



## wwPDB EM Validation Summary Report ⓘ

Aug 25, 2025 – 12:06 am BST

PDB ID : 9EVS / pdb\_00009evs  
EMDB ID : EMD-50011  
Title : Structure of the flowering plant mitoribosome with P-site tRNA  
Authors : Waltz, F.; Skaltsogiannis, V.; Giege, P.  
Deposited on : 2024-04-02  
Resolution : 3.05 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev126  
Mogul : 1.8.4, CSD as541be (2020)  
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) : 2.45.1



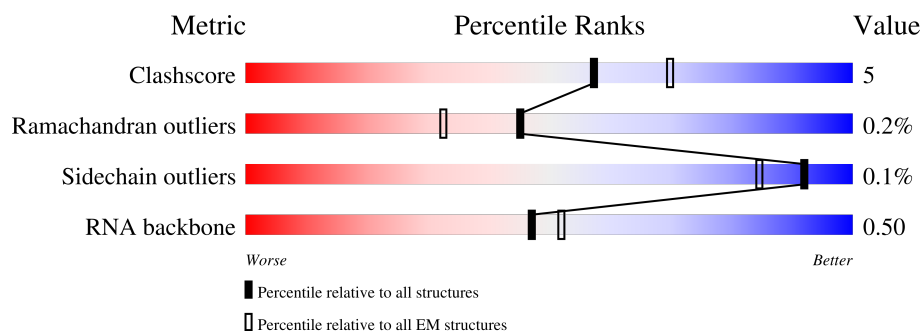
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.05 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<br>(#Entries) | EM structures<br>(#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Clashscore            | 210492                      | 15764                       |
| Ramachandran outliers | 207382                      | 16835                       |
| Sidechain outliers    | 206894                      | 16415                       |
| RNA backbone          | 6643                        | 2191                        |



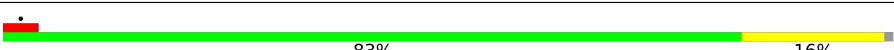
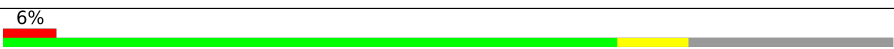

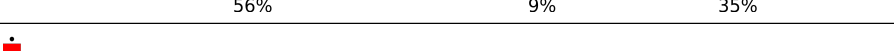
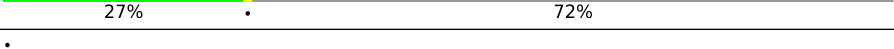





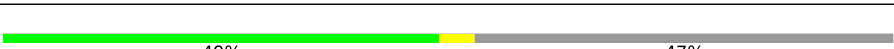
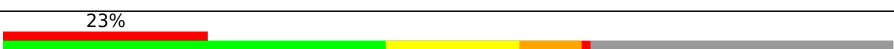
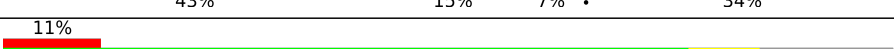
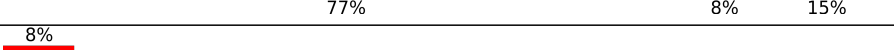



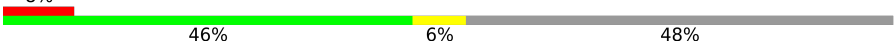




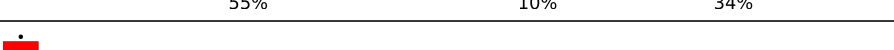
The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey 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   | B     | 554    | <div> <div>25%</div> <div>71%</div> <div>13%</div> <div>16%</div> </div> |
| 2   | C     | 362    | <div> <div>9%</div> <div>81%</div> <div>10%</div> <div>8%</div> </div>   |
| 3   | D     | 501    | <div> <div>13%</div> <div>75%</div> <div>8%</div> <div>17%</div> </div>  |
| 4   | E     | 138    | <div> <div>•</div> <div>67%</div> <div>7%</div> <div>27%</div> </div>    |
| 5   | F     | 157    | <div> <div>5%</div> <div>87%</div> <div>13%</div> </div>                 |
| 6   | G     | 129    | <div> <div>88%</div> <div>11%</div> <div>•</div> </div>                  |
| 7   | H     | 383    | <div> <div>11%</div> <div>47%</div> <div>8%</div> <div>44%</div> </div>  |

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| Mol | Chain | Length | Quality of chain   |
|-----|-------|--------|--|
| 8   | I     | 228    |    |
| 9   | J     | 304    |    |
| 10  | K     | 125    |    |
| 11  | L     | 154    |    |
| 12  | M     | 155    |    |
| 13  | N     | 414    |    |
| 14  | O     | 136    |    |
| 15  | P     | 110    |    |
| 16  | Q     | 237    |    |
| 17  | R     | 212    |    |
| 18  | S     | 100    |    |
| 19  | T     | 94     |    |
| 20  | U     | 192    |   |
| 21  | V     | 193    |  |
| 22  | W     | 483    |  |
| 23  | X     | 496    |  |
| 24  | Y     | 102    |  |
| 25  | Z     | 153    |  |
| 26  | 1     | 2922   |  |
| 27  | 3     | 118    |  |
| 28  | 1B    | 220    |  |
| 29  | 1C    | 327    |  |
| 30  | 1D    | 319    |  |
| 31  | 1E    | 297    |  |
| 32  | 1F    | 185    |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 33  | 1G    | 102    |                  |
| 34  | 1H    | 219    |                  |
| 35  | 1I    | 170    |                  |
| 36  | 1J    | 156    |                  |
| 37  | 1K    | 204    |                  |
| 38  | 1L    | 176    |                  |
| 39  | 1M    | 281    |                  |
| 40  | 1N    | 179    |                  |
| 41  | 1O    | 160    |                  |
| 42  | 1P    | 114    |                  |
| 43  | 1Q    | 233    |                  |
| 44  | 1R    | 126    |                  |
| 45  | 1S    | 270    |                  |
| 46  | 1T    | 264    |                  |
| 47  | 1U    | 180    |                  |
| 48  | 1V    | 159    |                  |
| 49  | 1W    | 249    |                  |
| 50  | 1X    | 271    |                  |
| 51  | 1Y    | 156    |                  |
| 52  | 1Z    | 212    |                  |
| 53  | 1a    | 144    |                  |
| 54  | 1b    | 109    |                  |
| 55  | 1c    | 135    |                  |
| 56  | 1d    | 139    |                  |
| 57  | 1e    | 63     |                  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 58  | 1f    | 146    |                  |
| 59  | 1g    | 162    |                  |
| 60  | 1h    | 103    |                  |
| 61  | 1i    | 247    |                  |
| 62  | 1j    | 90     |                  |
| 63  | 1k    | 119    |                  |
| 64  | 1l    | 233    |                  |
| 65  | 1m    | 128    |                  |
| 66  | 1o    | 125    |                  |
| 67  | 1p    | 130    |                  |
| 68  | 1q    | 79     |                  |
| 69  | 1r    | 167    |                  |
| 70  | 1s    | 181    |                  |
| 71  | 1t    | 491    |                  |
| 72  | 1u    | 757    |                  |
| 73  | 1v    | 521    |                  |
| 74  | 1x    | 4      |                  |
| 75  | 5     | 76     |                  |
| 76  | 2     | 1591   |                  |
| 77  | 6     | 6      |                  |
| 78  | a     | 424    |                  |
| 79  | b     | 80     |                  |
| 80  | c     | 128    |                  |
| 81  | d     | 110    |                  |
| 82  | e     | 383    |                  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 83  | f     | 410    |                  |
| 84  | h     | 384    |                  |
| 85  | i     | 725    |                  |
| 86  | j     | 408    |                  |
| 87  | k     | 155    |                  |
| 88  | A     | 212    |                  |



## 2 Entry composition

There are 93 unique types of molecules in this entry. The entry contains 211395 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 Small ribosomal subunit protein uS3m.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 1   | B     | 467      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3877  | 2520 | 701 | 643 | 13 |         |       |

There are 7 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference      |
|-------|---------|----------|--------|----------|----------------|
| B     | 22      | TRP      | ARG    | conflict | UNP A0A068BCX1 |
| B     | 172     | LEU      | SER    | conflict | UNP A0A068BCX1 |
| B     | 202     | LYS      | ARG    | conflict | UNP A0A068BCX1 |
| B     | 296     | LEU      | SER    | conflict | UNP A0A068BCX1 |
| B     | 512     | CYS      | ARG    | conflict | UNP A0A068BCX1 |
| B     | 524     | VAL      | ALA    | conflict | UNP A0A068BCX1 |
| B     | 533     | LEU      | SER    | conflict | UNP A0A068BCX1 |

- Molecule 2 is a protein called uS4m.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 2   | C     | 333      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2811  | 1798 | 540 | 462 | 11 |         |       |

- Molecule 3 is a protein called uS5m.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 3   | D     | 417      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3425  | 2146 | 603 | 664 | 12 |         |       |

- Molecule 4 is a protein called bS6m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 4   | E     | 101      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 823   | 535 | 145 | 138 | 5 |         |       |

- Molecule 5 is a protein called uS7m, Small ribosomal subunit protein uS7m.



| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 5   | F     | 157      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1254  | 793 | 244 | 213 | 4 |         |       |

- Molecule 6 is a protein called uS8m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 6   | G     | 128      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1037  | 652 | 193 | 189 | 3 |         |       |

- Molecule 7 is a protein called uS9m.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 7   | H     | 213      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1682  | 1054 | 312 | 311 | 5 |         |       |

- Molecule 8 is a protein called uS10m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 8   | I     | 113      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 941   | 602 | 174 | 159 | 6 |         |       |

- Molecule 9 is a protein called uS11m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 9   | J     | 127      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 988   | 608 | 195 | 181 | 4 |         |       |

- Molecule 10 is a protein called uS12m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10  | K     | 124      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 992   | 613 | 208 | 167 | 4 |         |       |

- Molecule 11 is a protein called uS13m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 11  | L     | 119      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 940   | 572 | 200 | 163 | 5 |         |       |

- Molecule 12 is a protein called uS14m.



| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12  | M     | 101      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 843   | 524 | 174 | 140 | 5 |         |       |

- Molecule 13 is a protein called uS15m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 13  | N     | 116      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 941   | 593 | 170 | 171 | 7 |         |       |

- Molecule 14 is a protein called bS16m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 14  | O     | 110      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 869   | 550 | 169 | 144 | 6 |         |       |

- Molecule 15 is a protein called uS17m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15  | P     | 91       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 717   | 455 | 135 | 124 | 3 |         |       |

- Molecule 16 is a protein called bS18m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16  | Q     | 90       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 724   | 460 | 127 | 134 | 3 |         |       |

- Molecule 17 is a protein called uS19m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17  | R     | 166      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1299  | 819 | 236 | 237 | 7 |         |       |

- Molecule 18 is a protein called bS21m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 18  | S     | 75       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 611   | 386 | 120 | 103 | 2 |         |       |

- Molecule 19 is a protein called bTHXm.



| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 19  | T     | 50       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 408   | 260 | 79 | 68 | 1 |         |       |

- Molecule 20 is a protein called mS23.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20  | U     | 127      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1014  | 647 | 184 | 178 | 5 |         |       |

- Molecule 21 is a protein called mS26.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21  | V     | 164      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1399  | 874 | 266 | 255 | 4 |         |       |

- Molecule 22 is a protein called mS29.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 22  | W     | 380      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3062  | 1955 | 535 | 559 | 13 |         |       |

- Molecule 23 is a protein called mS31/mS46.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 23  | X     | 204      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1613  | 1011 | 262 | 329 | 11 |         |       |

- Molecule 24 is a protein called mS33.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24  | Y     | 98       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 793   | 495 | 159 | 137 | 2 |         |       |

- Molecule 25 is a protein called mS34.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25  | Z     | 80       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 649   | 422 | 121 | 104 | 2 |         |       |

- Molecule 26 is a RNA chain called 26S rRNA.



| Mol | Chain | Residues | Atoms |       |       |       |      | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 26  | 1     | 2922     | Total | C     | N     | O     | P    | 5       | 0     |
|     |       |          | 62518 | 27942 | 11365 | 20289 | 2922 |         |       |

- Molecule 27 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 27  | 3     | 118      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 2513  | 1124 | 453 | 819 | 117 |         |       |

- Molecule 28 is a protein called uL2m C-ter.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 28  | 1B    | 177      | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 1325  | 819 | 259 | 233 | 14 |         |       |

- Molecule 29 is a protein called Large ribosomal subunit protein uL2mz, N-terminal part.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 29  | 1C    | 215      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1696  | 1078 | 316 | 296 | 6 |         |       |

There are 12 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference  |
|-------|---------|----------|--------|----------|------------|
| 1C    | 87      | LYS      | GLU    | conflict | UNP P93311 |
| 1C    | 89      | LEU      | PHE    | conflict | UNP P93311 |
| 1C    | 147     | TYR      | SER    | conflict | UNP P93311 |
| 1C    | 155     | SER      | GLY    | conflict | UNP P93311 |
| 1C    | 190     | ASP      | GLY    | conflict | UNP P93311 |
| 1C    | 195     | PRO      | ALA    | conflict | UNP P93311 |
| 1C    | 199     | VAL      | ALA    | conflict | UNP P93311 |
| 1C    | 200     | SER      | LYS    | conflict | UNP P93311 |
| 1C    | 201     | THR      | PRO    | conflict | UNP P93311 |
| 1C    | 221     | TYR      | CYS    | conflict | UNP P93311 |
| 1C    | 226     | TRP      | GLY    | conflict | UNP P93311 |
| 1C    | 238     | ASN      | LYS    | conflict | UNP P93311 |

- Molecule 30 is a protein called uL3m.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 30  | 1D    | 264      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2045  | 1309 | 367 | 358 | 11 |         |       |



- Molecule 31 is a protein called uL4m.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 31  | 1E    | 221      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1753  | 1104 | 334 | 308 | 7 |         |       |

- Molecule 32 is a protein called uL5m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32  | 1F    | 158      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1286  | 829 | 212 | 236 | 9 |         |       |

- Molecule 33 is a protein called uL6m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33  | 1G    | 98       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 779   | 508 | 136 | 130 | 5 |         |       |

- Molecule 34 is a protein called bL9m.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 34  | 1H    | 66       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 539   | 345 | 98 | 94 | 2 |         |       |

- Molecule 35 is a protein called uL10m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 35  | 1I    | 130      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1036  | 669 | 178 | 184 | 5 |         |       |

- Molecule 36 is a protein called uL11m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 36  | 1J    | 147      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1129  | 722 | 193 | 205 | 9 |         |       |

- Molecule 37 is a protein called uL13m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 37  | 1K    | 189      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1526  | 955 | 299 | 265 | 7 |         |       |

- Molecule 38 is a protein called uL14m.



| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 38  | 1L    | 127      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 966   | 609 | 184 | 168 | 5 |         |       |

- Molecule 39 is a protein called uL15m.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 39  | 1M    | 210      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1649  | 1052 | 321 | 273 | 3 |         |       |

- Molecule 40 is a protein called uL16m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 40  | 1N    | 148      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1160  | 731 | 230 | 192 | 7 |         |       |

- Molecule 41 is a protein called bL17m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 41  | 1O    | 151      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1231  | 767 | 244 | 214 | 6 |         |       |

- Molecule 42 is a protein called uL18m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42  | 1P    | 113      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 878   | 564 | 160 | 149 | 5 |         |       |

- Molecule 43 is a protein called bL19m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 43  | 1Q    | 122      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1008  | 641 | 198 | 166 | 3 |         |       |

- Molecule 44 is a protein called bL20m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 44  | 1R    | 110      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 915   | 572 | 184 | 154 | 5 |         |       |

- Molecule 45 is a protein called bL21m.



| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 45  | 1S    | 145      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1170  | 750 | 207 | 211 | 2 |         |       |

- Molecule 46 is a protein called uL22m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 46  | 1T    | 155      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1241  | 782 | 249 | 205 | 5 |         |       |

- Molecule 47 is a protein called uL23m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 47  | 1U    | 130      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1048  | 675 | 190 | 181 | 2 |         |       |

- Molecule 48 is a protein called uL24m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 48  | 1V    | 158      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1223  | 770 | 229 | 220 | 4 |         |       |

- Molecule 49 is a protein called bL25-2m.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 49  | 1W    | 205      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1588  | 1006 | 284 | 294 | 4 |         |       |

- Molecule 50 is a protein called bL25m.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 50  | 1X    | 216      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1670  | 1069 | 298 | 302 | 1 |         |       |

- Molecule 51 is a protein called bL27m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 51  | 1Y    | 98       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 768   | 484 | 152 | 131 | 1 |         |       |

- Molecule 52 is a protein called bL28m.



| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 52  | 1Z    | 177      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1441  | 911 | 266 | 255 | 9 |         |       |

- Molecule 53 is a protein called uL29m.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 53  | 1a    | 110      | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 928   | 588 | 172 | 158 | 10 |         |       |

- Molecule 54 is a protein called uL30m.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 54  | 1b    | 100      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 803   | 504 | 160 | 134 | 5 |         |       |

- Molecule 55 is a protein called bL31m.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 55  | 1c    | 59       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 489   | 313 | 98 | 73 | 5 |         |       |

- Molecule 56 is a protein called bL32m.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 56  | 1d    | 49       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 379   | 240 | 80 | 55 | 4 |         |       |

- Molecule 57 is a protein called bL33m.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 57  | 1e    | 54       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 459   | 300 | 85 | 72 | 2 |         |       |

- Molecule 58 is a protein called bL34m.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 58  | 1f    | 44       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 364   | 224 | 88 | 52 |         |       |

- Molecule 59 is a protein called bL35m.



| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 59  | 1g    | 91       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 770   | 496 | 152 | 119 | 3 |         |       |

- Molecule 60 is a protein called bL36m.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 60  | 1h    | 38       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 309   | 190 | 65 | 49 | 5 |         |       |

- Molecule 61 is a protein called mL40.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 61  | 1i    | 183      | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 1424  | 885 | 255 | 274 | 10 |         |       |

- Molecule 62 is a protein called mL41.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 62  | 1j    | 71       | Total | C   | N   | O  | S | 0       | 0     |
|     |       |          | 570   | 369 | 102 | 97 | 2 |         |       |

- Molecule 63 is a protein called mL43.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 63  | 1k    | 118      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 952   | 599 | 184 | 165 | 4 |         |       |

- Molecule 64 is a protein called mL46.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 64  | 1l    | 211      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1741  | 1131 | 286 | 316 | 8 |         |       |

- Molecule 65 is a protein called mL53.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 65  | 1m    | 122      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 970   | 610 | 170 | 184 | 6 |         |       |

- Molecule 66 is a protein called mL54.



| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 66  | 1o    | 76       | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 626   | 397 | 114 | 115 |         |       |

- Molecule 67 is a protein called mL59/mL64.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 67  | 1p    | 117      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 992   | 626 | 189 | 169 | 8 |         |       |

- Molecule 68 is a protein called mL60.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 68  | 1q    | 50       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 390   | 243 | 79 | 67 | 1 |         |       |

- Molecule 69 is a protein called mL80.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 69  | 1r    | 92       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 735   | 469 | 139 | 122 | 5 |         |       |

- Molecule 70 is a protein called mL87.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 70  | 1s    | 118      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 985   | 617 | 203 | 163 | 2 |         |       |

- Molecule 71 is a protein called mL101 (rPPR4).

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 71  | 1t    | 484      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3856  | 2433 | 665 | 733 | 25 |         |       |

- Molecule 72 is a protein called mL102 (rPPR5).

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 72  | 1u    | 666      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 5264  | 3316 | 915 | 991 | 42 |         |       |

- Molecule 73 is a protein called mL104 (rPPR9).



| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 73  | 1v    | 433      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3440  | 2173 | 599 | 640 | 28 |         |       |

- Molecule 74 is a protein called Nascent peptide.

| Mol | Chain | Residues | Atoms |    |   |   | AltConf | Trace |
|-----|-------|----------|-------|----|---|---|---------|-------|
| 74  | 1x    | 4        | Total | C  | N | O | 0       | 0     |
|     |       |          | 19    | 11 | 4 | 4 |         |       |

- Molecule 75 is a RNA chain called tRNA.

| Mol | Chain | Residues | Atoms |     |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---|---------|-------|
| 75  | 5     | 76       | Total | C   | N   | O   | P  | S | 0       | 0     |
|     |       |          | 1625  | 725 | 294 | 529 | 76 | 1 |         |       |

- Molecule 76 is a RNA chain called 18S rRNA.

| Mol | Chain | Residues | Atoms |       |      |       |      | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 76  | 2     | 1591     | Total | C     | N    | O     | P    | 0       | 0     |
|     |       |          | 34081 | 15222 | 6213 | 11055 | 1591 |         |       |

- Molecule 77 is a RNA chain called mRNA.

| Mol | Chain | Residues | Atoms |    |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---|---------|-------|
| 77  | 6     | 6        | Total | C  | N  | O  | P | 0       | 0     |
|     |       |          | 130   | 59 | 27 | 38 | 6 |         |       |

- Molecule 78 is a protein called mS35.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 78  | a     | 315      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2487  | 1547 | 448 | 482 | 10 |         |       |

- Molecule 79 is a protein called mS37.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 79  | b     | 77       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 610   | 378 | 116 | 108 | 8 |         |       |

- Molecule 80 is a protein called mS38.



| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 80  | c     | 26       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 232   | 145 | 54 | 32 | 1 |         |       |

- Molecule 81 is a protein called mS41.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 81  | d     | 78       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 616   | 403 | 110 | 102 | 1 |         |       |

- Molecule 82 is a protein called mS45.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 82  | e     | 246      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2074  | 1310 | 374 | 380 | 10 |         |       |

- Molecule 83 is a protein called mS47.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 83  | f     | 377      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2922  | 1843 | 486 | 573 | 20 |         |       |

- Molecule 84 is a protein called mS83 (rPPR10).

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 84  | h     | 310      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2460  | 1551 | 436 | 458 | 15 |         |       |

- Molecule 85 is a protein called mS77 (NFD5).

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 85  | i     | 306      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2487  | 1567 | 419 | 487 | 14 |         |       |

- Molecule 86 is a protein called mS76 (rPPR1).

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 86  | j     | 381      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2984  | 1885 | 510 | 567 | 22 |         |       |

- Molecule 87 is a protein called mS86.



| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 87  | k     | 47       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 314   | 194 | 61 | 55 | 4 |         |       |

- Molecule 88 is a protein called uS2m.

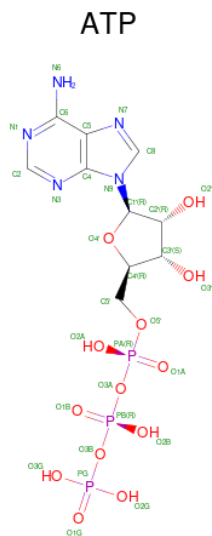
| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 88  | A     | 204      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1611  | 1032 | 284 | 285 | 10 |         |       |

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms |     | AltConf |
|-----|-------|----------|-------|-----|---------|
| 89  | T     | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 89  | W     | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 89  | 1     | 249      | Total | Mg  | 0       |
|     |       |          | 249   | 249 |         |
| 89  | 3     | 3        | Total | Mg  | 0       |
|     |       |          | 3     | 3   |         |
| 89  | 1D    | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 89  | 1h    | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 89  | 1j    | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 89  | 1q    | 2        | Total | Mg  | 0       |
|     |       |          | 2     | 2   |         |
| 89  | 2     | 98       | Total | Mg  | 0       |
|     |       |          | 98    | 98  |         |

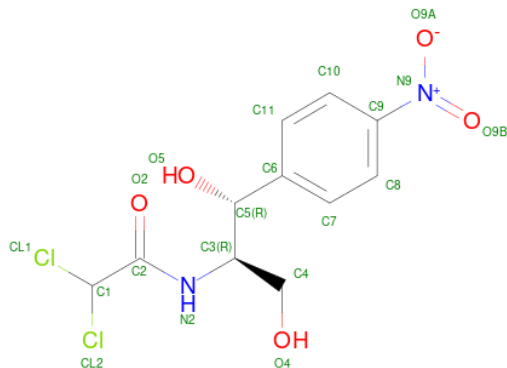
- Molecule 90 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).





| Mol | Chain | Residues | Atoms       |         |        |         |        | AltConf |
|-----|-------|----------|-------------|---------|--------|---------|--------|---------|
| 90  | W     | 1        | Total<br>31 | C<br>10 | N<br>5 | O<br>13 | P<br>3 | 0       |

- Molecule 91 is CHLORAMPHENICOL (CCD ID: CLM) (formula:  $C_{11}H_{12}Cl_2N_2O_5$ ).



| Mol | Chain | Residues | Atoms |    |    |   |   | AltConf |
|-----|-------|----------|-------|----|----|---|---|---------|
| 91  | 1     | 1        | Total | C  | Cl | N | O | 0       |
|     |       |          | 20    | 11 | 2  | 2 | 5 |         |

- Molecule 92 is POTASSIUM ION (CCD ID: K) (formula: K).



| Mol | Chain | Residues | Atoms       |         | AltConf |
|-----|-------|----------|-------------|---------|---------|
| 92  | 1     | 56       | Total<br>56 | K<br>56 | 0       |
| 92  | 1B    | 3        | Total<br>3  | K<br>3  | 0       |
| 92  | 1E    | 1        | Total<br>1  | K<br>1  | 0       |
| 92  | 2     | 14       | Total<br>14 | K<br>14 | 0       |

- Molecule 93 is ZINC ION (CCD ID: ZN) (formula: Zn).

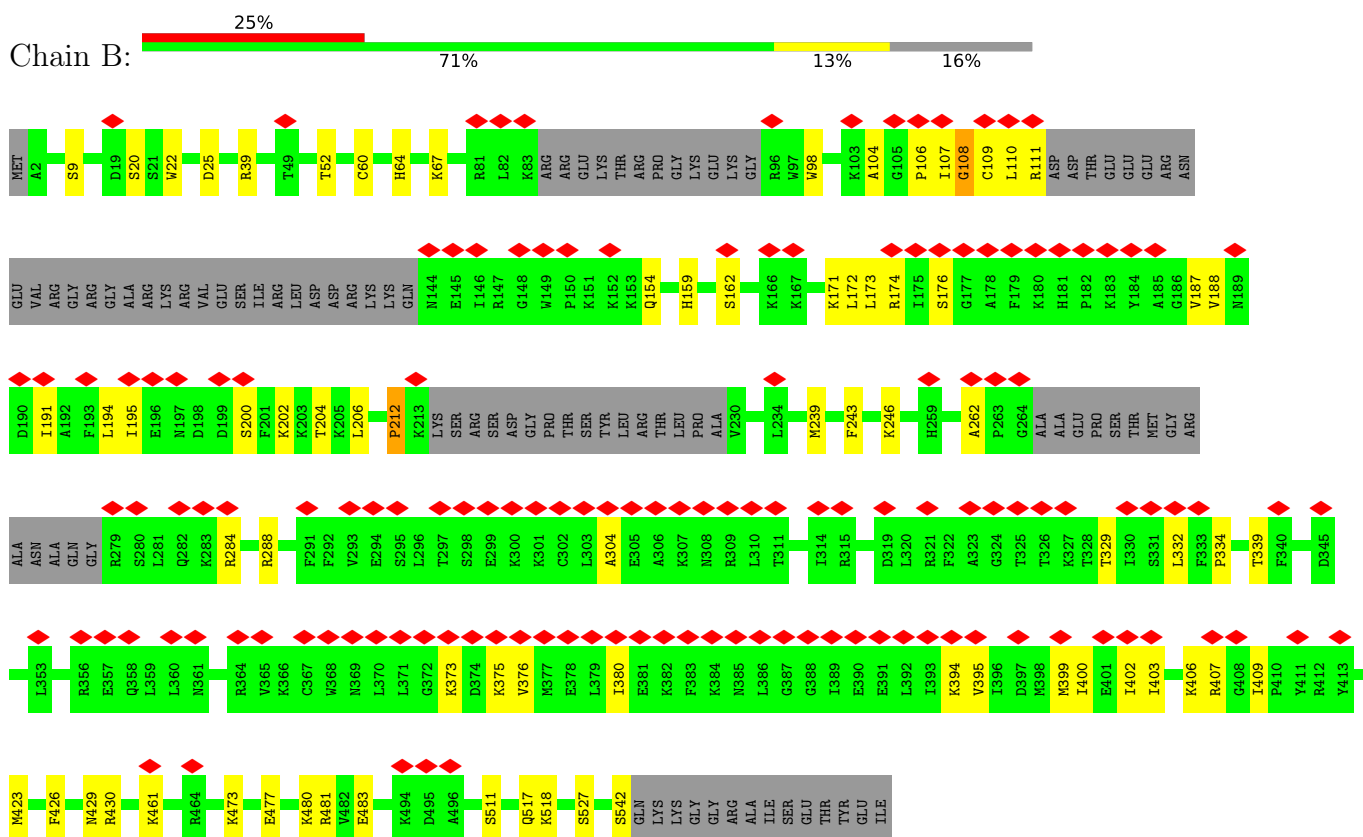
| Mol | Chain | Residues | Atoms      |         | AltConf |
|-----|-------|----------|------------|---------|---------|
| 93  | 1d    | 1        | Total<br>1 | Zn<br>1 | 0       |
| 93  | 1h    | 1        | Total<br>1 | Zn<br>1 | 0       |



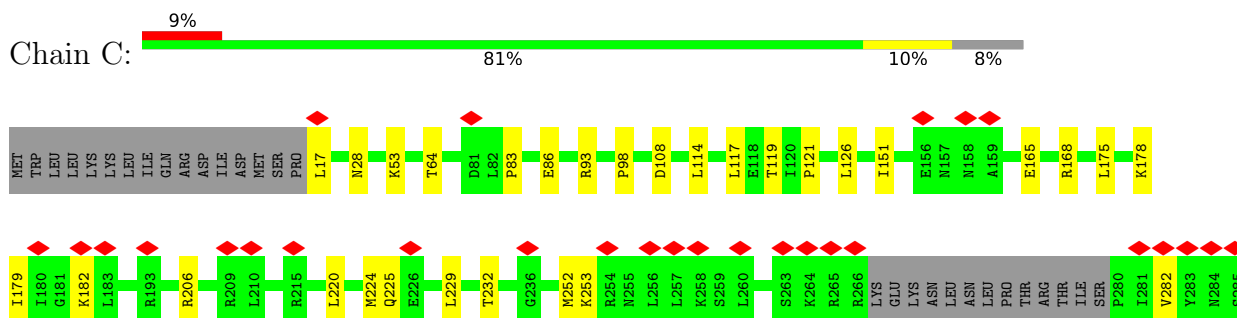
### 3 Residue-property plots

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.

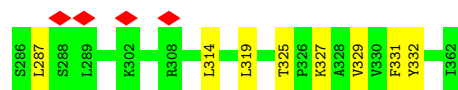
- Molecule 1: Small ribosomal subunit protein uS3m



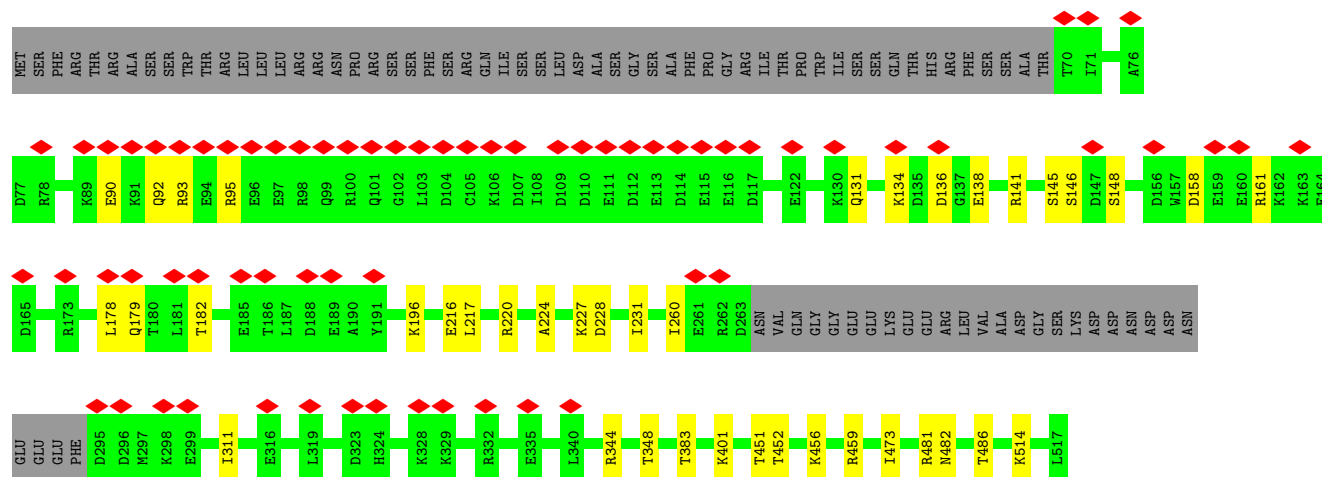
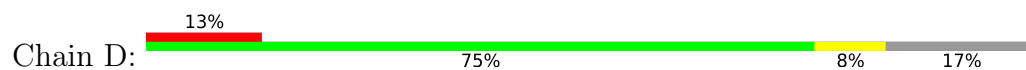
- Molecule 2: uS4m



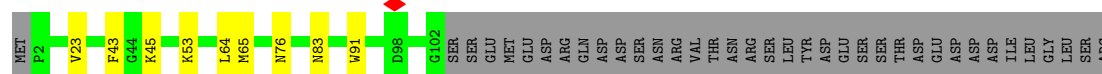




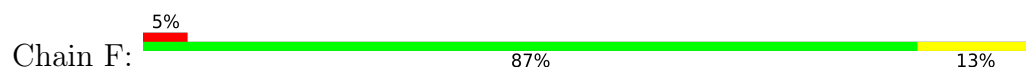
- Molecule 3: uS5m



- Molecule 4: bS6m



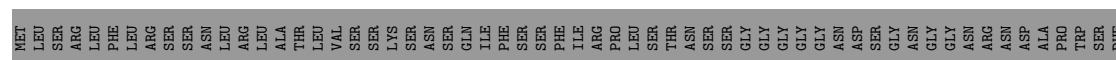
- Molecule 5: uS7m, Small ribosomal subunit protein uS7m



- Molecule 6: uS8m



- Molecule 7: uS9m









Chain L: 

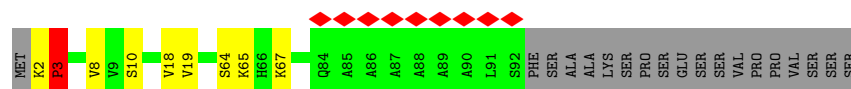
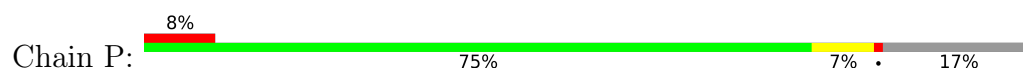
Chain M: 

Chain N:  27% 72%

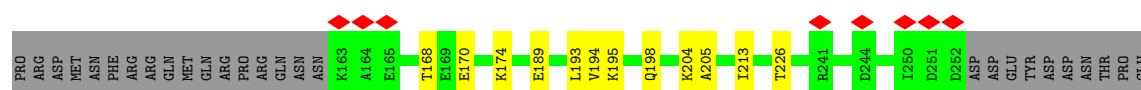
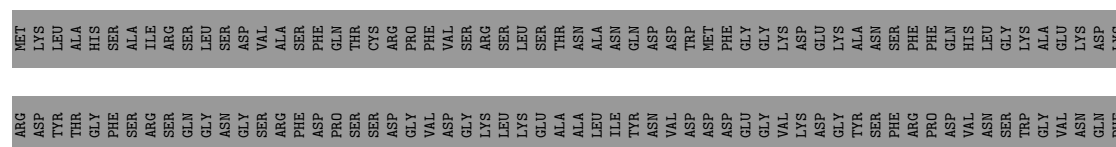
Chain O:  70% 11% 19%



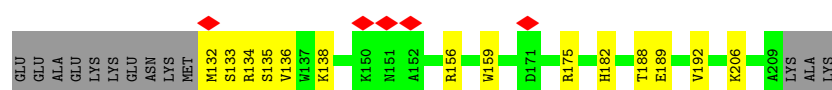
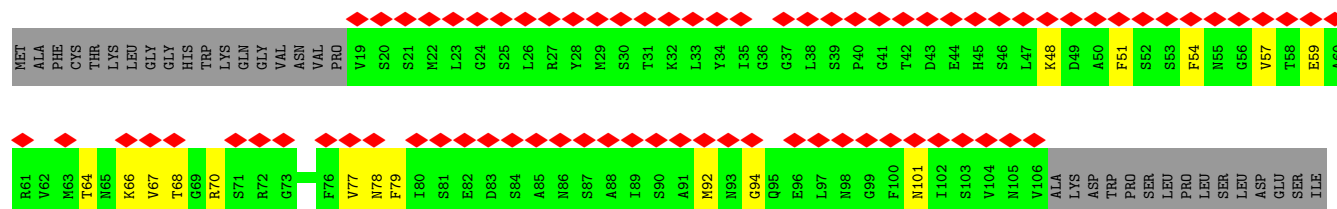
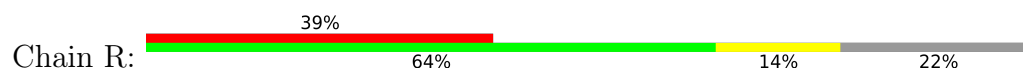




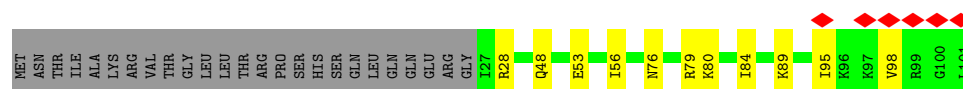
• Molecule 16: bS18m



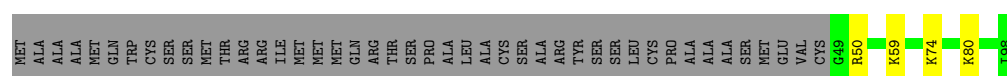
• Molecule 17: uS19m



• Molecule 18: bS21m



• Molecule 19: bTHXm



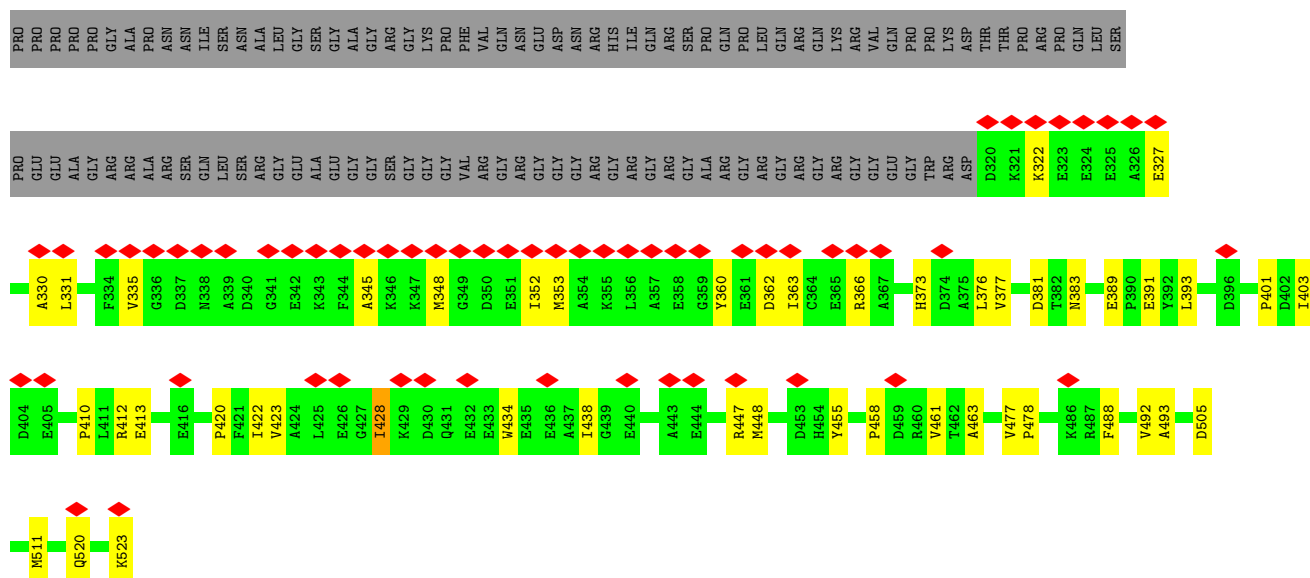
• Molecule 20: mS23



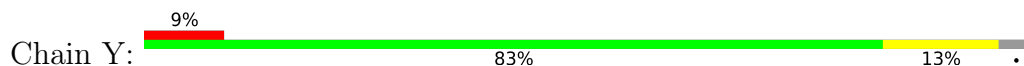




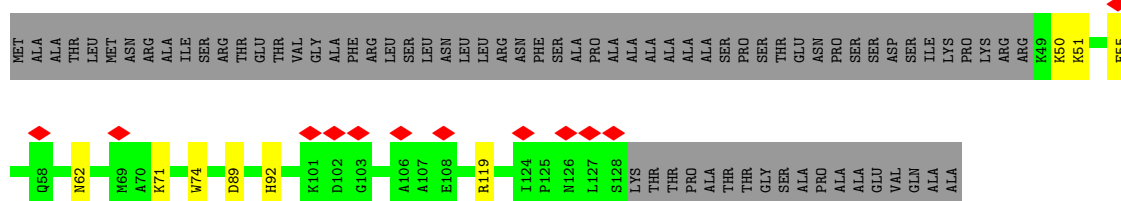




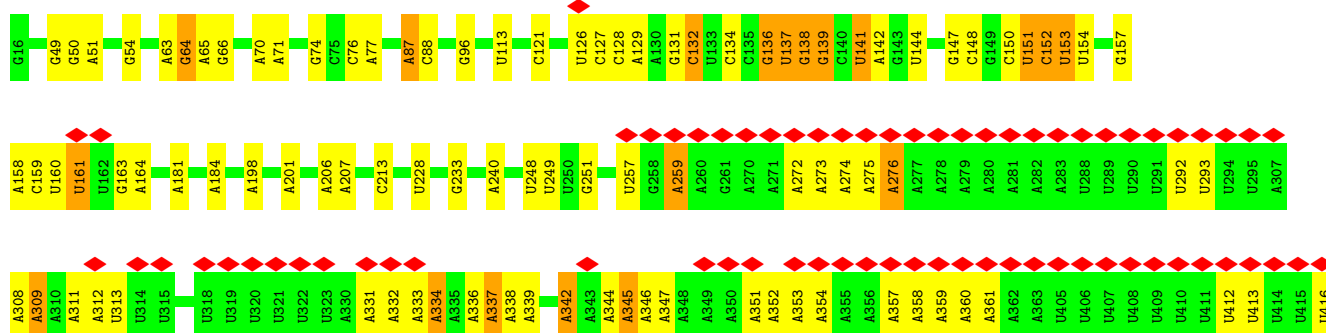
### • Molecule 24: mS33



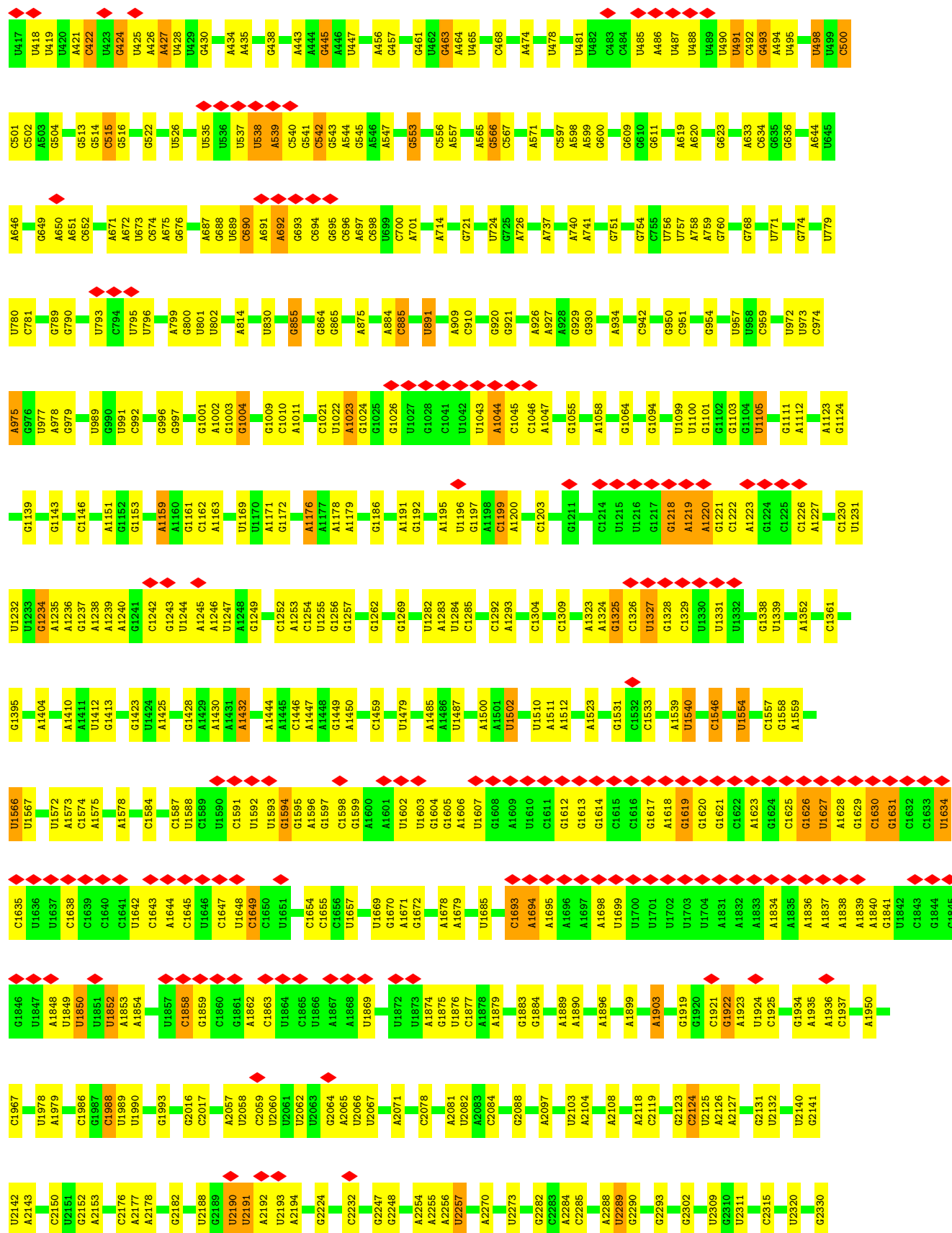
### • Molecule 25: mS34



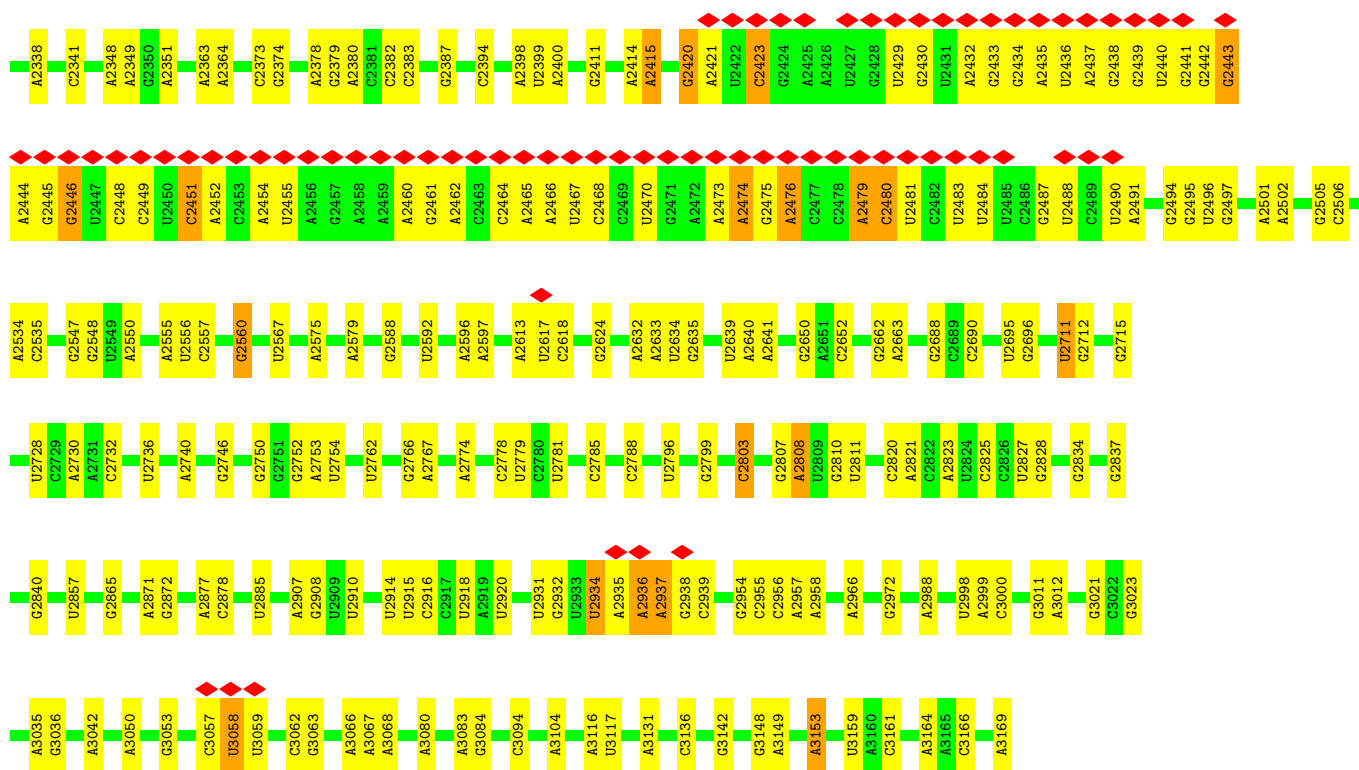
### • Molecule 26: 26S rRNA





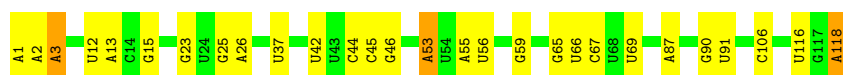






• Molecule 27: 5S rRNA

Chain 3: 76% 21% .



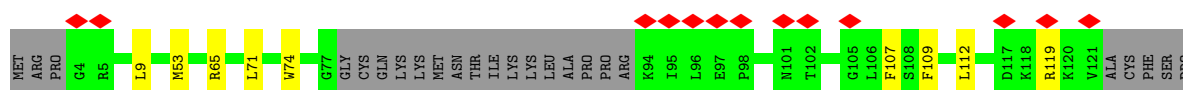
• Molecule 28: uL2m C-ter

Chain 1B: 73% 7% 20%

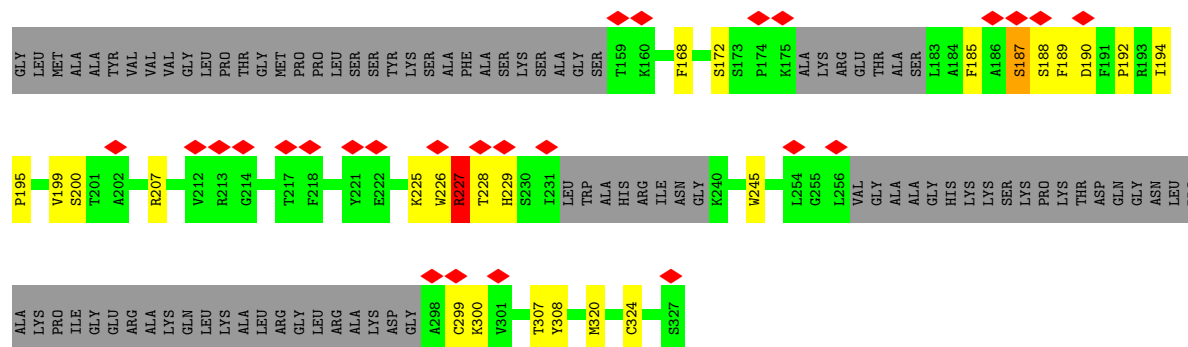


• Molecule 29: Large ribosomal subunit protein uL2mz, N-terminal part

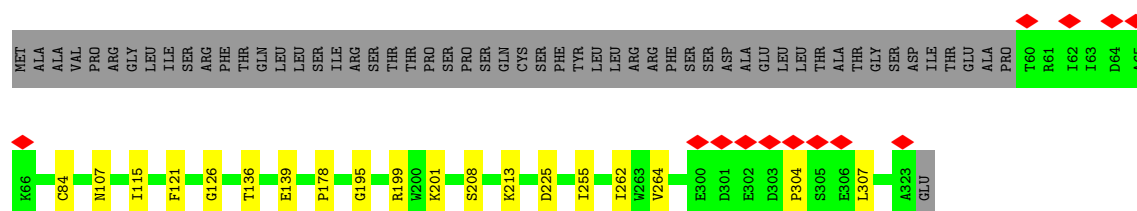
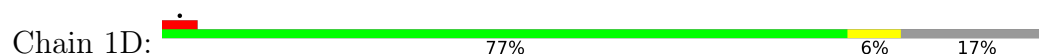
Chain 1C: 12% 55% 10% 34%



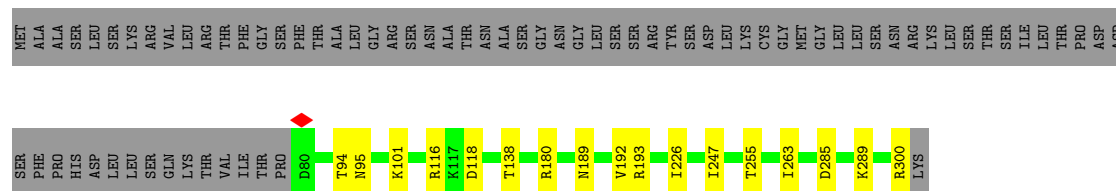




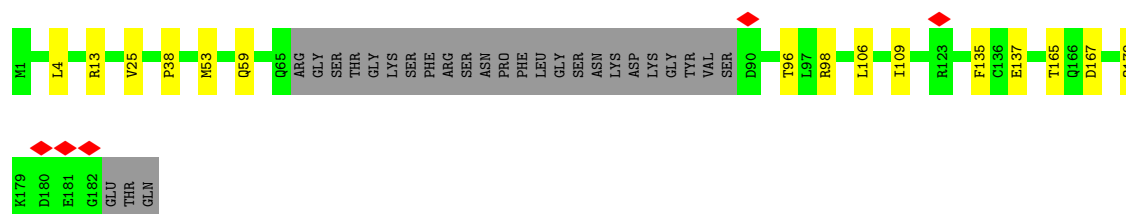
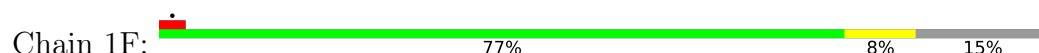
• Molecule 30: uL3m



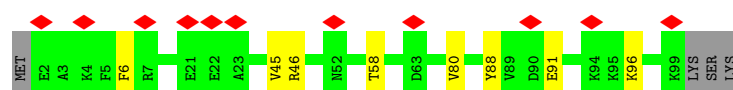
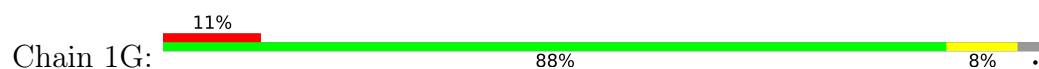
• Molecule 31: uL4m



• Molecule 32: uL5m

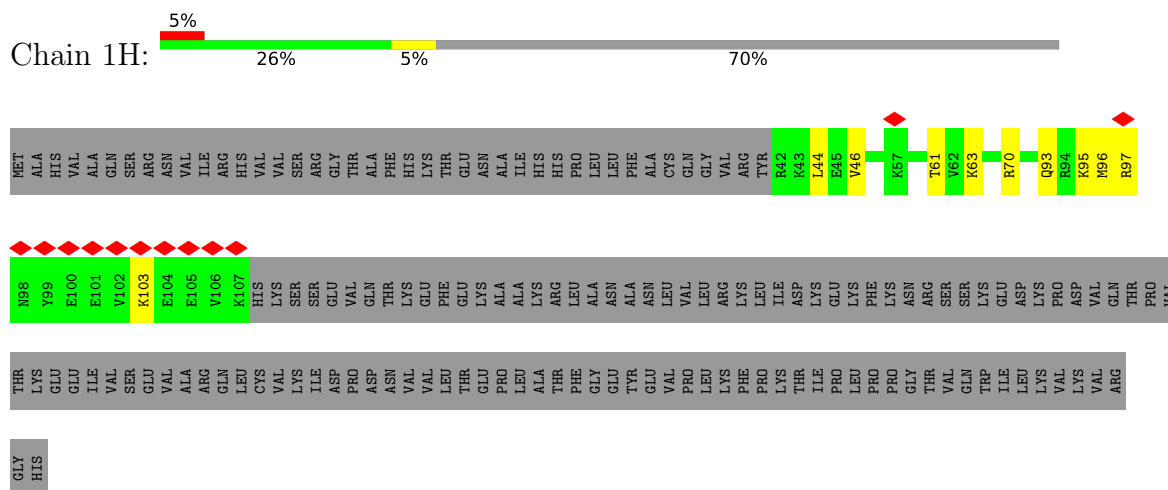


• Molecule 33: uL6m

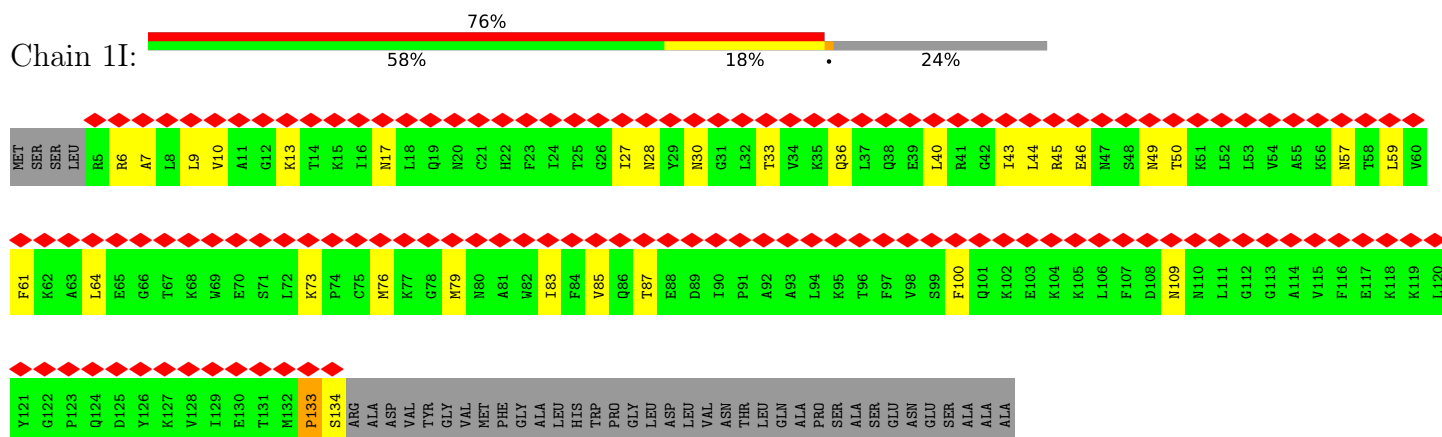




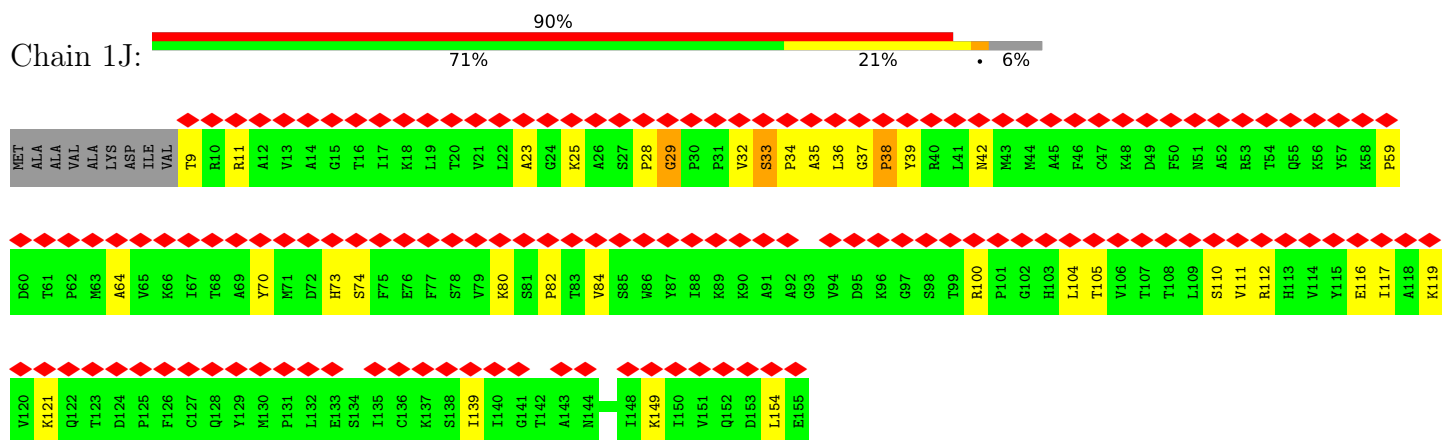
- Molecule 34: bL9m



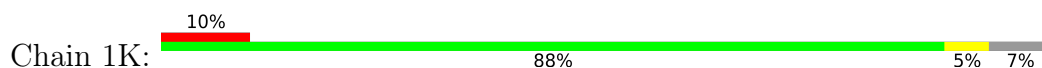
- Molecule 35: uL10m



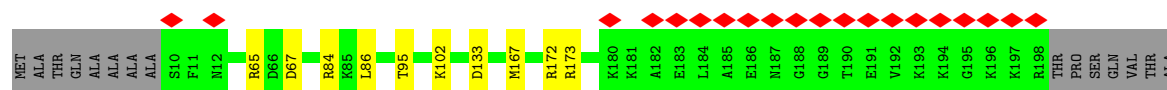
- Molecule 36: uL11m



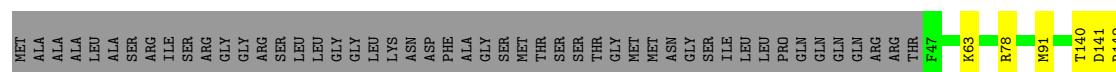
- Molecule 37: uL13m



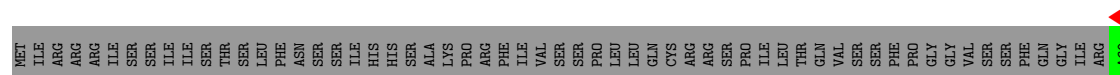




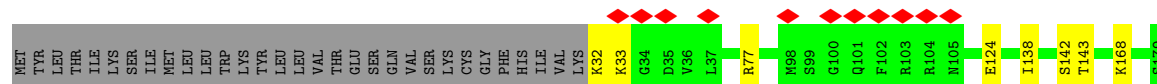
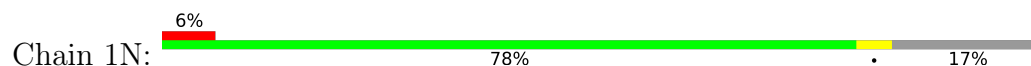
## • Molecule 38: uL14m



## • Molecule 39: uL15m



## • Molecule 40: uL16m



## • Molecule 41: bL17m



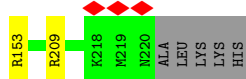
## • Molecule 42: uL18m




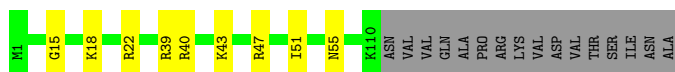
## • Molecule 43: bL19m



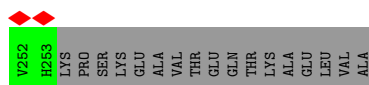
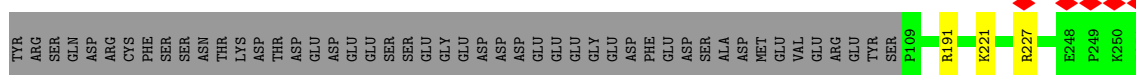




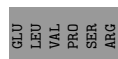
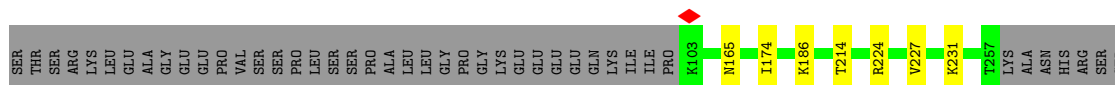
Chain 1R:  80% 7% 13%



Chain 1S:  53% . 46%



Chain 1T:  56% . 41%



Chain 1U: 

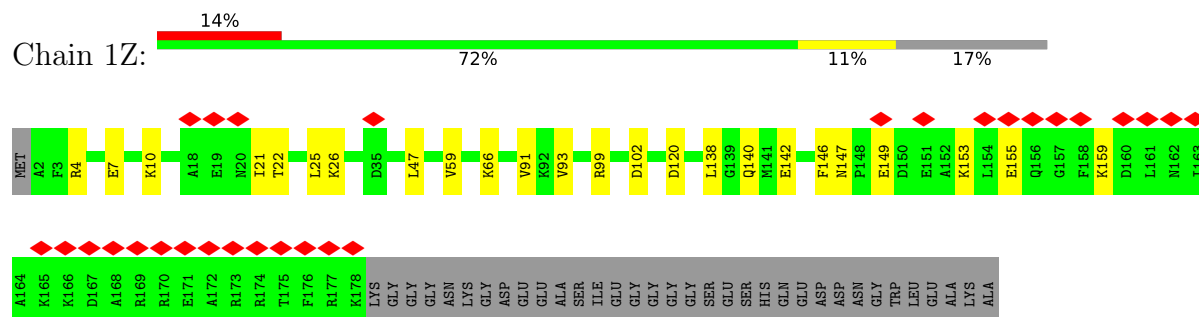




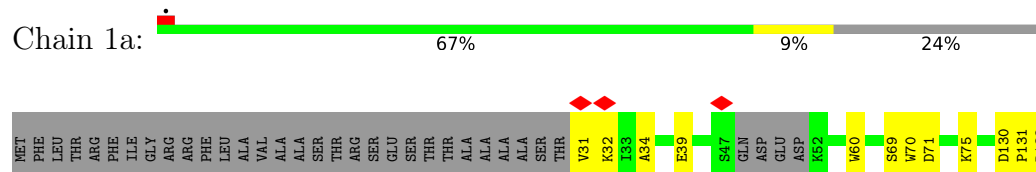




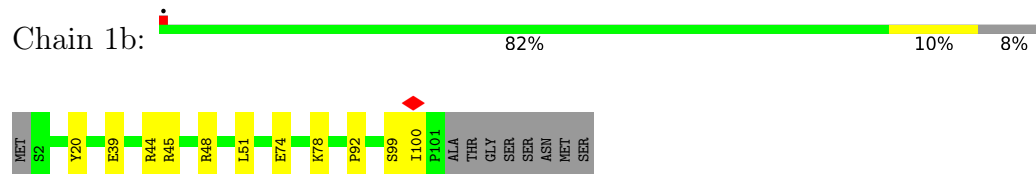
- Molecule 52: bL28m



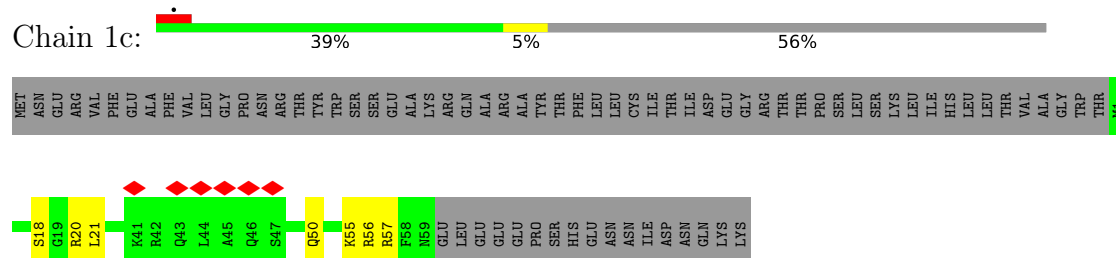
- Molecule 53: uL29m



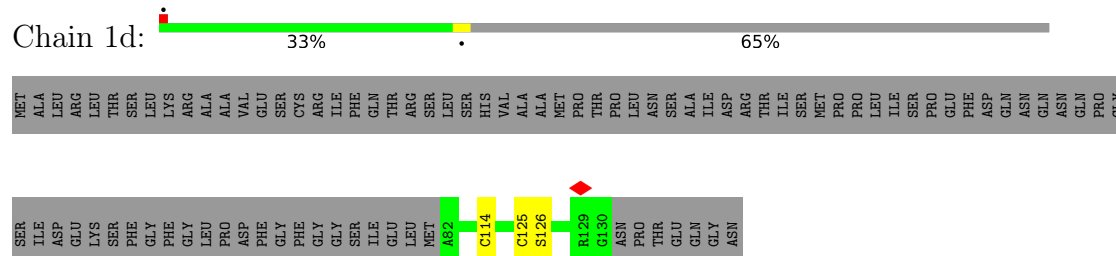
- Molecule 54: uL30m



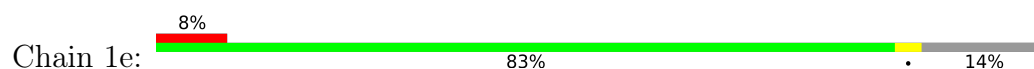
- Molecule 55: bL31m



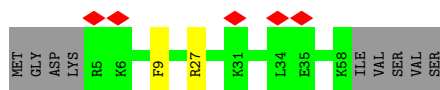
- Molecule 56: bL32m



- Molecule 57: bL33m

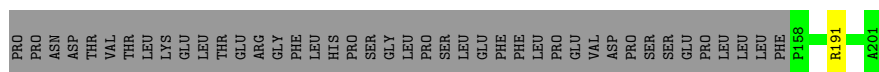






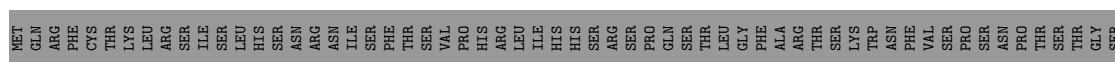
• Molecule 58: bL34m

Chain 1f: 29% 70%



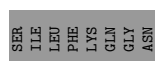
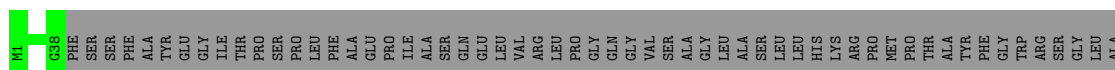
• Molecule 59: bL35m

Chain 1g: 51% 6% 44%



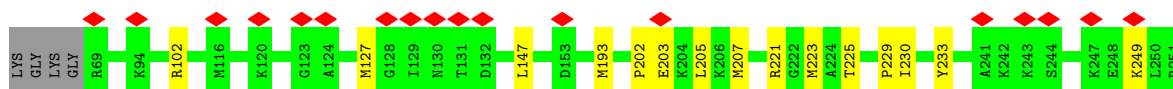
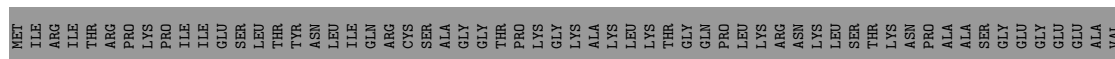
• Molecule 60: bL36m

Chain 1h: 37% 63%



• Molecule 61: mL40

Chain 1i: 7% 68% 6% 26%



• Molecule 62: mL41

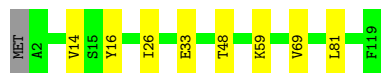
Chain 1j: 71% 8% 21%






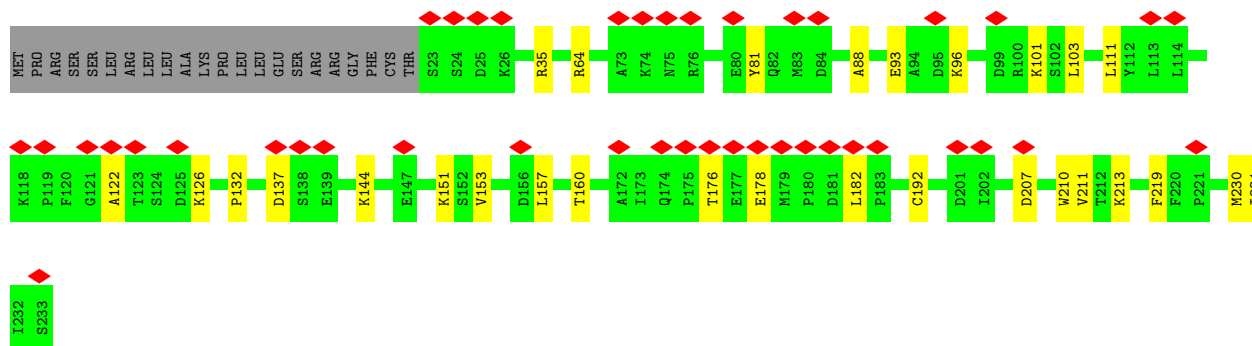
- Molecule 63: mL43

Chain 1k: 




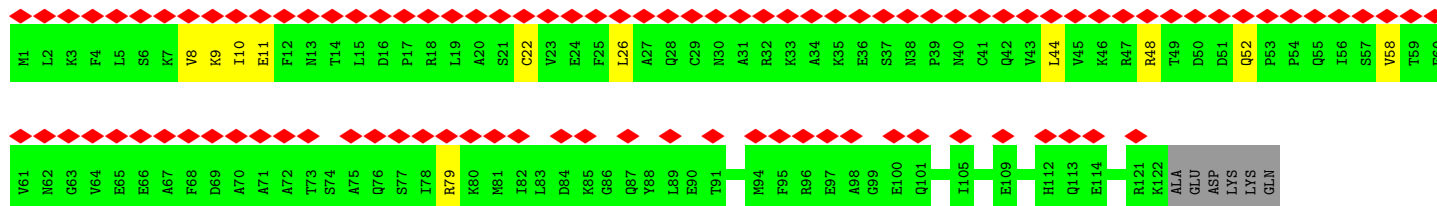
- Molecule 64: mL46

Chain 1l: 

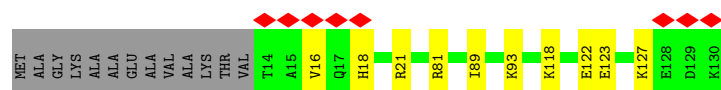


- Molecule 65: mL53

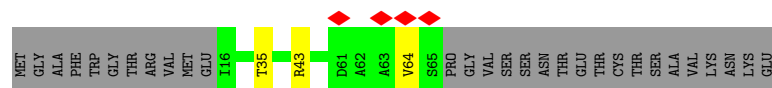
Chain 1m: 



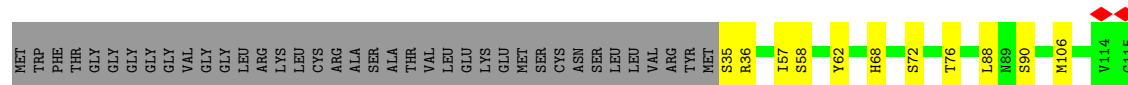




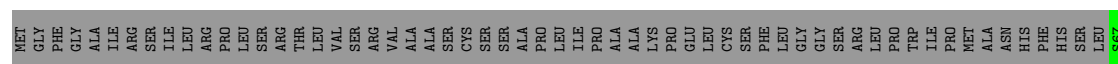
- Molecule 68: mL60



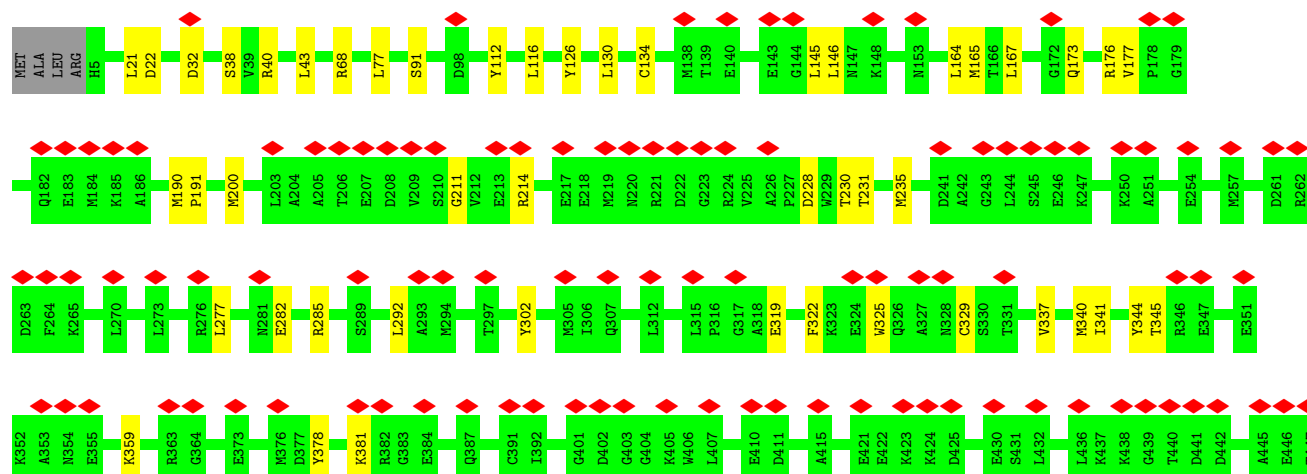
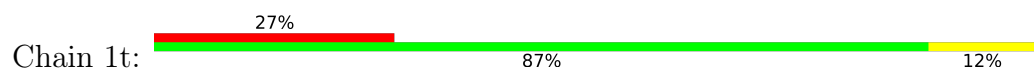
- Molecule 69: mL80



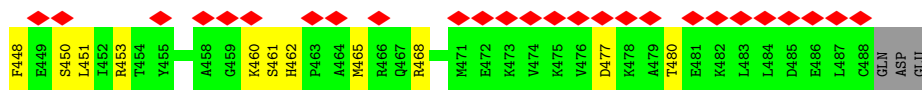
- Molecule 70: mL87



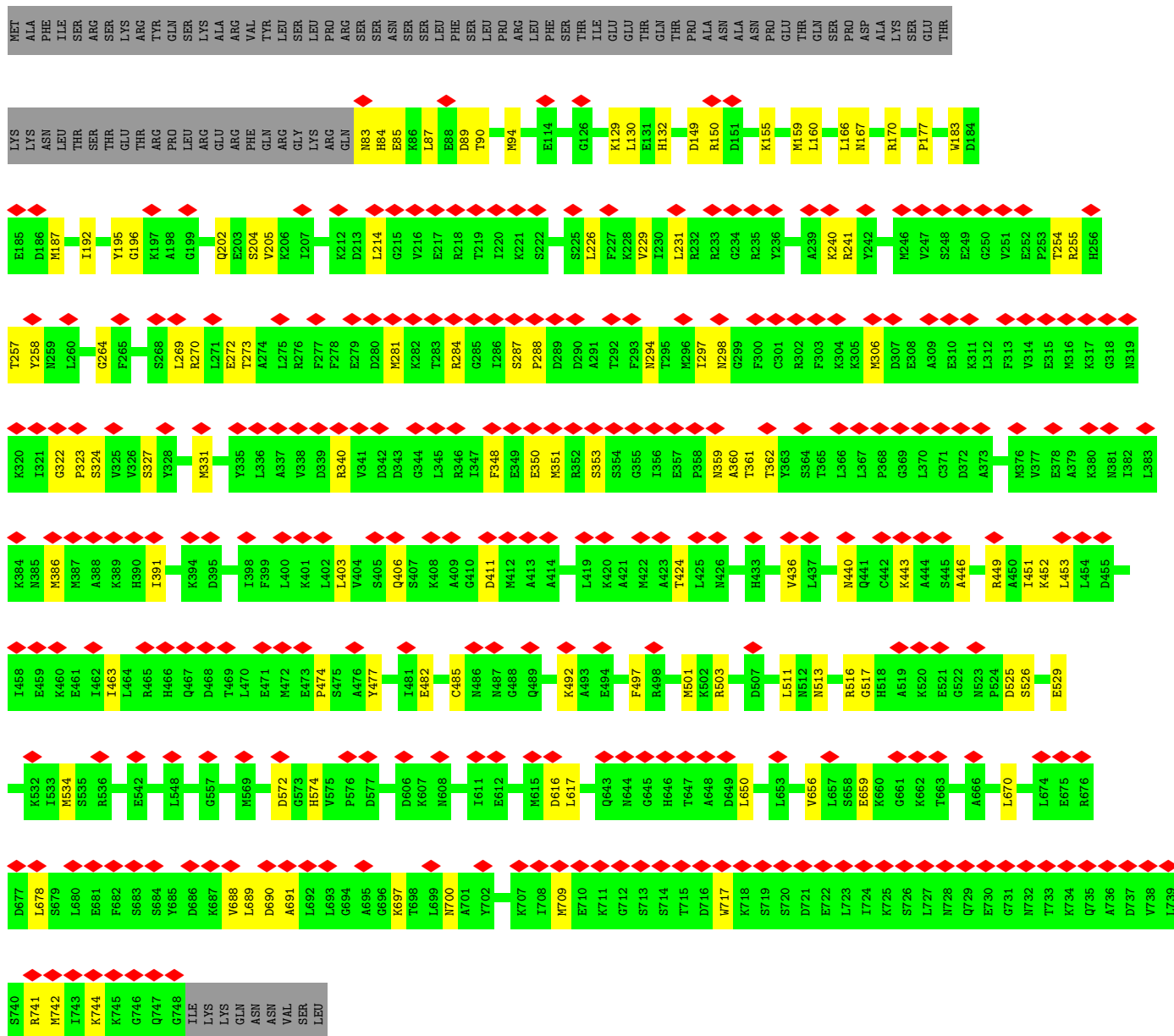
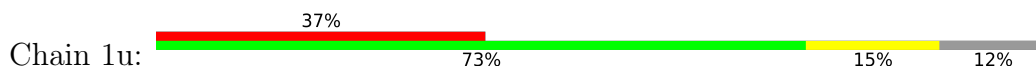
- Molecule 71: mL101 (rPPR4)



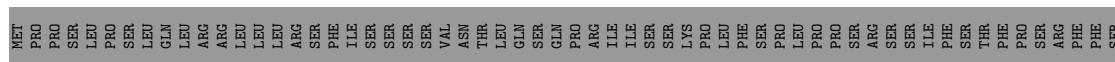
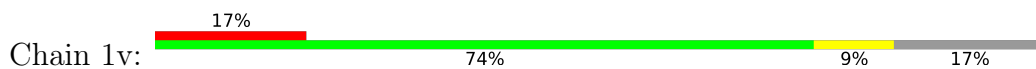




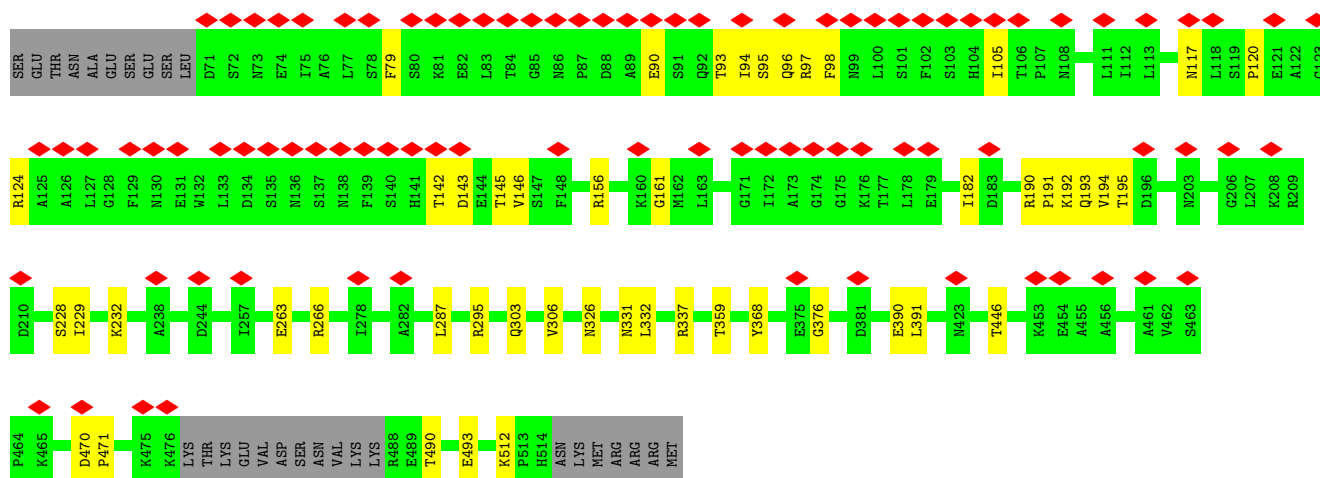
• Molecule 72: mL102 (rPPR5)



• Molecule 73: mL104 (rPPR9)







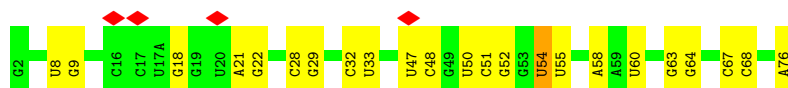
- Molecule 74: Nascent peptide

Chain 1x: 100%

There are no outlier residues recorded for this chain.

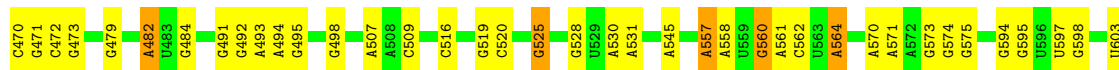
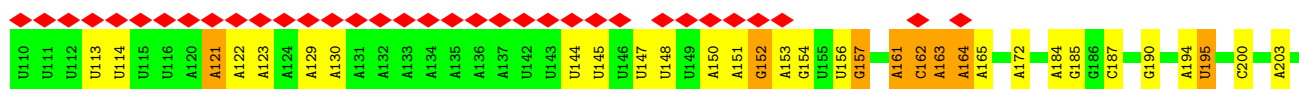
- Molecule 75: tRNA

Chain 5: 5% 70% 29%

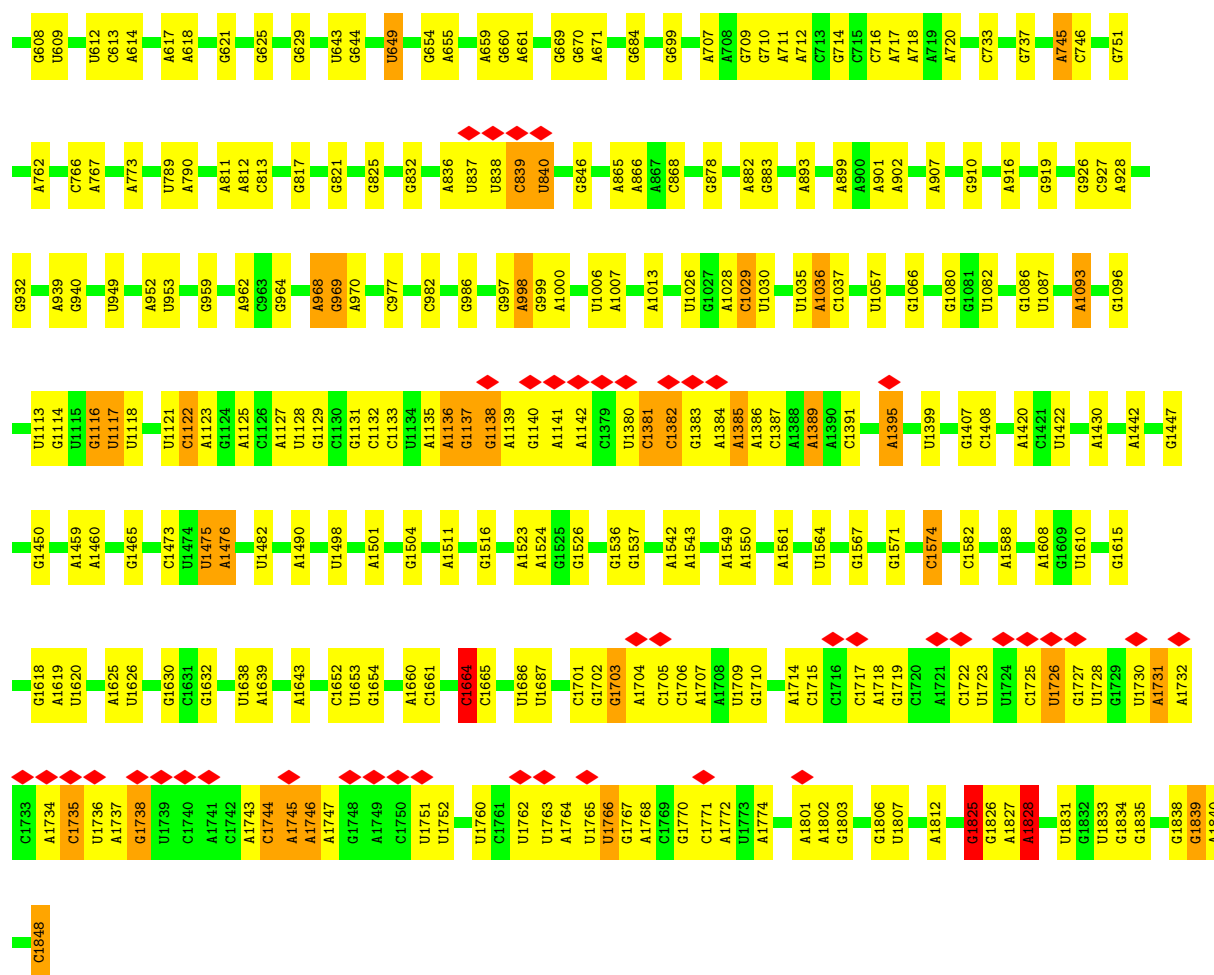


- Molecule 76: 18S rRNA

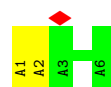
Chain 2: 7% 72% 25%



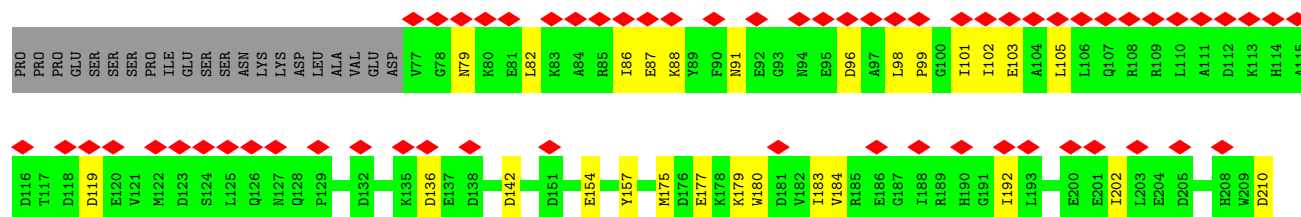
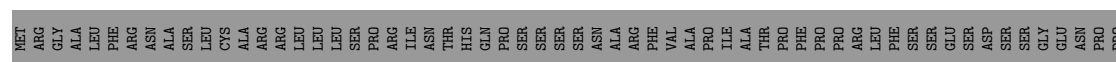




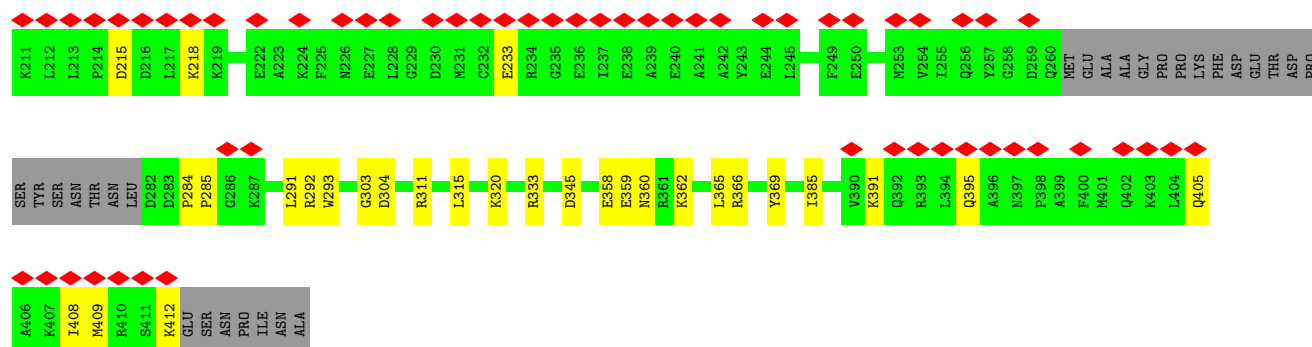
- Molecule 77: mRNA



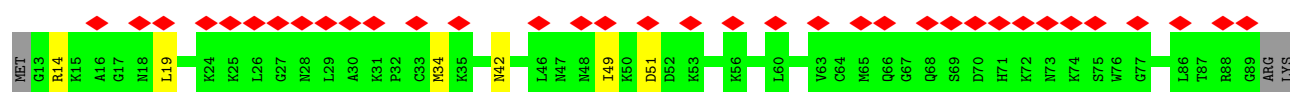
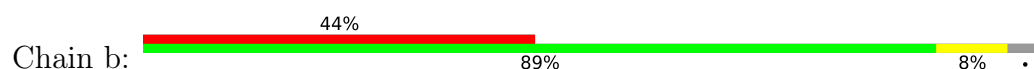
- Molecule 78: mS35



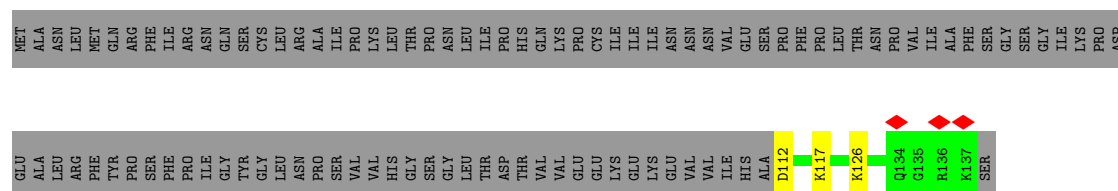




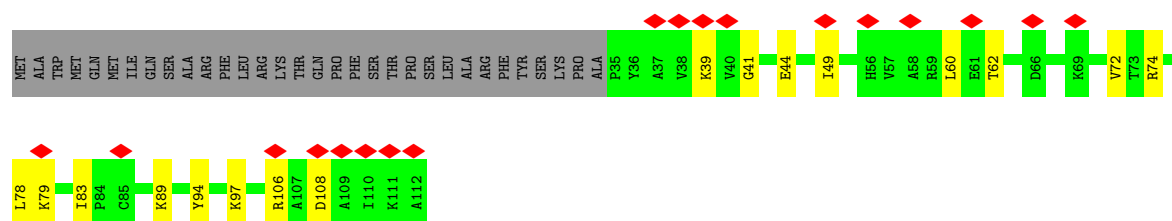
• Molecule 79: mS37



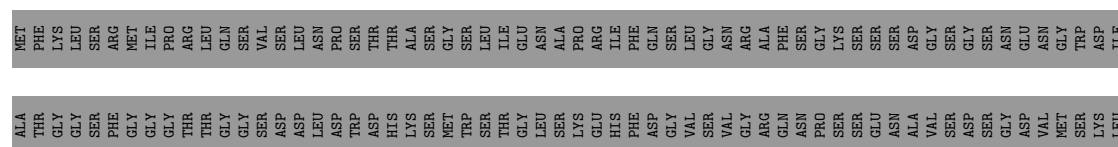
• Molecule 80: mS38



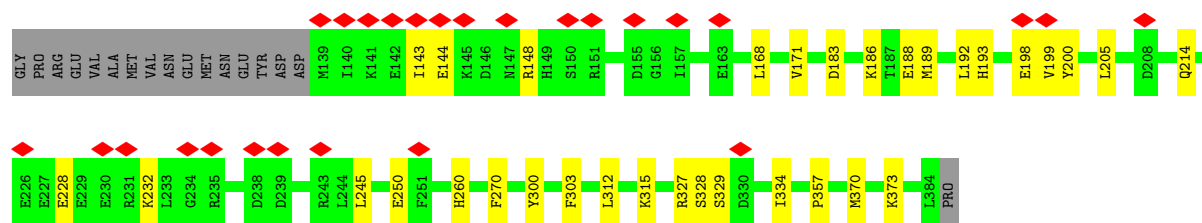
• Molecule 81: mS41



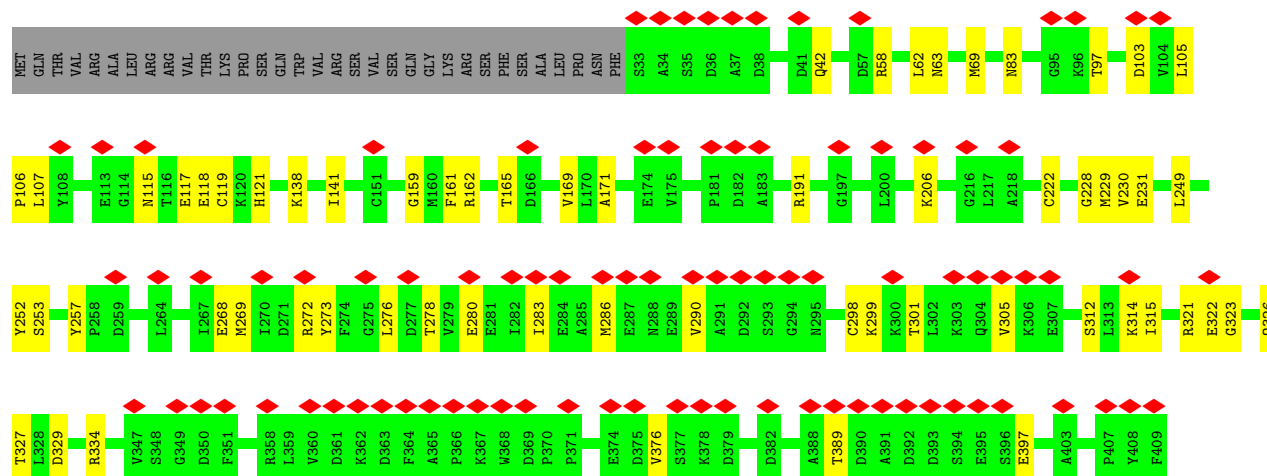
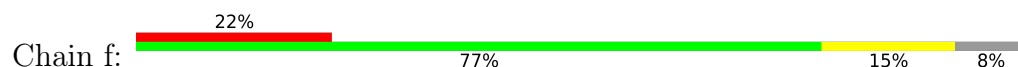
• Molecule 82: mS45



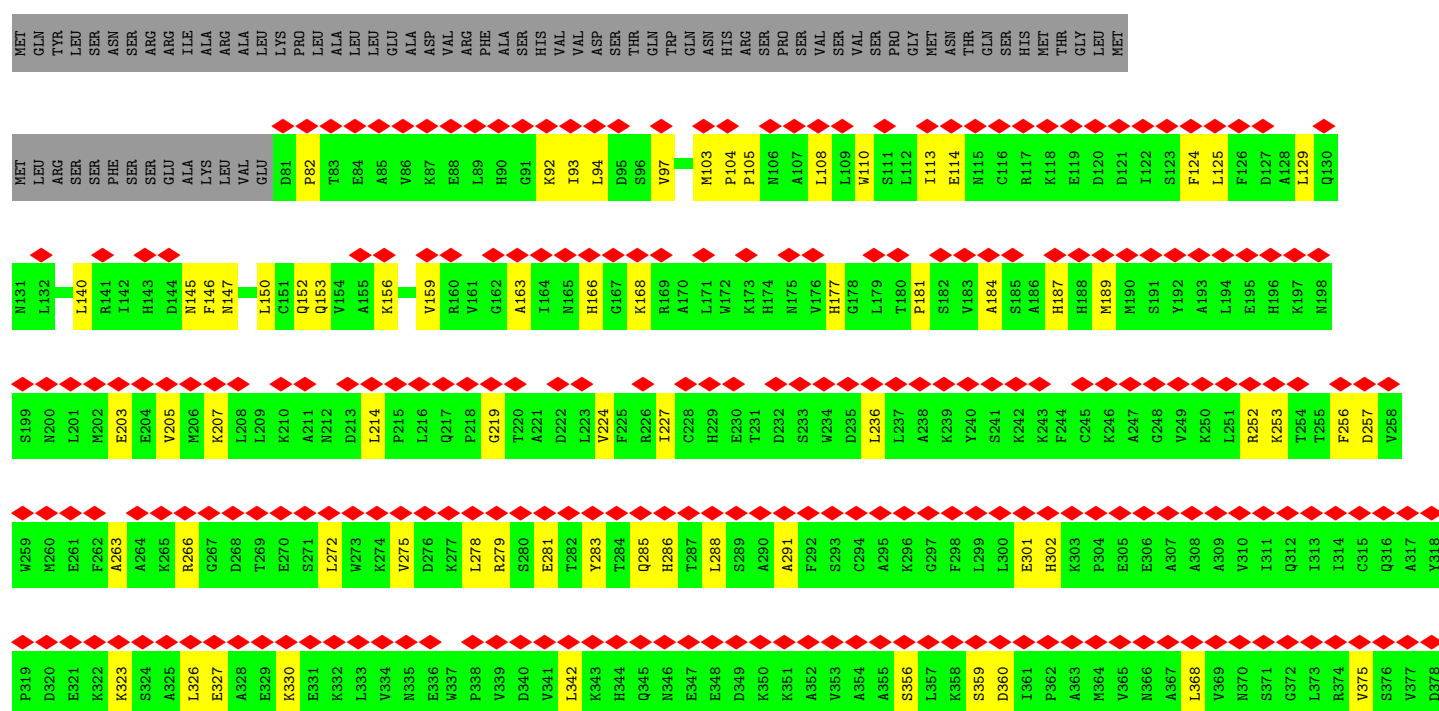




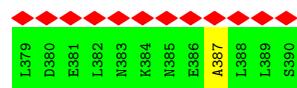
• Molecule 83: mS47



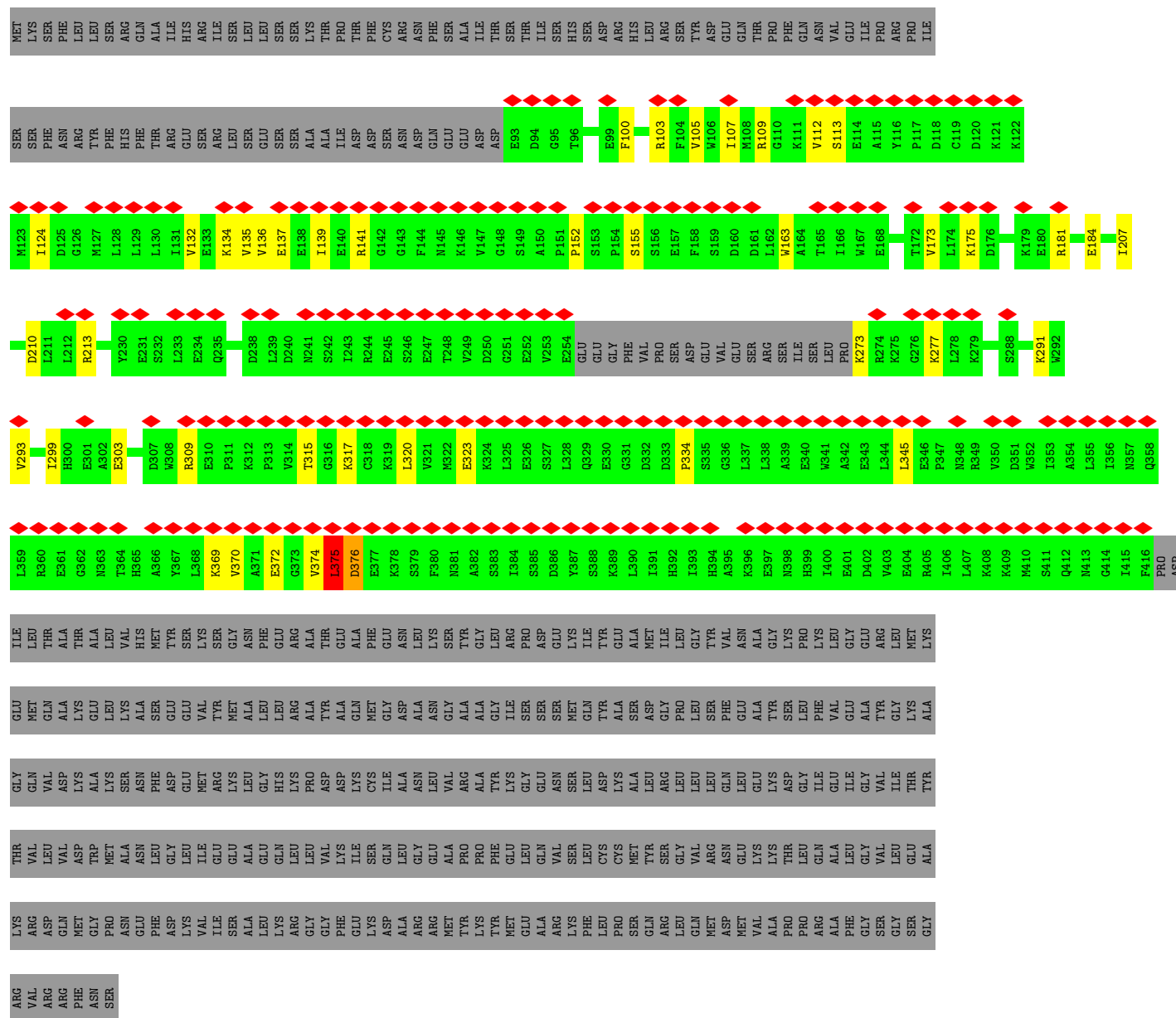
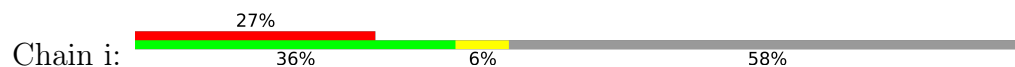
• Molecule 84: mS83 (rPPR10)



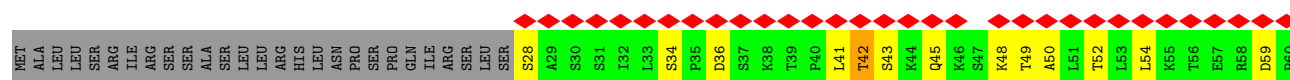




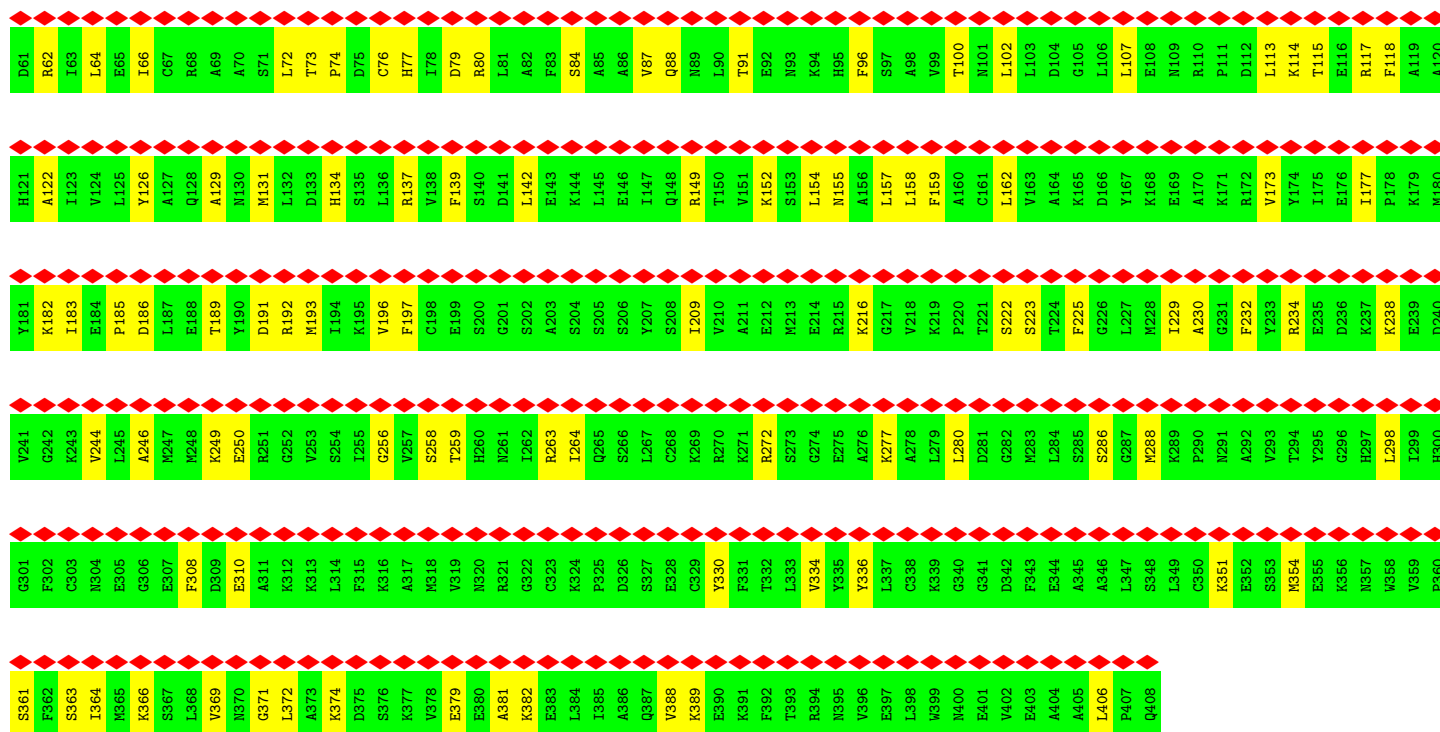
• Molecule 85: mS77 (NFD5)



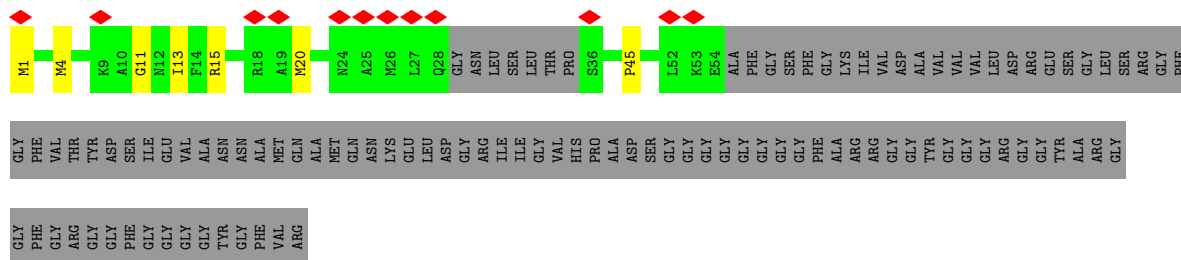
• Molecule 86: mS76 (rPPR1)



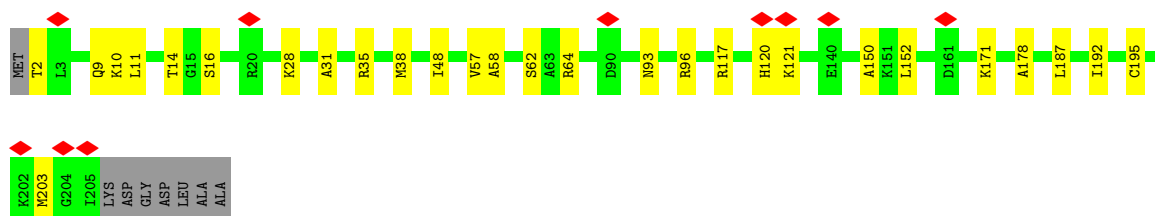
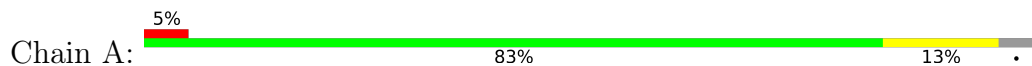




• Molecule 87: mS86



• Molecule 88: uS2m





## 4 Experimental information

| Property                             | Value                                   | Source    |
|--------------------------------------|---|-----------|
| EM reconstruction method             | SINGLE PARTICLE                         | Depositor |
| Imposed symmetry                     | POINT, Not provided                     |           |
| Number of particles used             | 34964                                   | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF                       | Depositor |
| CTF correction method                | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope                           | TFS KRIOS                               | Depositor |
| Voltage (kV)                         | 300                                     | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 45                                      | Depositor |
| Minimum defocus (nm)                 | 1000                                    | Depositor |
| Maximum defocus (nm)                 | 2500                                    | Depositor |
| Magnification                        | Not provided                            |           |
| Image detector                       | GATAN K2 QUANTUM (4k x 4k)              | Depositor |
| Maximum map value                    | 0.541                                   | Depositor |
| Minimum map value                    | -0.257                                  | Depositor |
| Average map value                    | -0.000                                  | Depositor |
| Map value standard deviation         | 0.019                                   | Depositor |
| Recommended contour level            | 0.0796                                  | Depositor |
| Map size (Å)                         | 596.712, 596.712, 596.712               | wwPDB     |
| Map dimensions                       | 564, 564, 564                           | wwPDB     |
| Map angles (°)                       | 90.0, 90.0, 90.0                        | wwPDB     |
| Pixel spacing (Å)                    | 1.058, 1.058, 1.058                     | Depositor |



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: K, 5MC, G7M, H2U, OMU, 2MA, PSU, OMG, 5MU, ZN, ATP, 4OC, 4SU, MA6, CLM, UR3, 2MG, OMC, MG

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   | B     | 0.26         | 0/3969        | 0.54        | 2/5320 (0.0%)   |
| 2   | C     | 0.27         | 0/2865        | 0.45        | 0/3836          |
| 3   | D     | 0.27         | 0/3474        | 0.46        | 0/4647          |
| 4   | E     | 0.27         | 0/838         | 0.41        | 0/1121          |
| 5   | F     | 0.27         | 0/1225        | 0.53        | 0/1641          |
| 6   | G     | 0.27         | 0/1054        | 0.44        | 0/1418          |
| 7   | H     | 0.37         | 1/1707 (0.1%) | 0.59        | 1/2287 (0.0%)   |
| 8   | I     | 0.27         | 0/964         | 0.46        | 0/1293          |
| 9   | J     | 0.38         | 0/1000        | 0.50        | 0/1340          |
| 10  | K     | 0.24         | 0/1009        | 0.39        | 0/1345          |
| 11  | L     | 0.32         | 0/950         | 0.52        | 0/1263          |
| 12  | M     | 0.44         | 0/856         | 0.52        | 0/1134          |
| 13  | N     | 0.26         | 0/958         | 0.41        | 0/1280          |
| 14  | O     | 0.30         | 0/890         | 0.50        | 0/1196          |
| 15  | P     | 0.28         | 0/730         | 0.48        | 1/984 (0.1%)    |
| 16  | Q     | 0.23         | 0/733         | 0.41        | 0/978           |
| 17  | R     | 0.24         | 0/1323        | 0.48        | 0/1772          |
| 18  | S     | 0.27         | 0/614         | 0.41        | 0/809           |
| 19  | T     | 0.28         | 0/416         | 0.40        | 0/547           |
| 20  | U     | 0.51         | 1/1036 (0.1%) | 0.90        | 8/1395 (0.6%)   |
| 21  | V     | 0.19         | 0/1423        | 0.39        | 0/1895          |
| 22  | W     | 0.22         | 0/3139        | 0.41        | 0/4250          |
| 23  | X     | 0.27         | 0/1644        | 0.53        | 0/2216          |
| 24  | Y     | 0.37         | 0/807         | 0.46        | 0/1077          |
| 25  | Z     | 0.18         | 0/669         | 0.39        | 0/900           |
| 26  | 1     | 0.35         | 0/69733       | 0.40        | 1/108691 (0.0%) |
| 27  | 3     | 0.31         | 0/2810        | 0.39        | 0/4378          |
| 28  | 1B    | 0.31         | 0/1347        | 0.43        | 0/1797          |
| 29  | 1C    | 0.38         | 0/1727        | 0.57        | 4/2311 (0.2%)   |
| 30  | 1D    | 0.32         | 0/2099        | 0.43        | 0/2836          |
| 31  | 1E    | 0.31         | 0/1786        | 0.41        | 0/2412          |



| Mol | Chain | Bond lengths |         | Bond angles |               |
|-----|-------|--------------|---------|-------------|---------------|
|     |       | RMSZ         | # Z  >5 | RMSZ        | # Z  >5       |
| 32  | 1F    | 0.26         | 0/1313  | 0.48        | 0/1772        |
| 33  | 1G    | 0.22         | 0/796   | 0.43        | 0/1067        |
| 34  | 1H    | 0.27         | 0/547   | 0.47        | 0/731         |
| 35  | 1I    | 0.24         | 0/1054  | 0.56        | 0/1417        |
| 36  | 1J    | 0.27         | 0/1155  | 0.61        | 1/1563 (0.1%) |
| 37  | 1K    | 0.29         | 0/1553  | 0.36        | 0/2080        |
| 38  | 1L    | 0.30         | 0/976   | 0.47        | 0/1304        |
| 39  | 1M    | 0.32         | 0/1682  | 0.46        | 2/2248 (0.1%) |
| 40  | 1N    | 0.28         | 0/1184  | 0.42        | 0/1580        |
| 41  | 1O    | 0.30         | 0/1255  | 0.43        | 0/1687        |
| 42  | 1P    | 0.28         | 0/895   | 0.47        | 0/1206        |
| 43  | 1Q    | 0.30         | 0/1022  | 0.39        | 0/1368        |
| 44  | 1R    | 0.37         | 0/930   | 0.41        | 0/1234        |
| 45  | 1S    | 0.31         | 0/1192  | 0.39        | 0/1602        |
| 46  | 1T    | 0.32         | 0/1259  | 0.41        | 0/1687        |
| 47  | 1U    | 0.28         | 0/1065  | 0.39        | 0/1421        |
| 48  | 1V    | 0.28         | 0/1247  | 0.37        | 0/1681        |
| 49  | 1W    | 0.24         | 0/1613  | 0.49        | 0/2180        |
| 50  | 1X    | 0.24         | 0/1703  | 0.41        | 0/2307        |
| 51  | 1Y    | 0.32         | 0/785   | 0.38        | 0/1051        |
| 52  | 1Z    | 0.31         | 0/1466  | 0.47        | 2/1954 (0.1%) |
| 53  | 1a    | 0.32         | 0/946   | 0.43        | 0/1262        |
| 54  | 1b    | 0.30         | 0/818   | 0.47        | 0/1099        |
| 55  | 1c    | 0.29         | 0/501   | 0.44        | 0/666         |
| 56  | 1d    | 0.44         | 0/387   | 0.63        | 1/514 (0.2%)  |
| 57  | 1e    | 0.33         | 0/468   | 0.39        | 0/618         |
| 58  | 1f    | 0.40         | 0/370   | 0.43        | 0/486         |
| 59  | 1g    | 0.37         | 0/789   | 0.45        | 0/1048        |
| 60  | 1h    | 0.29         | 0/312   | 0.38        | 0/409         |
| 61  | 1i    | 0.24         | 0/1440  | 0.38        | 0/1927        |
| 62  | 1j    | 0.35         | 0/586   | 0.41        | 0/789         |
| 63  | 1k    | 0.32         | 0/970   | 0.45        | 0/1309        |
| 64  | 1l    | 0.26         | 0/1792  | 0.45        | 0/2423        |
| 65  | 1m    | 0.23         | 0/987   | 0.48        | 0/1331        |
| 66  | 1o    | 0.17         | 0/637   | 0.43        | 0/860         |
| 67  | 1p    | 0.26         | 0/1014  | 0.39        | 0/1349        |
| 68  | 1q    | 0.31         | 0/394   | 0.40        | 0/527         |
| 69  | 1r    | 0.26         | 0/750   | 0.45        | 0/1005        |
| 70  | 1s    | 0.27         | 0/1001  | 0.41        | 0/1327        |
| 71  | 1t    | 0.26         | 0/3919  | 0.48        | 0/5272        |
| 72  | 1u    | 0.24         | 0/5345  | 0.51        | 0/7180        |
| 73  | 1v    | 0.25         | 0/3497  | 0.46        | 0/4681        |
| 74  | 1x    | 0.19         | 0/18    | 0.26        | 0/23          |



| Mol | Chain | Bond lengths |                 | Bond angles |                  |
|-----|-------|--------------|-----------------|-------------|------------------|
|     |       | RMSZ         | # Z  >5         | RMSZ        | # Z  >5          |
| 75  | 5     | 0.24         | 0/1725          | 0.33        | 0/2689           |
| 76  | 2     | 0.29         | 0/37992         | 0.37        | 0/59224          |
| 77  | 6     | 0.19         | 0/146           | 0.22        | 0/225            |
| 78  | a     | 0.25         | 0/2524          | 0.54        | 2/3387 (0.1%)    |
| 79  | b     | 0.29         | 0/618           | 0.68        | 0/822            |
| 80  | c     | 0.27         | 0/233           | 0.40        | 0/296            |
| 81  | d     | 0.26         | 0/628           | 0.47        | 0/840            |
| 82  | e     | 0.25         | 0/2118          | 0.48        | 0/2828           |
| 83  | f     | 0.25         | 0/2981          | 0.50        | 0/4033           |
| 84  | h     | 0.29         | 0/2507          | 0.54        | 0/3384           |
| 85  | i     | 0.24         | 0/2532          | 0.49        | 1/3400 (0.0%)    |
| 86  | j     | 0.24         | 0/3032          | 0.56        | 1/4073 (0.0%)    |
| 87  | k     | 0.25         | 0/317           | 0.58        | 1/424 (0.2%)     |
| 88  | A     | 0.25         | 0/1647          | 0.47        | 0/2227           |
| All | All   | 0.31         | 2/224428 (0.0%) | 0.43        | 28/325466 (0.0%) |

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

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 7   | H     | 0                   | 1                   |
| 11  | L     | 0                   | 1                   |
| 30  | 1D    | 0                   | 1                   |
| 71  | 1t    | 0                   | 1                   |
| All | All   | 0                   | 4                   |

All (2) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms  | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|--------|-------|-------------|----------|
| 7   | H     | 404 | LEU  | CG-CD2 | -5.93 | 1.32        | 1.52     |
| 20  | U     | 81  | PRO  | N-CD   | 5.13  | 1.54        | 1.47     |

The worst 5 of 28 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms   | Z      | Observed(°) | Ideal(°) |
|-----|-------|-----|------|---------|--------|-------------|----------|
| 20  | U     | 80  | ASP  | C-N-CD  | -14.93 | 63.78       | 125.00   |
| 20  | U     | 71  | PRO  | N-CA-C  | -9.97  | 99.67       | 113.53   |
| 20  | U     | 81  | PRO  | CA-N-CD | -9.66  | 98.47       | 112.00   |
| 36  | 1J    | 38  | PRO  | CA-N-CD | -9.01  | 99.39       | 112.00   |
| 20  | U     | 61  | ARG  | N-CA-C  | -8.98  | 101.90      | 113.12   |



There are no chirality outliers.

All (4) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group     |
|-----|-------|-----|------|-----------|
| 30  | 1D    | 225 | ASP  | Peptide   |
| 71  | 1t    | 462 | HIS  | Peptide   |
| 7   | H     | 225 | ILE  | Peptide   |
| 11  | L     | 136 | ARG  | Sidechain |

## 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   | B     | 3877  | 0        | 4008     | 100     | 0            |
| 2   | C     | 2811  | 0        | 2986     | 26      | 0            |
| 3   | D     | 3425  | 0        | 3453     | 28      | 0            |
| 4   | E     | 823   | 0        | 879      | 6       | 0            |
| 5   | F     | 1254  | 0        | 1268     | 14      | 0            |
| 6   | G     | 1037  | 0        | 1058     | 9       | 0            |
| 7   | H     | 1682  | 0        | 1726     | 27      | 0            |
| 8   | I     | 941   | 0        | 970      | 15      | 0            |
| 9   | J     | 988   | 0        | 1022     | 13      | 0            |
| 10  | K     | 992   | 0        | 1051     | 15      | 0            |
| 11  | L     | 940   | 0        | 989      | 9       | 0            |
| 12  | M     | 843   | 0        | 884      | 11      | 0            |
| 13  | N     | 941   | 0        | 978      | 4       | 0            |
| 14  | O     | 869   | 0        | 898      | 12      | 0            |
| 15  | P     | 717   | 0        | 755      | 10      | 0            |
| 16  | Q     | 724   | 0        | 744      | 10      | 0            |
| 17  | R     | 1299  | 0        | 1307     | 21      | 0            |
| 18  | S     | 611   | 0        | 687      | 7       | 0            |
| 19  | T     | 408   | 0        | 444      | 4       | 0            |
| 20  | U     | 1014  | 0        | 1061     | 62      | 0            |
| 21  | V     | 1399  | 0        | 1427     | 10      | 0            |
| 22  | W     | 3062  | 0        | 3030     | 23      | 0            |
| 23  | X     | 1613  | 0        | 1559     | 57      | 0            |
| 24  | Y     | 793   | 0        | 834      | 12      | 0            |
| 25  | Z     | 649   | 0        | 662      | 5       | 0            |
| 26  | 1     | 62518 | 0        | 31499    | 260     | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 27  | 3     | 2513  | 0        | 1275     | 4       | 0            |
| 28  | 1B    | 1325  | 0        | 1398     | 12      | 0            |
| 29  | 1C    | 1696  | 0        | 1745     | 51      | 0            |
| 30  | 1D    | 2045  | 0        | 2080     | 18      | 0            |
| 31  | 1E    | 1753  | 0        | 1815     | 19      | 0            |
| 32  | 1F    | 1286  | 0        | 1280     | 10      | 0            |
| 33  | 1G    | 779   | 0        | 810      | 5       | 0            |
| 34  | 1H    | 539   | 0        | 574      | 22      | 0            |
| 35  | 1I    | 1036  | 0        | 1084     | 40      | 0            |
| 36  | 1J    | 1129  | 0        | 1166     | 52      | 0            |
| 37  | 1K    | 1526  | 0        | 1586     | 8       | 0            |
| 38  | 1L    | 966   | 0        | 1048     | 6       | 0            |
| 39  | 1M    | 1649  | 0        | 1765     | 10      | 0            |
| 40  | 1N    | 1160  | 0        | 1206     | 6       | 0            |
| 41  | 1O    | 1231  | 0        | 1262     | 7       | 0            |
| 42  | 1P    | 878   | 0        | 939      | 3       | 0            |
| 43  | 1Q    | 1008  | 0        | 1101     | 5       | 0            |
| 44  | 1R    | 915   | 0        | 946      | 6       | 0            |
| 45  | 1S    | 1170  | 0        | 1226     | 3       | 0            |
| 46  | 1T    | 1241  | 0        | 1346     | 5       | 0            |
| 47  | 1U    | 1048  | 0        | 1123     | 14      | 0            |
| 48  | 1V    | 1223  | 0        | 1278     | 12      | 0            |
| 49  | 1W    | 1588  | 0        | 1663     | 23      | 0            |
| 50  | 1X    | 1670  | 0        | 1751     | 10      | 0            |
| 51  | 1Y    | 768   | 0        | 792      | 7       | 0            |
| 52  | 1Z    | 1441  | 0        | 1485     | 17      | 0            |
| 53  | 1a    | 928   | 0        | 959      | 9       | 0            |
| 54  | 1b    | 803   | 0        | 845      | 12      | 0            |
| 55  | 1c    | 489   | 0        | 511      | 10      | 0            |
| 56  | 1d    | 379   | 0        | 416      | 1       | 0            |
| 57  | 1e    | 459   | 0        | 491      | 1       | 0            |
| 58  | 1f    | 364   | 0        | 398      | 1       | 0            |
| 59  | 1g    | 770   | 0        | 841      | 6       | 0            |
| 60  | 1h    | 309   | 0        | 337      | 0       | 0            |
| 61  | 1i    | 1424  | 0        | 1482     | 16      | 0            |
| 62  | 1j    | 570   | 0        | 593      | 9       | 0            |
| 63  | 1k    | 952   | 0        | 987      | 5       | 0            |
| 64  | 1l    | 1741  | 0        | 1707     | 19      | 0            |
| 65  | 1m    | 970   | 0        | 979      | 8       | 0            |
| 66  | 1o    | 626   | 0        | 657      | 11      | 0            |
| 67  | 1p    | 992   | 0        | 1027     | 8       | 0            |
| 68  | 1q    | 390   | 0        | 421      | 2       | 0            |

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| Mol | Chain | Non-H  | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 69  | 1r    | 735    | 0        | 781      | 16      | 0            |
| 70  | 1s    | 985    | 0        | 1072     | 8       | 0            |
| 71  | 1t    | 3856   | 0        | 3912     | 37      | 0            |
| 72  | 1u    | 5264   | 0        | 5353     | 74      | 0            |
| 73  | 1v    | 3440   | 0        | 3497     | 29      | 0            |
| 74  | 1x    | 19     | 0        | 14       | 0       | 0            |
| 75  | 5     | 1625   | 0        | 828      | 5       | 0            |
| 76  | 2     | 34081  | 0        | 17178    | 192     | 0            |
| 77  | 6     | 130    | 0        | 66       | 1       | 0            |
| 78  | a     | 2487   | 0        | 2382     | 69      | 0            |
| 79  | b     | 610    | 0        | 626      | 6       | 0            |
| 80  | c     | 232    | 0        | 278      | 3       | 0            |
| 81  | d     | 616    | 0        | 674      | 11      | 0            |
| 82  | e     | 2074   | 0        | 2074     | 24      | 0            |
| 83  | f     | 2922   | 0        | 2868     | 73      | 0            |
| 84  | h     | 2460   | 0        | 2478     | 73      | 0            |
| 85  | i     | 2487   | 0        | 2450     | 39      | 0            |
| 86  | j     | 2984   | 0        | 3044     | 84      | 0            |
| 87  | k     | 314    | 0        | 261      | 12      | 0            |
| 88  | A     | 1611   | 0        | 1633     | 22      | 0            |
| 89  | 1     | 249    | 0        | 0        | 0       | 0            |
| 89  | 1D    | 1      | 0        | 0        | 0       | 0            |
| 89  | 1h    | 1      | 0        | 0        | 0       | 0            |
| 89  | 1j    | 1      | 0        | 0        | 0       | 0            |
| 89  | 1q    | 2      | 0        | 0        | 0       | 0            |
| 89  | 2     | 98     | 0        | 0        | 0       | 0            |
| 89  | 3     | 3      | 0        | 0        | 0       | 0            |
| 89  | T     | 1      | 0        | 0        | 0       | 0            |
| 89  | W     | 1      | 0        | 0        | 0       | 0            |
| 90  | W     | 31     | 0        | 12       | 0       | 0            |
| 91  | 1     | 20     | 0        | 11       | 0       | 0            |
| 92  | 1     | 56     | 0        | 0        | 0       | 0            |
| 92  | 1B    | 3      | 0        | 0        | 0       | 0            |
| 92  | 1E    | 1      | 0        | 0        | 0       | 0            |
| 92  | 2     | 14     | 0        | 0        | 0       | 0            |
| 93  | 1d    | 1      | 0        | 0        | 0       | 0            |
| 93  | 1h    | 1      | 0        | 0        | 0       | 0            |
| All | All   | 211395 | 0        | 164066   | 1717    | 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 5.

The worst 5 of 1717 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) |
|-------------------|-------------------|--------------------------|-------------------|
| 75:5:54:5MU:C4    | 75:5:54:5MU:C5    | 1.82                     | 1.65              |
| 36:1J:42:ASN:HB2  | 36:1J:73:HIS:CE1  | 1.37                     | 1.60              |
| 29:1C:227:ARG:NH2 | 29:1C:229:HIS:HB2 | 1.21                     | 1.44              |
| 36:1J:42:ASN:HB2  | 36:1J:73:HIS:NE2  | 1.33                     | 1.41              |
| 29:1C:199:VAL:CG1 | 34:1H:97:ARG:HD2  | 1.53                     | 1.39              |

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

| Mol | Chain | Analysed      | Favoured  | Allowed | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 1   | B     | 457/554 (82%) | 425 (93%) | 31 (7%) | 1 (0%)   | 44          | 71  |
| 2   | C     | 329/362 (91%) | 317 (96%) | 12 (4%) | 0        | 100         | 100 |
| 3   | D     | 413/501 (82%) | 397 (96%) | 15 (4%) | 1 (0%)   | 44          | 71  |
| 4   | E     | 99/138 (72%)  | 96 (97%)  | 3 (3%)  | 0        | 100         | 100 |
| 5   | F     | 146/157 (93%) | 140 (96%) | 6 (4%)  | 0        | 100         | 100 |
| 6   | G     | 126/129 (98%) | 122 (97%) | 4 (3%)  | 0        | 100         | 100 |
| 7   | H     | 209/383 (55%) | 197 (94%) | 11 (5%) | 1 (0%)   | 25          | 54  |
| 8   | I     | 111/228 (49%) | 107 (96%) | 4 (4%)  | 0        | 100         | 100 |
| 9   | J     | 125/304 (41%) | 121 (97%) | 4 (3%)  | 0        | 100         | 100 |
| 10  | K     | 122/125 (98%) | 118 (97%) | 4 (3%)  | 0        | 100         | 100 |
| 11  | L     | 117/154 (76%) | 110 (94%) | 7 (6%)  | 0        | 100         | 100 |
| 12  | M     | 99/155 (64%)  | 96 (97%)  | 3 (3%)  | 0        | 100         | 100 |
| 13  | N     | 114/414 (28%) | 113 (99%) | 1 (1%)  | 0        | 100         | 100 |
| 14  | O     | 108/136 (79%) | 104 (96%) | 4 (4%)  | 0        | 100         | 100 |
| 15  | P     | 89/110 (81%)  | 84 (94%)  | 4 (4%)  | 1 (1%)   | 12          | 35  |
| 16  | Q     | 88/237 (37%)  | 87 (99%)  | 1 (1%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Favoured  | Allowed | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 17  | R     | 162/212 (76%) | 152 (94%) | 10 (6%) | 0        | 100         | 100 |
| 18  | S     | 73/100 (73%)  | 72 (99%)  | 1 (1%)  | 0        | 100         | 100 |
| 19  | T     | 48/94 (51%)   | 44 (92%)  | 4 (8%)  | 0        | 100         | 100 |
| 20  | U     | 125/192 (65%) | 109 (87%) | 9 (7%)  | 7 (6%)   | 1           | 7   |
| 21  | V     | 162/193 (84%) | 160 (99%) | 2 (1%)  | 0        | 100         | 100 |
| 22  | W     | 376/483 (78%) | 368 (98%) | 8 (2%)  | 0        | 100         | 100 |
| 23  | X     | 202/496 (41%) | 191 (95%) | 8 (4%)  | 3 (2%)   | 8           | 29  |
| 24  | Y     | 96/102 (94%)  | 95 (99%)  | 1 (1%)  | 0        | 100         | 100 |
| 25  | Z     | 78/153 (51%)  | 74 (95%)  | 4 (5%)  | 0        | 100         | 100 |
| 28  | 1B    | 175/220 (80%) | 171 (98%) | 4 (2%)  | 0        | 100         | 100 |
| 29  | 1C    | 203/327 (62%) | 194 (96%) | 7 (3%)  | 2 (1%)   | 13          | 38  |
| 30  | 1D    | 262/319 (82%) | 257 (98%) | 5 (2%)  | 0        | 100         | 100 |
| 31  | 1E    | 219/297 (74%) | 217 (99%) | 2 (1%)  | 0        | 100         | 100 |
| 32  | 1F    | 154/185 (83%) | 148 (96%) | 6 (4%)  | 0        | 100         | 100 |
| 33  | 1G    | 96/102 (94%)  | 95 (99%)  | 1 (1%)  | 0        | 100         | 100 |
| 34  | 1H    | 64/219 (29%)  | 63 (98%)  | 1 (2%)  | 0        | 100         | 100 |
| 35  | 1I    | 128/170 (75%) | 119 (93%) | 8 (6%)  | 1 (1%)   | 16          | 43  |
| 36  | 1J    | 145/156 (93%) | 132 (91%) | 11 (8%) | 2 (1%)   | 9           | 30  |
| 37  | 1K    | 187/204 (92%) | 184 (98%) | 3 (2%)  | 0        | 100         | 100 |
| 38  | 1L    | 125/176 (71%) | 119 (95%) | 6 (5%)  | 0        | 100         | 100 |
| 39  | 1M    | 208/281 (74%) | 195 (94%) | 13 (6%) | 0        | 100         | 100 |
| 40  | 1N    | 146/179 (82%) | 143 (98%) | 3 (2%)  | 0        | 100         | 100 |
| 41  | 1O    | 149/160 (93%) | 141 (95%) | 8 (5%)  | 0        | 100         | 100 |
| 42  | 1P    | 111/114 (97%) | 102 (92%) | 9 (8%)  | 0        | 100         | 100 |
| 43  | 1Q    | 120/233 (52%) | 116 (97%) | 4 (3%)  | 0        | 100         | 100 |
| 44  | 1R    | 108/126 (86%) | 107 (99%) | 1 (1%)  | 0        | 100         | 100 |
| 45  | 1S    | 143/270 (53%) | 139 (97%) | 4 (3%)  | 0        | 100         | 100 |
| 46  | 1T    | 153/264 (58%) | 148 (97%) | 5 (3%)  | 0        | 100         | 100 |
| 47  | 1U    | 126/180 (70%) | 120 (95%) | 6 (5%)  | 0        | 100         | 100 |
| 48  | 1V    | 156/159 (98%) | 152 (97%) | 4 (3%)  | 0        | 100         | 100 |
| 49  | 1W    | 203/249 (82%) | 192 (95%) | 11 (5%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Favoured  | Allowed | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 50  | 1X    | 214/271 (79%) | 209 (98%) | 5 (2%)  | 0        | 100         | 100 |
| 51  | 1Y    | 96/156 (62%)  | 94 (98%)  | 2 (2%)  | 0        | 100         | 100 |
| 52  | 1Z    | 175/212 (82%) | 174 (99%) | 1 (1%)  | 0        | 100         | 100 |
| 53  | 1a    | 106/144 (74%) | 104 (98%) | 2 (2%)  | 0        | 100         | 100 |
| 54  | 1b    | 98/109 (90%)  | 94 (96%)  | 4 (4%)  | 0        | 100         | 100 |
| 55  | 1c    | 57/135 (42%)  | 54 (95%)  | 3 (5%)  | 0        | 100         | 100 |
| 56  | 1d    | 47/139 (34%)  | 47 (100%) | 0       | 0        | 100         | 100 |
| 57  | 1e    | 52/63 (82%)   | 51 (98%)  | 1 (2%)  | 0        | 100         | 100 |
| 58  | 1f    | 42/146 (29%)  | 42 (100%) | 0       | 0        | 100         | 100 |
| 59  | 1g    | 89/162 (55%)  | 89 (100%) | 0       | 0        | 100         | 100 |
| 60  | 1h    | 36/103 (35%)  | 34 (94%)  | 2 (6%)  | 0        | 100         | 100 |
| 61  | 1i    | 181/247 (73%) | 176 (97%) | 5 (3%)  | 0        | 100         | 100 |
| 62  | 1j    | 69/90 (77%)   | 68 (99%)  | 1 (1%)  | 0        | 100         | 100 |
| 63  | 1k    | 116/119 (98%) | 111 (96%) | 5 (4%)  | 0        | 100         | 100 |
| 64  | 1l    | 209/233 (90%) | 198 (95%) | 11 (5%) | 0        | 100         | 100 |
| 65  | 1m    | 120/128 (94%) | 119 (99%) | 1 (1%)  | 0        | 100         | 100 |
| 66  | 1o    | 74/125 (59%)  | 70 (95%)  | 4 (5%)  | 0        | 100         | 100 |
| 67  | 1p    | 115/130 (88%) | 112 (97%) | 3 (3%)  | 0        | 100         | 100 |
| 68  | 1q    | 48/79 (61%)   | 47 (98%)  | 0       | 1 (2%)   | 5           | 21  |
| 69  | 1r    | 90/167 (54%)  | 84 (93%)  | 6 (7%)  | 0        | 100         | 100 |
| 70  | 1s    | 116/181 (64%) | 113 (97%) | 3 (3%)  | 0        | 100         | 100 |
| 71  | 1t    | 482/491 (98%) | 468 (97%) | 14 (3%) | 0        | 100         | 100 |
| 72  | 1u    | 664/757 (88%) | 624 (94%) | 40 (6%) | 0        | 100         | 100 |
| 73  | 1v    | 429/521 (82%) | 412 (96%) | 17 (4%) | 0        | 100         | 100 |
| 74  | 1x    | 2/4 (50%)     | 2 (100%)  | 0       | 0        | 100         | 100 |
| 78  | a     | 311/424 (73%) | 305 (98%) | 6 (2%)  | 0        | 100         | 100 |
| 79  | b     | 75/80 (94%)   | 68 (91%)  | 7 (9%)  | 0        | 100         | 100 |
| 80  | c     | 24/128 (19%)  | 23 (96%)  | 1 (4%)  | 0        | 100         | 100 |
| 81  | d     | 76/110 (69%)  | 74 (97%)  | 2 (3%)  | 0        | 100         | 100 |
| 82  | e     | 244/383 (64%) | 236 (97%) | 8 (3%)  | 0        | 100         | 100 |
| 83  | f     | 375/410 (92%) | 361 (96%) | 14 (4%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed          | Favoured    | Allowed  | Outliers | Percentiles |     |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 84  | h     | 308/384 (80%)     | 301 (98%)   | 7 (2%)   | 0        | 100         | 100 |
| 85  | i     | 302/725 (42%)     | 290 (96%)   | 10 (3%)  | 2 (1%)   | 19          | 46  |
| 86  | j     | 379/408 (93%)     | 365 (96%)   | 14 (4%)  | 0        | 100         | 100 |
| 87  | k     | 43/155 (28%)      | 37 (86%)    | 6 (14%)  | 0        | 100         | 100 |
| 88  | A     | 202/212 (95%)     | 196 (97%)   | 6 (3%)   | 0        | 100         | 100 |
| All | All   | 13521/19033 (71%) | 13005 (96%) | 494 (4%) | 22 (0%)  | 45          | 71  |

5 of 22 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 7   | H     | 225 | ILE  |
| 20  | U     | 64  | PRO  |
| 20  | U     | 81  | PRO  |
| 29  | 1C    | 227 | ARG  |
| 35  | 1I    | 133 | PRO  |

### 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   | B     | 421/492 (86%)  | 421 (100%) | 0        | 100         | 100 |
| 2   | C     | 314/343 (92%)  | 314 (100%) | 0        | 100         | 100 |
| 3   | D     | 370/444 (83%)  | 370 (100%) | 0        | 100         | 100 |
| 4   | E     | 90/126 (71%)   | 90 (100%)  | 0        | 100         | 100 |
| 5   | F     | 124/124 (100%) | 124 (100%) | 0        | 100         | 100 |
| 6   | G     | 112/113 (99%)  | 112 (100%) | 0        | 100         | 100 |
| 7   | H     | 176/320 (55%)  | 175 (99%)  | 1 (1%)   | 84          | 90  |
| 8   | I     | 104/197 (53%)  | 104 (100%) | 0        | 100         | 100 |
| 9   | J     | 108/256 (42%)  | 107 (99%)  | 1 (1%)   | 75          | 86  |
| 10  | K     | 107/108 (99%)  | 107 (100%) | 0        | 100         | 100 |
| 11  | L     | 99/128 (77%)   | 99 (100%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Rotameric  | Outliers | Percentiles |     |
|-----|-------|---------------|------------|----------|-------------|-----|
| 12  | M     | 90/137 (66%)  | 90 (100%)  | 0        | 100         | 100 |
| 13  | N     | 107/362 (30%) | 107 (100%) | 0        | 100         | 100 |
| 14  | O     | 93/117 (80%)  | 93 (100%)  | 0        | 100         | 100 |
| 15  | P     | 78/95 (82%)   | 78 (100%)  | 0        | 100         | 100 |
| 16  | Q     | 75/203 (37%)  | 75 (100%)  | 0        | 100         | 100 |
| 17  | R     | 141/180 (78%) | 141 (100%) | 0        | 100         | 100 |
| 18  | S     | 68/90 (76%)   | 68 (100%)  | 0        | 100         | 100 |
| 19  | T     | 44/79 (56%)   | 44 (100%)  | 0        | 100         | 100 |
| 20  | U     | 109/170 (64%) | 104 (95%)  | 5 (5%)   | 23          | 49  |
| 21  | V     | 147/173 (85%) | 147 (100%) | 0        | 100         | 100 |
| 22  | W     | 328/410 (80%) | 328 (100%) | 0        | 100         | 100 |
| 23  | X     | 174/395 (44%) | 174 (100%) | 0        | 100         | 100 |
| 24  | Y     | 84/86 (98%)   | 84 (100%)  | 0        | 100         | 100 |
| 25  | Z     | 65/119 (55%)  | 65 (100%)  | 0        | 100         | 100 |
| 28  | 1B    | 141/176 (80%) | 141 (100%) | 0        | 100         | 100 |
| 29  | 1C    | 184/268 (69%) | 183 (100%) | 1 (0%)   | 86          | 91  |
| 30  | 1D    | 216/264 (82%) | 216 (100%) | 0        | 100         | 100 |
| 31  | 1E    | 192/257 (75%) | 192 (100%) | 0        | 100         | 100 |
| 32  | 1F    | 145/168 (86%) | 145 (100%) | 0        | 100         | 100 |
| 33  | 1G    | 82/86 (95%)   | 82 (100%)  | 0        | 100         | 100 |
| 34  | 1H    | 58/195 (30%)  | 58 (100%)  | 0        | 100         | 100 |
| 35  | 1I    | 113/143 (79%) | 113 (100%) | 0        | 100         | 100 |
| 36  | 1J    | 125/131 (95%) | 125 (100%) | 0        | 100         | 100 |
| 37  | 1K    | 161/170 (95%) | 161 (100%) | 0        | 100         | 100 |
| 38  | 1L    | 103/140 (74%) | 103 (100%) | 0        | 100         | 100 |
| 39  | 1M    | 169/235 (72%) | 169 (100%) | 0        | 100         | 100 |
| 40  | 1N    | 116/146 (80%) | 116 (100%) | 0        | 100         | 100 |
| 41  | 1O    | 129/139 (93%) | 129 (100%) | 0        | 100         | 100 |
| 42  | 1P    | 94/95 (99%)   | 94 (100%)  | 0        | 100         | 100 |
| 43  | 1Q    | 110/208 (53%) | 110 (100%) | 0        | 100         | 100 |
| 44  | 1R    | 96/110 (87%)  | 96 (100%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Rotameric  | Outliers | Percentiles |     |
|-----|-------|---------------|------------|----------|-------------|-----|
| 45  | 1S    | 130/244 (53%) | 130 (100%) | 0        | 100         | 100 |
| 46  | 1T    | 133/229 (58%) | 133 (100%) | 0        | 100         | 100 |
| 47  | 1U    | 114/147 (78%) | 114 (100%) | 0        | 100         | 100 |
| 48  | 1V    | 132/133 (99%) | 132 (100%) | 0        | 100         | 100 |
| 49  | 1W    | 181/216 (84%) | 181 (100%) | 0        | 100         | 100 |
| 50  | 1X    | 186/235 (79%) | 186 (100%) | 0        | 100         | 100 |
| 51  | 1Y    | 80/127 (63%)  | 80 (100%)  | 0        | 100         | 100 |
| 52  | 1Z    | 150/173 (87%) | 150 (100%) | 0        | 100         | 100 |
| 53  | 1a    | 102/128 (80%) | 102 (100%) | 0        | 100         | 100 |
| 54  | 1b    | 88/95 (93%)   | 88 (100%)  | 0        | 100         | 100 |
| 55  | 1c    | 51/119 (43%)  | 51 (100%)  | 0        | 100         | 100 |
| 56  | 1d    | 42/119 (35%)  | 42 (100%)  | 0        | 100         | 100 |
| 57  | 1e    | 49/57 (86%)   | 49 (100%)  | 0        | 100         | 100 |
| 58  | 1f    | 35/129 (27%)  | 35 (100%)  | 0        | 100         | 100 |
| 59  | 1g    | 84/152 (55%)  | 84 (100%)  | 0        | 100         | 100 |
| 60  | 1h    | 36/87 (41%)   | 36 (100%)  | 0        | 100         | 100 |
| 61  | 1i    | 152/203 (75%) | 152 (100%) | 0        | 100         | 100 |
| 62  | 1j    | 64/79 (81%)   | 64 (100%)  | 0        | 100         | 100 |
| 63  | 1k    | 105/106 (99%) | 105 (100%) | 0        | 100         | 100 |
| 64  | 1l    | 189/209 (90%) | 189 (100%) | 0        | 100         | 100 |
| 65  | 1m    | 107/112 (96%) | 107 (100%) | 0        | 100         | 100 |
| 66  | 1o    | 71/105 (68%)  | 71 (100%)  | 0        | 100         | 100 |
| 67  | 1p    | 101/108 (94%) | 101 (100%) | 0        | 100         | 100 |
| 68  | 1q    | 41/65 (63%)   | 41 (100%)  | 0        | 100         | 100 |
| 69  | 1r    | 83/138 (60%)  | 82 (99%)   | 1 (1%)   | 67          | 82  |
| 70  | 1s    | 103/155 (66%) | 103 (100%) | 0        | 100         | 100 |
| 71  | 1t    | 417/423 (99%) | 417 (100%) | 0        | 100         | 100 |
| 72  | 1u    | 578/663 (87%) | 578 (100%) | 0        | 100         | 100 |
| 73  | 1v    | 374/461 (81%) | 374 (100%) | 0        | 100         | 100 |
| 78  | a     | 252/374 (67%) | 252 (100%) | 0        | 100         | 100 |
| 79  | b     | 68/71 (96%)   | 68 (100%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed          | Rotameric    | Outliers | Percentiles |     |
|-----|-------|-------------------|--------------|----------|-------------|-----|
| 80  | c     | 25/116 (22%)      | 25 (100%)    | 0        | 100         | 100 |
| 81  | d     | 65/93 (70%)       | 65 (100%)    | 0        | 100         | 100 |
| 82  | e     | 226/339 (67%)     | 226 (100%)   | 0        | 100         | 100 |
| 83  | f     | 321/351 (92%)     | 321 (100%)   | 0        | 100         | 100 |
| 84  | h     | 271/337 (80%)     | 271 (100%)   | 0        | 100         | 100 |
| 85  | i     | 272/629 (43%)     | 271 (100%)   | 1 (0%)   | 89          | 93  |
| 86  | j     | 330/355 (93%)     | 330 (100%)   | 0        | 100         | 100 |
| 87  | k     | 22/106 (21%)      | 22 (100%)    | 0        | 100         | 100 |
| 88  | A     | 177/182 (97%)     | 177 (100%)   | 0        | 100         | 100 |
| All | All   | 11869/16368 (72%) | 11859 (100%) | 10 (0%)  | 92          | 96  |

5 of 10 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 29  | 1C    | 227 | ARG  |
| 69  | 1r    | 68  | HIS  |
| 85  | i     | 375 | LEU  |
| 20  | U     | 65  | GLU  |
| 20  | U     | 69  | VAL  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 65  | 1m    | 13  | ASN  |
| 73  | 1v    | 330 | ASN  |
| 68  | 1q    | 49  | GLN  |
| 72  | 1u    | 83  | ASN  |
| 78  | a     | 397 | ASN  |

### 5.3.3 RNA [i](#)

| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 26  | 1     | 2910/2922 (99%) | 539 (18%)         | 28 (0%)         |
| 27  | 3     | 117/118 (99%)   | 24 (20%)          | 1 (0%)          |
| 75  | 5     | 75/76 (98%)     | 12 (16%)          | 0               |
| 76  | 2     | 1583/1591 (99%) | 267 (16%)         | 11 (0%)         |
| 77  | 6     | 5/6 (83%)       | 0                 | 0               |

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| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| All | All   | 4690/4713 (99%) | 842 (17%)         | 40 (0%)         |

5 of 842 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 26  | 1     | 49  | G    |
| 26  | 1     | 50  | G    |
| 26  | 1     | 51  | A    |
| 26  | 1     | 54  | G    |
| 26  | 1     | 63  | A    |

5 of 40 RNA pucker outliers are listed below:

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 27  | 3     | 12   | U    |
| 76  | 2     | 1701 | C    |
| 76  | 2     | 103  | A    |
| 76  | 2     | 493  | A    |
| 76  | 2     | 1706 | C    |

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

21 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$ |
| 26  | 2MA  | 1     | 2808 | 26,89 | 19,25,26     | 3.40 | 6 (31%)     | 21,37,40    | 2.31 | 4 (19%)     |
| 76  | MA6  | 2     | 1827 | 76    | 18,26,27     | 1.30 | 2 (11%)     | 19,38,41    | 3.60 | 3 (15%)     |
| 26  | OMU  | 1     | 2857 | 26,89 | 19,22,23     | 2.97 | 8 (42%)     | 26,31,34    | 1.72 | 4 (15%)     |
| 26  | PSU  | 1     | 2910 | 26    | 18,21,22     | 1.00 | 2 (11%)     | 22,30,33    | 1.70 | 2 (9%)      |
| 26  | OMC  | 1     | 2803 | 26,89 | 19,22,23     | 2.73 | 7 (36%)     | 26,31,34    | 0.98 | 1 (3%)      |
| 76  | 4OC  | 2     | 1664 | 76    | 20,23,24     | 3.16 | 8 (40%)     | 26,32,35    | 0.88 | 1 (3%)      |
| 26  | PSU  | 1     | 2885 | 26,92 | 18,21,22     | 1.05 | 3 (16%)     | 22,30,33    | 1.83 | 5 (22%)     |



| Mol | Type | Chain | Res  | Link     | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|------|----------|--------------|------|----------|-------------|------|----------|
|     |      |       |      |          | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 26  | PSU  | 1     | 1105 | 26       | 18,21,22     | 1.03 | 2 (11%)  | 22,30,33    | 1.78 | 3 (13%)  |
| 76  | 2MG  | 2     | 1825 | 76       | 18,26,27     | 2.56 | 6 (33%)  | 16,38,41    | 1.71 | 3 (18%)  |
| 75  | 5MU  | 5     | 54   | 75       | 19,22,23     | 7.67 | 9 (47%)  | 28,32,35    | 3.49 | 10 (35%) |
| 26  | PSU  | 1     | 891  | 26,89    | 18,21,22     | 1.07 | 2 (11%)  | 22,30,33    | 1.84 | 4 (18%)  |
| 26  | H2U  | 1     | 2754 | 26       | 18,21,22     | 0.69 | 0        | 21,30,33    | 1.15 | 1 (4%)   |
| 76  | G7M  | 2     | 525  | 76       | 20,26,27     | 2.09 | 5 (25%)  | 17,39,42    | 1.24 | 2 (11%)  |
| 76  | UR3  | 2     | 1807 | 76       | 19,22,23     | 2.58 | 6 (31%)  | 26,32,35    | 1.34 | 1 (3%)   |
| 75  | PSU  | 5     | 55   | 75       | 18,21,22     | 1.10 | 1 (5%)   | 22,30,33    | 1.77 | 4 (18%)  |
| 26  | PSU  | 1     | 2762 | 26       | 18,21,22     | 0.98 | 2 (11%)  | 22,30,33    | 1.75 | 4 (18%)  |
| 76  | MA6  | 2     | 1828 | 76       | 18,26,27     | 1.30 | 2 (11%)  | 19,38,41    | 3.53 | 2 (10%)  |
| 26  | OMG  | 1     | 2560 | 26,75,92 | 18,26,27     | 2.40 | 8 (44%)  | 19,38,41    | 1.46 | 4 (21%)  |
| 75  | 4SU  | 5     | 8    | 75       | 18,21,22     | 3.97 | 7 (38%)  | 26,30,33    | 2.36 | 4 (15%)  |
| 75  | 5MC  | 5     | 32   | 75       | 18,22,23     | 3.42 | 7 (38%)  | 26,32,35    | 1.15 | 2 (7%)   |
| 26  | 5MU  | 1     | 2257 | 26,92    | 19,22,23     | 1.47 | 4 (21%)  | 28,32,35    | 2.38 | 6 (21%)  |

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   |
|-----|------|-------|------|-------|---------|-----------|---------|
| 26  | 2MA  | 1     | 2808 | 26,89 | -       | 2/3/25/26 | 0/3/3/3 |
| 76  | MA6  | 2     | 1827 | 76    | -       | 0/7/29/30 | 0/3/3/3 |
| 26  | OMU  | 1     | 2857 | 26,89 | -       | 0/9/27/28 | 0/2/2/2 |
| 26  | PSU  | 1     | 2910 | 26    | -       | 0/7/25/26 | 0/2/2/2 |
| 26  | OMC  | 1     | 2803 | 26,89 | -       | 0/9/27/28 | 0/2/2/2 |
| 76  | 4OC  | 2     | 1664 | 76    | -       | 2/9/29/30 | 0/2/2/2 |
| 26  | PSU  | 1     | 2885 | 26,92 | -       | 1/7/25/26 | 0/2/2/2 |
| 26  | PSU  | 1     | 1105 | 26    | -       | 0/7/25/26 | 0/2/2/2 |
| 76  | 2MG  | 2     | 1825 | 76    | -       | 2/5/27/28 | 0/3/3/3 |
| 75  | 5MU  | 5     | 54   | 75    | -       | 0/7/25/26 | 0/2/2/2 |
| 26  | PSU  | 1     | 891  | 26,89 | -       | 1/7/25/26 | 0/2/2/2 |
| 26  | H2U  | 1     | 2754 | 26    | -       | 0/7/38/39 | 0/2/2/2 |
| 76  | G7M  | 2     | 525  | 76    | -       | 3/3/25/26 | 0/3/3/3 |
| 76  | UR3  | 2     | 1807 | 76    | -       | 0/7/25/26 | 0/2/2/2 |
| 75  | PSU  | 5     | 55   | 75    | -       | 0/7/25/26 | 0/2/2/2 |
| 26  | PSU  | 1     | 2762 | 26    | -       | 0/7/25/26 | 0/2/2/2 |
| 76  | MA6  | 2     | 1828 | 76    | -       | 0/7/29/30 | 0/3/3/3 |

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| Mol | Type | Chain | Res  | Link     | Chirals | Torsions  | Rings   |
|-----|------|-------|------|----------|---------|-----------|---------|
| 26  | OMG  | 1     | 2560 | 26,75,92 | -       | 1/5/27/28 | 0/3/3/3 |
| 75  | 4SU  | 5     | 8    | 75       | -       | 0/7/25/26 | 0/2/2/2 |
| 75  | 5MC  | 5     | 32   | 75       | -       | 0/7/25/26 | 0/2/2/2 |
| 26  | 5MU  | 1     | 2257 | 26,92    | -       | 2/7/25/26 | 0/2/2/2 |

The worst 5 of 97 bond length outliers are listed below:

| Mol | Chain | Res  | Type | Atoms | Z      | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|--------|-------------|----------|
| 75  | 5     | 54   | 5MU  | C4-C5 | 22.55  | 1.82        | 1.44     |
| 75  | 5     | 54   | 5MU  | C6-N1 | 15.59  | 1.64        | 1.38     |
| 75  | 5     | 54   | 5MU  | C4-N3 | -12.11 | 1.16        | 1.38     |
| 75  | 5     | 54   | 5MU  | C6-C5 | -12.08 | 1.14        | 1.34     |
| 26  | 1     | 2808 | 2MA  | C4-N3 | 9.19   | 1.50        | 1.35     |

The worst 5 of 70 bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms    | Z      | Observed(°) | Ideal(°) |
|-----|-------|------|------|----------|--------|-------------|----------|
| 76  | 2     | 1828 | MA6  | N1-C6-N6 | -13.99 | 102.33      | 117.06   |
| 76  | 2     | 1827 | MA6  | N1-C6-N6 | -13.99 | 102.34      | 117.06   |
| 75  | 5     | 54   | 5MU  | C5-C4-N3 | 11.05  | 124.75      | 115.31   |
| 75  | 5     | 8    | 4SU  | C4-N3-C2 | -8.22  | 119.36      | 127.34   |
| 75  | 5     | 54   | 5MU  | C5-C6-N1 | -7.86  | 115.25      | 123.34   |

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

| Mol | Chain | Res  | Type | Atoms           |
|-----|-------|------|------|-----------------|
| 26  | 1     | 2560 | OMG  | C1'-C2'-O2'-CM2 |
| 76  | 2     | 525  | G7M  | C3'-C4'-C5'-O5' |
| 76  | 2     | 1664 | 4OC  | O4'-C4'-C5'-O5' |
| 76  | 2     | 1825 | 2MG  | O4'-C4'-C5'-O5' |
| 26  | 1     | 2808 | 2MA  | O4'-C4'-C5'-O5' |

There are no ring outliers.

7 monomers are involved in 10 short contacts:

| Mol | Chain | Res  | Type | Clashes | Symm-Clashes |
|-----|-------|------|------|---------|--------------|
| 76  | 2     | 1664 | 4OC  | 2       | 0            |
| 26  | 1     | 1105 | PSU  | 1       | 0            |
| 76  | 2     | 1825 | 2MG  | 1       | 0            |
| 75  | 5     | 54   | 5MU  | 1       | 0            |

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| Mol | Chain | Res  | Type | Clashes | Symm-Clashes |
|-----|-------|------|------|---------|--------------|
| 26  | 1     | 891  | PSU  | 2       | 0            |
| 76  | 2     | 1828 | MA6  | 2       | 0            |
| 26  | 1     | 2560 | OMG  | 2       | 0            |

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 435 ligands modelled in this entry, 433 are monoatomic - leaving 2 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 | $\# Z  > 2$ |
| 90  | ATP  | W     | 501  | 89   | 26,33,33     | 0.91 | 1 (3%)      | 31,52,52    | 1.56 | 5 (16%)     |
| 91  | CLM  | 1     | 3201 | -    | 19,20,20     | 1.64 | 3 (15%)     | 23,27,27    | 1.14 | 2 (8%)      |

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   |
|-----|------|-------|------|------|---------|------------|---------|
| 90  | ATP  | W     | 501  | 89   | -       | 0/18/38/38 | 0/3/3/3 |
| 91  | CLM  | 1     | 3201 | -    | -       | 2/20/22/22 | 0/1/1/1 |

All (4) bond length outliers are listed below:

| Mol | Chain | Res  | Type | Atoms  | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|--------|-------|-------------|----------|
| 91  | 1     | 3201 | CLM  | C2-N2  | 4.63  | 1.44        | 1.34     |
| 91  | 1     | 3201 | CLM  | O9B-N9 | -3.16 | 1.17        | 1.22     |
| 91  | 1     | 3201 | CLM  | O2-C2  | -2.90 | 1.17        | 1.23     |
| 90  | W     | 501  | ATP  | C5-C4  | 2.22  | 1.46        | 1.40     |



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

| Mol | Chain | Res  | Type | Atoms       | Z     | Observed(°) | Ideal(°) |
|-----|-------|------|------|-------------|-------|-------------|----------|
| 90  | W     | 501  | ATP  | PA-O3A-PB   | -3.90 | 119.45      | 132.83   |
| 90  | W     | 501  | ATP  | C3'-C2'-C1' | 3.52  | 106.28      | 100.98   |
| 90  | W     | 501  | ATP  | PB-O3B-PG   | -3.33 | 121.39      | 132.83   |
| 90  | W     | 501  | ATP  | N3-C2-N1    | -3.17 | 123.72      | 128.68   |
| 91  | 1     | 3201 | CLM  | C5-C3-N2    | -2.92 | 104.52      | 110.05   |

There are no chirality outliers.

All (2) torsion outliers are listed below:

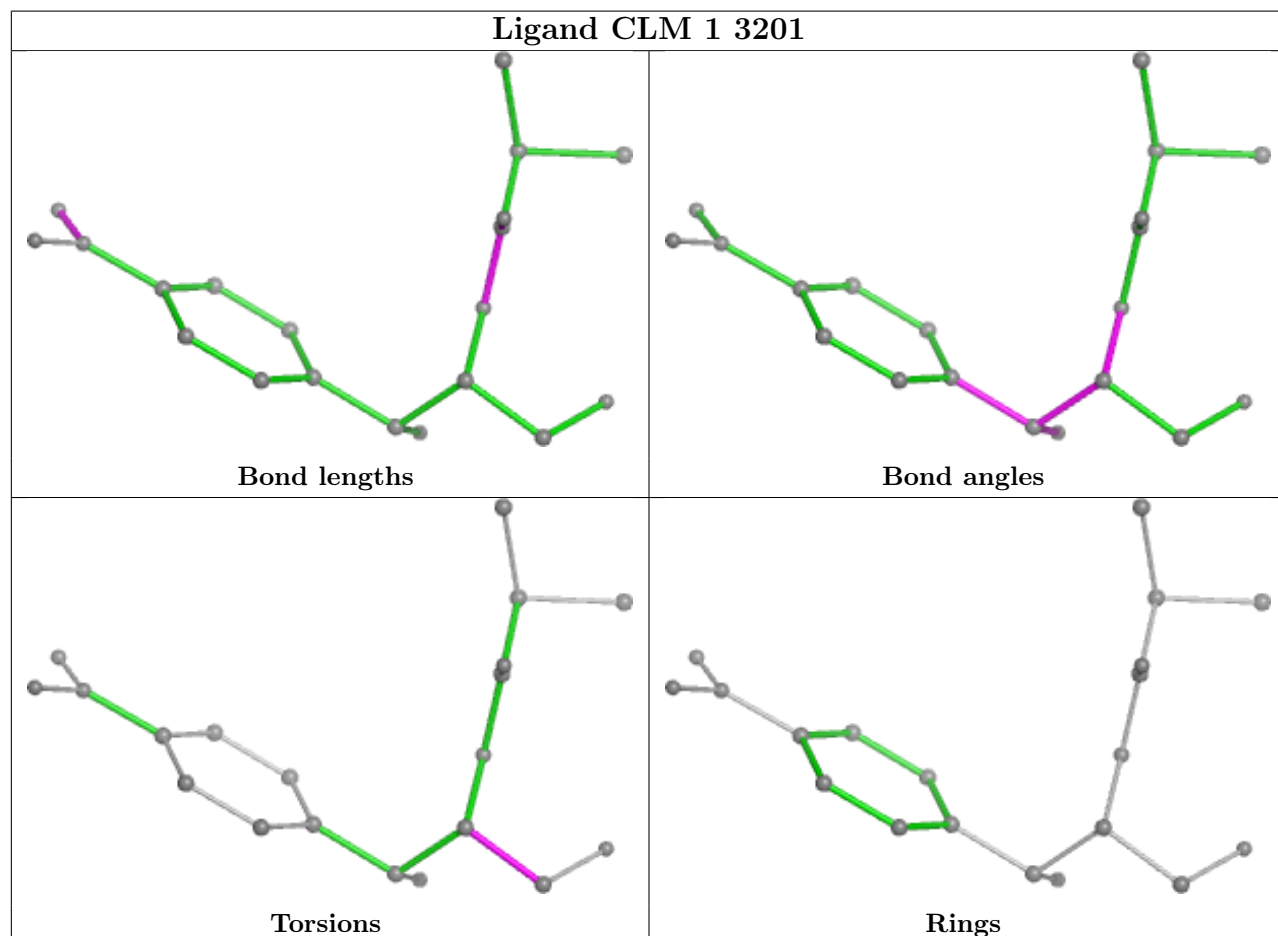
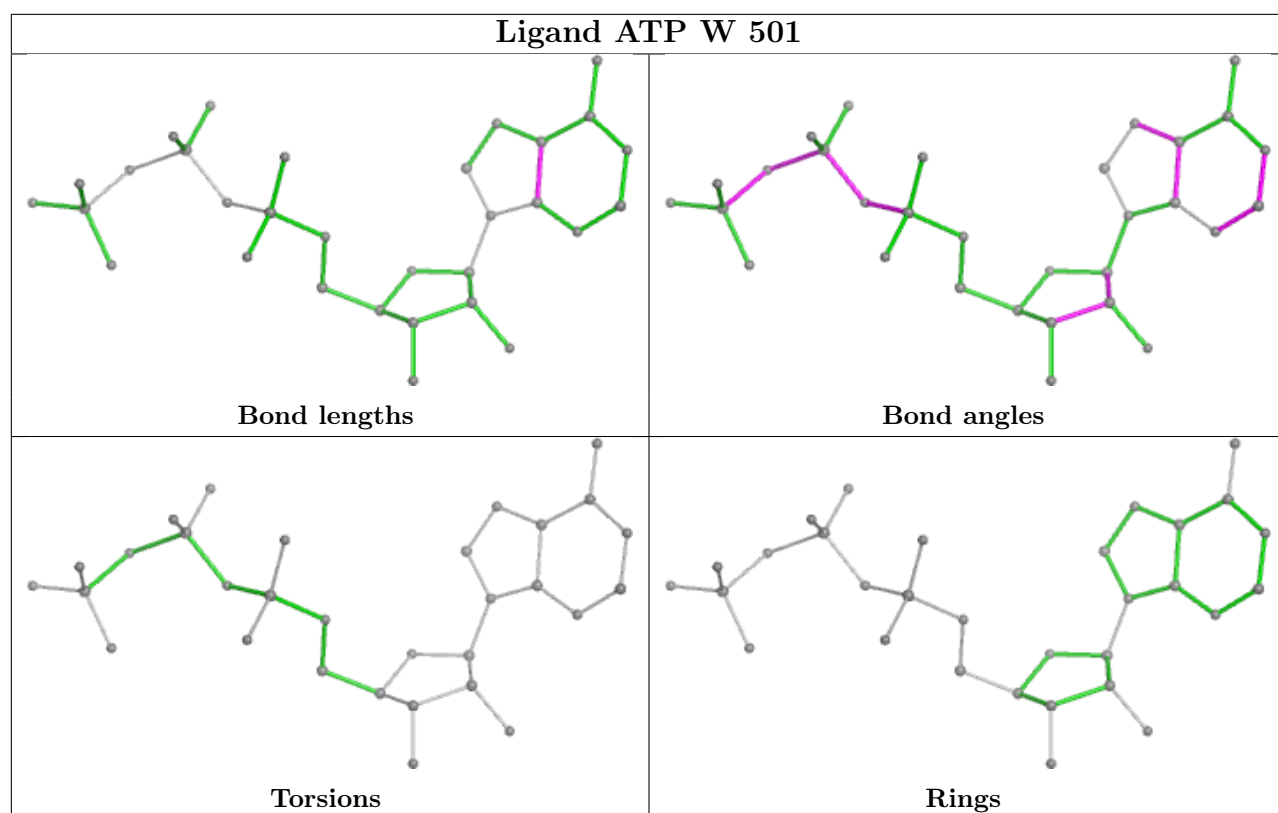
| Mol | Chain | Res  | Type | Atoms       |
|-----|-------|------|------|-------------|
| 91  | 1     | 3201 | CLM  | N2-C3-C4-O4 |
| 91  | 1     | 3201 | CLM  | C5-C3-C4-O4 |

There are no ring outliers.

No monomer is involved in short contacts.

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







## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 26  | 1     | 11               |
| 76  | 2     | 7                |

The worst 5 of 18 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1     | 1     | 295:U     | O3'    | 307:A     | P      | 27.62        |
| 1     | 1     | 261:G     | O3'    | 270:A     | P      | 26.81        |
| 1     | 2     | 95:A      | O3'    | 101:A     | P      | 23.00        |
| 1     | 1     | 1704:U    | O3'    | 1831:A    | P      | 17.44        |
| 1     | 1     | 363:A     | O3'    | 405:U     | P      | 17.26        |



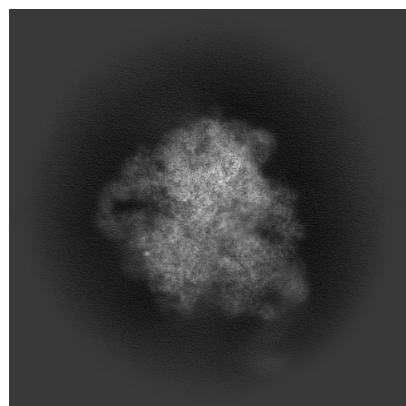
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50011. These allow visual inspection of the internal detail of the map and identification of artifacts.

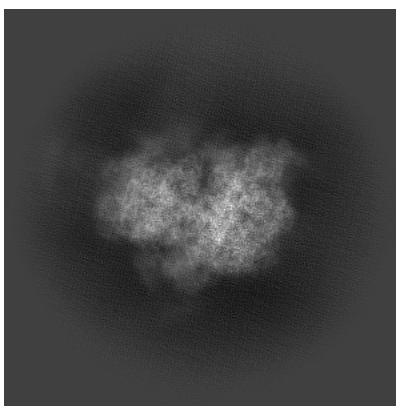
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

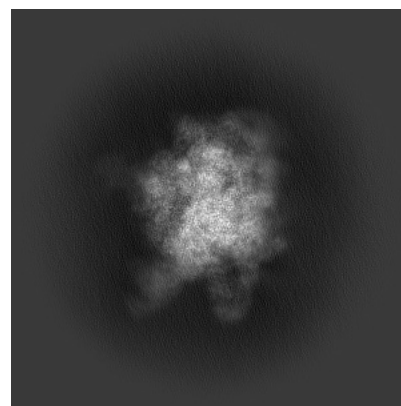
#### 6.1.1 Primary map



X

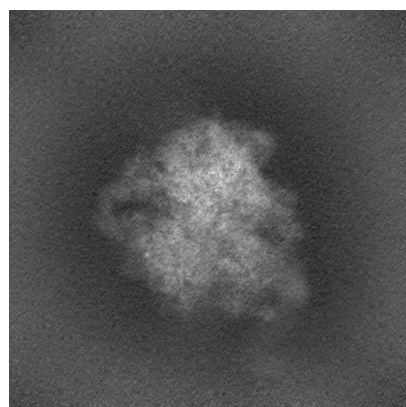


Y

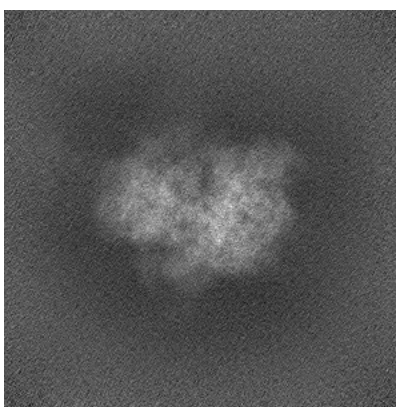


Z

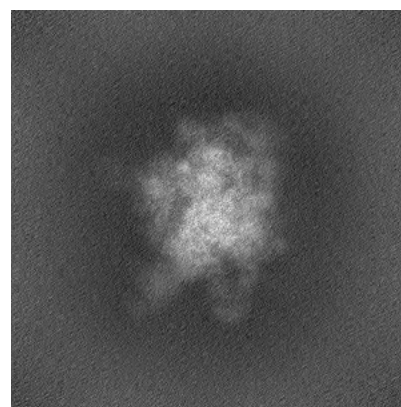
#### 6.1.2 Raw map



X



Y



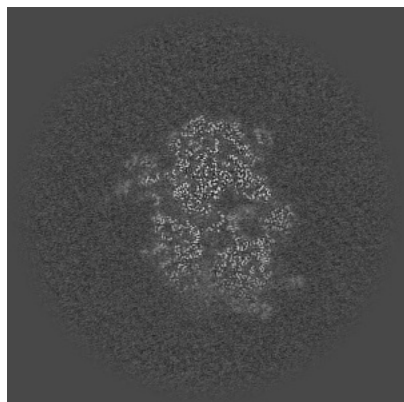
Z

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

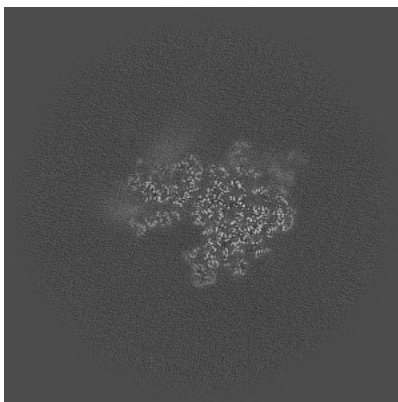


## 6.2 Central slices [i](#)

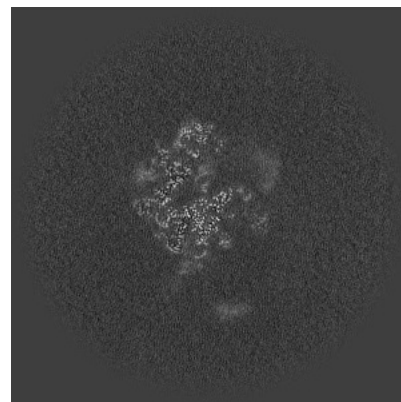
### 6.2.1 Primary map



X Index: 282

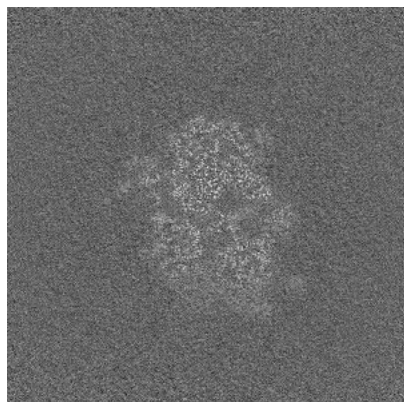


Y Index: 282

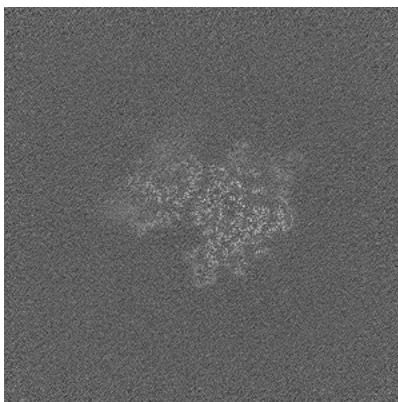


Z Index: 282

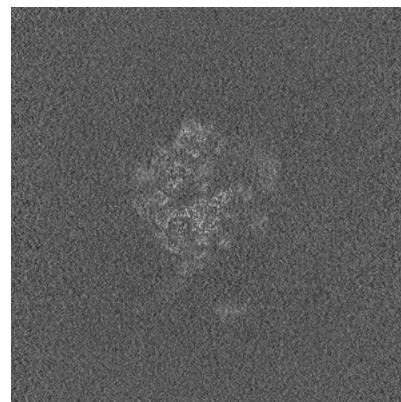
### 6.2.2 Raw map



X Index: 282



Y Index: 282



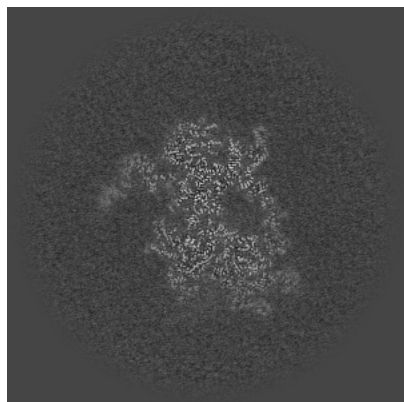
Z Index: 282

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

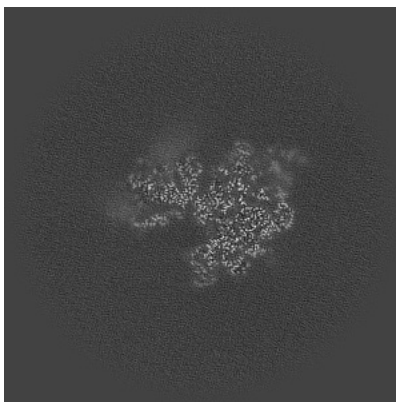


## 6.3 Largest variance slices [i](#)

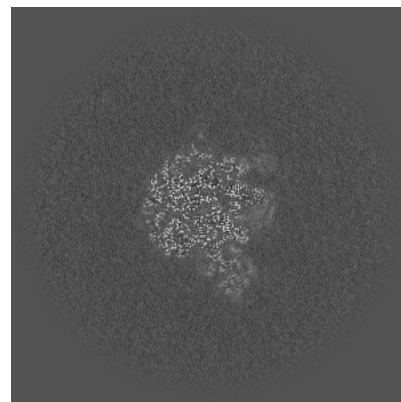
### 6.3.1 Primary map



X Index: 293

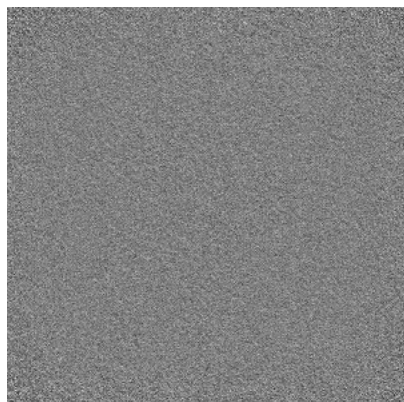


Y Index: 285

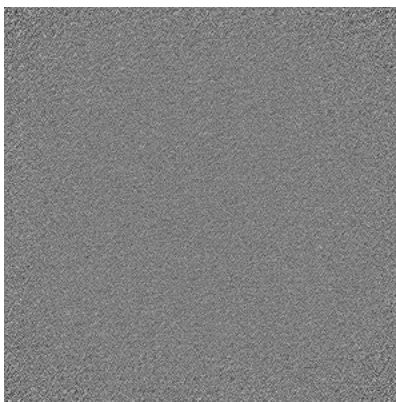


Z Index: 325

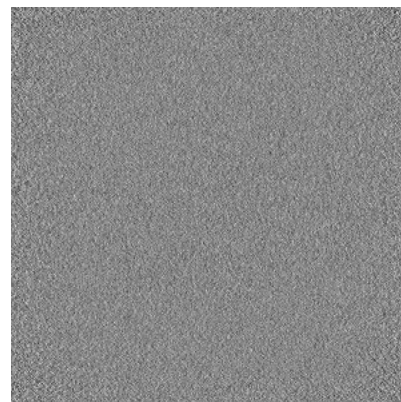
### 6.3.2 Raw map



X Index: 0



Y Index: 0



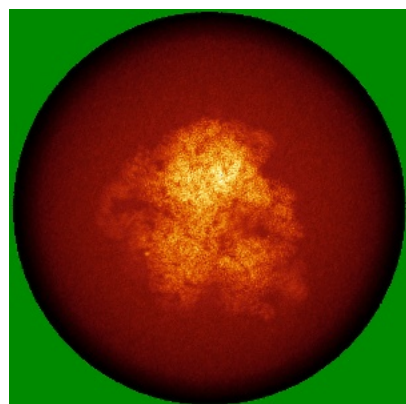
Z Index: 0

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

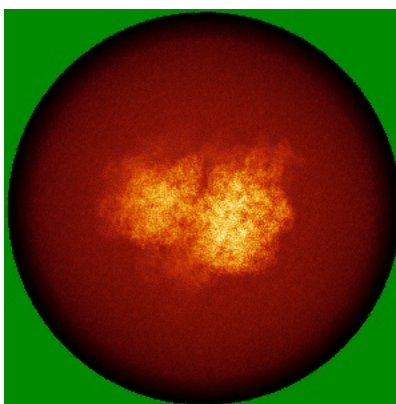


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

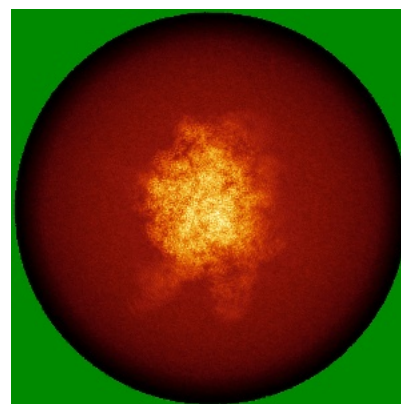
### 6.4.1 Primary map



X

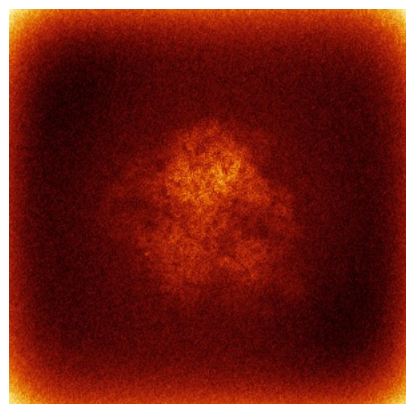


Y

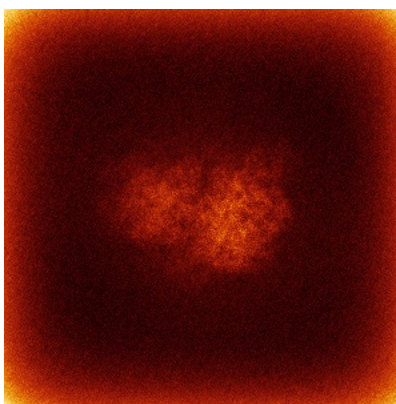


Z

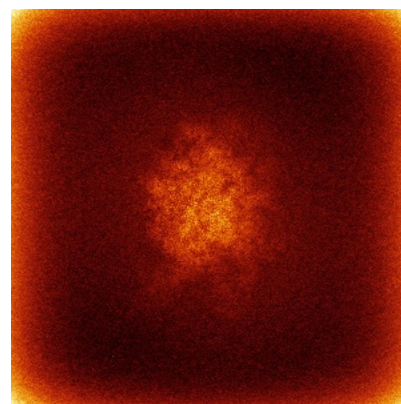
### 6.4.2 Raw map



X



Y



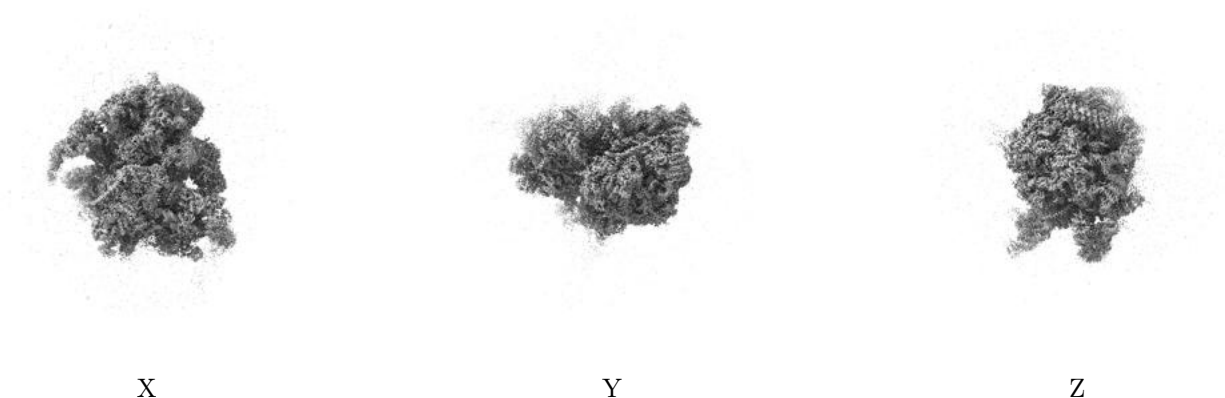
Z

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.



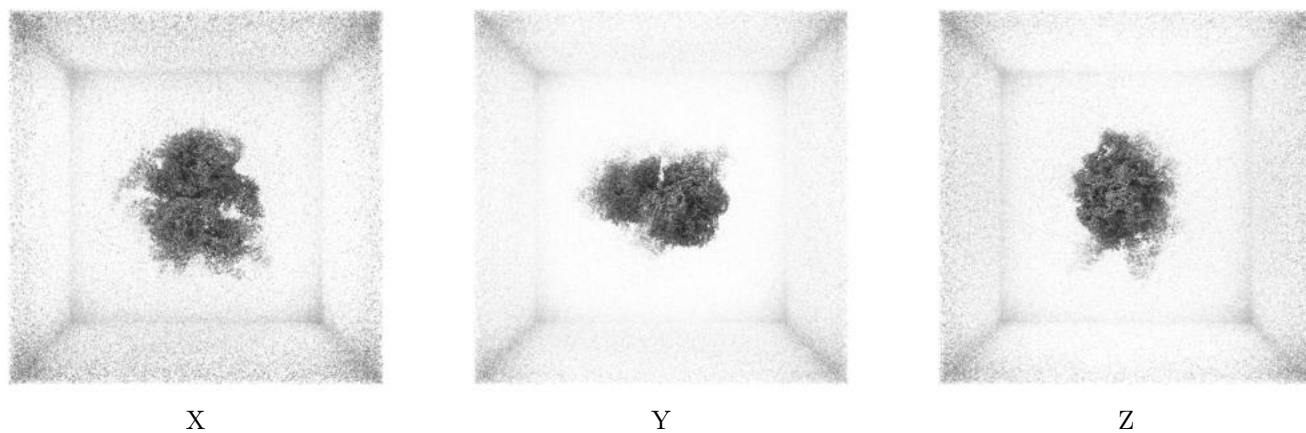
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0796. 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.



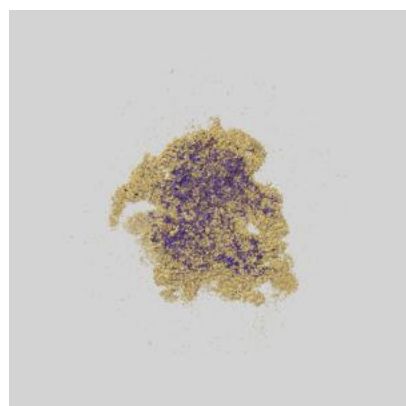
## 6.6 Mask visualisation [i](#)

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

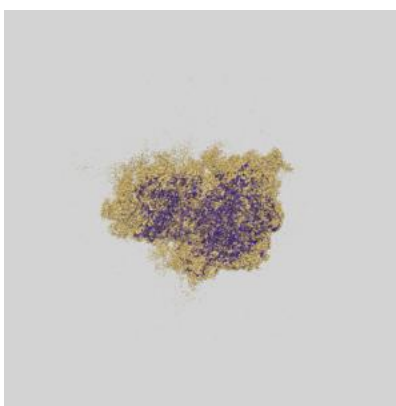
A mask typically either:

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

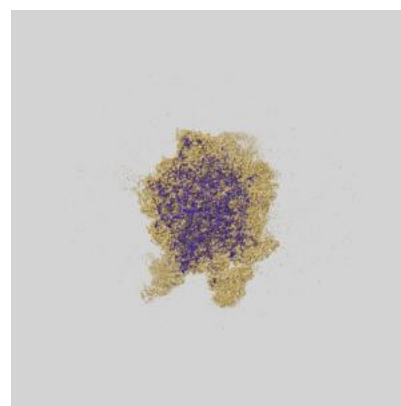
### 6.6.1 emd\_50011\_msk\_1.map [i](#)



X



Y



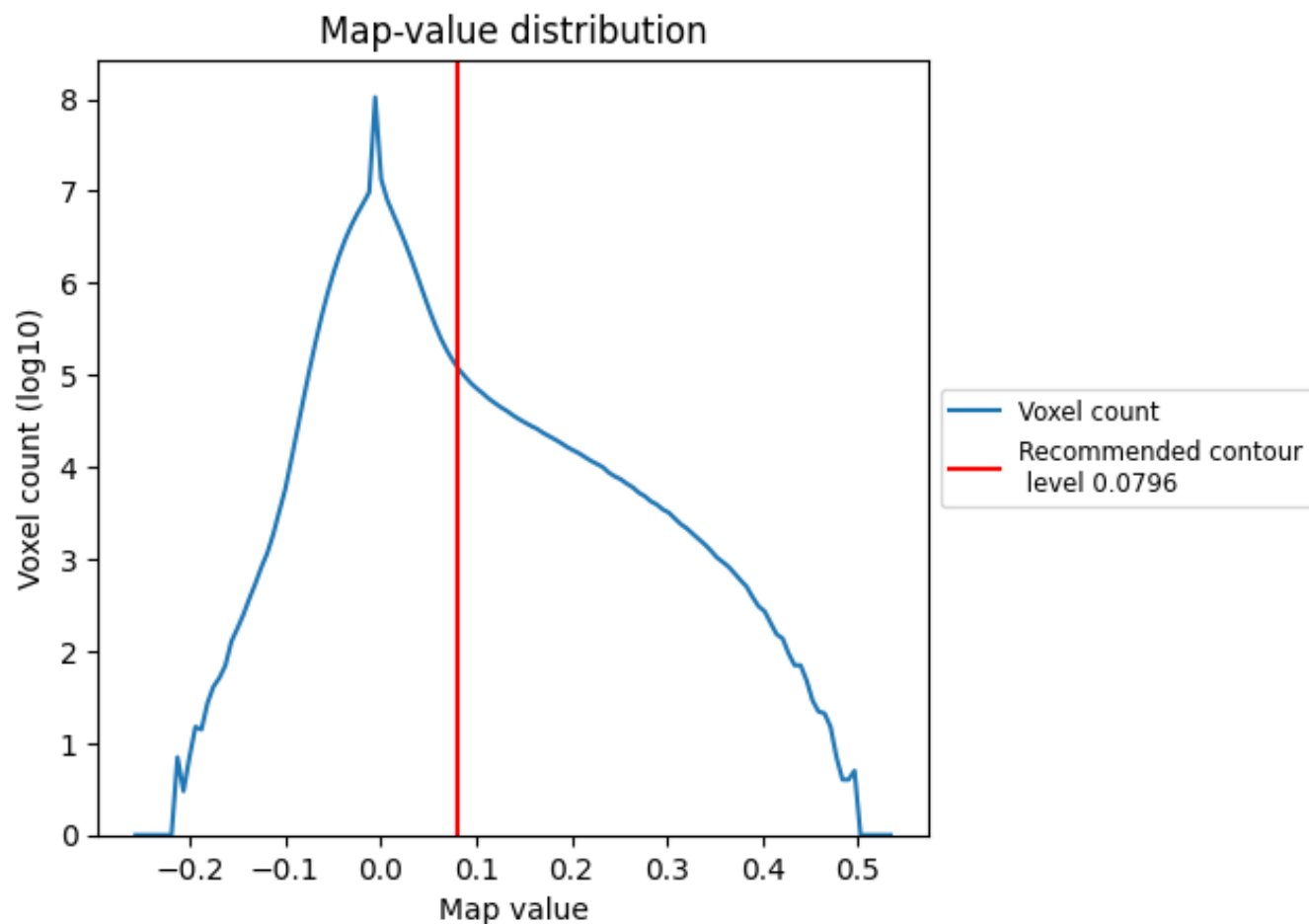
Z



## 7 Map analysis [i](#)

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

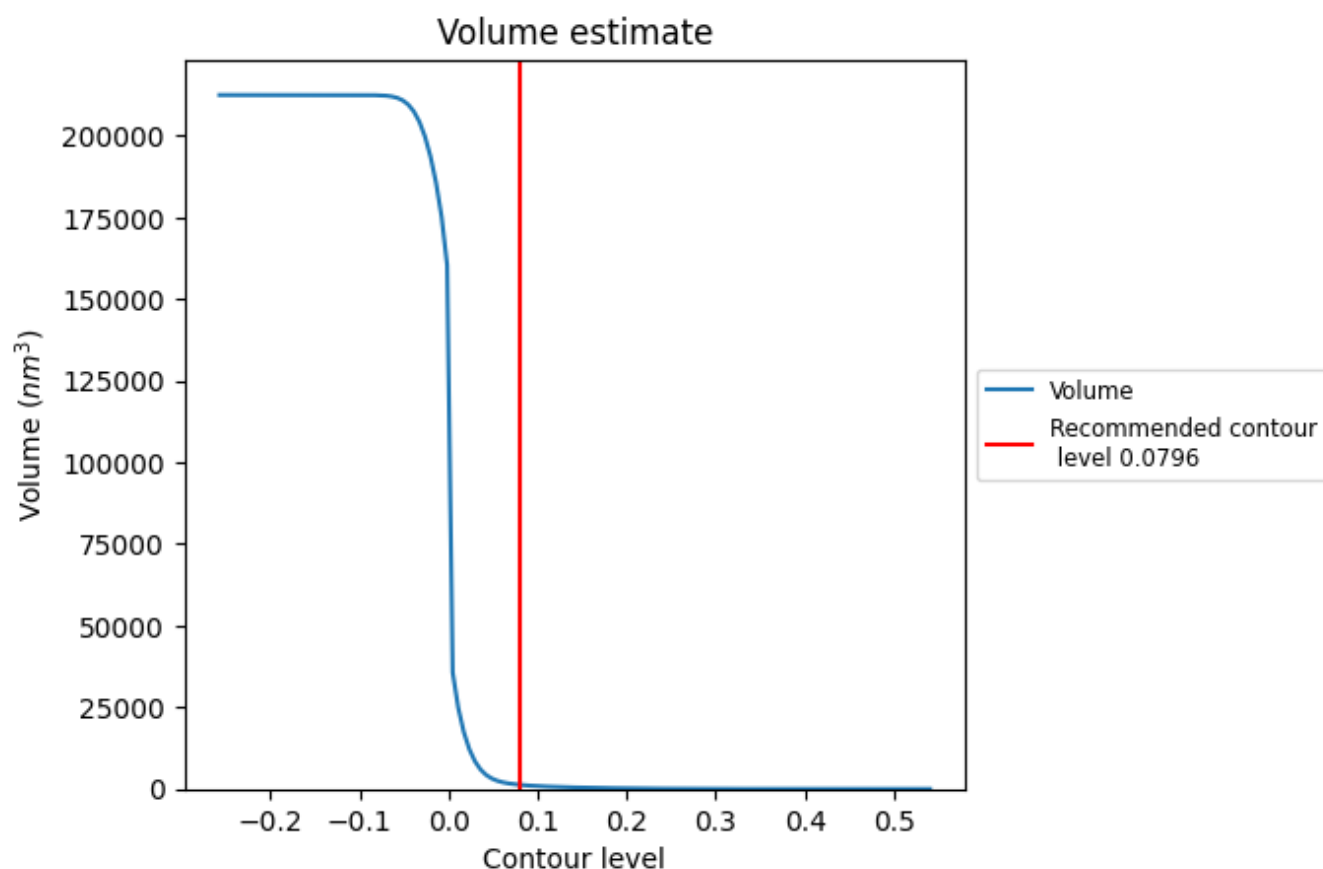
### 7.1 Map-value distribution [i](#)



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



## 7.2 Volume estimate [i](#)

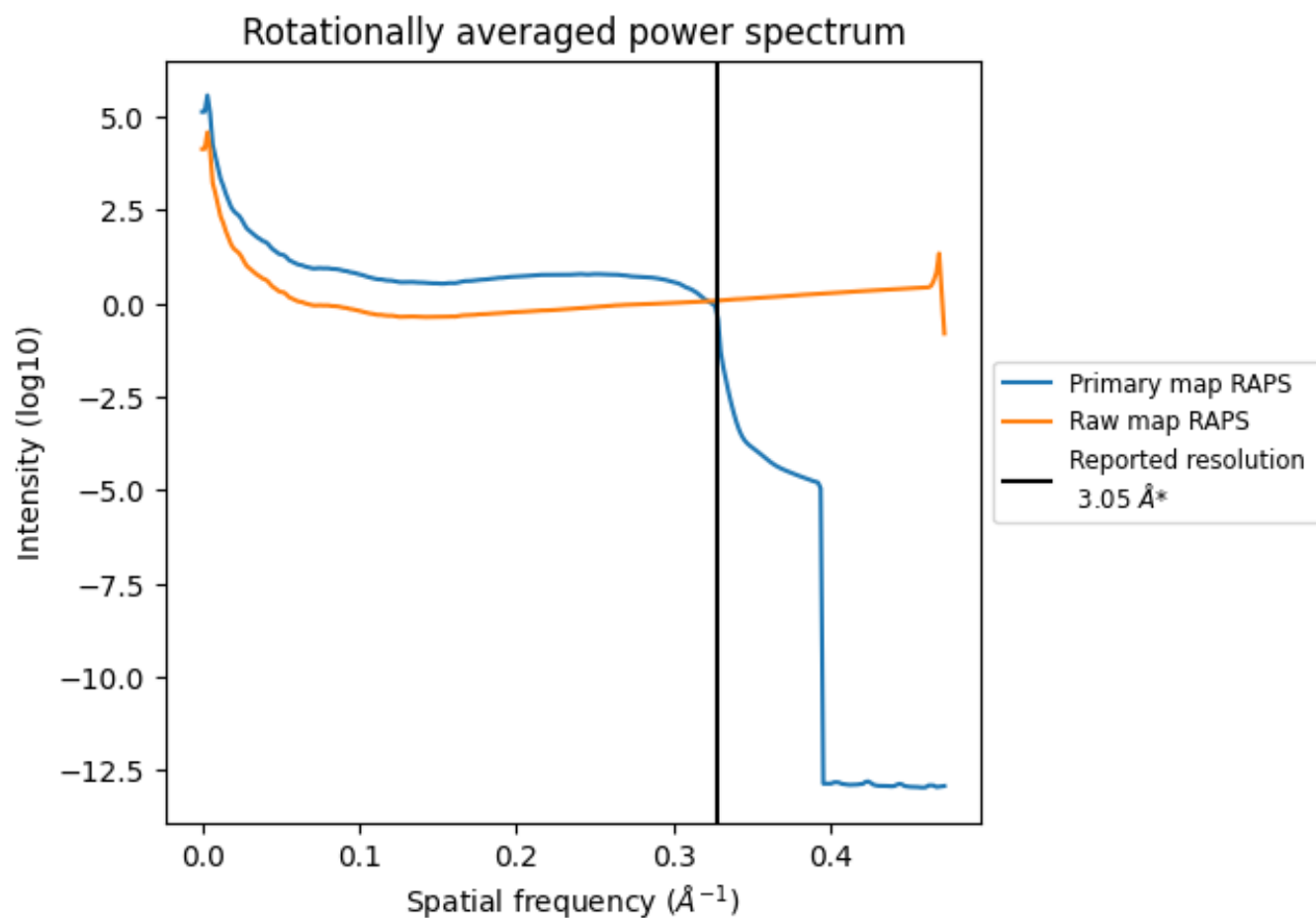


The volume at the recommended contour level is 1277  $\text{nm}^3$ ; this corresponds to an approximate mass of 1154 kDa.

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 ⓘ



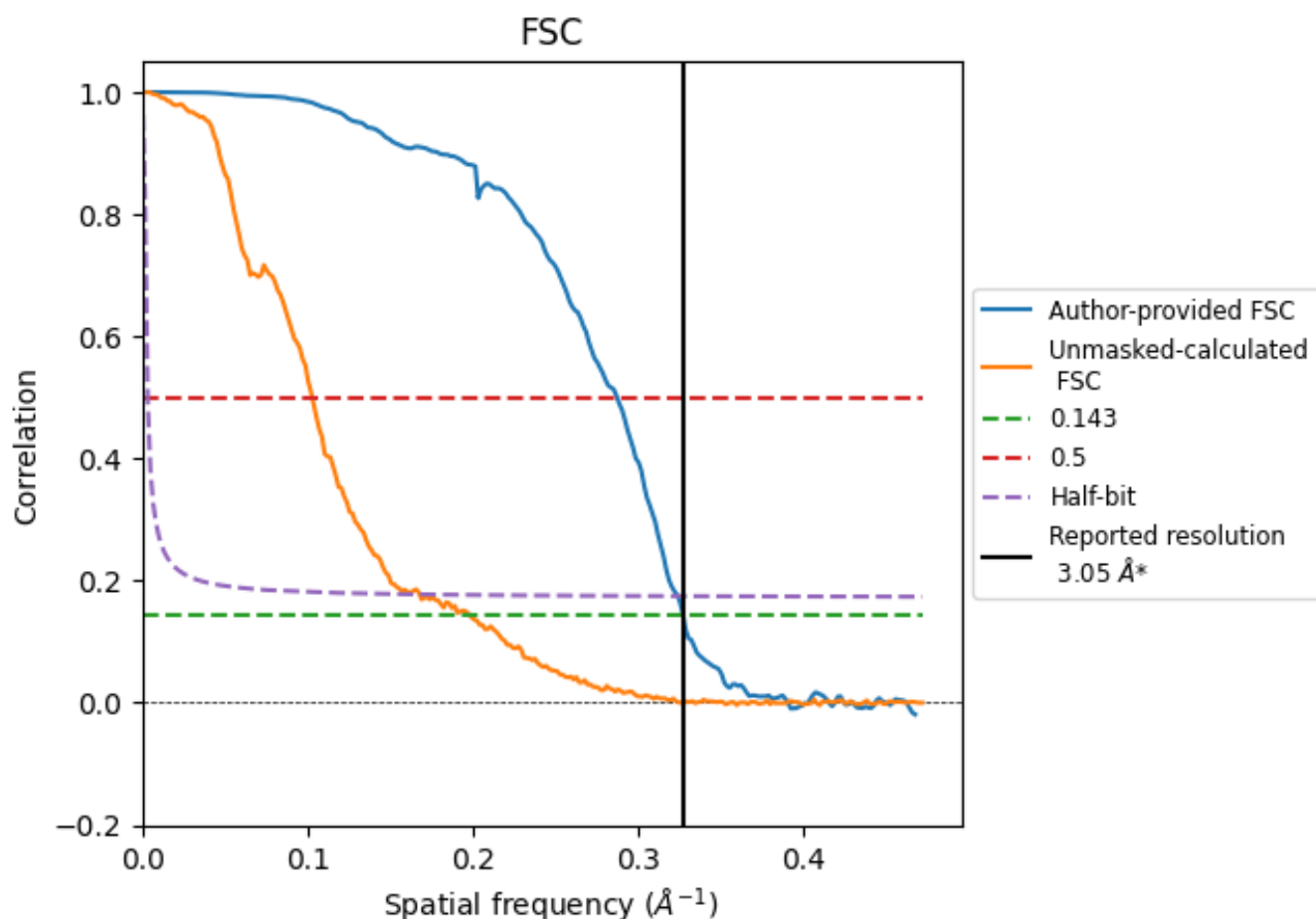
\*Reported resolution corresponds to spatial frequency of 0.328  $\text{\AA}^{-1}$



## 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 0.328  $\text{\AA}^{-1}$



## 8.2 Resolution estimates [i](#)

| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 3.05                               | -    | -        |
| Author-provided FSC curve | 3.05                               | 3.48 | 3.08     |
| Unmasked-calculated*      | 5.04                               | 9.71 | 5.95     |

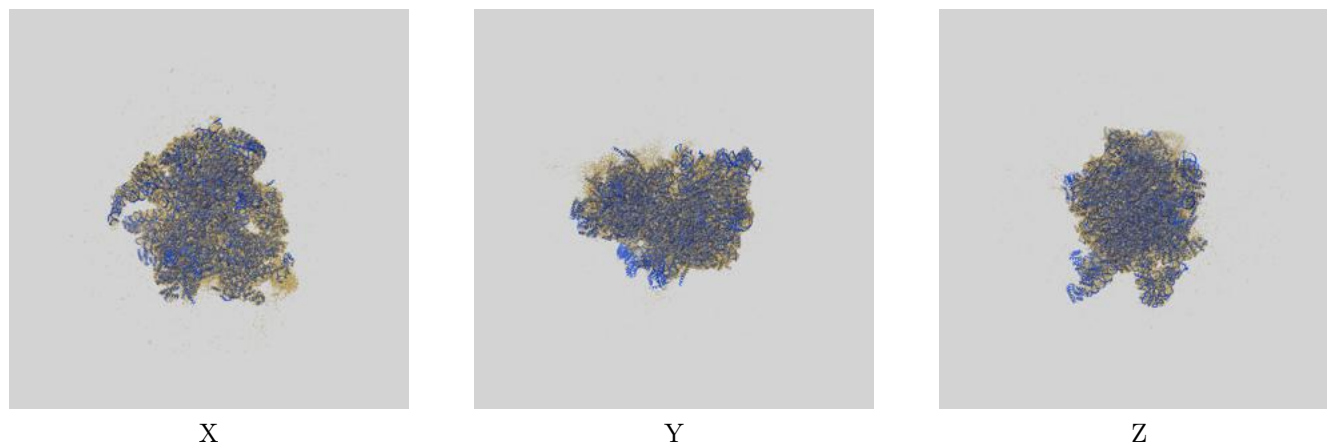
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.04 differs from the reported value 3.05 by more than 10 %



## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-50011 and PDB model 9EVS. Per-residue inclusion information can be found in [section 3](#) on [page 23](#).

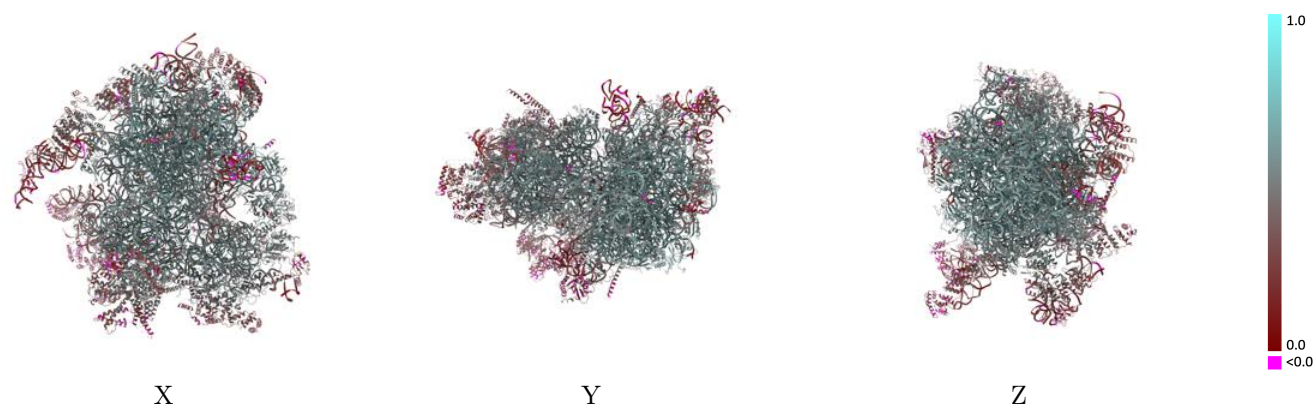
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0796 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

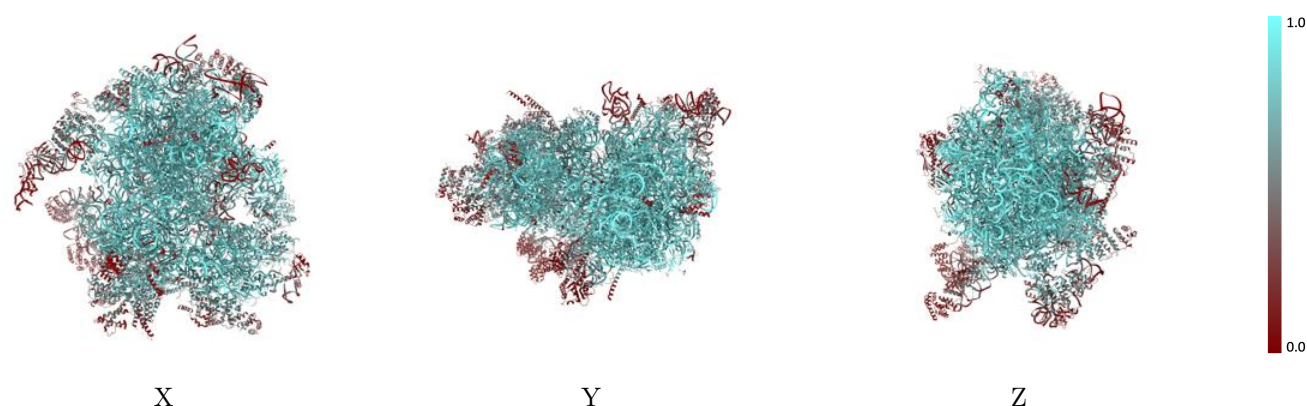


## 9.2 Q-score mapped to coordinate model [i](#)



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

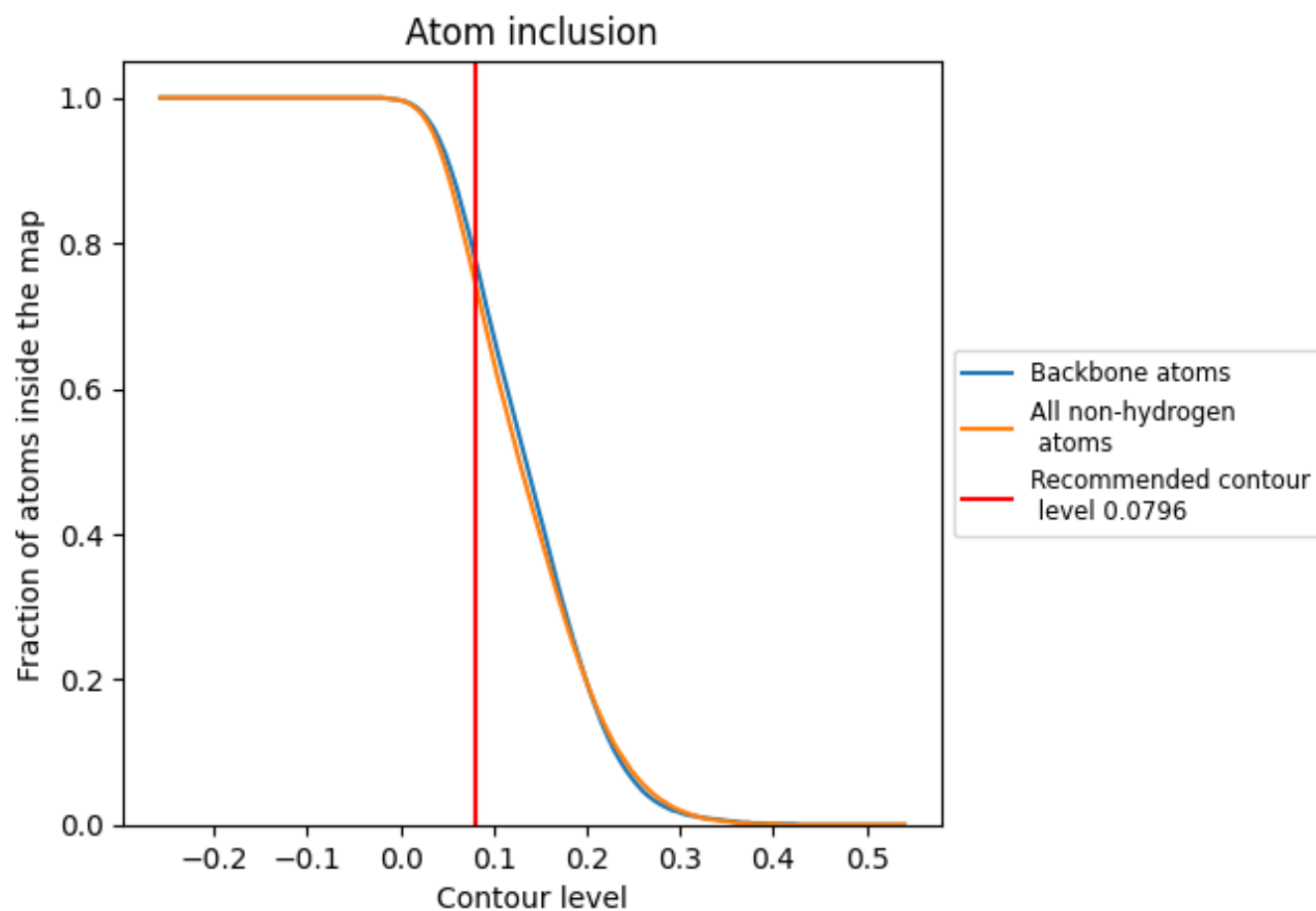
## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0796).



## 9.4 Atom inclusion [i](#)









































































At the recommended contour level, 78% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.



## 9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0796) and Q-score for the entire model and for each chain.





















































































| Chain | Atom inclusion   | Q-score  |
|-------|--|--|
| All   |  0.7490   |  0.4830   |
| 1     |  0.8610   |  0.5200   |
| 1B    |  0.8510   |  0.5650   |
| 1C    |  0.7010   |  0.5050   |
| 1D    |  0.8610   |  0.5710   |
| 1E    |  0.8800   |  0.5720   |
| 1F    |  0.7420   |  0.5240   |
| 1G    |  0.6510   |  0.4930   |
| 1H    |  0.6770   |  0.4830   |
| 1I    |  0.0220   |  0.1690   |
| 1J    |  0.0920   |  0.1880   |
| 1K    |  0.8180   |  0.5400   |
| 1L    |  0.8220   |  0.5680   |
| 1M    |  0.8570   |  0.5660   |
| 1N    |  0.7890  |  0.5350  |
| 1O    |  0.8840 |  0.5740 |
| 1P    |  0.8430 |  0.5530 |
| 1Q    |  0.8110 |  0.5530 |
| 1R    |  0.9310 |  0.5900 |
| 1S    |  0.8270 |  0.5670 |
| 1T    |  0.8840 |  0.5750 |
| 1U    |  0.8200 |  0.5590 |
| 1V    |  0.8360 |  0.5640 |
| 1W    |  0.2130 |  0.2470 |
| 1X    |  0.7670 |  0.5210 |
| 1Y    |  0.8280 |  0.5540 |
| 1Z    |  0.7440 |  0.5130 |
| 1a    |  0.8600 |  0.5550 |
| 1b    |  0.8710 |  0.5680 |
| 1c    |  0.8050 |  0.5300 |
| 1d    |  0.9210 |  0.5750 |
| 1e    |  0.8200 |  0.5520 |
| 1f    |  0.9770 |  0.6090 |
| 1g    |  0.8910 |  0.5810 |
| 1h    |  0.8770 |  0.5720 |



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





















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| Chain | Atom inclusion   | Q-score  |
|-------|--|--|
| 1i    |  0.6960   |  0.5070   |
| 1j    |  0.8940   |  0.5730   |
| 1k    |  0.8810   |  0.5730   |
| 1l    |  0.6310   |  0.4620   |
| 1m    |  0.2300   |  0.2880   |
| 1o    |  0.1180   |  0.2320   |
| 1p    |  0.7760   |  0.5430   |
| 1q    |  0.8400   |  0.5550   |
| 1r    |  0.8000   |  0.5250   |
| 1s    |  0.7830   |  0.5280   |
| 1t    |  0.5730   |  0.4040   |
| 1u    |  0.4600   |  0.3640   |
| 1v    |  0.6100   |  0.4180   |
| 1x    |  0.8950   |  0.6300   |
| 2     |  0.8760   |  0.5060   |
| 3     |  0.9400   |  0.5490   |
| 5     |  0.7550   |  0.4260   |
| 6     |  0.6610  |  0.5240  |
| A     |  0.7660 |  0.5170 |
| B     |  0.5750 |  0.4150 |
| C     |  0.7130 |  0.4830 |
| D     |  0.6730 |  0.4740 |
| E     |  0.7820 |  0.5330 |
| F     |  0.7040 |  0.4850 |
| G     |  0.8330 |  0.5470 |
| H     |  0.6380 |  0.4690 |
| I     |  0.8060 |  0.5270 |
| J     |  0.7400 |  0.5030 |
| K     |  0.7660 |  0.5340 |
| L     |  0.7530 |  0.5200 |
| M     |  0.8250 |  0.5460 |
| N     |  0.7780 |  0.5340 |
| O     |  0.8180 |  0.5280 |
| P     |  0.7660 |  0.5260 |
| Q     |  0.7350 |  0.5030 |
| R     |  0.4240 |  0.3540 |
| S     |  0.6830 |  0.5110 |
| T     |  0.8410 |  0.5580 |
| U     |  0.5330 |  0.3830 |
| V     |  0.6440 |  0.4420 |
| W     |  0.7000 |  0.4850 |
| X     |  0.5160 |  0.3830 |

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| Chain | Atom inclusion   | Q-score  |
|-------|--|--|
| Y     |  0.6910 |  0.4800 |
| Z     |  0.5970 |  0.3770 |
| a     |  0.5220 |  0.3680 |
| b     |  0.4680 |  0.3790 |
| c     |  0.8340 |  0.5570 |
| d     |  0.5750 |  0.4190 |
| e     |  0.6980 |  0.4680 |
| f     |  0.5830 |  0.4150 |
| h     |  0.1910 |  0.2040 |
| i     |  0.2840 |  0.2850 |
| j     |  0.0290 |  0.1450 |
| k     |  0.5630 |  0.4150 |