



wwPDB EM Validation Summary Report ⓘ

Jul 21, 2025 – 09:40 PM EDT

PDB ID : 8VUU / pdb_00008vuu
EMDB ID : EMD-43569
Title : Anisomycin-bound mammalian ribosome with partially accommodated A-site tRNA
Authors : Loerch, S.; Petrossian, E.; Smith, P.R.; Campbell, Z.T.
Deposited on : 2024-01-31
Resolution : 3.80 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

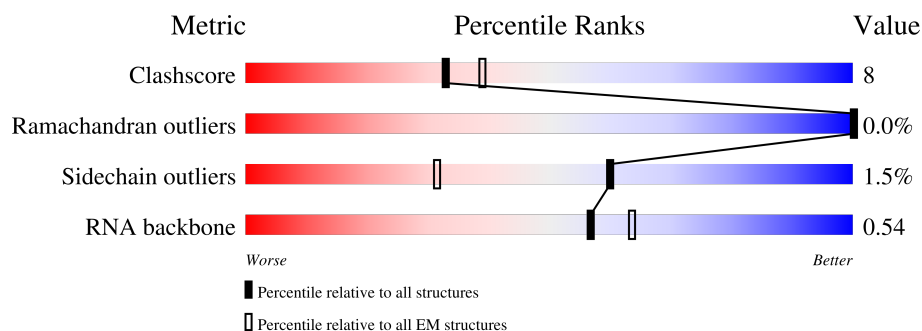
EMDB validation analysis : 0.0.1.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

1 Overall quality at a glance

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

The reported resolution of this entry is 3.80 Å.

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



| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|--------------------------|--------------------------|
| Clashscore | 210492 | 15764 |
| Ramachandran outliers | 207382 | 16835 |
| Sidechain outliers | 206894 | 16415 |
| RNA backbone | 6643 | 2191 |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 1 | A | 257 | <div> <div>63%</div> <div>75%</div> <div>22%</div> <div>.</div> </div> |
| 2 | B | 403 | <div> <div>59%</div> <div>75%</div> <div>23%</div> <div>.</div> </div> |
| 3 | C | 413 | <div> <div>49%</div> <div>70%</div> <div>17%</div> <div>12%</div> </div> |
| 4 | D | 297 | <div> <div>64%</div> <div>85%</div> <div>14%</div> <div>.</div> </div> |
| 5 | E | 291 | <div> <div>57%</div> <div>62%</div> <div>16%</div> <div>22%</div> </div> |
| 6 | F | 249 | <div> <div>55%</div> <div>72%</div> <div>19%</div> <div>9%</div> </div> |
| 7 | G | 319 | <div> <div>41%</div> <div>61%</div> <div>11%</div> <div>28%</div> </div> |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 8 | H | 192 | |
| 9 | I | 214 | |
| 10 | J | 178 | |
| 11 | K | 211 | |
| 12 | L | 218 | |
| 13 | M | 204 | |
| 14 | N | 203 | |
| 15 | O | 213 | |
| 16 | P | 188 | |
| 17 | Q | 212 | |
| 18 | R | 224 | |
| 19 | S | 160 | |
| 20 | T | 128 | |
| 21 | U | 140 | |
| 22 | V | 157 | |
| 23 | W | 156 | |
| 24 | X | 145 | |
| 25 | Y | 136 | |
| 26 | Z | 148 | |
| 27 | AA | 245 | |
| 28 | BA | 115 | |
| 29 | CA | 125 | |
| 30 | DA | 135 | |
| 31 | EA | 110 | |
| 32 | FA | 129 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 33 | GA | 123 | |
| 34 | HA | 105 | |
| 35 | IA | 97 | |
| 36 | JA | 70 | |
| 37 | KA | 51 | |
| 38 | LA | 128 | |
| 39 | MA | 25 | |
| 40 | NA | 106 | |
| 41 | OA | 92 | |
| 42 | PA | 137 | |
| 43 | RA | 165 | |
| 44 | SA | 76 | |
| 45 | TA | 76 | |
| 46 | VA | 12 | |
| 47 | WA | 3584 | |
| 48 | XA | 120 | |
| 49 | YA | 156 | |
| 50 | ZA | 1869 | |
| 51 | AB | 295 | |
| 52 | BB | 264 | |
| 53 | CB | 293 | |
| 54 | DB | 281 | |
| 55 | EB | 263 | |
| 56 | FB | 204 | |
| 57 | GB | 249 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 58 | HB | 432 | |
| 59 | IB | 208 | |
| 60 | JB | 194 | |
| 61 | KB | 165 | |
| 62 | LB | 158 | |
| 63 | MB | 132 | |
| 64 | NB | 151 | |
| 65 | OB | 151 | |
| 66 | PB | 145 | |
| 67 | QB | 172 | |
| 68 | RB | 135 | |
| 69 | SB | 152 | |
| 70 | TB | 145 | |
| 71 | UB | 119 | |
| 72 | VB | 83 | |
| 73 | WB | 130 | |
| 74 | XB | 143 | |
| 75 | YB | 131 | |
| 76 | ZB | 124 | |
| 77 | AC | 115 | |
| 78 | BC | 84 | |
| 79 | CC | 69 | |
| 80 | DC | 56 | |
| 81 | EC | 133 | |
| 82 | FC | 188 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 83 | GC | 317 | <div><div></div><div>95%</div><div>69%</div><div>29%</div><div>••</div></div> |
| 84 | IC | 4 | <div><div></div><div>100%</div><div>75%</div><div>25%</div></div> |
| 85 | b | 318 | <div><div></div><div>52%</div><div>39%</div><div>12%</div><div>•</div><div>47%</div></div> |
| 86 | At | 74 | <div><div></div><div>81%</div><div>51%</div><div>41%</div><div>5%</div><div>•</div></div> |

2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 218724 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called uL2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 1 | A | 250 | Total | C | N | O | S | 0 | 0 |
| | | | 1914 | 1199 | 392 | 317 | 6 | | |

- Molecule 2 is a protein called uL3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 2 | B | 397 | Total | C | N | O | S | 0 | 0 |
| | | | 3196 | 2035 | 603 | 545 | 13 | | |

- Molecule 3 is a protein called uL4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 3 | C | 362 | Total | C | N | O | S | 0 | 0 |
| | | | 2883 | 1812 | 577 | 480 | 14 | | |

- Molecule 4 is a protein called uL18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 4 | D | 294 | Total | C | N | O | S | 0 | 0 |
| | | | 2395 | 1514 | 439 | 428 | 14 | | |

- Molecule 5 is a protein called L6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 5 | E | 228 | Total | C | N | O | S | 0 | 0 |
| | | | 1823 | 1173 | 349 | 298 | 3 | | |

- Molecule 6 is a protein called uL30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 6 | F | 227 | Total | C | N | O | S | 0 | 0 |
| | | | 1897 | 1217 | 366 | 305 | 9 | | |

- Molecule 7 is a protein called L7A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 7 | G | 229 | Total | C | N | O | S | 0 | 0 |
| | | | 1850 | 1181 | 356 | 309 | 4 | | |

- Molecule 8 is a protein called L9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 8 | H | 190 | Total | C | N | O | S | 0 | 0 |
| | | | 1516 | 954 | 284 | 272 | 6 | | |

- Molecule 9 is a protein called L10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 9 | I | 205 | Total | C | N | O | S | 0 | 0 |
| | | | 1664 | 1056 | 321 | 274 | 13 | | |

- Molecule 10 is a protein called uL5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10 | J | 171 | Total | C | N | O | S | 0 | 0 |
| | | | 1372 | 867 | 256 | 243 | 6 | | |

- Molecule 11 is a protein called eL13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 11 | K | 210 | Total | C | N | O | S | 0 | 0 |
| | | | 1702 | 1065 | 354 | 279 | 4 | | |

There are 9 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------|------------|
| K | 46 | ILE | - | insertion | UNP G1TPV0 |
| K | 47 | ALA | - | insertion | UNP G1TPV0 |
| K | 48 | PRO | - | insertion | UNP G1TPV0 |
| K | 49 | ARG | - | insertion | UNP G1TPV0 |
| K | 50 | PRO | - | insertion | UNP G1TPV0 |
| K | 51 | ALA | - | insertion | UNP G1TPV0 |
| K | 52 | ALA | - | insertion | UNP G1TPV0 |
| K | 53 | GLY | - | insertion | UNP G1TPV0 |
| K | 54 | PRO | - | insertion | UNP G1TPV0 |

- Molecule 12 is a protein called eL14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12 | L | 138 | Total | C | N | O | S | 0 | 0 |
| | | | 1137 | 727 | 221 | 182 | 7 | | |

- Molecule 13 is a protein called L15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 13 | M | 203 | Total | C | N | O | S | 0 | 0 |
| | | | 1701 | 1072 | 359 | 266 | 4 | | |

- Molecule 14 is a protein called uL13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 14 | N | 199 | Total | C | N | O | S | 0 | 0 |
| | | | 1630 | 1051 | 319 | 255 | 5 | | |

- Molecule 15 is a protein called uL22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15 | O | 156 | Total | C | N | O | S | 0 | 0 |
| | | | 1266 | 793 | 245 | 219 | 9 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| O | 43 | SER | ALA | conflict | UNP G1TVT6 |

- Molecule 16 is a protein called eL18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16 | P | 187 | Total | C | N | O | S | 0 | 0 |
| | | | 1515 | 946 | 315 | 250 | 4 | | |

There are 12 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| P | 4 | ASP | ASN | conflict | UNP G1TFE0 |
| P | 14 | ARG | TRP | conflict | UNP G1TFE0 |
| P | 53 | MET | LEU | conflict | UNP G1TFE0 |
| P | 58 | ARG | TRP | conflict | UNP G1TFE0 |
| P | 75 | ARG | GLN | conflict | UNP G1TFE0 |
| P | 80 | ALA | PRO | conflict | UNP G1TFE0 |
| P | 86 | VAL | ILE | conflict | UNP G1TFE0 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| P | 104 | ARG | HIS | conflict | UNP G1TFE0 |
| P | 110 | ARG | CYS | conflict | UNP G1TFE0 |
| P | 137 | VAL | GLY | conflict | UNP G1TFE0 |
| P | 157 | GLY | ARG | conflict | UNP G1TFE0 |
| P | 181 | ARG | TRP | conflict | UNP G1TFE0 |

- Molecule 17 is a protein called eL19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17 | Q | 180 | Total | C | N | O | S | 0 | 0 |
| | | | 1508 | 933 | 328 | 238 | 9 | | |

- Molecule 18 is a protein called L18A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 18 | R | 176 | Total | C | N | O | S | 0 | 0 |
| | | | 1462 | 930 | 285 | 236 | 11 | | |

- Molecule 19 is a protein called eL21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19 | S | 159 | Total | C | N | O | S | 0 | 0 |
| | | | 1298 | 823 | 252 | 217 | 6 | | |

- Molecule 20 is a protein called eL22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20 | T | 101 | Total | C | N | O | S | 0 | 0 |
| | | | 826 | 530 | 144 | 150 | 2 | | |

There are 11 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| T | 18 | LEU | VAL | conflict | UNP G1TSG1 |
| T | 32 | GLY | ARG | conflict | UNP G1TSG1 |
| T | 36 | ALA | GLU | conflict | UNP G1TSG1 |
| T | 39 | PHE | SER | conflict | UNP G1TSG1 |
| T | 54 | GLY | ARG | conflict | UNP G1TSG1 |
| T | 60 | VAL | ALA | conflict | UNP G1TSG1 |
| T | 62 | SER | THR | conflict | UNP G1TSG1 |
| T | 63 | LEU | ILE | conflict | UNP G1TSG1 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| T | 97 | ARG | HIS | conflict | UNP G1TSG1 |
| T | 106 | THR | SER | conflict | UNP G1TSG1 |
| T | 126 | GLU | ASP | conflict | UNP G1TSG1 |

- Molecule 21 is a protein called L23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21 | U | 135 | Total | C | N | O | S | 0 | 0 |
| | | | 1004 | 631 | 191 | 177 | 5 | | |

- Molecule 22 is a protein called uL24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 22 | V | 110 | Total | C | N | O | S | 0 | 0 |
| | | | 887 | 555 | 179 | 149 | 4 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| V | 78 | SER | PHE | conflict | UNP G1SE28 |

- Molecule 23 is a protein called uL23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23 | W | 118 | Total | C | N | O | S | 0 | 0 |
| | | | 967 | 618 | 181 | 167 | 1 | | |

- Molecule 24 is a protein called L26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24 | X | 134 | Total | C | N | O | S | 0 | 0 |
| | | | 1115 | 700 | 226 | 186 | 3 | | |

- Molecule 25 is a protein called L27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25 | Y | 135 | Total | C | N | O | S | 0 | 0 |
| | | | 1107 | 714 | 208 | 182 | 3 | | |

- Molecule 26 is a protein called L27A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 26 | Z | 147 | Total | C | N | O | S | 0 | 0 |
| | | | 1162 | 734 | 239 | 185 | 4 | | |

- Molecule 27 is a protein called L29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27 | AA | 107 | Total | C | N | O | S | 0 | 0 |
| | | | 873 | 542 | 195 | 133 | 3 | | |

- Molecule 28 is a protein called eL30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 28 | BA | 99 | Total | C | N | O | S | 0 | 0 |
| | | | 769 | 486 | 135 | 141 | 7 | | |

- Molecule 29 is a protein called L31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29 | CA | 108 | Total | C | N | O | S | 0 | 0 |
| | | | 893 | 563 | 172 | 156 | 2 | | |

- Molecule 30 is a protein called L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 30 | DA | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1064 | 673 | 220 | 166 | 5 | | |

- Molecule 31 is a protein called eL33.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 31 | EA | 109 | Total | C | N | O | S | 0 | 0 |
| | | | 876 | 555 | 174 | 143 | 4 | | |

- Molecule 32 is a protein called L34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32 | FA | 114 | Total | C | N | O | S | 0 | 0 |
| | | | 906 | 566 | 187 | 147 | 6 | | |

- Molecule 33 is a protein called L35.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33 | GA | 121 | Total | C | N | O | S | 0 | 0 |
| | | | 1008 | 637 | 203 | 167 | 1 | | |

- Molecule 34 is a protein called L36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 34 | HA | 102 | Total | C | N | O | S | 0 | 0 |
| | | | 830 | 520 | 176 | 129 | 5 | | |

- Molecule 35 is a protein called L37.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 35 | IA | 87 | Total | C | N | O | S | 0 | 0 |
| | | | 716 | 440 | 159 | 112 | 5 | | |

- Molecule 36 is a protein called eL38.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 36 | JA | 69 | Total | C | N | O | S | 0 | 0 |
| | | | 569 | 366 | 103 | 99 | 1 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| JA | 24 | LYS | ASN | conflict | UNP G1U001 |

- Molecule 37 is a protein called eL39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 37 | KA | 50 | Total | C | N | O | S | 0 | 0 |
| | | | 447 | 286 | 96 | 64 | 1 | | |

- Molecule 38 is a protein called eL40.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 38 | LA | 52 | Total | C | N | O | S | 0 | 0 |
| | | | 429 | 266 | 90 | 67 | 6 | | |

- Molecule 39 is a protein called eL41.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 39 | MA | 25 | Total | C | N | O | S | 0 | 0 |
| | | | 239 | 145 | 64 | 27 | 3 | | |

- Molecule 40 is a protein called eL42.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 40 | NA | 104 | Total | C | N | O | S | 0 | 0 |
| | | | 851 | 533 | 174 | 138 | 6 | | |

- Molecule 41 is a protein called eL43.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 41 | OA | 91 | Total | C | N | O | S | 0 | 0 |
| | | | 708 | 445 | 136 | 120 | 7 | | |

- Molecule 42 is a protein called L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42 | PA | 124 | Total | C | N | O | S | 0 | 0 |
| | | | 994 | 616 | 205 | 167 | 6 | | |

- Molecule 43 is a protein called L12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 43 | RA | 153 | Total | C | N | O | S | 0 | 0 |
| | | | 1160 | 722 | 218 | 217 | 3 | | |

- Molecule 44 is a RNA chain called P-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 44 | SA | 76 | Total | C | N | O | P | 0 | 0 |
| | | | 1622 | 726 | 300 | 521 | 75 | | |

- Molecule 45 is a RNA chain called E-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 45 | TA | 76 | Total | C | N | O | P | 0 | 0 |
| | | | 1615 | 722 | 286 | 532 | 75 | | |

- Molecule 46 is a RNA chain called mRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|----|---------|-------|
| 46 | VA | 12 | Total | C | N | O | P | 0 | 0 |
| | | | 249 | 112 | 39 | 86 | 12 | | |

- Molecule 47 is a RNA chain called 28S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 47 | WA | 3578 | Total | C | N | O | P | 0 | 0 |
| | | | 76735 | 34173 | 14061 | 24923 | 3578 | | |

- Molecule 48 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 48 | XA | 119 | Total | C | N | O | P | 0 | 0 |
| | | | 2538 | 1132 | 454 | 834 | 118 | | |

There are 7 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|-------------|
| XA | 2 | U | N | conflict | GB X06789.1 |
| XA | 36 | C | N | conflict | GB X06789.1 |
| XA | 102 | U | N | conflict | GB X06789.1 |
| XA | 112 | U | N | conflict | GB X06789.1 |
| XA | 114 | U | N | conflict | GB X06789.1 |
| XA | 119 | U | C | conflict | GB X06789.1 |
| XA | 120 | U | N | conflict | GB X06789.1 |

- Molecule 49 is a RNA chain called 5.8S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|---------|-------|
| 49 | YA | 156 | Total | C | N | O | P | 0 | 0 |
| | | | 3314 | 1480 | 585 | 1094 | 155 | | |

- Molecule 50 is a RNA chain called 18S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 50 | ZA | 1716 | Total | C | N | O | P | 0 | 0 |
| | | | 36623 | 16347 | 6572 | 11989 | 1715 | | |

- Molecule 51 is a protein called RPSA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 51 | AB | 217 | Total | C | N | O | S | 0 | 0 |
| | | | 1710 | 1086 | 300 | 316 | 8 | | |

- Molecule 52 is a protein called S3A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 52 | BB | 213 | Total | C | N | O | S | 0 | 0 |
| | | | 1729 | 1098 | 309 | 308 | 14 | | |

- Molecule 53 is a protein called S2-like.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 53 | CB | 220 | Total | C | N | O | S | 0 | 0 |
| | | | 1707 | 1105 | 293 | 300 | 9 | | |

- Molecule 54 is a protein called S3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 54 | DB | 228 | Total | C | N | O | S | 0 | 0 |
| | | | 1768 | 1126 | 318 | 316 | 8 | | |

- Molecule 55 is a protein called S4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 55 | EB | 262 | Total | C | N | O | S | 0 | 0 |
| | | | 2076 | 1324 | 386 | 358 | 8 | | |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| EB | 25 | GLY | SER | conflict | UNP G1TK17 |
| EB | 51 | ARG | LYS | conflict | UNP G1TK17 |
| EB | 78 | THR | ALA | conflict | UNP G1TK17 |
| EB | 156 | VAL | MET | conflict | UNP G1TK17 |

- Molecule 56 is a protein called S5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 56 | FB | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1471 | 921 | 277 | 266 | 7 | | |

- Molecule 57 is a protein called eS6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 57 | GB | 237 | Total | C | N | O | S | 0 | 0 |
| | | | 1923 | 1200 | 387 | 329 | 7 | | |

- Molecule 58 is a protein called eS7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 58 | HB | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1489 | 952 | 271 | 265 | 1 | | |

- Molecule 59 is a protein called S8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 59 | IB | 206 | Total | C | N | O | S | 0 | 0 |
| | | | 1686 | 1058 | 332 | 291 | 5 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| IB | 47 | ARG | GLY | conflict | UNP G1TJW1 |

- Molecule 60 is a protein called S9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 60 | JB | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1525 | 969 | 306 | 248 | 2 | | |

- Molecule 61 is a protein called S10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 61 | KB | 96 | Total | C | N | O | S | 0 | 0 |
| | | | 810 | 530 | 143 | 131 | 6 | | |

- Molecule 62 is a protein called S11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 62 | LB | 144 | Total | C | N | O | S | 0 | 0 |
| | | | 1180 | 752 | 223 | 199 | 6 | | |

- Molecule 63 is a protein called S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 63 | MB | 117 | Total | C | N | O | S | 0 | 0 |
| | | | 908 | 570 | 161 | 169 | 8 | | |

- Molecule 64 is a protein called uS15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 64 | NB | 149 | Total | C | N | O | S | 0 | 0 |
| | | | 1202 | 770 | 228 | 203 | 1 | | |

- Molecule 65 is a protein called S14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 65 | OB | 136 | Total | C | N | O | S | 0 | 0 |
| | | | 1016 | 621 | 199 | 190 | 6 | | |

- Molecule 66 is a protein called S15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 66 | PB | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1058 | 670 | 201 | 180 | 7 | | |

- Molecule 67 is a protein called uS9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 67 | QB | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1128 | 717 | 213 | 195 | 3 | | |

- Molecule 68 is a protein called eS17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 68 | RB | 132 | Total | C | N | O | S | 0 | 0 |
| | | | 1068 | 670 | 199 | 195 | 4 | | |

- Molecule 69 is a protein called S18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 69 | SB | 144 | Total | C | N | O | S | 0 | 0 |
| | | | 1190 | 746 | 241 | 202 | 1 | | |

- Molecule 70 is a protein called S19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 70 | TB | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1104 | 693 | 212 | 196 | 3 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| TB | 119 | GLY | TRP | conflict | UNP G1TN62 |

- Molecule 71 is a protein called uS10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 71 | UB | 102 | Total | C | N | O | S | 0 | 0 |
| | | | 808 | 507 | 154 | 143 | 4 | | |

- Molecule 72 is a protein called S21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 72 | VB | 83 | Total | C | N | O | S | 0 | 0 |
| | | | 636 | 393 | 117 | 121 | 5 | | |

There are 7 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| VB | 3 | ASN | SER | conflict | UNP G1TM82 |
| VB | 4 | ASP | ASN | conflict | UNP G1TM82 |
| VB | 33 | GLN | PRO | conflict | UNP G1TM82 |
| VB | 50 | PHE | SER | conflict | UNP G1TM82 |
| VB | 75 | ALA | SER | conflict | UNP G1TM82 |
| VB | 76 | ASP | HIS | conflict | UNP G1TM82 |
| VB | 81 | LYS | GLN | conflict | UNP G1TM82 |

- Molecule 73 is a protein called S15A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 73 | WB | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1034 | 659 | 193 | 176 | 6 | | |

- Molecule 74 is a protein called S23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 74 | XB | 141 | Total | C | N | O | S | 0 | 0 |
| | | | 1098 | 693 | 219 | 183 | 3 | | |

- Molecule 75 is a protein called S24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 75 | YB | 124 | Total | C | N | O | S | 0 | 0 |
| | | | 1011 | 640 | 198 | 168 | 5 | | |

- Molecule 76 is a protein called eS25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 76 | ZB | 85 | Total | C | N | O | S | 0 | 0 |
| | | | 683 | 439 | 128 | 115 | 1 | | |

- Molecule 77 is a protein called S26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 77 | AC | 101 | Total | C | N | O | S | 0 | 0 |
| | | | 814 | 507 | 170 | 132 | 5 | | |

There are 3 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| AC | 28 | ARG | CYS | conflict | UNP G1TFE8 |
| AC | 56 | ALA | VAL | conflict | UNP G1TFE8 |
| AC | 109 | ARG | PRO | conflict | UNP G1TFE8 |

- Molecule 78 is a protein called S27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 78 | BC | 83 | Total | C | N | O | S | 0 | 0 |
| | | | 651 | 408 | 121 | 115 | 7 | | |

- Molecule 79 is a protein called S28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 79 | CC | 62 | Total | C | N | O | S | 0 | 0 |
| | | | 488 | 297 | 97 | 92 | 2 | | |

- Molecule 80 is a protein called uS14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 80 | DC | 55 | Total | C | N | O | S | 0 | 0 |
| | | | 459 | 286 | 94 | 74 | 5 | | |

- Molecule 81 is a protein called S30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 81 | EC | 55 | Total | C | N | O | S | 0 | 0 |
| | | | 443 | 274 | 97 | 71 | 1 | | |

- Molecule 82 is a protein called S27A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 82 | FC | 69 | Total | C | N | O | S | 0 | 0 |
| | | | 564 | 357 | 105 | 95 | 7 | | |

- Molecule 83 is a protein called RACK1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 83 | GC | 313 | Total | C | N | O | S | 0 | 0 |
| | | | 2436 | 1535 | 424 | 465 | 12 | | |

- Molecule 84 is a protein called nascent chain.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|----|---|---|---------|-------|
| 84 | IC | 4 | Total | C | N | O | 0 | 0 |
| | | | 20 | 12 | 4 | 4 | | |

- Molecule 85 is a protein called RPLP0.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 85 | b | 167 | Total | C | N | O | S | 0 | 0 |
| | | | 1279 | 813 | 228 | 229 | 9 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| b | 82 | LEU | ILE | conflict | UNP G1SPK4 |

- Molecule 86 is a RNA chain called A-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---|---------|-------|
| 86 | At | 74 | Total | C | N | O | P | S | 0 | 0 |
| | | | 1582 | 705 | 282 | 520 | 74 | 1 | | |

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 87 | I | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 87 | FA | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 87 | WA | 80 | Total | Mg | 0 |
| | | | 80 | 80 | |

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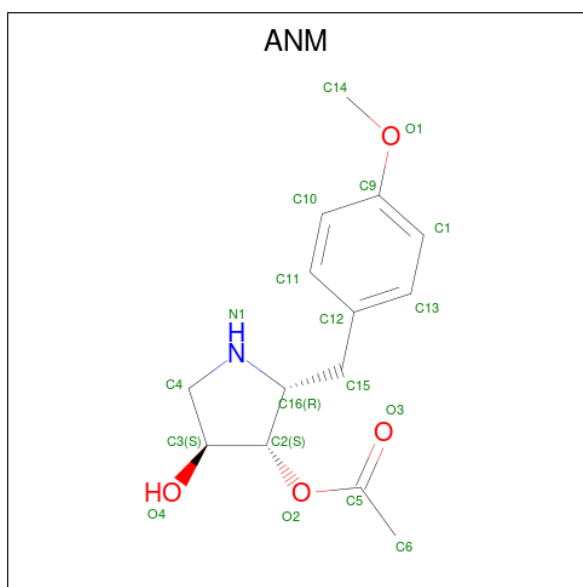
Continued from previous page...

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------------|----------|---------|
| 87 | XA | 1 | Total 1 | Mg 1 | 0 |
| 87 | ZA | 18 | Total 18 | Mg 18 | 0 |
| 87 | AC | 1 | Total 1 | Mg 1 | 0 |

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

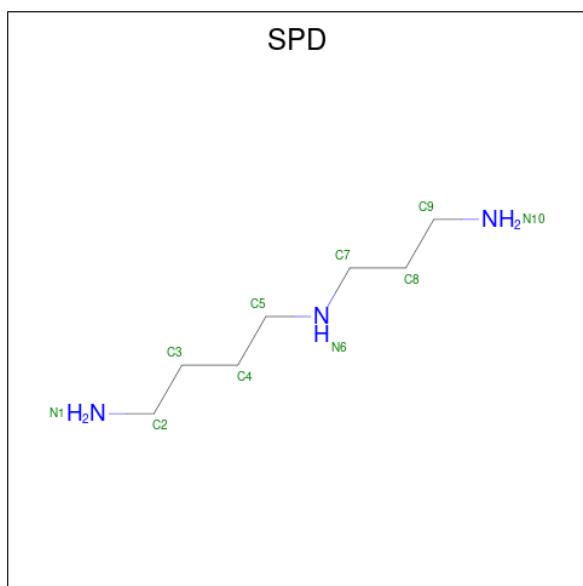
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|---------|---------|
| 88 | FA | 1 | Total 1 | Zn 1 | 0 |
| 88 | IA | 1 | Total 1 | Zn 1 | 0 |
| 88 | LA | 1 | Total 1 | Zn 1 | 0 |
| 88 | NA | 1 | Total 1 | Zn 1 | 0 |
| 88 | OA | 1 | Total 1 | Zn 1 | 0 |
| 88 | AC | 1 | Total 1 | Zn 1 | 0 |
| 88 | DC | 1 | Total 1 | Zn 1 | 0 |
| 88 | FC | 1 | Total 1 | Zn 1 | 0 |

- Molecule 89 is ANISOMYCIN (CCD ID: ANM) (formula: C₁₄H₁₉NO₄).



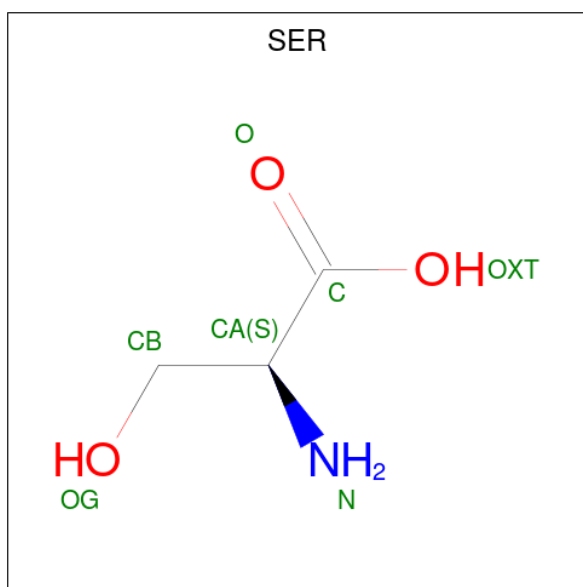
| Mol | Chain | Residues | Atoms | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---------|
| 89 | WA | 1 | Total | C | N | O | 0 |
| | | | 19 | 14 | 1 | 4 | |

- Molecule 90 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



| Mol | Chain | Residues | Atoms | | | AltConf |
|-----|-------|----------|-------|---|---|---------|
| 90 | WA | 1 | Total | C | N | 0 |
| | | | 10 | 7 | 3 | |

- Molecule 91 is SERINE (CCD ID: SER) (formula: $C_3H_7NO_3$).

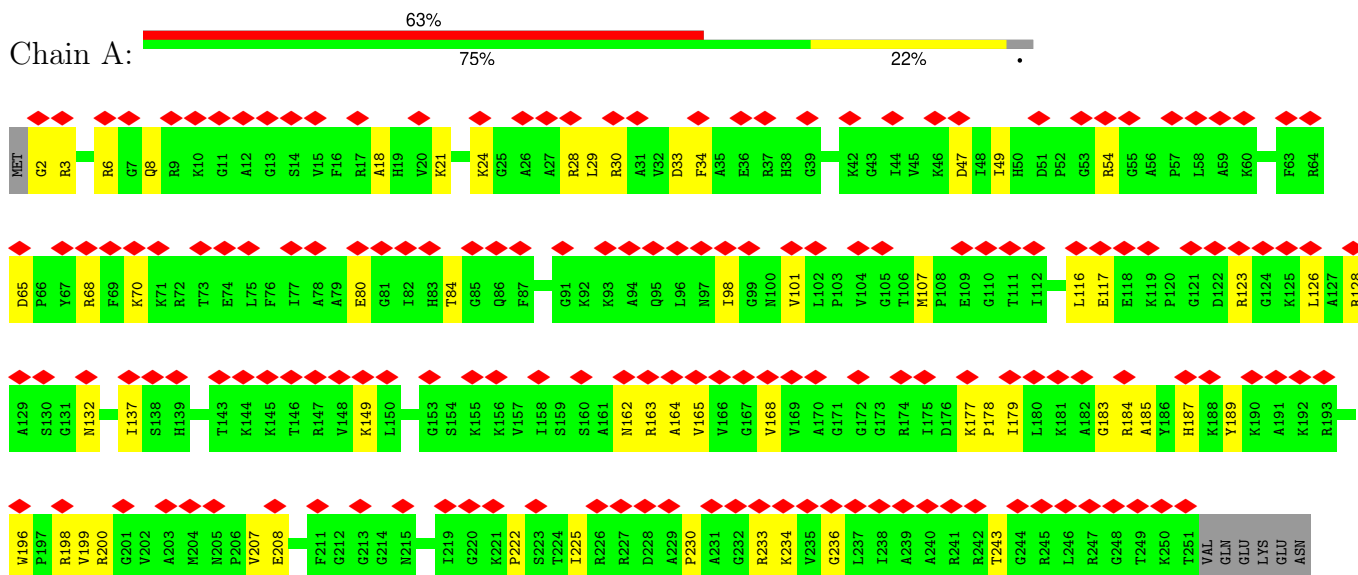


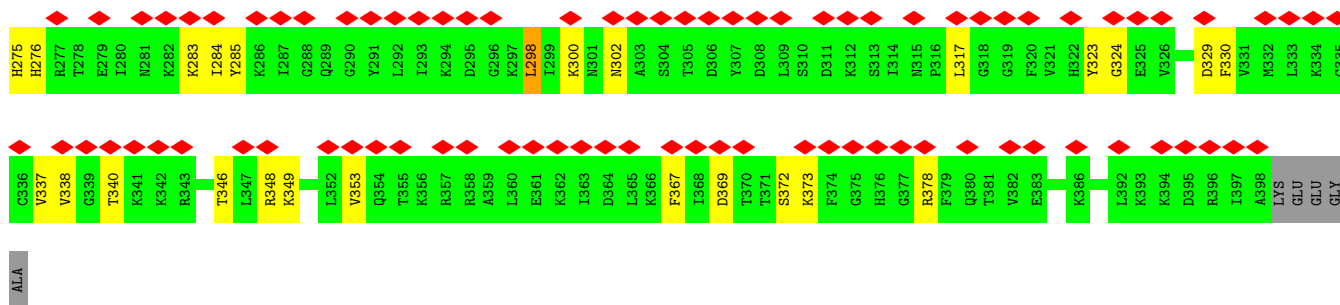
| Mol | Chain | Residues | Atoms | | | | AltConf |
|-----|-------|----------|-------|---|---|---|---------|
| | | | Total | C | N | O | |
| 91 | ZA | 1 | 6 | 3 | 1 | 2 | 0 |

3 Residue-property plots

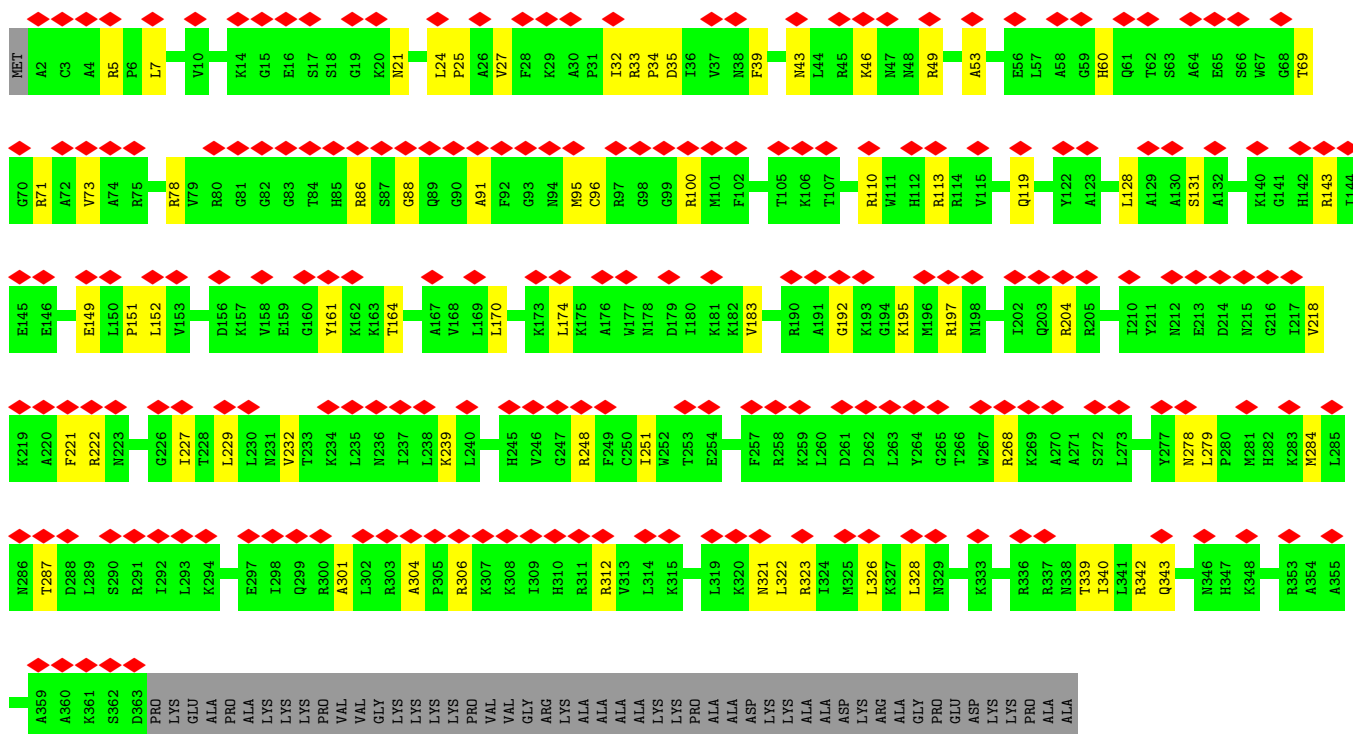
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: uL2

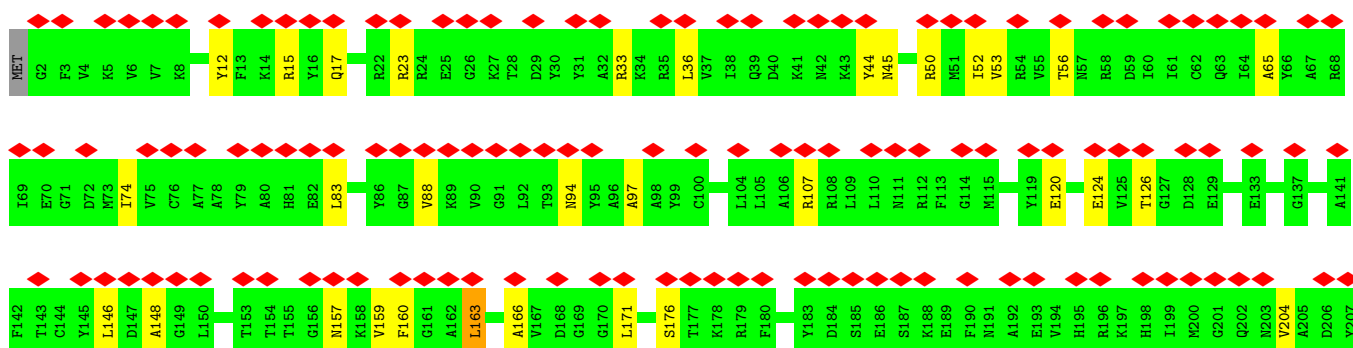
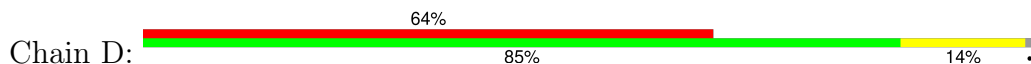


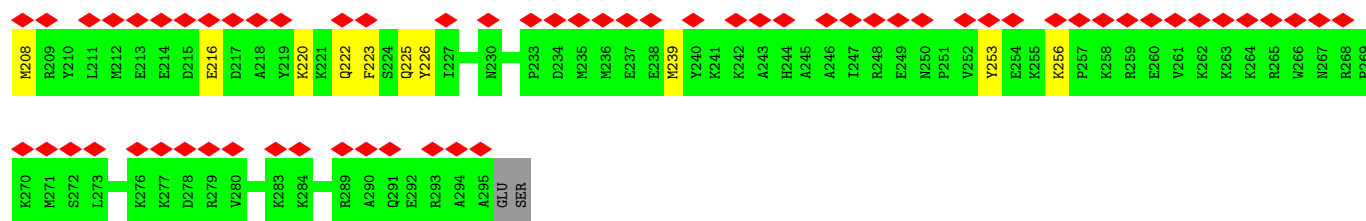


• Molecule 3: uL4

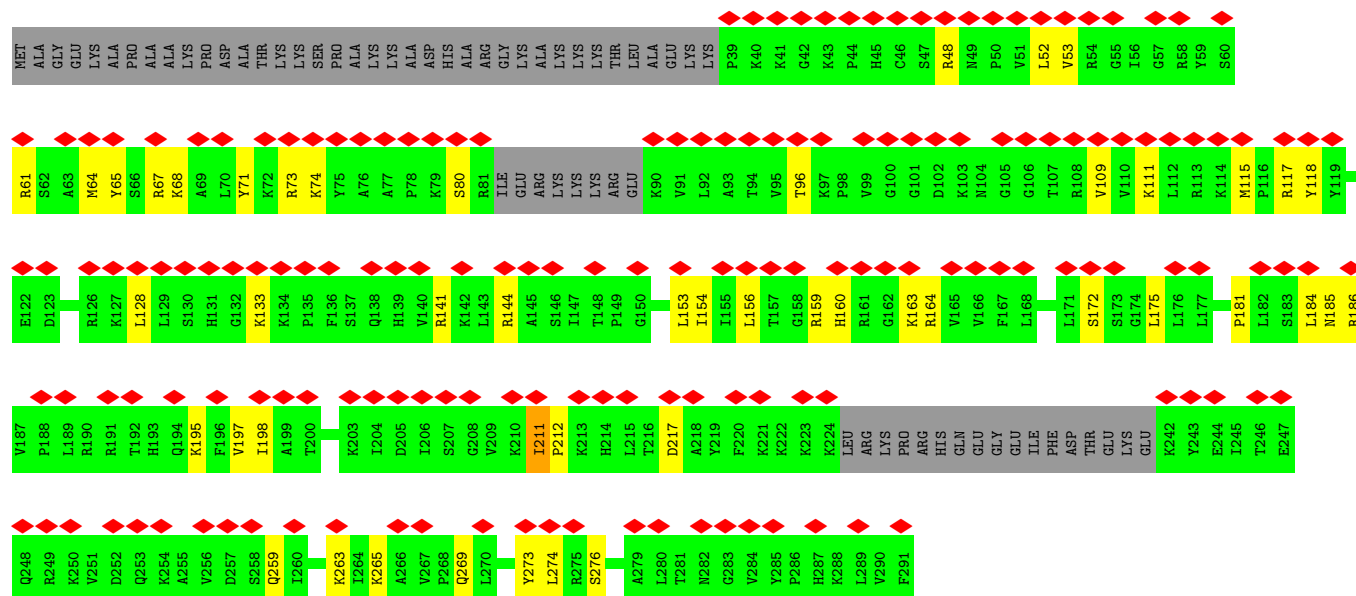


• Molecule 4: uL18

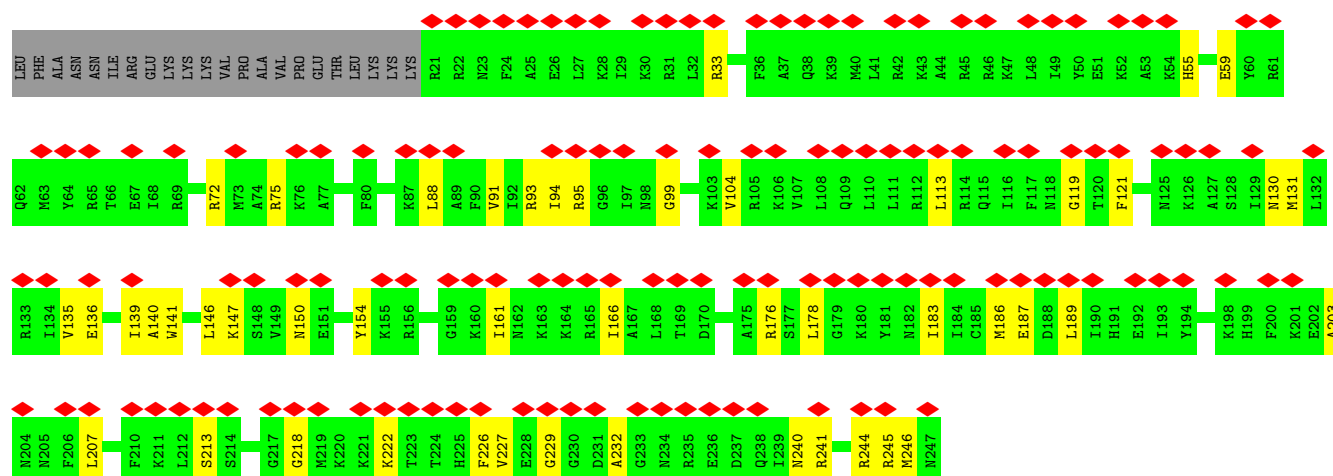




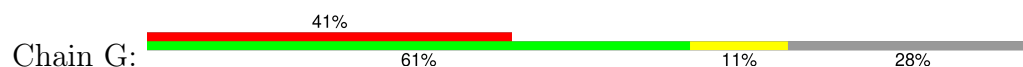
• Molecule 5: L6

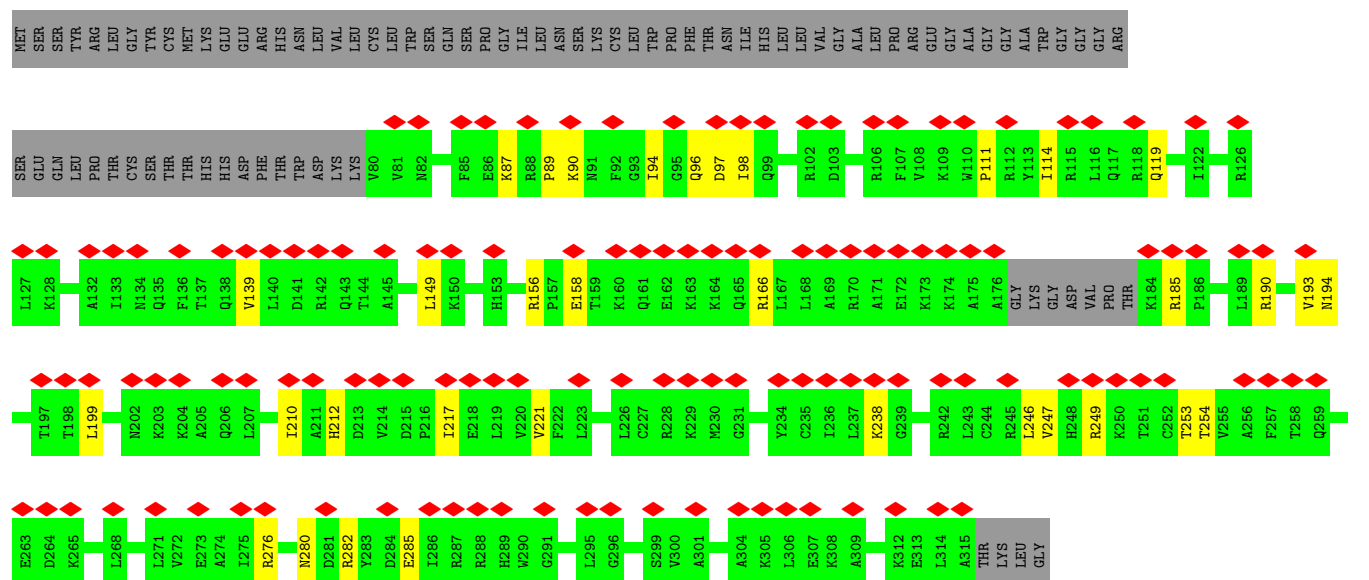


• Molecule 6: uL30

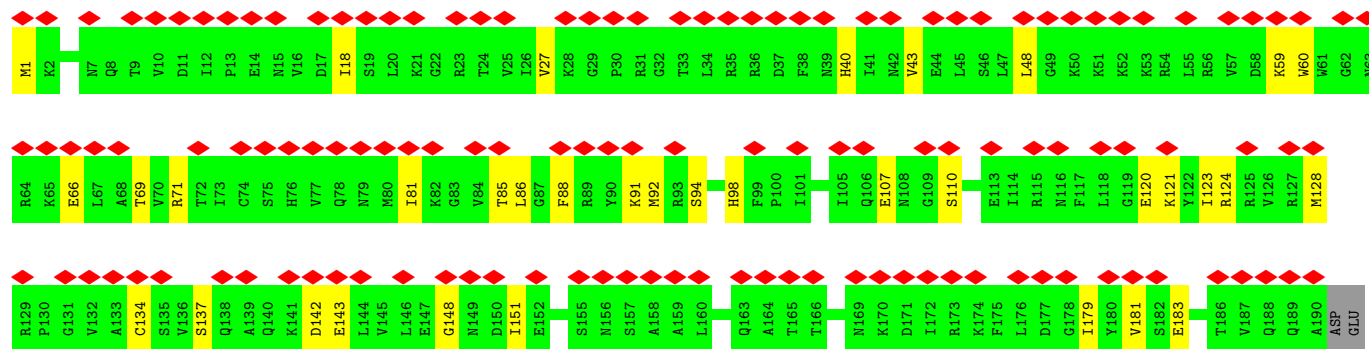
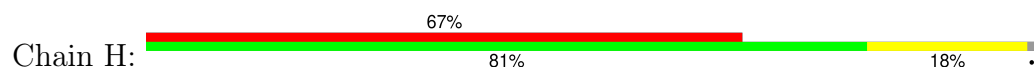


• Molecule 7: L7A

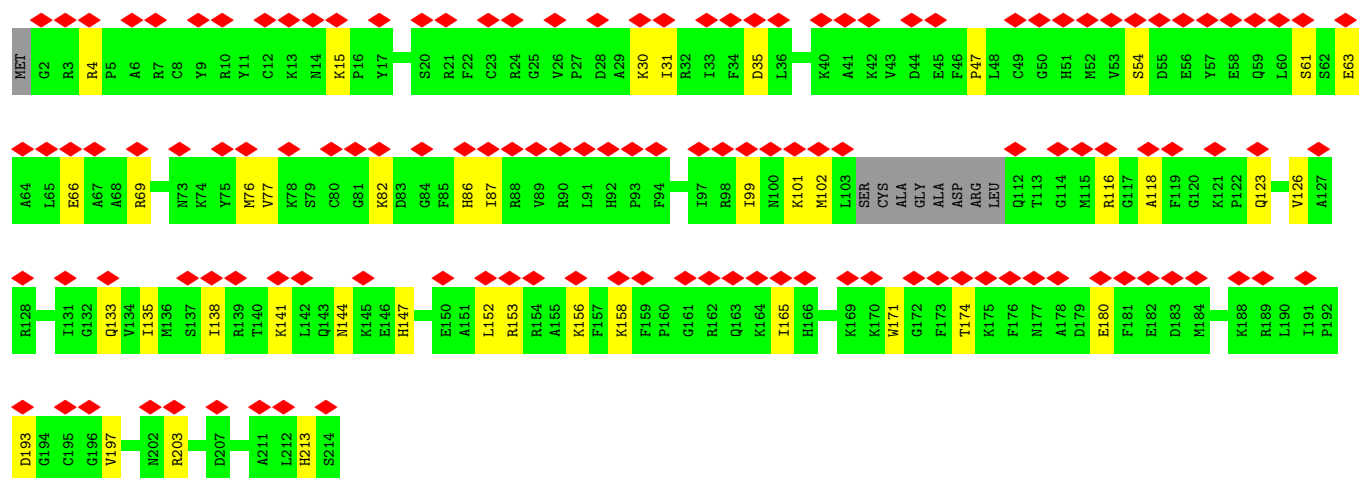
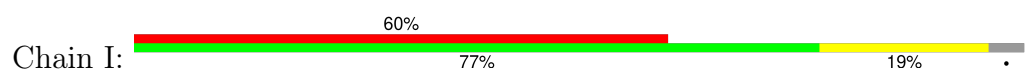




• Molecule 8: L9

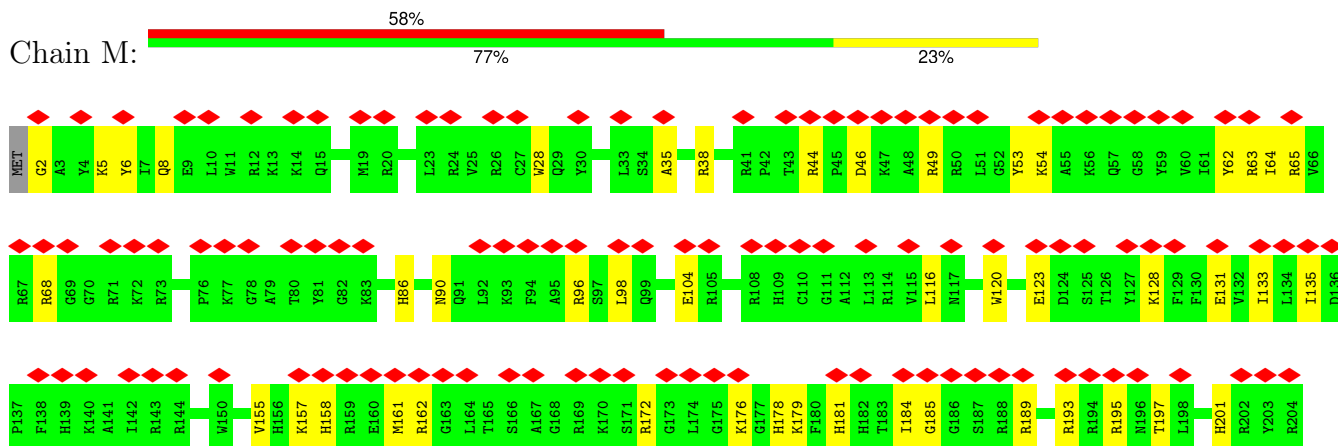


• Molecule 9: L10



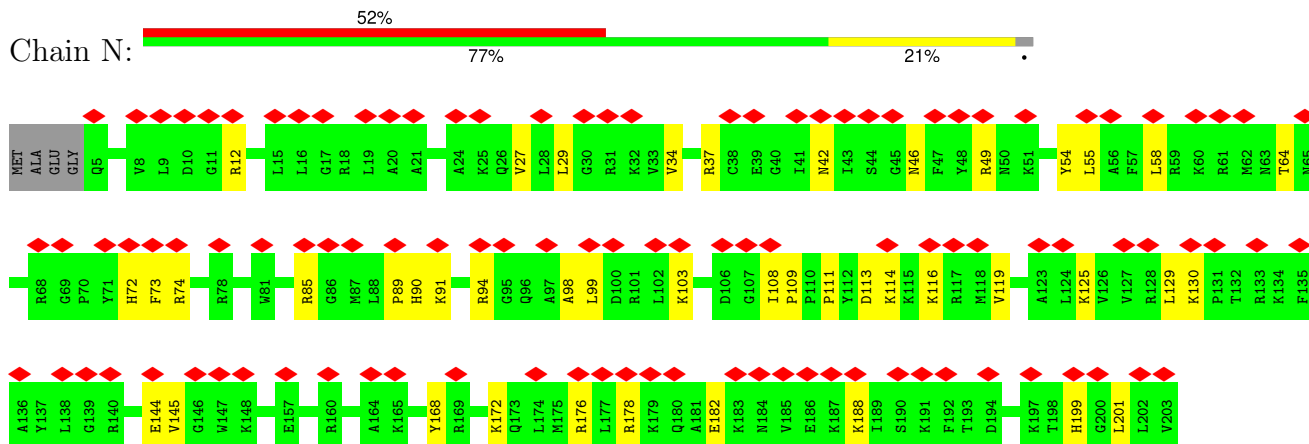
- Molecule 13: L15

Chain M:



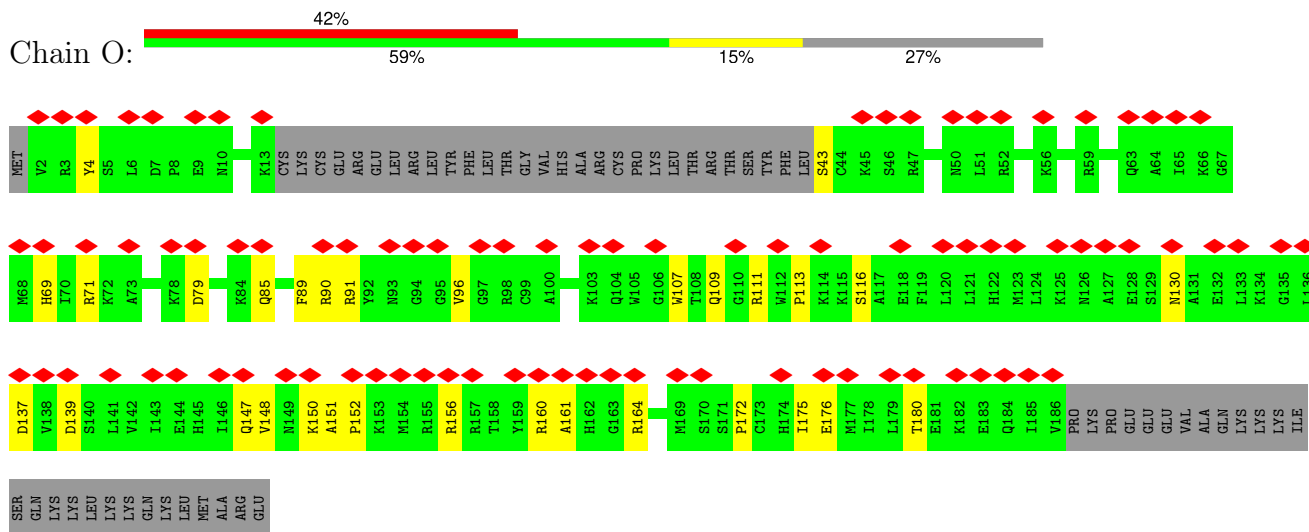
- Molecule 14: uL13

Chain N:



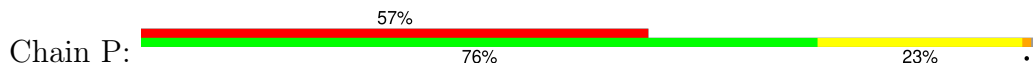
- Molecule 15: uL22

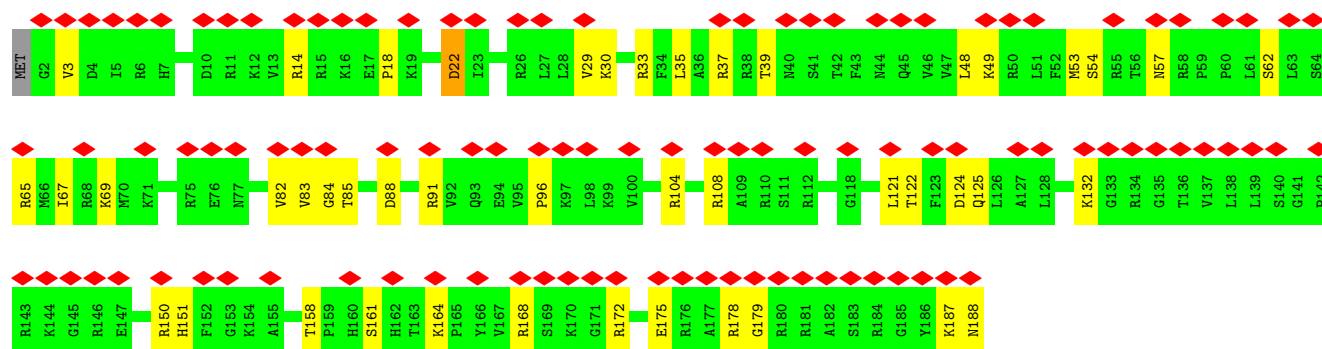
Chain O:



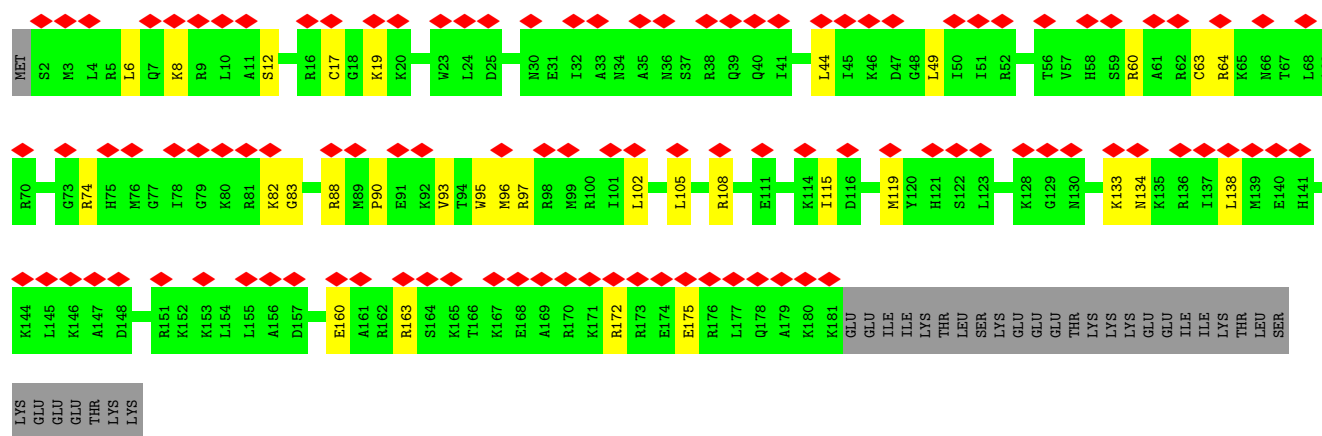
- Molecule 16: eL18

Chain P:

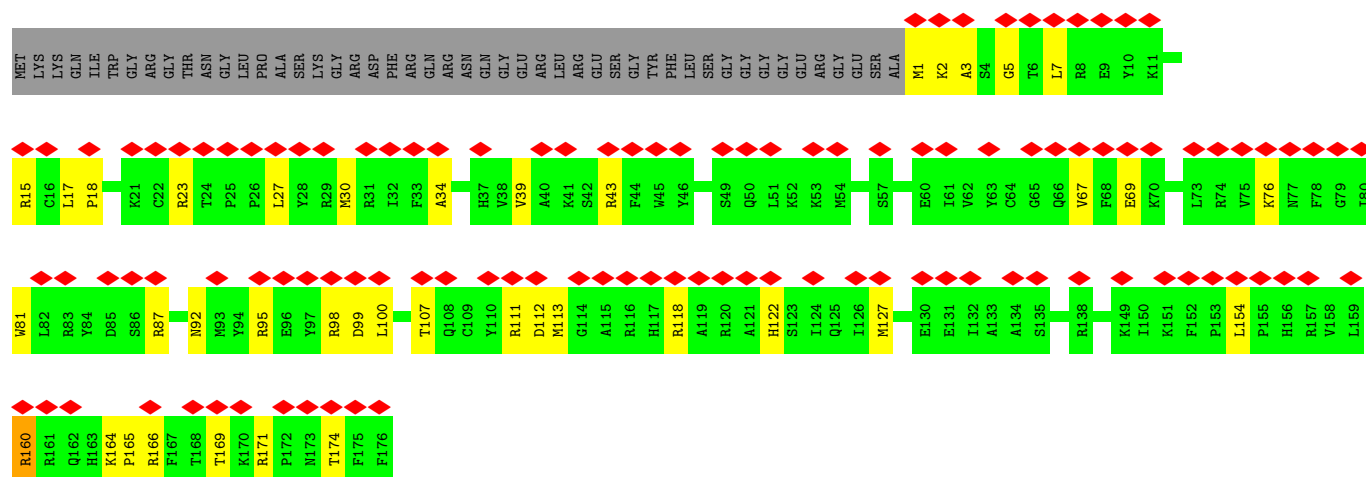




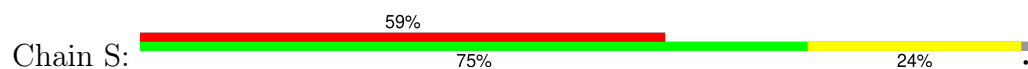
• Molecule 17: eL19

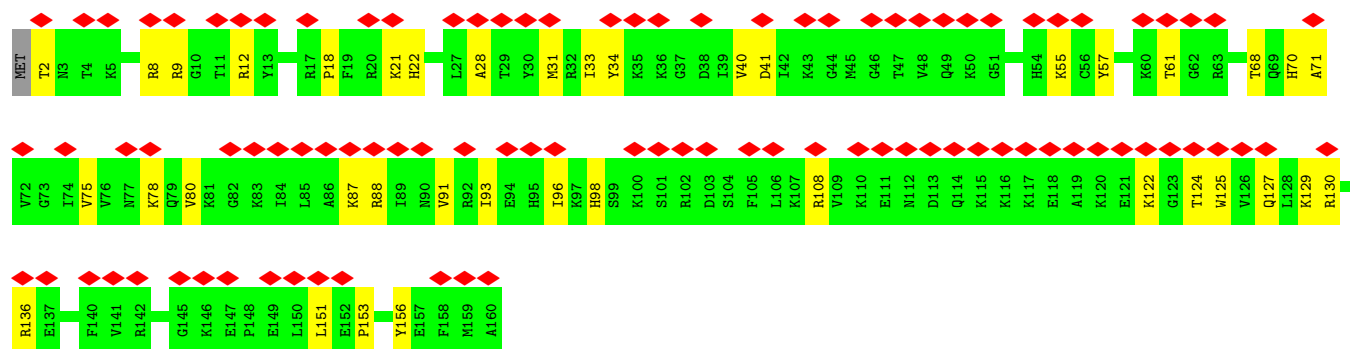


• Molecule 18: L18A

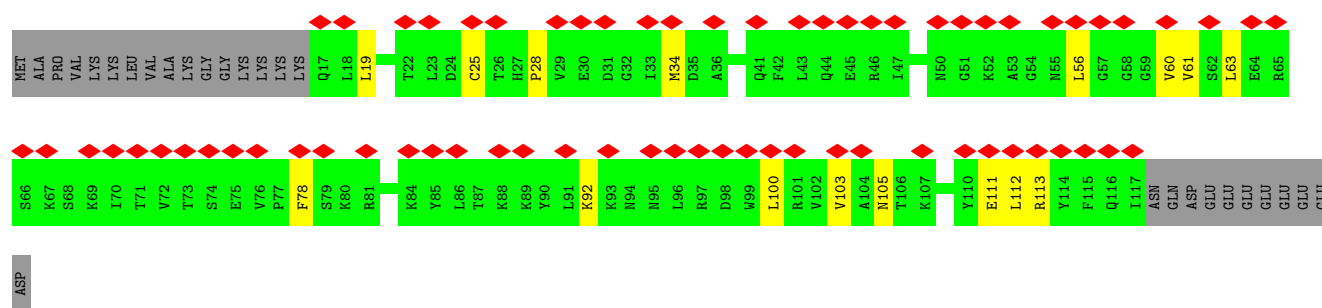


• Molecule 19: eL21

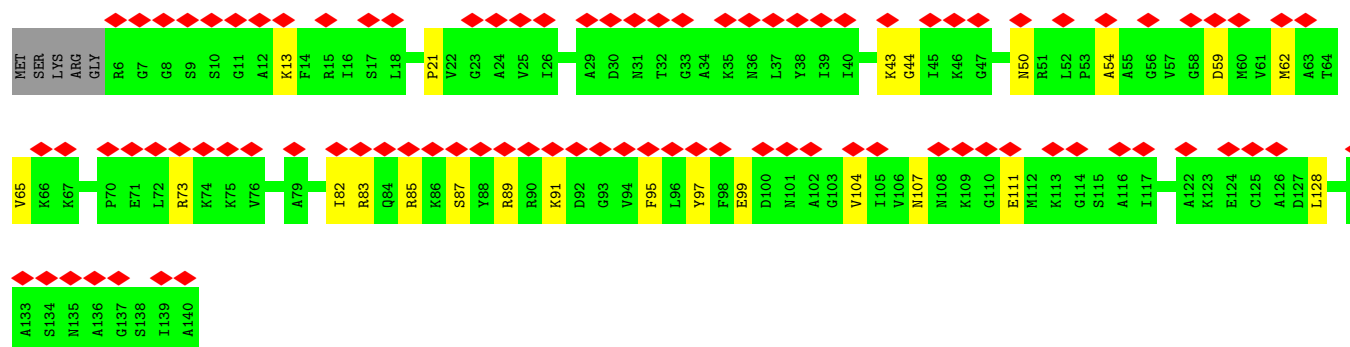
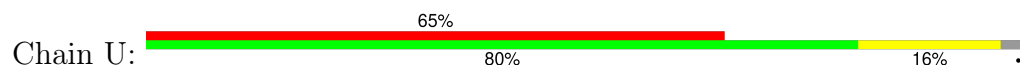




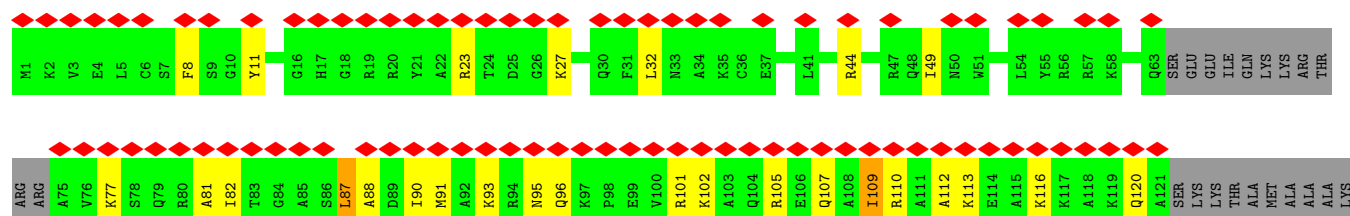
• Molecule 20: eL22



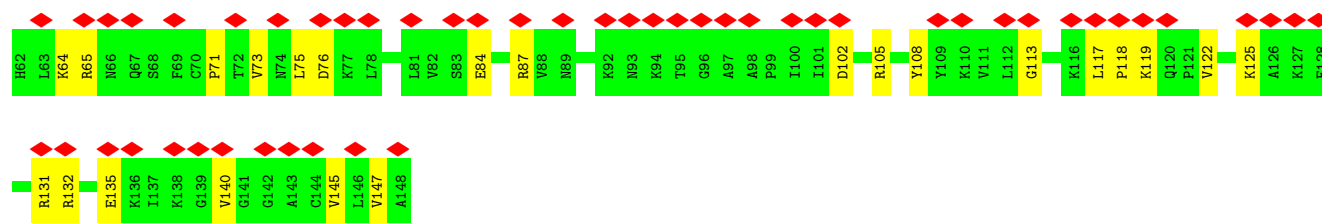
• Molecule 21: L23



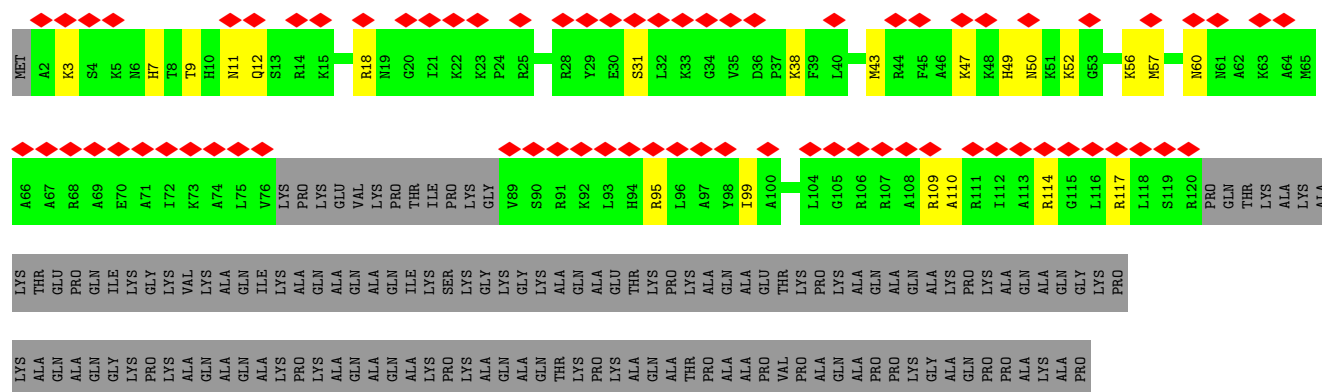
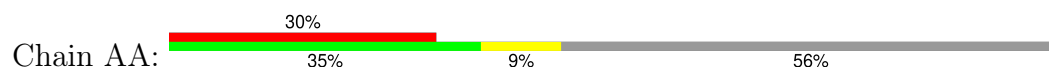
• Molecule 22: uL24



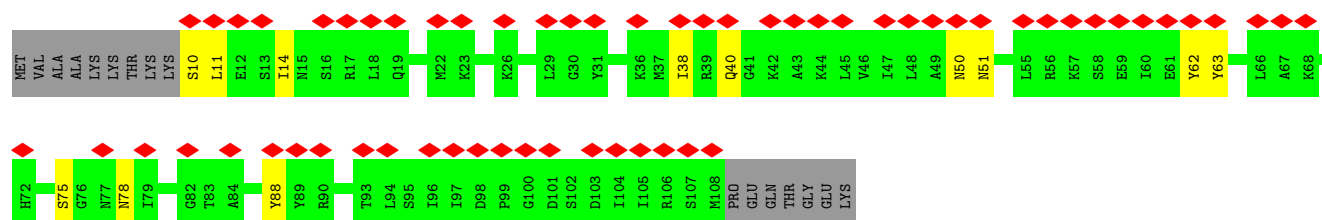
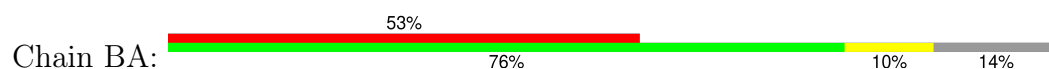
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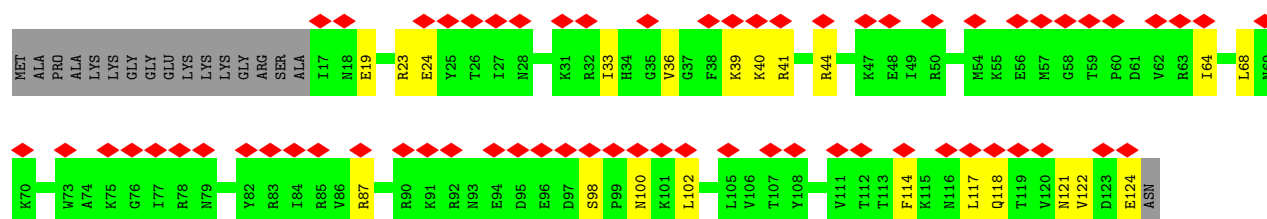
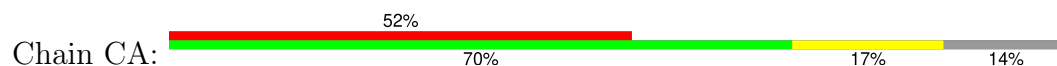
• Molecule 27: L29



• Molecule 28: eL30

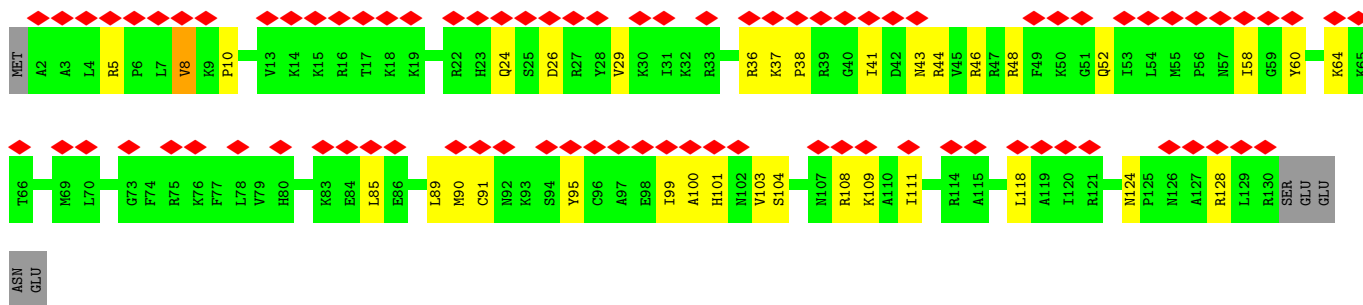


• Molecule 29: L31

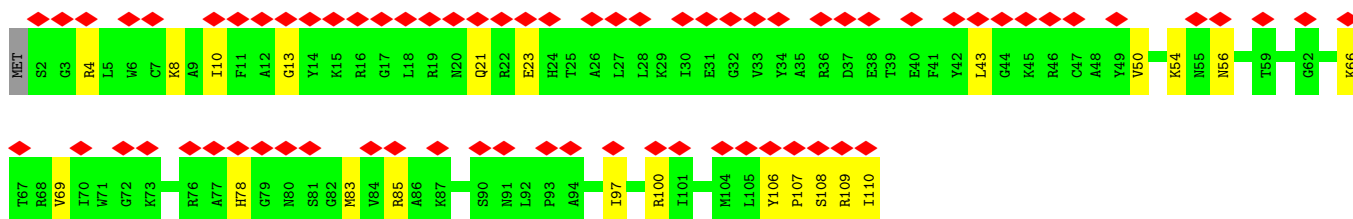
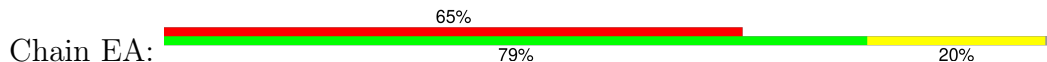


• Molecule 30: L32

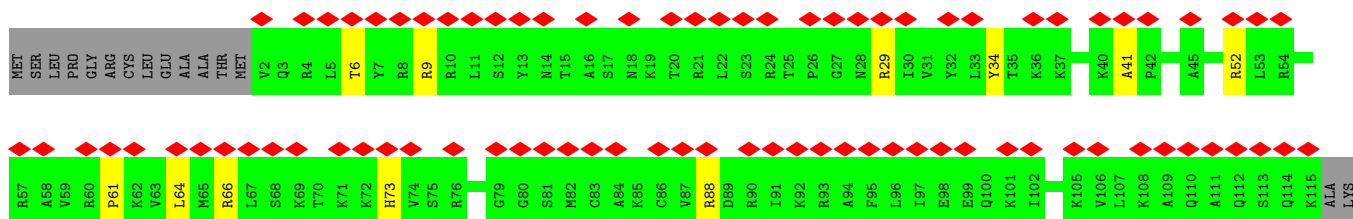
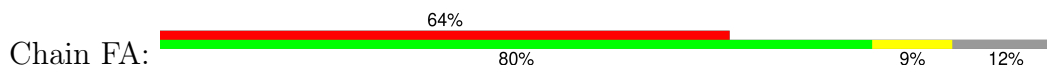




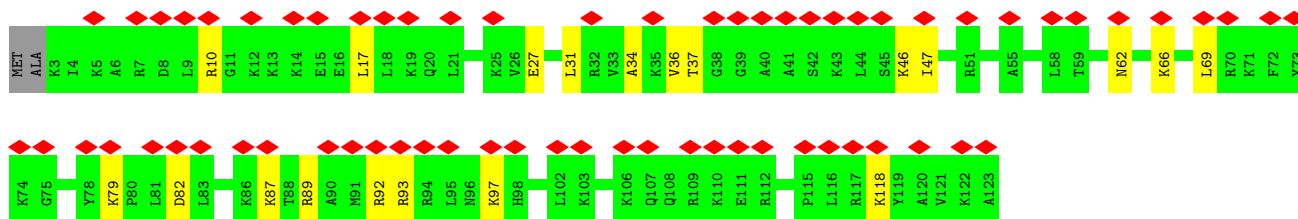
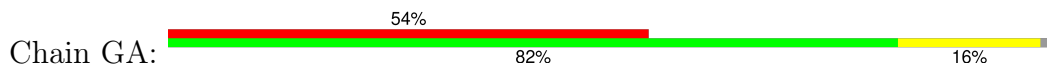
• Molecule 31: eL33



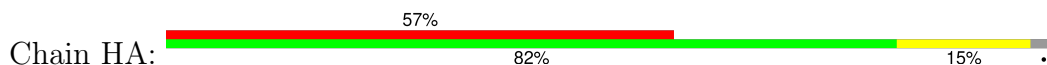
• Molecule 32: L34

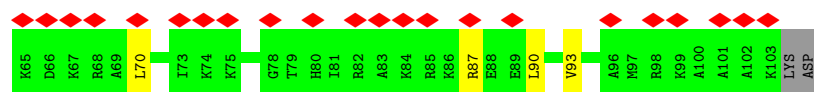


• Molecule 33: L35

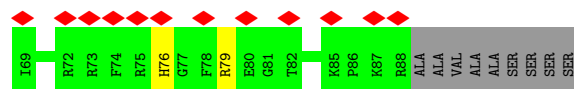
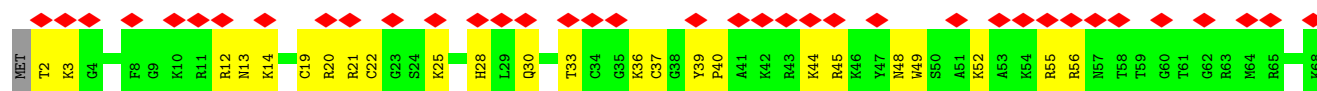


• Molecule 34: L36

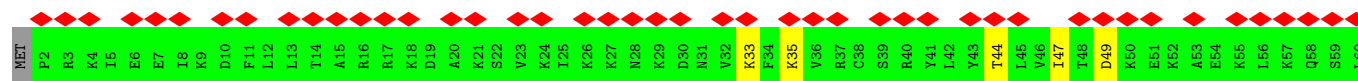
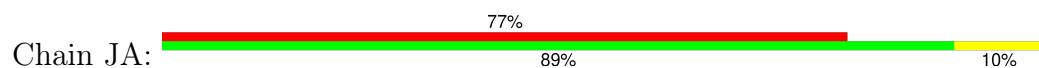




• Molecule 35: L37



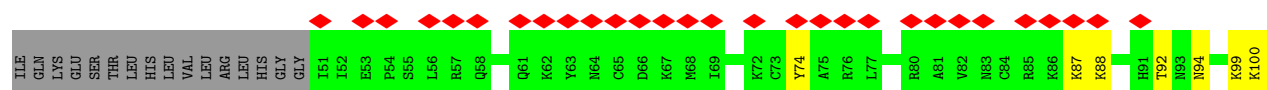
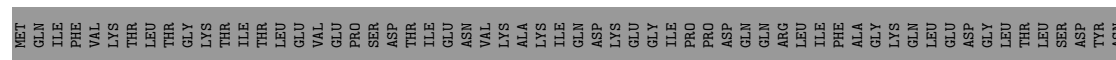
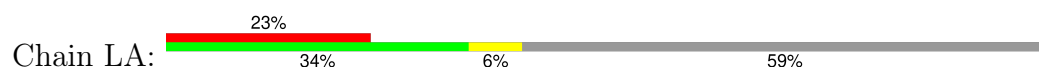
• Molecule 36: eL38



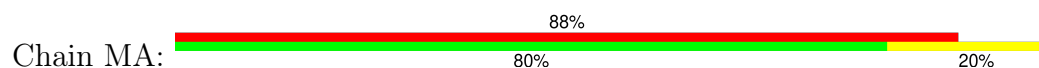
• Molecule 37: eL39



• Molecule 38: eL40

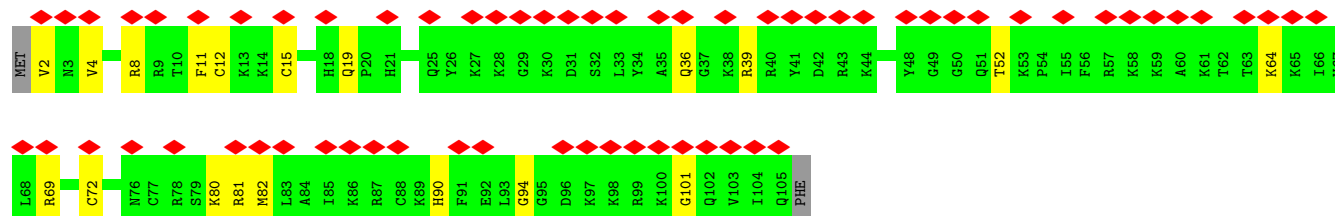
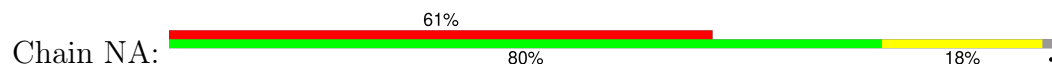


• Molecule 39: eL41

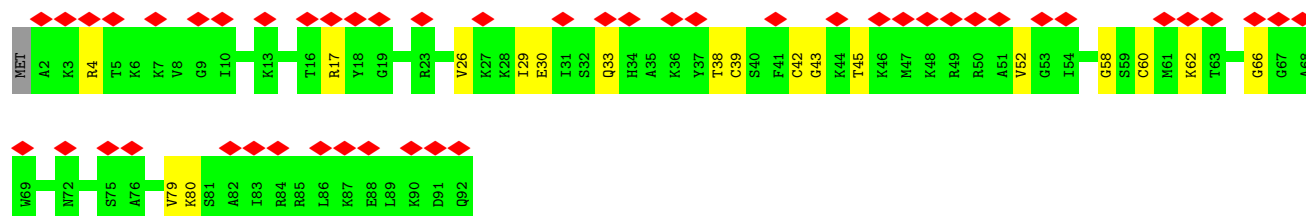
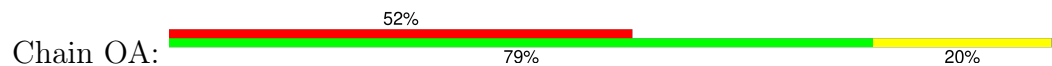




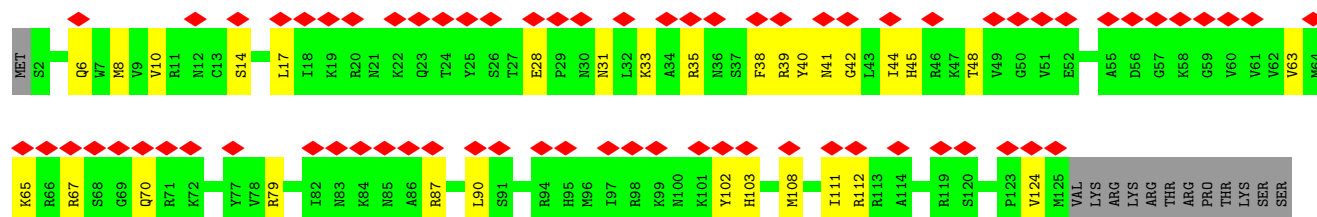
• Molecule 40: eL42



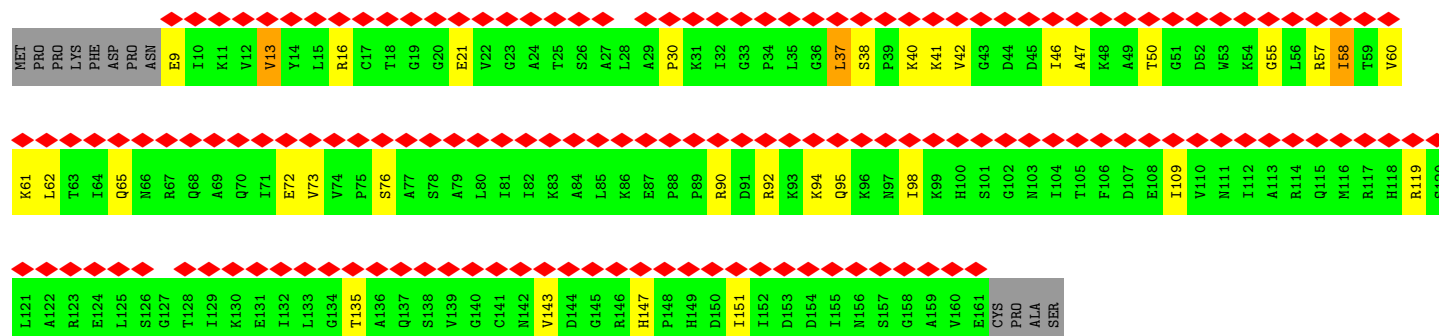
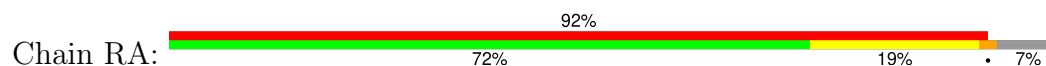
• Molecule 41: eL43



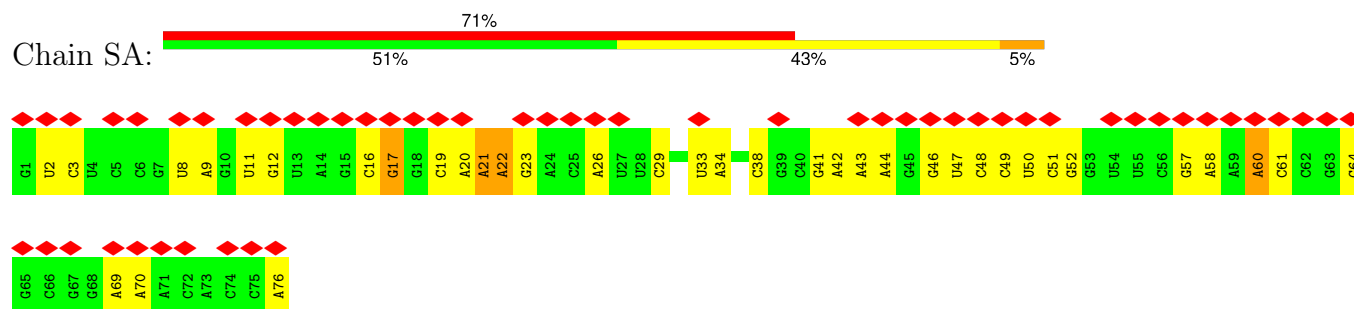
• Molecule 42: L28



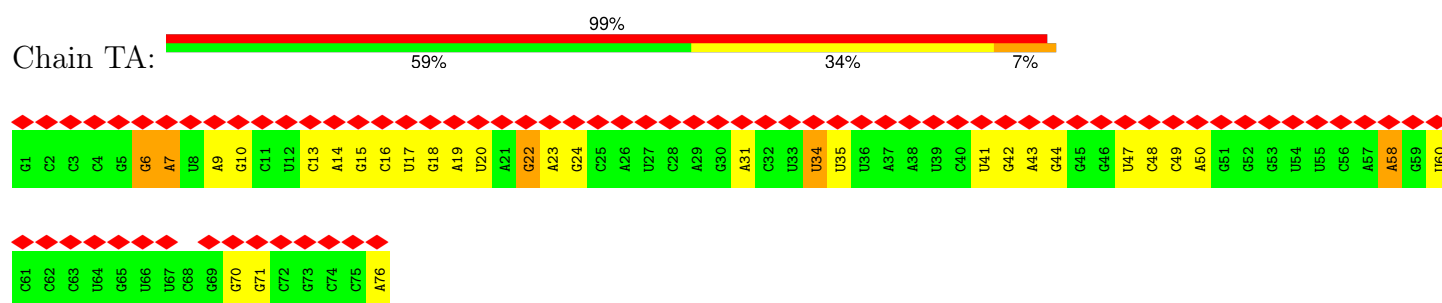
• Molecule 43: L12



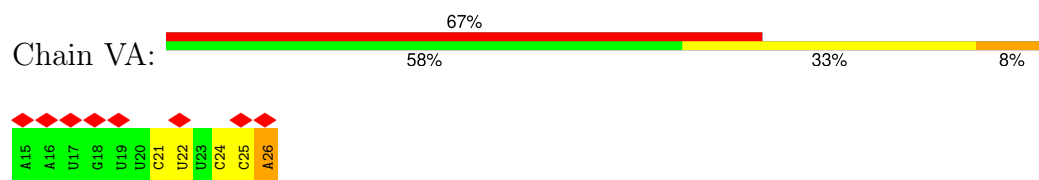
- Molecule 44: P-site tRNA



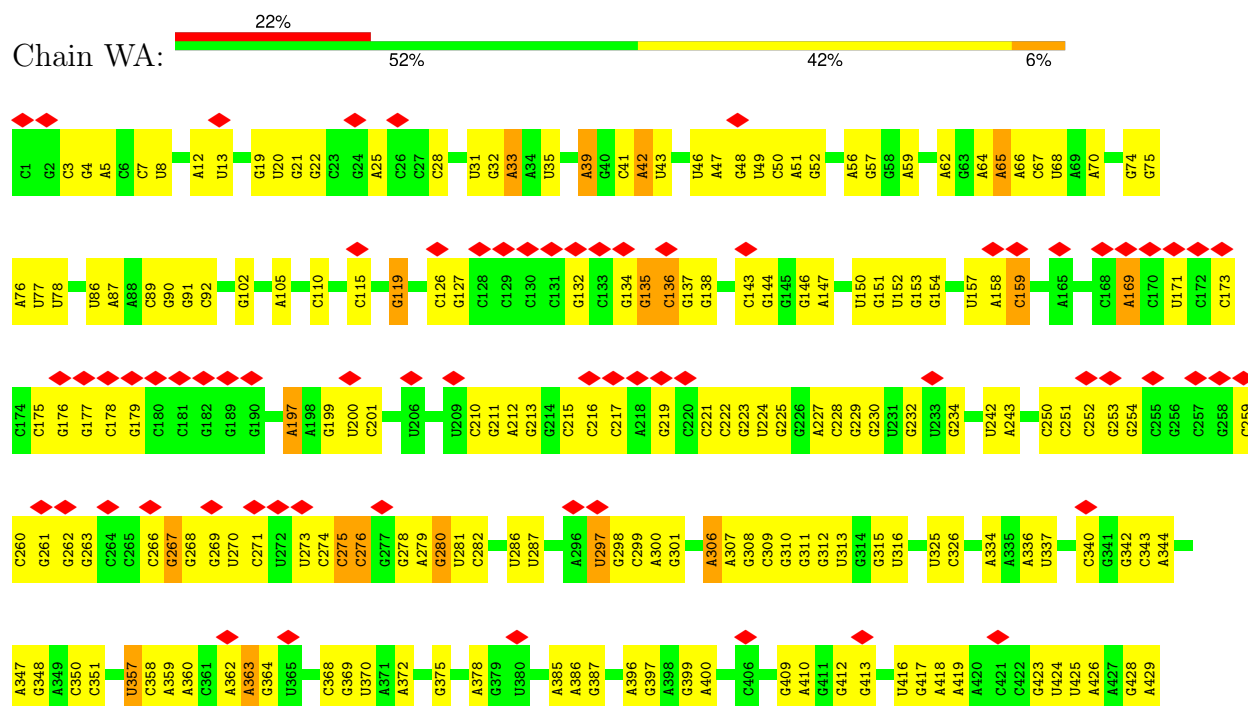
- Molecule 45: E-site tRNA

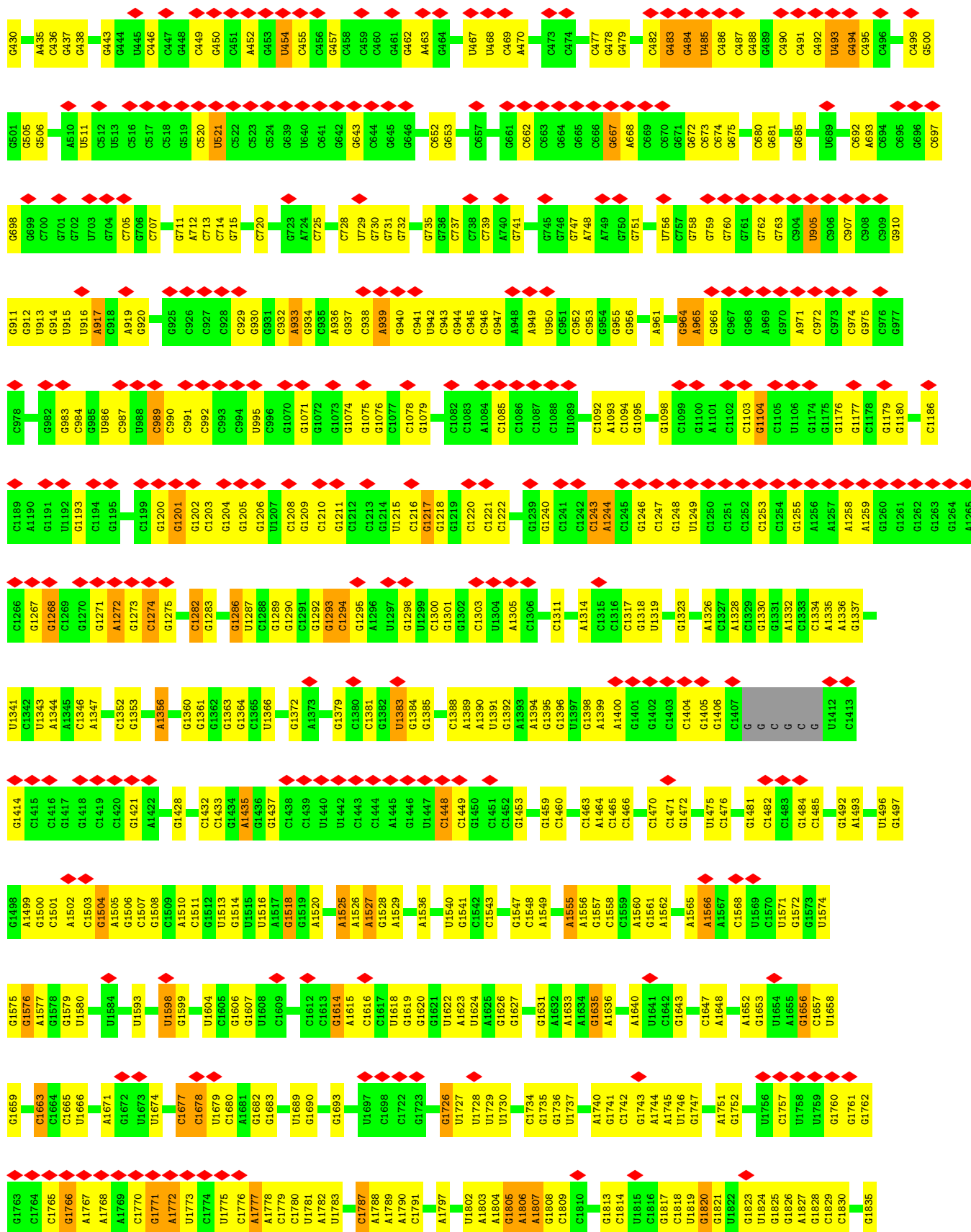


- Molecule 46: mRNA

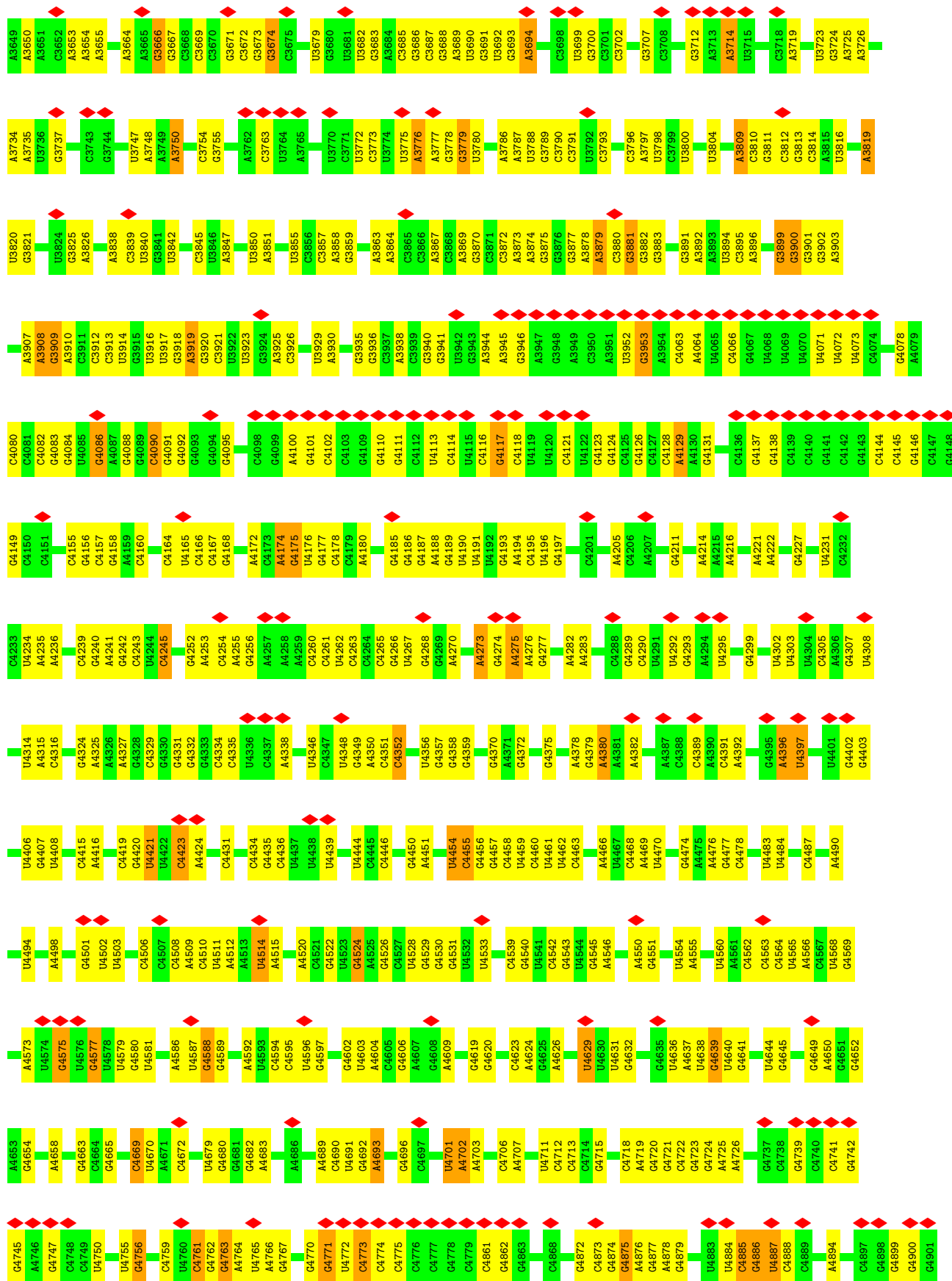


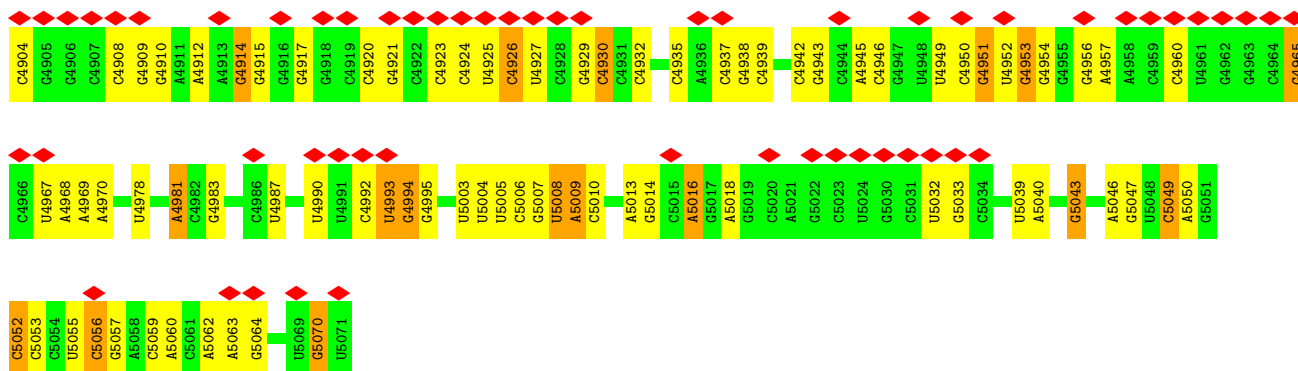
- Molecule 47: 28S rRNA



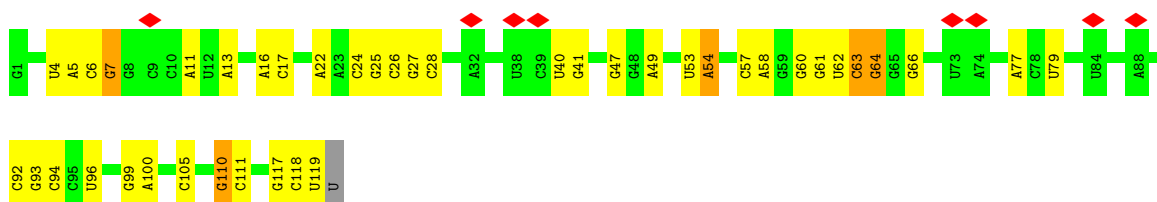


| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
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| G2778 | G2779 | G2780 | C2786 | C2787 | C2788 | A2789 | U2790 | U2791 | U2792 | C2793 | C2796 | A2797 | G2798 | G2799 | A2800 | C2807 | A2808 | G2813 | G2814 | A2815 | G2816 | C2819 | A2827 | U2828 | G2829 | U2830 | G2832 | A2833 | A2834 | A2835 | U2836 | A2837 | U2838 | G2839 | G2840 | G2844 | U2845 | A2846 | A2847 | G2850 | A2851 | G2857 | G2858 | A2859 | A2860 | G2861 | G2862 | G2863 | G2864 | | | | | | | | |
| G2704 | G2705 | G2708 | G2709 | U2710 | G2711 | G2712 | G2713 | G2714 | G2715 | G2716 | G2721 | G2722 | G2723 | G2724 | U2725 | G2726 | A2727 | G2728 | U2729 | U2730 | G2731 | U2732 | G2733 | G2734 | G2737 | G2738 | G2739 | G2740 | G2741 | U2742 | U2743 | G2744 | A2745 | A2746 | G2751 | G2752 | G2753 | G2754 | G2755 | G2756 | A2759 | G2760 | G2761 | U2762 | U2763 | G2764 | U2765 | A2766 | A2767 | A2768 | U2771 | G2777 | | | | | |
| U2633 | U2634 | U2635 | C2636 | G2640 | U2641 | G2642 | A2643 | A2644 | G2645 | A2649 | G2650 | G2651 | G2654 | G2655 | G2656 | G2657 | U2658 | G2659 | A2660 | A2661 | A2662 | U2663 | G2664 | C2669 | G2670 | C2671 | G2674 | G2675 | G2676 | G2677 | A2678 | G2679 | G2682 | G2683 | G2684 | G2685 | G2686 | G2687 | G2688 | U2689 | G2690 | G2691 | G2692 | U2693 | U2694 | G2695 | G2696 | A2697 | A2698 | A2699 | G2700 | G2701 | U2627 | U2703 | | | |
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| C2327 | G2328 | G2329 | G2330 | U2331 | G2332 | G2333 | A2334 | G2335 | C2336 | C2337 | G2338 | C2342 | A2343 | U2346 | G2347 | G2348 | A2349 | G2350 | A2351 | U2352 | G2353 | U2354 | A2362 | G2363 | U2364 | A2365 | U2371 | A2372 | U2373 | U2374 | C2375 | A2376 | A2377 | A2378 | C2379 | G2380 | A2383 | A2384 | C2385 | U2386 | U2387 | U2388 | G2389 | A2390 | A2391 | G2392 | G2396 | A2397 | A2398 | G2399 | G2402 | | | | | | |
| A2109 | G2110 | A2111 | G2112 | U2113 | G2114 | G2115 | A2116 | G2117 | G2118 | G2260 | G2261 | G2262 | A2265 | G2266 | G2267 | G2268 | U2269 | A2270 | G2277 | A2278 | G2279 | G2280 | A2281 | G2285 | G2286 | A2287 | G2288 | C2291 | G2297 | G2298 | A2302 | G2303 | G2304 | G2305 | G2308 | A2309 | A2310 | G2311 | G2312 | G2313 | U2314 | A2315 | G2316 | G2317 | G2318 | G2319 | G2320 | G2321 | G2322 | G2323 | G2324 | | | | | | |
| U2040 | G2041 | A2042 | A2043 | G2048 | A2049 | U2050 | G2053 | G2054 | C2055 | U2056 | G2057 | G2058 | A2059 | G2060 | C2061 | G2062 | U2063 | C2064 | G2067 | G2068 | G2069 | C2070 | A2071 | U2072 | A2073 | G2077 | G2078 | C2079 | G2080 | G2081 | U2082 | C2083 | G2084 | G2085 | U2086 | C2089 | U2092 | G2093 | G2094 | G2095 | G2096 | A2097 | G2098 | A2099 | G2100 | G2101 | G2102 | A2103 | G2104 | A2105 | A2106 | A2107 | G2108 | | | | |
| G1978 | C1979 | C1980 | A1981 | U1982 | G1983 | G1984 | A1985 | A1986 | A1987 | U1988 | C1989 | G1990 | G1991 | A1992 | A1993 | U1994 | C1995 | C1996 | G1997 | C1998 | U1999 | A2000 | A2001 | G2002 | G2003 | A2004 | G2005 | U2006 | G2007 | U2008 | G2009 | U2010 | A2011 | A2012 | C2013 | A2014 | A2015 | G2016 | U2017 | G2018 | A2019 | C2020 | U2021 | U2022 | G2023 | G2026 | A2027 | A2028 | U2029 | A2030 | A2031 | A2032 | G2033 | U2034 | A2035 | G2036 | C2039 |
| C1915 | G1916 | C1917 | G1918 | A1919 | U1920 | G1921 | C1922 | G1923 | A1924 | U1925 | C1926 | G1927 | C1928 | U1929 | C1930 | A1931 | C1932 | C1933 | A1934 | G1935 | A1936 | C1937 | C1938 | C1939 | C1940 | A1941 | G1942 | A1943 | A1944 | A1945 | U1949 | G1950 | U1951 | U1952 | G1953 | U1956 | G1957 | A1958 | U1959 | A1960 | U1961 | A1962 | G1963 | A1964 | C1965 | A1966 | G1967 | C1968 | A1969 | G1970 | G1971 | A1972 | U1973 | G1974 | C1975 | G1976 | G1977 |
| U1836 | G1837 | G1838 | A1839 | G1843 | G1844 | G1848 | C1849 | U1850 | U1851 | A1852 | G1853 | U1854 | U1855 | G1856 | G1857 | U1864 | U1865 | G1866 | G1870 | U1871 | C1872 | A1873 | G1874 | U1878 | G1879 | G1880 | C1881 | G1882 | C1883 | U1884 | G1885 | C1886 | G1887 | A1890 | A1893 | G1897 | A1898 | A1899 | C1900 | G1901 | C1902 | C1903 | G1904 | U1908 | A1909 | G1912 | C1913 | G1914 | | | | | | | | | |

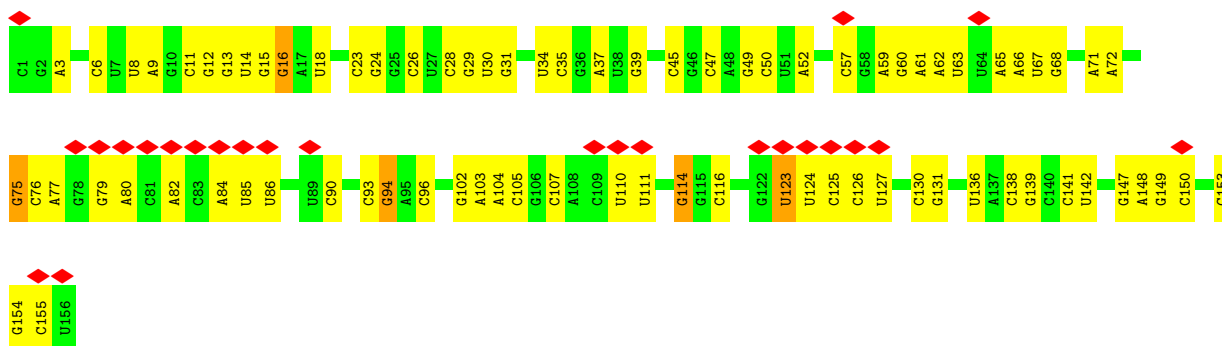




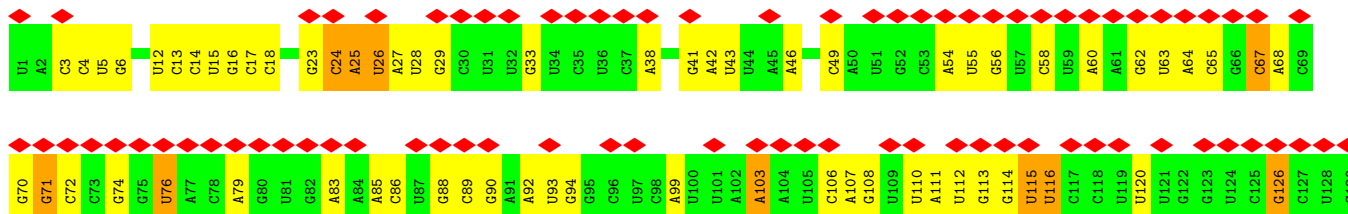
• Molecule 48: 5S rRNA



• Molecule 49: 5.8S rRNA



• Molecule 50: 18S rRNA

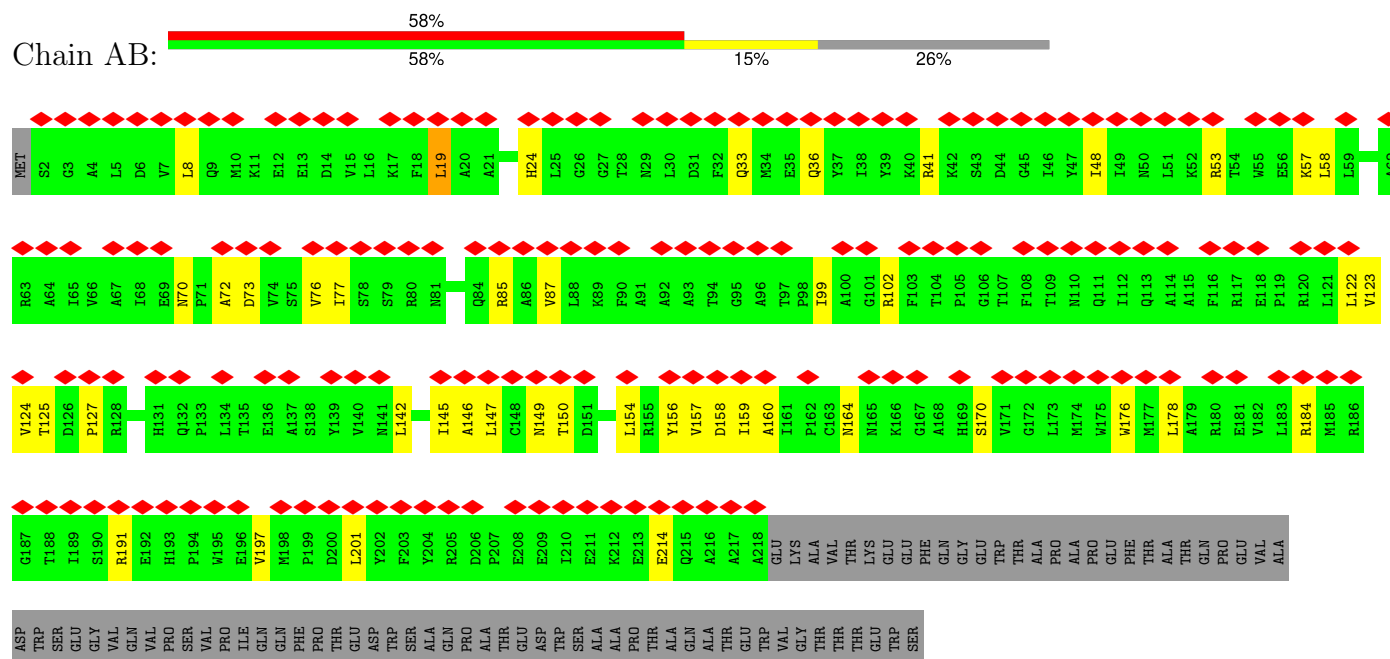






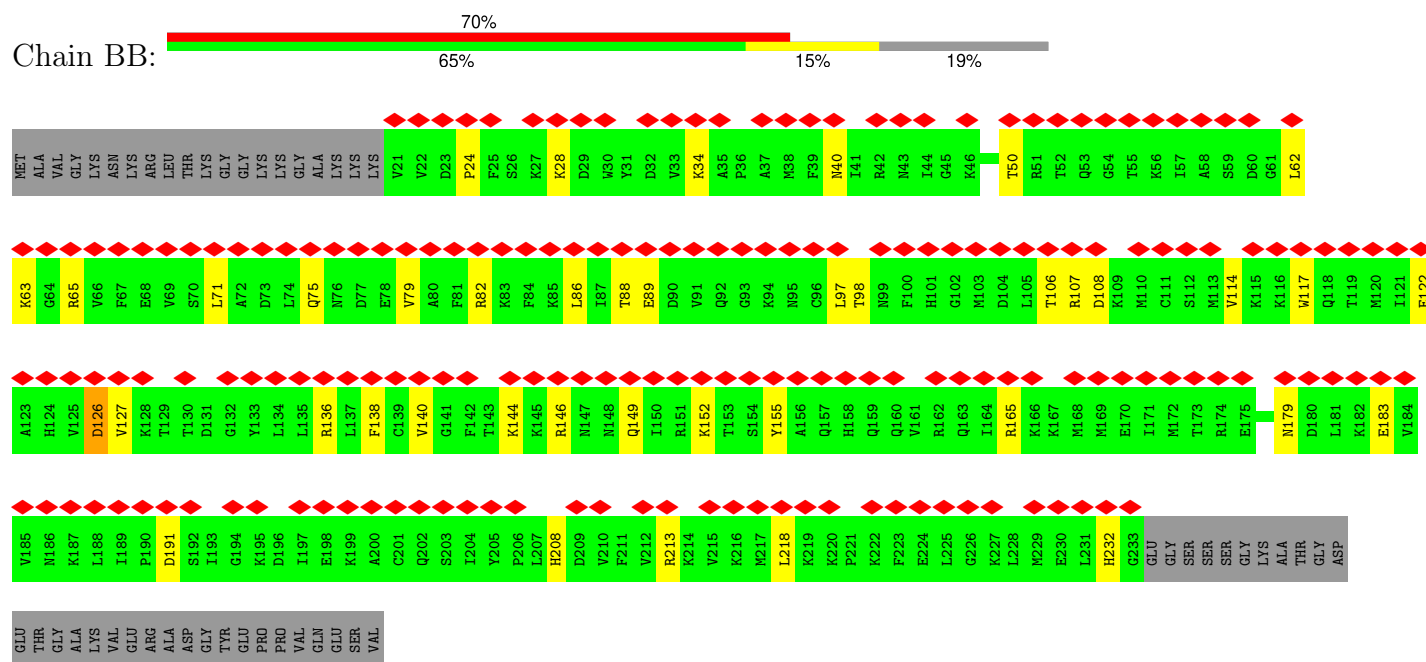
- Molecule 51: RPSA

Chain AB:



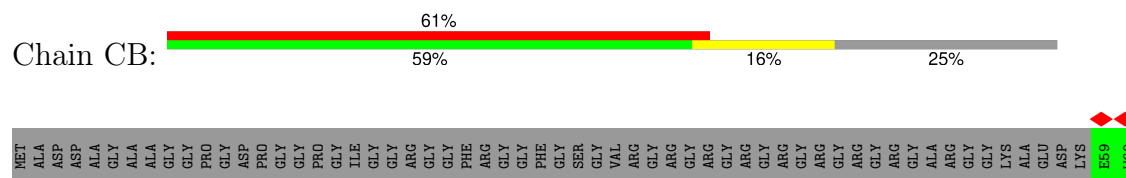
- Molecule 52: S3A

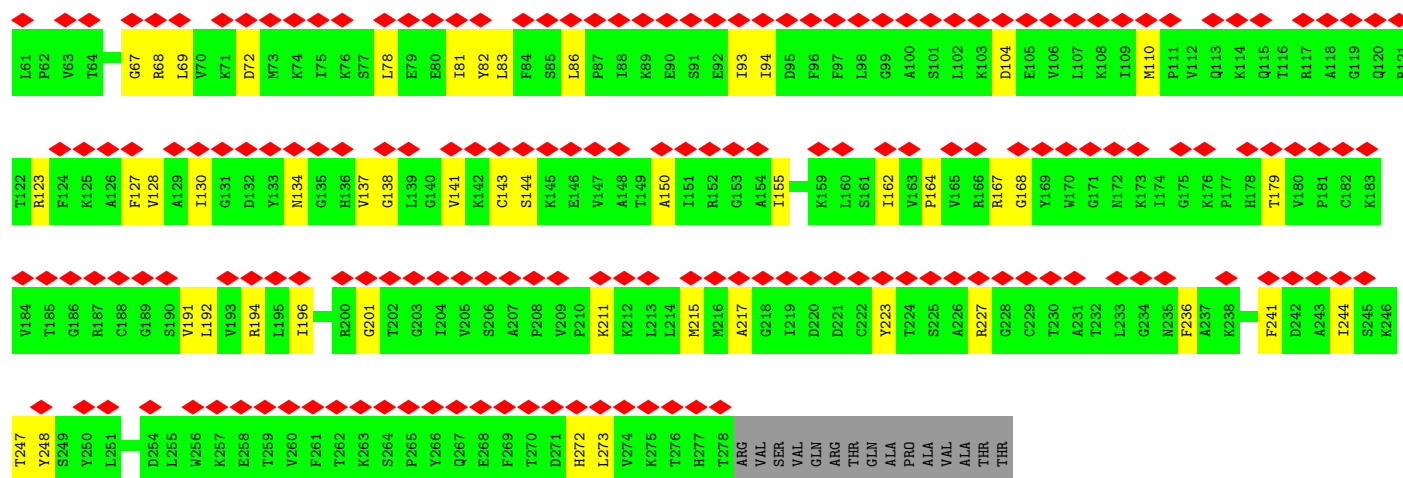
Chain BB:



- Molecule 53: S2-like

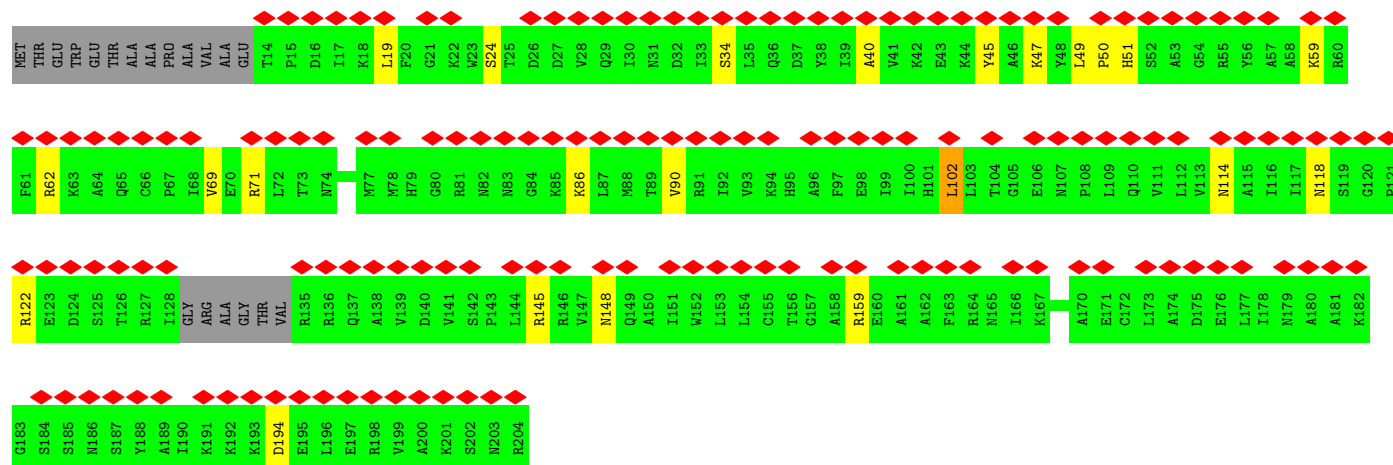
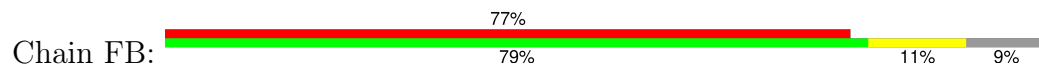
Chain CB:



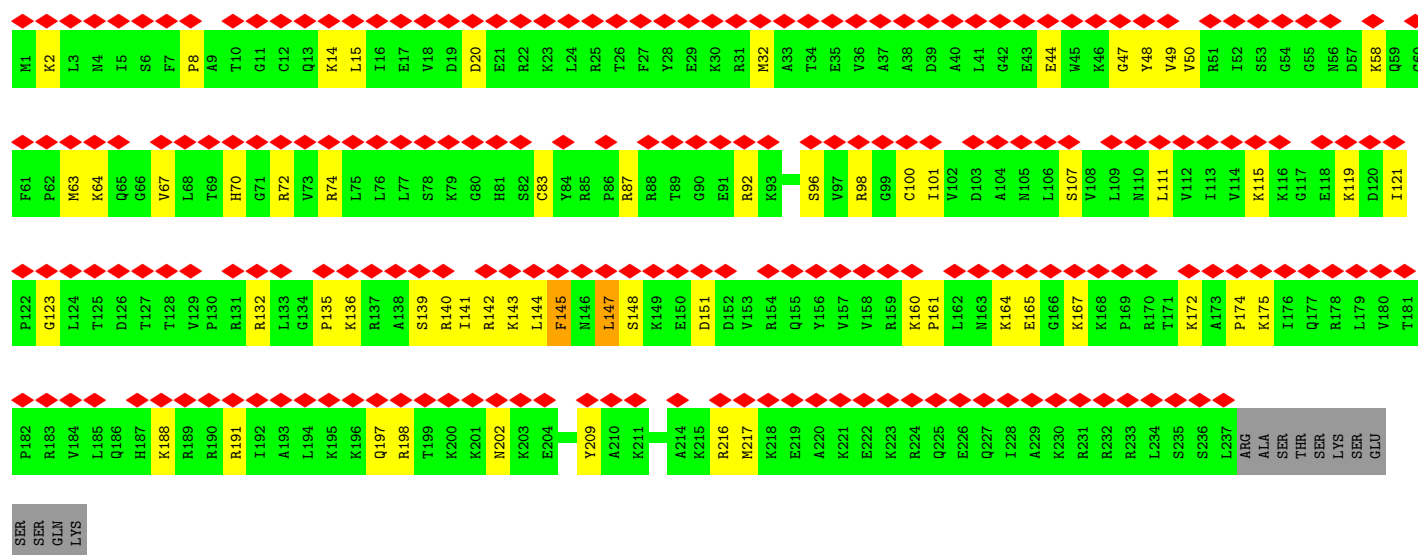
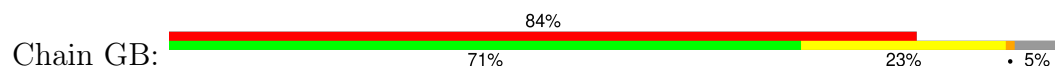




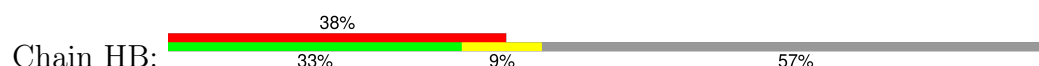
• Molecule 56: S5



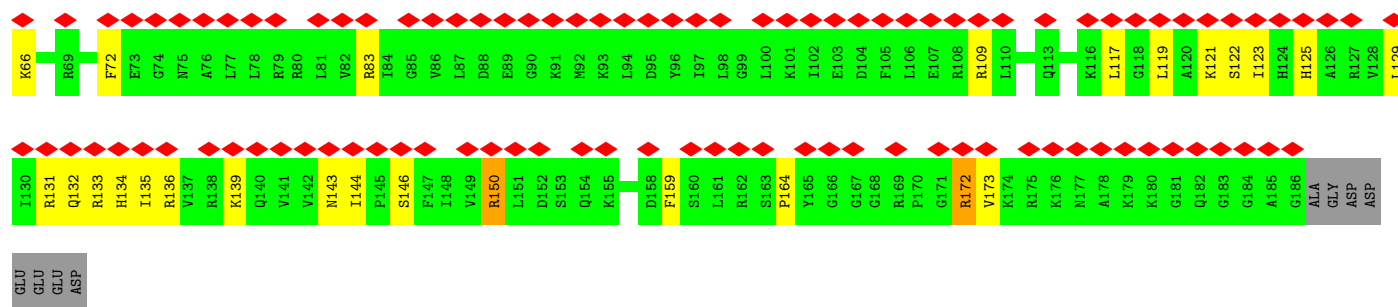
• Molecule 57: eS6



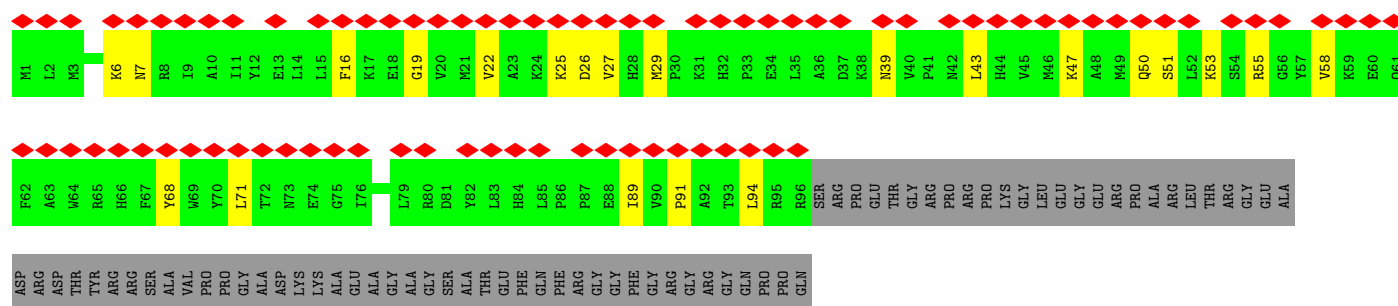
• Molecule 58: eS7



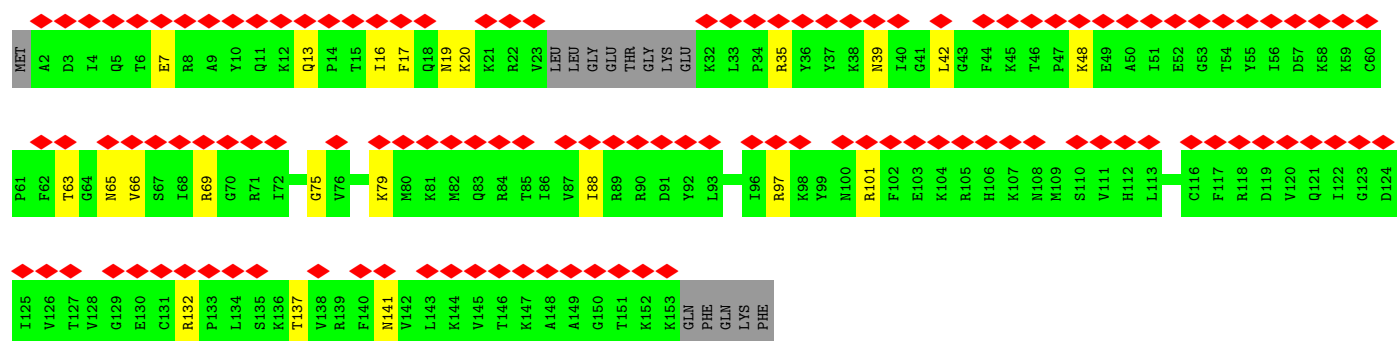
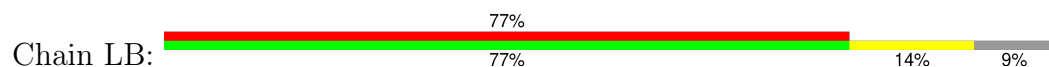




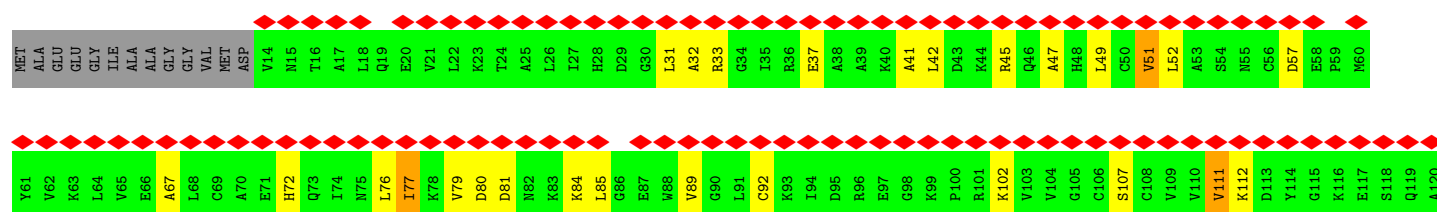
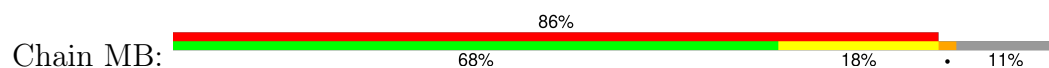
• Molecule 61: S10



• Molecule 62: S11

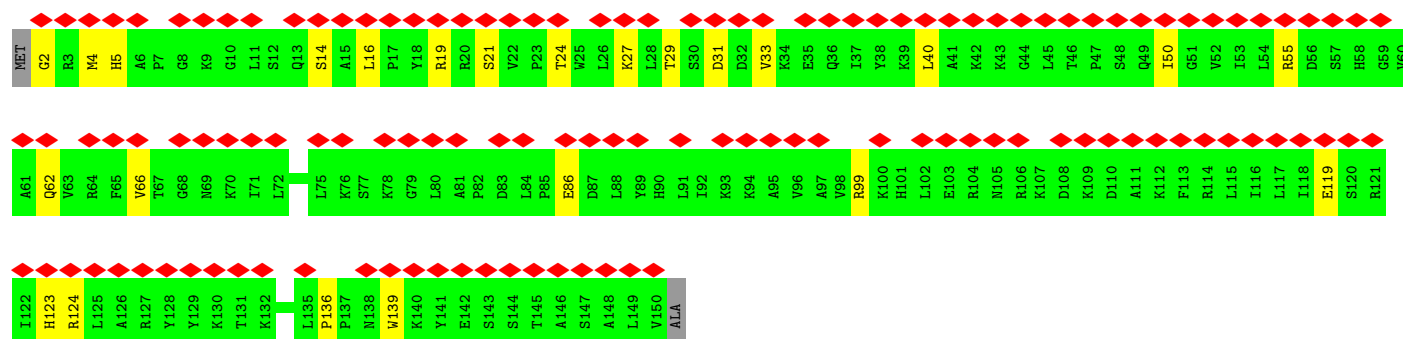
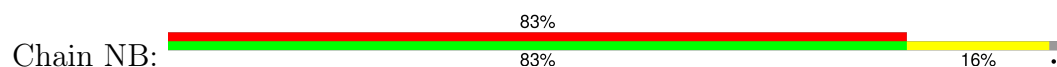


• Molecule 63: S12

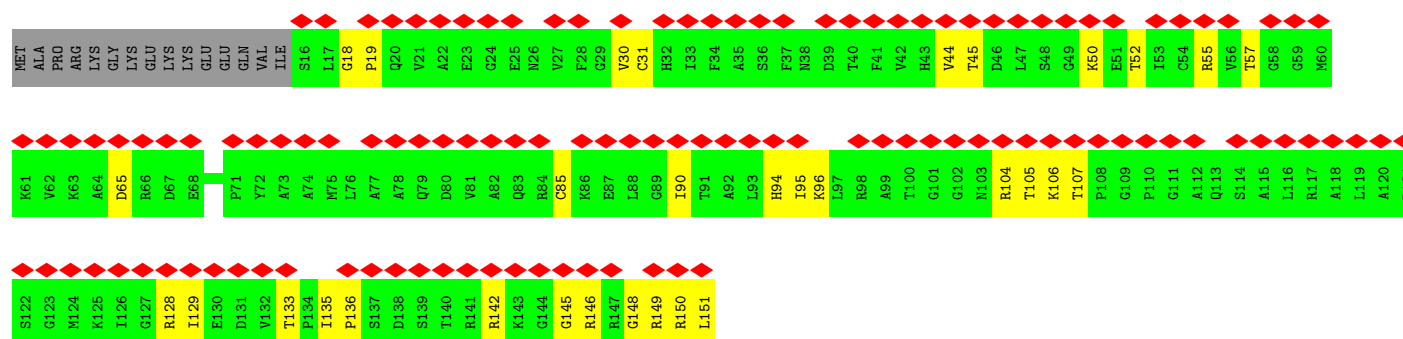
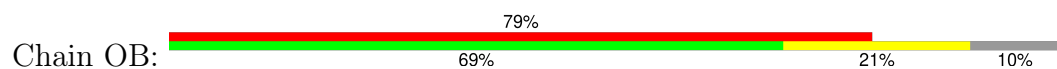




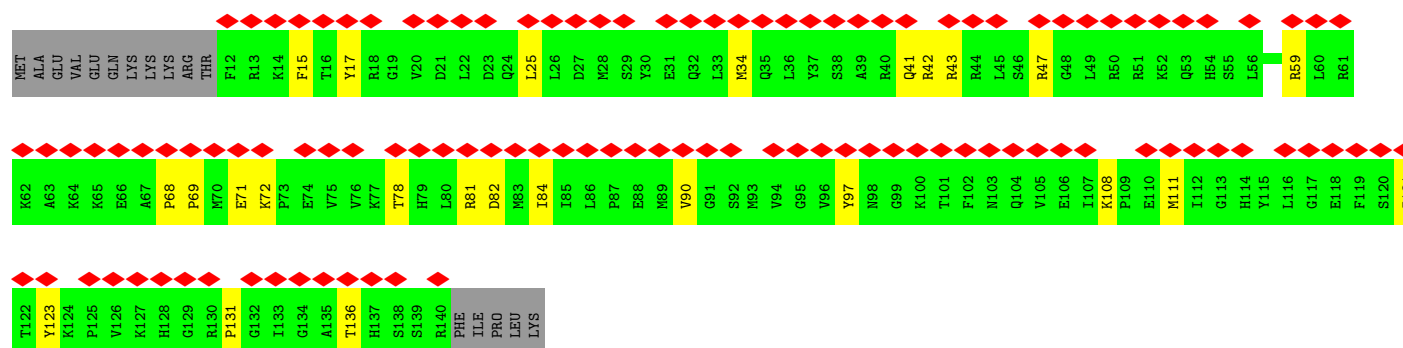
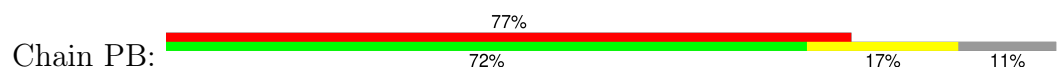
• Molecule 64: uS15



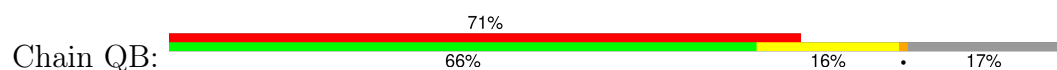
• Molecule 65: S14

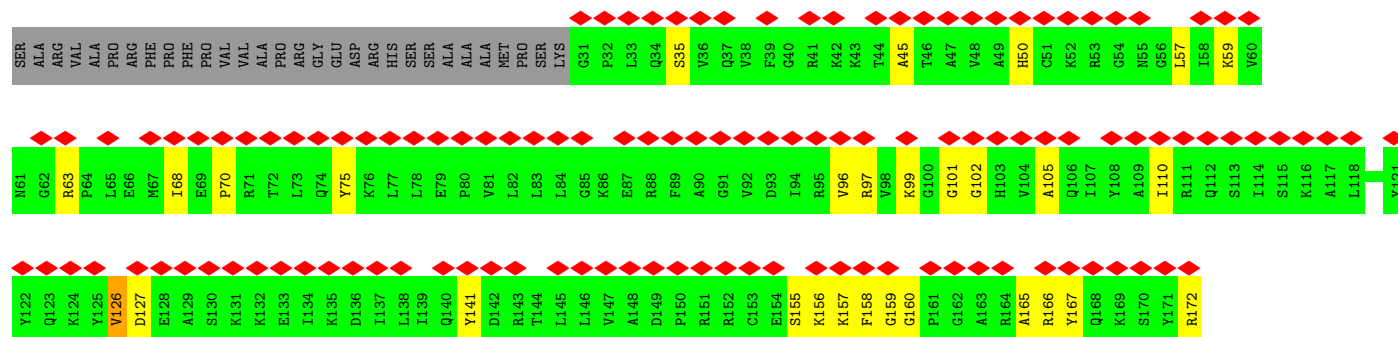


• Molecule 66: S15

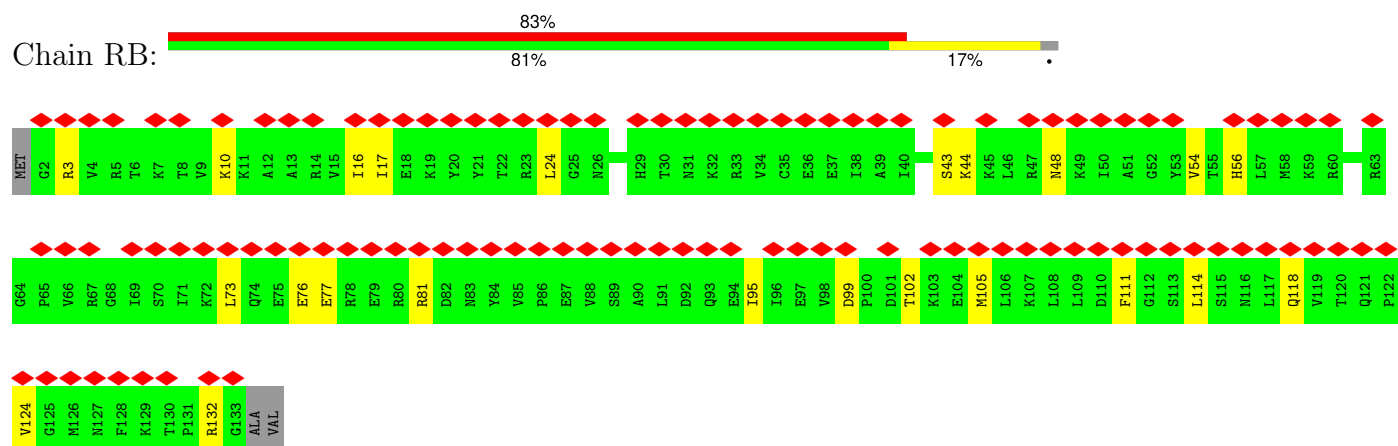


• Molecule 67: uS9

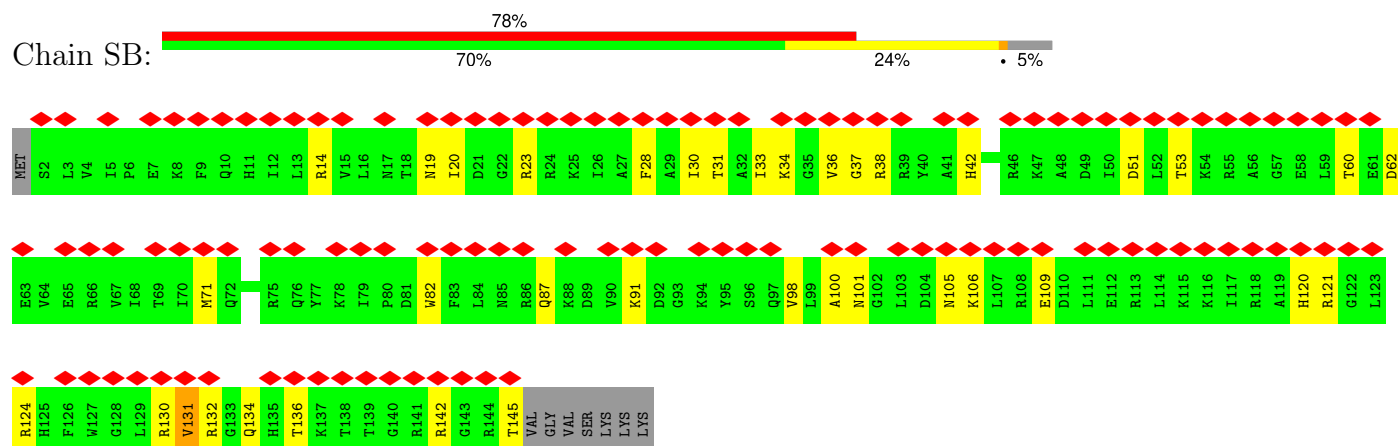




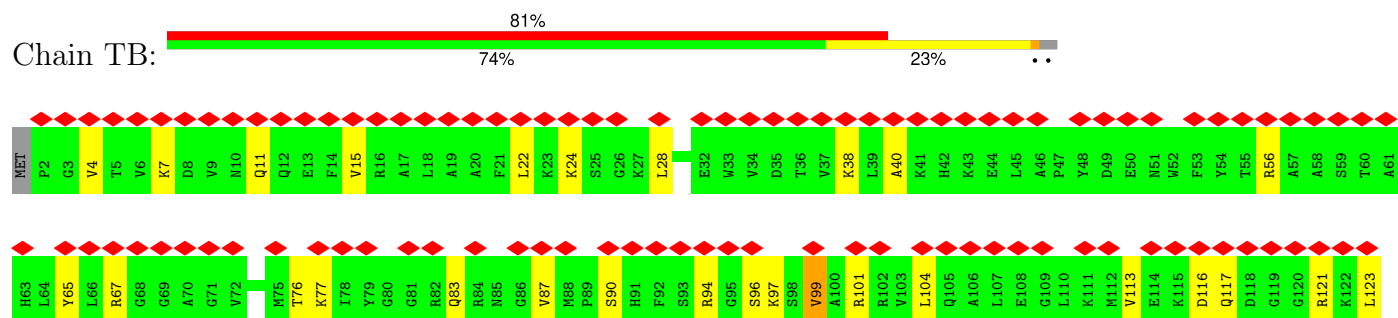
• Molecule 68: eS17



• Molecule 69: S18

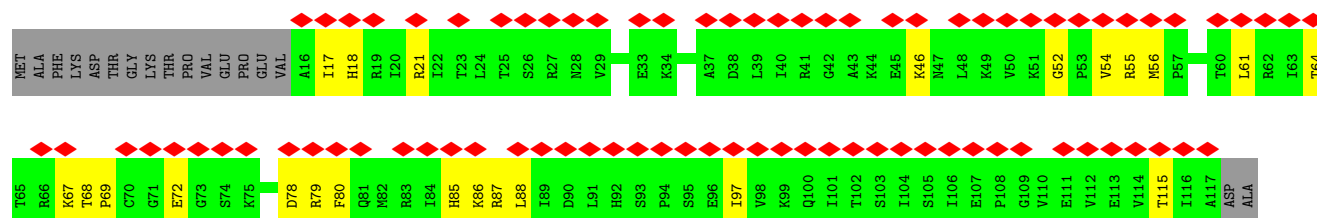


• Molecule 70: S19

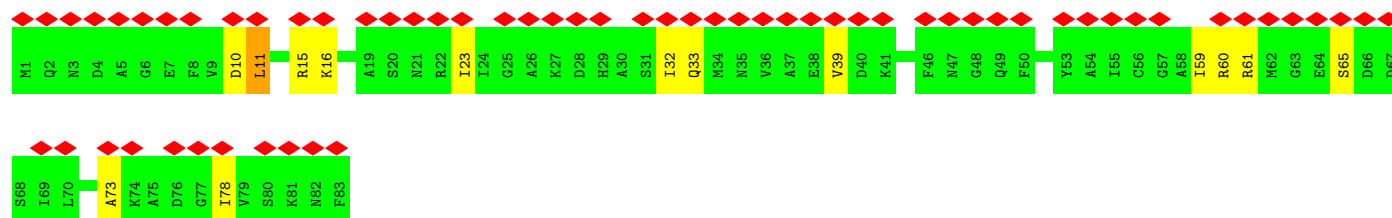
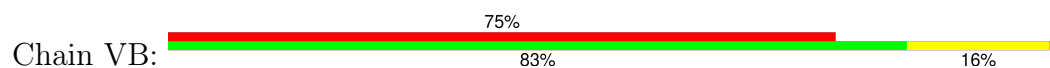




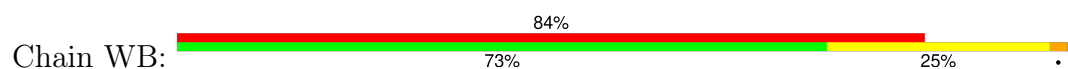
• Molecule 71: uS10



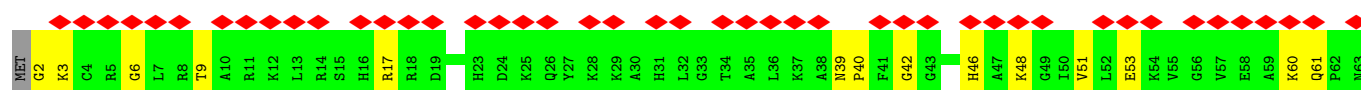
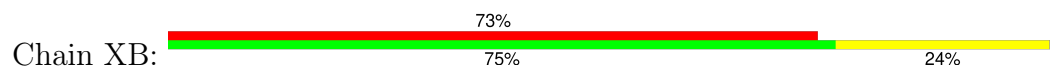
• Molecule 72: S21

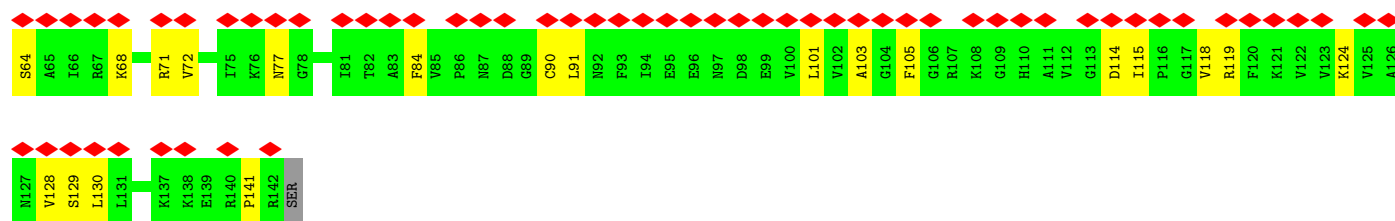


• Molecule 73: S15A

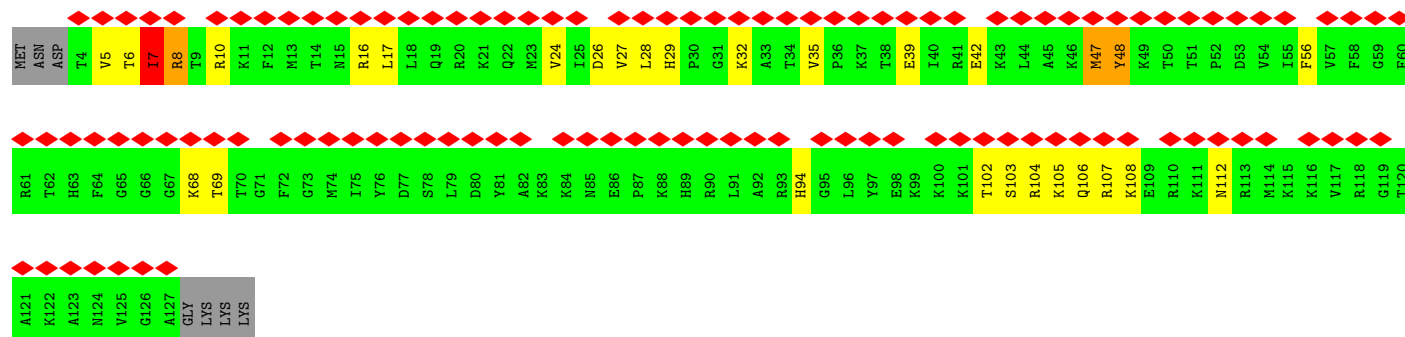
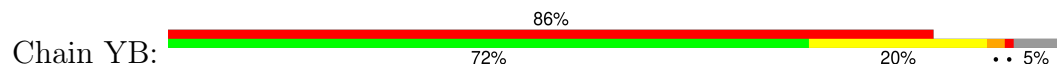


• Molecule 74: S23

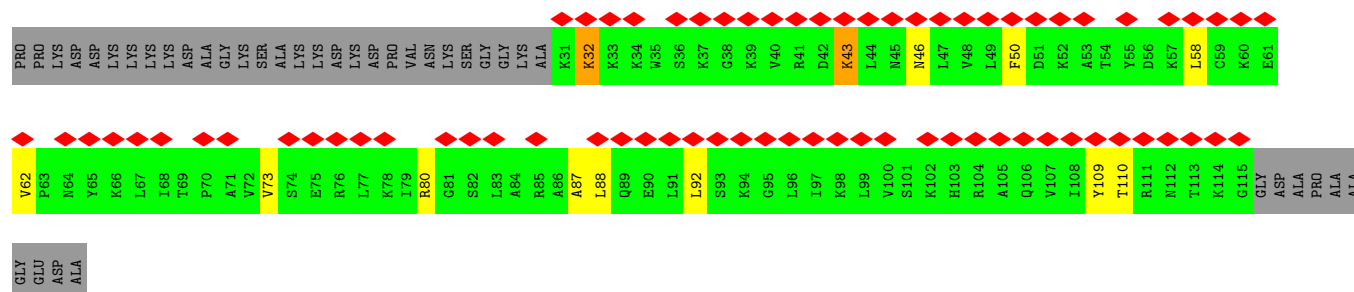




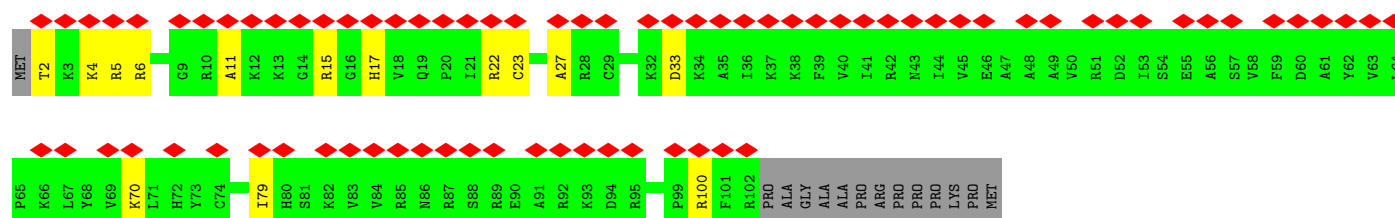
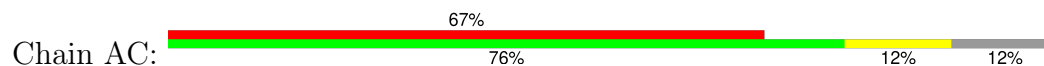
• Molecule 75: S24



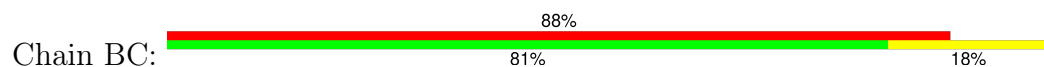
• Molecule 76: eS25

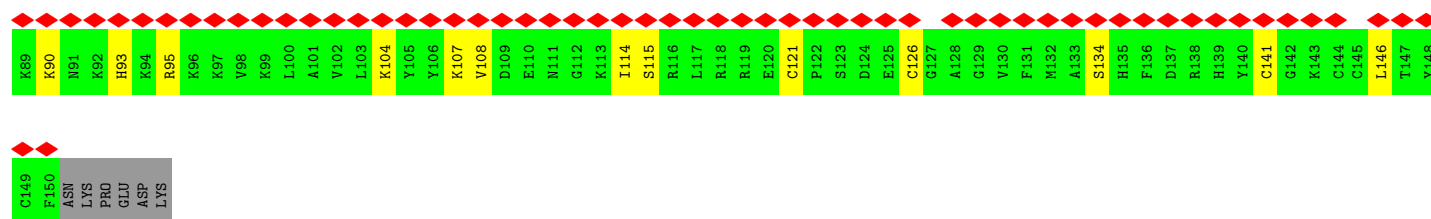


• Molecule 77: S26

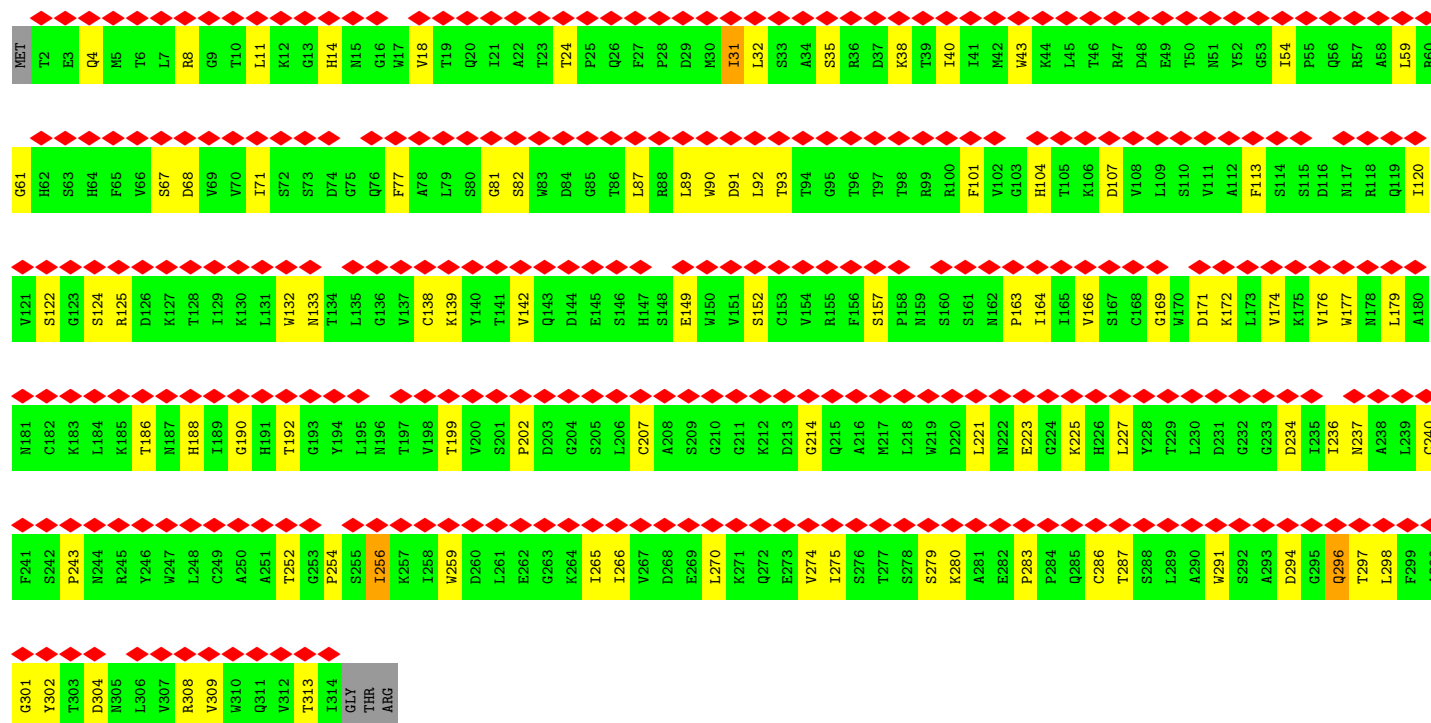
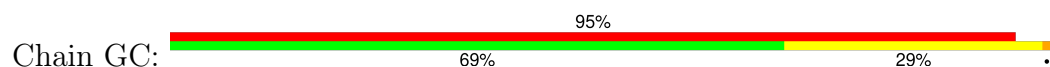


• Molecule 78: S27

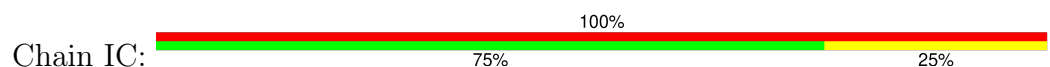




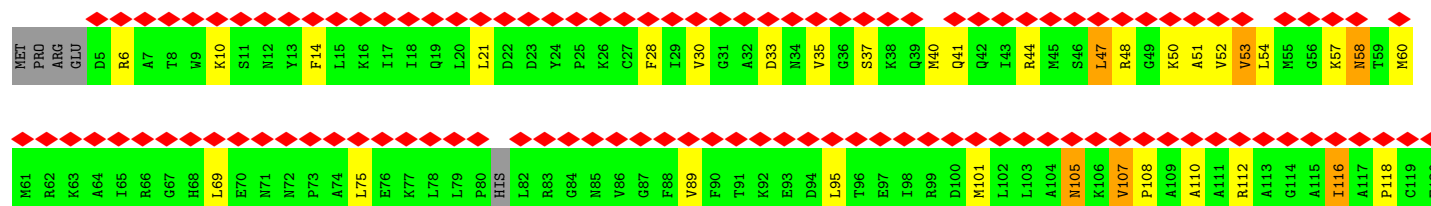
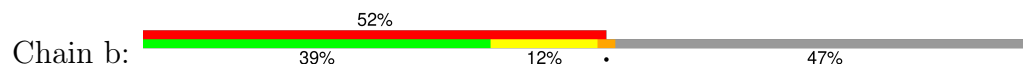
• Molecule 83: RACK1



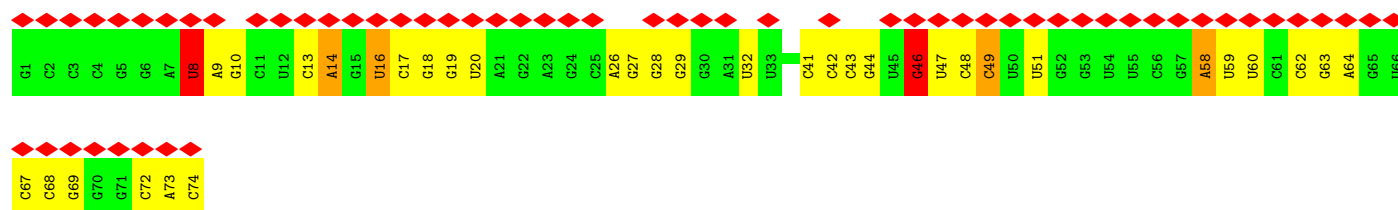
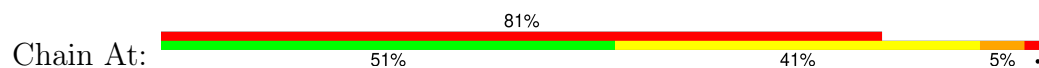
• Molecule 84: nascent chain



• Molecule 85: RPLP0



- Molecule 86: A-site tRNA



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 1508 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 75 | Depositor |
| Minimum defocus (nm) | 500 | Depositor |
| Maximum defocus (nm) | 2500 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K3 (6k x 4k) | Depositor |
| Maximum map value | 24.363 | Depositor |
| Minimum map value | -18.068 | Depositor |
| Average map value | 0.008 | Depositor |
| Map value standard deviation | 1.504 | Depositor |
| Recommended contour level | 7 | Depositor |
| Map size (Å) | 686.87994, 686.87994, 686.87994 | wwPDB |
| Map dimensions | 648, 648, 648 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.06, 1.06, 1.06 | Depositor |

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 4SU, SPD, ANM, PSU, H2U, MG, 7MG, ZN

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

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-------------|-------------|-------------|
| | | RMSZ | $\# Z > 5$ | RMSZ | $\# Z > 5$ |
| 1 | A | 0.07 | 0/1952 | 0.21 | 0/2617 |
| 2 | B | 0.08 | 0/3264 | 0.22 | 0/4371 |
| 3 | C | 0.07 | 0/2937 | 0.20 | 0/3946 |
| 4 | D | 0.08 | 0/2441 | 0.21 | 0/3269 |
| 5 | E | 0.08 | 0/1859 | 0.22 | 0/2491 |
| 6 | F | 0.08 | 0/1933 | 0.22 | 0/2577 |
| 7 | G | 0.08 | 0/1881 | 0.20 | 0/2532 |
| 8 | H | 0.07 | 0/1535 | 0.24 | 0/2063 |
| 9 | I | 0.07 | 0/1702 | 0.19 | 0/2272 |
| 10 | J | 0.07 | 0/1395 | 0.23 | 0/1863 |
| 11 | K | 0.08 | 0/1733 | 0.21 | 0/2316 |
| 12 | L | 0.08 | 0/1158 | 0.20 | 0/1547 |
| 13 | M | 0.08 | 0/1746 | 0.22 | 0/2338 |
| 14 | N | 0.09 | 0/1662 | 0.22 | 0/2222 |
| 15 | O | 0.07 | 0/1292 | 0.22 | 0/1733 |
| 16 | P | 0.07 | 0/1539 | 0.23 | 0/2054 |
| 17 | Q | 0.08 | 0/1524 | 0.19 | 0/2013 |
| 18 | R | 0.08 | 0/1501 | 0.23 | 0/2012 |
| 19 | S | 0.07 | 0/1326 | 0.20 | 0/1770 |
| 20 | T | 0.08 | 0/840 | 0.25 | 0/1127 |
| 21 | U | 0.08 | 0/1018 | 0.23 | 0/1364 |
| 22 | V | 0.11 | 0/900 | 0.29 | 0/1194 |
| 23 | W | 0.07 | 0/984 | 0.20 | 0/1323 |
| 24 | X | 0.06 | 0/1132 | 0.19 | 0/1504 |
| 25 | Y | 0.07 | 0/1130 | 0.20 | 0/1507 |
| 26 | Z | 0.08 | 0/1191 | 0.21 | 0/1590 |
| 27 | AA | 0.06 | 0/886 | 0.16 | 0/1171 |
| 28 | BA | 0.07 | 0/779 | 0.18 | 0/1044 |
| 29 | CA | 0.08 | 0/908 | 0.20 | 0/1223 |
| 30 | DA | 0.07 | 0/1082 | 0.20 | 0/1443 |
| 31 | EA | 0.08 | 0/895 | 0.21 | 0/1198 |
| 32 | FA | 0.07 | 0/916 | 0.22 | 0/1220 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|----------------|-------------|---------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 33 | GA | 0.07 | 0/1016 | 0.19 | 0/1341 |
| 34 | HA | 0.07 | 0/841 | 0.20 | 0/1112 |
| 35 | IA | 0.08 | 0/731 | 0.21 | 0/966 |
| 36 | JA | 0.07 | 0/575 | 0.20 | 0/761 |
| 37 | KA | 0.07 | 0/459 | 0.19 | 0/608 |
| 38 | LA | 0.08 | 0/435 | 0.24 | 0/575 |
| 39 | MA | 0.07 | 0/240 | 0.16 | 0/305 |
| 40 | NA | 0.07 | 0/864 | 0.20 | 0/1140 |
| 41 | OA | 0.08 | 0/718 | 0.20 | 0/953 |
| 42 | PA | 0.07 | 0/1010 | 0.22 | 0/1354 |
| 43 | RA | 0.10 | 0/1174 | 0.27 | 0/1582 |
| 44 | SA | 0.08 | 0/1815 | 0.21 | 0/2828 |
| 45 | TA | 0.09 | 0/1804 | 0.21 | 0/2810 |
| 46 | VA | 0.06 | 0/276 | 0.18 | 0/426 |
| 47 | WA | 0.09 | 0/85840 | 0.21 | 0/133885 |
| 48 | XA | 0.08 | 0/2836 | 0.18 | 0/4421 |
| 49 | YA | 0.09 | 0/3701 | 0.22 | 0/5766 |
| 50 | ZA | 0.40 | 6/40949 (0.0%) | 0.22 | 0/63819 |
| 51 | AB | 0.09 | 0/1747 | 0.21 | 0/2374 |
| 52 | BB | 0.07 | 0/1756 | 0.22 | 0/2350 |
| 53 | CB | 0.07 | 0/1744 | 0.23 | 0/2358 |
| 54 | DB | 0.08 | 0/1796 | 0.21 | 0/2417 |
| 55 | EB | 0.09 | 0/2118 | 0.26 | 0/2849 |
| 56 | FB | 0.08 | 0/1492 | 0.23 | 0/2005 |
| 57 | GB | 0.10 | 0/1946 | 0.26 | 0/2590 |
| 58 | HB | 0.09 | 0/1511 | 0.24 | 0/2022 |
| 59 | IB | 0.08 | 0/1715 | 0.21 | 0/2287 |
| 60 | JB | 0.09 | 0/1550 | 0.23 | 0/2069 |
| 61 | KB | 0.08 | 0/834 | 0.23 | 0/1125 |
| 62 | LB | 0.07 | 0/1200 | 0.24 | 0/1604 |
| 63 | MB | 0.08 | 0/918 | 0.23 | 0/1233 |
| 64 | NB | 0.07 | 0/1226 | 0.20 | 0/1649 |
| 65 | OB | 0.07 | 0/1029 | 0.23 | 0/1380 |
| 66 | PB | 0.08 | 0/1079 | 0.21 | 0/1441 |
| 67 | QB | 0.09 | 0/1146 | 0.25 | 0/1534 |
| 68 | RB | 0.09 | 0/1082 | 0.24 | 0/1452 |
| 69 | SB | 0.08 | 0/1208 | 0.23 | 0/1618 |
| 70 | TB | 0.07 | 0/1123 | 0.20 | 0/1504 |
| 71 | UB | 0.08 | 0/818 | 0.23 | 0/1099 |
| 72 | VB | 0.06 | 0/643 | 0.20 | 0/860 |
| 73 | WB | 0.08 | 0/1051 | 0.25 | 0/1406 |
| 74 | XB | 0.07 | 0/1116 | 0.21 | 0/1490 |
| 75 | YB | 1.33 | 3/1028 (0.3%) | 0.96 | 6/1366 (0.4%) |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-----------------|-------------|-----------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 76 | ZB | 0.07 | 0/691 | 0.21 | 0/922 |
| 77 | AC | 0.08 | 0/828 | 0.23 | 0/1109 |
| 78 | BC | 0.06 | 0/665 | 0.19 | 0/891 |
| 79 | CC | 0.09 | 0/490 | 0.25 | 0/656 |
| 80 | DC | 0.06 | 0/470 | 0.19 | 0/623 |
| 81 | EC | 0.07 | 0/447 | 0.20 | 0/587 |
| 82 | FC | 0.06 | 0/576 | 0.20 | 0/764 |
| 83 | GC | 0.09 | 0/2493 | 0.28 | 0/3394 |
| 84 | IC | 0.05 | 0/19 | 0.14 | 0/25 |
| 85 | b | 0.12 | 0/1298 | 0.28 | 0/1752 |
| 86 | At | 0.14 | 0/1652 | 0.19 | 0/2573 |
| All | All | 0.21 | 9/234830 (0.0%) | 0.22 | 6/344944 (0.0%) |

The worst 5 of 9 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 75 | YB | 7 | ILE | CA-CB | 38.96 | 1.99 | 1.54 |
| 50 | ZA | 836 | G | N1-C2 | 34.92 | 2.07 | 1.37 |
| 50 | ZA | 836 | G | C6-N1 | 34.13 | 2.07 | 1.39 |
| 50 | ZA | 836 | G | C2-N3 | 33.58 | 2.00 | 1.32 |
| 50 | ZA | 836 | G | C5-C6 | 32.20 | 2.06 | 1.42 |

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

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|------------|--------|-------------|----------|
| 75 | YB | 7 | ILE | CA-CB-CG1 | 19.95 | 144.31 | 110.40 |
| 75 | YB | 7 | ILE | CA-CB-CG2 | 14.62 | 135.35 | 110.50 |
| 75 | YB | 7 | ILE | CG1-CB-CG2 | -12.87 | 72.10 | 110.70 |
| 75 | YB | 7 | ILE | N-CA-C | -11.20 | 91.64 | 107.99 |
| 75 | YB | 7 | ILE | CB-CA-C | 10.78 | 125.75 | 110.98 |

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 1914 | 0 | 2013 | 48 | 0 |
| 2 | B | 3196 | 0 | 3339 | 70 | 0 |
| 3 | C | 2883 | 0 | 3053 | 50 | 0 |
| 4 | D | 2395 | 0 | 2427 | 32 | 0 |
| 5 | E | 1823 | 0 | 1995 | 38 | 0 |
| 6 | F | 1897 | 0 | 2021 | 37 | 0 |
| 7 | G | 1850 | 0 | 1991 | 22 | 0 |
| 8 | H | 1516 | 0 | 1597 | 20 | 0 |
| 9 | I | 1664 | 0 | 1712 | 26 | 0 |
| 10 | J | 1372 | 0 | 1412 | 20 | 0 |
| 11 | K | 1702 | 0 | 1820 | 25 | 0 |
| 12 | L | 1137 | 0 | 1211 | 21 | 0 |
| 13 | M | 1701 | 0 | 1749 | 35 | 0 |
| 14 | N | 1630 | 0 | 1778 | 35 | 0 |
| 15 | O | 1266 | 0 | 1302 | 23 | 0 |
| 16 | P | 1515 | 0 | 1634 | 32 | 0 |
| 17 | Q | 1508 | 0 | 1664 | 22 | 0 |
| 18 | R | 1462 | 0 | 1508 | 31 | 0 |
| 19 | S | 1298 | 0 | 1366 | 31 | 0 |
| 20 | T | 826 | 0 | 852 | 12 | 0 |
| 21 | U | 1004 | 0 | 1063 | 16 | 0 |
| 22 | V | 887 | 0 | 935 | 27 | 0 |
| 23 | W | 967 | 0 | 1040 | 13 | 0 |
| 24 | X | 1115 | 0 | 1205 | 19 | 0 |
| 25 | Y | 1107 | 0 | 1182 | 27 | 0 |
| 26 | Z | 1162 | 0 | 1209 | 30 | 0 |
| 27 | AA | 873 | 0 | 949 | 18 | 0 |
| 28 | BA | 769 | 0 | 803 | 8 | 0 |
| 29 | CA | 893 | 0 | 932 | 12 | 0 |
| 30 | DA | 1064 | 0 | 1160 | 27 | 0 |
| 31 | EA | 876 | 0 | 912 | 18 | 0 |
| 32 | FA | 906 | 0 | 998 | 9 | 0 |
| 33 | GA | 1008 | 0 | 1142 | 17 | 0 |
| 34 | HA | 830 | 0 | 916 | 11 | 0 |
| 35 | IA | 716 | 0 | 750 | 24 | 0 |
| 36 | JA | 569 | 0 | 637 | 5 | 0 |
| 37 | KA | 447 | 0 | 480 | 14 | 0 |
| 38 | LA | 429 | 0 | 465 | 5 | 0 |
| 39 | MA | 239 | 0 | 289 | 5 | 0 |
| 40 | NA | 851 | 0 | 920 | 13 | 0 |
| 41 | OA | 708 | 0 | 757 | 16 | 0 |
| 42 | PA | 994 | 0 | 1051 | 21 | 0 |
| 43 | RA | 1160 | 0 | 1218 | 23 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 44 | SA | 1622 | 0 | 825 | 21 | 0 |
| 45 | TA | 1615 | 0 | 820 | 15 | 0 |
| 46 | VA | 249 | 0 | 128 | 3 | 0 |
| 47 | WA | 76735 | 0 | 38764 | 1133 | 0 |
| 48 | XA | 2538 | 0 | 1286 | 31 | 0 |
| 49 | YA | 3314 | 0 | 1683 | 48 | 0 |
| 50 | ZA | 36623 | 0 | 18504 | 679 | 0 |
| 51 | AB | 1710 | 0 | 1711 | 26 | 0 |
| 52 | BB | 1729 | 0 | 1803 | 24 | 0 |
| 53 | CB | 1707 | 0 | 1793 | 26 | 0 |
| 54 | DB | 1768 | 0 | 1863 | 18 | 0 |
| 55 | EB | 2076 | 0 | 2177 | 55 | 0 |
| 56 | FB | 1471 | 0 | 1522 | 18 | 0 |
| 57 | GB | 1923 | 0 | 2089 | 48 | 0 |
| 58 | HB | 1489 | 0 | 1582 | 25 | 0 |
| 59 | IB | 1686 | 0 | 1772 | 27 | 0 |
| 60 | JB | 1525 | 0 | 1640 | 37 | 0 |
| 61 | KB | 810 | 0 | 836 | 15 | 0 |
| 62 | LB | 1180 | 0 | 1254 | 18 | 0 |
| 63 | MB | 908 | 0 | 939 | 17 | 0 |
| 64 | NB | 1202 | 0 | 1289 | 16 | 0 |
| 65 | OB | 1016 | 0 | 1039 | 22 | 0 |
| 66 | PB | 1058 | 0 | 1104 | 17 | 0 |
| 67 | QB | 1128 | 0 | 1195 | 24 | 0 |
| 68 | RB | 1068 | 0 | 1121 | 16 | 0 |
| 69 | SB | 1190 | 0 | 1249 | 25 | 0 |
| 70 | TB | 1104 | 0 | 1140 | 24 | 0 |
| 71 | UB | 808 | 0 | 878 | 17 | 0 |
| 72 | VB | 636 | 0 | 637 | 12 | 0 |
| 73 | WB | 1034 | 0 | 1080 | 21 | 0 |
| 74 | XB | 1098 | 0 | 1167 | 22 | 0 |
| 75 | YB | 1011 | 0 | 1083 | 72 | 0 |
| 76 | ZB | 683 | 0 | 761 | 10 | 0 |
| 77 | AC | 814 | 0 | 864 | 13 | 0 |
| 78 | BC | 651 | 0 | 672 | 9 | 0 |
| 79 | CC | 488 | 0 | 514 | 8 | 0 |
| 80 | DC | 459 | 0 | 449 | 13 | 0 |
| 81 | EC | 443 | 0 | 492 | 11 | 0 |
| 82 | FC | 564 | 0 | 577 | 11 | 0 |
| 83 | GC | 2436 | 0 | 2393 | 51 | 0 |
| 84 | IC | 20 | 0 | 10 | 1 | 0 |
| 85 | b | 1279 | 0 | 1344 | 27 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 86 | At | 1582 | 0 | 807 | 18 | 0 |
| 87 | AC | 1 | 0 | 0 | 0 | 0 |
| 87 | FA | 1 | 0 | 0 | 0 | 0 |
| 87 | I | 1 | 0 | 0 | 0 | 0 |
| 87 | WA | 80 | 0 | 0 | 0 | 0 |
| 87 | XA | 1 | 0 | 0 | 0 | 0 |
| 87 | ZA | 18 | 0 | 0 | 0 | 0 |
| 88 | AC | 1 | 0 | 0 | 0 | 0 |
| 88 | DC | 1 | 0 | 0 | 0 | 0 |
| 88 | FA | 1 | 0 | 0 | 0 | 0 |
| 88 | FC | 1 | 0 | 0 | 0 | 0 |
| 88 | IA | 1 | 0 | 0 | 0 | 0 |
| 88 | LA | 1 | 0 | 0 | 0 | 0 |
| 88 | NA | 1 | 0 | 0 | 0 | 0 |
| 88 | OA | 1 | 0 | 0 | 0 | 0 |
| 89 | WA | 19 | 0 | 19 | 1 | 0 |
| 90 | WA | 10 | 0 | 19 | 1 | 0 |
| 91 | ZA | 6 | 0 | 4 | 0 | 0 |
| All | All | 218724 | 0 | 162355 | 3038 | 0 |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 3038 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|----------------|-----------------|--------------------------|-------------------|
| 75:YB:7:ILE:CB | 75:YB:7:ILE:CG2 | 1.94 | 1.45 |
| 50:ZA:836:G:C4 | 50:ZA:836:G:C5 | 1.96 | 1.44 |
| 50:ZA:836:G:N1 | 75:YB:7:ILE:HA | 1.22 | 1.43 |
| 50:ZA:836:G:C5 | 50:ZA:836:G:C6 | 2.06 | 1.42 |
| 75:YB:7:ILE:CA | 75:YB:7:ILE:HB | 1.49 | 1.40 |

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|------------|---------|----------|-------------|-----|
| 1 | A | 248/257 (96%) | 243 (98%) | 5 (2%) | 0 | 100 | 100 |
| 2 | B | 395/403 (98%) | 386 (98%) | 9 (2%) | 0 | 100 | 100 |
| 3 | C | 360/413 (87%) | 353 (98%) | 7 (2%) | 0 | 100 | 100 |
| 4 | D | 292/297 (98%) | 286 (98%) | 6 (2%) | 0 | 100 | 100 |
| 5 | E | 222/291 (76%) | 220 (99%) | 2 (1%) | 0 | 100 | 100 |
| 6 | F | 225/249 (90%) | 219 (97%) | 6 (3%) | 0 | 100 | 100 |
| 7 | G | 225/319 (70%) | 222 (99%) | 3 (1%) | 0 | 100 | 100 |
| 8 | H | 188/192 (98%) | 183 (97%) | 5 (3%) | 0 | 100 | 100 |
| 9 | I | 201/214 (94%) | 196 (98%) | 5 (2%) | 0 | 100 | 100 |
| 10 | J | 169/178 (95%) | 168 (99%) | 1 (1%) | 0 | 100 | 100 |
| 11 | K | 208/211 (99%) | 201 (97%) | 7 (3%) | 0 | 100 | 100 |
| 12 | L | 136/218 (62%) | 131 (96%) | 5 (4%) | 0 | 100 | 100 |
| 13 | M | 201/204 (98%) | 196 (98%) | 5 (2%) | 0 | 100 | 100 |
| 14 | N | 197/203 (97%) | 195 (99%) | 2 (1%) | 0 | 100 | 100 |
| 15 | O | 154/213 (72%) | 151 (98%) | 3 (2%) | 0 | 100 | 100 |
| 16 | P | 185/188 (98%) | 182 (98%) | 3 (2%) | 0 | 100 | 100 |
| 17 | Q | 178/212 (84%) | 174 (98%) | 4 (2%) | 0 | 100 | 100 |
| 18 | R | 174/224 (78%) | 171 (98%) | 3 (2%) | 0 | 100 | 100 |
| 19 | S | 157/160 (98%) | 154 (98%) | 3 (2%) | 0 | 100 | 100 |
| 20 | T | 99/128 (77%) | 95 (96%) | 4 (4%) | 0 | 100 | 100 |
| 21 | U | 133/140 (95%) | 130 (98%) | 3 (2%) | 0 | 100 | 100 |
| 22 | V | 106/157 (68%) | 106 (100%) | 0 | 0 | 100 | 100 |
| 23 | W | 116/156 (74%) | 114 (98%) | 2 (2%) | 0 | 100 | 100 |
| 24 | X | 132/145 (91%) | 130 (98%) | 2 (2%) | 0 | 100 | 100 |
| 25 | Y | 133/136 (98%) | 133 (100%) | 0 | 0 | 100 | 100 |
| 26 | Z | 145/148 (98%) | 142 (98%) | 3 (2%) | 0 | 100 | 100 |
| 27 | AA | 103/245 (42%) | 100 (97%) | 3 (3%) | 0 | 100 | 100 |
| 28 | BA | 97/115 (84%) | 96 (99%) | 1 (1%) | 0 | 100 | 100 |
| 29 | CA | 106/125 (85%) | 105 (99%) | 1 (1%) | 0 | 100 | 100 |
| 30 | DA | 127/135 (94%) | 125 (98%) | 2 (2%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|------------|---------|----------|-------------|-----|
| 31 | EA | 107/110 (97%) | 107 (100%) | 0 | 0 | 100 | 100 |
| 32 | FA | 112/129 (87%) | 110 (98%) | 2 (2%) | 0 | 100 | 100 |
| 33 | GA | 119/123 (97%) | 117 (98%) | 2 (2%) | 0 | 100 | 100 |
| 34 | HA | 100/105 (95%) | 96 (96%) | 4 (4%) | 0 | 100 | 100 |
| 35 | IA | 85/97 (88%) | 83 (98%) | 2 (2%) | 0 | 100 | 100 |
| 36 | JA | 67/70 (96%) | 66 (98%) | 1 (2%) | 0 | 100 | 100 |
| 37 | KA | 48/51 (94%) | 48 (100%) | 0 | 0 | 100 | 100 |
| 38 | LA | 50/128 (39%) | 49 (98%) | 1 (2%) | 0 | 100 | 100 |
| 39 | MA | 23/25 (92%) | 23 (100%) | 0 | 0 | 100 | 100 |
| 40 | NA | 102/106 (96%) | 100 (98%) | 2 (2%) | 0 | 100 | 100 |
| 41 | OA | 89/92 (97%) | 87 (98%) | 2 (2%) | 0 | 100 | 100 |
| 42 | PA | 122/137 (89%) | 118 (97%) | 4 (3%) | 0 | 100 | 100 |
| 43 | RA | 151/165 (92%) | 140 (93%) | 11 (7%) | 0 | 100 | 100 |
| 51 | AB | 215/295 (73%) | 211 (98%) | 4 (2%) | 0 | 100 | 100 |
| 52 | BB | 211/264 (80%) | 207 (98%) | 4 (2%) | 0 | 100 | 100 |
| 53 | CB | 218/293 (74%) | 215 (99%) | 3 (1%) | 0 | 100 | 100 |
| 54 | DB | 226/281 (80%) | 225 (100%) | 1 (0%) | 0 | 100 | 100 |
| 55 | EB | 260/263 (99%) | 252 (97%) | 8 (3%) | 0 | 100 | 100 |
| 56 | FB | 181/204 (89%) | 176 (97%) | 5 (3%) | 0 | 100 | 100 |
| 57 | GB | 235/249 (94%) | 231 (98%) | 4 (2%) | 0 | 100 | 100 |
| 58 | HB | 181/432 (42%) | 177 (98%) | 4 (2%) | 0 | 100 | 100 |
| 59 | IB | 204/208 (98%) | 199 (98%) | 5 (2%) | 0 | 100 | 100 |
| 60 | JB | 183/194 (94%) | 182 (100%) | 1 (0%) | 0 | 100 | 100 |
| 61 | KB | 94/165 (57%) | 92 (98%) | 2 (2%) | 0 | 100 | 100 |
| 62 | LB | 140/158 (89%) | 139 (99%) | 1 (1%) | 0 | 100 | 100 |
| 63 | MB | 115/132 (87%) | 109 (95%) | 6 (5%) | 0 | 100 | 100 |
| 64 | NB | 147/151 (97%) | 146 (99%) | 1 (1%) | 0 | 100 | 100 |
| 65 | OB | 134/151 (89%) | 130 (97%) | 4 (3%) | 0 | 100 | 100 |
| 66 | PB | 127/145 (88%) | 125 (98%) | 2 (2%) | 0 | 100 | 100 |
| 67 | QB | 140/172 (81%) | 136 (97%) | 4 (3%) | 0 | 100 | 100 |
| 68 | RB | 130/135 (96%) | 129 (99%) | 1 (1%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 69 | SB | 142/152 (93%) | 140 (99%) | 2 (1%) | 0 | 100 | 100 |
| 70 | TB | 140/145 (97%) | 136 (97%) | 4 (3%) | 0 | 100 | 100 |
| 71 | UB | 100/119 (84%) | 97 (97%) | 3 (3%) | 0 | 100 | 100 |
| 72 | VB | 81/83 (98%) | 81 (100%) | 0 | 0 | 100 | 100 |
| 73 | WB | 127/130 (98%) | 125 (98%) | 2 (2%) | 0 | 100 | 100 |
| 74 | XB | 139/143 (97%) | 136 (98%) | 3 (2%) | 0 | 100 | 100 |
| 75 | YB | 122/131 (93%) | 118 (97%) | 4 (3%) | 0 | 100 | 100 |
| 76 | ZB | 83/124 (67%) | 82 (99%) | 1 (1%) | 0 | 100 | 100 |
| 77 | AC | 99/115 (86%) | 97 (98%) | 2 (2%) | 0 | 100 | 100 |
| 78 | BC | 81/84 (96%) | 78 (96%) | 3 (4%) | 0 | 100 | 100 |
| 79 | CC | 60/69 (87%) | 60 (100%) | 0 | 0 | 100 | 100 |
| 80 | DC | 53/56 (95%) | 53 (100%) | 0 | 0 | 100 | 100 |
| 81 | EC | 53/133 (40%) | 50 (94%) | 3 (6%) | 0 | 100 | 100 |
| 82 | FC | 67/188 (36%) | 66 (98%) | 1 (2%) | 0 | 100 | 100 |
| 83 | GC | 311/317 (98%) | 299 (96%) | 12 (4%) | 0 | 100 | 100 |
| 84 | IC | 2/4 (50%) | 2 (100%) | 0 | 0 | 100 | 100 |
| 85 | b | 165/318 (52%) | 154 (93%) | 10 (6%) | 1 (1%) | 22 | 55 |
| All | All | 11553/13817 (84%) | 11306 (98%) | 246 (2%) | 1 (0%) | 100 | 100 |

All (1) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 85 | b | 225 | VAL |

5.3.2 Protein sidechains ⓘ

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|---------------|------------|----------|-------------|-----|
| 1 | A | 192/199 (96%) | 192 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|---------------|------------|----------|-------------|-----|
| 2 | B | 344/348 (99%) | 340 (99%) | 4 (1%) | 67 | 77 |
| 3 | C | 302/337 (90%) | 301 (100%) | 1 (0%) | 91 | 92 |
| 4 | D | 247/250 (99%) | 246 (100%) | 1 (0%) | 89 | 91 |
| 5 | E | 201/251 (80%) | 200 (100%) | 1 (0%) | 86 | 90 |
| 6 | F | 198/218 (91%) | 198 (100%) | 0 | 100 | 100 |
| 7 | G | 197/273 (72%) | 196 (100%) | 1 (0%) | 86 | 90 |
| 8 | H | 169/171 (99%) | 165 (98%) | 4 (2%) | 44 | 62 |
| 9 | I | 175/181 (97%) | 173 (99%) | 2 (1%) | 70 | 79 |
| 10 | J | 144/149 (97%) | 140 (97%) | 4 (3%) | 38 | 59 |
| 11 | K | 175/176 (99%) | 174 (99%) | 1 (1%) | 84 | 88 |
| 12 | L | 117/161 (73%) | 117 (100%) | 0 | 100 | 100 |
| 13 | M | 171/172 (99%) | 169 (99%) | 2 (1%) | 67 | 77 |
| 14 | N | 171/173 (99%) | 171 (100%) | 0 | 100 | 100 |
| 15 | O | 137/190 (72%) | 137 (100%) | 0 | 100 | 100 |
| 16 | P | 164/165 (99%) | 162 (99%) | 2 (1%) | 67 | 77 |
| 17 | Q | 159/191 (83%) | 159 (100%) | 0 | 100 | 100 |
| 18 | R | 157/192 (82%) | 156 (99%) | 1 (1%) | 84 | 88 |
| 19 | S | 139/140 (99%) | 138 (99%) | 1 (1%) | 81 | 86 |
| 20 | T | 91/114 (80%) | 91 (100%) | 0 | 100 | 100 |
| 21 | U | 103/107 (96%) | 103 (100%) | 0 | 100 | 100 |
| 22 | V | 89/126 (71%) | 87 (98%) | 2 (2%) | 47 | 64 |
| 23 | W | 106/134 (79%) | 106 (100%) | 0 | 100 | 100 |
| 24 | X | 124/135 (92%) | 121 (98%) | 3 (2%) | 44 | 62 |
| 25 | Y | 117/118 (99%) | 116 (99%) | 1 (1%) | 75 | 82 |
| 26 | Z | 119/120 (99%) | 118 (99%) | 1 (1%) | 79 | 84 |
| 27 | AA | 87/184 (47%) | 87 (100%) | 0 | 100 | 100 |
| 28 | BA | 85/98 (87%) | 84 (99%) | 1 (1%) | 67 | 77 |
| 29 | CA | 98/110 (89%) | 98 (100%) | 0 | 100 | 100 |
| 30 | DA | 115/121 (95%) | 114 (99%) | 1 (1%) | 75 | 82 |
| 31 | EA | 88/89 (99%) | 88 (100%) | 0 | 100 | 100 |
| 32 | FA | 98/109 (90%) | 98 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 33 | GA | 109/110 (99%) | 108 (99%) | 1 (1%) | 75 | 82 |
| 34 | HA | 86/89 (97%) | 85 (99%) | 1 (1%) | 67 | 77 |
| 35 | IA | 74/80 (92%) | 74 (100%) | 0 | 100 | 100 |
| 36 | JA | 64/65 (98%) | 64 (100%) | 0 | 100 | 100 |
| 37 | KA | 47/48 (98%) | 47 (100%) | 0 | 100 | 100 |
| 38 | LA | 48/116 (41%) | 46 (96%) | 2 (4%) | 25 | 49 |
| 39 | MA | 24/24 (100%) | 24 (100%) | 0 | 100 | 100 |
| 40 | NA | 92/94 (98%) | 92 (100%) | 0 | 100 | 100 |
| 41 | OA | 74/75 (99%) | 73 (99%) | 1 (1%) | 62 | 75 |
| 42 | PA | 108/121 (89%) | 106 (98%) | 2 (2%) | 52 | 69 |
| 43 | RA | 126/137 (92%) | 119 (94%) | 7 (6%) | 17 | 43 |
| 51 | AB | 180/244 (74%) | 177 (98%) | 3 (2%) | 56 | 72 |
| 52 | BB | 194/231 (84%) | 192 (99%) | 2 (1%) | 73 | 80 |
| 53 | CB | 186/225 (83%) | 185 (100%) | 1 (0%) | 86 | 90 |
| 54 | DB | 190/232 (82%) | 187 (98%) | 3 (2%) | 58 | 73 |
| 55 | EB | 224/225 (100%) | 219 (98%) | 5 (2%) | 47 | 64 |
| 56 | FB | 158/170 (93%) | 156 (99%) | 2 (1%) | 65 | 76 |
| 57 | GB | 207/218 (95%) | 204 (99%) | 3 (1%) | 62 | 75 |
| 58 | HB | 165/360 (46%) | 162 (98%) | 3 (2%) | 54 | 71 |
| 59 | IB | 178/180 (99%) | 177 (99%) | 1 (1%) | 84 | 88 |
| 60 | JB | 161/168 (96%) | 154 (96%) | 7 (4%) | 25 | 49 |
| 61 | KB | 87/136 (64%) | 86 (99%) | 1 (1%) | 70 | 79 |
| 62 | LB | 130/142 (92%) | 129 (99%) | 1 (1%) | 79 | 84 |
| 63 | MB | 99/108 (92%) | 95 (96%) | 4 (4%) | 27 | 50 |
| 64 | NB | 130/131 (99%) | 130 (100%) | 0 | 100 | 100 |
| 65 | OB | 106/119 (89%) | 105 (99%) | 1 (1%) | 75 | 82 |
| 66 | PB | 115/130 (88%) | 113 (98%) | 2 (2%) | 56 | 72 |
| 67 | QB | 117/140 (84%) | 116 (99%) | 1 (1%) | 75 | 82 |
| 68 | RB | 119/121 (98%) | 118 (99%) | 1 (1%) | 79 | 84 |
| 69 | SB | 125/132 (95%) | 123 (98%) | 2 (2%) | 58 | 73 |
| 70 | TB | 112/115 (97%) | 109 (97%) | 3 (3%) | 40 | 60 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-------------------|------------|----------|-------------|-----|
| 71 | UB | 93/107 (87%) | 90 (97%) | 3 (3%) | 34 | 56 |
| 72 | VB | 67/67 (100%) | 66 (98%) | 1 (2%) | 60 | 74 |
| 73 | WB | 112/113 (99%) | 109 (97%) | 3 (3%) | 40 | 60 |
| 74 | XB | 113/115 (98%) | 109 (96%) | 4 (4%) | 31 | 54 |
| 75 | YB | 107/113 (95%) | 102 (95%) | 5 (5%) | 22 | 46 |
| 76 | ZB | 75/102 (74%) | 73 (97%) | 2 (3%) | 40 | 60 |
| 77 | AC | 88/98 (90%) | 87 (99%) | 1 (1%) | 70 | 79 |
| 78 | BC | 75/76 (99%) | 74 (99%) | 1 (1%) | 65 | 76 |
| 79 | CC | 55/62 (89%) | 55 (100%) | 0 | 100 | 100 |
| 80 | DC | 48/49 (98%) | 47 (98%) | 1 (2%) | 48 | 66 |
| 81 | EC | 46/106 (43%) | 45 (98%) | 1 (2%) | 47 | 64 |
| 82 | FC | 62/154 (40%) | 60 (97%) | 2 (3%) | 34 | 56 |
| 83 | GC | 272/275 (99%) | 255 (94%) | 17 (6%) | 15 | 40 |
| 85 | b | 138/258 (54%) | 119 (86%) | 19 (14%) | 3 | 17 |
| All | All | 10065/11683 (86%) | 9911 (98%) | 154 (2%) | 60 | 74 |

5 of 154 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 81 | EC | 124 | LYS |
| 85 | b | 69 | LEU |
| 83 | GC | 14 | HIS |
| 83 | GC | 274 | VAL |
| 85 | b | 149 | ARG |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 72 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 68 | RB | 29 | HIS |
| 85 | b | 71 | ASN |
| 70 | TB | 51 | ASN |
| 77 | AC | 43 | ASN |
| 28 | BA | 15 | ASN |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 44 | SA | 75/76 (98%) | 17 (22%) | 3 (4%) |
| 45 | TA | 75/76 (98%) | 15 (20%) | 0 |
| 46 | VA | 11/12 (91%) | 3 (27%) | 0 |
| 47 | WA | 3558/3584 (99%) | 607 (17%) | 22 (0%) |
| 48 | XA | 118/120 (98%) | 9 (7%) | 0 |
| 49 | YA | 155/156 (99%) | 35 (22%) | 0 |
| 50 | ZA | 1707/1869 (91%) | 311 (18%) | 10 (0%) |
| 86 | At | 73/74 (98%) | 15 (20%) | 0 |
| All | All | 5772/5967 (96%) | 1012 (17%) | 35 (0%) |

5 of 1012 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 44 | SA | 9 | A |
| 44 | SA | 16 | C |
| 44 | SA | 17 | G |
| 44 | SA | 19 | C |
| 44 | SA | 20 | A |

5 of 35 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 50 | ZA | 561 | A |
| 50 | ZA | 752 | G |
| 50 | ZA | 890 | U |
| 47 | WA | 1820 | G |
| 47 | WA | 1806 | A |

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

5 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 | $\# Z > 2$ |
| 86 | H2U | At | 20 | 86 | 18,21,22 | 0.44 | 0 | 19,30,33 | 1.05 | 1 (5%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 86 | H2U | At | 16 | 86 | 18,21,22 | 0.47 | 0 | 19,30,33 | 1.02 | 1 (5%) |
| 86 | 7MG | At | 46 | 86 | 23,26,27 | 3.44 | 10 (43%) | 27,39,42 | 2.22 | 9 (33%) |
| 86 | PSU | At | 32 | 86 | 18,21,22 | 4.57 | 6 (33%) | 21,30,33 | 2.95 | 5 (23%) |
| 86 | 4SU | At | 8 | 86 | 18,21,22 | 3.87 | 8 (44%) | 25,30,33 | 2.32 | 4 (16%) |

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 |
|-----|------|-------|-----|------|---------|-----------|---------|
| 86 | H2U | At | 20 | 86 | - | 1/7/38/39 | 0/2/2/2 |
| 86 | H2U | At | 16 | 86 | - | 1/7/38/39 | 0/2/2/2 |
| 86 | 7MG | At | 46 | 86 | - | 3/7/37/38 | 0/3/3/3 |
| 86 | PSU | At | 32 | 86 | - | 0/7/25/26 | 0/2/2/2 |
| 86 | 4SU | At | 8 | 86 | - | 0/7/25/26 | 0/2/2/2 |

The worst 5 of 24 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 86 | At | 32 | PSU | C6-C5 | 12.62 | 1.49 | 1.35 |
| 86 | At | 32 | PSU | C2-N1 | 10.00 | 1.49 | 1.36 |
| 86 | At | 46 | 7MG | C8-N9 | 8.71 | 1.51 | 1.45 |
| 86 | At | 8 | 4SU | C4-N3 | 8.22 | 1.46 | 1.37 |
| 86 | At | 32 | PSU | C2-N3 | 7.55 | 1.49 | 1.37 |

The worst 5 of 20 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|-------|-------------|----------|
| 86 | At | 8 | 4SU | C4-N3-C2 | -7.97 | 119.68 | 127.31 |
| 86 | At | 32 | PSU | N1-C2-N3 | 7.70 | 123.29 | 115.17 |
| 86 | At | 32 | PSU | C4-N3-C2 | -6.30 | 117.69 | 126.37 |
| 86 | At | 46 | 7MG | C2-N3-C4 | 5.68 | 122.08 | 112.30 |
| 86 | At | 8 | 4SU | C5-C4-N3 | 5.59 | 119.95 | 114.75 |

There are no chirality outliers.

All (5) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|-----------------|
| 86 | At | 46 | 7MG | O4'-C4'-C5'-O5' |

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| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|-----------------|
| 86 | At | 46 | 7MG | C3'-C4'-C5'-O5' |
| 86 | At | 16 | H2U | C4'-C5'-O5'-P |
| 86 | At | 46 | 7MG | C4'-C5'-O5'-P |
| 86 | At | 20 | H2U | O4'-C4'-C5'-O5' |

There are no ring outliers.

2 monomers are involved in 2 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 86 | At | 46 | 7MG | 1 | 0 |
| 86 | At | 8 | 4SU | 1 | 0 |

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 113 ligands modelled in this entry, 110 are monoatomic - leaving 3 for Mogul analysis.

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

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|------|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 89 | ANM | WA | 5178 | - | 20,20,20 | 4.07 | 7 (35%) | 24,27,27 | 1.47 | 2 (8%) |
| 90 | SPD | WA | 5179 | - | 9,9,9 | 0.27 | 0 | 8,8,8 | 0.26 | 0 |
| 91 | SER | ZA | 1919 | - | 4,5,6 | 0.58 | 0 | 1,5,7 | 0.56 | 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 |
|-----|------|-------|------|------|---------|------------|---------|
| 89 | ANM | WA | 5178 | - | - | 4/10/23/23 | 0/2/2/2 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|------|------|---------|----------|-------|
| 90 | SPD | WA | 5179 | - | - | 0/7/7/7 | - |
| 91 | SER | ZA | 1919 | - | - | 0/2/4/6 | - |

The worst 5 of 7 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|--------|--------|-------------|----------|
| 89 | WA | 5178 | ANM | C3-C2 | -11.63 | 1.32 | 1.53 |
| 89 | WA | 5178 | ANM | C16-N1 | -8.79 | 1.30 | 1.47 |
| 89 | WA | 5178 | ANM | C2-C16 | 7.55 | 1.68 | 1.53 |
| 89 | WA | 5178 | ANM | C4-C3 | 4.06 | 1.58 | 1.53 |
| 89 | WA | 5178 | ANM | C4-N1 | 3.88 | 1.60 | 1.47 |

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-------------|-------|-------------|----------|
| 89 | WA | 5178 | ANM | O2-C5-C6 | 5.41 | 120.73 | 111.09 |
| 89 | WA | 5178 | ANM | C12-C15-C16 | -2.05 | 109.93 | 113.40 |

There are no chirality outliers.

All (4) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|------|------|---------------|
| 89 | WA | 5178 | ANM | C6-C5-O2-C2 |
| 89 | WA | 5178 | ANM | O3-C5-O2-C2 |
| 89 | WA | 5178 | ANM | C1-C9-O1-C14 |
| 89 | WA | 5178 | ANM | C10-C9-O1-C14 |

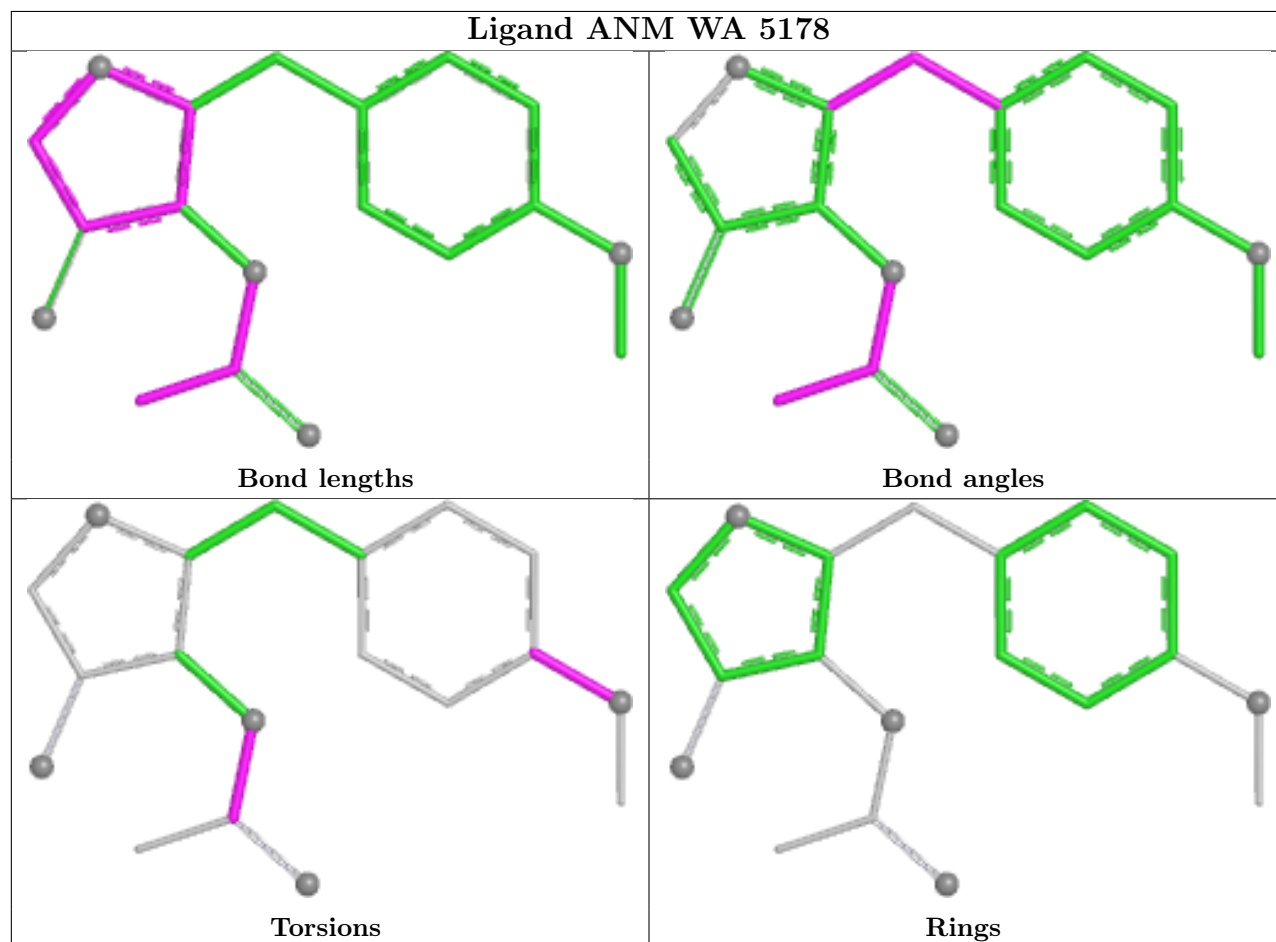
There are no ring outliers.

2 monomers are involved in 2 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|------|------|---------|--------------|
| 89 | WA | 5178 | ANM | 1 | 0 |
| 90 | WA | 5179 | SPD | 1 | 0 |

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 47 | WA | 20 |

The worst 5 of 20 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | WA | 2118:C | O3' | 2260:C | P | 37.44 |
| 1 | WA | 1225:G | O3' | 1239:G | P | 19.90 |
| 1 | WA | 763:G | O3' | 904:C | P | 18.09 |
| 1 | WA | 996:C | O3' | 1070:G | P | 17.05 |
| 1 | WA | 524:C | O3' | 639:G | P | 16.87 |

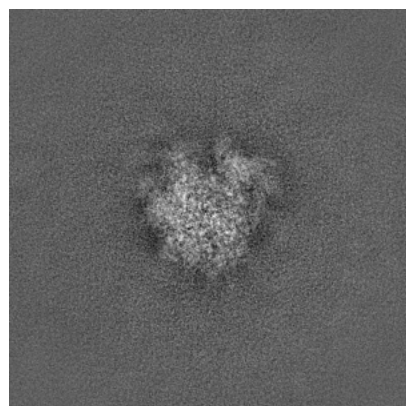
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43569. These allow visual inspection of the internal detail of the map and identification of artifacts.

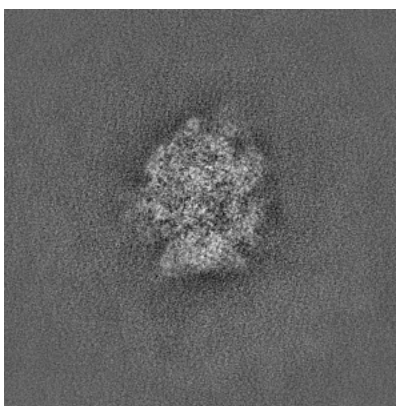
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

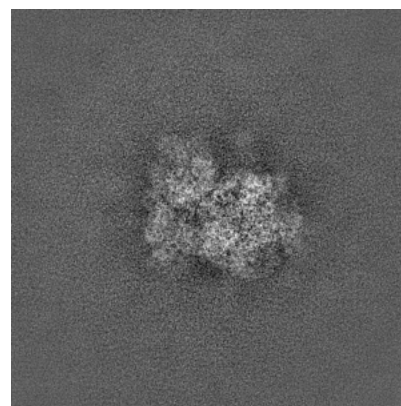
6.1.1 Primary map



X

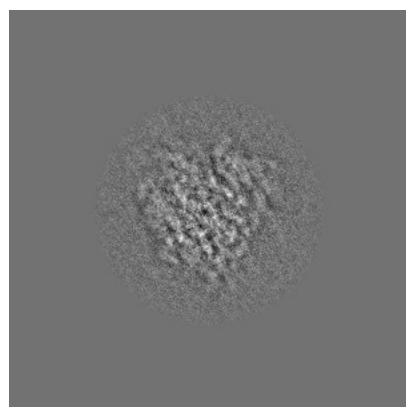


Y

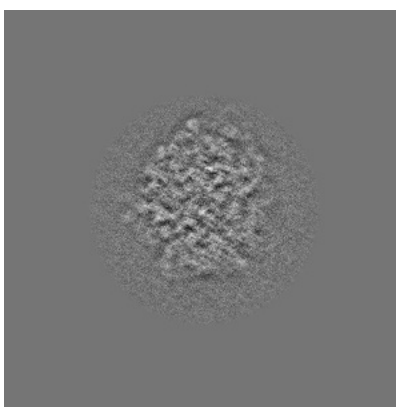


Z

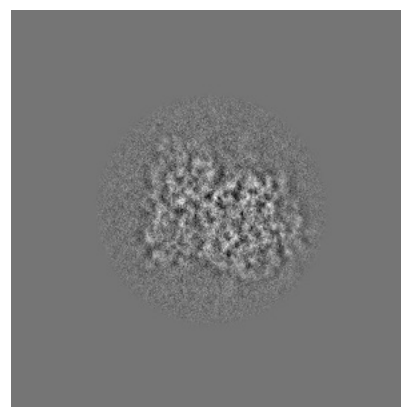
6.1.2 Raw map



X



Y

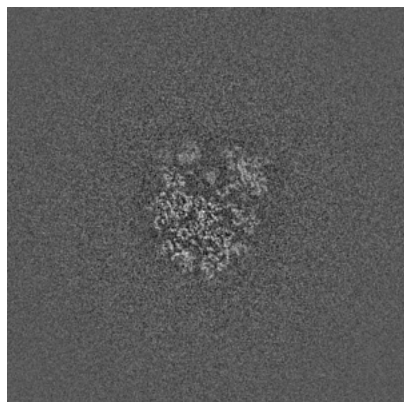


Z

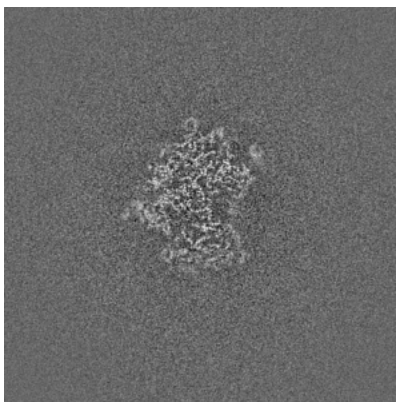
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

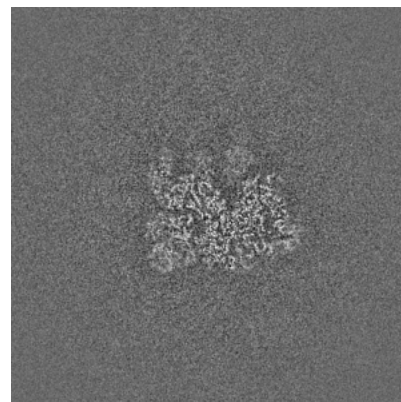
6.2.1 Primary map



X Index: 324

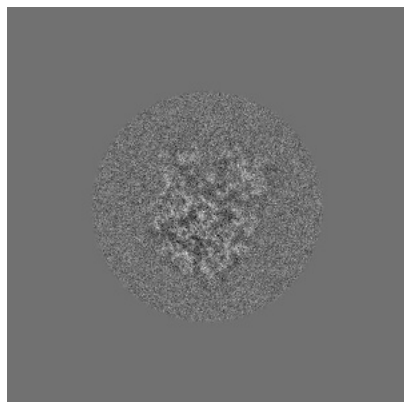


Y Index: 324

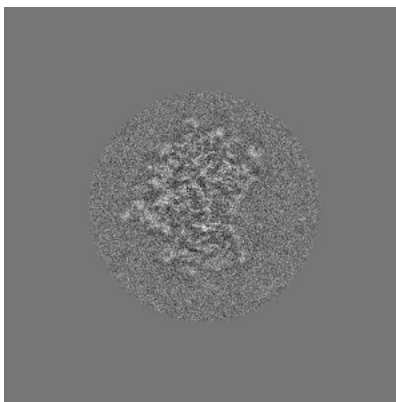


Z Index: 324

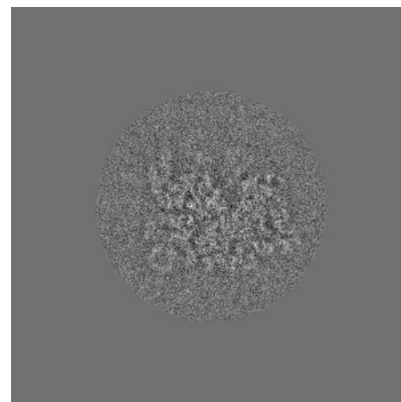
6.2.2 Raw map



X Index: 324



Y Index: 324

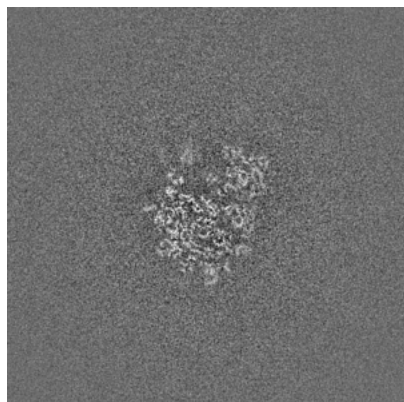


Z Index: 324

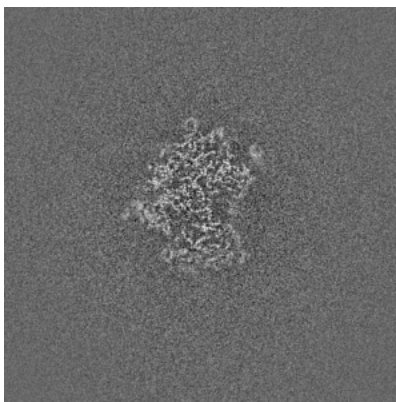
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

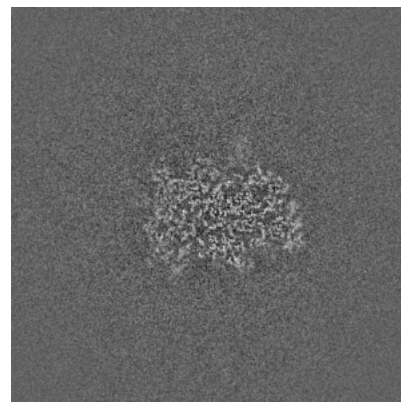
6.3.1 Primary map



X Index: 320

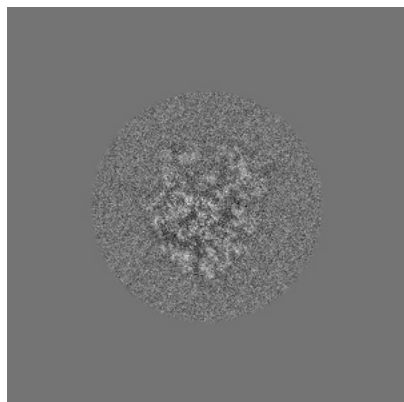


Y Index: 324

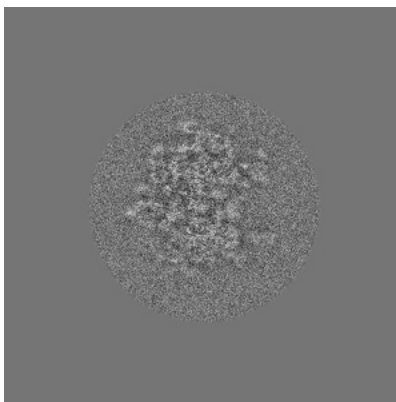


Z Index: 311

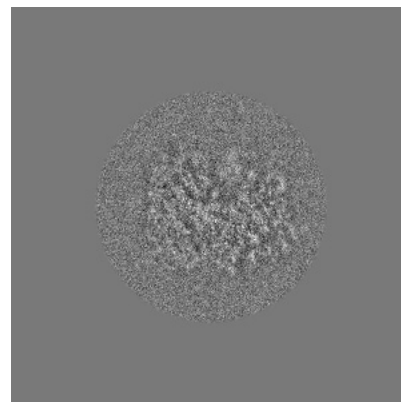
6.3.2 Raw map



X Index: 325



Y Index: 333

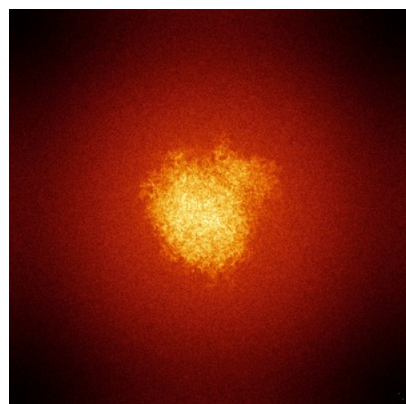


Z Index: 331

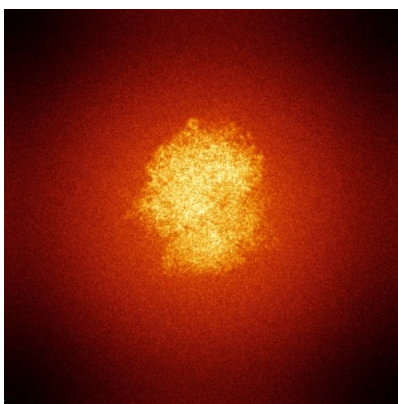
The images above show the largest variance slices of the map in three orthogonal directions.

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

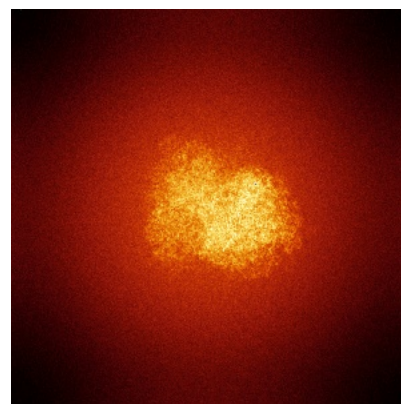
6.4.1 Primary map



X

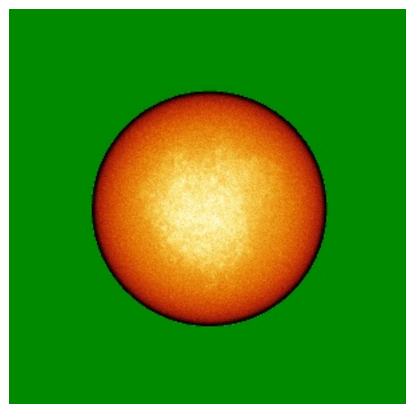


Y

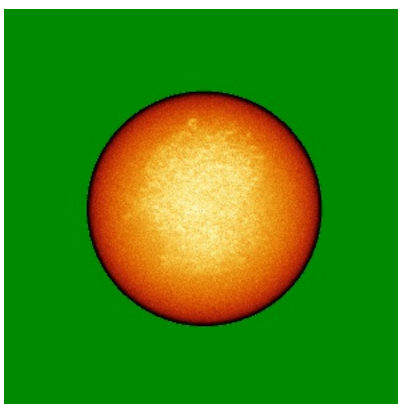


Z

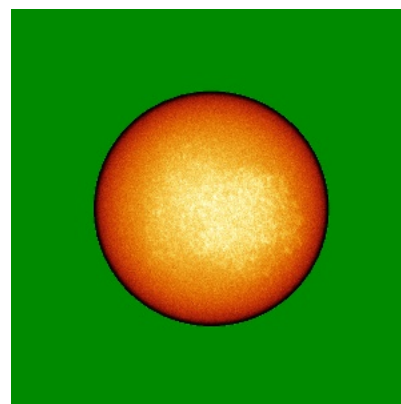
6.4.2 Raw map



X



Y



Z

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

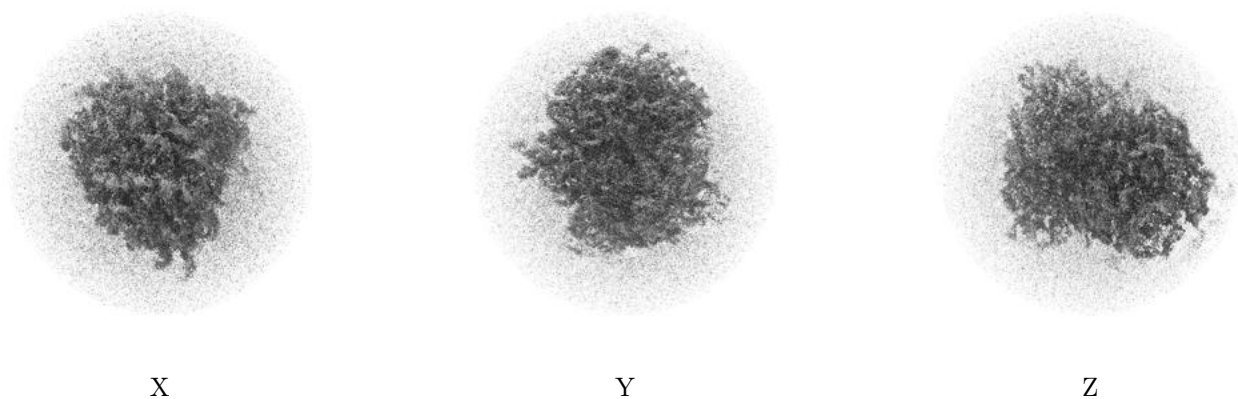
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 7.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

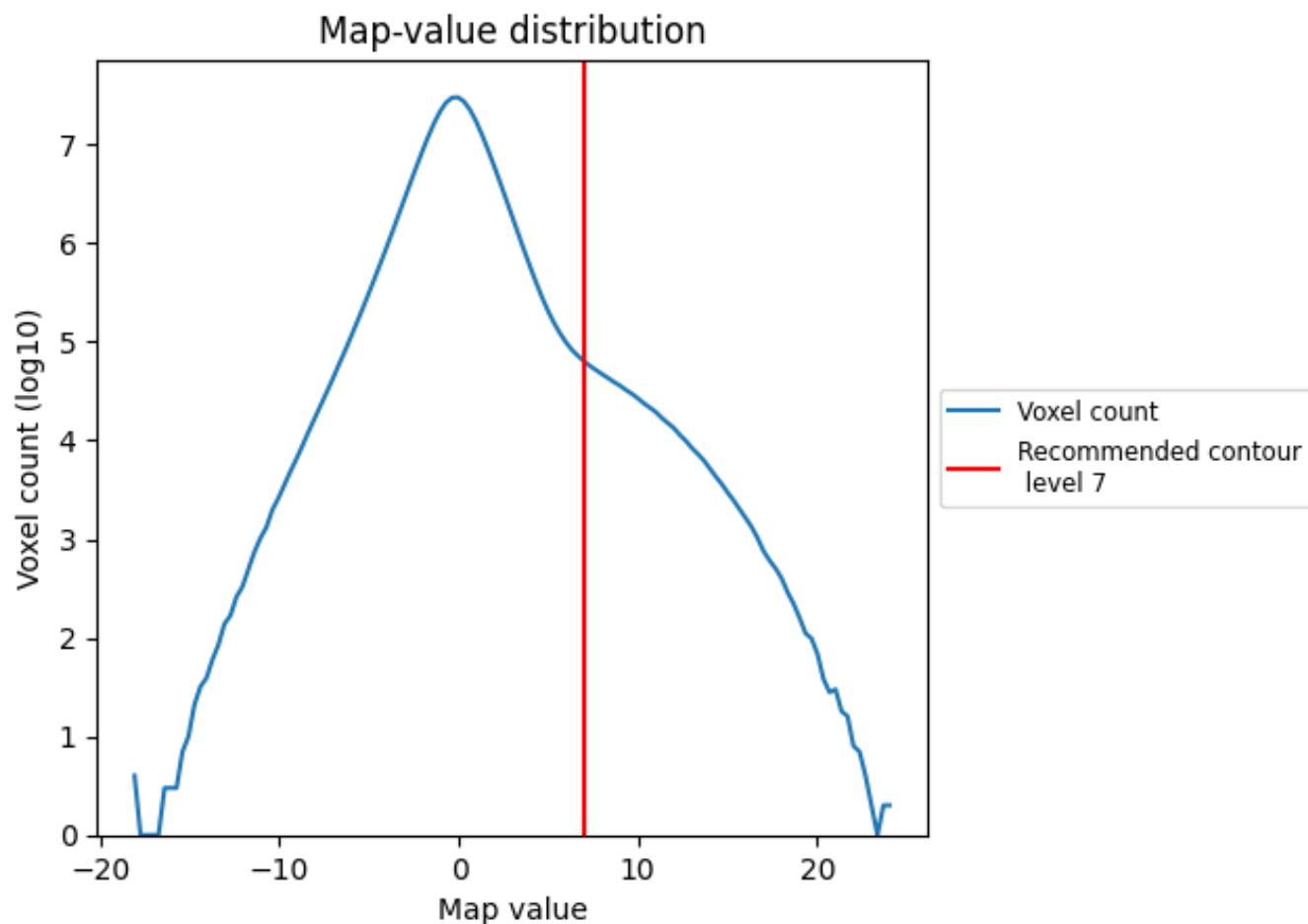
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

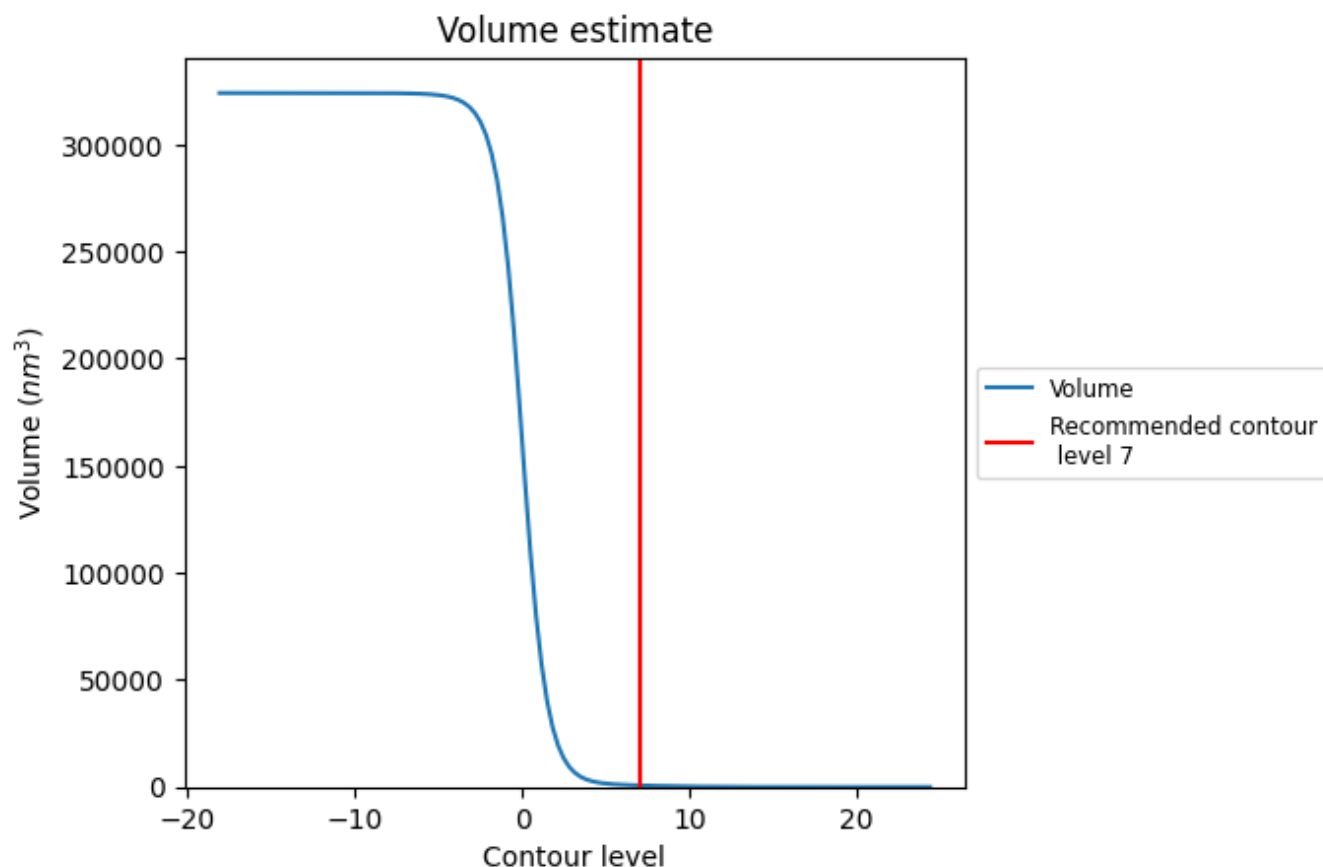
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

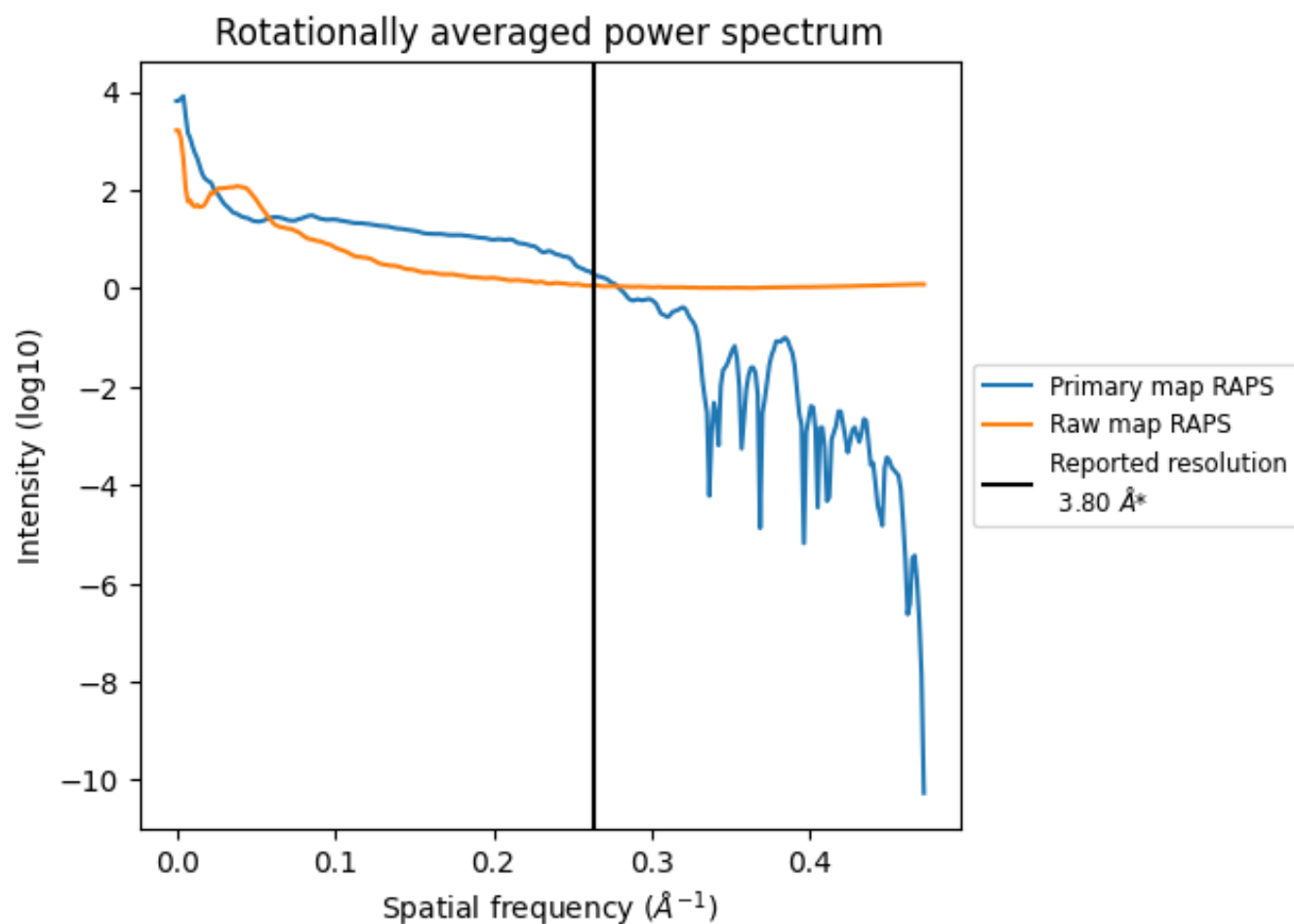
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 724 nm^3 ; this corresponds to an approximate mass of 654 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

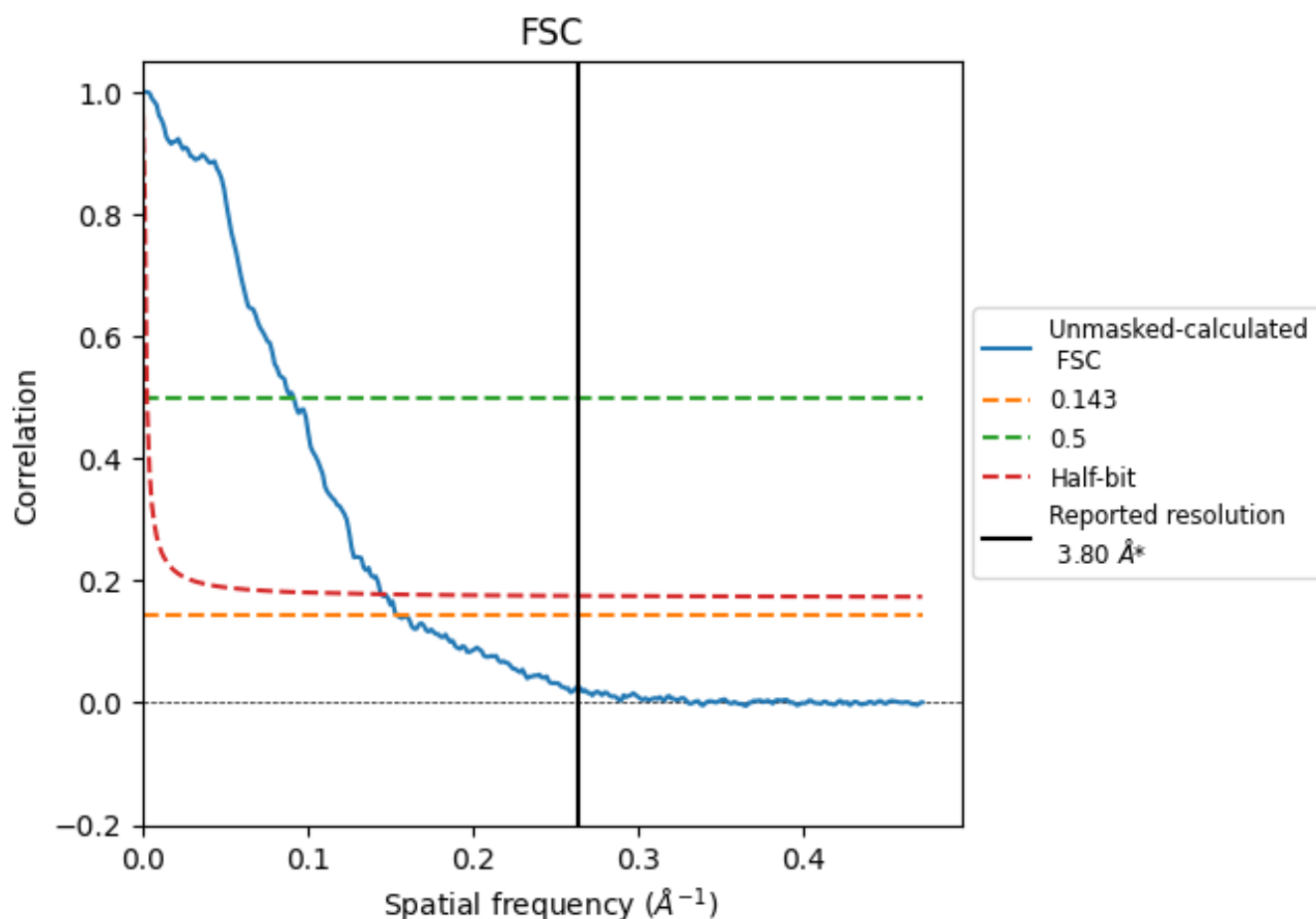


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

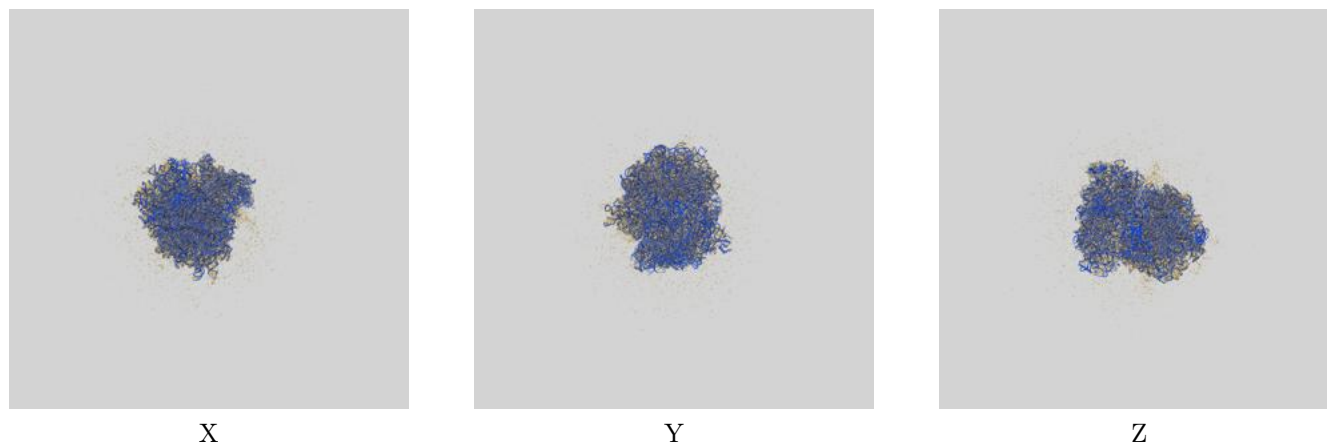
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|-------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.80 | - | - |
| Author-provided FSC curve | - | - | - |
| Unmasked-calculated* | 6.49 | 10.93 | 6.91 |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.49 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

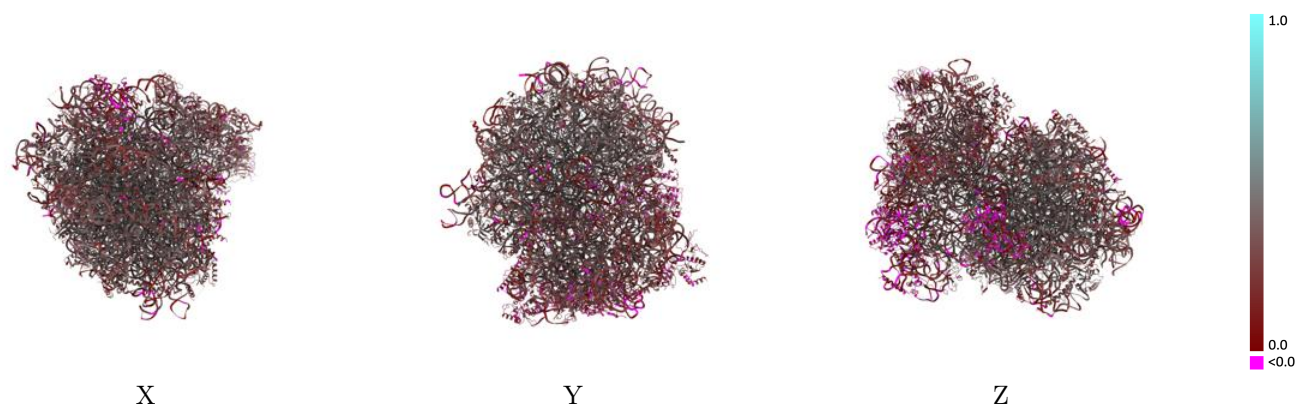
This section contains information regarding the fit between EMDB map EMD-43569 and PDB model 8VVU. Per-residue inclusion information can be found in section [3](#) on page [25](#).

9.1 Map-model overlay [i](#)



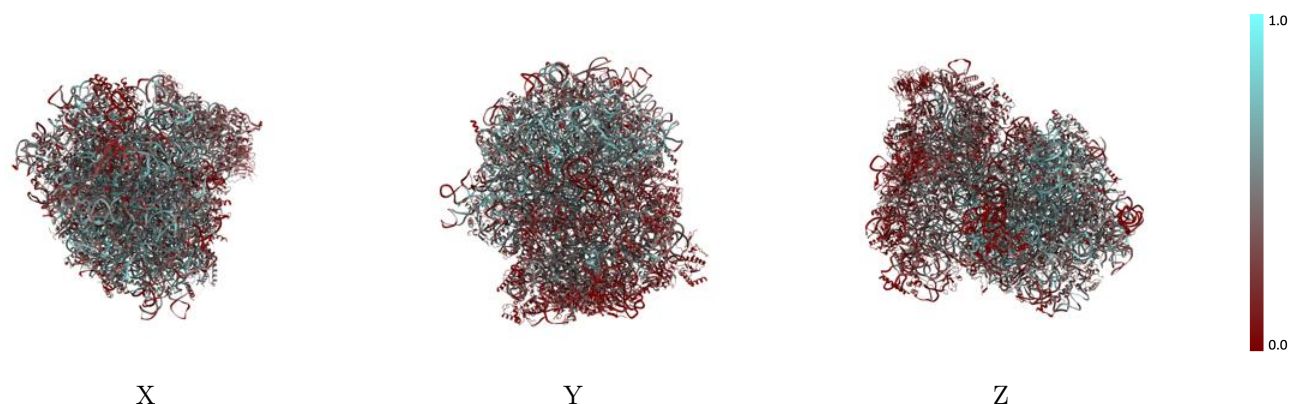
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



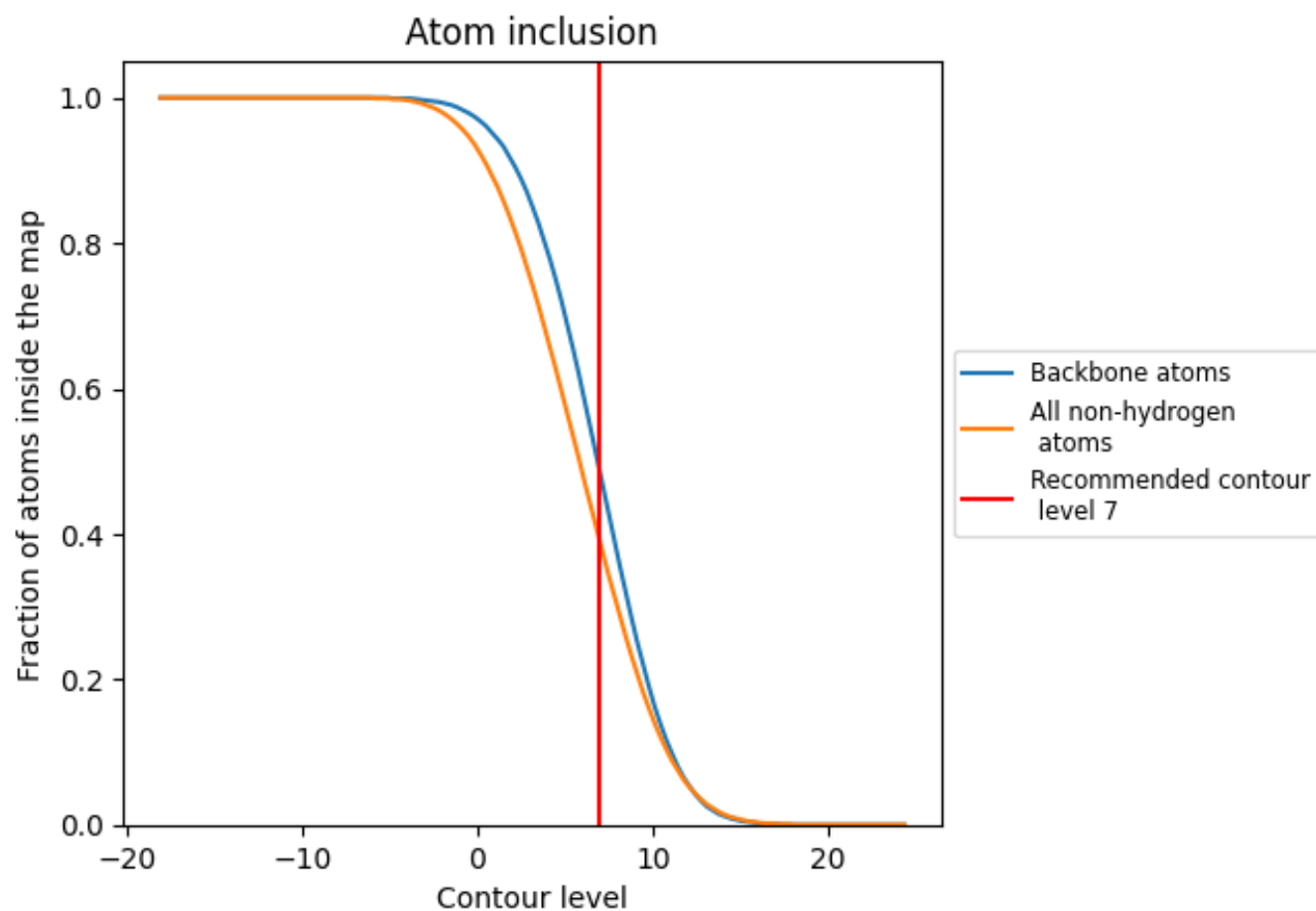
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 39% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (7) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|----------------|---------|
| All | 0.3890 | 0.3110 |
| A | 0.3430 | 0.3890 |
| AA | 0.3150 | 0.2980 |
| AB | 0.2230 | 0.2650 |
| AC | 0.2340 | 0.3270 |
| At | 0.2220 | 0.2100 |
| B | 0.3600 | 0.3730 |
| BA | 0.3320 | 0.3210 |
| BB | 0.1800 | 0.2300 |
| BC | 0.1630 | 0.2540 |
| C | 0.3800 | 0.3740 |
| CA | 0.3550 | 0.3570 |
| CB | 0.2250 | 0.3050 |
| CC | 0.1790 | 0.2500 |
| D | 0.3380 | 0.3140 |
| DA | 0.3380 | 0.3840 |
| DB | 0.2270 | 0.2860 |
| DC | 0.2530 | 0.3310 |
| E | 0.2860 | 0.3230 |
| EA | 0.3490 | 0.3990 |
| EB | 0.0810 | 0.0240 |
| EC | 0.2230 | 0.2220 |
| F | 0.3760 | 0.3640 |
| FA | 0.3160 | 0.3660 |
| FB | 0.2190 | 0.2640 |
| FC | 0.0960 | 0.2040 |
| G | 0.3590 | 0.3140 |
| GA | 0.3970 | 0.3440 |
| GB | 0.1510 | 0.1960 |
| GC | 0.1170 | 0.2140 |
| H | 0.3320 | 0.3310 |
| HA | 0.3730 | 0.3390 |
| HB | 0.1480 | 0.2150 |
| I | 0.3490 | 0.3780 |
| IA | 0.3900 | 0.3970 |























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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| IB |  0.2110 |  0.2780 |
| IC |  0.1000 |  0.3680 |
| J |  0.2820 |  0.2820 |
| JA |  0.2710 |  0.3010 |
| JB |  0.2530 |  0.2520 |
| K |  0.3810 |  0.3560 |
| KA |  0.3610 |  0.3550 |
| KB |  0.2220 |  0.2430 |
| L |  0.3720 |  0.3480 |
| LA |  0.3800 |  0.3530 |
| LB |  0.2170 |  0.3180 |
| M |  0.3680 |  0.3950 |
| MA |  0.2940 |  0.3540 |
| MB |  0.0780 |  0.1740 |
| N |  0.3890 |  0.3610 |
| NA |  0.3320 |  0.3760 |
| NB |  0.2250 |  0.2840 |
| O |  0.3880 |  0.3750 |
| OA |  0.3880 |  0.3580 |
| OB |  0.1800 |  0.2650 |
| P |  0.3920 |  0.3870 |
| PA |  0.3750 |  0.3780 |
| PB |  0.2040 |  0.2490 |
| Q |  0.3680 |  0.3140 |
| QB |  0.2110 |  0.2720 |
| R |  0.3500 |  0.3790 |
| RA |  0.0250 |  0.0600 |
| RB |  0.2000 |  0.2580 |
| S |  0.3380 |  0.3630 |
| SA |  0.3190 |  0.2880 |
| SB |  0.2400 |  0.2660 |
| T |  0.3070 |  0.2930 |
| TA |  0.0660 |  0.1450 |
| TB |  0.2060 |  0.2670 |
| U |  0.3190 |  0.3800 |
| UB |  0.2150 |  0.2810 |
| V |  0.2310 |  0.2420 |
| VA |  0.3330 |  0.3430 |
| VB |  0.2150 |  0.2990 |
| W |  0.3630 |  0.3520 |
| WA |  0.5260 |  0.3490 |
| WB |  0.1980 |  0.3130 |

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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| X |  0.3530 |  0.3570 |
| XA |  0.6260 |  0.3690 |
| XB |  0.2690 |  0.3310 |
| Y |  0.3700 |  0.3410 |
| YA |  0.5590 |  0.3550 |
| YB |  0.0960 |  0.0590 |
| Z |  0.3600 |  0.3980 |
| ZA |  0.3750 |  0.2630 |
| ZB |  0.1990 |  0.2260 |
| b |  0.0220 |  0.0650 |