) | 3 (3%) | 43 | 65 |
| 3 | J | 108/127 (85%) | 105 (97%) | 3 (3%) | 43 | 65 |
| 3 | R | 108/127 (85%) | 105 (97%) | 3 (3%) | 43 | 65 |
| 4 | B | 178/178 (100%) | 175 (98%) | 3 (2%) | 60 | 78 |
| 4 | K | 178/178 (100%) | 174 (98%) | 4 (2%) | 52 | 71 |
| 4 | S | 178/178 (100%) | 176 (99%) | 2 (1%) | 73 | 84 |
| 5 | C | 198/202 (98%) | 194 (98%) | 4 (2%) | 55 | 74 |
| 5 | L | 198/202 (98%) | 194 (98%) | 4 (2%) | 55 | 74 |
| 5 | T | 198/202 (98%) | 195 (98%) | 3 (2%) | 65 | 80 |
| 6 | H | 205/205 (100%) | 204 (100%) | 1 (0%) | 88 | 93 |
| 6 | M | 205/205 (100%) | 204 (100%) | 1 (0%) | 88 | 93 |
| 6 | U | 205/205 (100%) | 204 (100%) | 1 (0%) | 88 | 93 |
| 7 | I | 182/186 (98%) | 181 (100%) | 1 (0%) | 88 | 93 |
| 7 | N | 186/186 (100%) | 184 (99%) | 2 (1%) | 73 | 84 |
| 7 | V | 186/186 (100%) | 185 (100%) | 1 (0%) | 88 | 93 |
| All | All | 4373/4545 (96%) | 4292 (98%) | 81 (2%) | 57 | 75 |

All (81) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | G | 123 | THR |
| 1 | G | 125 | LEU |
| 1 | G | 137 | ASN |
| 1 | G | 138 | ILE |
| 1 | G | 236 | THR |
| 1 | G | 463 | THR |
| 1 | G | 474 | ASP |
| 1 | G | 503 | ARG |
| 1 | G | 504 | ARG |
| 2 | D | 38 | ARG |
| 2 | D | 51 | LEU |
| 2 | D | 72 | ARG |
| 2 | D | 125 | VAL |
| 2 | D | 205 | VAL |
| 2 | D | 212 | GLU |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | F | 123 | THR |
| 1 | F | 125 | LEU |
| 1 | F | 137 | ASN |
| 1 | F | 138 | ILE |
| 1 | F | 236 | THR |
| 1 | F | 463 | THR |
| 1 | F | 474 | ASP |
| 1 | F | 503 | ARG |
| 1 | F | 504 | ARG |
| 2 | O | 38 | ARG |
| 2 | O | 51 | LEU |
| 2 | O | 58 | VAL |
| 2 | O | 72 | ARG |
| 2 | O | 125 | VAL |
| 2 | O | 205 | VAL |
| 2 | O | 212 | GLU |
| 1 | Q | 123 | THR |
| 1 | Q | 125 | LEU |
| 1 | Q | 137 | ASN |
| 1 | Q | 138 | ILE |
| 1 | Q | 236 | THR |
| 1 | Q | 463 | THR |
| 1 | Q | 474 | ASP |
| 1 | Q | 503 | ARG |
| 1 | Q | 504 | ARG |
| 2 | W | 38 | ARG |
| 2 | W | 51 | LEU |
| 2 | W | 72 | ARG |
| 2 | W | 205 | VAL |
| 2 | W | 212 | GLU |
| 3 | A | 536 | THR |
| 3 | A | 570 | VAL |
| 3 | A | 606 | THR |
| 4 | B | 54 | ARG |
| 4 | B | 108 | SER |
| 4 | B | 201 | SER |
| 5 | C | 23 | ASN |
| 5 | C | 100(J) | TRP |
| 5 | C | 114 | THR |
| 5 | C | 139 | LEU |
| 6 | H | 80 | MET |
| 7 | I | 96 | CYS |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 3 | J | 536 | THR |
| 3 | J | 570 | VAL |
| 3 | J | 606 | THR |
| 4 | K | 54 | ARG |
| 4 | K | 109 | GLN |
| 4 | K | 111 | LYS |
| 4 | K | 129 | ASN |
| 5 | L | 23 | ASN |
| 5 | L | 100(J) | TRP |
| 5 | L | 114 | THR |
| 5 | L | 139 | LEU |
| 6 | M | 80 | MET |
| 7 | N | 93 | HIS |
| 7 | N | 96 | CYS |
| 3 | R | 536 | THR |
| 3 | R | 570 | VAL |
| 3 | R | 606 | THR |
| 4 | S | 54 | ARG |
| 4 | S | 111 | LYS |
| 5 | T | 100(J) | TRP |
| 5 | T | 114 | THR |
| 5 | T | 139 | LEU |
| 6 | U | 80 | MET |
| 7 | V | 96 | CYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 5 | C | 197 | ASN |
| 5 | C | 198 | HIS |
| 6 | M | 33 | HIS |
| 3 | R | 616 | ASN |
| 4 | S | 37 | GLN |
| 4 | S | 129 | ASN |

### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 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 | $\#\|Z\| > 2$ |
| 2 | PCA | W | 1 | 2 | 7,8,9 | 1.81 | 1 (14%) | 9,10,12 | 2.15 | 5 (55%) |
| 2 | PCA | D | 1 | 2 | 7,8,9 | 1.81 | 1 (14%) | 9,10,12 | 2.13 | 5 (55%) |

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 |
|---|---|---|---|---|---|---|---|
| 2 | PCA | W | 1 | 2 | - | 0/0/11/13 | 0/1/1/1 |
| 2 | PCA | D | 1 | 2 | - | 0/0/11/13 | 0/1/1/1 |

All (2) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 2 | D | 1 | PCA | CD-N | 4.68 | 1.46 | 1.34 |
| 2 | W | 1 | PCA | CD-N | 4.66 | 1.46 | 1.34 |

All (10) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | W | 1 | PCA | OE-CD-CG | -3.09 | 121.37 | 126.76 |
| 2 | D | 1 | PCA | OE-CD-CG | -3.09 | 121.37 | 126.76 |
| 2 | W | 1 | PCA | CA-N-CD | -2.87 | 103.74 | 113.58 |
| 2 | D | 1 | PCA | CA-N-CD | -2.84 | 103.86 | 113.58 |
| 2 | W | 1 | PCA | CB-CA-C | -2.63 | 109.08 | 112.70 |
| 2 | W | 1 | PCA | CB-CA-N | 2.57 | 110.68 | 103.30 |
| 2 | D | 1 | PCA | CB-CA-C | -2.56 | 109.17 | 112.70 |
| 2 | D | 1 | PCA | CB-CA-N | 2.55 | 110.63 | 103.30 |
| 2 | W | 1 | PCA | CG-CD-N | 2.45 | 114.72 | 108.39 |
| 2 | D | 1 | PCA | CG-CD-N | 2.40 | 114.61 | 108.39 |

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates (i)

135 monosaccharides 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 | $\#\|Z\| > 2$ |
| 8 | NAG | E | 1 | 1,8 | 14,14,15 | 1.95 | 1 (7%) | 17,19,21 | 1.48 | 3 (17%) |
| 8 | NAG | E | 2 | 8 | 14,14,15 | 2.27 | 2 (14%) | 17,19,21 | 1.84 | 3 (17%) |
| 8 | BMA | E | 3 | 8 | 11,11,12 | 2.80 | 6 (54%) | 15,15,17 | 2.18 | 6 (40%) |
| 8 | MAN | E | 4 | 8 | 11,11,12 | 0.76 | 0 | 15,15,17 | 1.18 | 2 (13%) |
| 8 | MAN | E | 5 | 8 | 11,11,12 | 1.71 | 3 (27%) | 15,15,17 | 3.22 | 9 (60%) |
| 9 | NAG | P | 1 | 1,9 | 14,14,15 | 0.88 | 1 (7%) | 17,19,21 | 0.77 | 1 (5%) |
| 9 | NAG | P | 2 | 9 | 14,14,15 | 1.03 | 1 (7%) | 17,19,21 | 0.66 | 0 |
| 9 | BMA | P | 3 | 9 | 11,11,12 | 0.74 | 0 | 15,15,17 | 0.77 | 0 |
| 8 | NAG | X | 1 | 1,8 | 14,14,15 | 2.15 | 2 (14%) | 17,19,21 | 1.78 | 3 (17%) |
| 8 | NAG | X | 2 | 8 | 14,14,15 | 0.69 | 1 (7%) | 17,19,21 | 0.53 | 0 |
| 8 | BMA | X | 3 | 8 | 11,11,12 | 0.61 | 0 | 15,15,17 | 0.77 | 0 |
| 8 | MAN | X | 4 | 8 | 11,11,12 | 0.60 | 0 | 15,15,17 | 1.03 | 2 (13%) |
| 8 | MAN | X | 5 | 8 | 11,11,12 | 0.71 | 0 | 15,15,17 | 0.98 | 1 (6%) |
| 10 | NAG | Y | 1 | 1,10 | 14,14,15 | 0.38 | 0 | 17,19,21 | 0.59 | 0 |
| 10 | NAG | Y | 2 | 10 | 14,14,15 | 0.38 | 0 | 17,19,21 | 0.42 | 0 |
| 10 | BMA | Y | 3 | 10 | 11,11,12 | 0.63 | 0 | 15,15,17 | 0.78 | 0 |
| 10 | MAN | Y | 4 | 10 | 11,11,12 | 0.67 | 0 | 15,15,17 | 1.07 | 2 (13%) |
| 11 | NAG | Z | 1 | 1,11 | 14,14,15 | 1.92 | 2 (14%) | 17,19,21 | 1.58 | 3 (17%) |
| 11 | NAG | Z | 2 | 11 | 14,14,15 | 2.26 | 2 (14%) | 17,19,21 | 1.90 | 4 (23%) |
| 11 | BMA | Z | 3 | 11 | 11,11,12 | 2.45 | 5 (45%) | 15,15,17 | 2.25 | 4 (26%) |
| 11 | MAN | Z | 4 | 11 | 11,11,12 | 1.48 | 1 (9%) | 15,15,17 | 3.23 | 7 (46%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\| > 2$ | Counts | RMSZ | $\#\|Z\| > 2$ |
| 11 | MAN | Z | 5 | 11 | 11,11,12 | 1.49 | 2 (18%) | 15,15,17 | 2.93 | 6 (40%) |
| 11 | MAN | Z | 6 | 11 | 11,11,12 | 1.38 | 2 (18%) | 15,15,17 | 3.39 | 8 (53%) |
| 11 | MAN | Z | 7 | 11 | 11,11,12 | 2.41 | 2 (18%) | 15,15,17 | 3.76 | 6 (40%) |
| 12 | NAG | a | 1 | 1,12 | 14,14,15 | 0.69 | 1 (7%) | 17,19,21 | 0.43 | 0 |
| 12 | NAG | a | 2 | 12 | 14,14,15 | 1.87 | 1 (7%) | 17,19,21 | 1.76 | 3 (17%) |
| 12 | BMA | a | 3 | 12 | 11,11,12 | 1.48 | 3 (27%) | 15,15,17 | 1.29 | 3 (20%) |
| 12 | MAN | a | 4 | 12 | 11,11,12 | 1.57 | 3 (27%) | 15,15,17 | 1.85 | 3 (20%) |
| 12 | MAN | a | 5 | 12 | 11,11,12 | 1.39 | 2 (18%) | 15,15,17 | 1.41 | 3 (20%) |
| 12 | MAN | a | 6 | 12 | 11,11,12 | 1.22 | 1 (9%) | 15,15,17 | 1.82 | 3 (20%) |
| 13 | NAG | b | 1 | 13,1 | 14,14,15 | 0.23 | 0 | 17,19,21 | 0.47 | 0 |
| 13 | NAG | b | 2 | 13 | 14,14,15 | 0.22 | 0 | 17,19,21 | 0.43 | 0 |
| 8 | NAG | c | 1 | 1,8 | 14,14,15 | 0.25 | 0 | 17,19,21 | 0.39 | 0 |
| 8 | NAG | c | 2 | 8 | 14,14,15 | 0.19 | 0 | 17,19,21 | 0.46 | 0 |
| 8 | BMA | c | 3 | 8 | 11,11,12 | 0.51 | 0 | 15,15,17 | 0.73 | 0 |
| 8 | MAN | c | 4 | 8 | 11,11,12 | 0.65 | 0 | 15,15,17 | 1.07 | 2 (13%) |
| 8 | MAN | c | 5 | 8 | 11,11,12 | 0.67 | 0 | 15,15,17 | 1.05 | 2 (13%) |
| 14 | NAG | d | 1 | 1,14 | 14,14,15 | 0.43 | 0 | 17,19,21 | 1.46 | 2 (11%) |
| 14 | NAG | d | 2 | 14 | 14,14,15 | 0.22 | 0 | 17,19,21 | 0.45 | 0 |
| 14 | BMA | d | 3 | 14 | 11,11,12 | 0.99 | 1 (9%) | 15,15,17 | 0.99 | 1 (6%) |
| 14 | MAN | d | 4 | 14 | 11,11,12 | 1.09 | 0 | 15,15,17 | 2.46 | 5 (33%) |
| 14 | MAN | d | 5 | 14 | 11,11,12 | 0.79 | 0 | 15,15,17 | 1.18 | 2 (13%) |
| 14 | MAN | d | 6 | 14 | 11,11,12 | 0.67 | 0 | 15,15,17 | 1.05 | 2 (13%) |
| 14 | MAN | d | 7 | 14 | 11,11,12 | 0.77 | 1 (9%) | 15,15,17 | 1.27 | 2 (13%) |
| 14 | MAN | d | 8 | 14 | 11,11,12 | 0.76 | 1 (9%) | 15,15,17 | 1.14 | 2 (13%) |
| 8 | NAG | e | 1 | 1,8 | 14,14,15 | 2.74 | 2 (14%) | 17,19,21 | 1.45 | 3 (17%) |
| 8 | NAG | e | 2 | 8 | 14,14,15 | 1.71 | 2 (14%) | 17,19,21 | 2.11 | 2 (11%) |
| 8 | BMA | e | 3 | 8 | 11,11,12 | 2.19 | 5 (45%) | 15,15,17 | 2.04 | 7 (46%) |
| 8 | MAN | e | 4 | 8 | 11,11,12 | 1.21 | 1 (9%) | 15,15,17 | 1.69 | 3 (20%) |
| 8 | MAN | e | 5 | 8 | 11,11,12 | 1.61 | 4 (36%) | 15,15,17 | 2.36 | 6 (40%) |
| 9 | NAG | f | 1 | 1,9 | 14,14,15 | 0.91 | 1 (7%) | 17,19,21 | 0.76 | 1 (5%) |
| 9 | NAG | f | 2 | 9 | 14,14,15 | 1.05 | 1 (7%) | 17,19,21 | 0.68 | 0 |
| 9 | BMA | f | 3 | 9 | 11,11,12 | 0.75 | 0 | 15,15,17 | 0.78 | 0 |
| 8 | NAG | g | 1 | 1,8 | 14,14,15 | 2.13 | 2 (14%) | 17,19,21 | 1.63 | 3 (17%) |
| 8 | NAG | g | 2 | 8 | 14,14,15 | 0.67 | 1 (7%) | 17,19,21 | 0.55 | 0 |
| 8 | BMA | g | 3 | 8 | 11,11,12 | 0.61 | 0 | 15,15,17 | 0.76 | 0 |
| 8 | MAN | g | 4 | 8 | 11,11,12 | 0.61 | 0 | 15,15,17 | 1.03 | 2 (13%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\| > 2$ | Counts | RMSZ | $\#\|Z\| > 2$ |
| 8 | MAN | g | 5 | 8 | 11,11,12 | 0.68 | 0 | 15,15,17 | 0.98 | 2 (13%) |
| 10 | NAG | h | 1 | 1,10 | 14,14,15 | 0.69 | 1 (7%) | 17,19,21 | 0.79 | 0 |
| 10 | NAG | h | 2 | 10 | 14,14,15 | 0.21 | 0 | 17,19,21 | 0.43 | 0 |
| 10 | BMA | h | 3 | 10 | 11,11,12 | 0.63 | 0 | 15,15,17 | 0.80 | 0 |
| 10 | MAN | h | 4 | 10 | 11,11,12 | 0.66 | 0 | 15,15,17 | 1.04 | 2 (13%) |
| 11 | NAG | i | 1 | 1,11 | 14,14,15 | 1.92 | 2 (14%) | 17,19,21 | 1.69 | 3 (17%) |
| 11 | NAG | i | 2 | 11 | 14,14,15 | 2.35 | 2 (14%) | 17,19,21 | 1.90 | 4 (23%) |
| 11 | BMA | i | 3 | 11 | 11,11,12 | 0.23 | 0 | 15,15,17 | 0.72 | 0 |
| 11 | MAN | i | 4 | 11 | 11,11,12 | 0.86 | 1 (9%) | 15,15,17 | 1.70 | 2 (13%) |
| 11 | MAN | i | 5 | 11 | 11,11,12 | 1.50 | 2 (18%) | 15,15,17 | 2.90 | 5 (33%) |
| 11 | MAN | i | 6 | 11 | 11,11,12 | 1.44 | 2 (18%) | 15,15,17 | 3.13 | 7 (46%) |
| 11 | MAN | i | 7 | 11 | 11,11,12 | 1.07 | 1 (9%) | 15,15,17 | 2.91 | 6 (40%) |
| 12 | NAG | j | 1 | 1,12 | 14,14,15 | 0.16 | 0 | 17,19,21 | 0.57 | 0 |
| 12 | NAG | j | 2 | 12 | 14,14,15 | 1.22 | 1 (7%) | 17,19,21 | 1.96 | 5 (29%) |
| 12 | BMA | j | 3 | 12 | 11,11,12 | 1.68 | 3 (27%) | 15,15,17 | 1.41 | 3 (20%) |
| 12 | MAN | j | 4 | 12 | 11,11,12 | 1.56 | 3 (27%) | 15,15,17 | 1.93 | 3 (20%) |
| 12 | MAN | j | 5 | 12 | 11,11,12 | 1.31 | 1 (9%) | 15,15,17 | 1.45 | 3 (20%) |
| 12 | MAN | j | 6 | 12 | 11,11,12 | 1.25 | 2 (18%) | 15,15,17 | 1.89 | 4 (26%) |
| 13 | NAG | k | 1 | 13,1 | 14,14,15 | 0.20 | 0 | 17,19,21 | 0.47 | 0 |
| 13 | NAG | k | 2 | 13 | 14,14,15 | 0.24 | 0 | 17,19,21 | 0.42 | 0 |
| 8 | NAG | l | 1 | 1,8 | 14,14,15 | 0.27 | 0 | 17,19,21 | 0.39 | 0 |
| 8 | NAG | l | 2 | 8 | 14,14,15 | 0.20 | 0 | 17,19,21 | 0.45 | 0 |
| 8 | BMA | l | 3 | 8 | 11,11,12 | 0.52 | 0 | 15,15,17 | 0.72 | 0 |
| 8 | MAN | l | 4 | 8 | 11,11,12 | 0.63 | 0 | 15,15,17 | 1.05 | 2 (13%) |
| 8 | MAN | l | 5 | 8 | 11,11,12 | 0.67 | 0 | 15,15,17 | 1.04 | 2 (13%) |
| 14 | NAG | m | 1 | 1,14 | 14,14,15 | 0.44 | 0 | 17,19,21 | 1.48 | 2 (11%) |
| 14 | NAG | m | 2 | 14 | 14,14,15 | 0.25 | 0 | 17,19,21 | 0.45 | 0 |
| 14 | BMA | m | 3 | 14 | 11,11,12 | 0.94 | 1 (9%) | 15,15,17 | 0.99 | 1 (6%) |
| 14 | MAN | m | 4 | 14 | 11,11,12 | 1.11 | 1 (9%) | 15,15,17 | 2.53 | 5 (33%) |
| 14 | MAN | m | 5 | 14 | 11,11,12 | 0.69 | 0 | 15,15,17 | 1.13 | 2 (13%) |
| 14 | MAN | m | 6 | 14 | 11,11,12 | 0.69 | 0 | 15,15,17 | 1.06 | 2 (13%) |
| 14 | MAN | m | 7 | 14 | 11,11,12 | 0.78 | 1 (9%) | 15,15,17 | 1.28 | 2 (13%) |
| 14 | MAN | m | 8 | 14 | 11,11,12 | 0.77 | 1 (9%) | 15,15,17 | 1.13 | 2 (13%) |
| 8 | NAG | n | 1 | 1,8 | 14,14,15 | 1.94 | 2 (14%) | 17,19,21 | 1.49 | 3 (17%) |
| 8 | NAG | n | 2 | 8 | 14,14,15 | 2.66 | 2 (14%) | 17,19,21 | 1.87 | 4 (23%) |
| 8 | BMA | n | 3 | 8 | 11,11,12 | 3.30 | 6 (54%) | 15,15,17 | 1.90 | 6 (40%) |
| 8 | MAN | n | 4 | 8 | 11,11,12 | 0.62 | 0 | 15,15,17 | 1.19 | 2 (13%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\| > 2$ | Counts | RMSZ | $\#\|Z\| > 2$ |
| 8 | MAN | n | 5 | 8 | 11,11,12 | 1.80 | 4 (36%) | 15,15,17 | 3.26 | 10 (66%) |
| 9 | NAG | o | 1 | 1,9 | 14,14,15 | 0.82 | 1 (7%) | 17,19,21 | 0.79 | 1 (5%) |
| 9 | NAG | o | 2 | 9 | 14,14,15 | 1.02 | 1 (7%) | 17,19,21 | 0.67 | 0 |
| 9 | BMA | o | 3 | 9 | 11,11,12 | 0.75 | 0 | 15,15,17 | 0.77 | 0 |
| 8 | NAG | p | 1 | 1,8 | 14,14,15 | 2.16 | 2 (14%) | 17,19,21 | 1.64 | 3 (17%) |
| 8 | NAG | p | 2 | 8 | 14,14,15 | 0.65 | 1 (7%) | 17,19,21 | 0.55 | 0 |
| 8 | BMA | p | 3 | 8 | 11,11,12 | 0.60 | 0 | 15,15,17 | 0.77 | 0 |
| 8 | MAN | p | 4 | 8 | 11,11,12 | 0.60 | 0 | 15,15,17 | 1.03 | 2 (13%) |
| 8 | MAN | p | 5 | 8 | 11,11,12 | 0.70 | 0 | 15,15,17 | 0.97 | 2 (13%) |
| 10 | NAG | q | 1 | 1,10 | 14,14,15 | 0.50 | 0 | 17,19,21 | 0.66 | 0 |
| 10 | NAG | q | 2 | 10 | 14,14,15 | 0.28 | 0 | 17,19,21 | 0.50 | 0 |
| 10 | BMA | q | 3 | 10 | 11,11,12 | 0.64 | 0 | 15,15,17 | 0.80 | 0 |
| 10 | MAN | q | 4 | 10 | 11,11,12 | 0.70 | 0 | 15,15,17 | 1.06 | 2 (13%) |
| 11 | NAG | r | 1 | 1,11 | 14,14,15 | 1.94 | 2 (14%) | 17,19,21 | 1.72 | 3 (17%) |
| 11 | NAG | r | 2 | 11 | 14,14,15 | 2.29 | 2 (14%) | 17,19,21 | 1.89 | 4 (23%) |
| 11 | BMA | r | 3 | 11 | 11,11,12 | 2.22 | 4 (36%) | 15,15,17 | 2.17 | 3 (20%) |
| 11 | MAN | r | 4 | 11 | 11,11,12 | 1.91 | 3 (27%) | 15,15,17 | 3.30 | 8 (53%) |
| 11 | MAN | r | 5 | 11 | 11,11,12 | 1.40 | 2 (18%) | 15,15,17 | 2.85 | 6 (40%) |
| 11 | MAN | r | 6 | 11 | 11,11,12 | 2.20 | 6 (54%) | 15,15,17 | 3.94 | 8 (53%) |
| 11 | MAN | r | 7 | 11 | 11,11,12 | 1.87 | 4 (36%) | 15,15,17 | 1.64 | 4 (26%) |
| 12 | NAG | s | 1 | 1,12 | 14,14,15 | 0.38 | 0 | 17,19,21 | 0.49 | 0 |
| 12 | NAG | s | 2 | 12 | 14,14,15 | 1.79 | 1 (7%) | 17,19,21 | 1.82 | 3 (17%) |
| 12 | BMA | s | 3 | 12 | 11,11,12 | 1.46 | 3 (27%) | 15,15,17 | 1.23 | 3 (20%) |
| 12 | MAN | s | 4 | 12 | 11,11,12 | 2.82 | 4 (36%) | 15,15,17 | 2.01 | 5 (33%) |
| 12 | MAN | s | 5 | 12 | 11,11,12 | 1.46 | 2 (18%) | 15,15,17 | 2.52 | 6 (40%) |
| 12 | MAN | s | 6 | 12 | 11,11,12 | 1.23 | 1 (9%) | 15,15,17 | 1.80 | 3 (20%) |
| 13 | NAG | t | 1 | 13,1 | 14,14,15 | 0.21 | 0 | 17,19,21 | 0.48 | 0 |
| 13 | NAG | t | 2 | 13 | 14,14,15 | 0.23 | 0 | 17,19,21 | 0.42 | 0 |
| 8 | NAG | u | 1 | 1,8 | 14,14,15 | 0.28 | 0 | 17,19,21 | 0.41 | 0 |
| 8 | NAG | u | 2 | 8 | 14,14,15 | 0.21 | 0 | 17,19,21 | 0.45 | 0 |
| 8 | BMA | u | 3 | 8 | 11,11,12 | 0.53 | 0 | 15,15,17 | 0.74 | 0 |
| 8 | MAN | u | 4 | 8 | 11,11,12 | 0.64 | 0 | 15,15,17 | 1.06 | 2 (13%) |
| 8 | MAN | u | 5 | 8 | 11,11,12 | 0.64 | 0 | 15,15,17 | 1.04 | 2 (13%) |
| 14 | NAG | v | 1 | 1,14 | 14,14,15 | 0.60 | 1 (7%) | 17,19,21 | 1.47 | 2 (11%) |
| 14 | NAG | v | 2 | 14 | 14,14,15 | 0.27 | 0 | 17,19,21 | 0.47 | 0 |
| 14 | BMA | v | 3 | 14 | 11,11,12 | 0.80 | 0 | 15,15,17 | 1.04 | 1 (6%) |
| 14 | MAN | v | 4 | 14 | 11,11,12 | 0.75 | 1 (9%) | 15,15,17 | 1.25 | 2 (13%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\| > 2$ | Counts | RMSZ | $\#\|Z\| > 2$ |
| 14 | MAN | v | 5 | 14 | 11,11,12 | 0.64 | 0 | 15,15,17 | 0.97 | 2 (13%) |
| 14 | MAN | v | 6 | 14 | 11,11,12 | 0.92 | 1 (9%) | 15,15,17 | 1.06 | 1 (6%) |
| 14 | MAN | v | 7 | 14 | 11,11,12 | 2.39 | 5 (45%) | 15,15,17 | 3.83 | 7 (46%) |
| 14 | MAN | v | 8 | 14 | 11,11,12 | 0.78 | 1 (9%) | 15,15,17 | 1.14 | 2 (13%) |

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 |
|---|---|---|---|---|---|---|---|
| 8 | NAG | E | 1 | 1,8 | - | 3/6/23/26 | 0/1/1/1 |
| 8 | NAG | E | 2 | 8 | - | 1/6/23/26 | 0/1/1/1 |
| 8 | BMA | E | 3 | 8 | - | 1/2/19/22 | 0/1/1/1 |
| 8 | MAN | E | 4 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 8 | MAN | E | 5 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 9 | NAG | P | 1 | 1,9 | - | 1/6/23/26 | 0/1/1/1 |
| 9 | NAG | P | 2 | 9 | - | 0/6/23/26 | 0/1/1/1 |
| 9 | BMA | P | 3 | 9 | - | 1/2/19/22 | 0/1/1/1 |
| 8 | NAG | X | 1 | 1,8 | - | 0/6/23/26 | 0/1/1/1 |
| 8 | NAG | X | 2 | 8 | - | 2/6/23/26 | 0/1/1/1 |
| 8 | BMA | X | 3 | 8 | - | 2/2/19/22 | 0/1/1/1 |
| 8 | MAN | X | 4 | 8 | - | 1/2/19/22 | 0/1/1/1 |
| 8 | MAN | X | 5 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 10 | NAG | Y | 1 | 1,10 | - | 2/6/23/26 | 0/1/1/1 |
| 10 | NAG | Y | 2 | 10 | - | 0/6/23/26 | 0/1/1/1 |
| 10 | BMA | Y | 3 | 10 | - | 1/2/19/22 | 0/1/1/1 |
| 10 | MAN | Y | 4 | 10 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | NAG | Z | 1 | 1,11 | - | 2/6/23/26 | 0/1/1/1 |
| 11 | NAG | Z | 2 | 11 | - | 2/6/23/26 | 0/1/1/1 |
| 11 | BMA | Z | 3 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | MAN | Z | 4 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | MAN | Z | 5 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | MAN | Z | 6 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | MAN | Z | 7 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 12 | NAG | a | 1 | 1,12 | - | 2/6/23/26 | 0/1/1/1 |
| 12 | NAG | a | 2 | 12 | - | 1/6/23/26 | 0/1/1/1 |
| 12 | BMA | a | 3 | 12 | - | 0/2/19/22 | 0/1/1/1 |
| 12 | MAN | a | 4 | 12 | - | 2/2/19/22 | 0/1/1/1 |
| 12 | MAN | a | 5 | 12 | - | 2/2/19/22 | 0/1/1/1 |

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*Continued from previous page...*

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 12 | MAN | a | 6 | 12 | - | 1/2/19/22 | 0/1/1/1 |
| 13 | NAG | b | 1 | 13,1 | - | 0/6/23/26 | 0/1/1/1 |
| 13 | NAG | b | 2 | 13 | - | 0/6/23/26 | 0/1/1/1 |
| 8 | NAG | c | 1 | 1,8 | - | 1/6/23/26 | 0/1/1/1 |
| 8 | NAG | c | 2 | 8 | - | 0/6/23/26 | 0/1/1/1 |
| 8 | BMA | c | 3 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 8 | MAN | c | 4 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 8 | MAN | c | 5 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 14 | NAG | d | 1 | 1,14 | - | 5/6/23/26 | 0/1/1/1 |
| 14 | NAG | d | 2 | 14 | - | 2/6/23/26 | 0/1/1/1 |
| 14 | BMA | d | 3 | 14 | - | 0/2/19/22 | 0/1/1/1 |
| 14 | MAN | d | 4 | 14 | - | 2/2/19/22 | 0/1/1/1 |
| 14 | MAN | d | 5 | 14 | - | 2/2/19/22 | 0/1/1/1 |
| 14 | MAN | d | 6 | 14 | - | 0/2/19/22 | 0/1/1/1 |
| 14 | MAN | d | 7 | 14 | - | 0/2/19/22 | 0/1/1/1 |
| 14 | MAN | d | 8 | 14 | - | 0/2/19/22 | 0/1/1/1 |
| 8 | NAG | e | 1 | 1,8 | - | 2/6/23/26 | 0/1/1/1 |
| 8 | NAG | e | 2 | 8 | - | 2/6/23/26 | 0/1/1/1 |
| 8 | BMA | e | 3 | 8 | - | 1/2/19/22 | 0/1/1/1 |
| 8 | MAN | e | 4 | 8 | - | 1/2/19/22 | 0/1/1/1 |
| 8 | MAN | e | 5 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 9 | NAG | f | 1 | 1,9 | - | 1/6/23/26 | 0/1/1/1 |
| 9 | NAG | f | 2 | 9 | - | 0/6/23/26 | 0/1/1/1 |
| 9 | BMA | f | 3 | 9 | - | 1/2/19/22 | 0/1/1/1 |
| 8 | NAG | g | 1 | 1,8 | - | 0/6/23/26 | 0/1/1/1 |
| 8 | NAG | g | 2 | 8 | - | 2/6/23/26 | 0/1/1/1 |
| 8 | BMA | g | 3 | 8 | - | 2/2/19/22 | 0/1/1/1 |
| 8 | MAN | g | 4 | 8 | - | 1/2/19/22 | 0/1/1/1 |
| 8 | MAN | g | 5 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 10 | NAG | h | 1 | 1,10 | - | 2/6/23/26 | 0/1/1/1 |
| 10 | NAG | h | 2 | 10 | - | 1/6/23/26 | 0/1/1/1 |
| 10 | BMA | h | 3 | 10 | - | 1/2/19/22 | 0/1/1/1 |
| 10 | MAN | h | 4 | 10 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | NAG | i | 1 | 1,11 | - | 2/6/23/26 | 0/1/1/1 |
| 11 | NAG | i | 2 | 11 | - | 2/6/23/26 | 0/1/1/1 |
| 11 | BMA | i | 3 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | MAN | i | 4 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | MAN | i | 5 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | MAN | i | 6 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | MAN | i | 7 | 11 | - | 1/2/19/22 | 0/1/1/1 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 12 | NAG | j | 1 | 1,12 | - | 2/6/23/26 | 0/1/1/1 |
| 12 | NAG | j | 2 | 12 | - | 1/6/23/26 | 0/1/1/1 |
| 12 | BMA | j | 3 | 12 | - | 0/2/19/22 | 0/1/1/1 |
| 12 | MAN | j | 4 | 12 | - | 2/2/19/22 | 0/1/1/1 |
| 12 | MAN | j | 5 | 12 | - | 2/2/19/22 | 0/1/1/1 |
| 12 | MAN | j | 6 | 12 | - | 1/2/19/22 | 0/1/1/1 |
| 13 | NAG | k | 1 | 13,1 | - | 0/6/23/26 | 0/1/1/1 |
| 13 | NAG | k | 2 | 13 | - | 0/6/23/26 | 0/1/1/1 |
| 8 | NAG | l | 1 | 1,8 | - | 1/6/23/26 | 0/1/1/1 |
| 8 | NAG | l | 2 | 8 | - | 0/6/23/26 | 0/1/1/1 |
| 8 | BMA | l | 3 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 8 | MAN | l | 4 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 8 | MAN | l | 5 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 14 | NAG | m | 1 | 1,14 | - | 4/6/23/26 | 0/1/1/1 |
| 14 | NAG | m | 2 | 14 | - | 1/6/23/26 | 0/1/1/1 |
| 14 | BMA | m | 3 | 14 | - | 0/2/19/22 | 0/1/1/1 |
| 14 | MAN | m | 4 | 14 | - | 2/2/19/22 | 0/1/1/1 |
| 14 | MAN | m | 5 | 14 | - | 2/2/19/22 | 0/1/1/1 |
| 14 | MAN | m | 6 | 14 | - | 0/2/19/22 | 0/1/1/1 |
| 14 | MAN | m | 7 | 14 | - | 0/2/19/22 | 0/1/1/1 |
| 14 | MAN | m | 8 | 14 | - | 0/2/19/22 | 0/1/1/1 |
| 8 | NAG | n | 1 | 1,8 | - | 0/6/23/26 | 0/1/1/1 |
| 8 | NAG | n | 2 | 8 | - | 3/6/23/26 | 0/1/1/1 |
| 8 | BMA | n | 3 | 8 | - | 1/2/19/22 | 0/1/1/1 |
| 8 | MAN | n | 4 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 8 | MAN | n | 5 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 9 | NAG | o | 1 | 1,9 | - | 1/6/23/26 | 0/1/1/1 |
| 9 | NAG | o | 2 | 9 | - | 0/6/23/26 | 0/1/1/1 |
| 9 | BMA | o | 3 | 9 | - | 1/2/19/22 | 0/1/1/1 |
| 8 | NAG | p | 1 | 1,8 | - | 0/6/23/26 | 0/1/1/1 |
| 8 | NAG | p | 2 | 8 | - | 2/6/23/26 | 0/1/1/1 |
| 8 | BMA | p | 3 | 8 | - | 2/2/19/22 | 0/1/1/1 |
| 8 | MAN | p | 4 | 8 | - | 1/2/19/22 | 0/1/1/1 |
| 8 | MAN | p | 5 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 10 | NAG | q | 1 | 1,10 | - | 2/6/23/26 | 0/1/1/1 |
| 10 | NAG | q | 2 | 10 | - | 1/6/23/26 | 0/1/1/1 |
| 10 | BMA | q | 3 | 10 | - | 1/2/19/22 | 0/1/1/1 |
| 10 | MAN | q | 4 | 10 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | NAG | r | 1 | 1,11 | - | 2/6/23/26 | 0/1/1/1 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 11 | NAG | r | 2 | 11 | - | 2/6/23/26 | 0/1/1/1 |
| 11 | BMA | r | 3 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | MAN | r | 4 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | MAN | r | 5 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 11 | MAN | r | 6 | 11 | - | 1/2/19/22 | 0/1/1/1 |
| 11 | MAN | r | 7 | 11 | - | 0/2/19/22 | 0/1/1/1 |
| 12 | NAG | s | 1 | 1,12 | - | 2/6/23/26 | 0/1/1/1 |
| 12 | NAG | s | 2 | 12 | - | 2/6/23/26 | 0/1/1/1 |
| 12 | BMA | s | 3 | 12 | - | 0/2/19/22 | 0/1/1/1 |
| 12 | MAN | s | 4 | 12 | - | 0/2/19/22 | 0/1/1/1 |
| 12 | MAN | s | 5 | 12 | - | 1/2/19/22 | 0/1/1/1 |
| 12 | MAN | s | 6 | 12 | - | 1/2/19/22 | 0/1/1/1 |
| 13 | NAG | t | 1 | 13,1 | - | 0/6/23/26 | 0/1/1/1 |
| 13 | NAG | t | 2 | 13 | - | 0/6/23/26 | 0/1/1/1 |
| 8 | NAG | u | 1 | 1,8 | - | 1/6/23/26 | 0/1/1/1 |
| 8 | NAG | u | 2 | 8 | - | 0/6/23/26 | 0/1/1/1 |
| 8 | BMA | u | 3 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 8 | MAN | u | 4 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 8 | MAN | u | 5 | 8 | - | 0/2/19/22 | 0/1/1/1 |
| 14 | NAG | v | 1 | 1,14 | - | 3/6/23/26 | 0/1/1/1 |
| 14 | NAG | v | 2 | 14 | - | 2/6/23/26 | 0/1/1/1 |
| 14 | BMA | v | 3 | 14 | - | 0/2/19/22 | 0/1/1/1 |
| 14 | MAN | v | 4 | 14 | - | 2/2/19/22 | 0/1/1/1 |
| 14 | MAN | v | 5 | 14 | - | 2/2/19/22 | 0/1/1/1 |
| 14 | MAN | v | 6 | 14 | - | 0/2/19/22 | 0/1/1/1 |
| 14 | MAN | v | 7 | 14 | - | 0/2/19/22 | 0/1/1/1 |
| 14 | MAN | v | 8 | 14 | - | 0/2/19/22 | 0/1/1/1 |

All (153) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 8 | e | 1 | NAG | O5-C1 | -9.72 | 1.28 | 1.43 |
| 8 | n | 2 | NAG | O5-C1 | -9.29 | 1.28 | 1.43 |
| 11 | i | 2 | NAG | O5-C1 | -8.19 | 1.30 | 1.43 |
| 11 | r | 2 | NAG | O5-C1 | -8.02 | 1.30 | 1.43 |
| 11 | Z | 2 | NAG | O5-C1 | -7.87 | 1.31 | 1.43 |
| 8 | E | 2 | NAG | O5-C1 | -7.53 | 1.31 | 1.43 |
| 8 | X | 1 | NAG | O5-C1 | -7.48 | 1.31 | 1.43 |
| 8 | p | 1 | NAG | O5-C1 | -7.48 | 1.31 | 1.43 |
| 8 | g | 1 | NAG | O5-C1 | -7.39 | 1.31 | 1.43 |
| 12 | s | 4 | MAN | C2-C3 | 6.80 | 1.62 | 1.52 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 8 | E | 1 | NAG | O5-C1 | -6.74 | 1.33 | 1.43 |
| 11 | r | 1 | NAG | O5-C1 | -6.67 | 1.33 | 1.43 |
| 11 | Z | 1 | NAG | O5-C1 | -6.65 | 1.33 | 1.43 |
| 8 | n | 1 | NAG | O5-C1 | -6.63 | 1.33 | 1.43 |
| 11 | i | 1 | NAG | O5-C1 | -6.58 | 1.33 | 1.43 |
| 12 | a | 2 | NAG | O5-C1 | -6.47 | 1.33 | 1.43 |
| 11 | Z | 7 | MAN | C4-C5 | -6.34 | 1.39 | 1.53 |
| 12 | s | 2 | NAG | O5-C1 | -6.28 | 1.33 | 1.43 |
| 8 | n | 3 | BMA | C4-C5 | 5.24 | 1.64 | 1.53 |
| 12 | s | 4 | MAN | O2-C2 | 4.93 | 1.53 | 1.43 |
| 8 | n | 3 | BMA | C4-C3 | 4.88 | 1.64 | 1.52 |
| 8 | e | 2 | NAG | O5-C1 | 4.88 | 1.51 | 1.43 |
| 11 | r | 3 | BMA | C4-C3 | 4.80 | 1.64 | 1.52 |
| 11 | Z | 3 | BMA | C2-C3 | 4.64 | 1.59 | 1.52 |
| 8 | E | 3 | BMA | C4-C3 | 4.64 | 1.64 | 1.52 |
| 8 | n | 3 | BMA | O5-C5 | 4.59 | 1.52 | 1.43 |
| 11 | Z | 3 | BMA | C4-C3 | 4.36 | 1.63 | 1.52 |
| 11 | r | 4 | MAN | C4-C3 | 4.35 | 1.63 | 1.52 |
| 12 | j | 2 | NAG | O5-C1 | -4.17 | 1.37 | 1.43 |
| 8 | n | 3 | BMA | C1-C2 | -4.02 | 1.43 | 1.52 |
| 8 | E | 3 | BMA | O5-C5 | 3.98 | 1.51 | 1.43 |
| 14 | v | 7 | MAN | C2-C3 | -3.98 | 1.46 | 1.52 |
| 11 | r | 6 | MAN | C4-C5 | -3.96 | 1.44 | 1.53 |
| 8 | n | 3 | BMA | C2-C3 | 3.83 | 1.58 | 1.52 |
| 11 | Z | 5 | MAN | C4-C5 | -3.77 | 1.45 | 1.53 |
| 8 | e | 2 | NAG | C1-C2 | 3.72 | 1.57 | 1.52 |
| 14 | v | 7 | MAN | O5-C5 | 3.70 | 1.50 | 1.43 |
| 11 | Z | 7 | MAN | O4-C4 | 3.67 | 1.51 | 1.43 |
| 8 | E | 3 | BMA | C4-C5 | 3.66 | 1.60 | 1.53 |
| 9 | f | 2 | NAG | O5-C1 | -3.61 | 1.37 | 1.43 |
| 11 | r | 5 | MAN | C4-C5 | -3.57 | 1.45 | 1.53 |
| 14 | v | 7 | MAN | O2-C2 | -3.56 | 1.35 | 1.43 |
| 8 | e | 3 | BMA | C4-C3 | 3.56 | 1.61 | 1.52 |
| 9 | P | 2 | NAG | O5-C1 | -3.52 | 1.38 | 1.43 |
| 9 | o | 2 | NAG | O5-C1 | -3.51 | 1.38 | 1.43 |
| 8 | E | 3 | BMA | C2-C3 | 3.43 | 1.57 | 1.52 |
| 11 | r | 6 | MAN | C4-C3 | -3.41 | 1.43 | 1.52 |
| 8 | e | 3 | BMA | C4-C5 | 3.40 | 1.60 | 1.53 |
| 12 | a | 5 | MAN | C1-C2 | 3.40 | 1.60 | 1.52 |
| 11 | r | 7 | MAN | C4-C3 | 3.38 | 1.60 | 1.52 |
| 11 | r | 7 | MAN | O5-C5 | 3.34 | 1.50 | 1.43 |
| 12 | j | 5 | MAN | C1-C2 | 3.34 | 1.59 | 1.52 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 11 | r | 3 | BMA | O4-C4 | 3.34 | 1.50 | 1.43 |
| 11 | i | 5 | MAN | C4-C5 | -3.32 | 1.46 | 1.53 |
| 8 | E | 2 | NAG | C1-C2 | -3.31 | 1.47 | 1.52 |
| 8 | e | 3 | BMA | O5-C1 | -3.30 | 1.38 | 1.43 |
| 12 | j | 3 | BMA | O5-C1 | 3.26 | 1.48 | 1.43 |
| 8 | e | 5 | MAN | O5-C1 | -3.25 | 1.38 | 1.43 |
| 14 | v | 7 | MAN | O4-C4 | -3.23 | 1.35 | 1.43 |
| 9 | f | 1 | NAG | C1-C2 | 3.18 | 1.57 | 1.52 |
| 12 | j | 4 | MAN | O5-C1 | 3.11 | 1.48 | 1.43 |
| 12 | j | 4 | MAN | C1-C2 | 3.10 | 1.59 | 1.52 |
| 9 | P | 1 | NAG | C1-C2 | 3.10 | 1.57 | 1.52 |
| 11 | r | 3 | BMA | C2-C3 | 3.10 | 1.57 | 1.52 |
| 8 | E | 5 | MAN | C1-C2 | 3.10 | 1.59 | 1.52 |
| 12 | j | 3 | BMA | O5-C5 | 3.08 | 1.49 | 1.43 |
| 11 | r | 4 | MAN | O2-C2 | 3.08 | 1.49 | 1.43 |
| 8 | n | 3 | BMA | O5-C1 | -3.07 | 1.38 | 1.43 |
| 8 | n | 5 | MAN | C1-C2 | 3.03 | 1.59 | 1.52 |
| 8 | n | 2 | NAG | C1-C2 | -3.03 | 1.47 | 1.52 |
| 12 | a | 4 | MAN | O5-C1 | 3.03 | 1.48 | 1.43 |
| 12 | a | 4 | MAN | C1-C2 | 3.00 | 1.59 | 1.52 |
| 8 | n | 5 | MAN | O5-C1 | -2.99 | 1.38 | 1.43 |
| 11 | Z | 6 | MAN | C1-C2 | 2.98 | 1.59 | 1.52 |
| 12 | s | 3 | BMA | O5-C5 | 2.97 | 1.49 | 1.43 |
| 12 | s | 6 | MAN | C1-C2 | 2.95 | 1.58 | 1.52 |
| 11 | Z | 3 | BMA | O2-C2 | -2.94 | 1.37 | 1.43 |
| 8 | E | 5 | MAN | C4-C5 | -2.93 | 1.46 | 1.53 |
| 9 | o | 1 | NAG | C1-C2 | 2.88 | 1.56 | 1.52 |
| 8 | E | 3 | BMA | C1-C2 | -2.86 | 1.45 | 1.52 |
| 12 | s | 3 | BMA | O5-C1 | 2.84 | 1.48 | 1.43 |
| 11 | Z | 4 | MAN | C4-C5 | -2.81 | 1.47 | 1.53 |
| 12 | a | 3 | BMA | O5-C5 | 2.78 | 1.49 | 1.43 |
| 12 | a | 3 | BMA | O5-C1 | 2.76 | 1.48 | 1.43 |
| 11 | i | 2 | NAG | C1-C2 | -2.75 | 1.48 | 1.52 |
| 8 | e | 5 | MAN | C1-C2 | 2.75 | 1.58 | 1.52 |
| 8 | E | 3 | BMA | O5-C1 | -2.72 | 1.39 | 1.43 |
| 11 | i | 6 | MAN | C1-C2 | 2.71 | 1.58 | 1.52 |
| 12 | a | 6 | MAN | C1-C2 | 2.71 | 1.58 | 1.52 |
| 8 | e | 1 | NAG | C1-C2 | -2.65 | 1.48 | 1.52 |
| 11 | r | 6 | MAN | O5-C1 | -2.61 | 1.39 | 1.43 |
| 11 | Z | 2 | NAG | C1-C2 | -2.60 | 1.48 | 1.52 |
| 12 | s | 4 | MAN | O5-C5 | 2.59 | 1.48 | 1.43 |
| 12 | j | 6 | MAN | O5-C1 | 2.57 | 1.47 | 1.43 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 11 | Z | 3 | BMA | C6-C5 | 2.55 | 1.60 | 1.51 |
| 8 | e | 3 | BMA | C1-C2 | -2.55 | 1.46 | 1.52 |
| 8 | p | 1 | NAG | C1-C2 | -2.53 | 1.48 | 1.52 |
| 11 | i | 5 | MAN | O5-C1 | -2.49 | 1.39 | 1.43 |
| 8 | g | 1 | NAG | C1-C2 | -2.49 | 1.48 | 1.52 |
| 11 | Z | 3 | BMA | O4-C4 | 2.49 | 1.48 | 1.43 |
| 12 | j | 3 | BMA | C2-C3 | 2.48 | 1.56 | 1.52 |
| 11 | r | 2 | NAG | C1-C2 | -2.46 | 1.48 | 1.52 |
| 11 | i | 6 | MAN | C4-C3 | -2.45 | 1.46 | 1.52 |
| 12 | a | 1 | NAG | O5-C1 | -2.44 | 1.39 | 1.43 |
| 12 | s | 5 | MAN | C1-C2 | 2.40 | 1.57 | 1.52 |
| 11 | i | 7 | MAN | O5-C1 | -2.40 | 1.39 | 1.43 |
| 12 | s | 4 | MAN | O5-C1 | -2.39 | 1.39 | 1.43 |
| 8 | X | 1 | NAG | C1-C2 | -2.36 | 1.48 | 1.52 |
| 11 | i | 1 | NAG | C1-C2 | -2.35 | 1.48 | 1.52 |
| 11 | r | 6 | MAN | O4-C4 | 2.34 | 1.48 | 1.43 |
| 11 | r | 1 | NAG | C1-C2 | -2.33 | 1.48 | 1.52 |
| 8 | n | 5 | MAN | O2-C2 | 2.32 | 1.48 | 1.43 |
| 10 | h | 1 | NAG | O5-C1 | -2.32 | 1.40 | 1.43 |
| 11 | r | 6 | MAN | O5-C5 | 2.31 | 1.48 | 1.43 |
| 14 | d | 3 | BMA | C2-C3 | 2.31 | 1.55 | 1.52 |
| 8 | n | 5 | MAN | C4-C5 | -2.30 | 1.48 | 1.53 |
| 12 | s | 5 | MAN | C2-C3 | -2.30 | 1.49 | 1.52 |
| 11 | r | 7 | MAN | C2-C3 | 2.30 | 1.55 | 1.52 |
| 14 | v | 7 | MAN | C4-C5 | -2.29 | 1.48 | 1.53 |
| 11 | r | 4 | MAN | O5-C1 | -2.27 | 1.40 | 1.43 |
| 12 | j | 6 | MAN | C1-C2 | 2.27 | 1.57 | 1.52 |
| 8 | X | 2 | NAG | O5-C1 | 2.26 | 1.47 | 1.43 |
| 12 | a | 4 | MAN | C2-C3 | -2.25 | 1.49 | 1.52 |
| 12 | a | 3 | BMA | C2-C3 | 2.23 | 1.55 | 1.52 |
| 14 | m | 3 | BMA | C2-C3 | 2.23 | 1.55 | 1.52 |
| 14 | v | 4 | MAN | C1-C2 | 2.22 | 1.57 | 1.52 |
| 11 | r | 3 | BMA | O2-C2 | -2.19 | 1.38 | 1.43 |
| 12 | s | 3 | BMA | C2-C3 | 2.19 | 1.55 | 1.52 |
| 11 | Z | 1 | NAG | C1-C2 | -2.18 | 1.49 | 1.52 |
| 11 | Z | 5 | MAN | C2-C3 | -2.18 | 1.49 | 1.52 |
| 8 | g | 2 | NAG | O5-C1 | 2.17 | 1.47 | 1.43 |
| 8 | E | 5 | MAN | O5-C1 | -2.16 | 1.40 | 1.43 |
| 8 | e | 3 | BMA | O3-C3 | -2.16 | 1.37 | 1.43 |
| 12 | j | 4 | MAN | C2-C3 | -2.14 | 1.49 | 1.52 |
| 14 | m | 7 | MAN | C1-C2 | 2.13 | 1.57 | 1.52 |
| 14 | v | 8 | MAN | C1-C2 | 2.13 | 1.57 | 1.52 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 11 | Z | 6 | MAN | C4-C5 | -2.12 | 1.48 | 1.53 |
| 8 | n | 1 | NAG | C1-C2 | -2.11 | 1.49 | 1.52 |
| 8 | p | 2 | NAG | O5-C1 | 2.11 | 1.47 | 1.43 |
| 11 | r | 5 | MAN | C2-C3 | -2.10 | 1.49 | 1.52 |
| 14 | d | 8 | MAN | C1-C2 | 2.09 | 1.57 | 1.52 |
| 8 | e | 5 | MAN | C4-C3 | 2.08 | 1.57 | 1.52 |
| 14 | m | 8 | MAN | C1-C2 | 2.08 | 1.56 | 1.52 |
| 12 | a | 5 | MAN | O2-C2 | 2.07 | 1.47 | 1.43 |
| 11 | r | 7 | MAN | O5-C1 | 2.07 | 1.47 | 1.43 |
| 8 | e | 5 | MAN | O2-C2 | 2.06 | 1.47 | 1.43 |
| 14 | m | 4 | MAN | C4-C5 | -2.06 | 1.48 | 1.53 |
| 14 | d | 7 | MAN | C1-C2 | 2.04 | 1.56 | 1.52 |
| 11 | r | 6 | MAN | O3-C3 | -2.04 | 1.38 | 1.43 |
| 11 | i | 4 | MAN | O5-C5 | 2.03 | 1.47 | 1.43 |
| 14 | v | 1 | NAG | O5-C1 | -2.03 | 1.40 | 1.43 |
| 14 | v | 6 | MAN | C2-C3 | 2.02 | 1.55 | 1.52 |
| 8 | e | 4 | MAN | O5-C5 | 2.02 | 1.47 | 1.43 |

All (313) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 14 | v | 7 | MAN | O5-C5-C6 | -8.66 | 93.63 | 107.20 |
| 11 | r | 6 | MAN | O5-C1-C2 | 8.54 | 123.95 | 110.77 |
| 11 | Z | 6 | MAN | O3-C3-C4 | -7.86 | 92.17 | 110.35 |
| 8 | e | 2 | NAG | C1-O5-C5 | 7.86 | 122.84 | 112.19 |
| 11 | r | 4 | MAN | O5-C1-C2 | 7.40 | 122.19 | 110.77 |
| 11 | Z | 7 | MAN | C1-C2-C3 | -7.39 | 100.58 | 109.67 |
| 11 | Z | 4 | MAN | O5-C1-C2 | 7.29 | 122.03 | 110.77 |
| 14 | v | 7 | MAN | C1-O5-C5 | 7.22 | 121.97 | 112.19 |
| 11 | Z | 7 | MAN | O5-C1-C2 | 7.22 | 121.91 | 110.77 |
| 11 | i | 7 | MAN | O5-C1-C2 | 7.21 | 121.90 | 110.77 |
| 8 | n | 5 | MAN | O3-C3-C4 | -6.83 | 94.55 | 110.35 |
| 11 | r | 6 | MAN | C3-C4-C5 | 6.77 | 122.32 | 110.24 |
| 11 | r | 6 | MAN | O2-C2-C3 | -6.53 | 97.05 | 110.14 |
| 11 | Z | 7 | MAN | C3-C4-C5 | 6.50 | 121.84 | 110.24 |
| 11 | i | 6 | MAN | O3-C3-C4 | -6.31 | 95.76 | 110.35 |
| 11 | r | 4 | MAN | O3-C3-C4 | -6.28 | 95.82 | 110.35 |
| 11 | Z | 4 | MAN | O5-C5-C4 | -6.04 | 96.13 | 110.83 |
| 11 | Z | 5 | MAN | O5-C1-C2 | 5.73 | 119.62 | 110.77 |
| 11 | Z | 6 | MAN | O5-C1-C2 | 5.66 | 119.50 | 110.77 |
| 11 | Z | 3 | BMA | C3-C4-C5 | 5.60 | 120.22 | 110.24 |
| 11 | i | 6 | MAN | O5-C1-C2 | 5.59 | 119.41 | 110.77 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 12 | s | 5 | MAN | O5-C5-C4 | -5.59 | 97.23 | 110.83 |
| 12 | j | 6 | MAN | C1-O5-C5 | 5.58 | 119.75 | 112.19 |
| 11 | i | 5 | MAN | O5-C1-C2 | 5.43 | 119.16 | 110.77 |
| 11 | Z | 7 | MAN | O5-C5-C4 | -5.39 | 97.71 | 110.83 |
| 8 | n | 5 | MAN | O5-C1-C2 | 5.38 | 119.07 | 110.77 |
| 8 | E | 5 | MAN | O3-C3-C4 | -5.27 | 98.17 | 110.35 |
| 11 | i | 5 | MAN | O5-C5-C6 | -5.26 | 98.96 | 107.20 |
| 12 | j | 4 | MAN | C1-O5-C5 | 5.25 | 119.31 | 112.19 |
| 12 | a | 6 | MAN | C1-O5-C5 | 5.22 | 119.26 | 112.19 |
| 11 | r | 5 | MAN | O5-C1-C2 | 5.20 | 118.80 | 110.77 |
| 12 | s | 6 | MAN | C1-O5-C5 | 5.19 | 119.22 | 112.19 |
| 14 | v | 7 | MAN | O5-C5-C4 | -5.16 | 98.27 | 110.83 |
| 14 | m | 4 | MAN | C1-O5-C5 | 5.15 | 119.17 | 112.19 |
| 8 | E | 5 | MAN | O5-C1-C2 | 5.14 | 118.70 | 110.77 |
| 12 | j | 2 | NAG | C3-C4-C5 | 5.13 | 119.39 | 110.24 |
| 8 | E | 2 | NAG | O4-C4-C5 | 5.12 | 122.00 | 109.30 |
| 8 | E | 5 | MAN | O2-C2-C3 | -5.11 | 99.90 | 110.14 |
| 11 | r | 3 | BMA | C3-C4-C5 | 5.06 | 119.26 | 110.24 |
| 11 | Z | 5 | MAN | C1-O5-C5 | 5.05 | 119.03 | 112.19 |
| 11 | Z | 5 | MAN | O5-C5-C4 | -4.99 | 98.69 | 110.83 |
| 12 | a | 4 | MAN | C1-O5-C5 | 4.98 | 118.94 | 112.19 |
| 8 | e | 5 | MAN | O3-C3-C4 | -4.96 | 98.88 | 110.35 |
| 11 | i | 5 | MAN | O5-C5-C4 | -4.95 | 98.78 | 110.83 |
| 11 | r | 5 | MAN | O5-C5-C4 | -4.95 | 98.79 | 110.83 |
| 11 | i | 7 | MAN | O5-C5-C4 | -4.94 | 98.81 | 110.83 |
| 14 | d | 4 | MAN | C1-O5-C5 | 4.91 | 118.85 | 112.19 |
| 11 | r | 5 | MAN | O5-C5-C6 | -4.88 | 99.56 | 107.20 |
| 11 | r | 6 | MAN | O5-C5-C4 | -4.85 | 99.04 | 110.83 |
| 11 | i | 5 | MAN | C1-O5-C5 | 4.82 | 118.72 | 112.19 |
| 8 | n | 5 | MAN | O2-C2-C3 | -4.78 | 100.56 | 110.14 |
| 8 | e | 4 | MAN | C1-C2-C3 | -4.69 | 103.90 | 109.67 |
| 11 | Z | 6 | MAN | C1-C2-C3 | 4.63 | 115.36 | 109.67 |
| 14 | m | 1 | NAG | C2-N2-C7 | 4.62 | 129.48 | 122.90 |
| 11 | r | 5 | MAN | C1-O5-C5 | 4.60 | 118.43 | 112.19 |
| 14 | v | 1 | NAG | C2-N2-C7 | 4.57 | 129.41 | 122.90 |
| 14 | d | 1 | NAG | C2-N2-C7 | 4.56 | 129.40 | 122.90 |
| 12 | s | 2 | NAG | C3-C4-C5 | 4.55 | 118.36 | 110.24 |
| 12 | a | 2 | NAG | C3-C4-C5 | 4.54 | 118.34 | 110.24 |
| 12 | s | 5 | MAN | O5-C1-C2 | 4.54 | 117.78 | 110.77 |
| 8 | n | 2 | NAG | O4-C4-C5 | 4.52 | 120.53 | 109.30 |
| 14 | v | 7 | MAN | O5-C1-C2 | 4.49 | 117.71 | 110.77 |
| 11 | i | 6 | MAN | C3-C4-C5 | 4.49 | 118.24 | 110.24 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 11 | Z | 4 | MAN | C1-O5-C5 | 4.42 | 118.18 | 112.19 |
| 11 | i | 7 | MAN | C1-O5-C5 | 4.39 | 118.14 | 112.19 |
| 11 | Z | 5 | MAN | O5-C5-C6 | -4.36 | 100.37 | 107.20 |
| 14 | v | 7 | MAN | O2-C2-C3 | -4.36 | 101.41 | 110.14 |
| 14 | m | 4 | MAN | O5-C1-C2 | 4.34 | 117.48 | 110.77 |
| 12 | s | 4 | MAN | O3-C3-C2 | 4.34 | 118.31 | 109.99 |
| 11 | i | 2 | NAG | C3-C4-C5 | 4.32 | 117.95 | 110.24 |
| 14 | m | 4 | MAN | O5-C5-C4 | -4.32 | 100.33 | 110.83 |
| 14 | d | 4 | MAN | O5-C1-C2 | 4.31 | 117.43 | 110.77 |
| 11 | i | 4 | MAN | C1-O5-C5 | 4.31 | 118.03 | 112.19 |
| 14 | m | 4 | MAN | O2-C2-C3 | -4.26 | 101.61 | 110.14 |
| 8 | p | 1 | NAG | C3-C4-C5 | 4.25 | 117.83 | 110.24 |
| 8 | g | 1 | NAG | C3-C4-C5 | 4.25 | 117.82 | 110.24 |
| 14 | d | 4 | MAN | O2-C2-C3 | -4.24 | 101.64 | 110.14 |
| 8 | X | 1 | NAG | C3-C4-C5 | 4.23 | 117.79 | 110.24 |
| 11 | Z | 2 | NAG | C3-C4-C5 | 4.21 | 117.74 | 110.24 |
| 8 | e | 5 | MAN | O5-C1-C2 | 4.20 | 117.25 | 110.77 |
| 11 | i | 6 | MAN | C1-C2-C3 | 4.18 | 114.81 | 109.67 |
| 11 | r | 3 | BMA | O4-C4-C5 | 4.18 | 119.69 | 109.30 |
| 14 | d | 4 | MAN | O5-C5-C4 | -4.16 | 100.69 | 110.83 |
| 11 | i | 6 | MAN | O2-C2-C3 | -4.15 | 101.83 | 110.14 |
| 8 | X | 1 | NAG | O4-C4-C5 | 4.12 | 119.52 | 109.30 |
| 11 | Z | 4 | MAN | O2-C2-C3 | -4.11 | 101.91 | 110.14 |
| 11 | r | 6 | MAN | O2-C2-C1 | -4.09 | 100.79 | 109.15 |
| 8 | E | 5 | MAN | C3-C4-C5 | 4.05 | 117.47 | 110.24 |
| 11 | Z | 7 | MAN | O4-C4-C3 | -4.03 | 101.03 | 110.35 |
| 11 | Z | 6 | MAN | O2-C2-C3 | -4.01 | 102.10 | 110.14 |
| 11 | Z | 2 | NAG | O4-C4-C5 | 4.01 | 119.25 | 109.30 |
| 11 | r | 2 | NAG | C3-C4-C5 | 3.89 | 117.17 | 110.24 |
| 11 | Z | 5 | MAN | O2-C2-C3 | -3.86 | 102.40 | 110.14 |
| 11 | r | 5 | MAN | O2-C2-C3 | -3.85 | 102.43 | 110.14 |
| 8 | E | 3 | BMA | O3-C3-C2 | 3.83 | 117.33 | 109.99 |
| 12 | j | 4 | MAN | O2-C2-C3 | -3.83 | 102.47 | 110.14 |
| 11 | Z | 6 | MAN | C3-C4-C5 | 3.80 | 117.01 | 110.24 |
| 11 | r | 4 | MAN | C1-O5-C5 | 3.76 | 117.28 | 112.19 |
| 8 | n | 3 | BMA | O3-C3-C2 | 3.75 | 117.18 | 109.99 |
| 8 | E | 5 | MAN | O5-C5-C4 | -3.74 | 101.72 | 110.83 |
| 11 | Z | 3 | BMA | O4-C4-C5 | 3.74 | 118.59 | 109.30 |
| 12 | a | 4 | MAN | O2-C2-C3 | -3.73 | 102.66 | 110.14 |
| 12 | j | 2 | NAG | O4-C4-C5 | 3.71 | 118.50 | 109.30 |
| 14 | m | 7 | MAN | C1-O5-C5 | 3.71 | 117.21 | 112.19 |
| 8 | E | 2 | NAG | C3-C4-C5 | 3.68 | 116.81 | 110.24 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 8 | E | 5 | MAN | O5-C5-C6 | -3.67 | 101.45 | 107.20 |
| 14 | d | 7 | MAN | C1-O5-C5 | 3.67 | 117.16 | 112.19 |
| 11 | r | 2 | NAG | C1-O5-C5 | -3.66 | 107.23 | 112.19 |
| 11 | r | 1 | NAG | O4-C4-C5 | 3.66 | 118.38 | 109.30 |
| 11 | r | 2 | NAG | O4-C4-C5 | 3.65 | 118.36 | 109.30 |
| 11 | r | 7 | MAN | C2-C3-C4 | 3.64 | 117.19 | 110.89 |
| 11 | i | 1 | NAG | O4-C4-C5 | 3.59 | 118.22 | 109.30 |
| 8 | n | 5 | MAN | C2-C3-C4 | -3.59 | 104.68 | 110.89 |
| 11 | Z | 6 | MAN | C2-C3-C4 | -3.56 | 104.74 | 110.89 |
| 8 | e | 1 | NAG | C3-C4-C5 | 3.55 | 116.57 | 110.24 |
| 8 | p | 1 | NAG | O4-C4-C5 | 3.55 | 118.11 | 109.30 |
| 8 | g | 1 | NAG | O4-C4-C5 | 3.54 | 118.10 | 109.30 |
| 11 | i | 2 | NAG | O4-C4-C5 | 3.52 | 118.03 | 109.30 |
| 8 | e | 5 | MAN | O2-C2-C3 | -3.52 | 103.09 | 110.14 |
| 12 | s | 5 | MAN | O2-C2-C3 | -3.51 | 103.11 | 110.14 |
| 11 | i | 5 | MAN | O2-C2-C3 | -3.46 | 103.20 | 110.14 |
| 11 | r | 1 | NAG | C3-C4-C5 | 3.46 | 116.41 | 110.24 |
| 14 | v | 7 | MAN | C2-C3-C4 | 3.41 | 116.80 | 110.89 |
| 8 | n | 2 | NAG | C3-C4-C5 | 3.41 | 116.32 | 110.24 |
| 12 | s | 2 | NAG | O4-C4-C5 | 3.38 | 117.70 | 109.30 |
| 11 | i | 2 | NAG | C1-O5-C5 | -3.38 | 107.61 | 112.19 |
| 11 | Z | 2 | NAG | C1-O5-C5 | -3.38 | 107.62 | 112.19 |
| 11 | i | 7 | MAN | O5-C5-C6 | -3.37 | 101.93 | 107.20 |
| 11 | i | 1 | NAG | C3-C4-C5 | 3.35 | 116.21 | 110.24 |
| 14 | v | 4 | MAN | C1-O5-C5 | 3.34 | 116.72 | 112.19 |
| 8 | n | 4 | MAN | C1-O5-C5 | 3.33 | 116.70 | 112.19 |
| 11 | Z | 1 | NAG | O4-C4-C5 | 3.32 | 117.55 | 109.30 |
| 8 | n | 1 | NAG | C3-C4-C5 | 3.31 | 116.15 | 110.24 |
| 11 | r | 1 | NAG | O4-C4-C3 | 3.31 | 118.01 | 110.35 |
| 11 | i | 1 | NAG | O4-C4-C3 | 3.30 | 117.97 | 110.35 |
| 12 | j | 3 | BMA | C1-C2-C3 | 3.29 | 113.71 | 109.67 |
| 11 | r | 4 | MAN | O3-C3-C2 | 3.29 | 116.29 | 109.99 |
| 11 | Z | 1 | NAG | C3-C4-C5 | 3.28 | 116.09 | 110.24 |
| 8 | E | 5 | MAN | C1-O5-C5 | 3.28 | 116.63 | 112.19 |
| 8 | e | 3 | BMA | O3-C3-C2 | 3.27 | 116.26 | 109.99 |
| 11 | r | 4 | MAN | C2-C3-C4 | -3.26 | 105.25 | 110.89 |
| 8 | n | 2 | NAG | O4-C4-C3 | 3.25 | 117.86 | 110.35 |
| 11 | i | 7 | MAN | O2-C2-C3 | -3.23 | 103.67 | 110.14 |
| 8 | E | 3 | BMA | O4-C4-C5 | 3.22 | 117.29 | 109.30 |
| 14 | m | 5 | MAN | C1-O5-C5 | 3.20 | 116.52 | 112.19 |
| 12 | s | 4 | MAN | C1-C2-C3 | -3.18 | 105.75 | 109.67 |
| 8 | E | 3 | BMA | O4-C4-C3 | 3.17 | 117.67 | 110.35 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 8 | E | 4 | MAN | C1-O5-C5 | 3.15 | 116.46 | 112.19 |
| 14 | d | 5 | MAN | C1-O5-C5 | 3.13 | 116.44 | 112.19 |
| 12 | a | 2 | NAG | O4-C4-C5 | 3.13 | 117.08 | 109.30 |
| 14 | m | 4 | MAN | O5-C5-C6 | -3.13 | 102.30 | 107.20 |
| 11 | i | 6 | MAN | C2-C3-C4 | -3.12 | 105.49 | 110.89 |
| 11 | Z | 1 | NAG | O4-C4-C3 | 3.09 | 117.50 | 110.35 |
| 8 | e | 5 | MAN | C1-O5-C5 | 3.09 | 116.38 | 112.19 |
| 8 | n | 5 | MAN | O2-C2-C1 | -3.08 | 102.84 | 109.15 |
| 8 | n | 5 | MAN | O5-C5-C4 | -3.08 | 103.34 | 110.83 |
| 12 | s | 4 | MAN | O2-C2-C1 | 3.07 | 115.43 | 109.15 |
| 11 | r | 4 | MAN | O2-C2-C3 | -3.06 | 104.01 | 110.14 |
| 8 | E | 1 | NAG | C3-C4-C5 | 3.06 | 115.69 | 110.24 |
| 8 | e | 4 | MAN | C1-O5-C5 | 3.05 | 116.32 | 112.19 |
| 8 | E | 3 | BMA | O5-C1-C2 | -3.04 | 106.08 | 110.77 |
| 12 | a | 5 | MAN | O2-C2-C1 | 3.03 | 115.36 | 109.15 |
| 11 | i | 2 | NAG | O4-C4-C3 | 3.03 | 117.36 | 110.35 |
| 11 | r | 3 | BMA | O4-C4-C3 | 3.02 | 117.33 | 110.35 |
| 12 | j | 5 | MAN | O2-C2-C1 | 3.02 | 115.33 | 109.15 |
| 11 | r | 2 | NAG | O4-C4-C3 | 3.01 | 117.31 | 110.35 |
| 11 | r | 6 | MAN | C1-C2-C3 | 2.96 | 113.30 | 109.67 |
| 8 | e | 3 | BMA | O4-C4-C3 | 2.95 | 117.18 | 110.35 |
| 11 | i | 4 | MAN | O5-C1-C2 | 2.94 | 115.31 | 110.77 |
| 11 | Z | 3 | BMA | O4-C4-C3 | 2.93 | 117.12 | 110.35 |
| 11 | Z | 7 | MAN | C1-O5-C5 | 2.92 | 116.14 | 112.19 |
| 8 | e | 1 | NAG | O4-C4-C5 | 2.91 | 116.52 | 109.30 |
| 8 | n | 3 | BMA | O4-C4-C3 | 2.90 | 117.06 | 110.35 |
| 14 | d | 4 | MAN | O5-C5-C6 | -2.88 | 102.69 | 107.20 |
| 8 | E | 5 | MAN | O2-C2-C1 | -2.83 | 103.37 | 109.15 |
| 11 | r | 4 | MAN | O2-C2-C1 | -2.82 | 103.39 | 109.15 |
| 11 | Z | 3 | BMA | O3-C3-C2 | 2.81 | 115.38 | 109.99 |
| 8 | n | 5 | MAN | C3-C4-C5 | 2.81 | 115.25 | 110.24 |
| 8 | c | 4 | MAN | C1-O5-C5 | 2.81 | 116.00 | 112.19 |
| 11 | r | 4 | MAN | O5-C5-C4 | -2.81 | 104.00 | 110.83 |
| 8 | E | 2 | NAG | O4-C4-C3 | 2.80 | 116.81 | 110.35 |
| 12 | j | 2 | NAG | O3-C3-C2 | 2.79 | 115.24 | 109.47 |
| 8 | e | 5 | MAN | C2-C3-C4 | -2.79 | 106.07 | 110.89 |
| 8 | n | 1 | NAG | O4-C4-C3 | 2.79 | 116.80 | 110.35 |
| 8 | u | 4 | MAN | C1-O5-C5 | 2.78 | 115.95 | 112.19 |
| 14 | v | 6 | MAN | C1-O5-C5 | 2.77 | 115.95 | 112.19 |
| 14 | m | 6 | MAN | C1-O5-C5 | 2.77 | 115.94 | 112.19 |
| 8 | E | 1 | NAG | O4-C4-C5 | 2.76 | 116.14 | 109.30 |
| 12 | s | 4 | MAN | O3-C3-C4 | -2.75 | 103.99 | 110.35 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 14 | d | 6 | MAN | C1-O5-C5 | 2.73 | 115.89 | 112.19 |
| 11 | Z | 4 | MAN | O2-C2-C1 | -2.73 | 103.56 | 109.15 |
| 8 | E | 1 | NAG | O4-C4-C3 | 2.72 | 116.63 | 110.35 |
| 8 | E | 3 | BMA | C3-C4-C5 | 2.71 | 115.08 | 110.24 |
| 11 | r | 7 | MAN | C1-O5-C5 | 2.71 | 115.87 | 112.19 |
| 12 | a | 3 | BMA | C1-C2-C3 | 2.70 | 112.99 | 109.67 |
| 11 | Z | 2 | NAG | O4-C4-C3 | 2.70 | 116.59 | 110.35 |
| 8 | l | 4 | MAN | C1-O5-C5 | 2.70 | 115.85 | 112.19 |
| 8 | X | 1 | NAG | O4-C4-C3 | 2.70 | 116.58 | 110.35 |
| 12 | a | 5 | MAN | O2-C2-C3 | -2.70 | 104.74 | 110.14 |
| 10 | Y | 4 | MAN | C1-O5-C5 | 2.69 | 115.83 | 112.19 |
| 11 | Z | 4 | MAN | O5-C5-C6 | -2.69 | 102.99 | 107.20 |
| 14 | d | 1 | NAG | C1-C2-N2 | 2.67 | 115.05 | 110.49 |
| 14 | m | 1 | NAG | C1-C2-N2 | 2.66 | 115.03 | 110.49 |
| 12 | j | 3 | BMA | O5-C5-C6 | 2.65 | 111.36 | 107.20 |
| 12 | j | 5 | MAN | O2-C2-C3 | -2.65 | 104.82 | 110.14 |
| 8 | E | 5 | MAN | C2-C3-C4 | -2.65 | 106.31 | 110.89 |
| 14 | d | 8 | MAN | C1-O5-C5 | 2.63 | 115.76 | 112.19 |
| 14 | v | 8 | MAN | C1-O5-C5 | 2.63 | 115.76 | 112.19 |
| 11 | r | 6 | MAN | C2-C3-C4 | -2.62 | 106.35 | 110.89 |
| 8 | n | 3 | BMA | O5-C1-C2 | -2.62 | 106.72 | 110.77 |
| 12 | s | 5 | MAN | C3-C4-C5 | 2.61 | 114.89 | 110.24 |
| 14 | m | 8 | MAN | C1-O5-C5 | 2.60 | 115.71 | 112.19 |
| 10 | q | 4 | MAN | C1-O5-C5 | 2.59 | 115.71 | 112.19 |
| 14 | v | 1 | NAG | C1-C2-N2 | 2.59 | 114.91 | 110.49 |
| 8 | n | 1 | NAG | O4-C4-C5 | 2.58 | 115.71 | 109.30 |
| 12 | a | 2 | NAG | O3-C3-C2 | 2.58 | 114.81 | 109.47 |
| 10 | h | 4 | MAN | C1-O5-C5 | 2.57 | 115.68 | 112.19 |
| 8 | n | 5 | MAN | C1-O5-C5 | 2.57 | 115.67 | 112.19 |
| 8 | c | 5 | MAN | C1-O5-C5 | 2.55 | 115.65 | 112.19 |
| 8 | X | 4 | MAN | C1-O5-C5 | 2.55 | 115.64 | 112.19 |
| 8 | g | 4 | MAN | C1-O5-C5 | 2.55 | 115.64 | 112.19 |
| 12 | s | 2 | NAG | O3-C3-C2 | 2.54 | 114.72 | 109.47 |
| 8 | u | 5 | MAN | C1-O5-C5 | 2.53 | 115.62 | 112.19 |
| 8 | p | 4 | MAN | C1-O5-C5 | 2.52 | 115.61 | 112.19 |
| 11 | r | 6 | MAN | O4-C4-C3 | -2.52 | 104.51 | 110.35 |
| 8 | n | 5 | MAN | C1-C2-C3 | 2.52 | 112.77 | 109.67 |
| 8 | l | 5 | MAN | C1-O5-C5 | 2.52 | 115.60 | 112.19 |
| 12 | s | 5 | MAN | C1-O5-C5 | 2.49 | 115.56 | 112.19 |
| 11 | r | 7 | MAN | C3-C4-C5 | 2.48 | 114.67 | 110.24 |
| 12 | a | 3 | BMA | O5-C5-C6 | 2.48 | 111.09 | 107.20 |
| 12 | s | 5 | MAN | O3-C3-C2 | 2.47 | 114.73 | 109.99 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 12 | s | 3 | BMA | C1-C2-C3 | 2.47 | 112.70 | 109.67 |
| 12 | s | 6 | MAN | O2-C2-C3 | -2.45 | 105.22 | 110.14 |
| 8 | e | 3 | BMA | O6-C6-C5 | -2.45 | 102.88 | 111.29 |
| 14 | d | 5 | MAN | O2-C2-C3 | -2.45 | 105.23 | 110.14 |
| 8 | e | 3 | BMA | O4-C4-C5 | 2.45 | 115.38 | 109.30 |
| 11 | r | 7 | MAN | O2-C2-C1 | 2.44 | 114.14 | 109.15 |
| 12 | j | 5 | MAN | C1-O5-C5 | 2.42 | 115.48 | 112.19 |
| 8 | E | 4 | MAN | O2-C2-C3 | -2.42 | 105.30 | 110.14 |
| 11 | Z | 5 | MAN | C3-C4-C5 | 2.40 | 114.53 | 110.24 |
| 11 | i | 6 | MAN | O5-C5-C4 | -2.40 | 104.98 | 110.83 |
| 8 | e | 1 | NAG | O5-C5-C6 | -2.40 | 103.44 | 107.20 |
| 12 | j | 6 | MAN | O5-C1-C2 | 2.40 | 114.47 | 110.77 |
| 8 | e | 3 | BMA | C3-C4-C5 | 2.38 | 114.48 | 110.24 |
| 12 | a | 6 | MAN | O2-C2-C3 | -2.38 | 105.38 | 110.14 |
| 12 | s | 3 | BMA | O5-C5-C6 | 2.35 | 110.89 | 107.20 |
| 9 | o | 1 | NAG | C1-O5-C5 | 2.34 | 115.36 | 112.19 |
| 11 | Z | 6 | MAN | O5-C5-C4 | -2.34 | 105.15 | 110.83 |
| 8 | p | 1 | NAG | O4-C4-C3 | 2.33 | 115.75 | 110.35 |
| 9 | P | 1 | NAG | C1-O5-C5 | 2.32 | 115.33 | 112.19 |
| 14 | m | 3 | BMA | C1-O5-C5 | 2.31 | 115.32 | 112.19 |
| 12 | s | 4 | MAN | C1-O5-C5 | 2.29 | 115.30 | 112.19 |
| 8 | e | 3 | BMA | O5-C1-C2 | -2.29 | 107.24 | 110.77 |
| 8 | e | 4 | MAN | O2-C2-C3 | -2.28 | 105.56 | 110.14 |
| 14 | m | 7 | MAN | O2-C2-C3 | -2.28 | 105.56 | 110.14 |
| 14 | m | 5 | MAN | O2-C2-C3 | -2.28 | 105.56 | 110.14 |
| 8 | g | 1 | NAG | O4-C4-C3 | 2.27 | 115.60 | 110.35 |
| 12 | a | 5 | MAN | C1-O5-C5 | 2.27 | 115.26 | 112.19 |
| 14 | d | 7 | MAN | O2-C2-C3 | -2.26 | 105.62 | 110.14 |
| 11 | r | 5 | MAN | C3-C4-C5 | 2.25 | 114.26 | 110.24 |
| 12 | j | 3 | BMA | O2-C2-C3 | -2.25 | 105.63 | 110.14 |
| 8 | n | 4 | MAN | O2-C2-C3 | -2.25 | 105.63 | 110.14 |
| 14 | m | 6 | MAN | O2-C2-C3 | -2.25 | 105.63 | 110.14 |
| 8 | u | 5 | MAN | O2-C2-C3 | -2.24 | 105.65 | 110.14 |
| 14 | v | 3 | BMA | C1-O5-C5 | 2.24 | 115.23 | 112.19 |
| 12 | a | 3 | BMA | O2-C2-C3 | -2.24 | 105.66 | 110.14 |
| 14 | v | 5 | MAN | O2-C2-C3 | -2.24 | 105.66 | 110.14 |
| 10 | q | 4 | MAN | O2-C2-C3 | -2.23 | 105.66 | 110.14 |
| 14 | d | 3 | BMA | C1-O5-C5 | 2.23 | 115.22 | 112.19 |
| 8 | n | 5 | MAN | O5-C5-C6 | -2.23 | 103.70 | 107.20 |
| 8 | c | 5 | MAN | O2-C2-C3 | -2.23 | 105.68 | 110.14 |
| 11 | Z | 6 | MAN | O2-C2-C1 | -2.23 | 104.59 | 109.15 |
| 8 | E | 3 | BMA | O5-C5-C4 | -2.23 | 105.41 | 110.83 |

*Continued on next page...*

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 8 | n | 3 | BMA | O2-C2-C3 | -2.22 | 105.68 | 110.14 |
| 10 | Y | 4 | MAN | O2-C2-C3 | -2.22 | 105.69 | 110.14 |
| 12 | j | 6 | MAN | O2-C2-C3 | -2.22 | 105.69 | 110.14 |
| 14 | d | 6 | MAN | O2-C2-C3 | -2.22 | 105.69 | 110.14 |
| 11 | Z | 4 | MAN | O3-C3-C2 | 2.22 | 114.24 | 109.99 |
| 14 | v | 4 | MAN | O2-C2-C3 | -2.22 | 105.70 | 110.14 |
| 8 | l | 4 | MAN | O2-C2-C3 | -2.22 | 105.70 | 110.14 |
| 10 | h | 4 | MAN | O2-C2-C3 | -2.22 | 105.70 | 110.14 |
| 14 | v | 5 | MAN | C1-O5-C5 | 2.22 | 115.19 | 112.19 |
| 8 | n | 2 | NAG | C1-O5-C5 | -2.22 | 109.19 | 112.19 |
| 12 | j | 2 | NAG | C4-C3-C2 | 2.21 | 114.26 | 111.02 |
| 8 | u | 4 | MAN | O2-C2-C3 | -2.21 | 105.71 | 110.14 |
| 8 | X | 5 | MAN | O2-C2-C3 | -2.20 | 105.72 | 110.14 |
| 8 | g | 5 | MAN | O2-C2-C3 | -2.20 | 105.73 | 110.14 |
| 8 | X | 4 | MAN | O2-C2-C3 | -2.20 | 105.73 | 110.14 |
| 12 | a | 6 | MAN | O5-C1-C2 | 2.19 | 114.15 | 110.77 |
| 8 | c | 4 | MAN | O2-C2-C3 | -2.19 | 105.75 | 110.14 |
| 8 | p | 5 | MAN | O2-C2-C3 | -2.19 | 105.75 | 110.14 |
| 9 | f | 1 | NAG | C1-O5-C5 | 2.19 | 115.16 | 112.19 |
| 8 | l | 5 | MAN | O2-C2-C3 | -2.19 | 105.76 | 110.14 |
| 8 | g | 4 | MAN | O2-C2-C3 | -2.18 | 105.77 | 110.14 |
| 8 | e | 3 | BMA | C1-C2-C3 | -2.17 | 107.00 | 109.67 |
| 8 | p | 4 | MAN | O2-C2-C3 | -2.17 | 105.80 | 110.14 |
| 12 | j | 2 | NAG | O4-C4-C3 | 2.16 | 115.34 | 110.35 |
| 14 | d | 8 | MAN | O2-C2-C3 | -2.15 | 105.83 | 110.14 |
| 12 | s | 6 | MAN | O5-C1-C2 | 2.15 | 114.09 | 110.77 |
| 11 | i | 7 | MAN | O3-C3-C2 | 2.14 | 114.09 | 109.99 |
| 8 | g | 5 | MAN | C1-O5-C5 | 2.13 | 115.08 | 112.19 |
| 14 | v | 7 | MAN | C3-C4-C5 | 2.13 | 114.03 | 110.24 |
| 14 | m | 8 | MAN | O2-C2-C3 | -2.12 | 105.89 | 110.14 |
| 12 | s | 3 | BMA | O2-C2-C3 | -2.11 | 105.91 | 110.14 |
| 14 | v | 8 | MAN | O2-C2-C3 | -2.11 | 105.92 | 110.14 |
| 8 | p | 5 | MAN | C1-O5-C5 | 2.08 | 115.01 | 112.19 |
| 8 | n | 3 | BMA | C2-C3-C4 | 2.07 | 114.47 | 110.89 |
| 8 | e | 5 | MAN | O5-C5-C4 | -2.05 | 105.83 | 110.83 |
| 12 | j | 6 | MAN | O2-C2-C1 | 2.03 | 113.31 | 109.15 |
| 8 | n | 3 | BMA | O5-C5-C4 | -2.03 | 105.89 | 110.83 |
| 12 | a | 4 | MAN | C1-C2-C3 | 2.01 | 112.14 | 109.67 |
| 12 | j | 4 | MAN | C1-C2-C3 | 2.01 | 112.13 | 109.67 |
| 8 | e | 2 | NAG | C4-C3-C2 | 2.01 | 113.96 | 111.02 |

There are no chirality outliers.

All (115) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 8 | X | 3 | BMA | C4-C5-C6-O6 |
| 8 | g | 3 | BMA | C4-C5-C6-O6 |
| 8 | p | 3 | BMA | C4-C5-C6-O6 |
| 12 | j | 1 | NAG | C4-C5-C6-O6 |
| 11 | i | 7 | MAN | O5-C5-C6-O6 |
| 12 | a | 5 | MAN | O5-C5-C6-O6 |
| 12 | j | 5 | MAN | O5-C5-C6-O6 |
| 12 | s | 5 | MAN | O5-C5-C6-O6 |
| 8 | g | 3 | BMA | O5-C5-C6-O6 |
| 10 | Y | 1 | NAG | C4-C5-C6-O6 |
| 8 | X | 3 | BMA | O5-C5-C6-O6 |
| 8 | p | 3 | BMA | O5-C5-C6-O6 |
| 8 | n | 2 | NAG | C4-C5-C6-O6 |
| 10 | q | 1 | NAG | C4-C5-C6-O6 |
| 11 | r | 1 | NAG | C4-C5-C6-O6 |
| 8 | e | 1 | NAG | C1-C2-N2-C7 |
| 11 | i | 1 | NAG | C4-C5-C6-O6 |
| 11 | r | 2 | NAG | C4-C5-C6-O6 |
| 10 | h | 1 | NAG | C4-C5-C6-O6 |
| 11 | i | 2 | NAG | C4-C5-C6-O6 |
| 8 | X | 2 | NAG | C4-C5-C6-O6 |
| 11 | Z | 2 | NAG | C4-C5-C6-O6 |
| 8 | g | 2 | NAG | C4-C5-C6-O6 |
| 14 | d | 1 | NAG | C8-C7-N2-C2 |
| 14 | d | 1 | NAG | O7-C7-N2-C2 |
| 14 | m | 1 | NAG | C8-C7-N2-C2 |
| 14 | m | 1 | NAG | O7-C7-N2-C2 |
| 14 | v | 1 | NAG | C8-C7-N2-C2 |
| 14 | v | 1 | NAG | O7-C7-N2-C2 |
| 12 | j | 1 | NAG | O5-C5-C6-O6 |
| 14 | d | 4 | MAN | O5-C5-C6-O6 |
| 8 | p | 2 | NAG | C4-C5-C6-O6 |
| 10 | Y | 1 | NAG | O5-C5-C6-O6 |
| 12 | a | 4 | MAN | O5-C5-C6-O6 |
| 14 | m | 4 | MAN | O5-C5-C6-O6 |
| 12 | j | 4 | MAN | O5-C5-C6-O6 |
| 10 | q | 1 | NAG | O5-C5-C6-O6 |
| 11 | Z | 1 | NAG | C4-C5-C6-O6 |
| 14 | d | 2 | NAG | O5-C5-C6-O6 |
| 8 | X | 2 | NAG | O5-C5-C6-O6 |
| 8 | E | 1 | NAG | C1-C2-N2-C7 |
| 8 | g | 2 | NAG | O5-C5-C6-O6 |

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| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 12 | a | 4 | MAN | C4-C5-C6-O6 |
| 12 | j | 4 | MAN | C4-C5-C6-O6 |
| 10 | h | 1 | NAG | O5-C5-C6-O6 |
| 8 | e | 3 | BMA | O5-C5-C6-O6 |
| 12 | a | 6 | MAN | O5-C5-C6-O6 |
| 12 | s | 6 | MAN | O5-C5-C6-O6 |
| 8 | u | 1 | NAG | O5-C5-C6-O6 |
| 8 | p | 2 | NAG | O5-C5-C6-O6 |
| 11 | i | 1 | NAG | O5-C5-C6-O6 |
| 11 | i | 2 | NAG | O5-C5-C6-O6 |
| 11 | r | 1 | NAG | O5-C5-C6-O6 |
| 11 | r | 2 | NAG | O5-C5-C6-O6 |
| 8 | n | 2 | NAG | O5-C5-C6-O6 |
| 11 | Z | 2 | NAG | O5-C5-C6-O6 |
| 8 | l | 1 | NAG | O5-C5-C6-O6 |
| 14 | v | 2 | NAG | O5-C5-C6-O6 |
| 12 | j | 6 | MAN | O5-C5-C6-O6 |
| 12 | s | 2 | NAG | C4-C5-C6-O6 |
| 8 | c | 1 | NAG | O5-C5-C6-O6 |
| 14 | v | 4 | MAN | O5-C5-C6-O6 |
| 12 | a | 2 | NAG | C4-C5-C6-O6 |
| 12 | j | 2 | NAG | C4-C5-C6-O6 |
| 8 | n | 3 | BMA | O5-C5-C6-O6 |
| 10 | h | 3 | BMA | O5-C5-C6-O6 |
| 12 | s | 1 | NAG | C4-C5-C6-O6 |
| 8 | p | 4 | MAN | O5-C5-C6-O6 |
| 8 | e | 2 | NAG | C4-C5-C6-O6 |
| 14 | v | 4 | MAN | C4-C5-C6-O6 |
| 8 | X | 4 | MAN | O5-C5-C6-O6 |
| 8 | g | 4 | MAN | O5-C5-C6-O6 |
| 8 | e | 4 | MAN | C4-C5-C6-O6 |
| 8 | E | 3 | BMA | O5-C5-C6-O6 |
| 9 | P | 3 | BMA | O5-C5-C6-O6 |
| 9 | o | 3 | BMA | O5-C5-C6-O6 |
| 10 | Y | 3 | BMA | O5-C5-C6-O6 |
| 10 | q | 3 | BMA | O5-C5-C6-O6 |
| 8 | E | 1 | NAG | C4-C5-C6-O6 |
| 12 | j | 5 | MAN | C4-C5-C6-O6 |
| 9 | f | 3 | BMA | O5-C5-C6-O6 |
| 14 | d | 5 | MAN | O5-C5-C6-O6 |
| 12 | a | 5 | MAN | C4-C5-C6-O6 |
| 12 | s | 1 | NAG | O5-C5-C6-O6 |

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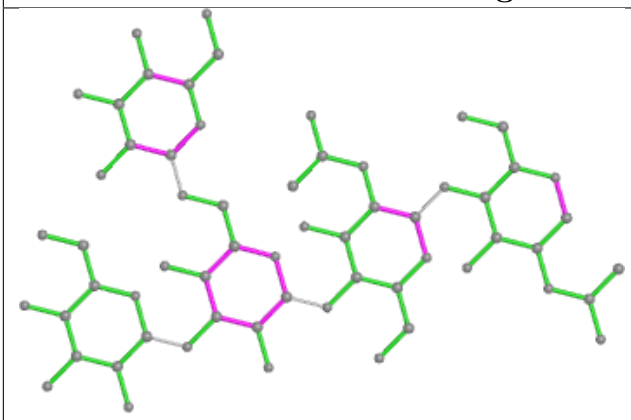
| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 12 | a | 1 | NAG | C4-C5-C6-O6 |
| 14 | m | 2 | NAG | O5-C5-C6-O6 |
| 14 | d | 5 | MAN | C4-C5-C6-O6 |
| 8 | e | 2 | NAG | O5-C5-C6-O6 |
| 14 | d | 2 | NAG | C4-C5-C6-O6 |
| 8 | n | 2 | NAG | C1-C2-N2-C7 |
| 8 | E | 2 | NAG | C1-C2-N2-C7 |
| 14 | v | 5 | MAN | C4-C5-C6-O6 |
| 14 | d | 1 | NAG | C4-C5-C6-O6 |
| 14 | v | 5 | MAN | O5-C5-C6-O6 |
| 14 | m | 4 | MAN | C4-C5-C6-O6 |
| 14 | d | 4 | MAN | C4-C5-C6-O6 |
| 12 | a | 1 | NAG | O5-C5-C6-O6 |
| 8 | E | 1 | NAG | C3-C2-N2-C7 |
| 9 | P | 1 | NAG | C3-C2-N2-C7 |
| 9 | f | 1 | NAG | C3-C2-N2-C7 |
| 9 | o | 1 | NAG | C3-C2-N2-C7 |
| 14 | d | 1 | NAG | C3-C2-N2-C7 |
| 11 | r | 6 | MAN | O5-C5-C6-O6 |
| 14 | m | 5 | MAN | O5-C5-C6-O6 |
| 11 | Z | 1 | NAG | O5-C5-C6-O6 |
| 14 | m | 5 | MAN | C4-C5-C6-O6 |
| 14 | m | 1 | NAG | C4-C5-C6-O6 |
| 10 | h | 2 | NAG | O5-C5-C6-O6 |
| 12 | s | 2 | NAG | C1-C2-N2-C7 |
| 14 | v | 2 | NAG | C4-C5-C6-O6 |
| 8 | e | 1 | NAG | C3-C2-N2-C7 |
| 10 | q | 2 | NAG | C3-C2-N2-C7 |
| 14 | m | 1 | NAG | C3-C2-N2-C7 |
| 14 | v | 1 | NAG | C3-C2-N2-C7 |
| 14 | d | 1 | NAG | O5-C5-C6-O6 |

There are no ring outliers.

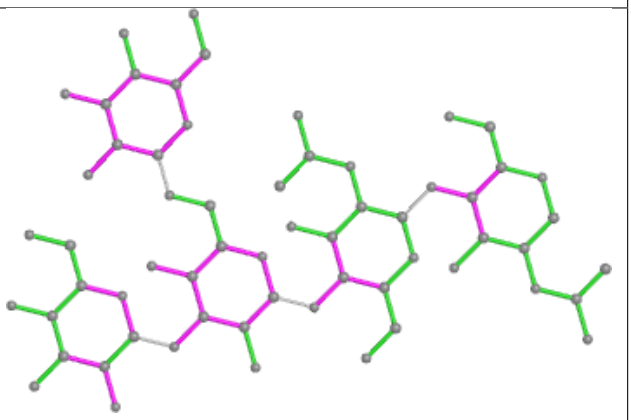
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

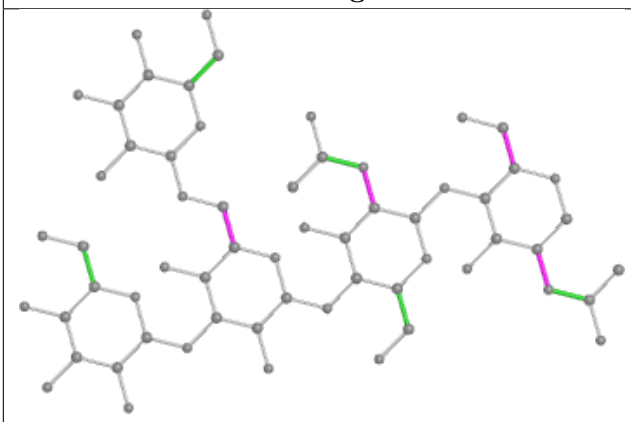
**Oligosaccharide Chain E**



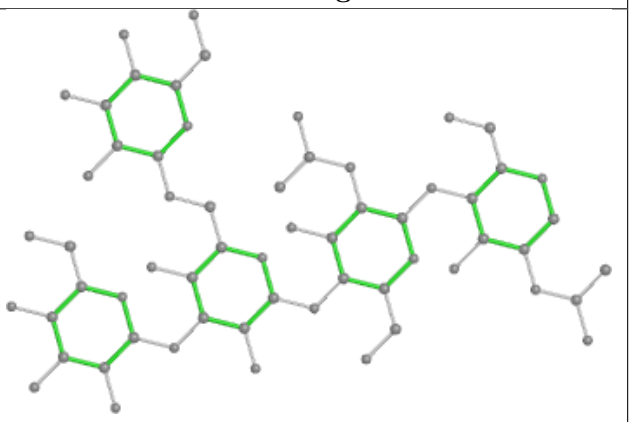
**Bond lengths**



**Bond angles**

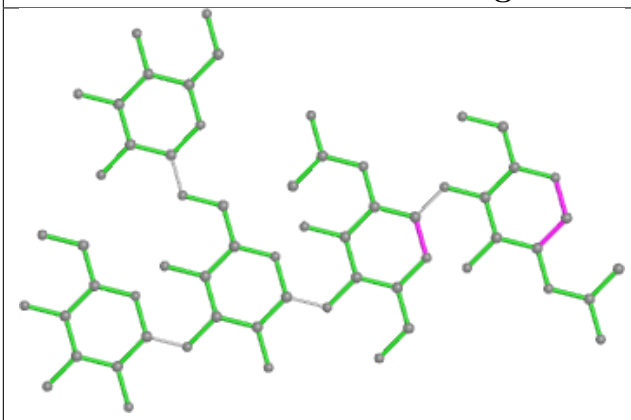


**Torsions**

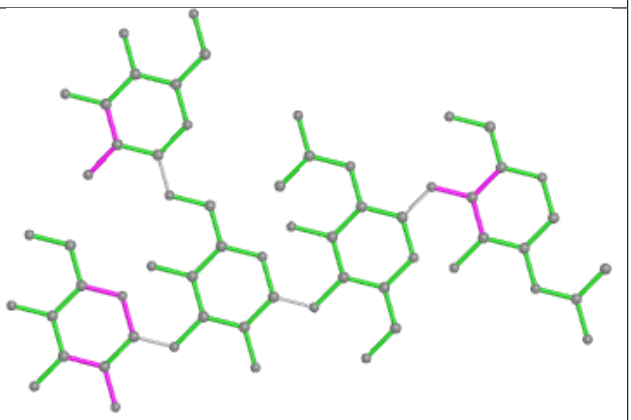


**Rings**

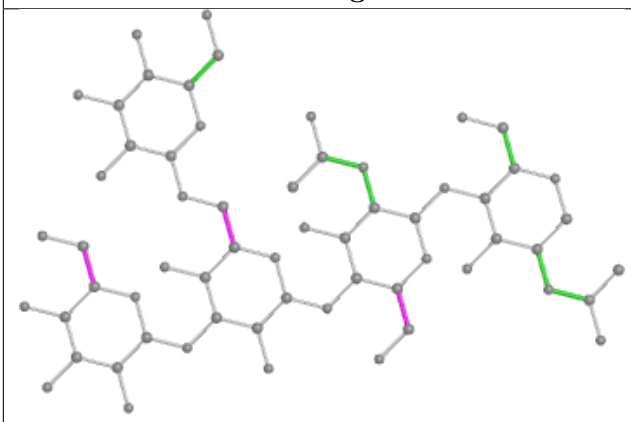
**Oligosaccharide Chain X**



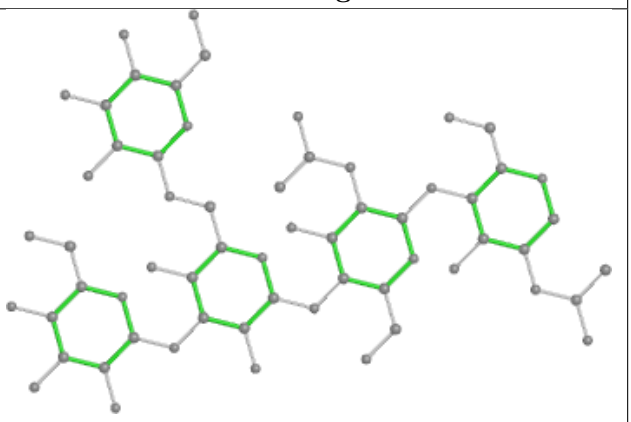
**Bond lengths**



**Bond angles**

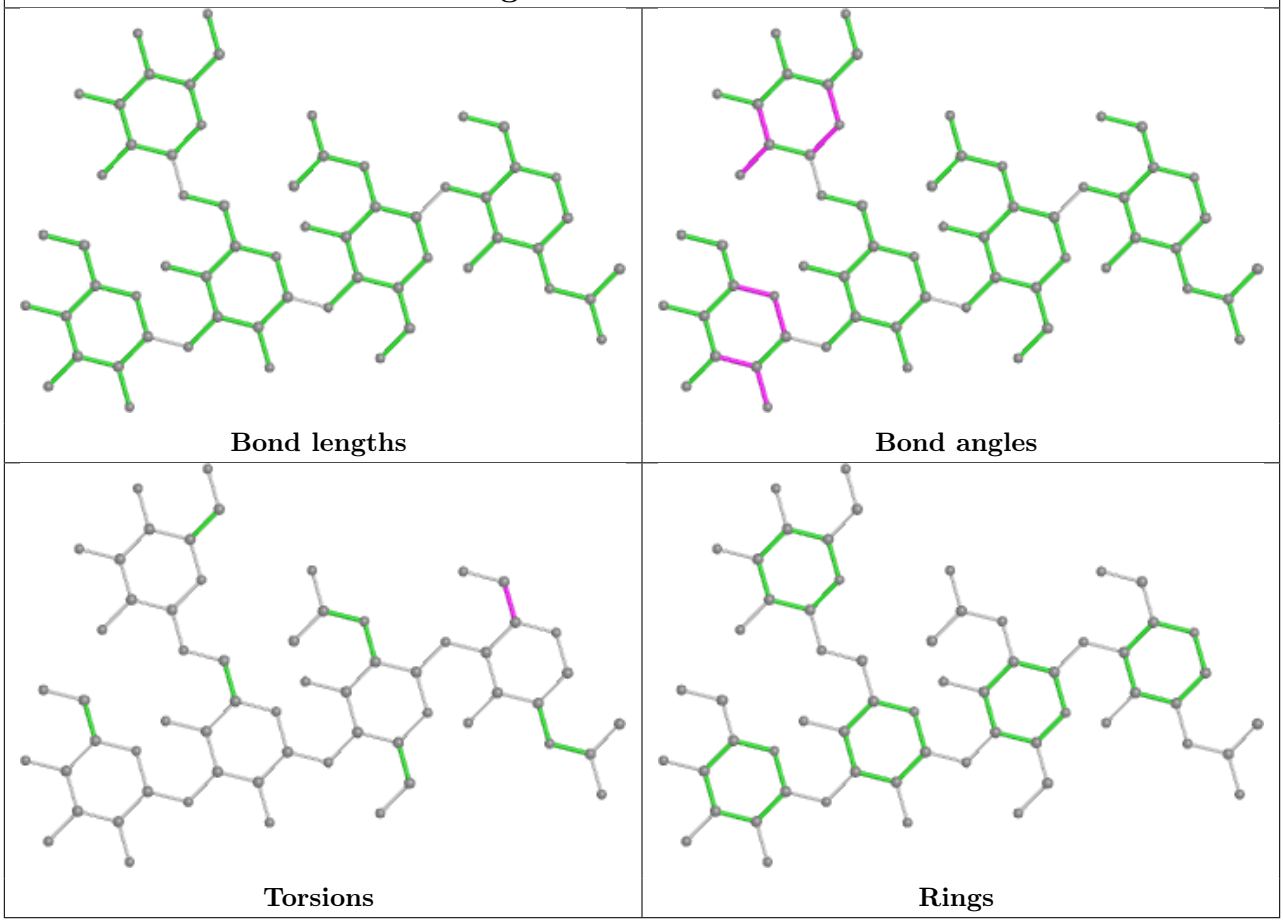


**Torsions**

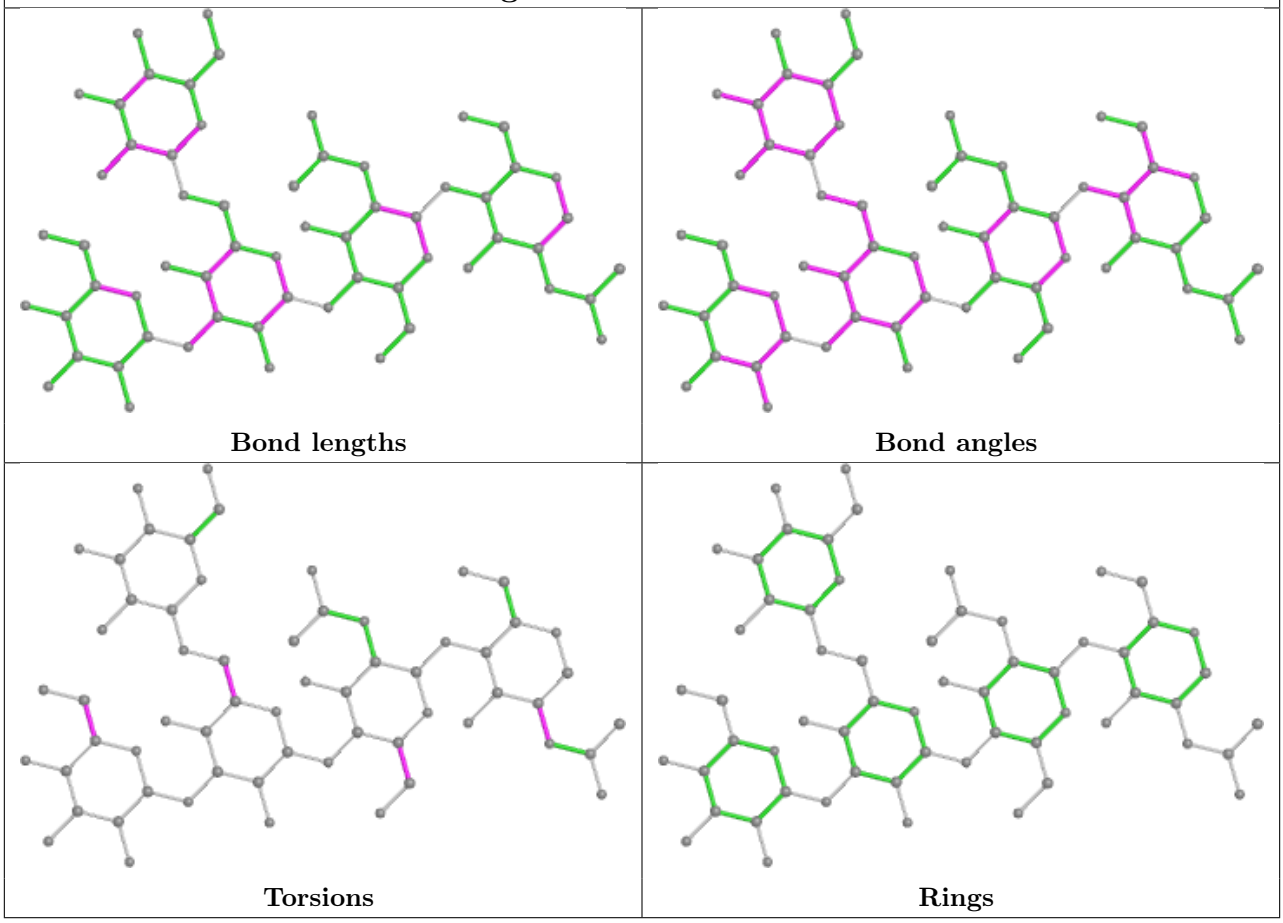


**Rings**

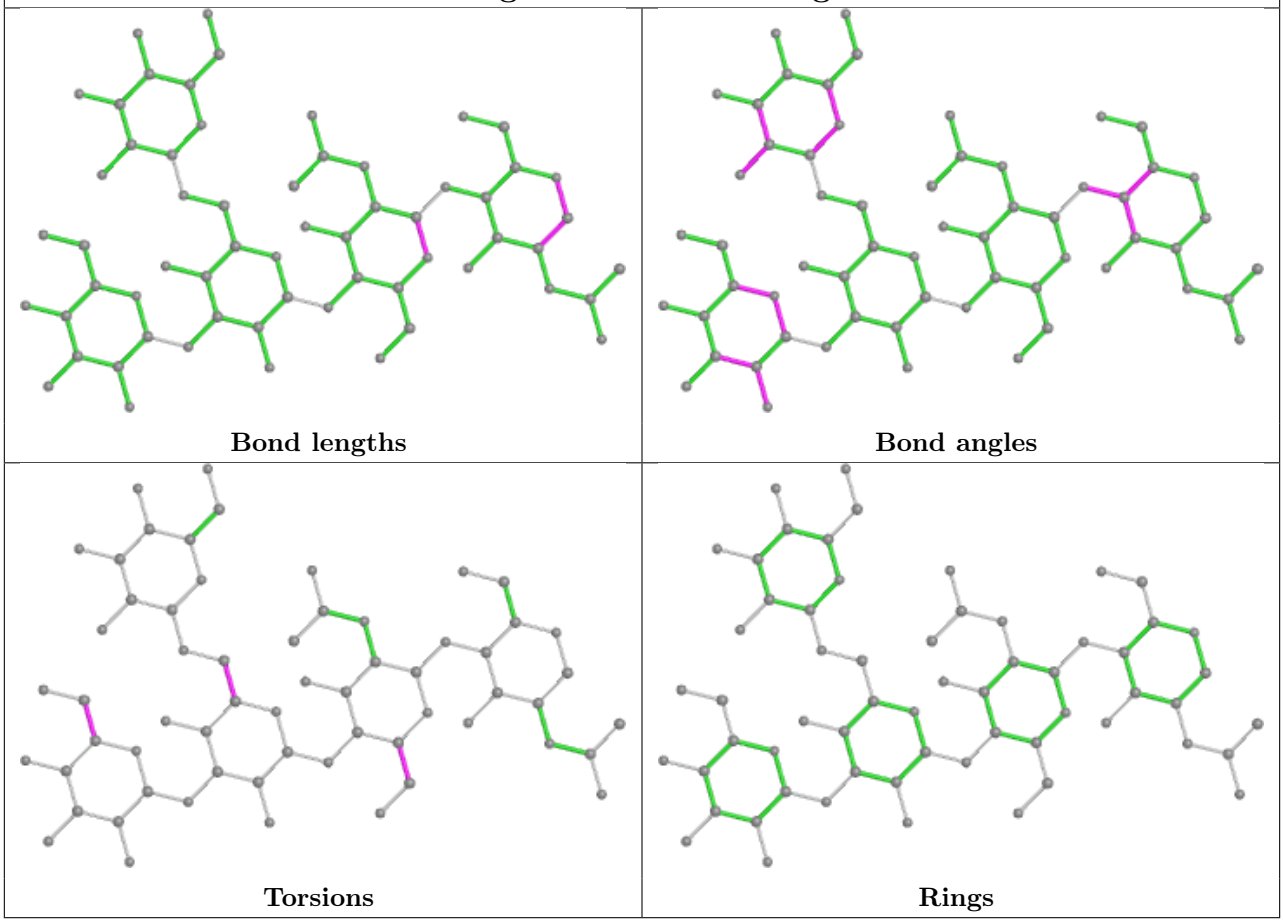
**Oligosaccharide Chain c**



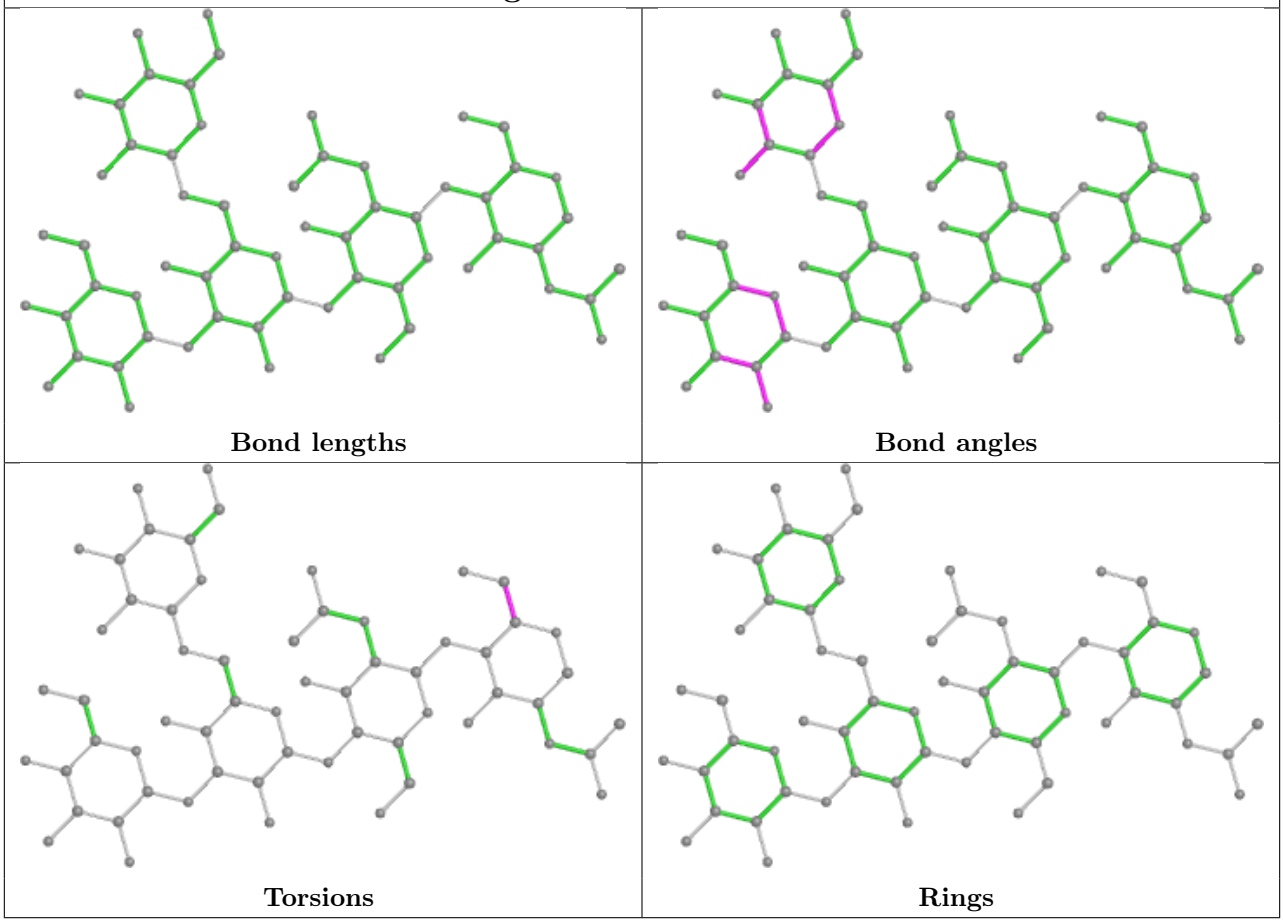
**Oligosaccharide Chain e**



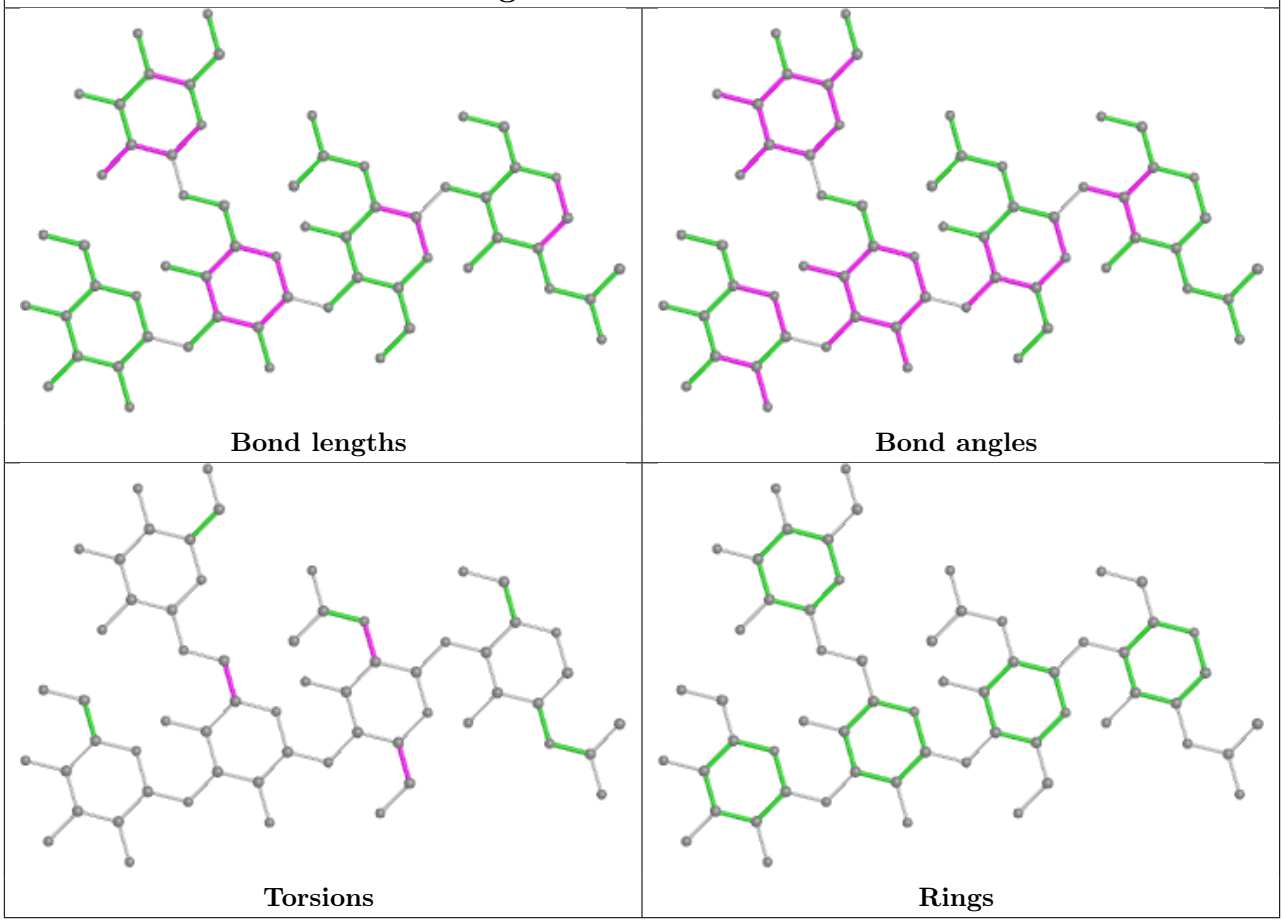
**Oligosaccharide Chain g**



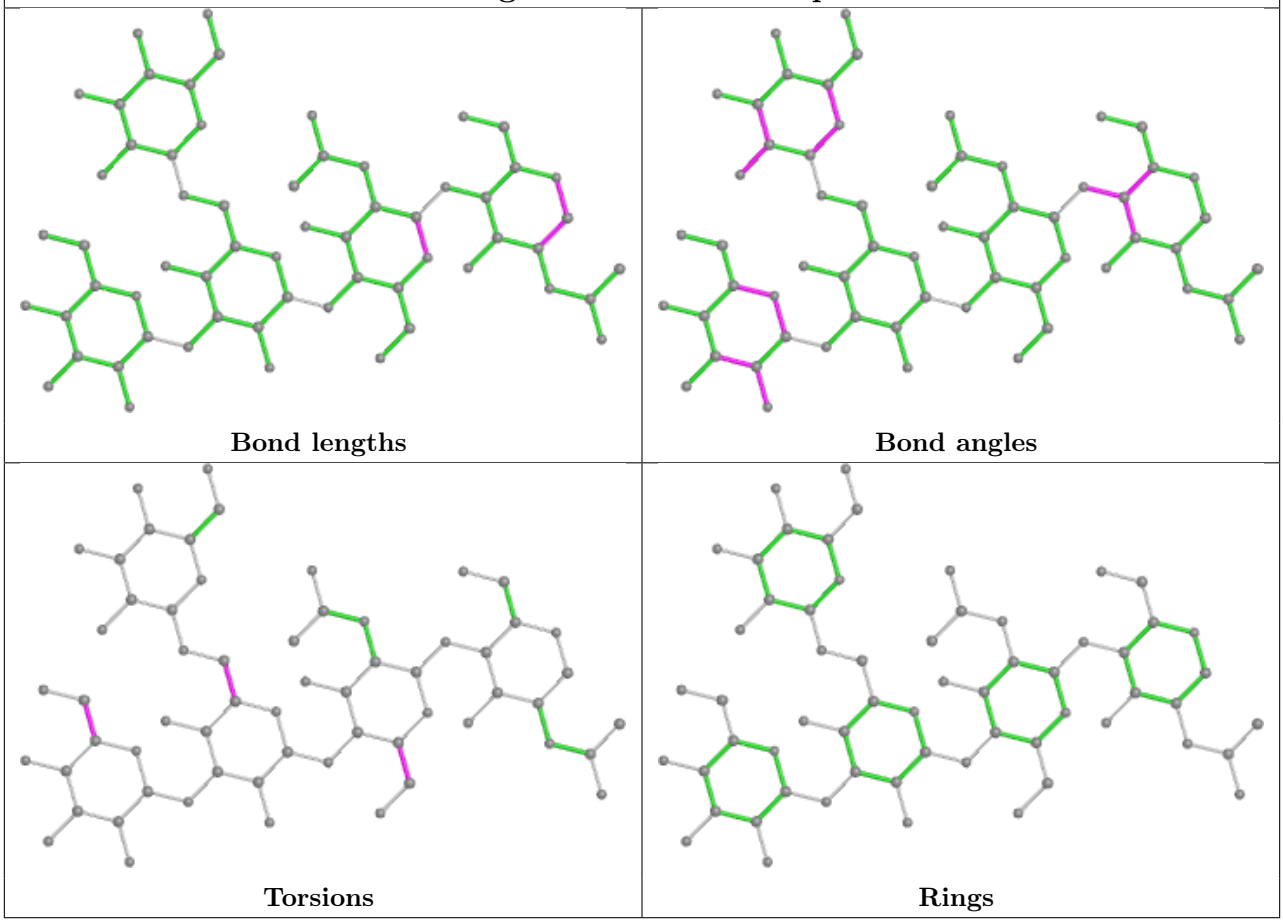
**Oligosaccharide Chain l**



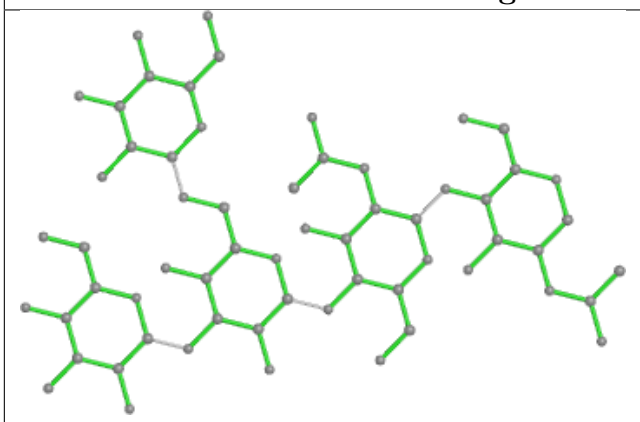
**Oligosaccharide Chain n**



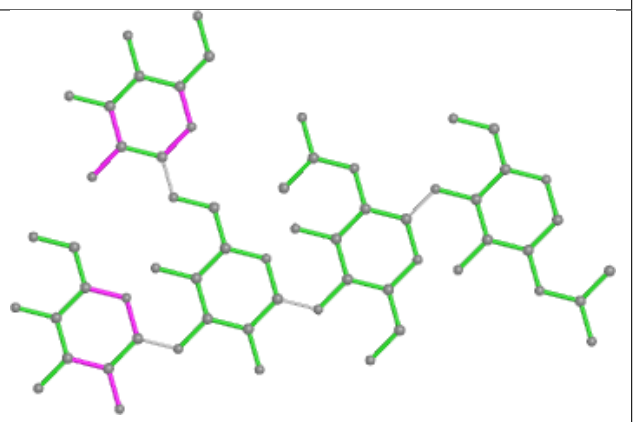
**Oligosaccharide Chain p**



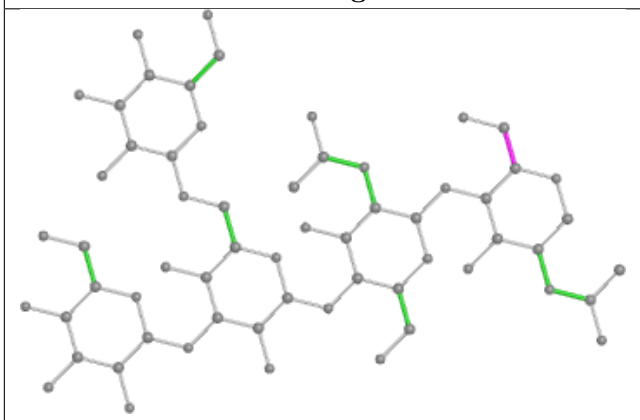
## Oligosaccharide Chain u



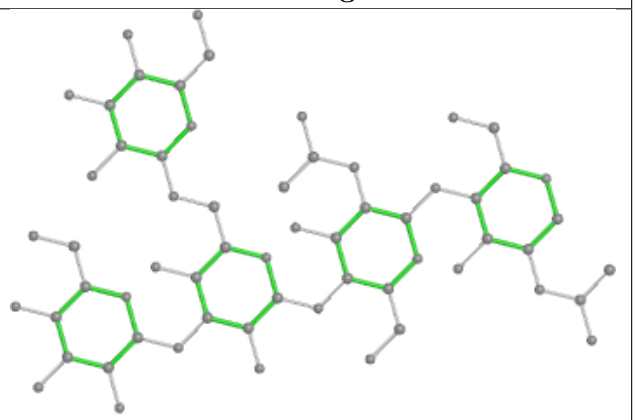
Bond lengths



Bond angles

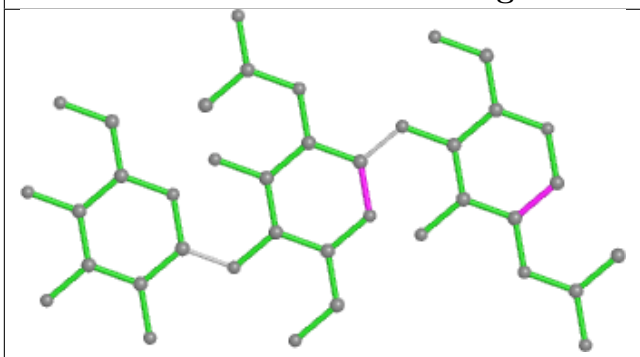


Torsions

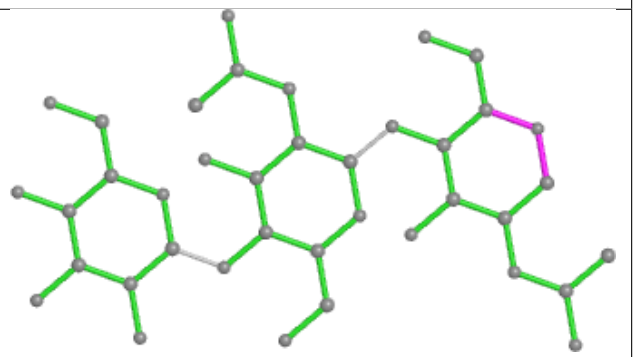


Rings

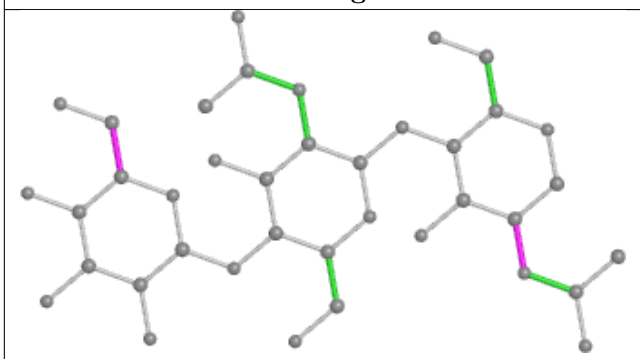
## Oligosaccharide Chain P



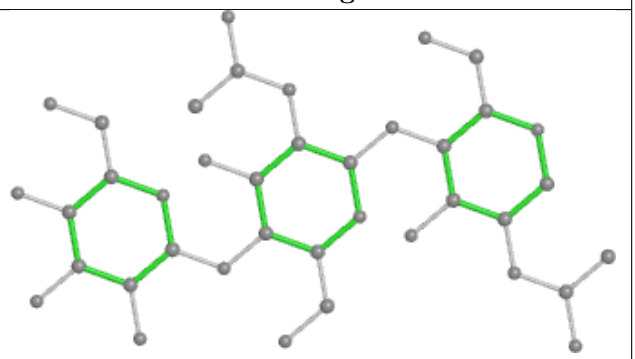
Bond lengths



Bond angles

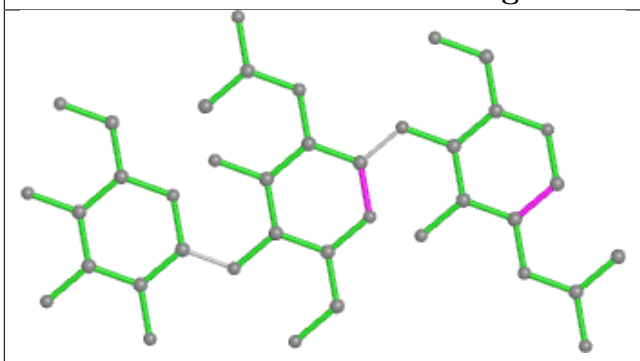


Torsions



Rings

## Oligosaccharide Chain f



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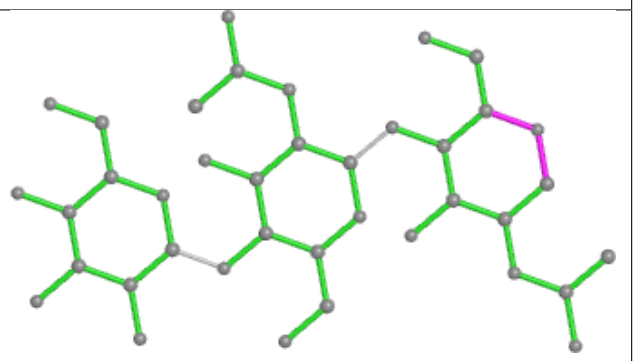
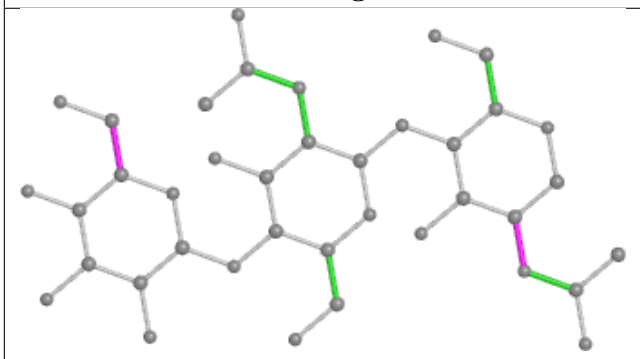


Bond angles



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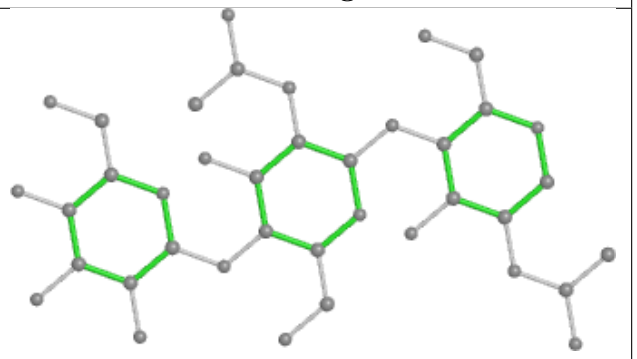
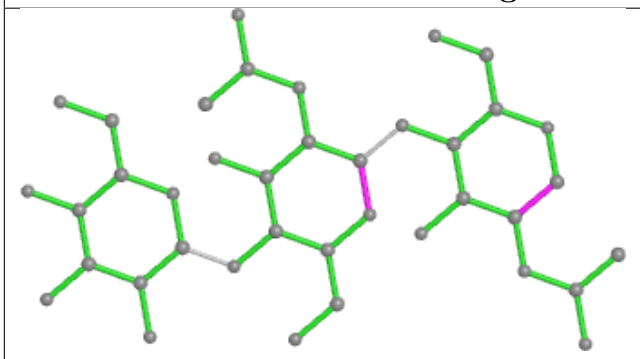


Rings

## Oligosaccharide Chain o



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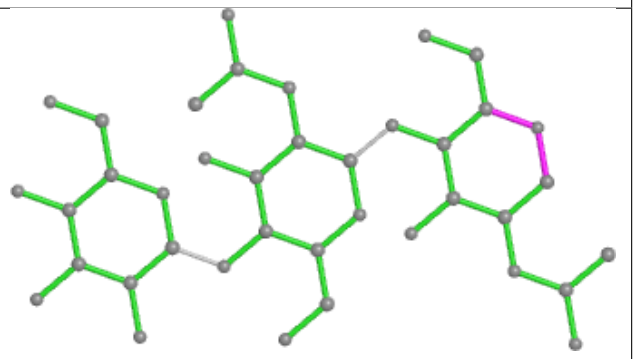
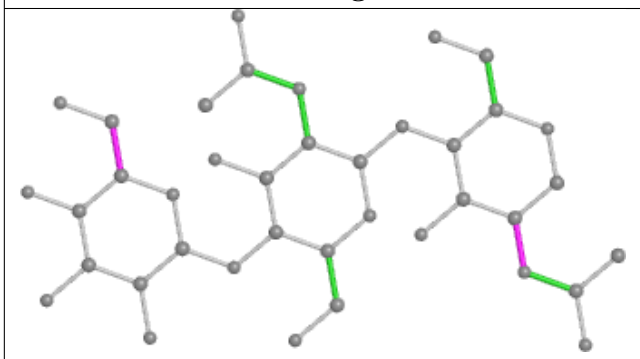


Bond angles



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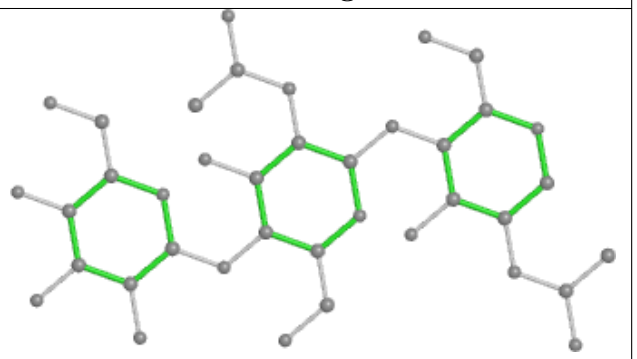
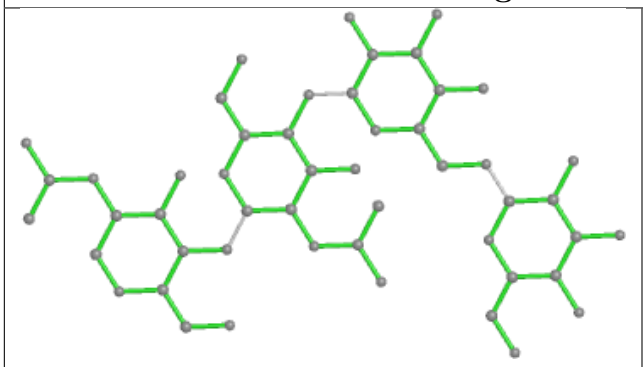


Rings

## Oligosaccharide Chain Y



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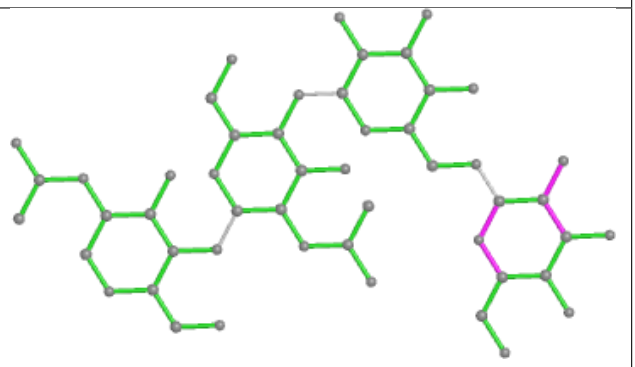

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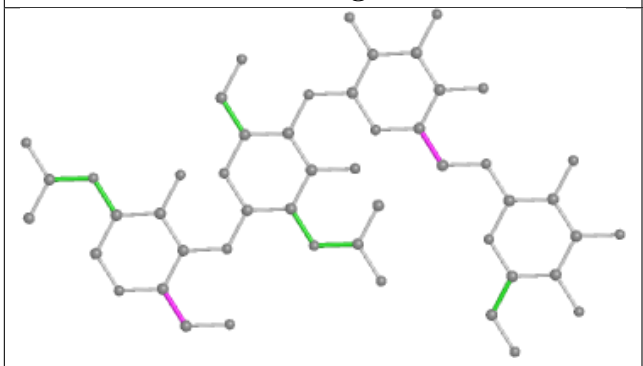
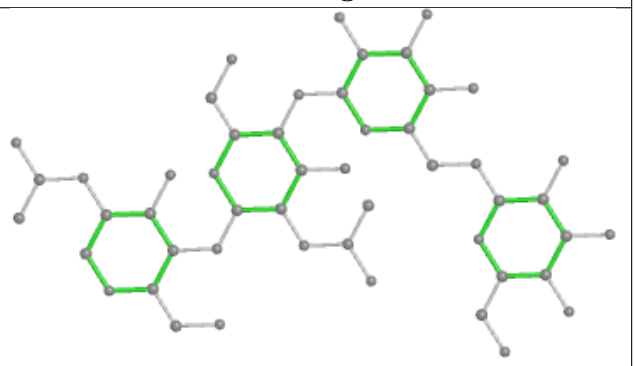
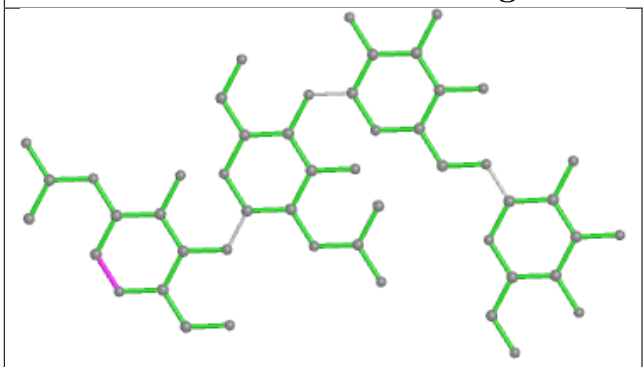


Torsions



Rings

## Oligosaccharide Chain h



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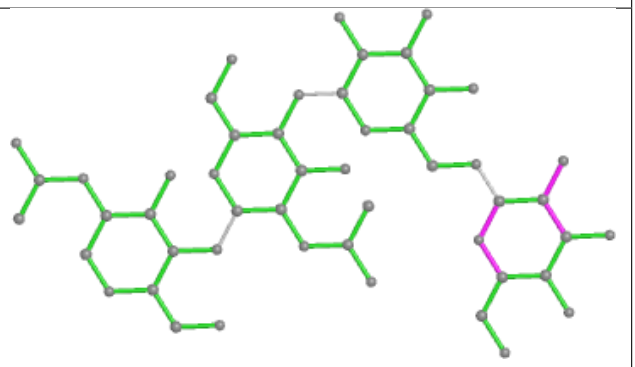

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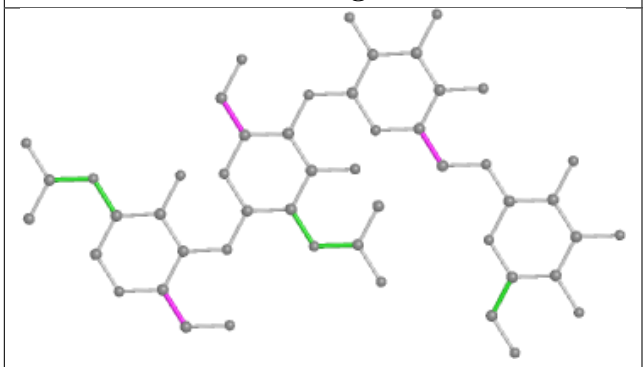

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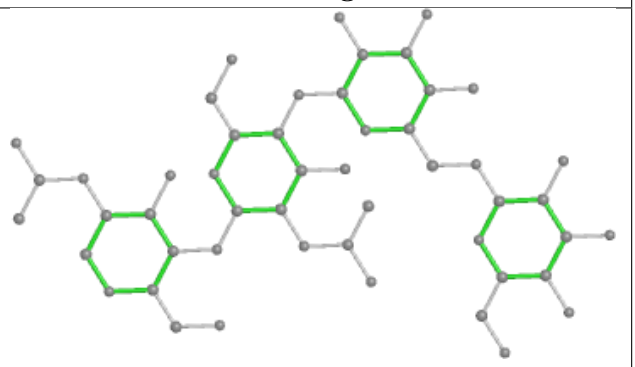
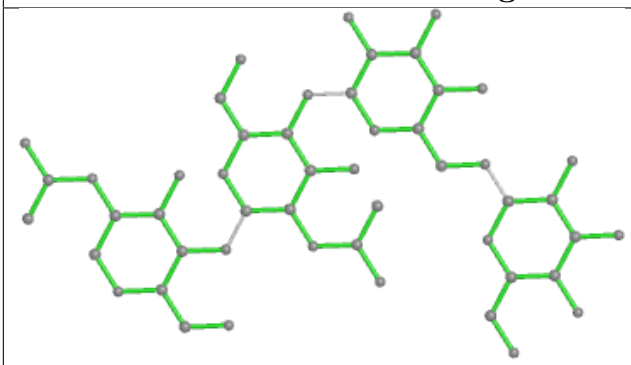
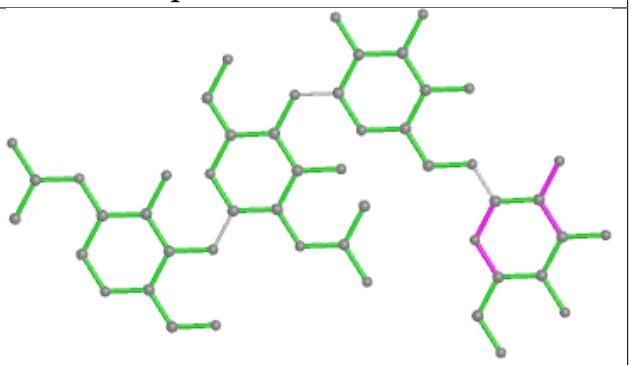
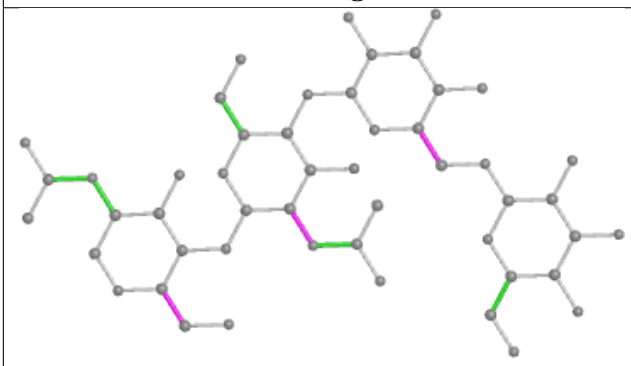
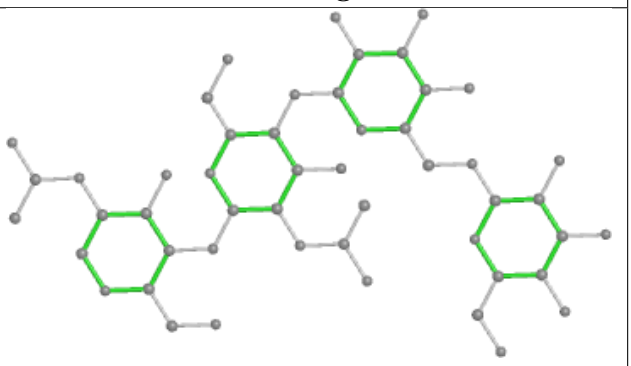


Rings

| Oligosaccharide Chain q | |
|---|---|
|  Bond lengths |  Bond angles |
|  Torsions |  Rings |

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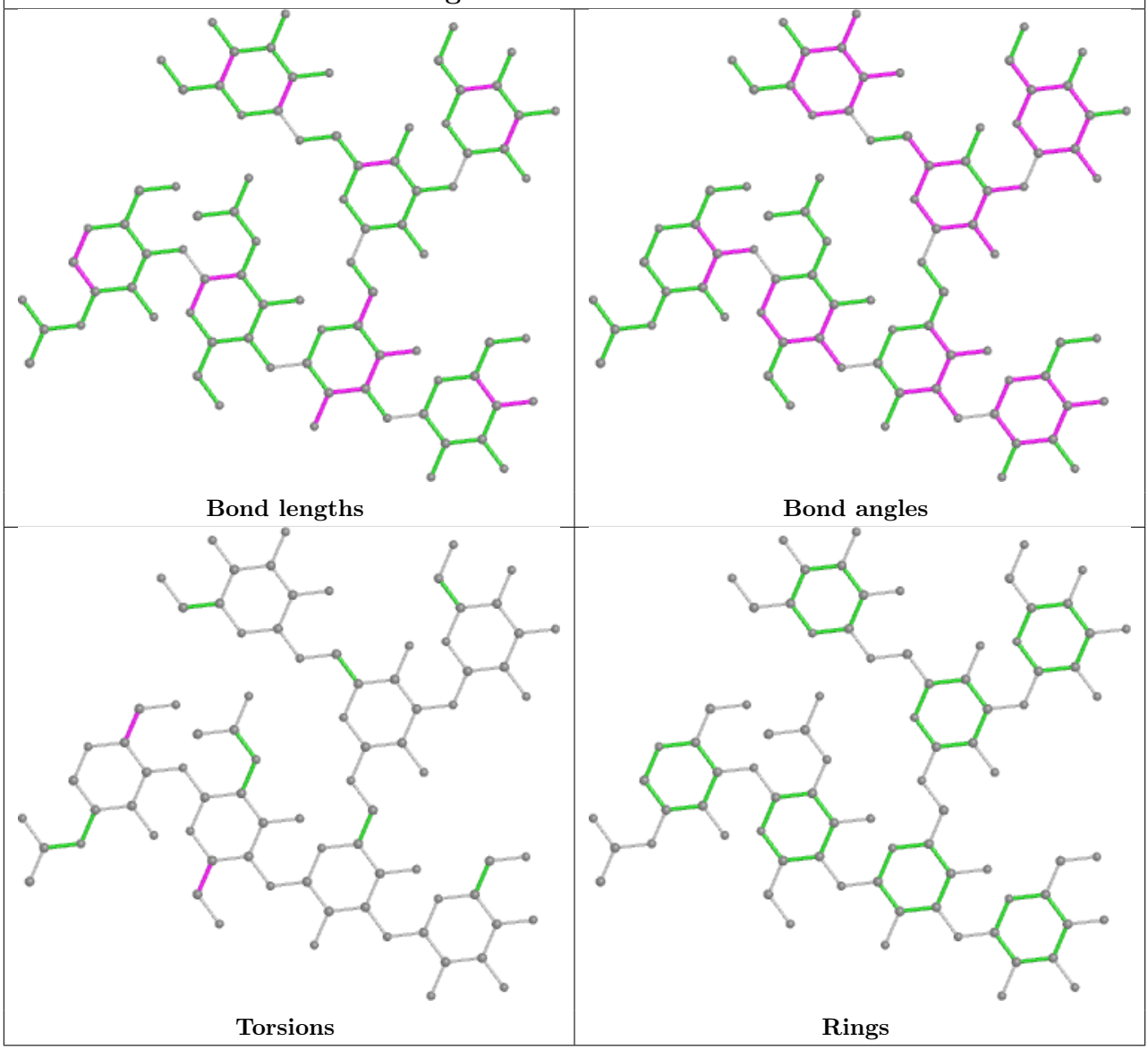
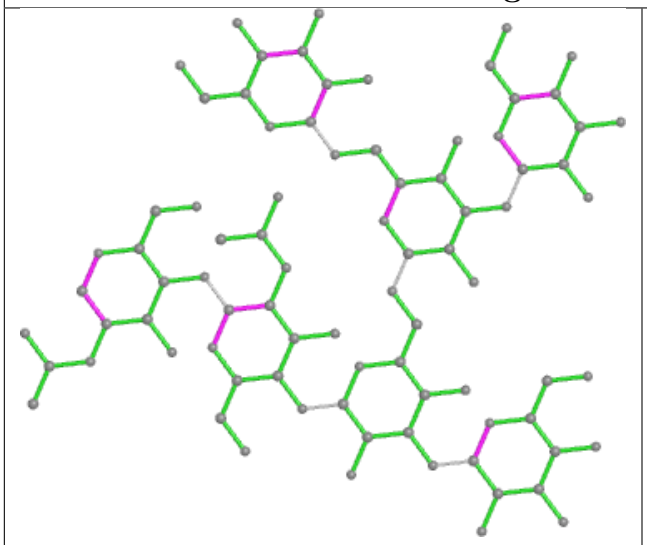
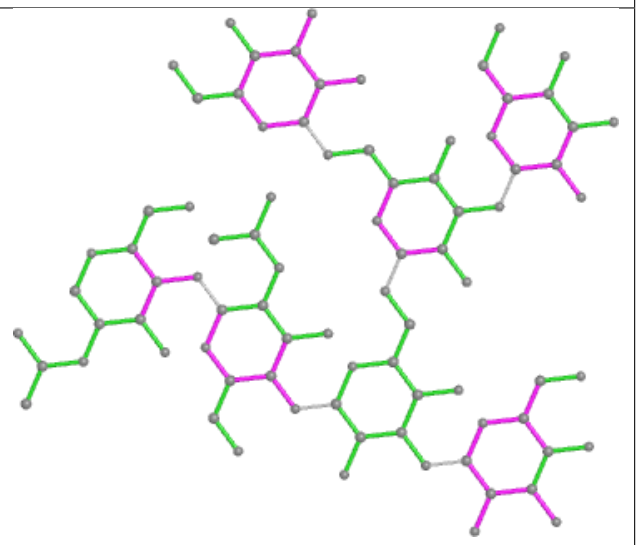


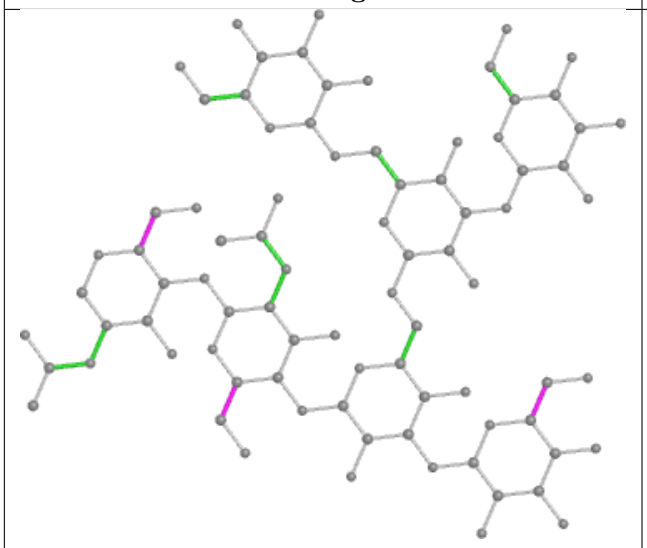
**Oligosaccharide Chain i**



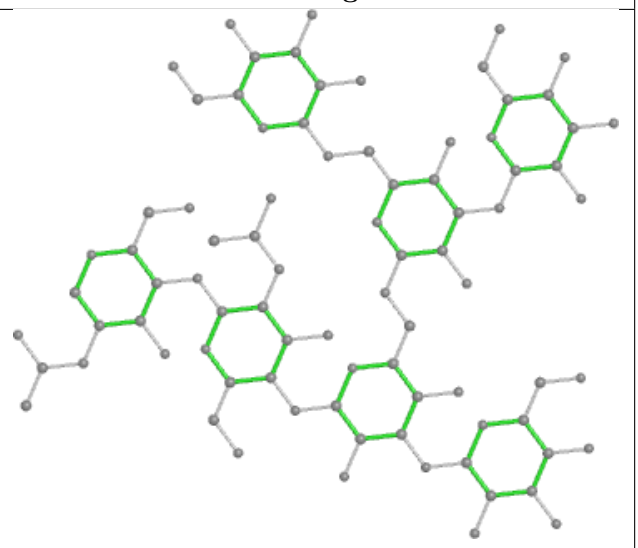
**Bond lengths**



**Bond angles**

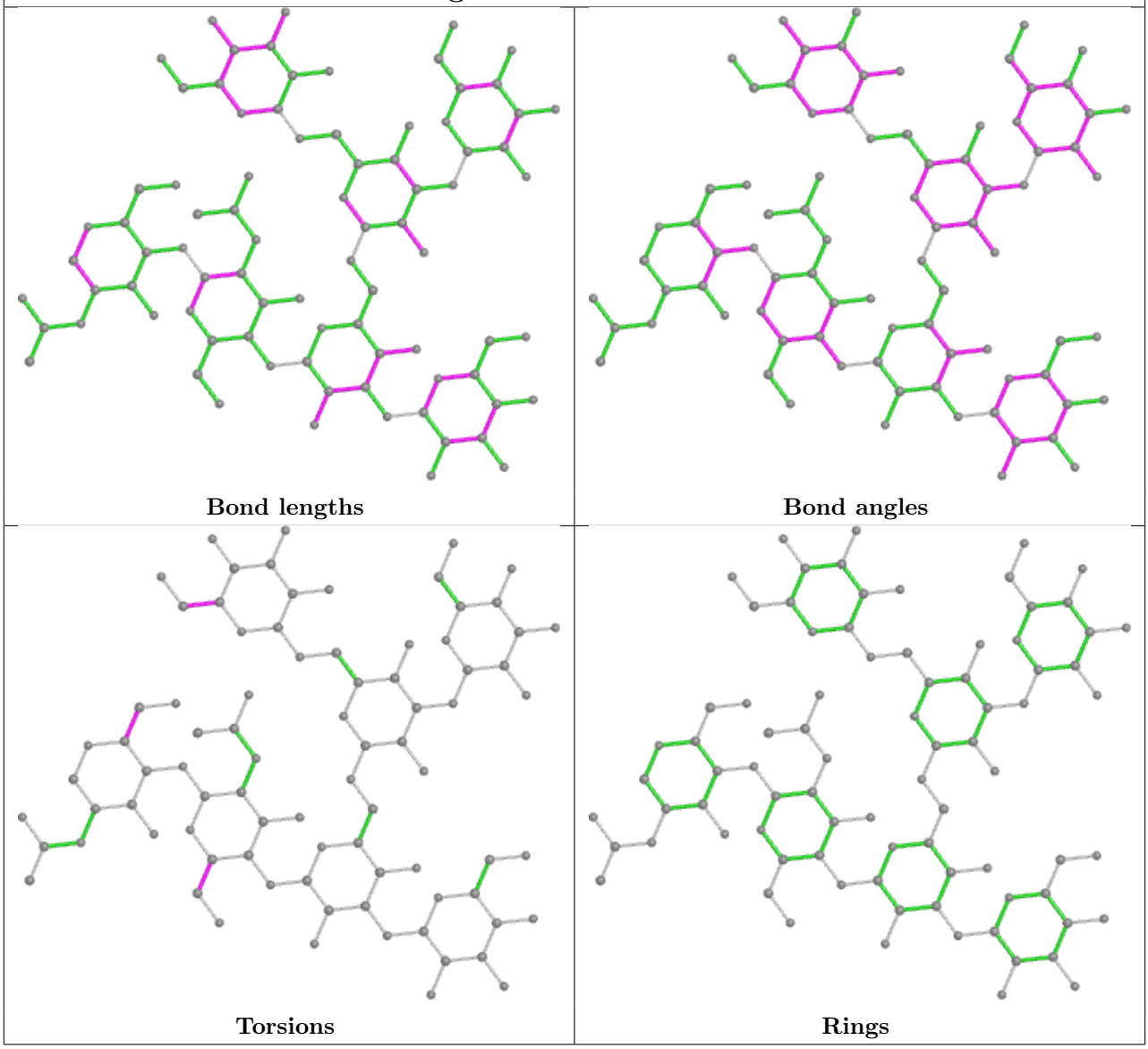


**Torsions**

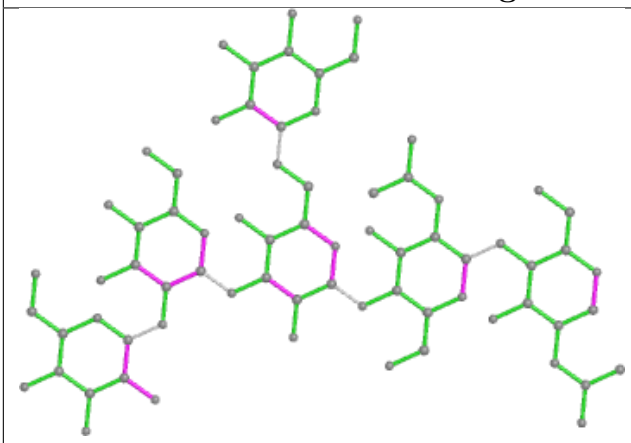


**Rings**

**Oligosaccharide Chain r**



**Oligosaccharide Chain a**



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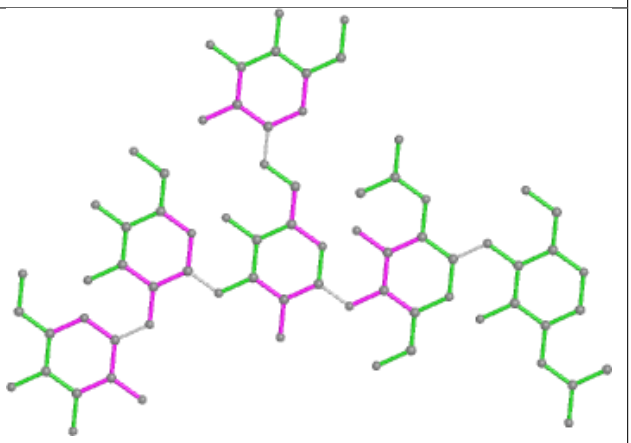

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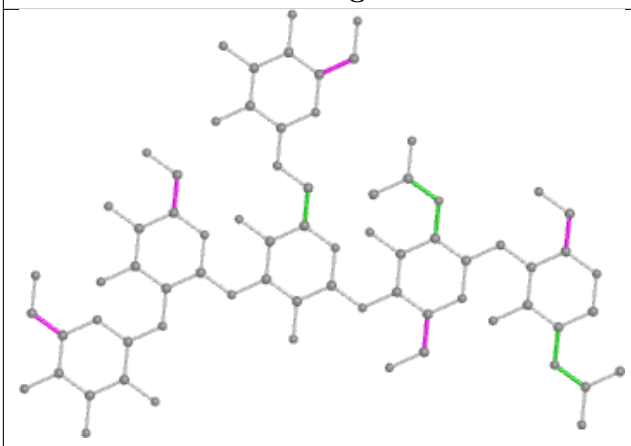

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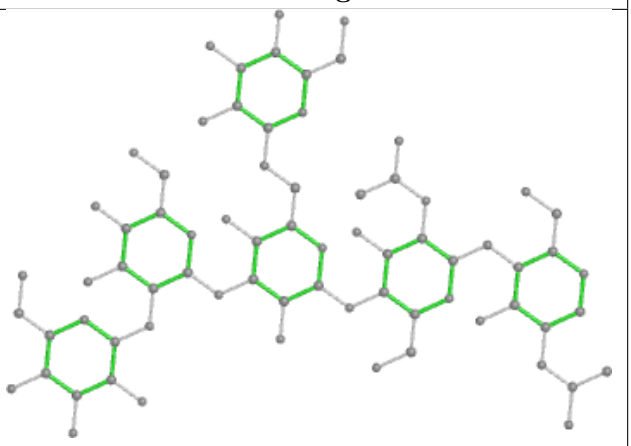
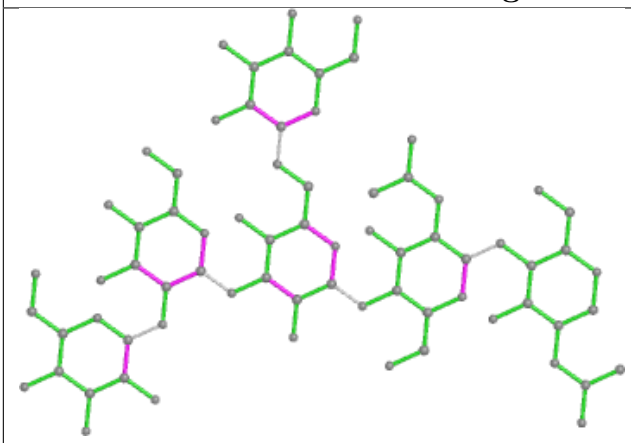


**Rings**

**Oligosaccharide Chain j**



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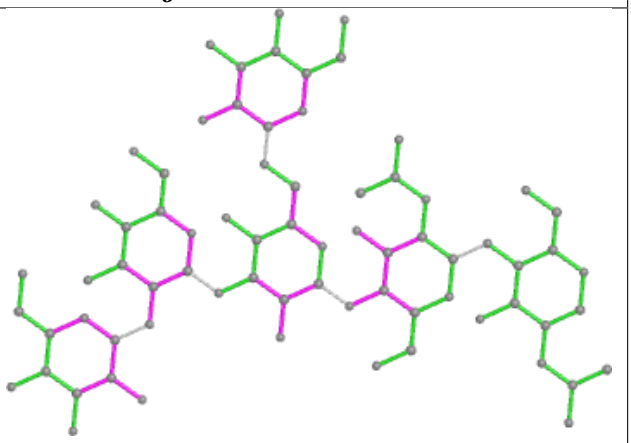

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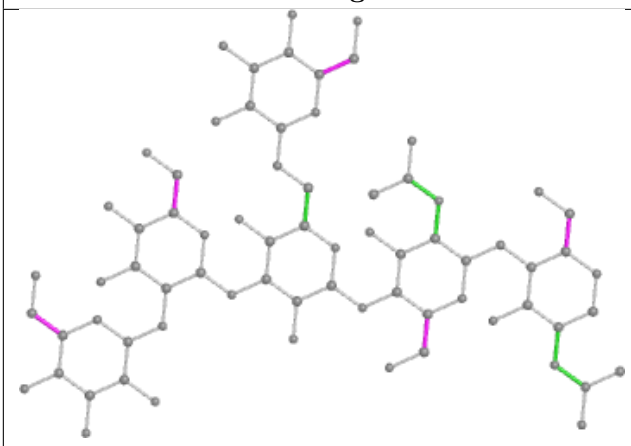

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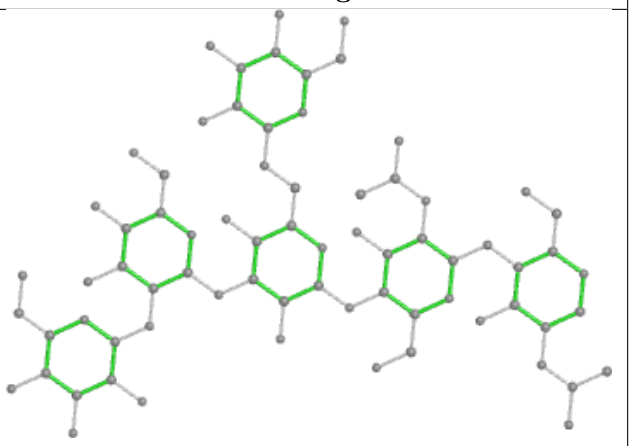
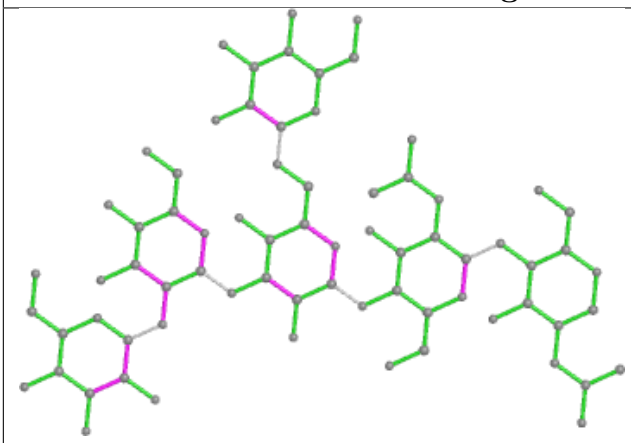


**Rings**

**Oligosaccharide Chain s**



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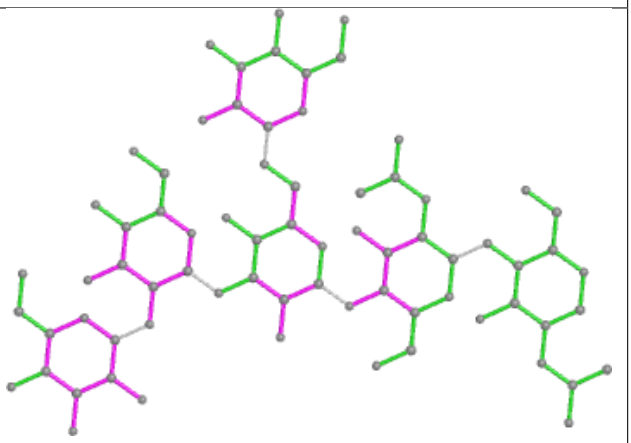
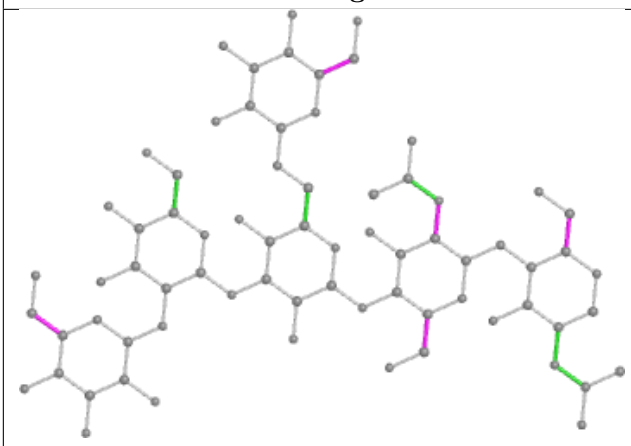
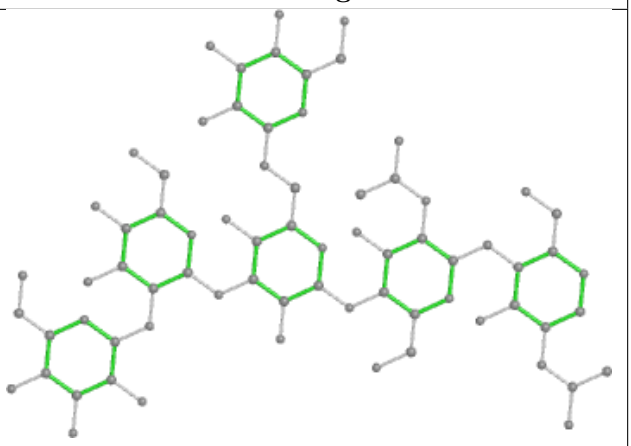


**Bond angles**

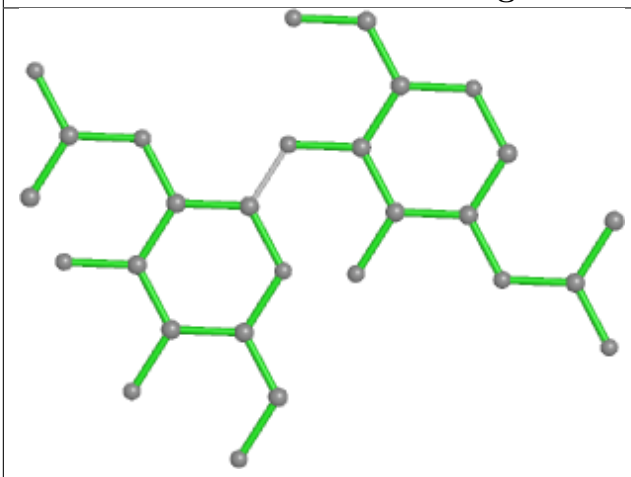


**Torsions**



**Rings**

**Oligosaccharide Chain b**



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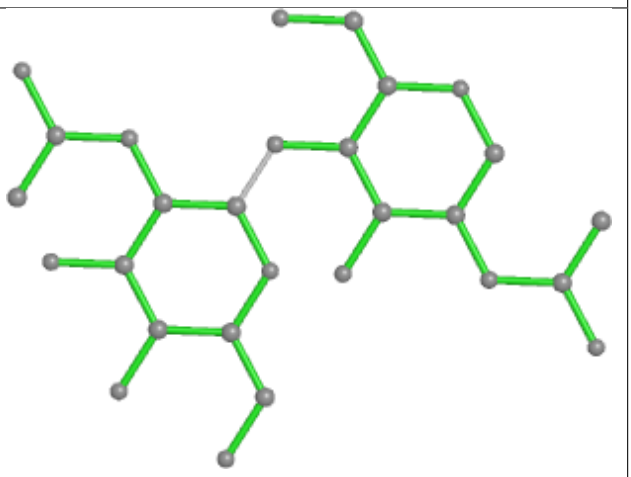
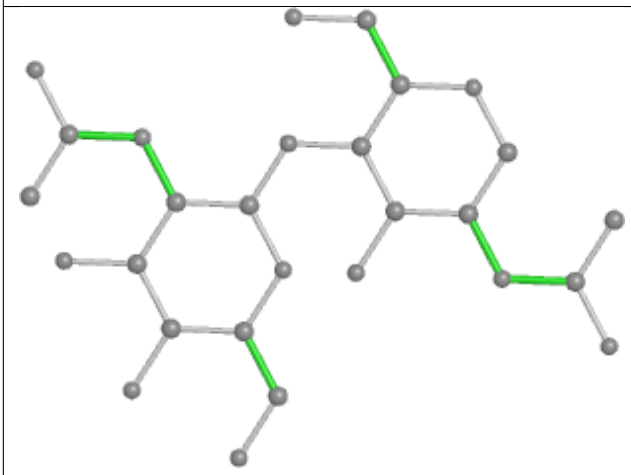
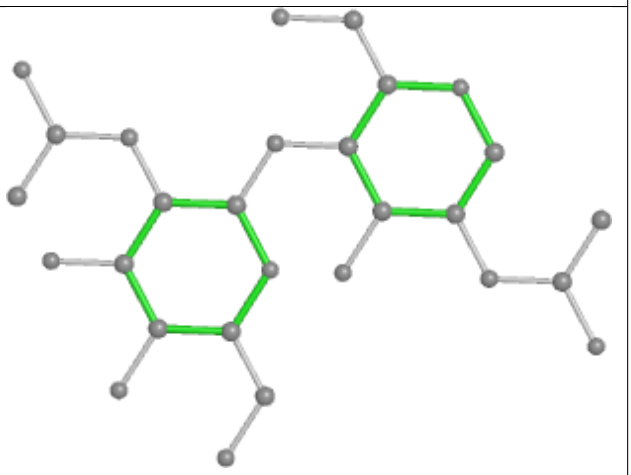


**Bond angles**

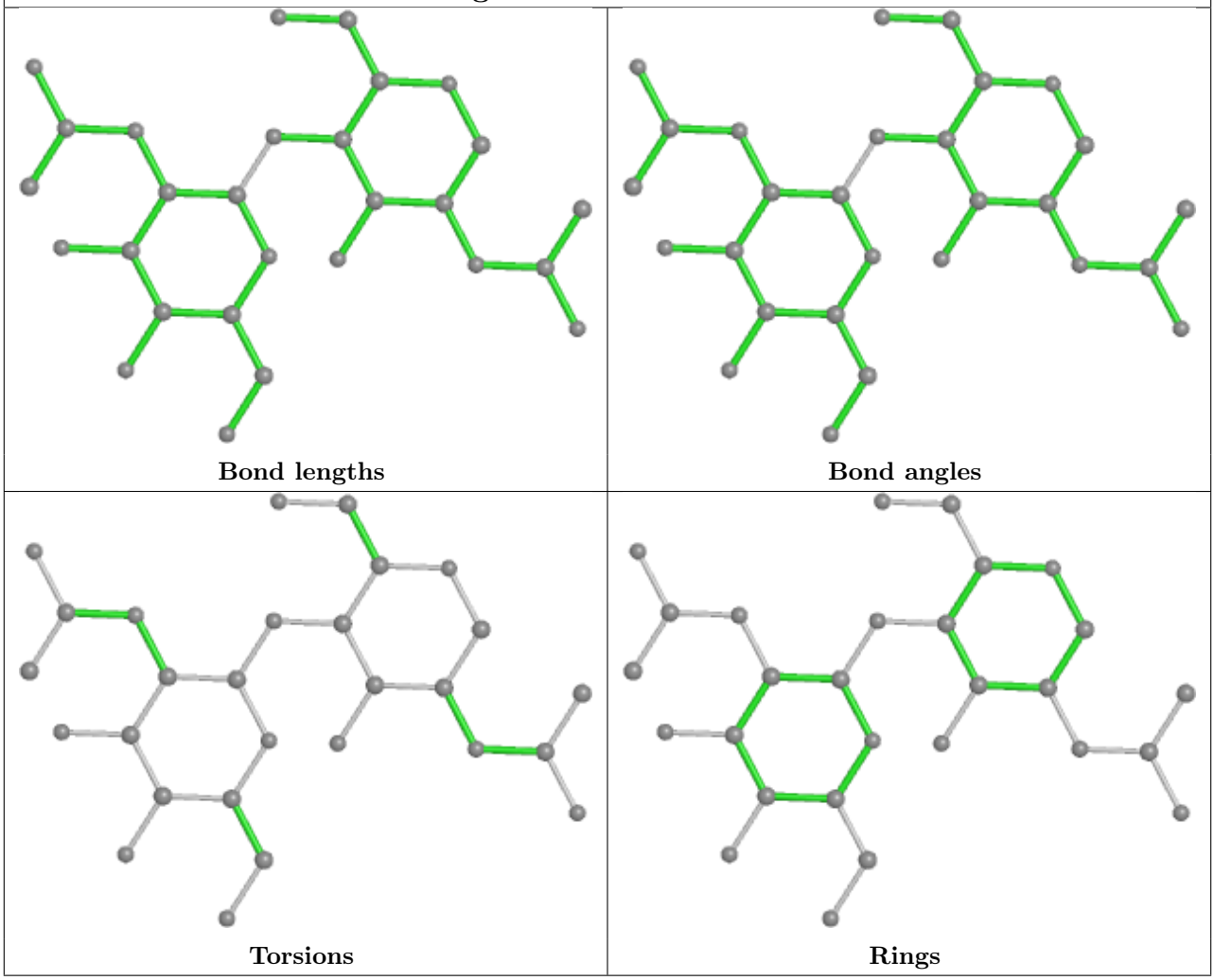


**Torsions**

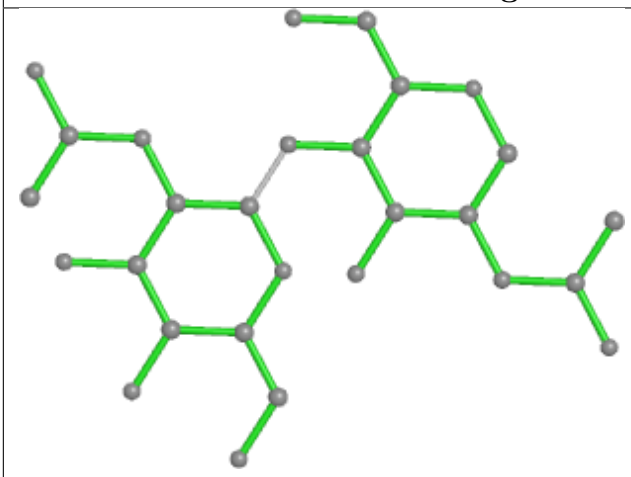


**Rings**

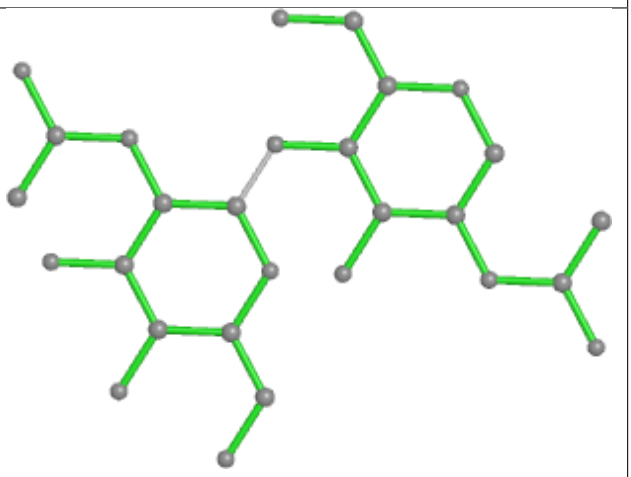
**Oligosaccharide Chain k**



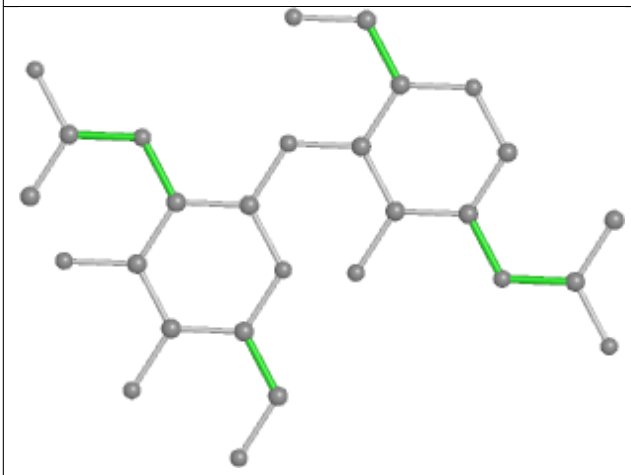
**Oligosaccharide Chain t**



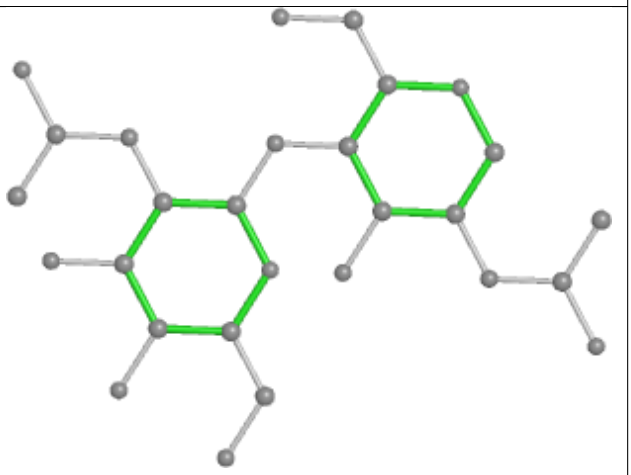
**Bond lengths**



**Bond angles**

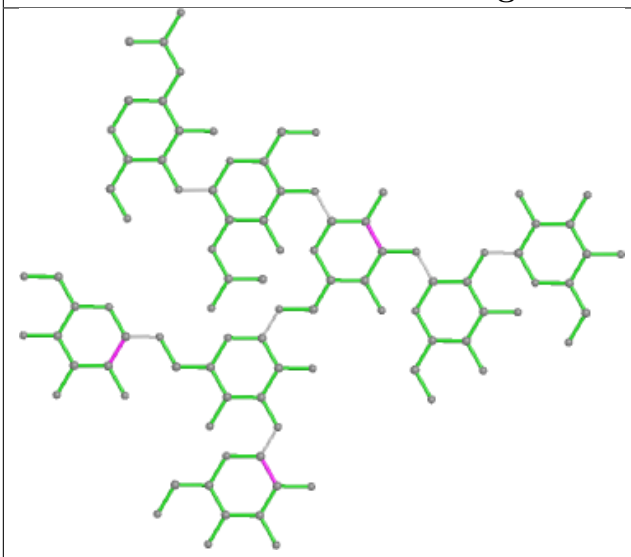


**Torsions**

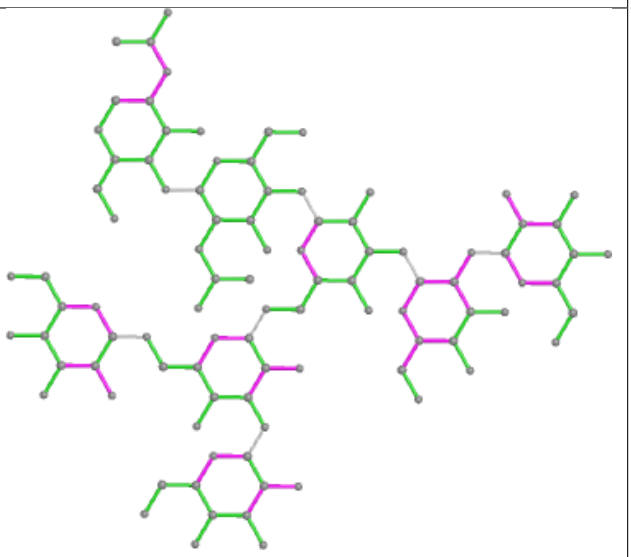


**Rings**

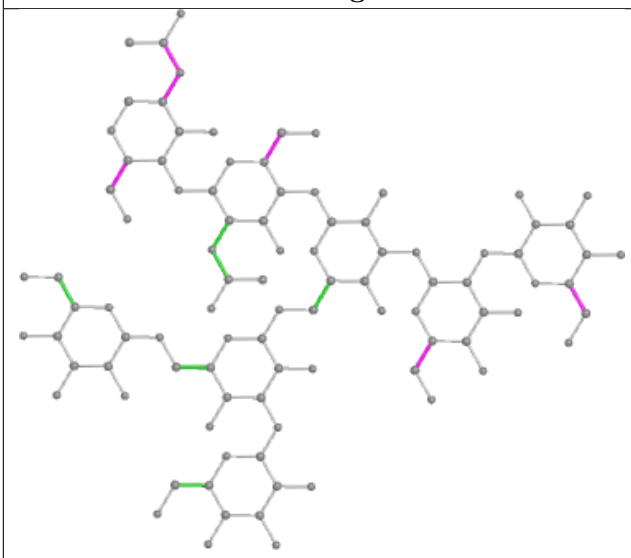
**Oligosaccharide Chain d**



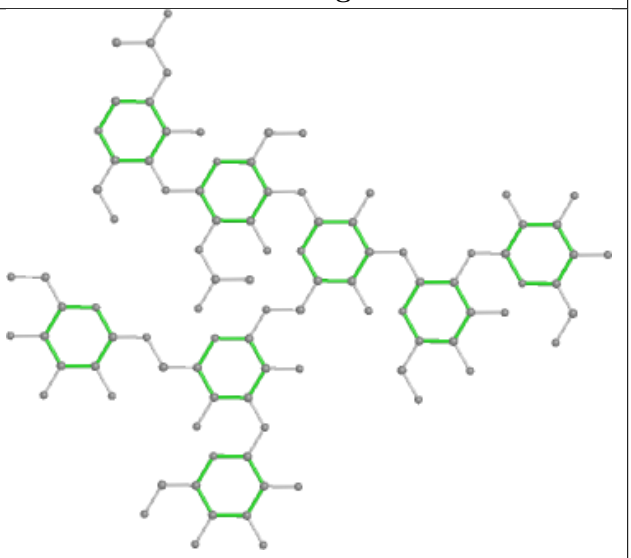
**Bond lengths**



**Bond angles**

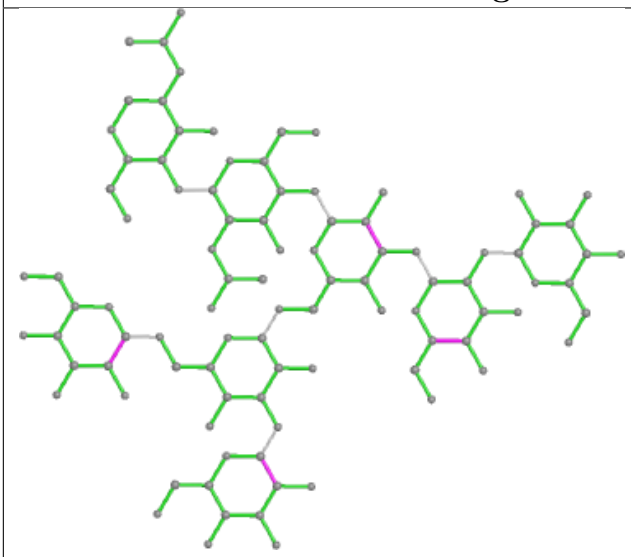


**Torsions**

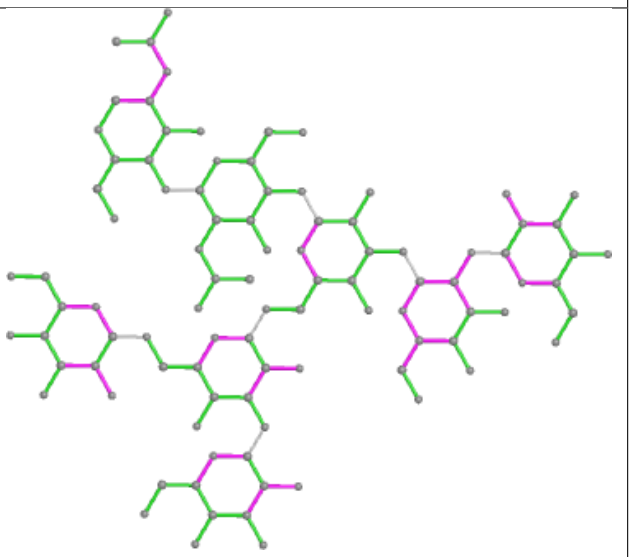


**Rings**

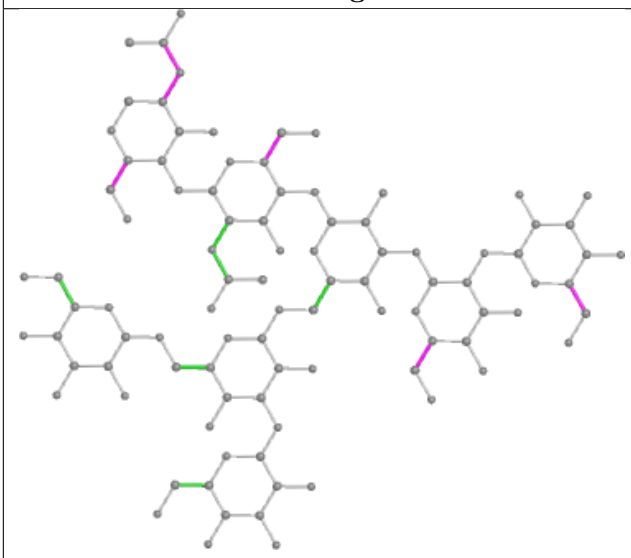
**Oligosaccharide Chain m**



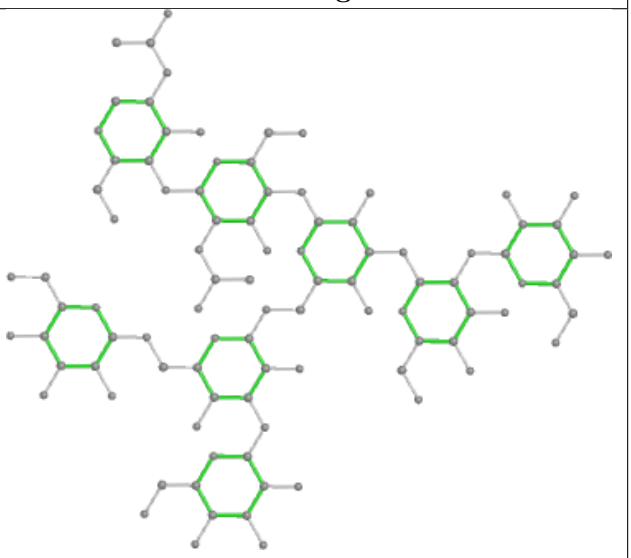
**Bond lengths**



**Bond angles**

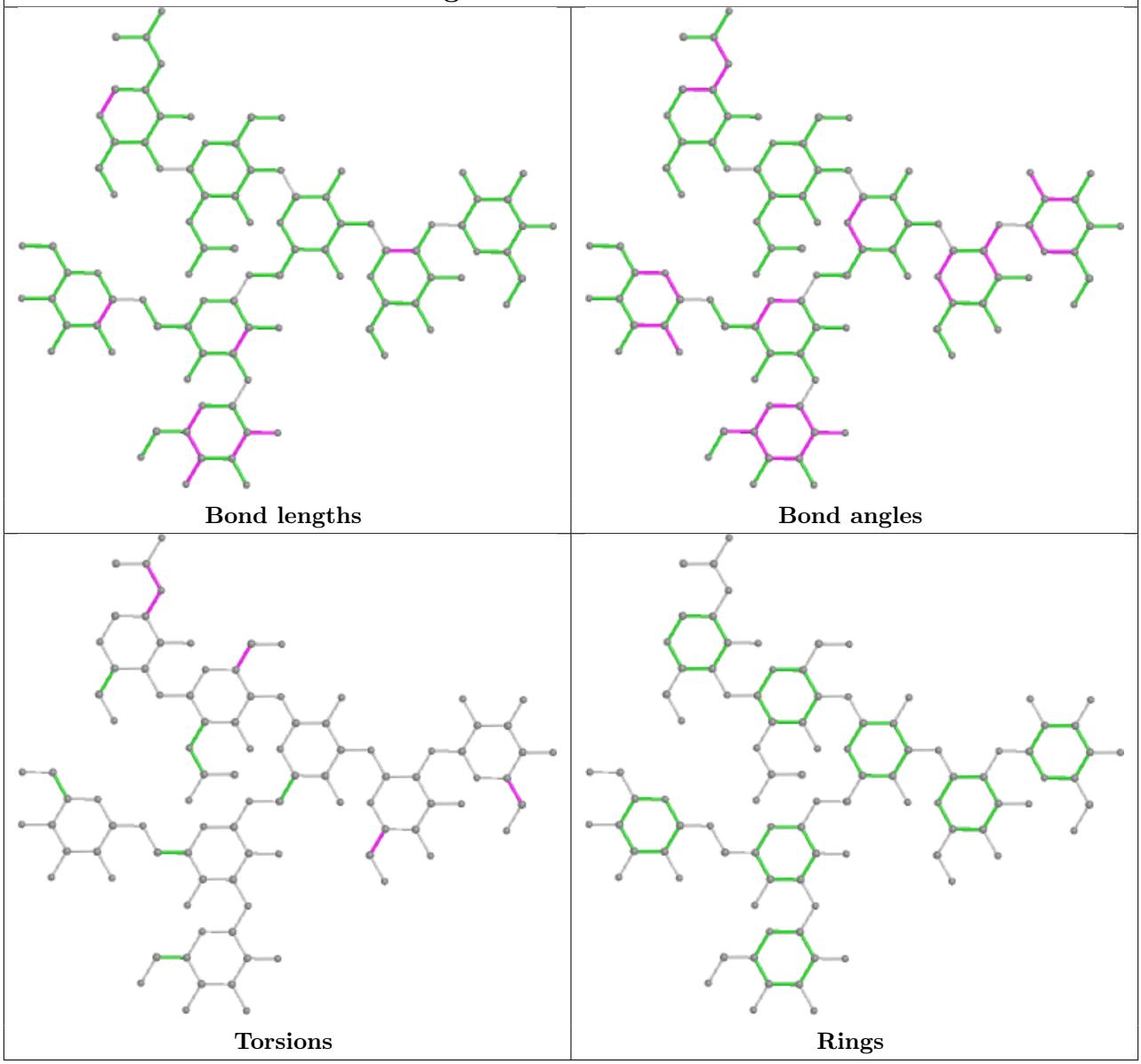


**Torsions**



**Rings**

**Oligosaccharide Chain v**




## 5.6 Ligand geometry (i)

33 ligands 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 | $\#\|Z\| > 2$ |
| 15 | NAG | A | 702 | 3 | 14,14,15 | 0.66 | 1 (7%) | 17,19,21 | 0.54 | 0 |
| 15 | NAG | Q | 606 | 1 | 14,14,15 | 0.41 | 0 | 17,19,21 | 0.55 | 0 |
| 15 | NAG | G | 652 | 1 | 14,14,15 | 0.18 | 0 | 17,19,21 | 0.33 | 0 |
| 15 | NAG | Q | 615 | 1 | 14,14,15 | 0.19 | 0 | 17,19,21 | 0.47 | 0 |
| 15 | NAG | F | 652 | 1 | 14,14,15 | 0.19 | 0 | 17,19,21 | 0.35 | 0 |
| 15 | NAG | G | 653 | 1 | 14,14,15 | 0.47 | 0 | 17,19,21 | 0.49 | 0 |
| 15 | NAG | G | 606 | 1 | 14,14,15 | 0.44 | 0 | 17,19,21 | 0.54 | 0 |
| 15 | NAG | R | 701 | 3 | 14,14,15 | 0.79 | 1 (7%) | 17,19,21 | 0.54 | 0 |
| 15 | NAG | F | 651 | 1 | 14,14,15 | 0.22 | 0 | 17,19,21 | 0.36 | 0 |
| 15 | NAG | Q | 649 | 1 | 14,14,15 | 0.34 | 0 | 17,19,21 | 0.73 | 1 (5%) |
| 15 | NAG | Q | 653 | 1 | 14,14,15 | 1.10 | 1 (7%) | 17,19,21 | 0.74 | 1 (5%) |
| 15 | NAG | Q | 633 | 1 | 14,14,15 | 0.21 | 0 | 17,19,21 | 0.40 | 0 |
| 15 | NAG | F | 649 | 1 | 14,14,15 | 1.67 | 3 (21%) | 17,19,21 | 2.38 | 8 (47%) |
| 15 | NAG | Q | 650 | 1 | 14,14,15 | 0.25 | 0 | 17,19,21 | 0.54 | 0 |
| 15 | NAG | F | 606 | 1 | 14,14,15 | 0.42 | 0 | 17,19,21 | 0.54 | 0 |
| 15 | NAG | F | 633 | 1 | 14,14,15 | 0.22 | 0 | 17,19,21 | 0.38 | 0 |
| 15 | NAG | F | 615 | 1 | 14,14,15 | 0.17 | 0 | 17,19,21 | 0.47 | 0 |
| 15 | NAG | G | 615 | 1 | 14,14,15 | 0.94 | 2 (14%) | 17,19,21 | 0.88 | 1 (5%) |
| 15 | NAG | F | 650 | 1 | 14,14,15 | 0.32 | 0 | 17,19,21 | 0.70 | 1 (5%) |
| 15 | NAG | G | 649 | 1 | 14,14,15 | 1.79 | 2 (14%) | 17,19,21 | 2.32 | 8 (47%) |
| 15 | NAG | G | 651 | 1 | 14,14,15 | 0.34 | 0 | 17,19,21 | 0.50 | 0 |
| 15 | NAG | G | 650 | 1 | 14,14,15 | 0.29 | 0 | 17,19,21 | 0.66 | 1 (5%) |
| 15 | NAG | A | 701 | 3 | 14,14,15 | 0.66 | 1 (7%) | 17,19,21 | 0.57 | 0 |
| 15 | NAG | F | 653 | 1 | 14,14,15 | 0.82 | 1 (7%) | 17,19,21 | 0.58 | 0 |
| 15 | NAG | Q | 651 | 1 | 14,14,15 | 2.08 | 1 (7%) | 17,19,21 | 2.09 | 6 (35%) |
| 15 | NAG | G | 633 | 1 | 14,14,15 | 0.24 | 0 | 17,19,21 | 0.38 | 0 |
| 15 | NAG | R | 702 | 3 | 14,14,15 | 0.77 | 1 (7%) | 17,19,21 | 0.60 | 0 |
| 15 | NAG | J | 702 | 3 | 14,14,15 | 0.91 | 1 (7%) | 17,19,21 | 0.57 | 0 |
| 15 | NAG | A | 703 | 3 | 14,14,15 | 0.62 | 0 | 17,19,21 | 0.83 | 0 |
| 15 | NAG | R | 703 | 3 | 14,14,15 | 0.65 | 0 | 17,19,21 | 0.81 | 0 |
| 15 | NAG | J | 703 | 3 | 14,14,15 | 0.69 | 1 (7%) | 17,19,21 | 0.83 | 0 |
| 15 | NAG | J | 701 | 3 | 14,14,15 | 0.65 | 1 (7%) | 17,19,21 | 0.60 | 0 |
| 15 | NAG | Q | 652 | 1 | 14,14,15 | 0.18 | 0 | 17,19,21 | 0.35 | 0 |

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

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 15 | NAG | A | 702 | 3 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | Q | 606 | 1 | - | 1/6/23/26 | 0/1/1/1 |
| 15 | NAG | G | 652 | 1 | - | 4/6/23/26 | 0/1/1/1 |
| 15 | NAG | Q | 615 | 1 | - | 4/6/23/26 | 0/1/1/1 |
| 15 | NAG | F | 652 | 1 | - | 4/6/23/26 | 0/1/1/1 |
| 15 | NAG | G | 653 | 1 | - | 2/6/23/26 | 0/1/1/1 |
| 15 | NAG | G | 606 | 1 | - | 1/6/23/26 | 0/1/1/1 |
| 15 | NAG | R | 701 | 3 | - | 2/6/23/26 | 0/1/1/1 |
| 15 | NAG | F | 651 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | Q | 649 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | Q | 653 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | Q | 633 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | F | 649 | 1 | - | 1/6/23/26 | 0/1/1/1 |
| 15 | NAG | Q | 650 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | F | 606 | 1 | - | 1/6/23/26 | 0/1/1/1 |
| 15 | NAG | F | 633 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | F | 615 | 1 | - | 4/6/23/26 | 0/1/1/1 |
| 15 | NAG | G | 615 | 1 | - | 3/6/23/26 | 0/1/1/1 |
| 15 | NAG | F | 650 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | G | 649 | 1 | - | 1/6/23/26 | 0/1/1/1 |
| 15 | NAG | G | 651 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | G | 650 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | A | 701 | 3 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | F | 653 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | Q | 651 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | G | 633 | 1 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | R | 702 | 3 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | J | 702 | 3 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | A | 703 | 3 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | R | 703 | 3 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | J | 703 | 3 | - | 0/6/23/26 | 0/1/1/1 |
| 15 | NAG | J | 701 | 3 | - | 2/6/23/26 | 0/1/1/1 |
| 15 | NAG | Q | 652 | 1 | - | 4/6/23/26 | 0/1/1/1 |

All (17) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 15 | Q | 651 | NAG | O5-C1 | -7.20 | 1.32 | 1.43 |
| 15 | G | 649 | NAG | O5-C1 | -5.53 | 1.34 | 1.43 |
| 15 | F | 649 | NAG | O5-C1 | -4.83 | 1.36 | 1.43 |
| 15 | Q | 653 | NAG | O5-C1 | -3.59 | 1.38 | 1.43 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 15 | J | 702 | NAG | O5-C1 | -3.07 | 1.38 | 1.43 |
| 15 | G | 615 | NAG | C1-C2 | 2.80 | 1.56 | 1.52 |
| 15 | G | 649 | NAG | C3-C2 | 2.61 | 1.58 | 1.52 |
| 15 | R | 701 | NAG | O5-C1 | -2.58 | 1.39 | 1.43 |
| 15 | F | 649 | NAG | C4-C5 | 2.52 | 1.58 | 1.53 |
| 15 | R | 702 | NAG | O5-C1 | -2.46 | 1.39 | 1.43 |
| 15 | F | 649 | NAG | C3-C2 | 2.26 | 1.57 | 1.52 |
| 15 | F | 653 | NAG | C8-C7 | -2.26 | 1.45 | 1.50 |
| 15 | J | 703 | NAG | O5-C1 | -2.21 | 1.40 | 1.43 |
| 15 | A | 701 | NAG | O5-C1 | -2.15 | 1.40 | 1.43 |
| 15 | J | 701 | NAG | O5-C1 | -2.15 | 1.40 | 1.43 |
| 15 | A | 702 | NAG | O5-C1 | -2.12 | 1.40 | 1.43 |
| 15 | G | 615 | NAG | O5-C1 | -2.04 | 1.40 | 1.43 |

All (27) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 15 | F | 649 | NAG | C3-C4-C5 | 4.73 | 118.67 | 110.24 |
| 15 | G | 649 | NAG | C3-C4-C5 | 4.44 | 118.16 | 110.24 |
| 15 | G | 649 | NAG | O4-C4-C5 | 4.07 | 119.41 | 109.30 |
| 15 | Q | 651 | NAG | O4-C4-C5 | 4.03 | 119.31 | 109.30 |
| 15 | F | 649 | NAG | O4-C4-C5 | 4.01 | 119.25 | 109.30 |
| 15 | Q | 651 | NAG | C3-C4-C5 | 3.84 | 117.09 | 110.24 |
| 15 | F | 649 | NAG | O4-C4-C3 | 3.82 | 119.19 | 110.35 |
| 15 | F | 649 | NAG | O3-C3-C4 | 3.67 | 118.83 | 110.35 |
| 15 | G | 649 | NAG | O4-C4-C3 | 3.62 | 118.72 | 110.35 |
| 15 | G | 649 | NAG | O3-C3-C4 | 3.51 | 118.46 | 110.35 |
| 15 | Q | 651 | NAG | C1-O5-C5 | -3.39 | 107.59 | 112.19 |
| 15 | G | 649 | NAG | C1-O5-C5 | -2.97 | 108.17 | 112.19 |
| 15 | Q | 651 | NAG | O4-C4-C3 | 2.93 | 117.13 | 110.35 |
| 15 | F | 649 | NAG | O5-C1-C2 | -2.79 | 106.89 | 111.29 |
| 15 | Q | 651 | NAG | O3-C3-C4 | 2.72 | 116.64 | 110.35 |
| 15 | Q | 649 | NAG | C1-O5-C5 | 2.70 | 115.86 | 112.19 |
| 15 | Q | 651 | NAG | O3-C3-C2 | 2.56 | 114.76 | 109.47 |
| 15 | G | 615 | NAG | C1-C2-N2 | 2.55 | 114.84 | 110.49 |
| 15 | F | 649 | NAG | O3-C3-C2 | 2.54 | 114.72 | 109.47 |
| 15 | F | 650 | NAG | C1-O5-C5 | 2.54 | 115.63 | 112.19 |
| 15 | F | 649 | NAG | C6-C5-C4 | 2.48 | 118.82 | 113.00 |
| 15 | G | 650 | NAG | C1-O5-C5 | 2.39 | 115.44 | 112.19 |
| 15 | G | 649 | NAG | O3-C3-C2 | 2.38 | 114.40 | 109.47 |
| 15 | G | 649 | NAG | O5-C1-C2 | -2.36 | 107.56 | 111.29 |
| 15 | G | 649 | NAG | C6-C5-C4 | 2.27 | 118.32 | 113.00 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 15 | Q | 653 | NAG | C1-O5-C5 | -2.13 | 109.31 | 112.19 |
| 15 | F | 649 | NAG | C1-O5-C5 | -2.09 | 109.36 | 112.19 |

There are no chirality outliers.

All (34) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 15 | F | 615 | NAG | O5-C5-C6-O6 |
| 15 | Q | 615 | NAG | O5-C5-C6-O6 |
| 15 | G | 653 | NAG | C4-C5-C6-O6 |
| 15 | G | 615 | NAG | O5-C5-C6-O6 |
| 15 | G | 652 | NAG | C8-C7-N2-C2 |
| 15 | G | 652 | NAG | O7-C7-N2-C2 |
| 15 | F | 652 | NAG | C8-C7-N2-C2 |
| 15 | F | 652 | NAG | O7-C7-N2-C2 |
| 15 | Q | 652 | NAG | C8-C7-N2-C2 |
| 15 | Q | 652 | NAG | O7-C7-N2-C2 |
| 15 | G | 615 | NAG | C4-C5-C6-O6 |
| 15 | G | 653 | NAG | O5-C5-C6-O6 |
| 15 | F | 652 | NAG | C4-C5-C6-O6 |
| 15 | J | 701 | NAG | C4-C5-C6-O6 |
| 15 | F | 615 | NAG | C4-C5-C6-O6 |
| 15 | Q | 652 | NAG | C4-C5-C6-O6 |
| 15 | R | 701 | NAG | C4-C5-C6-O6 |
| 15 | J | 701 | NAG | O5-C5-C6-O6 |
| 15 | Q | 615 | NAG | C4-C5-C6-O6 |
| 15 | R | 701 | NAG | O5-C5-C6-O6 |
| 15 | F | 652 | NAG | O5-C5-C6-O6 |
| 15 | G | 652 | NAG | C4-C5-C6-O6 |
| 15 | Q | 652 | NAG | O5-C5-C6-O6 |
| 15 | G | 615 | NAG | C3-C2-N2-C7 |
| 15 | G | 652 | NAG | O5-C5-C6-O6 |
| 15 | G | 606 | NAG | C3-C2-N2-C7 |
| 15 | F | 606 | NAG | C3-C2-N2-C7 |
| 15 | Q | 606 | NAG | C3-C2-N2-C7 |
| 15 | F | 649 | NAG | C4-C5-C6-O6 |
| 15 | F | 615 | NAG | C3-C2-N2-C7 |
| 15 | Q | 615 | NAG | C3-C2-N2-C7 |
| 15 | F | 615 | NAG | C1-C2-N2-C7 |
| 15 | Q | 615 | NAG | C1-C2-N2-C7 |
| 15 | G | 649 | NAG | C4-C5-C6-O6 |

There are no ring outliers.

No monomer is involved in short contacts.

## 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, $95^{th}$ 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 | F | 449/471 (95%) | 0.43 | 30 (6%) | 17 | 18 | 261, 419, 512, 568 | 0 |
| 1 | G | 449/471 (95%) | 0.35 | 16 (3%) | 42 | 38 | 251, 420, 504, 599 | 0 |
| 1 | Q | 449/471 (95%) | 0.43 | 24 (5%) | 26 | 26 | 240, 430, 527, 617 | 0 |
| 2 | D | 222/250 (88%) | 1.03 | 41 (18%) | 1 | 4 | 303, 478, 541, 600 | 0 |
| 2 | O | 222/250 (88%) | 0.92 | 34 (15%) | 2 | 5 | 285, 453, 530, 563 | 0 |
| 2 | W | 222/250 (88%) | 1.01 | 39 (17%) | 1 | 4 | 292, 497, 603, 637 | 0 |
| 3 | A | 126/147 (85%) | 0.07 | 3 (2%) | 59 | 52 | 241, 374, 496, 610 | 0 |
| 3 | J | 126/147 (85%) | 0.18 | 5 (3%) | 38 | 34 | 245, 378, 467, 584 | 0 |
| 3 | R | 126/147 (85%) | 0.28 | 5 (3%) | 38 | 34 | 209, 367, 476, 681 | 0 |
| 4 | B | 210/210 (100%) | 1.34 | 61 (29%) | 0 | 2 | 274, 470, 717, 766 | 0 |
| 4 | K | 210/210 (100%) | 1.66 | 67 (31%) | 0 | 2 | 308, 556, 766, 872 | 0 |
| 4 | S | 210/210 (100%) | 1.51 | 58 (27%) | 0 | 2 | 316, 507, 686, 716 | 0 |
| 5 | C | 228/232 (98%) | 1.73 | 70 (30%) | 0 | 2 | 328, 474, 737, 788 | 0 |
| 5 | L | 228/232 (98%) | 1.51 | 72 (31%) | 0 | 2 | 311, 467, 818, 919 | 0 |
| 5 | T | 228/232 (98%) | 2.14 | 94 (41%) | 0 | 1 | 367, 548, 770, 828 | 0 |
| 6 | H | 242/242 (100%) | 0.37 | 14 (5%) | 23 | 23 | 214, 360, 510, 653 | 0 |
| 6 | M | 242/242 (100%) | 1.37 | 68 (28%) | 0 | 2 | 272, 501, 677, 748 | 0 |
| 6 | U | 242/242 (100%) | 0.94 | 43 (17%) | 1 | 4 | 214, 438, 635, 673 | 0 |
| 7 | I | 207/213 (97%) | 0.32 | 5 (2%) | 59 | 52 | 139, 326, 450, 512 | 0 |
| 7 | N | 213/213 (100%) | 1.17 | 51 (23%) | 0 | 2 | 209, 470, 714, 764 | 0 |
| 7 | V | 213/213 (100%) | 0.69 | 24 (11%) | 5 | 9 | 175, 400, 572, 618 | 0 |
| All | All | 5064/5295 (95%) | 0.90 | 824 (16%) | 1 | 4 | 139, 441, 705, 919 | 0 |

All (824) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 5 | C | 178 | SER | 14.5 |
| 4 | K | 201 | SER | 13.9 |
| 4 | K | 200 | GLY | 11.9 |
| 5 | C | 185 | SER | 10.1 |
| 4 | K | 165 | PRO | 9.8 |
| 5 | C | 188 | GLY | 9.5 |
| 5 | T | 140 | VAL | 9.4 |
| 5 | T | 19 | SER | 9.1 |
| 7 | N | 150 | ALA | 9.1 |
| 5 | C | 179 | VAL | 9.0 |
| 4 | K | 202 | THR | 8.9 |
| 5 | T | 206 | ASP | 8.8 |
| 4 | S | 200 | GLY | 8.4 |
| 5 | C | 186 | SER | 8.4 |
| 5 | C | 187 | LEU | 8.3 |
| 5 | T | 138 | CYS | 8.1 |
| 5 | C | 156 | ALA | 7.9 |
| 4 | S | 202 | THR | 7.9 |
| 6 | M | 185 | PRO | 7.8 |
| 5 | C | 184 | SER | 7.6 |
| 5 | T | 196 | VAL | 7.5 |
| 5 | L | 153 | ASN | 7.5 |
| 2 | D | 134 | SER | 7.4 |
| 7 | N | 128 | ASN | 7.4 |
| 5 | C | 180 | VAL | 7.3 |
| 7 | N | 157 | ALA | 7.3 |
| 4 | K | 144 | ALA | 7.3 |
| 5 | T | 18 | LEU | 7.2 |
| 4 | K | 145 | VAL | 7.2 |
| 5 | T | 195 | ASN | 7.2 |
| 5 | T | 112 | ALA | 7.1 |
| 5 | T | 187 | LEU | 7.1 |
| 5 | T | 194 | CYS | 7.0 |
| 5 | T | 188 | GLY | 7.0 |
| 6 | M | 10 | GLU | 6.9 |
| 5 | L | 162 | HIS | 6.8 |
| 5 | L | 195 | ASN | 6.8 |
| 5 | L | 182 | VAL | 6.7 |
| 7 | N | 155 | VAL | 6.7 |
| 5 | C | 150 | VAL | 6.7 |
| 6 | M | 187 | SER | 6.6 |
| 7 | N | 154 | PRO | 6.6 |
| 5 | C | 158 | THR | 6.5 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 4 | B | 122 | SER | 6.5 |
| 7 | N | 151 | ASP | 6.4 |
| 4 | K | 108 | SER | 6.4 |
| 4 | S | 201 | SER | 6.4 |
| 6 | U | 188 | SER | 6.3 |
| 7 | N | 153 | SER | 6.3 |
| 6 | M | 186 | SER | 6.3 |
| 5 | T | 113 | SER | 6.2 |
| 1 | Q | 498 | PRO | 6.1 |
| 5 | T | 205 | VAL | 6.1 |
| 5 | T | 111 | SER | 6.1 |
| 5 | C | 190 | GLN | 6.1 |
| 5 | T | 137 | GLY | 6.0 |
| 7 | N | 191 | TYR | 6.0 |
| 4 | K | 203 | VAL | 5.9 |
| 4 | B | 134 | VAL | 5.9 |
| 5 | C | 153 | ASN | 5.9 |
| 7 | N | 156 | LYS | 5.9 |
| 5 | T | 159 | SER | 5.9 |
| 6 | M | 184 | VAL | 5.9 |
| 5 | T | 160 | GLY | 5.8 |
| 2 | W | 8 | GLY | 5.8 |
| 5 | C | 177 | SER | 5.8 |
| 2 | D | 223 | ASP | 5.8 |
| 5 | C | 157 | LEU | 5.7 |
| 5 | T | 142 | ASP | 5.7 |
| 7 | V | 80 | PRO | 5.6 |
| 5 | C | 152 | TRP | 5.6 |
| 4 | B | 197 | THR | 5.6 |
| 5 | L | 151 | SER | 5.6 |
| 4 | B | 182 | THR | 5.6 |
| 5 | L | 206 | ASP | 5.6 |
| 5 | C | 176 | LEU | 5.6 |
| 5 | T | 189 | THR | 5.5 |
| 5 | C | 135 | ALA | 5.5 |
| 5 | C | 175 | SER | 5.5 |
| 7 | N | 127 | ALA | 5.5 |
| 5 | L | 18 | LEU | 5.5 |
| 5 | T | 190 | GLN | 5.4 |
| 5 | T | 81 | ARG | 5.4 |
| 5 | T | 67 | VAL | 5.4 |
| 4 | K | 153 | SER | 5.4 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 6 | U | 114 | ALA | 5.4 |
| 5 | C | 189 | THR | 5.4 |
| 6 | U | 113 | SER | 5.4 |
| 1 | Q | 185 | ASN | 5.3 |
| 5 | L | 194 | CYS | 5.3 |
| 7 | N | 190 | SER | 5.3 |
| 4 | S | 207 | VAL | 5.3 |
| 4 | K | 135 | CYS | 5.3 |
| 5 | C | 155 | GLY | 5.3 |
| 7 | N | 109 | SER | 5.2 |
| 5 | T | 118 | SER | 5.2 |
| 4 | K | 116 | VAL | 5.2 |
| 2 | O | 8 | GLY | 5.2 |
| 4 | S | 181 | LEU | 5.2 |
| 2 | D | 210 | GLN | 5.2 |
| 5 | T | 210 | GLU | 5.2 |
| 6 | M | 211 | VAL | 5.2 |
| 5 | C | 134 | ALA | 5.2 |
| 4 | K | 109 | GLN | 5.1 |
| 5 | C | 191 | THR | 5.1 |
| 5 | T | 116 | GLY | 5.1 |
| 5 | T | 86 | ASP | 5.1 |
| 5 | T | 117 | PRO | 5.0 |
| 4 | B | 210 | THR | 5.0 |
| 6 | M | 210 | ARG | 5.0 |
| 7 | N | 110 | LYS | 5.0 |
| 5 | L | 134 | ALA | 5.0 |
| 6 | M | 165 | THR | 4.9 |
| 5 | L | 185 | SER | 4.9 |
| 1 | F | 398 | ASN | 4.9 |
| 6 | M | 17 | SER | 4.9 |
| 2 | D | 222 | VAL | 4.9 |
| 2 | D | 148 | SER | 4.9 |
| 4 | K | 136 | LEU | 4.9 |
| 5 | T | 82 | LEU | 4.9 |
| 5 | T | 191 | THR | 4.9 |
| 5 | C | 161 | VAL | 4.9 |
| 5 | T | 119 | VAL | 4.9 |
| 5 | T | 110 | SER | 4.9 |
| 5 | T | 165 | PRO | 4.9 |
| 5 | T | 171 | SER | 4.9 |
| 5 | T | 154 | SER | 4.9 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 2 | W | 202 | ASP | 4.8 |
| 5 | L | 156 | ALA | 4.8 |
| 5 | L | 154 | SER | 4.8 |
| 4 | S | 206 | THR | 4.8 |
| 4 | S | 157 | LYS | 4.8 |
| 4 | K | 197 | THR | 4.8 |
| 7 | N | 152 | SER | 4.7 |
| 6 | U | 213 | PRO | 4.7 |
| 4 | B | 126 | LEU | 4.7 |
| 6 | M | 172 | SER | 4.7 |
| 7 | N | 126 | GLN | 4.7 |
| 2 | D | 133 | LEU | 4.7 |
| 5 | T | 82(A) | THR | 4.7 |
| 4 | K | 177 | SER | 4.6 |
| 4 | K | 198 | HIS | 4.6 |
| 6 | U | 9 | ALA | 4.6 |
| 4 | B | 125 | GLU | 4.6 |
| 5 | C | 138 | CYS | 4.6 |
| 5 | C | 133 | THR | 4.6 |
| 5 | T | 68 | HIS | 4.6 |
| 4 | B | 127 | GLN | 4.5 |
| 5 | C | 166 | ALA | 4.5 |
| 5 | L | 17 | THR | 4.5 |
| 5 | T | 193 | ILE | 4.5 |
| 5 | L | 183 | PRO | 4.5 |
| 6 | M | 173 | SER | 4.5 |
| 6 | M | 188 | SER | 4.5 |
| 2 | W | 41 | PRO | 4.4 |
| 6 | M | 139 | GLY | 4.4 |
| 6 | M | 18 | VAL | 4.4 |
| 6 | M | 219 | GLY | 4.4 |
| 5 | L | 150 | VAL | 4.4 |
| 4 | K | 164 | THR | 4.4 |
| 2 | D | 147 | THR | 4.4 |
| 6 | M | 100 | GLY | 4.4 |
| 6 | U | 112 | SER | 4.3 |
| 5 | T | 209 | VAL | 4.3 |
| 5 | T | 175 | SER | 4.3 |
| 6 | U | 187 | SER | 4.3 |
| 5 | C | 92 | CYS | 4.3 |
| 2 | W | 200 | SER | 4.3 |
| 4 | S | 121 | PRO | 4.3 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 2 | O | 202 | ASP | 4.3 |
| 2 | D | 150 | SER | 4.3 |
| 5 | C | 162 | HIS | 4.2 |
| 5 | T | 208 | ARG | 4.2 |
| 5 | T | 186 | SER | 4.2 |
| 6 | U | 192 | GLN | 4.2 |
| 5 | T | 177 | SER | 4.2 |
| 4 | K | 110 | PRO | 4.2 |
| 5 | L | 27 | THR | 4.2 |
| 1 | G | 283 | ASN | 4.2 |
| 4 | B | 13 | VAL | 4.2 |
| 4 | K | 127 | GLN | 4.2 |
| 5 | L | 180 | VAL | 4.2 |
| 5 | L | 196 | VAL | 4.1 |
| 4 | S | 170 | ASN | 4.1 |
| 5 | L | 19 | SER | 4.1 |
| 5 | L | 211 | PRO | 4.1 |
| 5 | L | 152 | TRP | 4.1 |
| 6 | M | 138 | LEU | 4.1 |
| 2 | W | 7 | SER | 4.1 |
| 6 | M | 100(A) | SER | 4.1 |
| 4 | S | 185 | GLN | 4.1 |
| 1 | Q | 504 | ARG | 4.1 |
| 6 | M | 100(B) | SER | 4.0 |
| 2 | D | 189 | ALA | 4.0 |
| 1 | F | 411 | ASN | 4.0 |
| 1 | G | 220 | PRO | 4.0 |
| 6 | H | 9 | ALA | 4.0 |
| 5 | C | 126 | SER | 4.0 |
| 4 | K | 121 | PRO | 4.0 |
| 4 | B | 146 | THR | 4.0 |
| 5 | T | 141 | LYS | 4.0 |
| 4 | K | 176 | SER | 4.0 |
| 4 | S | 192 | TYR | 4.0 |
| 5 | L | 181 | THR | 4.0 |
| 2 | O | 184 | GLY | 4.0 |
| 6 | U | 51 | ILE | 4.0 |
| 2 | W | 199 | GLU | 3.9 |
| 5 | L | 161 | VAL | 3.9 |
| 4 | S | 48 | ILE | 3.9 |
| 1 | Q | 411 | ASN | 3.9 |
| 4 | K | 162 | THR | 3.9 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 4 | B | 6 | ALA | 3.9 |
| 3 | R | 547 | GLY | 3.9 |
| 5 | C | 160 | GLY | 3.9 |
| 5 | T | 207 | LYS | 3.9 |
| 4 | S | 163 | THR | 3.9 |
| 4 | S | 184 | GLU | 3.9 |
| 2 | D | 7 | SER | 3.9 |
| 5 | L | 155 | GLY | 3.9 |
| 4 | S | 43 | ALA | 3.9 |
| 1 | F | 60 | ALA | 3.9 |
| 6 | M | 9 | ALA | 3.9 |
| 2 | O | 18 | MET | 3.8 |
| 4 | K | 161 | GLU | 3.8 |
| 2 | D | 151 | GLY | 3.8 |
| 5 | C | 151 | SER | 3.8 |
| 4 | B | 184 | GLU | 3.8 |
| 6 | U | 159 | LEU | 3.8 |
| 4 | S | 33 | VAL | 3.8 |
| 3 | J | 546 | SER | 3.8 |
| 5 | L | 70 | SER | 3.8 |
| 4 | K | 132 | THR | 3.8 |
| 5 | C | 132 | GLY | 3.8 |
| 6 | M | 8 | GLY | 3.8 |
| 7 | V | 208 | PRO | 3.8 |
| 1 | G | 219 | ALA | 3.8 |
| 6 | M | 171 | GLN | 3.8 |
| 6 | M | 125 | ALA | 3.7 |
| 5 | L | 160 | GLY | 3.7 |
| 4 | K | 20 | ARG | 3.7 |
| 6 | M | 174 | GLY | 3.7 |
| 5 | T | 66 | ARG | 3.7 |
| 7 | N | 42 | ARG | 3.7 |
| 5 | T | 176 | LEU | 3.7 |
| 3 | R | 600 | GLY | 3.7 |
| 7 | V | 120 | PRO | 3.7 |
| 5 | L | 190 | GLN | 3.7 |
| 2 | O | 185 | SER | 3.7 |
| 6 | U | 58 | ASN | 3.7 |
| 1 | Q | 462 | ASN | 3.7 |
| 5 | T | 197 | ASN | 3.7 |
| 6 | U | 150 | VAL | 3.7 |
| 6 | M | 126 | PRO | 3.7 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 7 | N | 207 | ALA | 3.7 |
| 5 | C | 18 | LEU | 3.6 |
| 5 | T | 178 | SER | 3.6 |
| 5 | L | 192 | TYR | 3.6 |
| 2 | D | 188 | GLY | 3.6 |
| 2 | D | 221 | GLN | 3.6 |
| 4 | S | 186 | TRP | 3.6 |
| 5 | L | 207 | LYS | 3.6 |
| 7 | N | 43 | ALA | 3.6 |
| 2 | D | 64 | PHE | 3.6 |
| 7 | N | 108 | GLN | 3.6 |
| 5 | C | 154 | SER | 3.6 |
| 1 | Q | 474 | ASP | 3.6 |
| 6 | M | 191 | THR | 3.6 |
| 6 | M | 212 | GLU | 3.6 |
| 4 | S | 169 | SER | 3.6 |
| 5 | T | 192 | TYR | 3.6 |
| 7 | N | 206 | VAL | 3.6 |
| 6 | M | 52(A) | PRO | 3.6 |
| 5 | T | 114 | THR | 3.6 |
| 5 | C | 140 | VAL | 3.5 |
| 5 | T | 211 | PRO | 3.5 |
| 4 | S | 133 | LEU | 3.5 |
| 4 | S | 47 | ILE | 3.5 |
| 5 | T | 153 | ASN | 3.5 |
| 2 | D | 153 | LEU | 3.5 |
| 6 | M | 202 | PRO | 3.5 |
| 5 | L | 82 | LEU | 3.5 |
| 4 | S | 35 | TRP | 3.5 |
| 4 | S | 109 | GLN | 3.5 |
| 5 | L | 69 | LEU | 3.5 |
| 5 | C | 181 | THR | 3.5 |
| 7 | N | 205 | THR | 3.5 |
| 6 | U | 147 | PRO | 3.5 |
| 6 | U | 191 | THR | 3.5 |
| 5 | T | 139 | LEU | 3.4 |
| 5 | T | 179 | VAL | 3.4 |
| 4 | B | 118 | LEU | 3.4 |
| 6 | U | 115 | SER | 3.4 |
| 2 | W | 9 | GLY | 3.4 |
| 6 | M | 190 | GLY | 3.4 |
| 5 | T | 136 | LEU | 3.4 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 5 | L | 169 | GLN | 3.4 |
| 4 | K | 154 | SER | 3.4 |
| 5 | C | 183 | PRO | 3.4 |
| 4 | K | 188 | SER | 3.4 |
| 5 | C | 68 | HIS | 3.4 |
| 4 | B | 62 | PHE | 3.4 |
| 7 | N | 149 | LYS | 3.4 |
| 4 | B | 119 | PHE | 3.4 |
| 4 | S | 42 | GLN | 3.4 |
| 6 | U | 190 | GLY | 3.3 |
| 2 | D | 187 | TRP | 3.3 |
| 5 | C | 182 | VAL | 3.3 |
| 6 | M | 158 | ALA | 3.3 |
| 4 | S | 120 | PRO | 3.3 |
| 4 | K | 199 | GLU | 3.3 |
| 5 | T | 145 | PRO | 3.3 |
| 6 | U | 194 | TYR | 3.3 |
| 4 | B | 209 | PRO | 3.3 |
| 5 | L | 121 | PRO | 3.3 |
| 5 | C | 159 | SER | 3.3 |
| 2 | D | 220 | VAL | 3.3 |
| 4 | S | 156 | VAL | 3.3 |
| 7 | N | 144 | VAL | 3.3 |
| 4 | K | 166 | SER | 3.3 |
| 2 | D | 132 | THR | 3.3 |
| 5 | L | 118 | SER | 3.3 |
| 5 | L | 186 | SER | 3.3 |
| 6 | M | 100(C) | THR | 3.3 |
| 5 | L | 81 | ARG | 3.3 |
| 4 | K | 123 | SER | 3.3 |
| 4 | K | 21 | ILE | 3.3 |
| 5 | C | 149 | THR | 3.3 |
| 5 | L | 68 | HIS | 3.3 |
| 1 | F | 458 | GLY | 3.2 |
| 5 | T | 30 | ARG | 3.2 |
| 2 | O | 7 | SER | 3.2 |
| 4 | B | 202 | THR | 3.2 |
| 4 | B | 130 | LYS | 3.2 |
| 4 | K | 19 | ALA | 3.2 |
| 7 | V | 79 | ARG | 3.2 |
| 5 | C | 131 | GLY | 3.2 |
| 5 | L | 149 | THR | 3.2 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 4 | B | 15 | PRO | 3.2 |
| 2 | W | 70 | MET | 3.2 |
| 7 | N | 210 | GLU | 3.2 |
| 4 | S | 203 | VAL | 3.2 |
| 6 | M | 218 | LYS | 3.2 |
| 5 | T | 93 | ALA | 3.2 |
| 5 | L | 138 | CYS | 3.2 |
| 4 | K | 131 | ALA | 3.2 |
| 2 | W | 90 | ASP | 3.2 |
| 2 | W | 189 | ALA | 3.2 |
| 5 | L | 133 | THR | 3.2 |
| 5 | L | 187 | LEU | 3.2 |
| 4 | K | 120 | PRO | 3.2 |
| 6 | M | 140 | CYS | 3.2 |
| 5 | L | 158 | THR | 3.2 |
| 5 | T | 29 | VAL | 3.2 |
| 5 | L | 110 | SER | 3.2 |
| 5 | L | 165 | PRO | 3.2 |
| 6 | H | 110 | THR | 3.2 |
| 1 | F | 460 | ALA | 3.2 |
| 7 | V | 207 | ALA | 3.2 |
| 1 | F | 366 | GLY | 3.1 |
| 4 | S | 155 | PRO | 3.1 |
| 2 | W | 2 | VAL | 3.1 |
| 4 | S | 154 | SER | 3.1 |
| 2 | D | 8 | GLY | 3.1 |
| 4 | B | 108 | SER | 3.1 |
| 5 | C | 67 | VAL | 3.1 |
| 5 | C | 206 | ASP | 3.1 |
| 2 | O | 25 | SER | 3.1 |
| 4 | B | 112 | ALA | 3.1 |
| 2 | O | 201 | GLY | 3.1 |
| 7 | N | 12 | SER | 3.1 |
| 7 | N | 41 | GLY | 3.1 |
| 6 | M | 161 | SER | 3.1 |
| 4 | B | 133 | LEU | 3.1 |
| 6 | M | 81 | GLU | 3.1 |
| 4 | B | 23 | CYS | 3.1 |
| 6 | H | 100(A) | SER | 3.1 |
| 4 | S | 32 | SER | 3.1 |
| 4 | S | 21 | ILE | 3.1 |
| 4 | B | 95(C) | ASN | 3.1 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 6 | H | 100 | GLY | 3.1 |
| 5 | T | 148 | VAL | 3.1 |
| 5 | C | 110 | SER | 3.1 |
| 2 | W | 190 | ASP | 3.1 |
| 7 | N | 112 | ASN | 3.1 |
| 4 | B | 149 | TRP | 3.1 |
| 5 | L | 191 | THR | 3.1 |
| 6 | M | 209 | LYS | 3.1 |
| 2 | W | 188 | GLY | 3.1 |
| 5 | L | 184 | SER | 3.1 |
| 1 | G | 183 | GLN | 3.0 |
| 5 | L | 92 | CYS | 3.0 |
| 4 | B | 206 | THR | 3.0 |
| 5 | C | 73 | LYS | 3.0 |
| 5 | L | 205 | VAL | 3.0 |
| 3 | R | 599 | SER | 3.0 |
| 4 | K | 152 | ASP | 3.0 |
| 2 | D | 10 | GLN | 3.0 |
| 1 | Q | 263 | GLY | 3.0 |
| 7 | N | 105 | SER | 3.0 |
| 5 | L | 163 | THR | 3.0 |
| 4 | B | 164 | THR | 3.0 |
| 4 | K | 124 | GLU | 3.0 |
| 2 | D | 20 | LEU | 3.0 |
| 5 | T | 34 | TRP | 3.0 |
| 6 | M | 182 | VAL | 3.0 |
| 7 | V | 82 | ASP | 3.0 |
| 6 | U | 185 | PRO | 3.0 |
| 7 | V | 130 | ALA | 3.0 |
| 5 | T | 163 | THR | 3.0 |
| 6 | U | 33 | HIS | 3.0 |
| 2 | D | 135 | LEU | 3.0 |
| 5 | L | 80 | LEU | 3.0 |
| 2 | O | 143 | ILE | 3.0 |
| 4 | B | 145 | VAL | 3.0 |
| 1 | F | 457 | ASP | 3.0 |
| 4 | K | 210 | THR | 3.0 |
| 7 | N | 111 | ALA | 3.0 |
| 2 | O | 153 | LEU | 3.0 |
| 5 | C | 211 | PRO | 2.9 |
| 1 | F | 364 | SER | 2.9 |
| 4 | S | 176 | SER | 2.9 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 4 | B | 188 | SER | 2.9 |
| 7 | N | 192 | SER | 2.9 |
| 2 | W | 117 | ARG | 2.9 |
| 4 | B | 120 | PRO | 2.9 |
| 5 | T | 149 | THR | 2.9 |
| 7 | I | 142 | GLY | 2.9 |
| 2 | D | 209 | GLN | 2.9 |
| 6 | M | 52 | SER | 2.9 |
| 6 | U | 189 | LEU | 2.9 |
| 6 | H | 147 | PRO | 2.9 |
| 6 | M | 82 | ILE | 2.9 |
| 6 | U | 193 | THR | 2.9 |
| 2 | O | 117 | ARG | 2.9 |
| 6 | U | 57 | LYS | 2.9 |
| 5 | C | 19 | SER | 2.9 |
| 5 | T | 92 | CYS | 2.9 |
| 4 | K | 24 | GLY | 2.9 |
| 4 | S | 197 | THR | 2.9 |
| 5 | T | 99 | ARG | 2.9 |
| 4 | B | 155 | PRO | 2.9 |
| 5 | T | 102 | GLY | 2.9 |
| 6 | M | 123 | PRO | 2.9 |
| 2 | W | 116 | GLY | 2.9 |
| 6 | M | 33 | HIS | 2.9 |
| 4 | B | 14 | ALA | 2.8 |
| 6 | M | 217 | ASP | 2.8 |
| 4 | B | 187 | LYS | 2.8 |
| 6 | U | 11 | LEU | 2.8 |
| 1 | G | 474 | ASP | 2.8 |
| 2 | D | 45 | PRO | 2.8 |
| 6 | M | 67 | VAL | 2.8 |
| 1 | F | 365 | SER | 2.8 |
| 4 | B | 79 | GLU | 2.8 |
| 2 | W | 38 | ARG | 2.8 |
| 4 | B | 163 | THR | 2.8 |
| 5 | T | 151 | SER | 2.8 |
| 1 | G | 176 | PHE | 2.8 |
| 4 | B | 185 | GLN | 2.8 |
| 5 | C | 195 | ASN | 2.8 |
| 3 | A | 547 | GLY | 2.8 |
| 4 | K | 146 | THR | 2.8 |
| 5 | C | 81 | ARG | 2.8 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 7 | N | 180 | LEU | 2.8 |
| 3 | J | 547 | GLY | 2.8 |
| 7 | V | 20 | THR | 2.8 |
| 7 | N | 113 | PRO | 2.8 |
| 5 | T | 82(B) | GLY | 2.8 |
| 6 | U | 50 | TRP | 2.8 |
| 5 | T | 97 | HIS | 2.8 |
| 4 | B | 156 | VAL | 2.8 |
| 5 | C | 192 | TYR | 2.8 |
| 2 | O | 171 | GLY | 2.8 |
| 4 | B | 179 | LEU | 2.8 |
| 4 | B | 123 | SER | 2.8 |
| 4 | K | 95(C) | ASN | 2.8 |
| 6 | U | 184 | VAL | 2.8 |
| 4 | B | 24 | GLY | 2.8 |
| 6 | M | 157 | GLY | 2.8 |
| 4 | S | 199 | GLU | 2.8 |
| 5 | T | 20 | LEU | 2.8 |
| 7 | I | 157 | ALA | 2.8 |
| 2 | O | 182 | PHE | 2.8 |
| 7 | V | 131 | THR | 2.8 |
| 6 | M | 220 | LEU | 2.8 |
| 6 | M | 11 | LEU | 2.8 |
| 7 | N | 198 | GLU | 2.8 |
| 5 | L | 78 | VAL | 2.8 |
| 1 | G | 368 | ASP | 2.7 |
| 2 | O | 90 | ASP | 2.7 |
| 4 | B | 59 | PRO | 2.7 |
| 1 | F | 61 | TYR | 2.7 |
| 6 | H | 191 | THR | 2.7 |
| 7 | N | 158 | GLY | 2.7 |
| 4 | B | 196 | VAL | 2.7 |
| 7 | V | 180 | LEU | 2.7 |
| 2 | W | 40 | ALA | 2.7 |
| 2 | D | 46 | GLU | 2.7 |
| 4 | K | 195 | GLN | 2.7 |
| 6 | M | 1 | GLN | 2.7 |
| 5 | C | 93 | ALA | 2.7 |
| 5 | T | 103 | LYS | 2.7 |
| 4 | S | 108 | SER | 2.7 |
| 5 | T | 83 | THR | 2.7 |
| 4 | S | 151 | ALA | 2.7 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 3 | R | 546 | SER | 2.7 |
| 4 | S | 131 | ALA | 2.7 |
| 2 | O | 116 | GLY | 2.7 |
| 7 | V | 13 | GLY | 2.7 |
| 4 | S | 90 | ILE | 2.7 |
| 5 | T | 82(C) | VAL | 2.7 |
| 5 | T | 158 | THR | 2.7 |
| 6 | H | 10 | GLU | 2.7 |
| 4 | S | 97 | VAL | 2.7 |
| 7 | V | 41 | GLY | 2.7 |
| 1 | Q | 32 | GLU | 2.7 |
| 5 | L | 157 | LEU | 2.7 |
| 2 | O | 203 | PHE | 2.7 |
| 4 | K | 180 | SER | 2.7 |
| 4 | S | 31 | ARG | 2.7 |
| 5 | C | 141 | LYS | 2.7 |
| 7 | N | 188 | HIS | 2.7 |
| 4 | B | 131 | ALA | 2.7 |
| 7 | N | 13 | GLY | 2.7 |
| 1 | G | 190 | GLU | 2.7 |
| 5 | C | 163 | THR | 2.7 |
| 6 | U | 222 | VAL | 2.7 |
| 4 | S | 153 | SER | 2.7 |
| 5 | L | 111 | SER | 2.7 |
| 5 | L | 178 | SER | 2.7 |
| 6 | M | 216 | CYS | 2.7 |
| 5 | T | 31 | ASP | 2.6 |
| 2 | D | 2 | VAL | 2.6 |
| 5 | T | 69 | LEU | 2.6 |
| 6 | U | 149 | PRO | 2.6 |
| 4 | K | 196 | VAL | 2.6 |
| 2 | D | 125 | VAL | 2.6 |
| 2 | W | 94 | TYR | 2.6 |
| 2 | W | 134 | SER | 2.6 |
| 2 | O | 172 | SER | 2.6 |
| 5 | C | 148 | VAL | 2.6 |
| 1 | F | 483 | LEU | 2.6 |
| 2 | O | 20 | LEU | 2.6 |
| 7 | I | 42 | ARG | 2.6 |
| 1 | Q | 365 | SER | 2.6 |
| 7 | N | 182 | PRO | 2.6 |
| 2 | D | 149 | GLN | 2.6 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 5 | L | 208 | ARG | 2.6 |
| 4 | K | 178 | TYR | 2.6 |
| 5 | L | 119 | VAL | 2.6 |
| 6 | H | 190 | GLY | 2.6 |
| 7 | N | 140 | TYR | 2.6 |
| 1 | F | 324 | GLY | 2.6 |
| 6 | M | 175 | LEU | 2.6 |
| 7 | N | 179 | SER | 2.6 |
| 5 | T | 9 | PRO | 2.6 |
| 7 | V | 206 | VAL | 2.6 |
| 4 | S | 88 | CYS | 2.6 |
| 4 | S | 182 | THR | 2.6 |
| 5 | L | 170 | SER | 2.6 |
| 4 | K | 115 | SER | 2.6 |
| 5 | T | 121 | PRO | 2.6 |
| 4 | S | 148 | ALA | 2.6 |
| 5 | T | 85 | ALA | 2.6 |
| 5 | T | 166 | ALA | 2.6 |
| 5 | L | 159 | SER | 2.6 |
| 1 | F | 334 | SER | 2.6 |
| 2 | O | 135 | LEU | 2.6 |
| 4 | B | 82 | ASP | 2.6 |
| 1 | F | 462 | ASN | 2.5 |
| 6 | M | 189 | LEU | 2.5 |
| 2 | W | 187 | TRP | 2.5 |
| 4 | S | 132 | THR | 2.5 |
| 5 | C | 34 | TRP | 2.5 |
| 6 | H | 121 | VAL | 2.5 |
| 6 | U | 116 | THR | 2.5 |
| 7 | V | 115 | VAL | 2.5 |
| 4 | B | 189 | HIS | 2.5 |
| 4 | K | 163 | THR | 2.5 |
| 1 | Q | 356 | ASN | 2.5 |
| 6 | M | 222 | VAL | 2.5 |
| 1 | Q | 60 | ALA | 2.5 |
| 2 | W | 119 | ALA | 2.5 |
| 3 | A | 591 | GLN | 2.5 |
| 4 | K | 143 | GLY | 2.5 |
| 5 | C | 119 | VAL | 2.5 |
| 6 | U | 69 | MET | 2.5 |
| 7 | N | 141 | PRO | 2.5 |
| 2 | D | 186 | ARG | 2.5 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 6 | M | 12 | LYS | 2.5 |
| 7 | I | 41 | GLY | 2.5 |
| 2 | W | 6 | GLN | 2.5 |
| 2 | D | 202 | ASP | 2.5 |
| 7 | V | 132 | LEU | 2.5 |
| 2 | D | 18 | MET | 2.5 |
| 4 | B | 203 | VAL | 2.5 |
| 4 | K | 114 | PRO | 2.5 |
| 5 | C | 136 | LEU | 2.5 |
| 7 | N | 44 | PRO | 2.5 |
| 3 | A | 600 | GLY | 2.5 |
| 1 | G | 471 | GLY | 2.5 |
| 5 | T | 150 | VAL | 2.5 |
| 7 | V | 185 | TRP | 2.5 |
| 2 | D | 124 | SER | 2.5 |
| 1 | F | 219 | ALA | 2.5 |
| 4 | K | 117 | THR | 2.5 |
| 5 | T | 181 | THR | 2.5 |
| 6 | M | 56 | ASP | 2.5 |
| 2 | D | 41 | PRO | 2.5 |
| 7 | V | 187 | SER | 2.5 |
| 3 | J | 614 | TRP | 2.5 |
| 6 | H | 71 | THR | 2.5 |
| 6 | U | 110 | THR | 2.5 |
| 5 | C | 9 | PRO | 2.4 |
| 2 | O | 2 | VAL | 2.4 |
| 4 | B | 208 | ALA | 2.4 |
| 6 | M | 7 | SER | 2.4 |
| 1 | F | 59 | LYS | 2.4 |
| 7 | V | 182 | PRO | 2.4 |
| 4 | B | 80 | ALA | 2.4 |
| 4 | K | 128 | ALA | 2.4 |
| 4 | K | 181 | LEU | 2.4 |
| 4 | S | 204 | GLU | 2.4 |
| 6 | M | 180 | SER | 2.4 |
| 1 | F | 276 | ASN | 2.4 |
| 7 | V | 57 | GLY | 2.4 |
| 4 | S | 41 | GLY | 2.4 |
| 7 | V | 108 | GLN | 2.4 |
| 1 | F | 212 | PRO | 2.4 |
| 5 | C | 170 | SER | 2.4 |
| 1 | Q | 283 | ASN | 2.4 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 6 | M | 221 | GLU | 2.4 |
| 7 | N | 159 | VAL | 2.4 |
| 4 | S | 95(C) | ASN | 2.4 |
| 5 | T | 28 | LEU | 2.4 |
| 5 | T | 87 | SER | 2.4 |
| 1 | F | 256 | SER | 2.4 |
| 1 | F | 397 | SER | 2.4 |
| 4 | K | 11 | VAL | 2.4 |
| 2 | W | 84 | ARG | 2.4 |
| 4 | B | 63 | SER | 2.3 |
| 5 | T | 80 | LEU | 2.3 |
| 5 | C | 125 | SER | 2.3 |
| 2 | O | 83 | LEU | 2.3 |
| 7 | N | 142 | GLY | 2.3 |
| 2 | O | 3 | ARG | 2.3 |
| 2 | W | 87 | THR | 2.3 |
| 2 | W | 27 | TYR | 2.3 |
| 6 | M | 115 | SER | 2.3 |
| 1 | F | 504 | ARG | 2.3 |
| 2 | D | 11 | MET | 2.3 |
| 2 | D | 141 | ALA | 2.3 |
| 4 | S | 99 | GLY | 2.3 |
| 4 | S | 164 | THR | 2.3 |
| 5 | C | 210 | GLU | 2.3 |
| 2 | O | 150 | SER | 2.3 |
| 2 | W | 42 | GLY | 2.3 |
| 3 | J | 599 | SER | 2.3 |
| 6 | U | 131 | THR | 2.3 |
| 7 | V | 110 | LYS | 2.3 |
| 1 | Q | 71 | THR | 2.3 |
| 5 | T | 17 | THR | 2.3 |
| 6 | M | 160 | THR | 2.3 |
| 4 | B | 121 | PRO | 2.3 |
| 4 | S | 196 | VAL | 2.3 |
| 5 | L | 202 | ASN | 2.3 |
| 5 | C | 71 | LEU | 2.3 |
| 6 | M | 116 | THR | 2.3 |
| 6 | U | 59 | LEU | 2.3 |
| 2 | O | 151 | GLY | 2.3 |
| 5 | C | 137 | GLY | 2.3 |
| 2 | O | 133 | LEU | 2.3 |
| 2 | O | 163 | ALA | 2.3 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 1 | Q | 63 | THR | 2.3 |
| 4 | B | 21 | ILE | 2.3 |
| 4 | B | 183 | PRO | 2.3 |
| 6 | U | 146 | PHE | 2.3 |
| 7 | V | 106 | VAL | 2.3 |
| 2 | W | 201 | GLY | 2.3 |
| 5 | L | 141 | LYS | 2.3 |
| 6 | U | 161 | SER | 2.3 |
| 4 | K | 129 | ASN | 2.3 |
| 4 | K | 130 | LYS | 2.3 |
| 7 | N | 189 | ARG | 2.3 |
| 1 | G | 185 | ASN | 2.2 |
| 1 | G | 247 | CYS | 2.2 |
| 4 | K | 6 | ALA | 2.2 |
| 2 | D | 38 | ARG | 2.2 |
| 4 | K | 157 | LYS | 2.2 |
| 5 | T | 202 | ASN | 2.2 |
| 5 | T | 170 | SER | 2.2 |
| 1 | F | 220 | PRO | 2.2 |
| 4 | K | 47 | ILE | 2.2 |
| 2 | W | 220 | VAL | 2.2 |
| 4 | B | 207 | VAL | 2.2 |
| 5 | L | 67 | VAL | 2.2 |
| 6 | M | 162 | GLY | 2.2 |
| 7 | N | 64 | GLY | 2.2 |
| 4 | B | 60 | ASP | 2.2 |
| 5 | L | 71 | LEU | 2.2 |
| 4 | K | 18 | THR | 2.2 |
| 1 | Q | 375 | SER | 2.2 |
| 2 | W | 85 | SER | 2.2 |
| 6 | H | 11 | LEU | 2.2 |
| 5 | T | 44 | GLN | 2.2 |
| 2 | W | 15 | GLY | 2.2 |
| 2 | W | 133 | LEU | 2.2 |
| 4 | K | 133 | LEU | 2.2 |
| 2 | W | 124 | SER | 2.2 |
| 4 | B | 169 | SER | 2.2 |
| 5 | L | 166 | ALA | 2.2 |
| 5 | L | 188 | GLY | 2.2 |
| 5 | L | 26 | GLY | 2.2 |
| 1 | Q | 496 | VAL | 2.2 |
| 5 | T | 115 | LYS | 2.2 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 5 | C | 142 | ASP | 2.2 |
| 2 | D | 12 | LYS | 2.2 |
| 5 | C | 17 | THR | 2.2 |
| 5 | L | 100(L) | THR | 2.2 |
| 6 | M | 149 | PRO | 2.2 |
| 7 | N | 208 | PRO | 2.2 |
| 6 | U | 186 | SER | 2.2 |
| 2 | O | 199 | GLU | 2.2 |
| 4 | K | 48 | ILE | 2.2 |
| 5 | L | 167 | VAL | 2.2 |
| 7 | N | 122 | SER | 2.2 |
| 1 | F | 325 | ASP | 2.2 |
| 2 | O | 94 | TYR | 2.2 |
| 2 | W | 218 | THR | 2.2 |
| 4 | B | 19 | ALA | 2.2 |
| 6 | U | 224 | PHE | 2.2 |
| 4 | B | 20 | ARG | 2.2 |
| 4 | B | 73 | LEU | 2.2 |
| 5 | L | 79 | SER | 2.2 |
| 6 | M | 196 | CYS | 2.2 |
| 6 | U | 138 | LEU | 2.2 |
| 2 | O | 96 | CYS | 2.2 |
| 4 | S | 24 | GLY | 2.1 |
| 1 | Q | 497 | ALA | 2.1 |
| 4 | K | 148 | ALA | 2.1 |
| 2 | O | 118 | GLY | 2.1 |
| 4 | B | 97 | VAL | 2.1 |
| 6 | U | 8 | GLY | 2.1 |
| 4 | K | 204 | GLU | 2.1 |
| 6 | M | 134 | GLY | 2.1 |
| 1 | F | 496 | VAL | 2.1 |
| 4 | B | 168 | GLN | 2.1 |
| 6 | U | 160 | THR | 2.1 |
| 5 | L | 135 | ALA | 2.1 |
| 1 | Q | 460 | ALA | 2.1 |
| 2 | W | 53 | PRO | 2.1 |
| 2 | W | 4 | LEU | 2.1 |
| 1 | Q | 476 | ARG | 2.1 |
| 4 | S | 177 | SER | 2.1 |
| 7 | V | 19 | VAL | 2.1 |
| 2 | W | 10 | GLN | 2.1 |
| 6 | H | 131 | THR | 2.1 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 6 | H | 72 | ASP | 2.1 |
| 5 | C | 29 | VAL | 2.1 |
| 4 | K | 126 | LEU | 2.1 |
| 4 | K | 151 | ALA | 2.1 |
| 1 | G | 498 | PRO | 2.1 |
| 1 | F | 257 | THR | 2.1 |
| 4 | S | 45 | SER | 2.1 |
| 2 | W | 177 | GLY | 2.1 |
| 4 | K | 25 | GLU | 2.1 |
| 4 | S | 162 | THR | 2.1 |
| 2 | O | 164 | PRO | 2.1 |
| 6 | U | 52 | SER | 2.1 |
| 6 | M | 13 | LYS | 2.1 |
| 5 | T | 161 | VAL | 2.1 |
| 6 | U | 71 | THR | 2.1 |
| 1 | F | 32 | GLU | 2.1 |
| 6 | U | 148 | GLU | 2.1 |
| 7 | N | 104 | VAL | 2.1 |
| 2 | D | 130 | PRO | 2.1 |
| 2 | W | 20 | LEU | 2.1 |
| 4 | S | 100 | GLU | 2.1 |
| 2 | D | 67 | ARG | 2.1 |
| 1 | F | 368 | ASP | 2.1 |
| 5 | L | 210 | GLU | 2.1 |
| 3 | R | 598 | CYS | 2.1 |
| 4 | K | 150 | LYS | 2.1 |
| 7 | N | 120 | PRO | 2.1 |
| 5 | L | 116 | GLY | 2.1 |
| 7 | I | 146 | VAL | 2.1 |
| 1 | G | 50 | THR | 2.1 |
| 1 | G | 264 | SER | 2.1 |
| 4 | S | 150 | LYS | 2.1 |
| 6 | M | 167 | PRO | 2.1 |
| 7 | N | 119 | PRO | 2.1 |
| 1 | Q | 49 | GLU | 2.1 |
| 2 | D | 146 | ARG | 2.1 |
| 4 | B | 132 | THR | 2.1 |
| 1 | F | 253 | PRO | 2.1 |
| 1 | Q | 59 | LYS | 2.1 |
| 3 | J | 523 | LEU | 2.1 |
| 5 | C | 165 | PRO | 2.1 |
| 1 | F | 280 | ASN | 2.1 |

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| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 5 | C | 194 | CYS | 2.0 |
| 1 | Q | 125 | LEU | 2.0 |
| 2 | D | 55 | GLY | 2.0 |
| 6 | M | 223 | LEU | 2.0 |
| 1 | F | 281 | ALA | 2.0 |
| 2 | O | 24 | ALA | 2.0 |
| 2 | W | 71 | THR | 2.0 |
| 5 | L | 193 | ILE | 2.0 |
| 6 | M | 193 | THR | 2.0 |
| 7 | N | 197 | HIS | 2.0 |
| 4 | S | 210 | THR | 2.0 |
| 5 | T | 203 | THR | 2.0 |
| 7 | V | 127 | ALA | 2.0 |
| 1 | Q | 264 | SER | 2.0 |
| 5 | T | 180 | VAL | 2.0 |
| 4 | K | 107 | LEU | 2.0 |
| 4 | S | 158 | ALA | 2.0 |
| 5 | T | 84 | ALA | 2.0 |
| 2 | O | 200 | SER | 2.0 |
| 6 | U | 34 | ILE | 2.0 |
| 1 | Q | 325 | ASP | 2.0 |
| 2 | O | 220 | VAL | 2.0 |
| 1 | G | 192 | ARG | 2.0 |
| 6 | H | 109 | LEU | 2.0 |
| 1 | G | 191 | TYR | 2.0 |

## 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, $95^{th}$ 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 |
|---|---|---|---|---|---|---|---|---|
| 2 | PCA | W | 1 | 8/9 | 0.51 | 0.94 | 355,368,480,481 | 0 |
| 2 | PCA | D | 1 | 8/9 | 0.56 | 0.90 | 434,443,508,513 | 0 |

## 6.3 Carbohydrates (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, $95^{th}$ 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 | BMA | o | 3 | 11/12 | 0.00 | 1.08 | 641,642,644,644 | 0 |
| 14 | MAN | m | 8 | 11/12 | 0.02 | 0.92 | 506,514,524,533 | 0 |
| 11 | MAN | Z | 6 | 11/12 | 0.06 | 0.58 | 708,709,711,711 | 0 |
| 11 | MAN | r | 7 | 11/12 | 0.22 | 0.89 | 620,620,620,620 | 0 |
| 11 | MAN | Z | 7 | 11/12 | 0.28 | 0.84 | 488,488,488,488 | 0 |
| 8 | MAN | p | 4 | 11/12 | 0.34 | 0.59 | 563,590,602,606 | 0 |
| 11 | BMA | r | 3 | 11/12 | 0.34 | 0.46 | 549,550,550,551 | 0 |
| 9 | BMA | P | 3 | 11/12 | 0.35 | 0.78 | 536,538,539,539 | 0 |
| 8 | MAN | g | 5 | 11/12 | 0.36 | 0.54 | 526,544,561,562 | 0 |
| 12 | MAN | s | 5 | 11/12 | 0.38 | 0.72 | 589,589,589,589 | 0 |
| 8 | MAN | X | 5 | 11/12 | 0.43 | 0.33 | 510,528,545,546 | 0 |
| 8 | MAN | e | 5 | 11/12 | 0.45 | 0.57 | 555,558,560,561 | 0 |
| 11 | BMA | Z | 3 | 11/12 | 0.45 | 0.43 | 541,543,545,545 | 0 |
| 8 | MAN | n | 4 | 11/12 | 0.49 | 0.56 | 422,422,423,424 | 0 |
| 14 | MAN | v | 8 | 11/12 | 0.49 | 0.62 | 480,486,493,502 | 0 |
| 11 | BMA | i | 3 | 11/12 | 0.50 | 0.62 | 485,487,490,492 | 0 |
| 8 | BMA | e | 3 | 11/12 | 0.50 | 0.66 | 558,559,560,562 | 0 |
| 8 | MAN | p | 5 | 11/12 | 0.51 | 0.59 | 546,563,582,583 | 0 |
| 10 | MAN | h | 4 | 11/12 | 0.52 | 0.57 | 519,522,525,526 | 0 |
| 10 | BMA | h | 3 | 11/12 | 0.54 | 0.50 | 437,440,442,443 | 0 |
| 8 | MAN | l | 5 | 11/12 | 0.55 | 0.61 | 622,623,625,625 | 0 |
| 8 | MAN | e | 4 | 11/12 | 0.56 | 0.53 | 508,509,512,512 | 0 |
| 9 | NAG | P | 2 | 14/15 | 0.57 | 0.43 | 511,513,515,517 | 0 |
| 8 | BMA | p | 3 | 11/12 | 0.57 | 0.54 | 527,544,557,575 | 0 |
| 8 | BMA | n | 3 | 11/12 | 0.58 | 0.52 | 470,471,471,471 | 0 |
| 8 | MAN | g | 4 | 11/12 | 0.58 | 0.52 | 637,667,676,683 | 0 |
| 10 | MAN | q | 4 | 11/12 | 0.58 | 0.36 | 526,527,528,529 | 0 |
| 8 | BMA | g | 3 | 11/12 | 0.59 | 0.36 | 626,642,653,670 | 0 |
| 8 | MAN | c | 5 | 11/12 | 0.59 | 0.50 | 540,543,547,549 | 0 |
| 8 | NAG | e | 2 | 14/15 | 0.60 | 0.66 | 499,504,507,509 | 0 |
| 10 | MAN | Y | 4 | 11/12 | 0.60 | 0.61 | 580,581,582,583 | 0 |
| 11 | NAG | i | 2 | 14/15 | 0.60 | 0.51 | 501,506,509,511 | 0 |
| 12 | MAN | j | 6 | 11/12 | 0.61 | 0.89 | 507,511,517,517 | 0 |
| 12 | MAN | j | 5 | 11/12 | 0.61 | 0.61 | 453,467,469,470 | 0 |
| 8 | MAN | n | 5 | 11/12 | 0.62 | 0.43 | 457,458,458,459 | 0 |
| 14 | MAN | m | 6 | 11/12 | 0.63 | 0.53 | 469,477,482,485 | 0 |
| 8 | BMA | c | 3 | 11/12 | 0.65 | 0.35 | 512,514,518,519 | 0 |
| 11 | MAN | r | 5 | 11/12 | 0.65 | 0.66 | 605,605,606,607 | 0 |
| 9 | NAG | f | 2 | 14/15 | 0.65 | 0.47 | 485,488,490,491 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 14 | MAN | d | 8 | 11/12 | 0.66 | 0.49 | 390,393,399,407 | 0 |
| 8 | MAN | X | 4 | 11/12 | 0.66 | 0.51 | 521,546,562,562 | 0 |
| 8 | MAN | E | 4 | 11/12 | 0.66 | 0.54 | 400,402,404,404 | 0 |
| 10 | NAG | Y | 1 | 14/15 | 0.66 | 0.45 | 401,402,404,405 | 0 |
| 9 | NAG | f | 1 | 14/15 | 0.67 | 0.57 | 473,478,482,482 | 0 |
| 9 | NAG | o | 2 | 14/15 | 0.68 | 0.50 | 620,622,625,626 | 0 |
| 8 | NAG | l | 1 | 14/15 | 0.68 | 0.50 | 477,479,481,483 | 0 |
| 8 | MAN | c | 4 | 11/12 | 0.69 | 0.52 | 502,506,510,511 | 0 |
| 11 | MAN | i | 7 | 11/12 | 0.69 | 0.67 | 448,448,448,448 | 0 |
| 14 | NAG | d | 1 | 14/15 | 0.70 | 0.47 | 456,462,468,471 | 0 |
| 11 | MAN | i | 4 | 11/12 | 0.71 | 0.31 | 489,492,496,496 | 0 |
| 12 | MAN | a | 5 | 11/12 | 0.71 | 0.41 | 502,517,520,521 | 0 |
| 11 | MAN | r | 4 | 11/12 | 0.71 | 0.30 | 576,577,579,579 | 0 |
| 10 | NAG | h | 2 | 14/15 | 0.71 | 0.44 | 419,421,424,425 | 0 |
| 11 | MAN | r | 6 | 11/12 | 0.71 | 0.28 | 454,455,456,457 | 0 |
| 8 | NAG | n | 1 | 14/15 | 0.72 | 0.36 | 426,428,429,430 | 0 |
| 11 | MAN | Z | 4 | 11/12 | 0.72 | 0.36 | 613,615,616,616 | 0 |
| 11 | NAG | r | 2 | 14/15 | 0.73 | 0.44 | 509,510,511,511 | 0 |
| 10 | BMA | q | 3 | 11/12 | 0.73 | 0.35 | 489,490,491,492 | 0 |
| 11 | NAG | Z | 2 | 14/15 | 0.73 | 0.40 | 470,472,474,476 | 0 |
| 11 | MAN | i | 5 | 11/12 | 0.74 | 0.50 | 507,509,513,514 | 0 |
| 8 | MAN | l | 4 | 11/12 | 0.74 | 0.38 | 512,515,515,517 | 0 |
| 14 | MAN | v | 6 | 11/12 | 0.74 | 0.25 | 481,485,491,492 | 0 |
| 14 | NAG | m | 2 | 14/15 | 0.74 | 0.46 | 427,437,446,456 | 0 |
| 9 | NAG | o | 1 | 14/15 | 0.75 | 0.41 | 542,543,544,545 | 0 |
| 11 | NAG | i | 1 | 14/15 | 0.75 | 0.40 | 417,419,420,421 | 0 |
| 11 | MAN | Z | 5 | 11/12 | 0.76 | 0.55 | 582,584,585,586 | 0 |
| 12 | MAN | s | 6 | 11/12 | 0.77 | 0.40 | 440,445,450,450 | 0 |
| 14 | MAN | d | 7 | 11/12 | 0.77 | 0.75 | 499,503,504,506 | 0 |
| 8 | BMA | l | 3 | 11/12 | 0.78 | 0.23 | 537,539,542,542 | 0 |
| 14 | MAN | v | 4 | 11/12 | 0.78 | 0.38 | 452,458,471,472 | 0 |
| 12 | MAN | s | 4 | 11/12 | 0.78 | 0.46 | 567,567,567,567 | 0 |
| 8 | NAG | n | 2 | 14/15 | 0.78 | 0.56 | 492,493,494,495 | 0 |
| 14 | BMA | m | 3 | 11/12 | 0.79 | 0.36 | 470,474,482,483 | 0 |
| 8 | BMA | X | 3 | 11/12 | 0.79 | 0.23 | 526,543,558,577 | 0 |
| 14 | NAG | m | 1 | 14/15 | 0.80 | 0.38 | 426,430,436,438 | 0 |
| 9 | NAG | P | 1 | 14/15 | 0.80 | 0.32 | 529,532,535,535 | 0 |
| 14 | MAN | v | 5 | 11/12 | 0.80 | 0.37 | 454,458,461,462 | 0 |
| 11 | MAN | i | 6 | 11/12 | 0.80 | 0.23 | 438,440,445,447 | 0 |
| 10 | BMA | Y | 3 | 11/12 | 0.80 | 0.46 | 467,469,470,471 | 0 |
| 11 | NAG | r | 1 | 14/15 | 0.81 | 0.34 | 388,390,392,393 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 8 | NAG | l | 2 | 14/15 | 0.81 | 0.29 | 461,463,465,465 | 0 |
| 8 | NAG | g | 2 | 14/15 | 0.81 | 0.33 | 531,555,576,580 | 0 |
| 12 | NAG | j | 1 | 14/15 | 0.81 | 0.58 | 433,439,447,461 | 0 |
| 14 | NAG | d | 2 | 14/15 | 0.81 | 0.54 | 452,460,471,473 | 0 |
| 12 | BMA | j | 3 | 11/12 | 0.81 | 0.29 | 407,417,420,424 | 0 |
| 8 | BMA | u | 3 | 11/12 | 0.81 | 0.19 | 480,480,481,481 | 0 |
| 10 | NAG | Y | 2 | 14/15 | 0.81 | 0.47 | 426,430,433,434 | 0 |
| 14 | BMA | v | 3 | 11/12 | 0.82 | 0.40 | 445,449,459,463 | 0 |
| 14 | MAN | d | 6 | 11/12 | 0.82 | 0.58 | 465,467,473,475 | 0 |
| 13 | NAG | t | 2 | 14/15 | 0.82 | 0.33 | 521,522,522,523 | 0 |
| 8 | NAG | p | 2 | 14/15 | 0.82 | 0.53 | 465,488,513,516 | 0 |
| 13 | NAG | t | 1 | 14/15 | 0.82 | 0.24 | 446,447,448,449 | 0 |
| 12 | MAN | a | 4 | 11/12 | 0.83 | 0.32 | 479,498,500,501 | 0 |
| 14 | BMA | d | 3 | 11/12 | 0.83 | 0.48 | 471,476,486,491 | 0 |
| 10 | NAG | q | 1 | 14/15 | 0.83 | 0.34 | 404,407,410,412 | 0 |
| 8 | BMA | E | 3 | 11/12 | 0.84 | 0.37 | 434,435,439,440 | 0 |
| 12 | BMA | a | 3 | 11/12 | 0.84 | 0.27 | 418,427,431,437 | 0 |
| 8 | MAN | u | 4 | 11/12 | 0.84 | 0.37 | 558,559,560,561 | 0 |
| 10 | NAG | h | 1 | 14/15 | 0.84 | 0.40 | 345,348,350,351 | 0 |
| 12 | MAN | a | 6 | 11/12 | 0.84 | 0.42 | 408,413,418,418 | 0 |
| 8 | NAG | X | 2 | 14/15 | 0.84 | 0.26 | 418,443,465,472 | 0 |
| 8 | NAG | c | 2 | 14/15 | 0.85 | 0.25 | 410,416,420,420 | 0 |
| 14 | MAN | v | 7 | 11/12 | 0.85 | 0.28 | 455,460,462,463 | 0 |
| 14 | MAN | m | 7 | 11/12 | 0.85 | 0.62 | 425,428,432,433 | 0 |
| 8 | MAN | E | 5 | 11/12 | 0.86 | 0.51 | 482,484,485,485 | 0 |
| 11 | NAG | Z | 1 | 14/15 | 0.86 | 0.31 | 401,403,404,404 | 0 |
| 8 | NAG | g | 1 | 14/15 | 0.86 | 0.27 | 414,418,440,441 | 0 |
| 13 | NAG | b | 1 | 14/15 | 0.86 | 0.19 | 374,378,381,382 | 0 |
| 13 | NAG | k | 1 | 14/15 | 0.86 | 0.23 | 367,370,375,376 | 0 |
| 12 | MAN | j | 4 | 11/12 | 0.87 | 0.65 | 469,484,487,488 | 0 |
| 9 | BMA | f | 3 | 11/12 | 0.87 | 0.27 | 435,438,442,444 | 0 |
| 8 | NAG | X | 1 | 14/15 | 0.87 | 0.27 | 395,399,426,427 | 0 |
| 12 | NAG | s | 1 | 14/15 | 0.87 | 0.36 | 420,425,434,447 | 0 |
| 12 | BMA | s | 3 | 11/12 | 0.87 | 0.25 | 508,516,520,524 | 0 |
| 12 | NAG | j | 2 | 14/15 | 0.88 | 0.43 | 366,376,381,387 | 0 |
| 12 | NAG | a | 2 | 14/15 | 0.88 | 0.28 | 366,377,383,390 | 0 |
| 8 | NAG | E | 1 | 14/15 | 0.88 | 0.26 | 366,367,368,369 | 0 |
| 12 | NAG | a | 1 | 14/15 | 0.88 | 0.36 | 324,331,339,351 | 0 |
| 14 | MAN | m | 5 | 11/12 | 0.89 | 0.18 | 384,389,393,393 | 0 |
| 10 | NAG | q | 2 | 14/15 | 0.89 | 0.27 | 485,487,489,489 | 0 |
| 8 | MAN | u | 5 | 11/12 | 0.89 | 0.24 | 435,435,438,438 | 0 |
| 14 | MAN | d | 4 | 11/12 | 0.89 | 0.24 | 410,421,430,432 | 0 |

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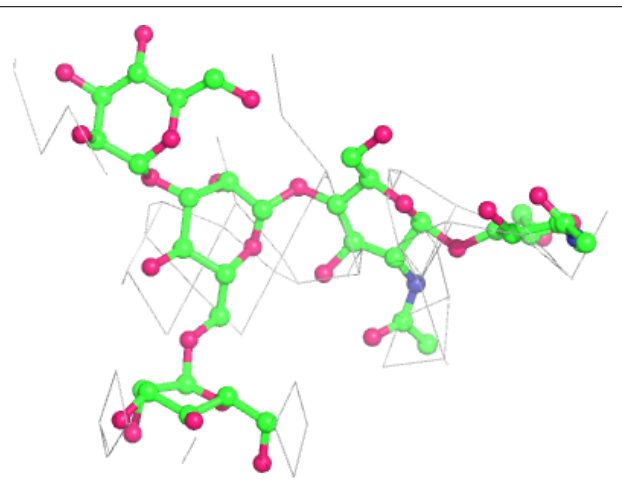
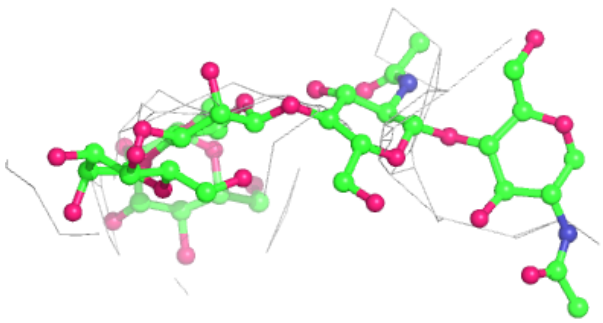
| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 14 | NAG | v | 1 | 14/15 | 0.89 | 0.23 | 374,381,388,390 | 0 |
| 14 | NAG | v | 2 | 14/15 | 0.89 | 0.31 | 432,437,446,450 | 0 |
| 8 | NAG | p | 1 | 14/15 | 0.90 | 0.28 | 364,371,393,395 | 0 |
| 8 | NAG | e | 1 | 14/15 | 0.90 | 0.28 | 444,448,454,455 | 0 |
| 8 | NAG | E | 2 | 14/15 | 0.90 | 0.23 | 430,433,437,437 | 0 |
| 13 | NAG | k | 2 | 14/15 | 0.91 | 0.23 | 416,421,426,426 | 0 |
| 14 | MAN | d | 5 | 11/12 | 0.91 | 0.24 | 392,395,397,399 | 0 |
| 13 | NAG | b | 2 | 14/15 | 0.91 | 0.33 | 398,401,404,406 | 0 |
| 8 | NAG | u | 2 | 14/15 | 0.91 | 0.18 | 352,353,354,354 | 0 |
| 8 | NAG | c | 1 | 14/15 | 0.92 | 0.23 | 348,350,351,353 | 0 |
| 8 | NAG | u | 1 | 14/15 | 0.93 | 0.21 | 345,347,349,350 | 0 |
| 14 | MAN | m | 4 | 11/12 | 0.93 | 0.17 | 400,403,419,420 | 0 |
| 12 | NAG | s | 2 | 14/15 | 0.94 | 0.25 | 434,446,451,458 | 0 |

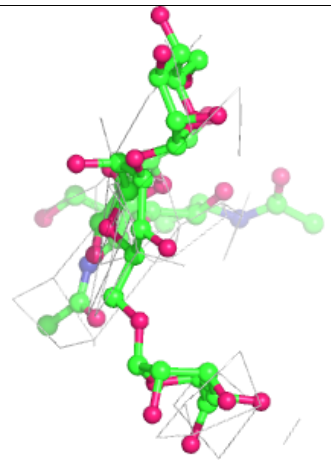
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around Chain E:**

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

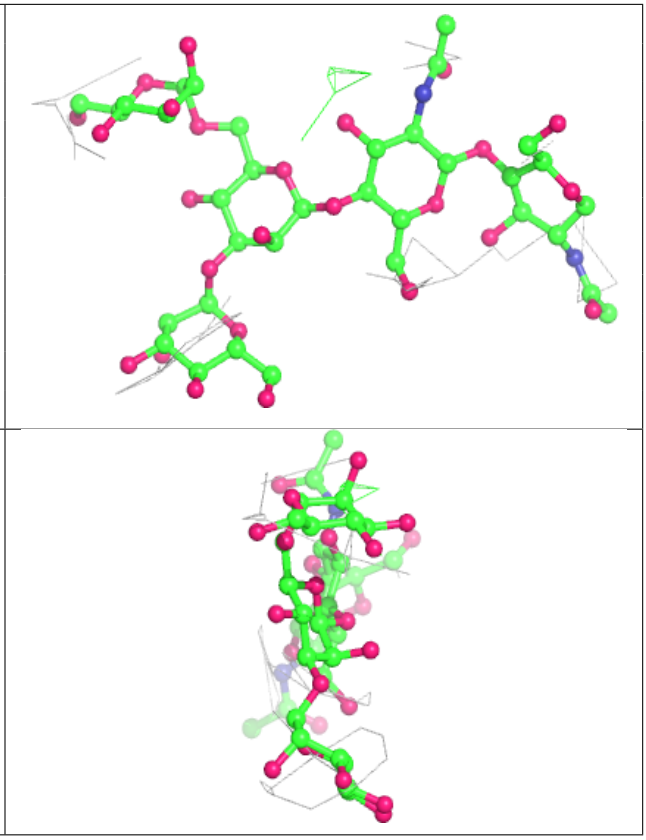






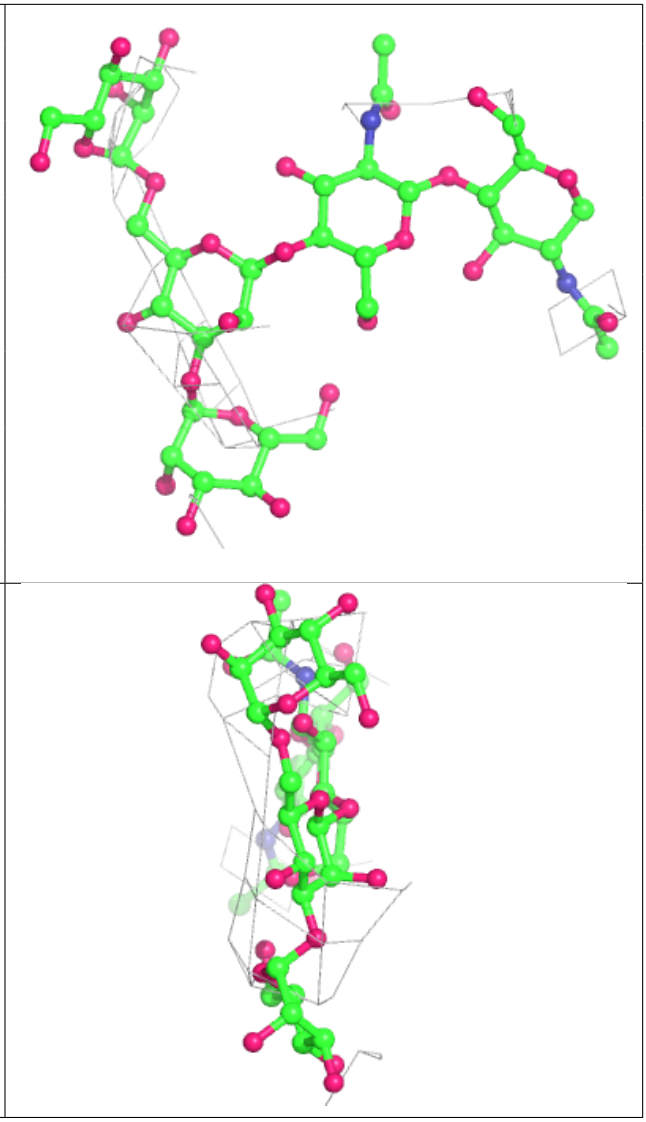
**Electron density around Chain X:**

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



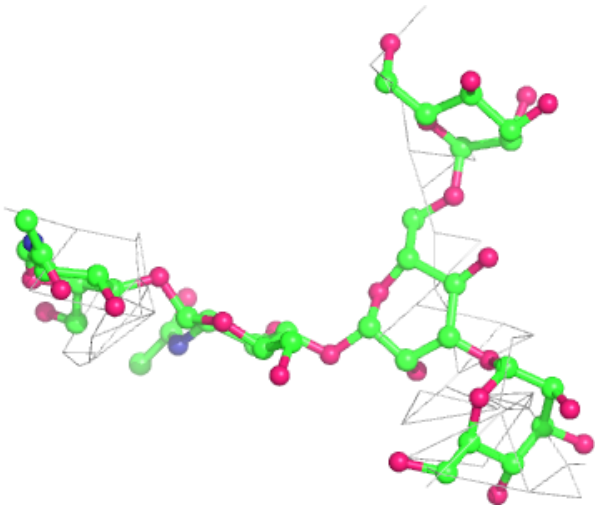
**Electron density around Chain c:**

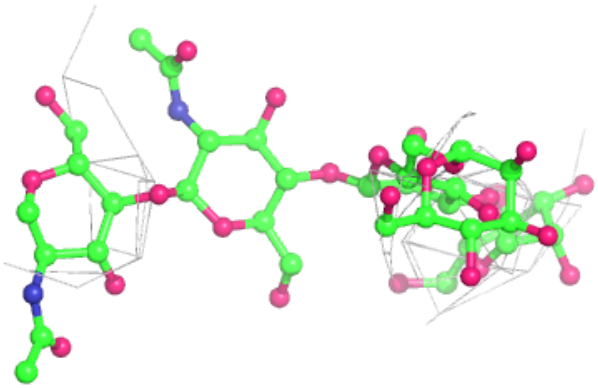
$2mF_o$-$DF_c$ (at 0.7 rmsd) in gray
$mF_o$-$DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

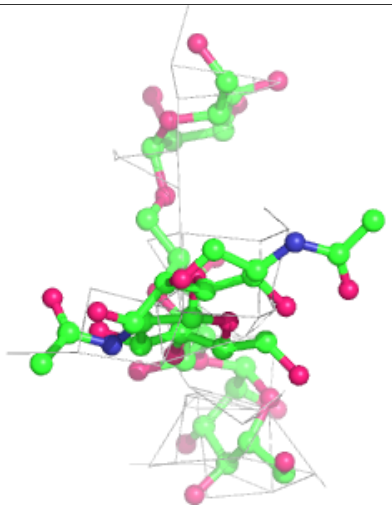


**Electron density around Chain e:**

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

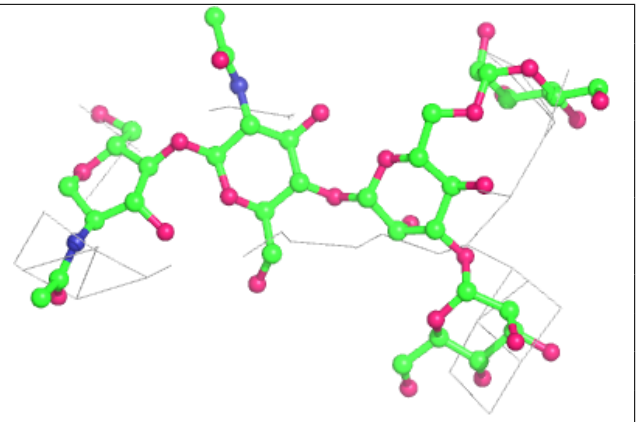


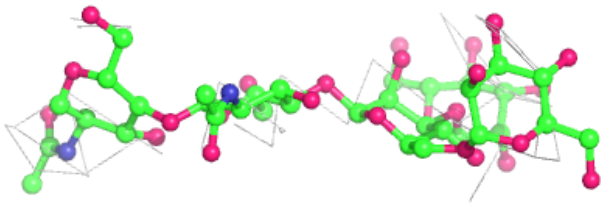


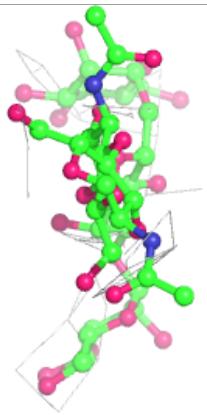


**Electron density around Chain g:**

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

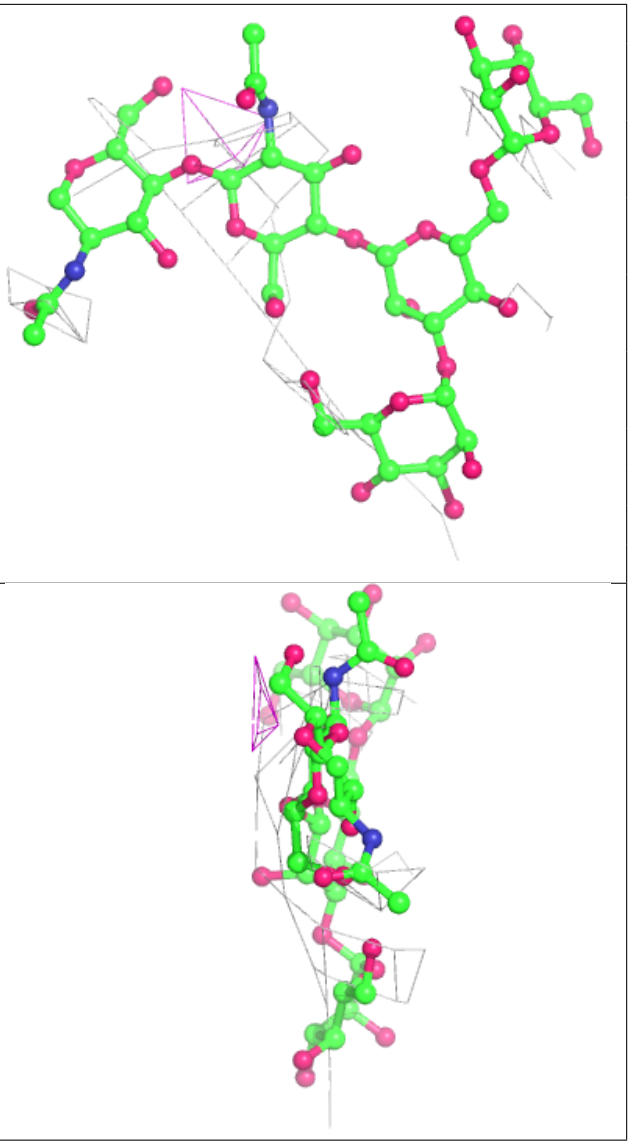






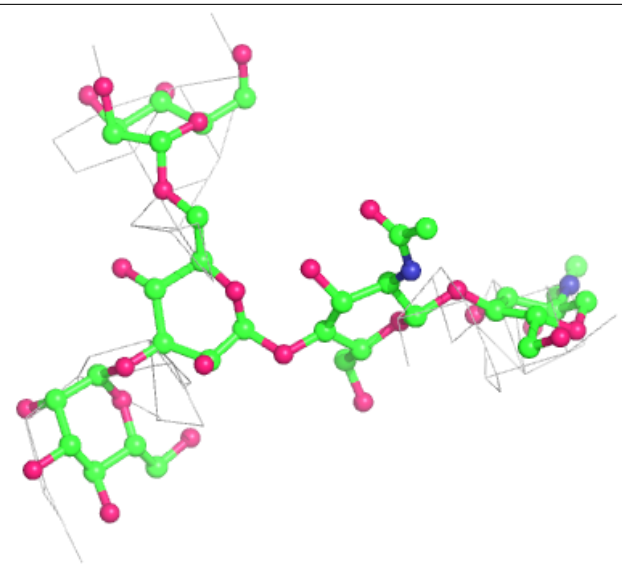
**Electron density around Chain l:**

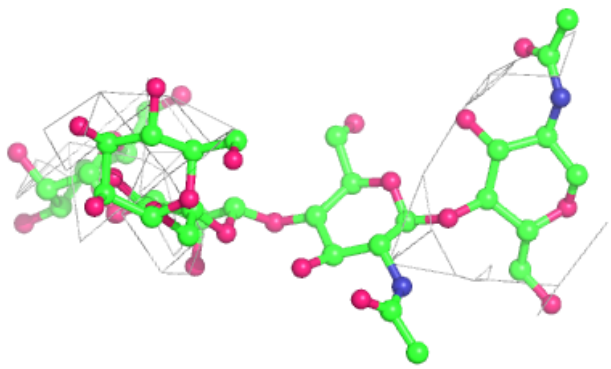
$2mF_o$-$DF_c$ (at 0.7 rmsd) in gray
$mF_o$-$DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

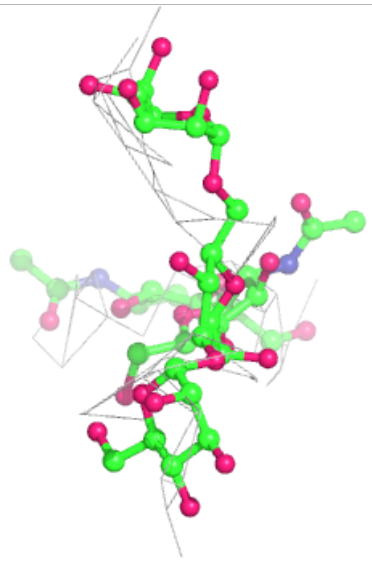


**Electron density around Chain n:**

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

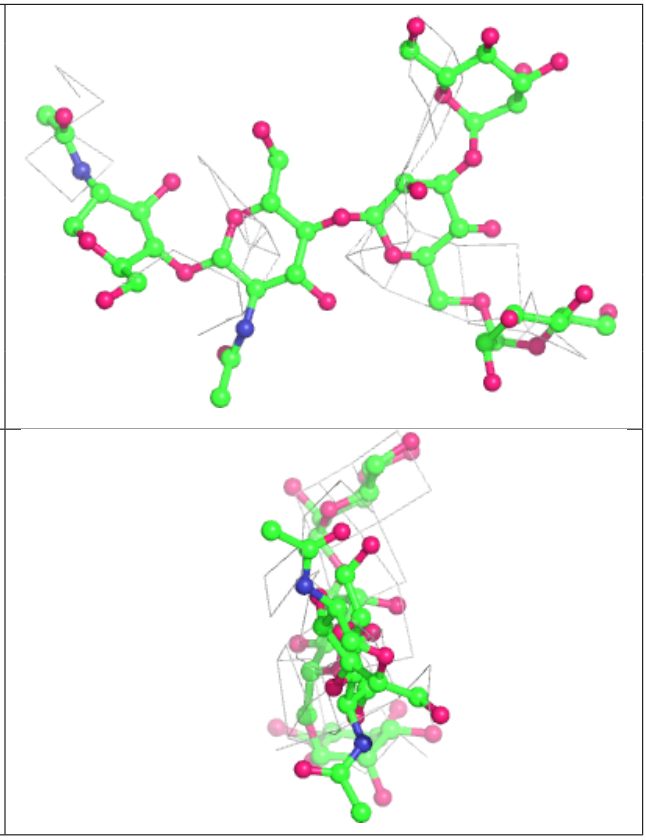






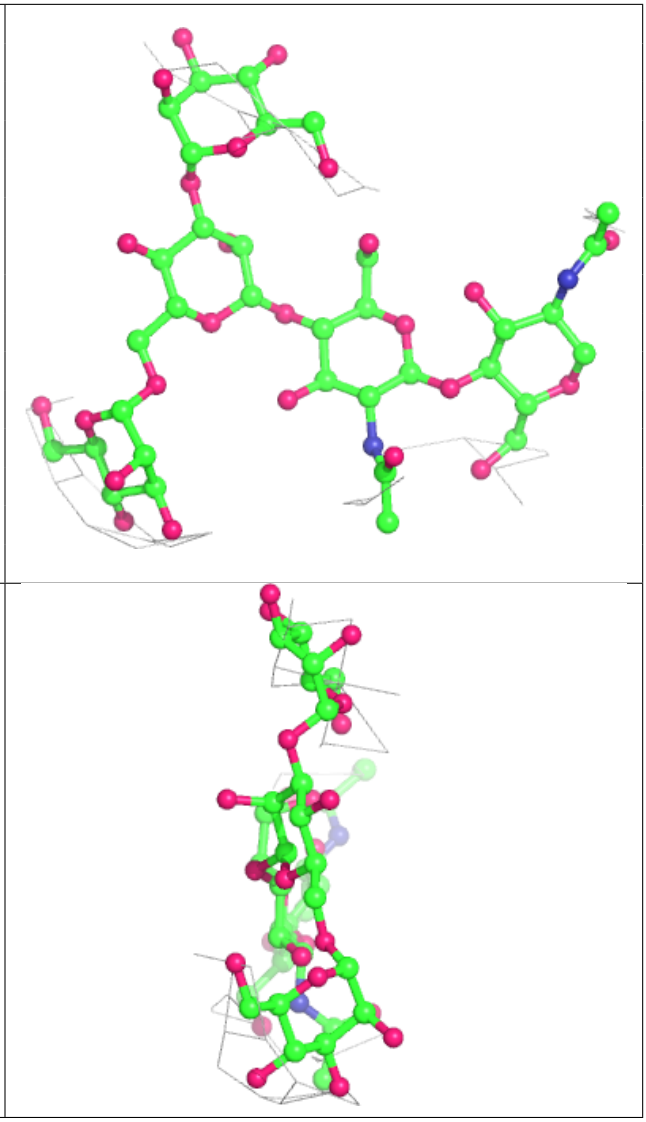
**Electron density around Chain p:**

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



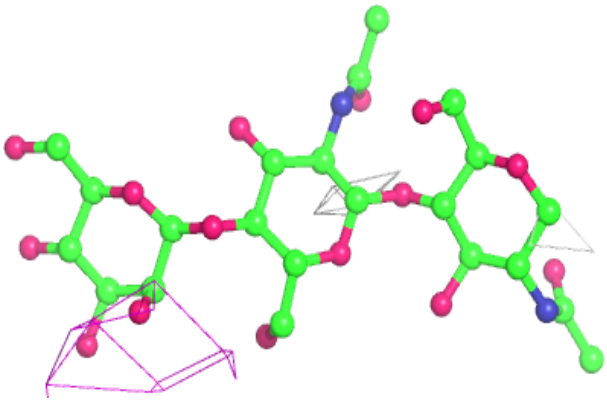
**Electron density around Chain u:**

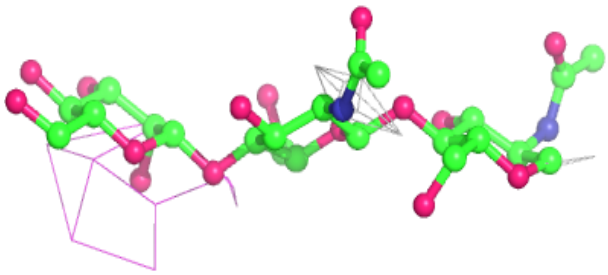
$2mF_o$-$DF_c$ (at 0.7 rmsd) in gray
$mF_o$-$DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

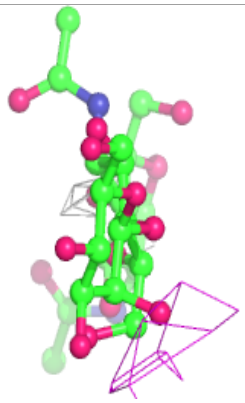


**Electron density around Chain P:**

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

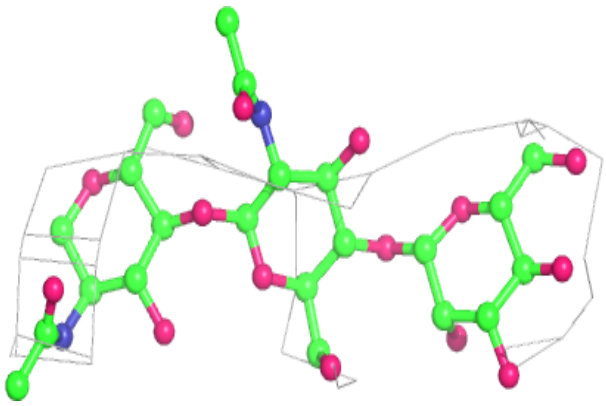


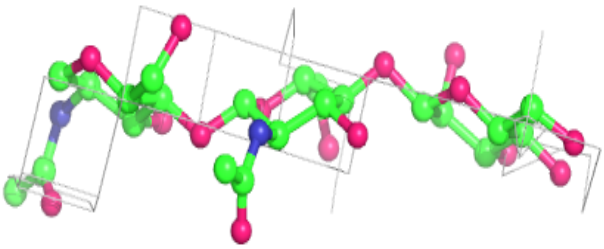


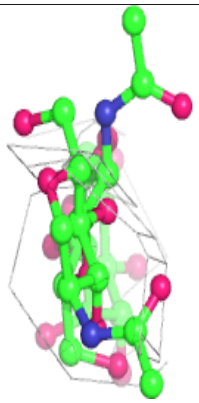


**Electron density around Chain f:**

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

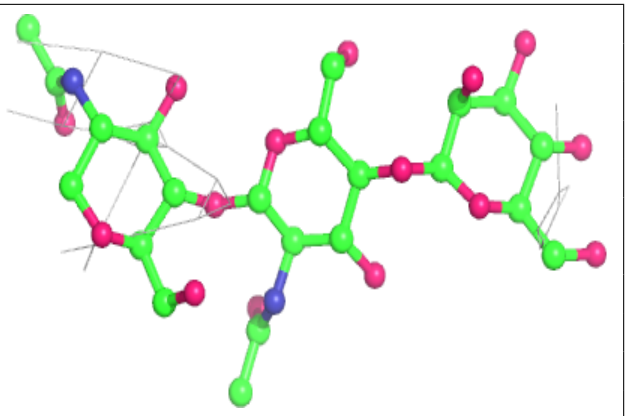


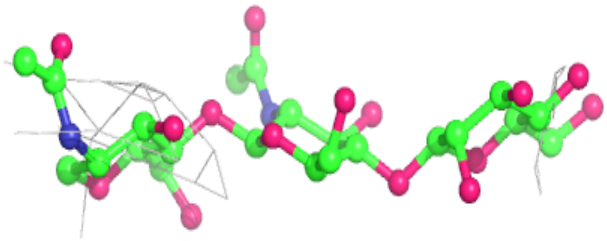


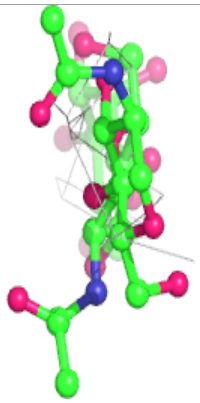


**Electron density around Chain o:**

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

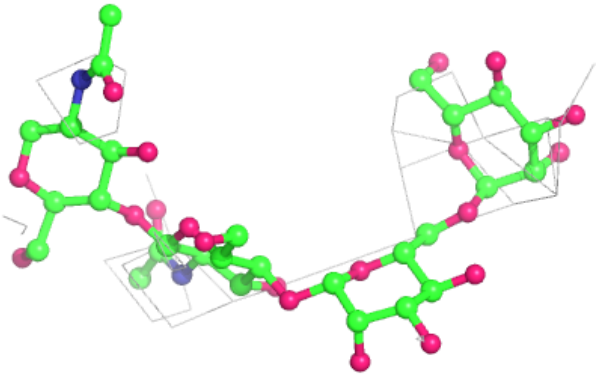


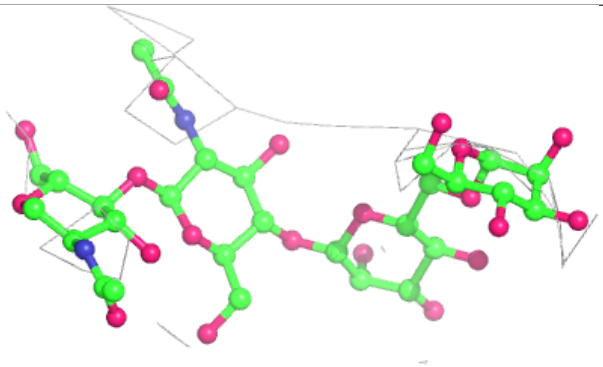


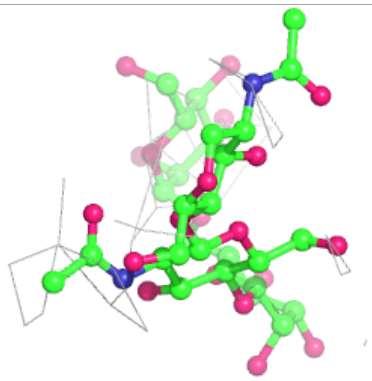


**Electron density around Chain Y:**

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

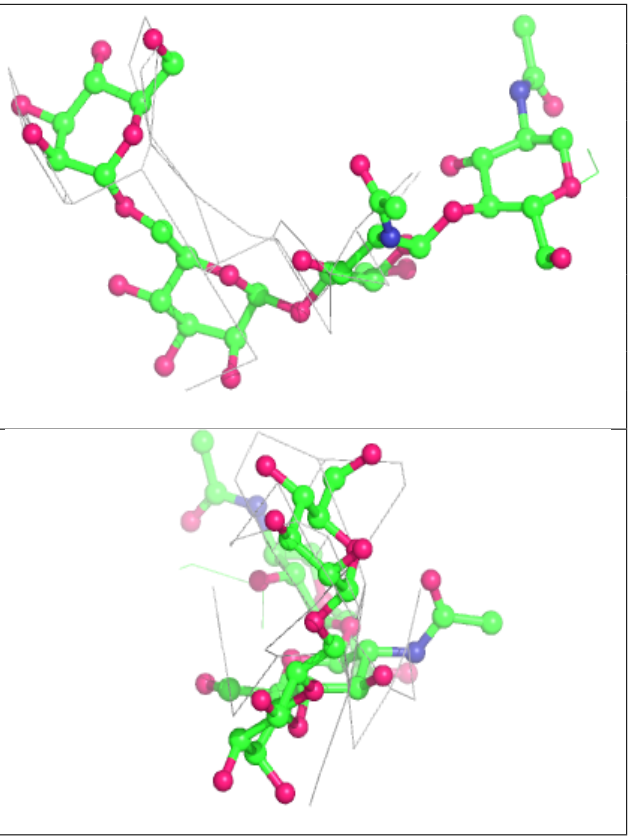






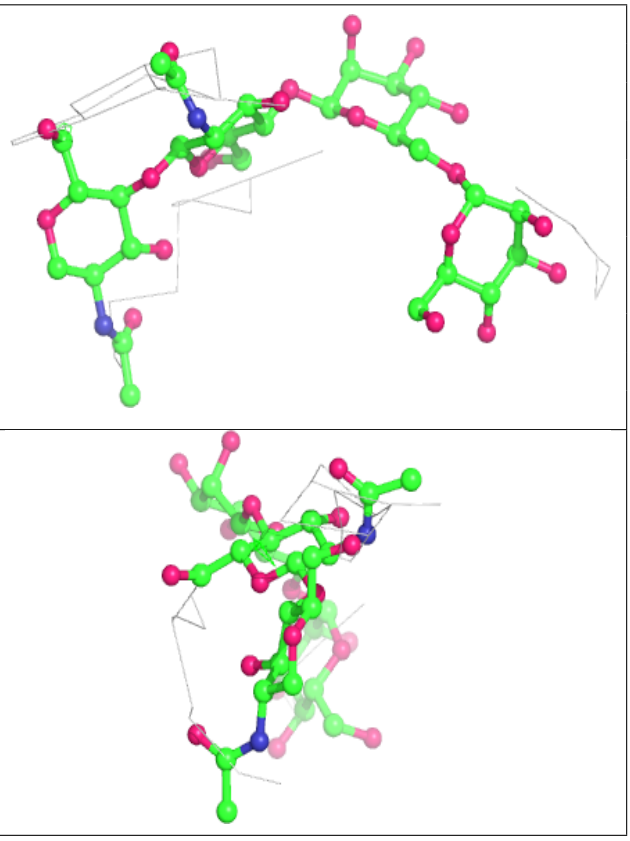
**Electron density around Chain h:**

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



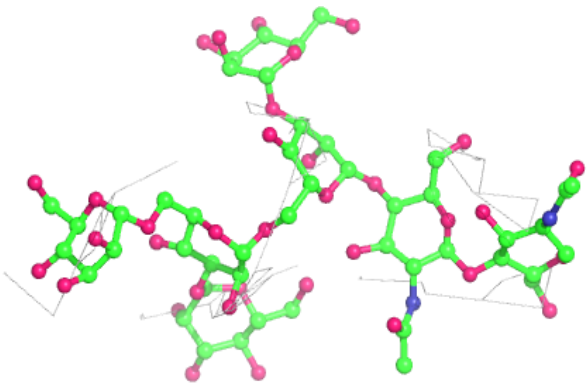
**Electron density around Chain q:**

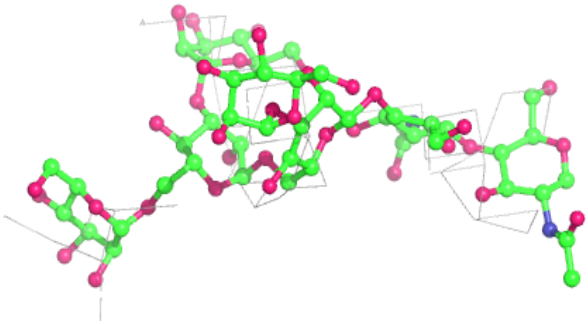
$2mF_o$-$DF_c$ (at 0.7 rmsd) in gray
$mF_o$-$DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

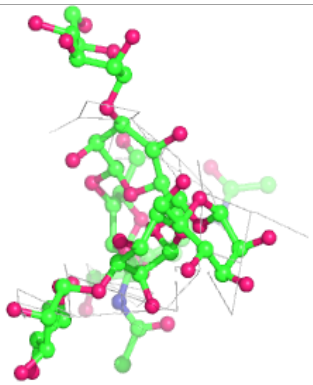


**Electron density around Chain Z:**

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

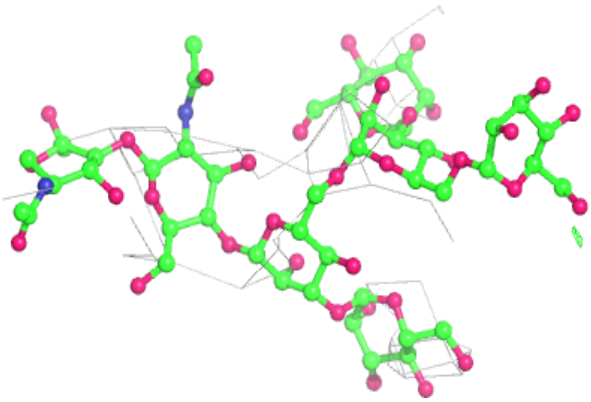


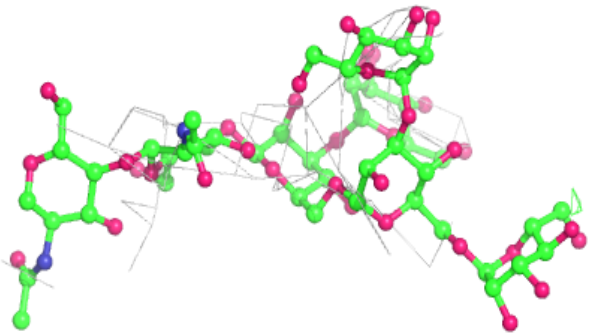


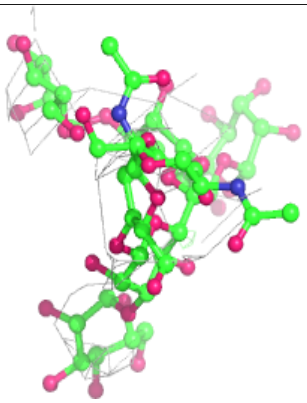


**Electron density around Chain i:**

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

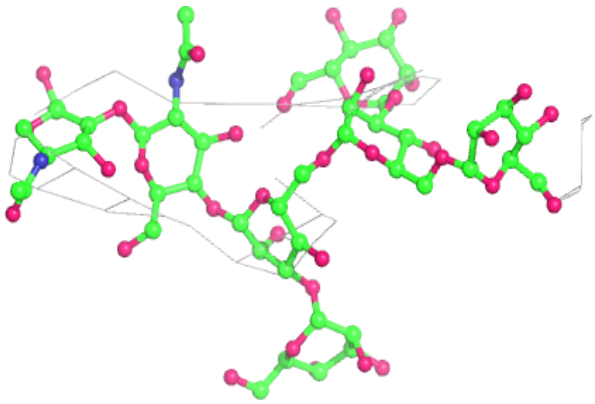


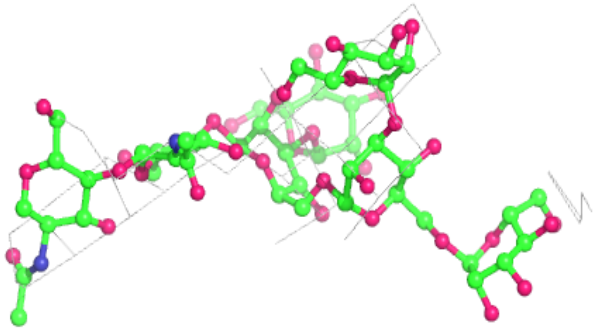


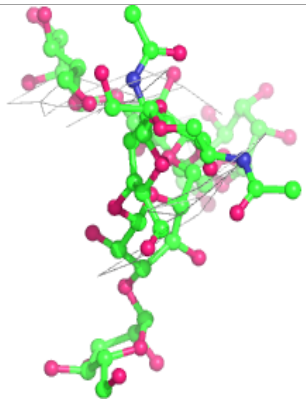


**Electron density around Chain r:**

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

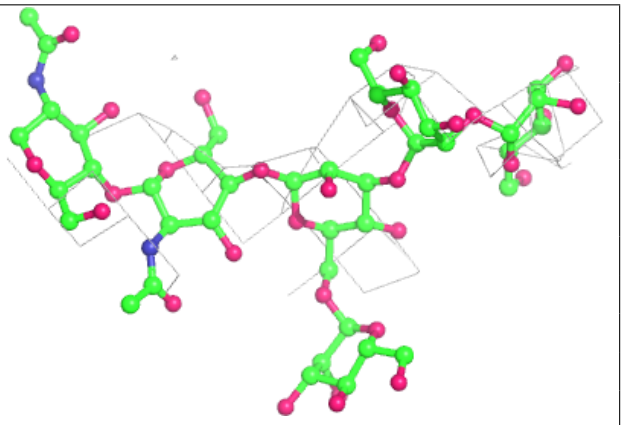


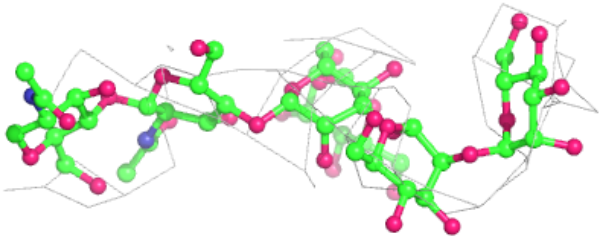


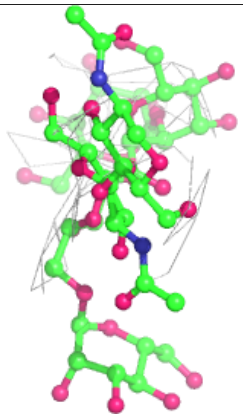


**Electron density around Chain a:**

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

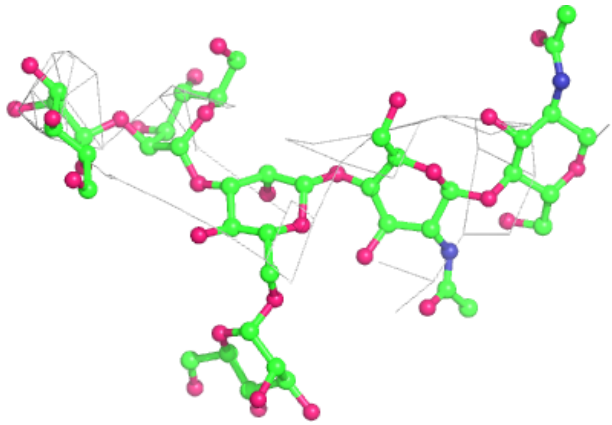


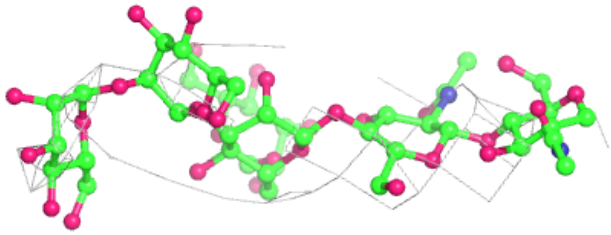


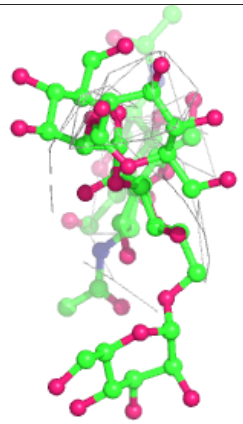


**Electron density around Chain j:**

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

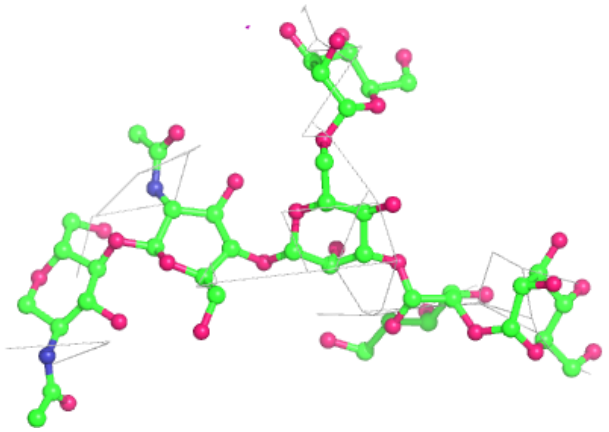


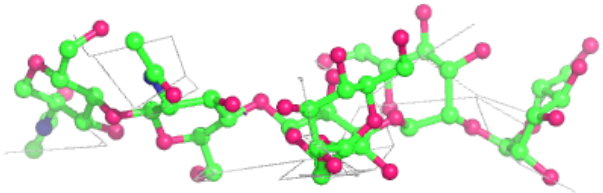


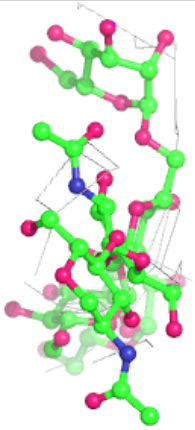


**Electron density around Chain s:**

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

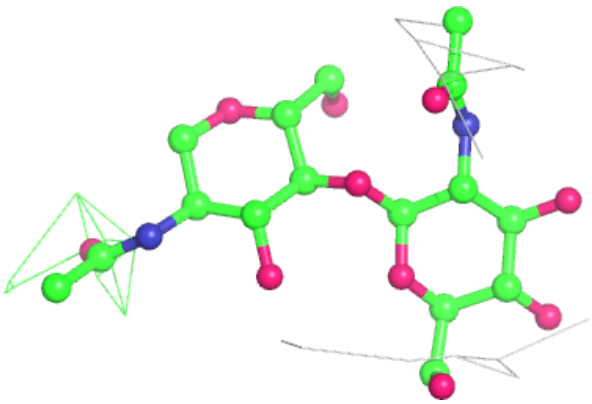


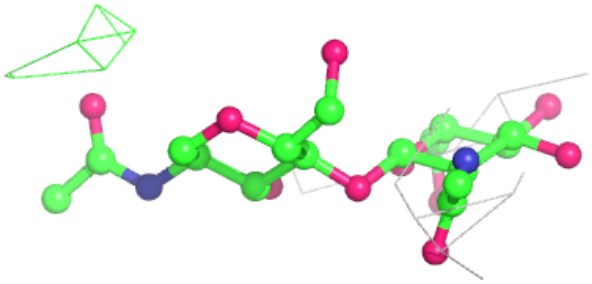


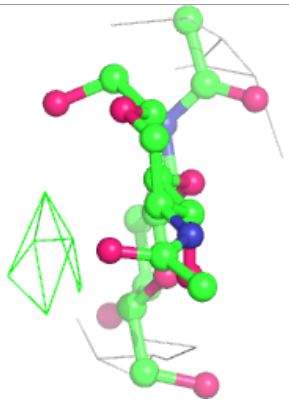


**Electron density around Chain b:**

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

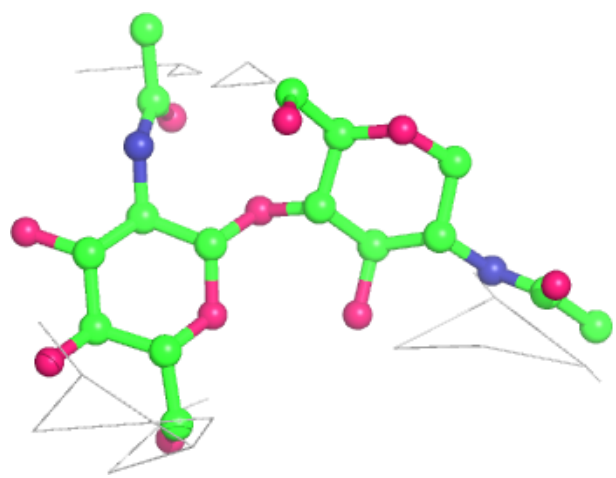


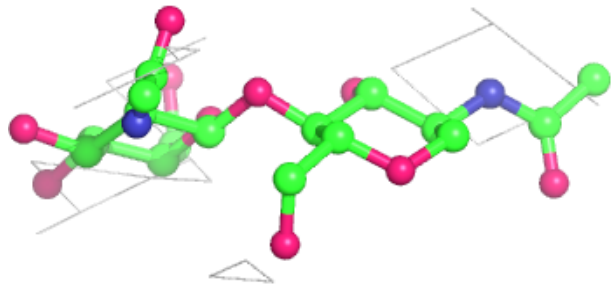


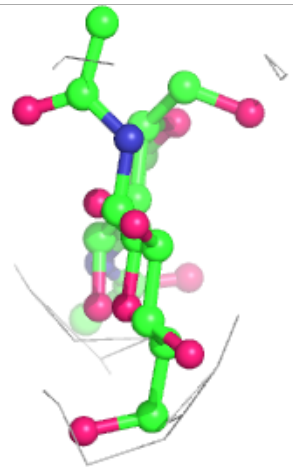


**Electron density around Chain k:**

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

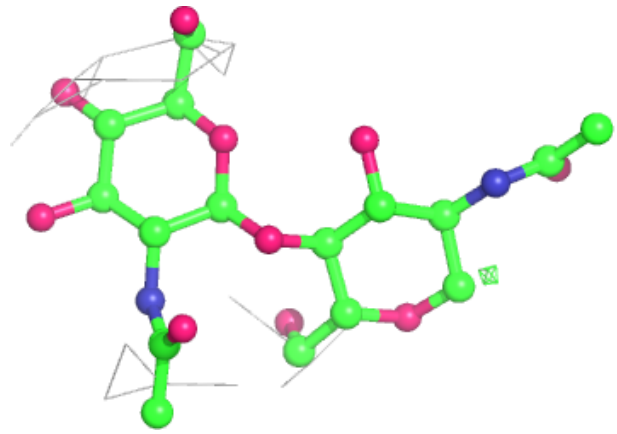


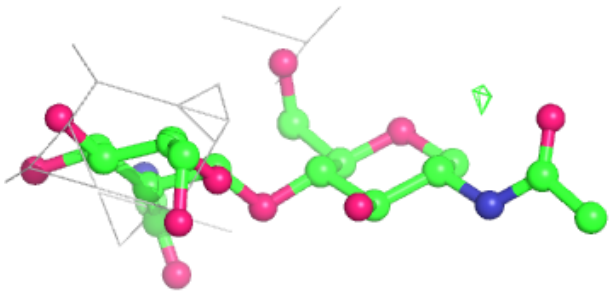


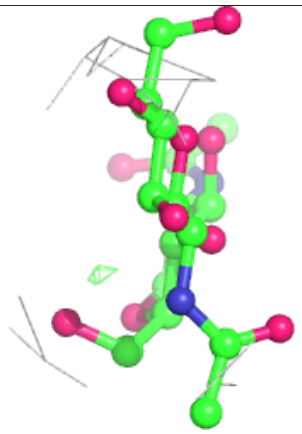


**Electron density around Chain t:**

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

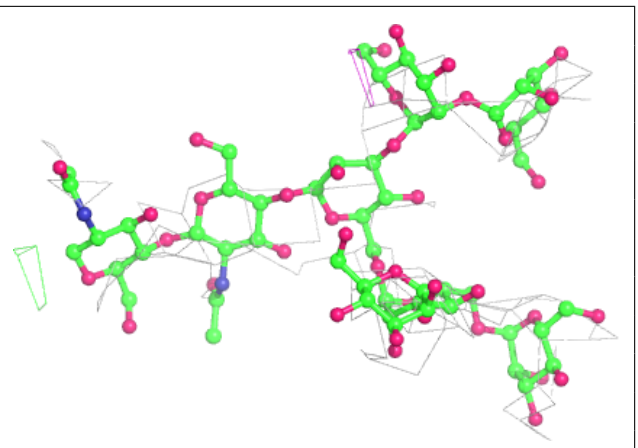


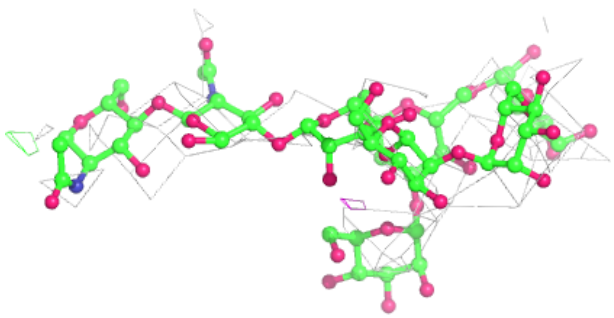


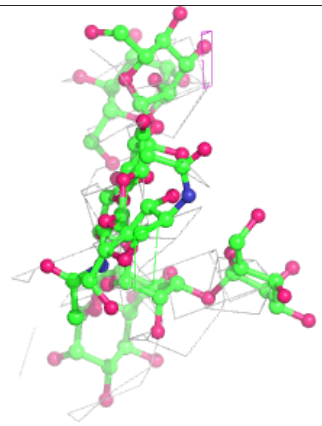


**Electron density around Chain d:**

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

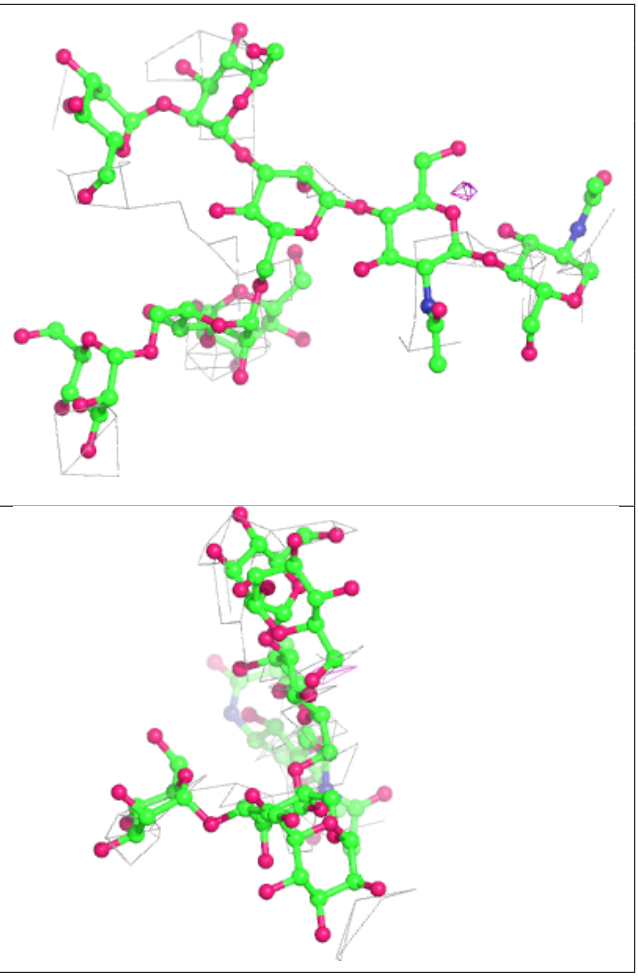






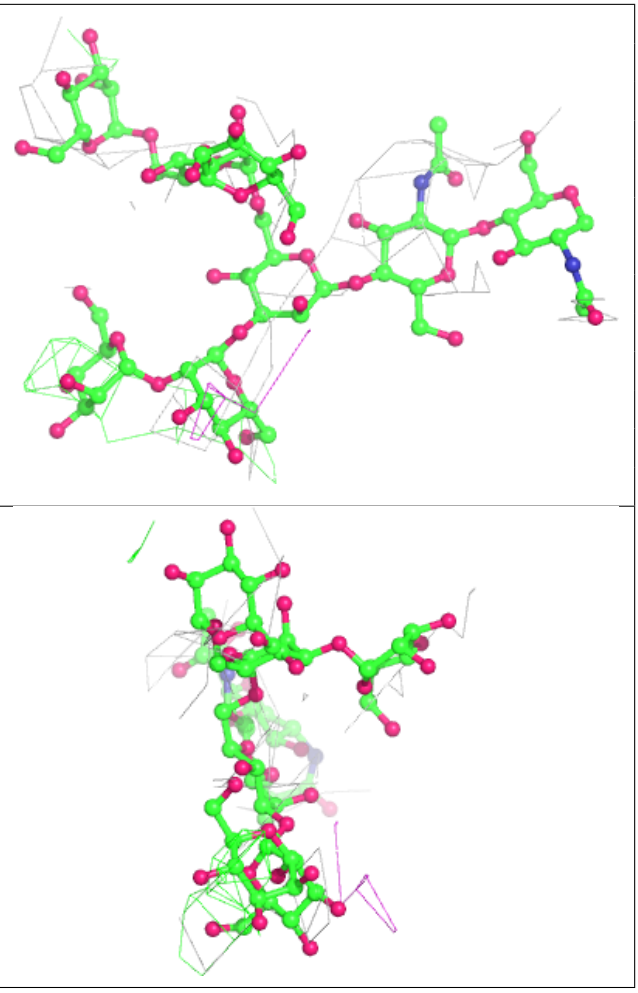
**Electron density around Chain m:**

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



**Electron density around Chain v:**

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



## 6.4 Ligands (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, $95^{th}$ 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 |
|---|---|---|---|---|---|---|---|---|
| 15 | NAG | G | 649 | 14/15 | 0.36 | 0.71 | 491,493,495,496 | 0 |
| 15 | NAG | Q | 615 | 14/15 | 0.46 | 0.77 | 499,500,501,502 | 0 |
| 15 | NAG | Q | 649 | 14/15 | 0.48 | 0.76 | 505,508,510,511 | 0 |
| 15 | NAG | F | 615 | 14/15 | 0.49 | 0.65 | 506,511,514,515 | 0 |
| 15 | NAG | R | 701 | 14/15 | 0.57 | 0.62 | 448,450,452,452 | 0 |
| 15 | NAG | F | 651 | 14/15 | 0.58 | 0.60 | 425,429,432,434 | 0 |
| 15 | NAG | Q | 651 | 14/15 | 0.59 | 0.82 | 446,448,449,449 | 0 |
| 15 | NAG | Q | 652 | 14/15 | 0.60 | 0.58 | 410,411,411,411 | 0 |
| 15 | NAG | G | 653 | 14/15 | 0.61 | 0.46 | 431,431,431,431 | 0 |
| 15 | NAG | R | 703 | 14/15 | 0.63 | 0.54 | 390,390,390,390 | 0 |

*Continued on next page...*

*Continued from previous page...*

| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 15 | NAG | G | 651 | 14/15 | 0.66 | 0.54 | 448,451,453,454 | 0 |
| 15 | NAG | J | 703 | 14/15 | 0.66 | 0.48 | 511,511,511,511 | 0 |
| 15 | NAG | F | 652 | 14/15 | 0.67 | 0.49 | 405,407,410,411 | 0 |
| 15 | NAG | Q | 633 | 14/15 | 0.67 | 0.46 | 517,518,519,519 | 0 |
| 15 | NAG | G | 606 | 14/15 | 0.68 | 0.27 | 449,452,455,456 | 0 |
| 15 | NAG | F | 649 | 14/15 | 0.68 | 0.53 | 468,470,474,474 | 0 |
| 15 | NAG | F | 606 | 14/15 | 0.68 | 0.42 | 460,464,467,468 | 0 |
| 15 | NAG | G | 615 | 14/15 | 0.69 | 0.43 | 429,431,432,434 | 0 |
| 15 | NAG | J | 701 | 14/15 | 0.71 | 0.64 | 503,510,514,514 | 0 |
| 15 | NAG | G | 633 | 14/15 | 0.73 | 0.37 | 475,477,480,480 | 0 |
| 15 | NAG | J | 702 | 14/15 | 0.74 | 0.64 | 480,482,485,487 | 0 |
| 15 | NAG | A | 702 | 14/15 | 0.74 | 0.41 | 410,413,414,415 | 0 |
| 15 | NAG | F | 633 | 14/15 | 0.75 | 0.48 | 511,516,521,523 | 0 |
| 15 | NAG | Q | 653 | 14/15 | 0.76 | 0.46 | 441,441,441,441 | 0 |
| 15 | NAG | G | 652 | 14/15 | 0.78 | 0.43 | 302,308,311,311 | 0 |
| 15 | NAG | A | 703 | 14/15 | 0.79 | 0.56 | 461,461,461,461 | 0 |
| 15 | NAG | R | 702 | 14/15 | 0.80 | 0.52 | 479,481,484,484 | 0 |
| 15 | NAG | F | 653 | 14/15 | 0.81 | 0.50 | 399,399,399,399 | 0 |
| 15 | NAG | Q | 606 | 14/15 | 0.82 | 0.29 | 474,477,479,480 | 0 |
| 15 | NAG | A | 701 | 14/15 | 0.89 | 0.56 | 406,407,409,409 | 0 |
| 15 | NAG | F | 650 | 14/15 | 0.90 | 0.32 | 345,348,352,354 | 0 |
| 15 | NAG | Q | 650 | 14/15 | 0.91 | 0.43 | 351,352,354,354 | 0 |
| 15 | NAG | G | 650 | 14/15 | 0.92 | 0.22 | 347,349,352,353 | 0 |

## 6.5 Other polymers (i)

There are no such residues in this entry.