



wwPDB EM Validation Summary Report ⓘ

Nov 10, 2024 – 12:54 am GMT

PDB ID : 7NQL
EMDB ID : EMD-12529
Title : 55S mammalian mitochondrial ribosome with ICT1 and P site tRNAMet
Authors : Kummer, E.; Schubert, K.; Ban, N.
Deposited on : 2021-03-01
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

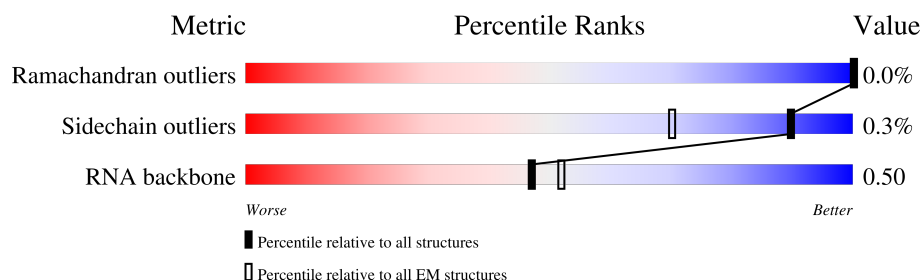
EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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 3.40 Å.

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



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

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

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | B7 | 95 | |
| 2 | B8 | 188 | |
| 3 | B9 | 100 | |
| 4 | BA | 1571 | |
| 5 | BB | 73 | |
| 6 | BD | 306 | |
| 7 | BE | 399 | |
| 8 | BF | 294 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 9 | BI | 268 | |
| 10 | BJ | 262 | |
| 11 | BK | 192 | |
| 12 | BL | 184 | |
| 13 | BN | 178 | |
| 14 | BO | 145 | |
| 15 | BP | 296 | |
| 16 | BQ | 251 | |
| 17 | BR | 169 | |
| 18 | BS | 180 | |
| 19 | BT | 292 | |
| 20 | BU | 149 | |
| 21 | BV | 209 | |
| 22 | BW | 210 | |
| 23 | BX | 150 | |
| 24 | BY | 216 | |
| 25 | Ba | 423 | |
| 26 | Bb | 380 | |
| 27 | Bc | 334 | |
| 28 | Bd | 206 | |
| 29 | Be | 135 | |
| 30 | Bf | 142 | |
| 31 | Bg | 159 | |
| 32 | Bh | 332 | |
| 33 | Bi | 306 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 34 | Bj | 279 | |
| 35 | Bk | 269 | |
| 36 | Bl | 166 | |
| 37 | Bm | 198 | |
| 38 | Bn | 128 | |
| 39 | Bo | 124 | |
| 40 | Bp | 112 | |
| 41 | Bq | 138 | |
| 42 | Bt | 102 | |
| 43 | Bu | 205 | |
| 44 | Bv | 222 | |
| 45 | Bw | 433 | |
| 46 | Bx | 196 | |
| 47 | AA | 962 | |
| 48 | CL | 198 | |
| 48 | DL | 198 | |
| 48 | EL | 198 | |
| 48 | FL | 198 | |
| 48 | GL | 198 | |
| 48 | HL | 198 | |
| 49 | AB | 289 | |
| 50 | AC | 167 | |
| 51 | AE | 430 | |
| 52 | AF | 276 | |
| 53 | AG | 242 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 54 | AI | 397 | |
| 55 | AJ | 200 | |
| 56 | AK | 196 | |
| 57 | AL | 139 | |
| 58 | AN | 128 | |
| 59 | AO | 239 | |
| 60 | AP | 135 | |
| 61 | AQ | 130 | |
| 62 | AR | 143 | |
| 63 | AU | 87 | |
| 64 | AV | 71 | |
| 65 | AX | 6 | |
| 66 | AZ | 18 | |
| 67 | Aa | 382 | |
| 68 | Ab | 190 | |
| 69 | Ac | 173 | |
| 70 | Ad | 205 | |
| 71 | Ae | 455 | |
| 72 | Af | 188 | |
| 73 | Ag | 410 | |
| 74 | Ah | 387 | |
| 75 | Ai | 106 | |
| 76 | Aj | 218 | |
| 77 | Ak | 325 | |
| 78 | Am | 118 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 79 | An | 199 | |
| 80 | Ao | 699 | |
| 81 | Ap | 258 | |
| 82 | B0 | 148 | |
| 83 | B1 | 256 | |
| 84 | B2 | 252 | |
| 85 | B3 | 161 | |
| 86 | B4 | 126 | |
| 87 | B5 | 188 | |
| 88 | B6 | 65 | |

2 Entry composition

There are 94 unique types of molecules in this entry. The entry contains 174319 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 Mitochondrial ribosomal protein L34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 1 | B7 | 46 | Total | C | N | O | S | 0 | 0 |
| | | | 387 | 239 | 89 | 58 | 1 | | |

- Molecule 2 is a protein called Mitochondrial ribosomal protein L35.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 2 | B8 | 95 | Total | C | N | O | S | 0 | 0 |
| | | | 833 | 539 | 163 | 129 | 2 | | |

- Molecule 3 is a protein called Ribosomal protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 3 | B9 | 38 | Total | C | N | O | S | 0 | 0 |
| | | | 335 | 214 | 70 | 47 | 4 | | |

- Molecule 4 is a RNA chain called 16S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 4 | BA | 1544 | Total | C | N | O | P | 0 | 0 |
| | | | 32844 | 14750 | 5972 | 10578 | 1544 | | |

- Molecule 5 is a RNA chain called CP tRNAPhe.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 5 | BB | 67 | Total | C | N | O | P | 0 | 0 |
| | | | 1427 | 640 | 261 | 459 | 67 | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------|-------------|
| BB | 72 | C | - | insertion | GB 76262549 |
| BB | 73 | A | - | insertion | GB 76262549 |

- Molecule 6 is a protein called uL2m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 6 | BD | 240 | Total | C | N | O | S | 0 | 0 |
| | | | 1860 | 1160 | 371 | 319 | 10 | | |

- Molecule 7 is a protein called ICT1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 7 | BE | 307 | Total | C | N | O | S | 0 | 0 |
| | | | 2420 | 1554 | 426 | 430 | 10 | | |

- Molecule 8 is a protein called Mitochondrial ribosomal protein L4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 8 | BF | 250 | Total | C | N | O | S | 0 | 0 |
| | | | 2011 | 1294 | 367 | 344 | 6 | | |

- Molecule 9 is a protein called Mitochondrial ribosomal protein L9.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 9 | BI | 98 | Total | C | N | O | 0 | 0 |
| | | | 805 | 509 | 155 | 141 | | |

- Molecule 10 is a protein called Mitochondrial ribosomal protein L10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 10 | BJ | 212 | Total | C | N | O | S | 0 | 0 |
| | | | 1705 | 1100 | 306 | 290 | 9 | | |

- Molecule 11 is a protein called Mitochondrial ribosomal protein L11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 11 | BK | 176 | Total | C | N | O | S | 0 | 0 |
| | | | 1303 | 830 | 236 | 235 | 2 | | |

- Molecule 12 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12 | BL | 137 | Total | C | N | O | S | 0 | 0 |
| | | | 1113 | 683 | 219 | 206 | 5 | | |

There are 7 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| BL | 23 | SER | - | expression tag | UNP Q14197 |
| BL | 24 | GLY | - | expression tag | UNP Q14197 |
| BL | 25 | GLY | - | expression tag | UNP Q14197 |
| BL | 26 | SER | - | expression tag | UNP Q14197 |
| BL | 27 | GLY | - | expression tag | UNP Q14197 |
| BL | 28 | SER | - | expression tag | UNP Q14197 |
| BL | 29 | GLY | - | expression tag | UNP Q14197 |

- Molecule 13 is a protein called uL13m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 13 | BN | 177 | Total | C | N | O | S | 0 | 0 |
| | | | 1444 | 926 | 258 | 253 | 7 | | |

- Molecule 14 is a protein called uL14m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 14 | BO | 115 | Total | C | N | O | S | 0 | 0 |
| | | | 896 | 562 | 176 | 154 | 4 | | |

- Molecule 15 is a protein called uL15m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 15 | BP | 288 | Total | C | N | O | S | 0 | 0 |
| | | | 2312 | 1473 | 430 | 403 | 6 | | |

- Molecule 16 is a protein called uL16m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 16 | BQ | 222 | Total | C | N | O | S | 0 | 0 |
| | | | 1803 | 1156 | 331 | 306 | 10 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| BQ | 237 | HIS | TYR | conflict | UNP F1RI89 |

- Molecule 17 is a protein called bL17m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17 | BR | 153 | Total | C | N | O | S | 0 | 0 |
| | | | 1240 | 777 | 236 | 222 | 5 | | |

- Molecule 18 is a protein called Mitochondrial ribosomal protein L18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 18 | BS | 143 | Total | C | N | O | S | 0 | 0 |
| | | | 1168 | 733 | 227 | 204 | 4 | | |

- Molecule 19 is a protein called Mitochondrial ribosomal protein L19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 19 | BT | 240 | Total | C | N | O | S | 0 | 0 |
| | | | 1954 | 1253 | 338 | 354 | 9 | | |

- Molecule 20 is a protein called Mitochondrial ribosomal protein L20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20 | BU | 140 | Total | C | N | O | S | 0 | 0 |
| | | | 1159 | 732 | 239 | 185 | 3 | | |

- Molecule 21 is a protein called Mitochondrial ribosomal protein L21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21 | BV | 155 | Total | C | N | O | S | 0 | 0 |
| | | | 1231 | 789 | 219 | 219 | 4 | | |

- Molecule 22 is a protein called uL22m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 22 | BW | 166 | Total | C | N | O | S | 0 | 0 |
| | | | 1374 | 876 | 258 | 234 | 6 | | |

- Molecule 23 is a protein called uL23m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23 | BX | 149 | Total | C | N | O | S | 0 | 0 |
| | | | 1181 | 752 | 227 | 200 | 2 | | |

- Molecule 24 is a protein called uL24m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 24 | BY | 206 | Total | C | N | O | S | 0 | 0 |
| | | | 1678 | 1056 | 308 | 309 | 5 | | |

- Molecule 25 is a protein called Mitochondrial ribosomal protein L37.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 25 | Ba | 393 | Total | C | N | O | S | 0 | 0 |
| | | | 3173 | 2040 | 556 | 565 | 12 | | |

- Molecule 26 is a protein called Mitochondrial ribosomal protein L38.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 26 | Bb | 354 | Total | C | N | O | S | 0 | 0 |
| | | | 2952 | 1876 | 542 | 525 | 9 | | |

- Molecule 27 is a protein called Mitochondrial ribosomal protein L39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 27 | Bc | 295 | Total | C | N | O | S | 0 | 0 |
| | | | 2408 | 1541 | 410 | 441 | 16 | | |

- Molecule 28 is a protein called Mitochondrial ribosomal protein L40.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 28 | Bd | 138 | Total | C | N | O | S | 0 | 0 |
| | | | 1158 | 729 | 211 | 217 | 1 | | |

- Molecule 29 is a protein called Mitochondrial ribosomal protein L41.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29 | Be | 122 | Total | C | N | O | S | 0 | 0 |
| | | | 972 | 628 | 168 | 173 | 3 | | |

- Molecule 30 is a protein called mL42.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 30 | Bf | 108 | Total | C | N | O | S | 0 | 0 |
| | | | 827 | 519 | 154 | 150 | 4 | | |

- Molecule 31 is a protein called Mitochondrial ribosomal protein L43.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 31 | Bg | 148 | Total | C | N | O | S | 0 | 0 |
| | | | 1167 | 727 | 225 | 212 | 3 | | |

- Molecule 32 is a protein called mL44.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 32 | Bh | 289 | Total | C | N | O | S | 0 | 0 |
| | | | 2319 | 1486 | 399 | 426 | 8 | | |

- Molecule 33 is a protein called Mitochondrial ribosomal protein L45.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 33 | Bi | 260 | Total | C | N | O | S | 0 | 0 |
| | | | 2138 | 1370 | 379 | 379 | 10 | | |

- Molecule 34 is a protein called Mitochondrial ribosomal protein L46.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 34 | Bj | 217 | Total | C | N | O | S | 0 | 0 |
| | | | 1775 | 1137 | 311 | 321 | 6 | | |

- Molecule 35 is a protein called 39S ribosomal protein L48, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 35 | Bk | 155 | Total | C | N | O | S | 0 | 0 |
| | | | 1246 | 796 | 214 | 231 | 5 | | |

- Molecule 36 is a protein called Mrpl34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 36 | Bl | 133 | Total | C | N | O | S | 0 | 0 |
| | | | 1097 | 709 | 192 | 194 | 2 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|----------------|
| Bl | 59 | ARG | LYS | conflict | UNP A0A0R4J8D6 |

- Molecule 37 is a protein called Mitochondrial ribosomal protein L50.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 37 | Bm | 109 | Total | C | N | O | S | 0 | 0 |
| | | | 893 | 568 | 160 | 162 | 3 | | |

- Molecule 38 is a protein called Mitochondrial ribosomal protein L51.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 38 | Bn | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 837 | 539 | 166 | 128 | 4 | | |

- Molecule 39 is a protein called mL52.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 39 | Bo | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 772 | 481 | 148 | 141 | 2 | | |

- Molecule 40 is a protein called mL53.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 40 | Bp | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 742 | 459 | 143 | 134 | 6 | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|----------------|
| Bp | 12 | ALA | SER | conflict | UNP A0A341D604 |
| Bp | 107 | SER | GLY | conflict | UNP A0A341D604 |

- Molecule 41 is a protein called mL54.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 41 | Bq | 54 | Total | C | N | O | S | 0 | 0 |
| | | | 474 | 304 | 88 | 81 | 1 | | |

- Molecule 42 is a protein called Mitochondrial ribosomal protein L57.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42 | Bt | 94 | Total | C | N | O | S | 0 | 0 |
| | | | 780 | 485 | 168 | 126 | 1 | | |

- Molecule 43 is a protein called mL62 (ICT1).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 43 | Bu | 151 | Total | C | N | O | S | 0 | 0 |
| | | | 1198 | 738 | 233 | 222 | 5 | | |

- Molecule 44 is a protein called mL64.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 44 | Bv | 135 | Total | C | N | O | S | 0 | 0 |
| | | | 1131 | 692 | 223 | 211 | 5 | | |

- Molecule 45 is a protein called 39S ribosomal protein S30, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 45 | Bw | 387 | Total | C | N | O | S | 0 | 0 |
| | | | 3126 | 2011 | 548 | 555 | 12 | | |

- Molecule 46 is a protein called Mitochondrial ribosomal protein S18A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 46 | Bx | 162 | Total | C | N | O | S | 0 | 0 |
| | | | 1325 | 845 | 249 | 224 | 7 | | |

- Molecule 47 is a RNA chain called 12S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|------|-----|---------|-------|
| 47 | AA | 960 | Total | C | N | O | P | 0 | 0 |
| | | | 20411 | 9162 | 3708 | 6581 | 960 | | |

- Molecule 48 is a protein called Mitochondrial ribosomal protein L12.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 48 | CL | 45 | Total | C | N | O | 0 | 0 |
| | | | 317 | 203 | 52 | 62 | | |
| 48 | DL | 27 | Total | C | N | O | 0 | 0 |
| | | | 213 | 137 | 33 | 43 | | |
| 48 | EL | 28 | Total | C | N | O | 0 | 0 |
| | | | 222 | 143 | 35 | 44 | | |
| 48 | FL | 27 | Total | C | N | O | 0 | 0 |
| | | | 213 | 137 | 33 | 43 | | |
| 48 | GL | 27 | Total | C | N | O | 0 | 0 |
| | | | 213 | 137 | 33 | 43 | | |
| 48 | HL | 26 | Total | C | N | O | 0 | 0 |
| | | | 205 | 131 | 32 | 42 | | |

- Molecule 49 is a protein called Mitochondrial ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 49 | AB | 220 | Total | C | N | O | S | 0 | 0 |
| | | | 1762 | 1126 | 326 | 304 | 6 | | |

- Molecule 50 is a protein called Mitochondrial ribosomal protein S24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 50 | AC | 132 | Total | C | N | O | S | 0 | 0 |
| | | | 1075 | 695 | 195 | 181 | 4 | | |

- Molecule 51 is a protein called Mitochondrial ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 51 | AE | 343 | Total | C | N | O | S | 0 | 0 |
| | | | 2732 | 1707 | 527 | 487 | 11 | | |

- Molecule 52 is a protein called bS6m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 52 | AF | 122 | Total | C | N | O | S | 0 | 0 |
| | | | 981 | 620 | 178 | 177 | 6 | | |

- Molecule 53 is a protein called Mitochondrial ribosomal protein S7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 53 | AG | 208 | Total | C | N | O | S | 0 | 0 |
| | | | 1721 | 1097 | 314 | 299 | 11 | | |

- Molecule 54 is a protein called uS9m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 54 | AI | 328 | Total | C | N | O | S | 0 | 0 |
| | | | 2650 | 1678 | 478 | 481 | 13 | | |

- Molecule 55 is a protein called Mitochondrial ribosomal protein S10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 55 | AJ | 140 | Total | C | N | O | S | 0 | 0 |
| | | | 1155 | 746 | 197 | 208 | 4 | | |

- Molecule 56 is a protein called uS11m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 56 | AK | 137 | Total | C | N | O | S | 0 | 0 |
| | | | 1007 | 631 | 193 | 180 | 3 | | |

- Molecule 57 is a protein called Mitochondrial ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 57 | AL | 109 | Total | C | N | O | S | 0 | 0 |
| | | | 840 | 524 | 172 | 138 | 6 | | |

- Molecule 58 is a protein called Mitochondrial ribosomal protein S14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 58 | AN | 101 | Total | C | N | O | S | 0 | 0 |
| | | | 858 | 534 | 174 | 144 | 6 | | |

- Molecule 59 is a protein called uS15m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 59 | AO | 175 | Total | C | N | O | S | 0 | 0 |
| | | | 1448 | 919 | 272 | 248 | 9 | | |

- Molecule 60 is a protein called 28S ribosomal protein S16, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 60 | AP | 117 | Total | C | N | O | S | 0 | 0 |
| | | | 932 | 588 | 184 | 155 | 5 | | |

- Molecule 61 is a protein called uS17m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 61 | AQ | 112 | Total | C | N | O | S | 0 | 0 |
| | | | 875 | 568 | 153 | 151 | 3 | | |

- Molecule 62 is a protein called Mitochondrial ribosomal protein S18C.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 62 | AR | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 784 | 507 | 132 | 138 | 7 | | |

- Molecule 63 is a protein called bS21m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 63 | AU | 86 | Total | C | N | O | S | 0 | 0 |
| | | | 734 | 453 | 148 | 125 | 8 | | |

- Molecule 64 is a RNA chain called fMet-tRNAMet (P site).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 64 | AV | 71 | Total | C | N | O | P | 0 | 0 |
| | | | 1498 | 673 | 264 | 491 | 70 | | |

There are 3 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------|---------------|
| AV | 69 | C | - | insertion | GB 1208989970 |
| AV | 70 | C | - | insertion | GB 1208989970 |
| AV | 71 | A | - | insertion | GB 1208989970 |

- Molecule 65 is a RNA chain called mRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---|---------|-------|
| 65 | AX | 6 | Total | C | N | O | P | 0 | 0 |
| | | | 131 | 59 | 27 | 39 | 6 | | |

- Molecule 66 is a protein called unknown.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---------|-------|
| 66 | AZ | 18 | Total | C | N | O | 0 | 0 |
| | | | 90 | 54 | 18 | 18 | | |

- Molecule 67 is a protein called Mitochondrial ribosomal protein S22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 67 | Aa | 292 | Total | C | N | O | S | 0 | 0 |
| | | | 2378 | 1518 | 409 | 442 | 9 | | |

- Molecule 68 is a protein called mS23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 68 | Ab | 135 | Total | C | N | O | S | 0 | 0 |
| | | | 1101 | 709 | 199 | 192 | 1 | | |

- Molecule 69 is a protein called Mitochondrial ribosomal protein S25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 69 | Ac | 169 | Total | C | N | O | S | 0 | 0 |
| | | | 1367 | 876 | 236 | 245 | 10 | | |

- Molecule 70 is a protein called Mitochondrial ribosomal protein S26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 70 | Ad | 177 | Total | C | N | O | S | 0 | 0 |
| | | | 1467 | 904 | 288 | 273 | 2 | | |

- Molecule 71 is a protein called Mitochondrial ribosomal protein S27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 71 | Ae | 388 | Total | C | N | O | S | 0 | 0 |
| | | | 3109 | 1971 | 535 | 589 | 14 | | |

- Molecule 72 is a protein called Mitoribosomal protein ms28, mrps28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 72 | Af | 99 | Total | C | N | O | S | 0 | 0 |
| | | | 778 | 494 | 134 | 146 | 4 | | |

- Molecule 73 is a protein called Death associated protein 3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 73 | Ag | 353 | Total | C | N | O | S | 0 | 0 |
| | | | 2875 | 1837 | 515 | 513 | 10 | | |

- Molecule 74 is a protein called Mitochondrial ribosomal protein S31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 74 | Ah | 120 | Total | C | N | O | S | 0 | 0 |
| | | | 1015 | 659 | 168 | 185 | 3 | | |

There are 10 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------|------------|
| Ah | 180 | UNK | - | insertion | UNP F1RME2 |
| Ah | 181 | GLN | - | insertion | UNP F1RME2 |
| Ah | 182 | LYS | - | insertion | UNP F1RME2 |
| Ah | 184 | GLY | - | insertion | UNP F1RME2 |
| Ah | 185 | GLU | LYS | conflict | UNP F1RME2 |
| Ah | 187 | PRO | LYS | conflict | UNP F1RME2 |
| Ah | 189 | ILE | LEU | conflict | UNP F1RME2 |
| Ah | 190 | SER | ILE | conflict | UNP F1RME2 |
| Ah | 237 | SER | - | insertion | UNP F1RME2 |
| Ah | 238 | PHE | - | insertion | UNP F1RME2 |

- Molecule 75 is a protein called mS33.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 75 | Ai | 99 | Total | C | N | O | S | 0 | 0 |
| | | | 824 | 522 | 156 | 143 | 3 | | |

- Molecule 76 is a protein called mS34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 76 | Aj | 213 | Total | C | N | O | S | 0 | 0 |
| | | | 1788 | 1131 | 338 | 311 | 8 | | |

- Molecule 77 is a protein called Mitochondrial ribosomal protein S35.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 77 | Ak | 275 | Total | C | N | O | S | 0 | 0 |
| | | | 2222 | 1414 | 380 | 419 | 9 | | |

- Molecule 78 is a protein called mS37.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 78 | Am | 116 | Total | C | N | O | S | 0 | 0 |
| | | | 930 | 577 | 185 | 160 | 8 | | |

- Molecule 79 is a protein called Aurora kinase A interacting protein 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 79 | An | 72 | Total | C | N | O | S | 0 | 0 |
| | | | 639 | 407 | 139 | 92 | 1 | | |

- Molecule 80 is a protein called Pentatricopeptide repeat domain 3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 80 | Ao | 572 | Total | C | N | O | S | 0 | 0 |
| | | | 4526 | 2898 | 770 | 834 | 24 | | |

- Molecule 81 is a protein called 28S ribosomal protein S18b, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 81 | Ap | 190 | Total | C | N | O | S | 0 | 0 |
| | | | 1564 | 991 | 292 | 273 | 8 | | |

- Molecule 82 is a protein called Mitochondrial ribosomal protein L27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 82 | B0 | 110 | Total | C | N | O | S | 0 | 0 |
| | | | 857 | 553 | 156 | 145 | 3 | | |

- Molecule 83 is a protein called Mitochondrial ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 83 | B1 | 244 | Total | C | N | O | S | 0 | 0 |
| | | | 2036 | 1315 | 363 | 353 | 5 | | |

- Molecule 84 is a protein called Mitochondrial ribosomal protein L47.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 84 | B2 | 179 | Total | C | N | O | S | 0 | 0 |
| | | | 1548 | 992 | 290 | 260 | 6 | | |

- Molecule 85 is a protein called uL30m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 85 | B3 | 118 | Total | C | N | O | S | 0 | 0 |
| | | | 968 | 622 | 178 | 165 | 3 | | |

- Molecule 86 is a protein called bL31m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 86 | B4 | 62 | Total | C | N | O | S | 0 | 0 |
| | | | 474 | 296 | 94 | 81 | 3 | | |

- Molecule 87 is a protein called bL32m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 87 | B5 | 110 | Total | C | N | O | S | 0 | 0 |
| | | | 902 | 553 | 181 | 162 | 6 | | |

- Molecule 88 is a protein called bL33m.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 88 | B6 | 52 | Total | C | N | O | S | 0 | 0 |
| | | | 425 | 274 | 78 | 71 | 2 | | |

- Molecule 89 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|---------|---------|
| 89 | B9 | 1 | Total 1 | Zn 1 | 0 |
| 89 | Bx | 1 | Total 1 | Zn 1 | 0 |
| 89 | AR | 1 | Total 1 | Zn 1 | 0 |
| 89 | Ac | 1 | Total 1 | Zn 1 | 0 |
| 89 | Ap | 1 | Total 1 | Zn 1 | 0 |
| 89 | B5 | 1 | Total 1 | Zn 1 | 0 |

- Molecule 90 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

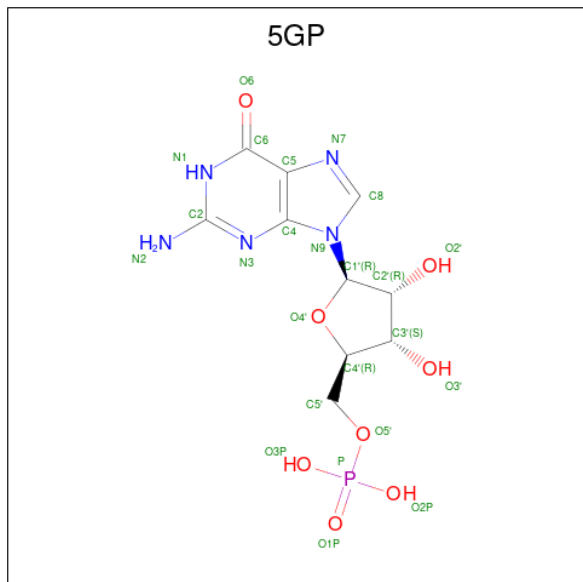
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|--------------|-----------|---------|
| 90 | BA | 212 | Total 212 | Mg 212 | 0 |
| 90 | BB | 1 | Total 1 | Mg 1 | 0 |
| 90 | BD | 3 | Total 3 | Mg 3 | 0 |
| 90 | BE | 1 | Total 1 | Mg 1 | 0 |
| 90 | BP | 3 | Total 3 | Mg 3 | 0 |
| 90 | BQ | 1 | Total 1 | Mg 1 | 0 |
| 90 | BR | 1 | Total 1 | Mg 1 | 0 |
| 90 | Be | 2 | Total 2 | Mg 2 | 0 |
| 90 | Bl | 1 | Total 1 | Mg 1 | 0 |
| 90 | Bt | 1 | Total 1 | Mg 1 | 0 |
| 90 | AA | 101 | Total 101 | Mg 101 | 0 |
| 90 | AB | 1 | Total 1 | Mg 1 | 0 |
| 90 | AL | 1 | Total 1 | Mg 1 | 0 |
| 90 | AV | 1 | Total 1 | Mg 1 | 0 |

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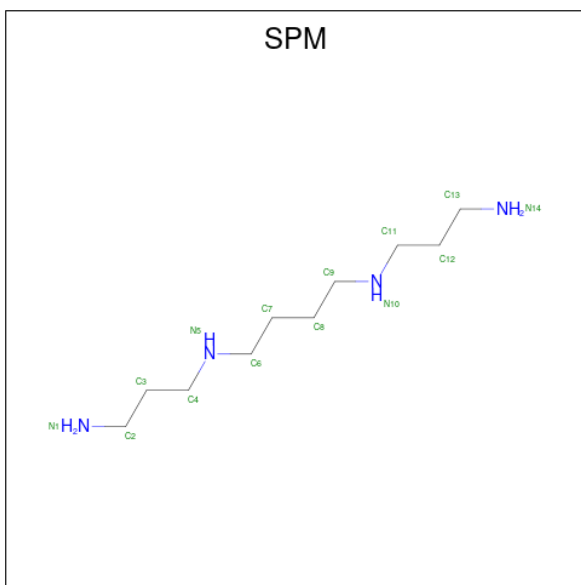
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 90 | AX | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 90 | Ag | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 90 | Am | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 90 | An | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 90 | B3 | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |

- Molecule 91 is GUANOSINE-5'-MONOPHOSPHATE (three-letter code: 5GP) (formula: $C_{10}H_{14}N_5O_8P$).



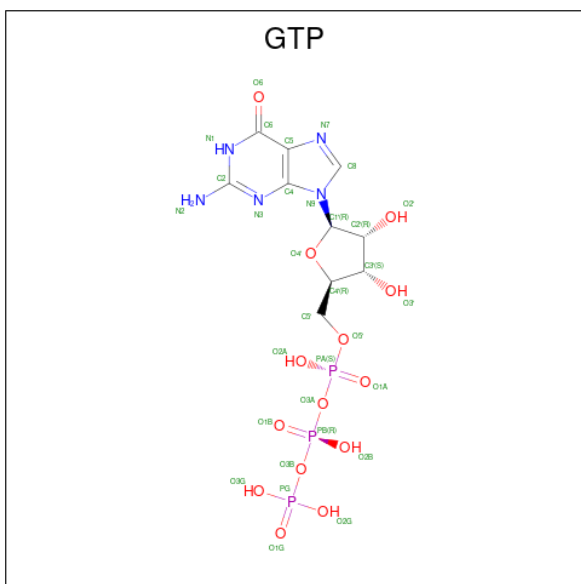
| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---|---------|
| 91 | BA | 1 | Total | C | N | O | P | 0 |
| | | | 24 | 10 | 5 | 8 | 1 | |
| 91 | BA | 1 | Total | C | N | O | P | 0 |
| | | | 24 | 10 | 5 | 8 | 1 | |

- Molecule 92 is SPERMINE (three-letter code: SPM) (formula: $C_{10}H_{26}N_4$).



| Mol | Chain | Residues | Atoms | | | AltConf |
|-----|-------|----------|-------------|---------|--------|---------|
| 92 | BA | 1 | Total 14 | C 10 | N 4 | 0 |
| 92 | BA | 1 | Total 14 | C 10 | N 4 | 0 |
| 92 | AA | 1 | Total 14 | C 10 | N 4 | 0 |

- Molecule 93 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{14}\text{P}_3$).



| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|----|---|---------|
| 93 | Ag | 1 | Total | C | N | O | P | 0 |
| | | | 32 | 10 | 5 | 14 | 3 | |

- Molecule 94 is water.

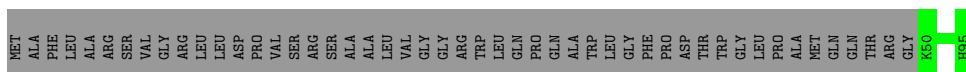
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|---|---------|
| 94 | Ag | 3 | Total | O | 0 |
| | | | 3 | 3 | |

3 Residue-property plots [i](#)

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

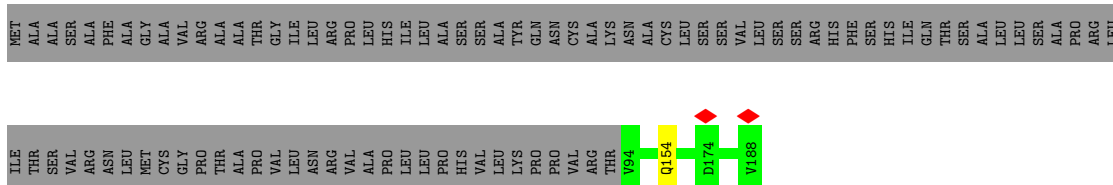
- Molecule 1: Mitochondrial ribosomal protein L34

Chain B7: 



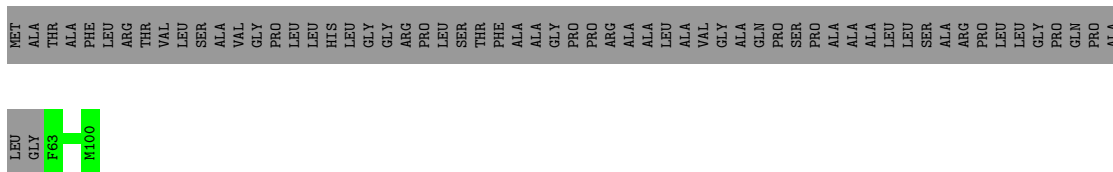
- Molecule 2: Mitochondrial ribosomal protein L35

Chain B8: 



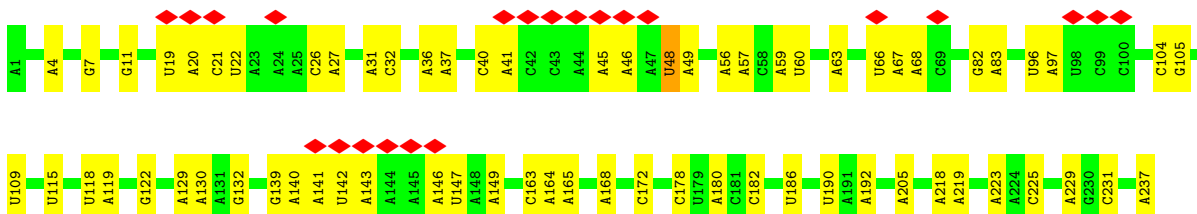
- Molecule 3: Ribosomal protein

Chain B9: 

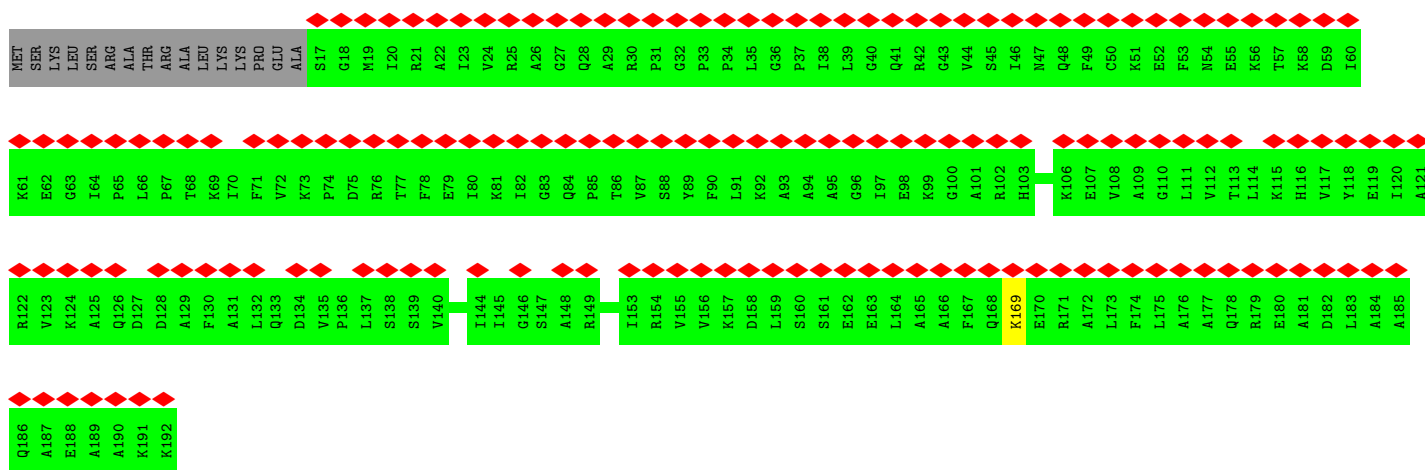
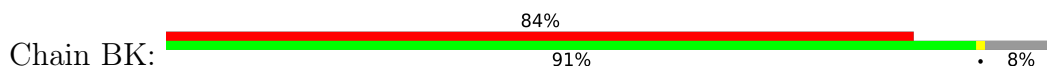


- Molecule 4: 16S rRNA

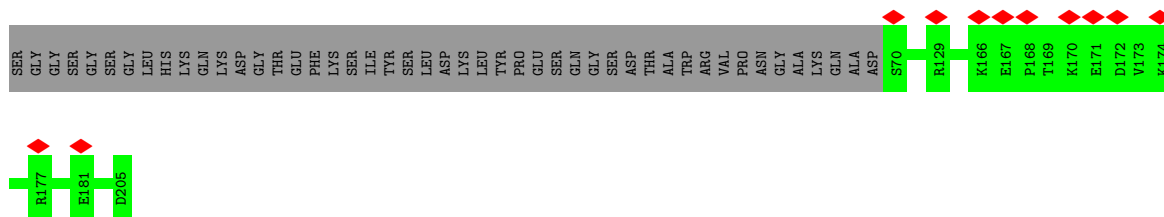
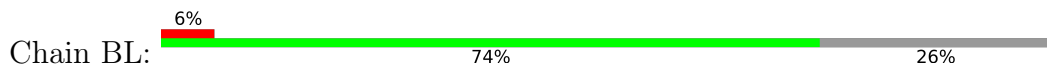
Chain BA: 



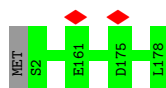
- Molecule 11: Mitochondrial ribosomal protein L11




- Molecule 12: Peptidyl-tRNA hydrolase ICT1, mitochondrial

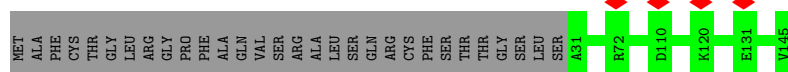


- Molecule 13: uL13m



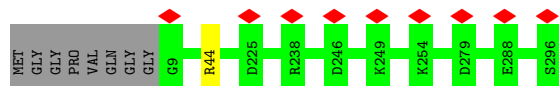
- Molecule 14: uL14m

Chain BO:  79% 21%



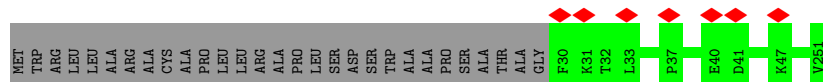
- Molecule 15: uL15m

Chain BP:  97% .



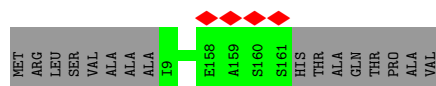
- Molecule 16: uL16m

Chain BQ:  88% 12%




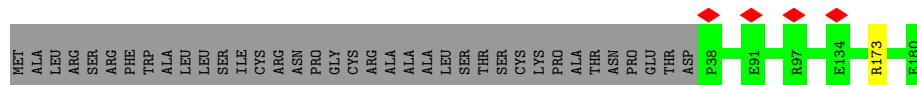
- Molecule 17: bL17m

Chain BR:  91% 9%




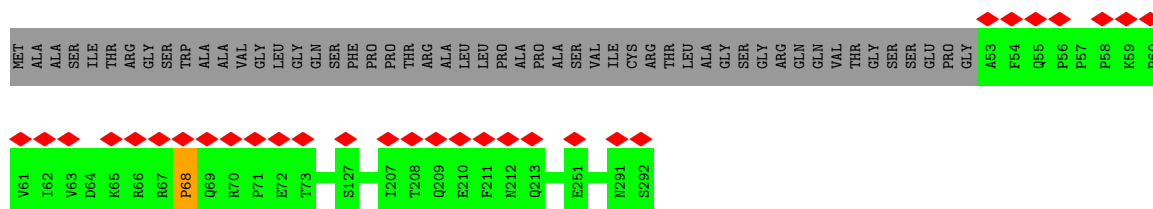
- Molecule 18: Mitochondrial ribosomal protein L18

Chain BS:  79% 21%



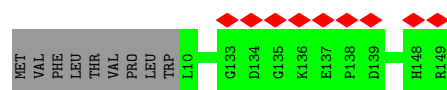
- Molecule 19: Mitochondrial ribosomal protein L19

Chain BT:  10% 82% 18%



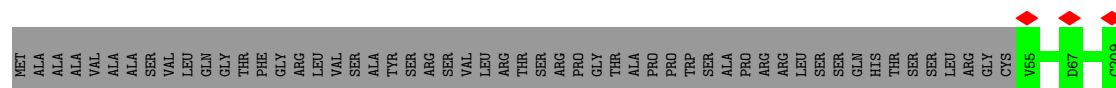
- Molecule 20: Mitochondrial ribosomal protein L20

Chain BU:  6% 94% 6%



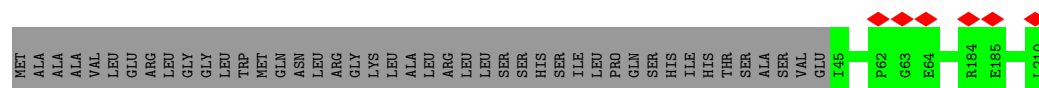
- Molecule 21: Mitochondrial ribosomal protein L21

Chain BV: 74% 26%



- Molecule 22: uL22m

Chain BW: 79% 21%



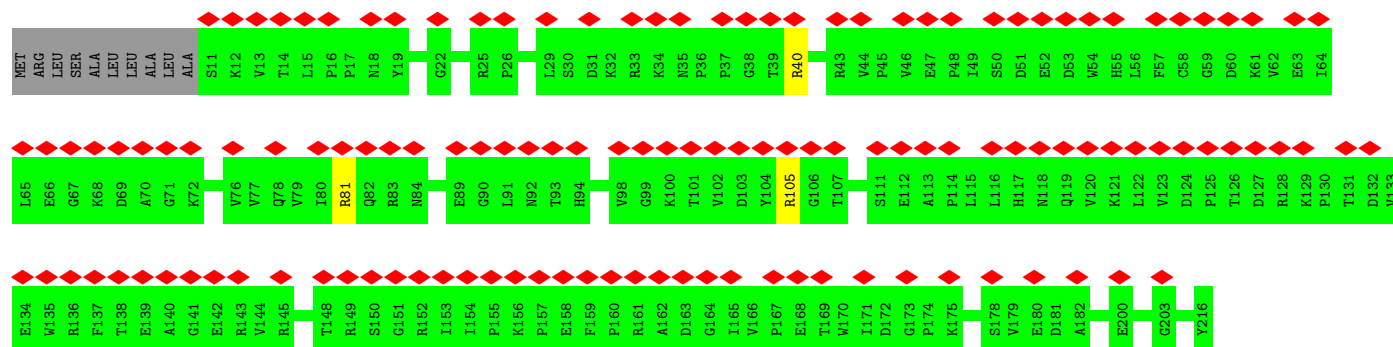
- Molecule 23: uL23m

Chain BX: 22% 99%



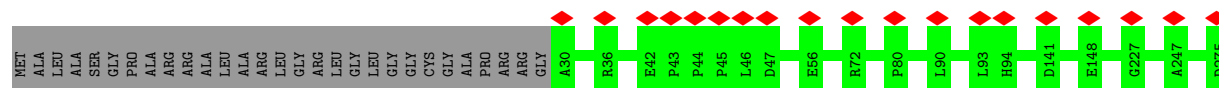
- Molecule 24: uL24m

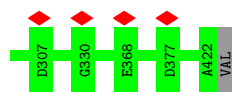
Chain BY: 60% 94% 5%



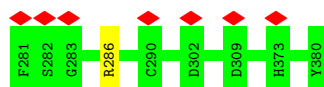
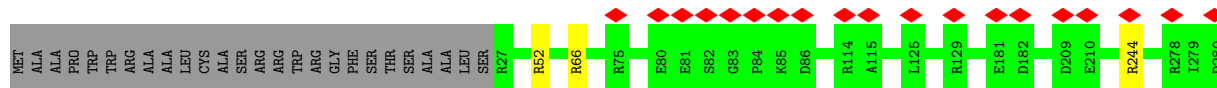
- Molecule 25: Mitochondrial ribosomal protein L37

Chain Ba: 5% 93% 7%

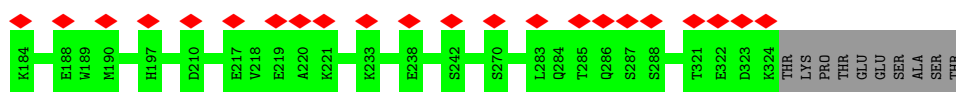
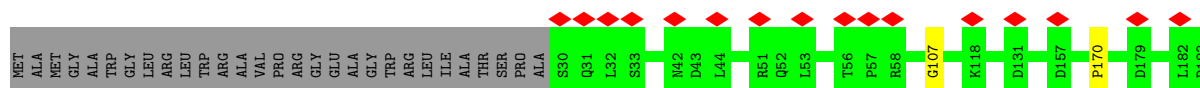
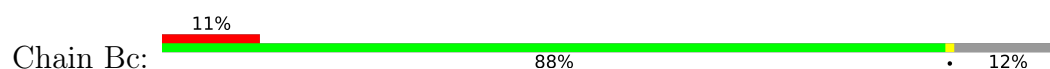




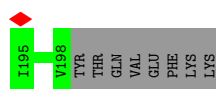
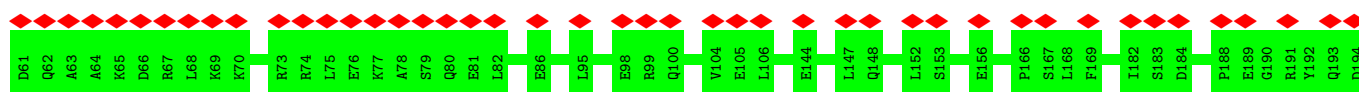
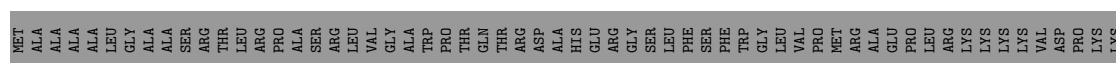
• Molecule 26: Mitochondrial ribosomal protein L38



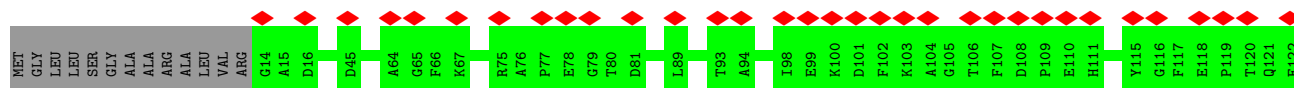
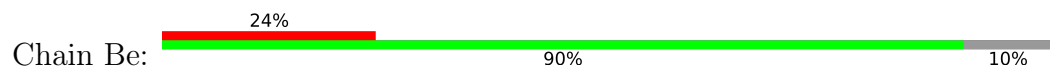
• Molecule 27: Mitochondrial ribosomal protein L39



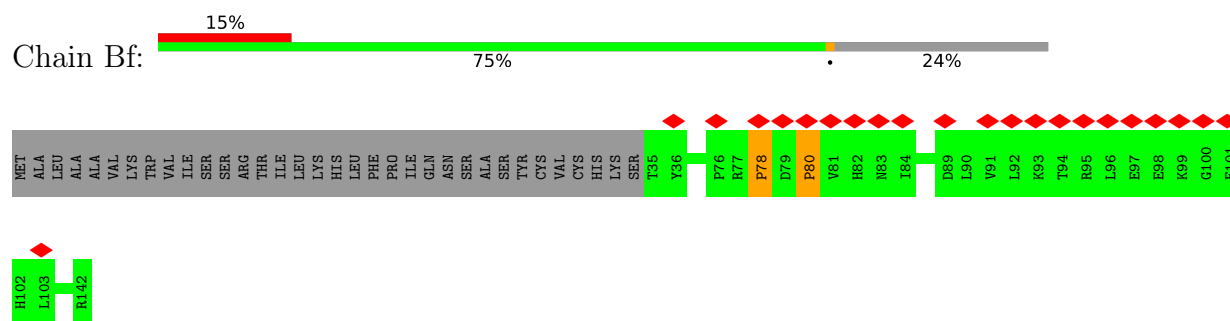
• Molecule 28: Mitochondrial ribosomal protein L40



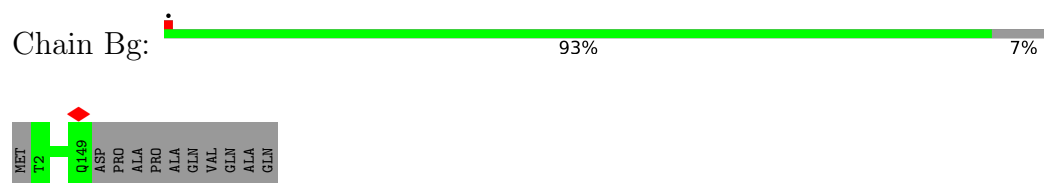
• Molecule 29: Mitochondrial ribosomal protein L41



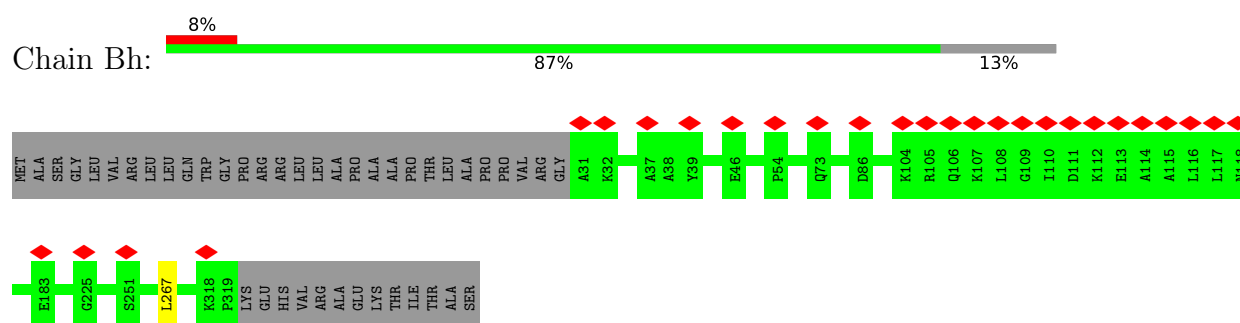
- Molecule 30: mL42



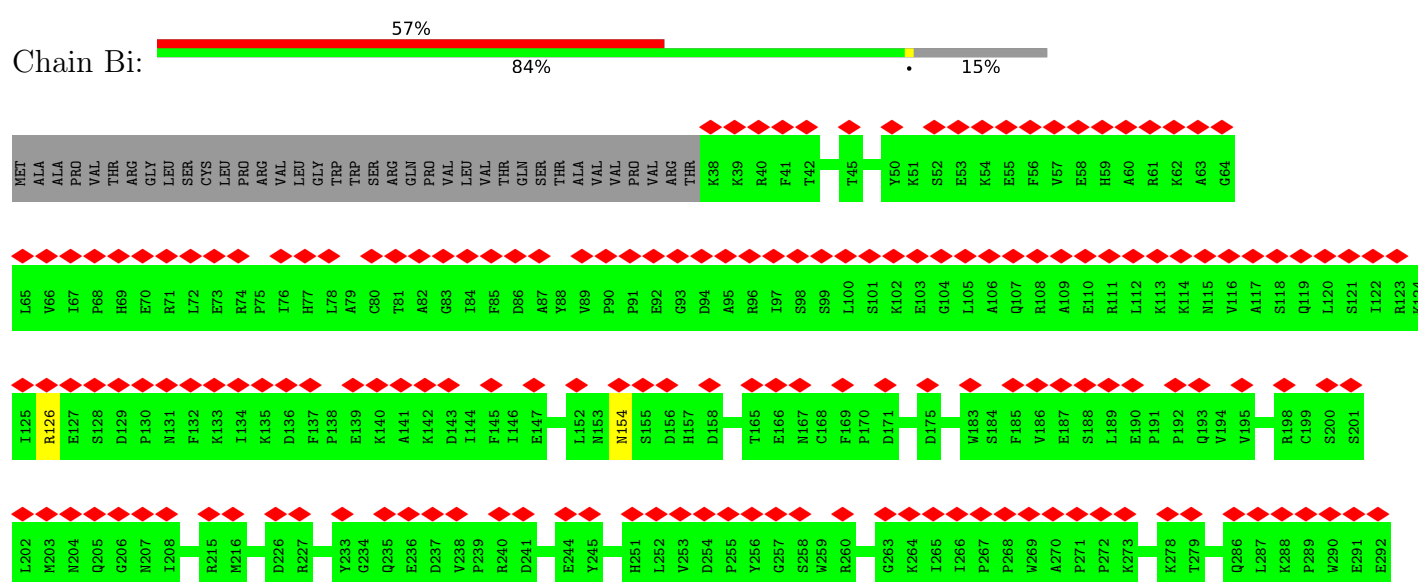
- Molecule 31: Mitochondrial ribosomal protein L43

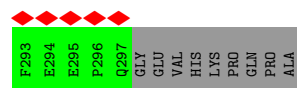


- Molecule 32: mL44

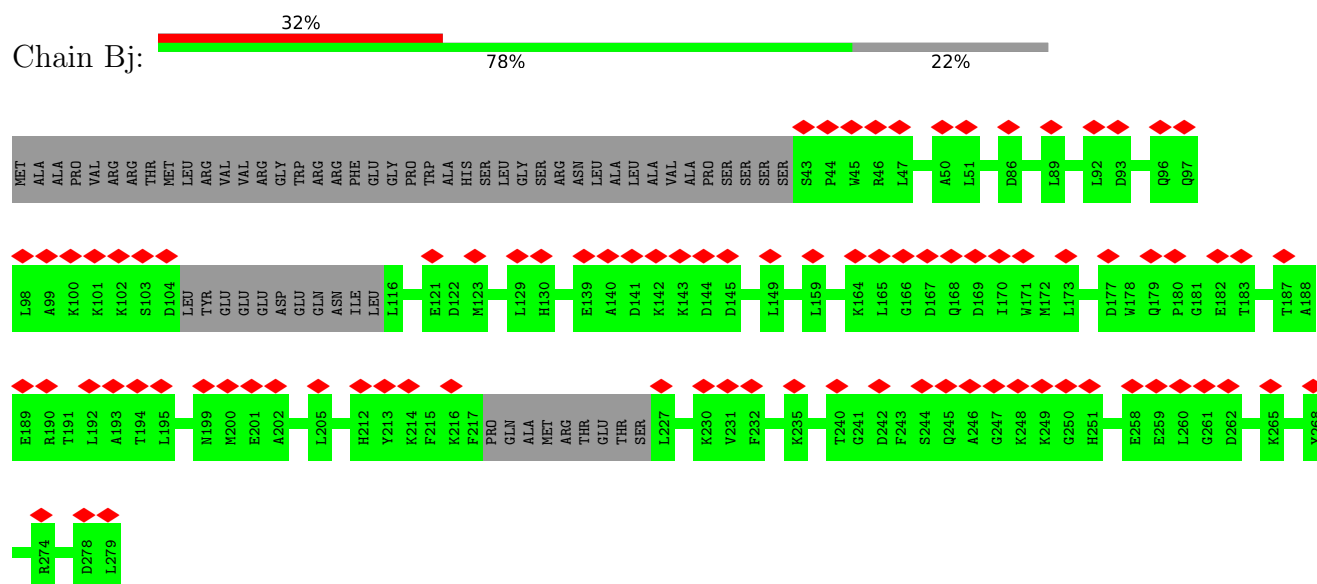


- Molecule 33: Mitochondrial ribosomal protein L45

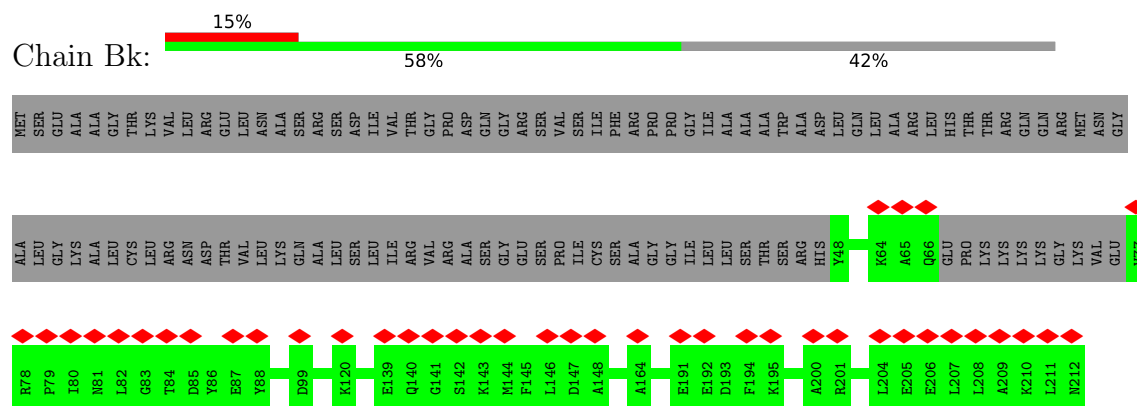




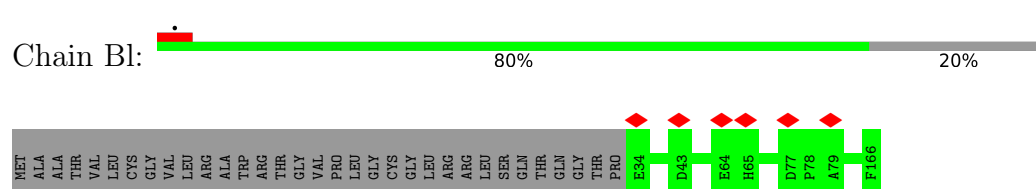
• Molecule 34: Mitochondrial ribosomal protein L46



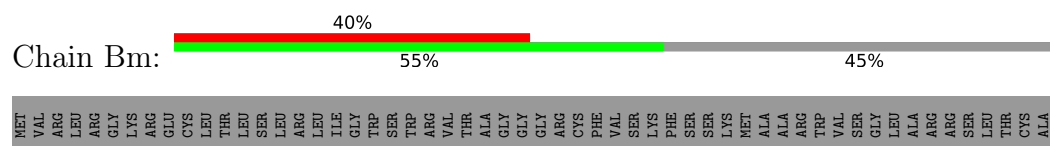
• Molecule 35: 39S ribosomal protein L48, mitochondrial

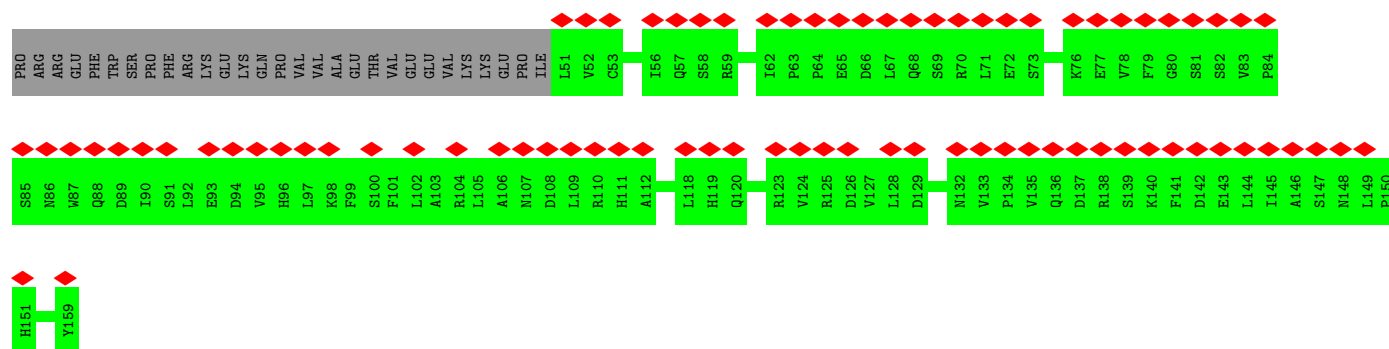


• Molecule 36: Mrpl34

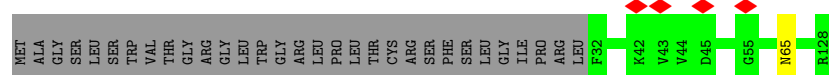
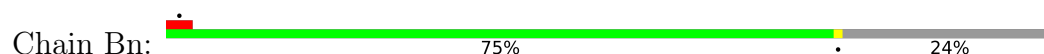


• Molecule 37: Mitochondrial ribosomal protein L50

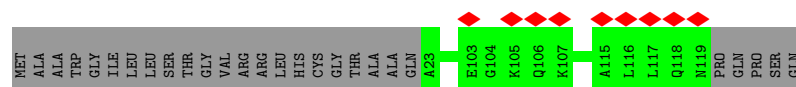
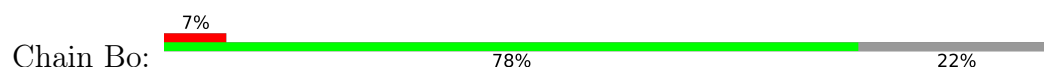




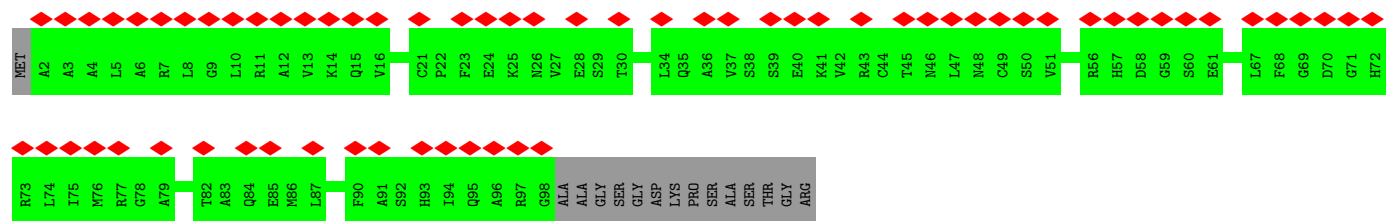
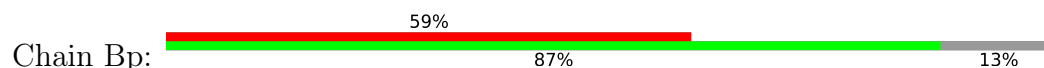
- Molecule 38: Mitochondrial ribosomal protein L51



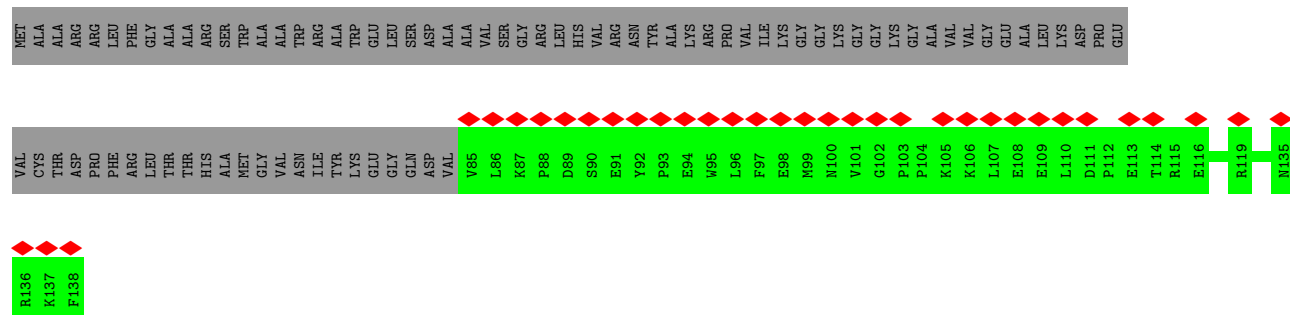
- Molecule 39: mL52

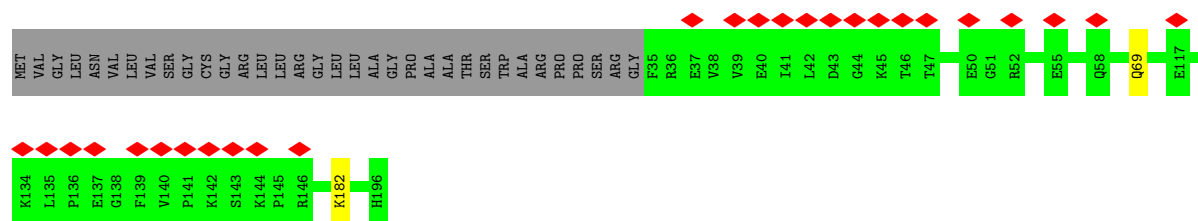


- Molecule 40: mL53

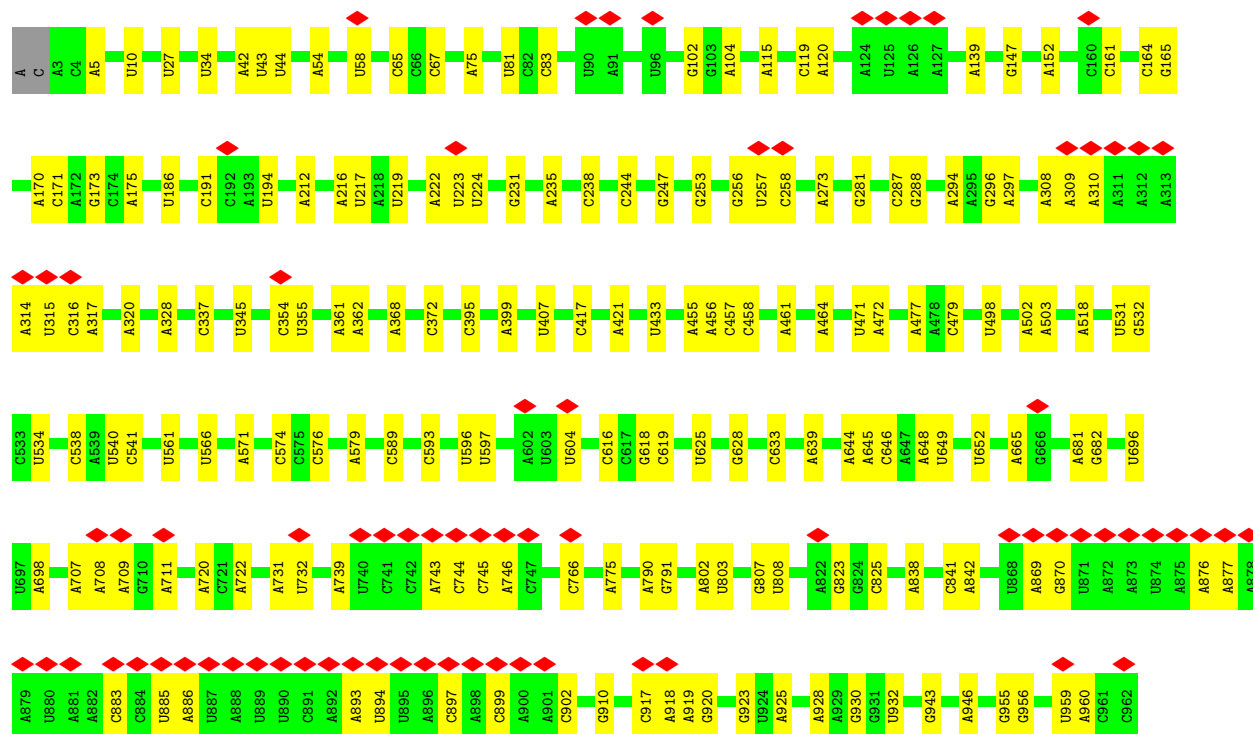
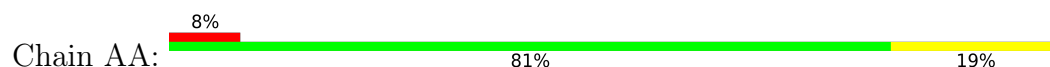


- Molecule 41: mL54

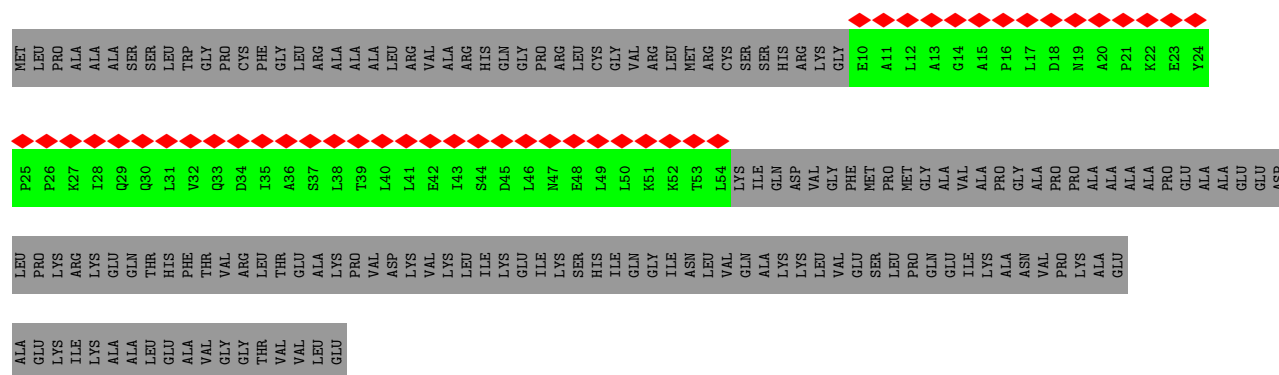




• Molecule 47: 12S rRNA

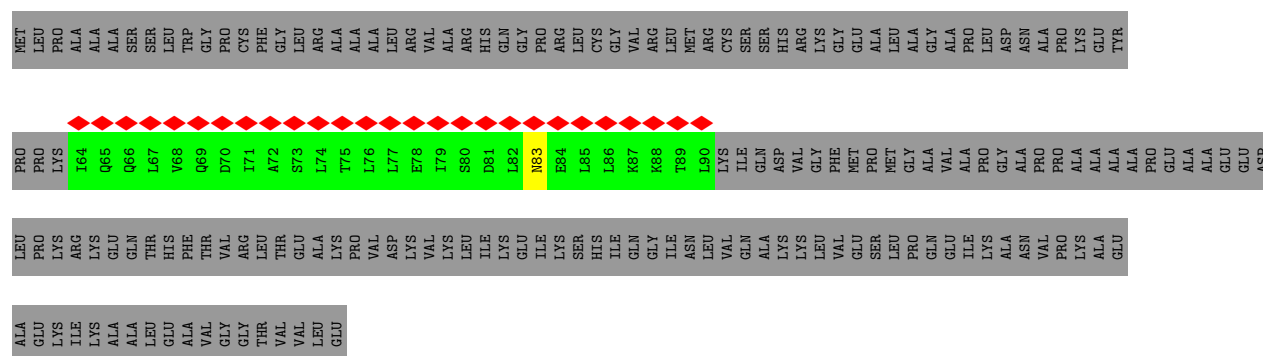


• Molecule 48: Mitochondrial ribosomal protein L12



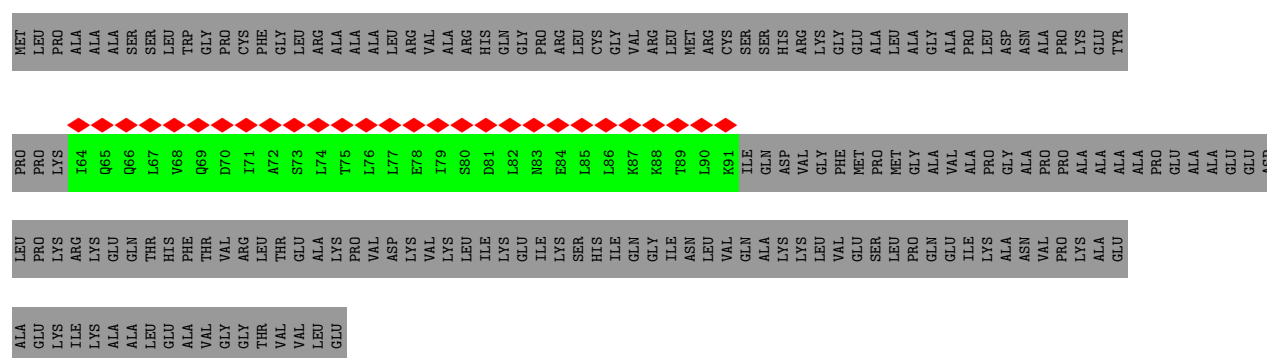
• Molecule 48: Mitochondrial ribosomal protein L12

Chain DL:  14%
13% 86%



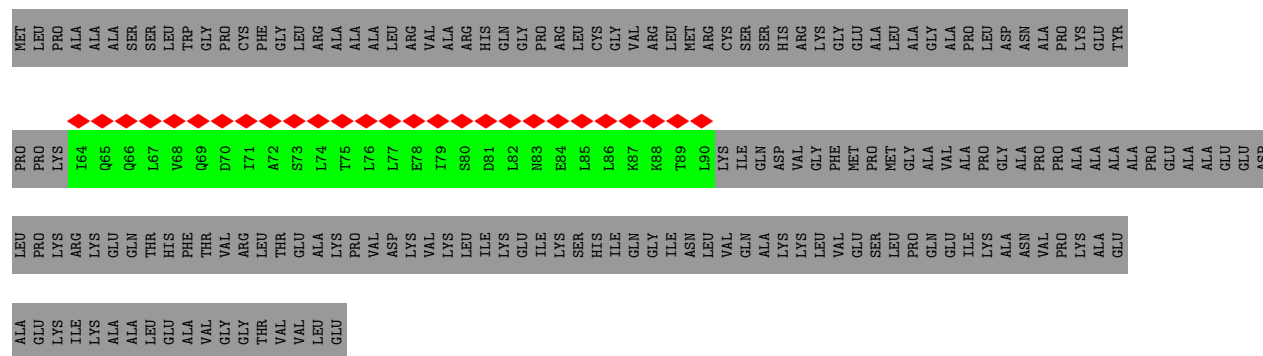
- Molecule 48: Mitochondrial ribosomal protein L12

Chain EL: 



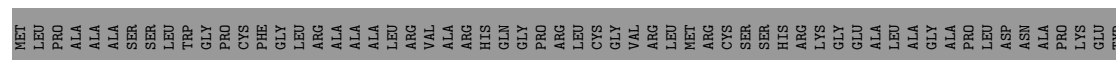
- Molecule 48: Mitochondrial ribosomal protein L12

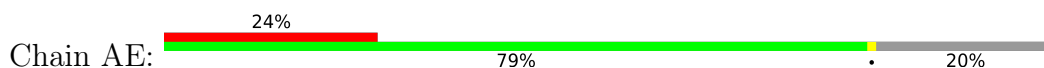
Chain FL:  14% 86%



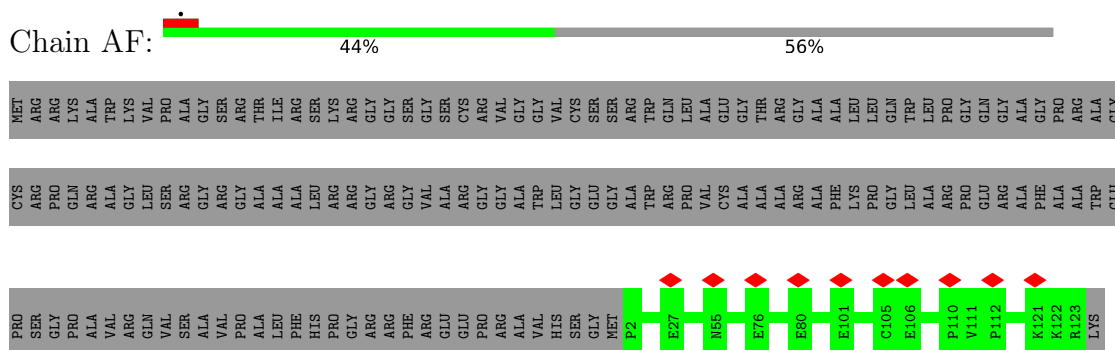
- Molecule 48: Mitochondrial ribosomal protein L12

Chain GL: 

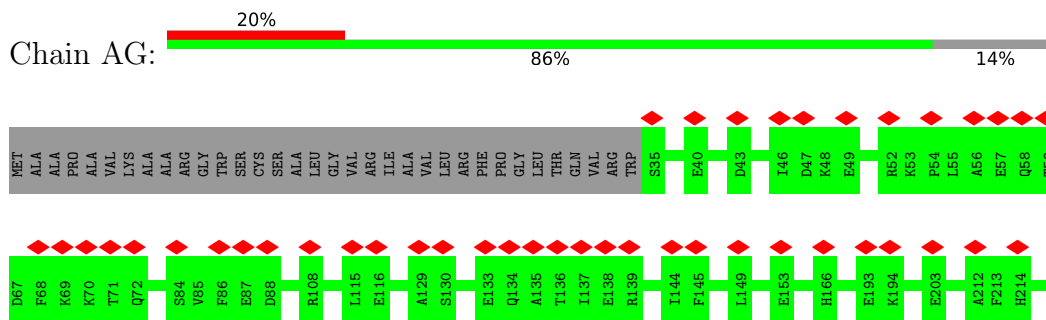




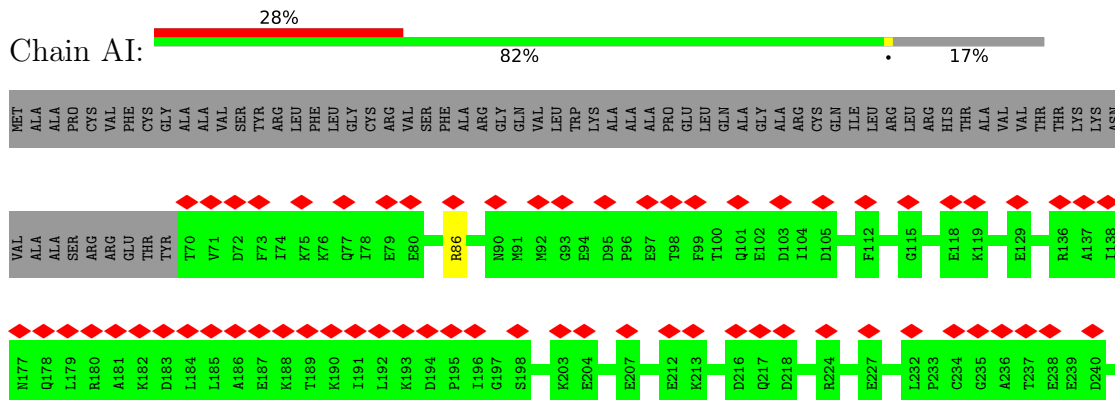
- Molecule 52: bS6m

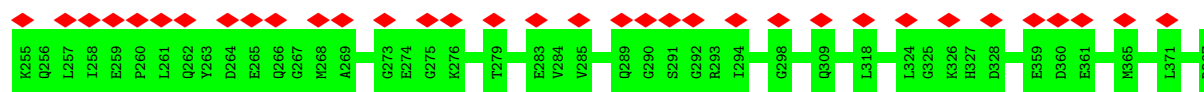


- Molecule 53: Mitochondrial ribosomal protein S7

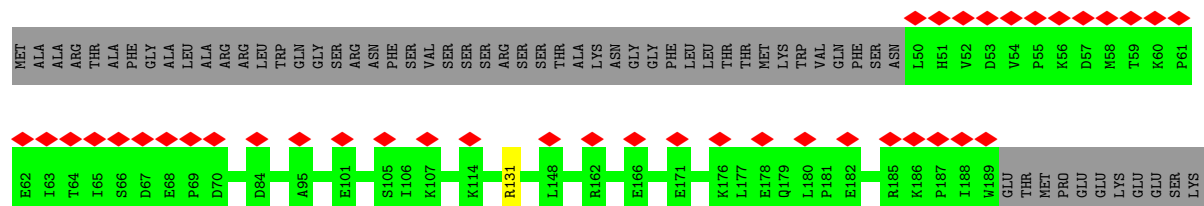


- Molecule 54: uS9m

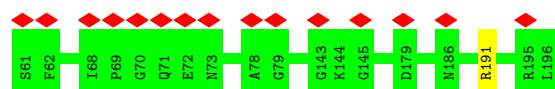
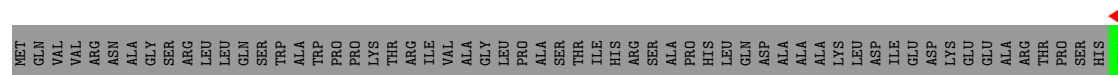




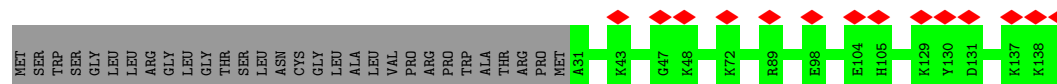
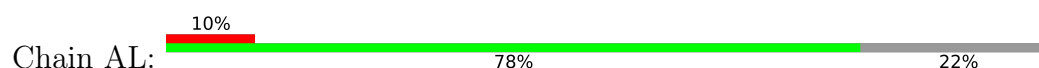
- Molecule 55: Mitochondrial ribosomal protein S10



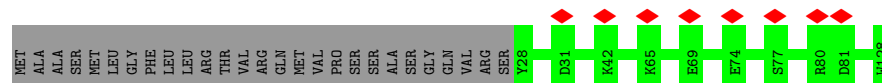
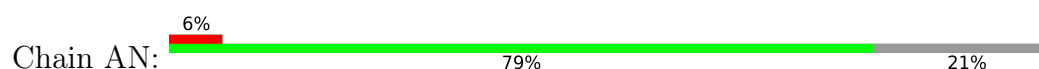
- Molecule 56: uS11m



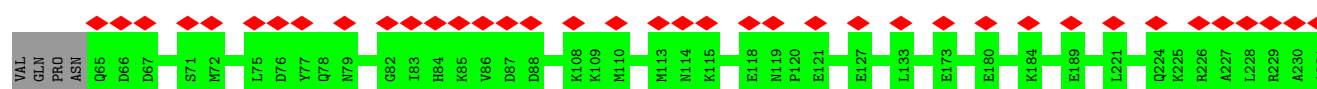
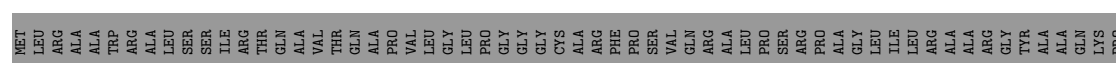
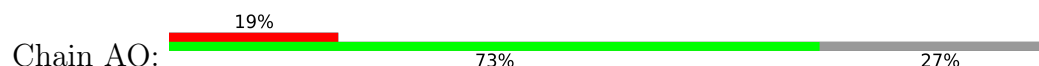
- Molecule 57: Mitochondrial ribosomal protein S12

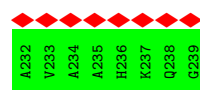


- Molecule 58: Mitochondrial ribosomal protein S14

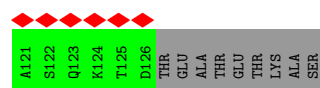
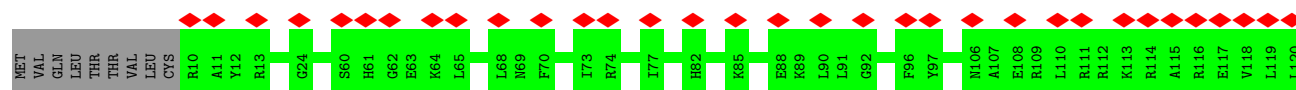
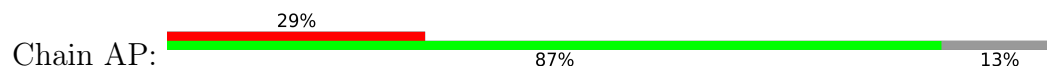


- Molecule 59: uS15m

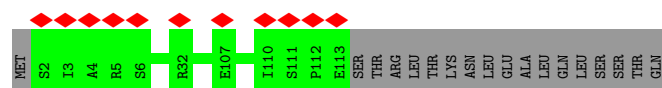
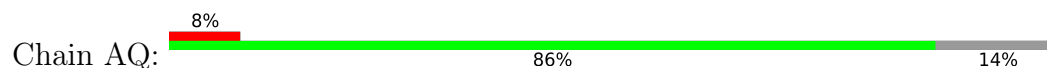




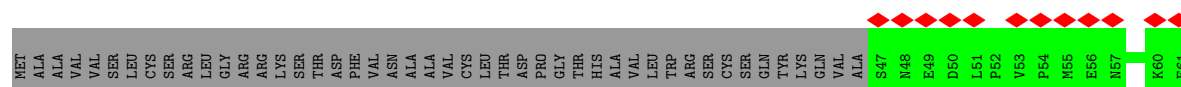
- Molecule 60: 28S ribosomal protein S16, mitochondrial



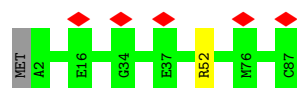
- Molecule 61: uS17m



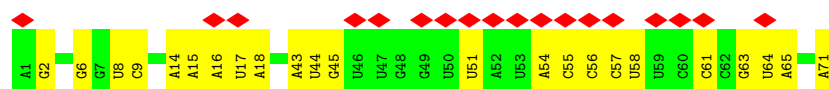
- Molecule 62: Mitochondrial ribosomal protein S18C



- Molecule 63: bS21m



- Molecule 64: fMet-tRNA^{Met} (P site)




- Molecule 65: mRNA

Chain AX:  67% 33%




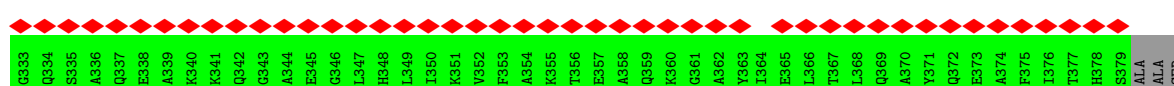
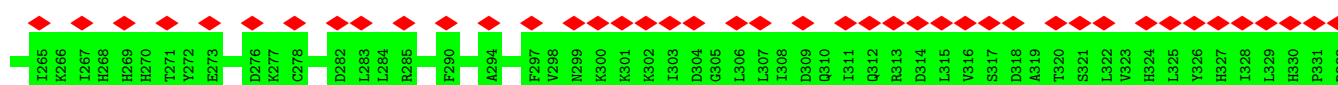
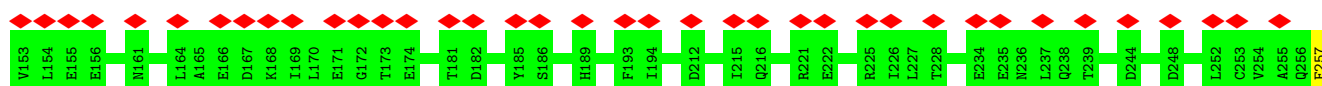
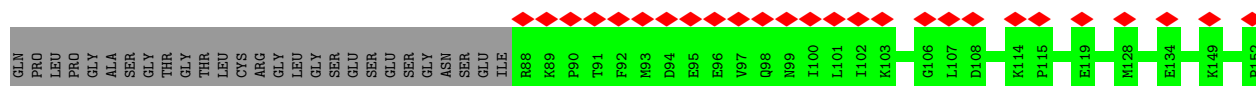
- Molecule 66: unknown

Chain AZ:  78% 100%




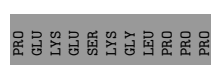
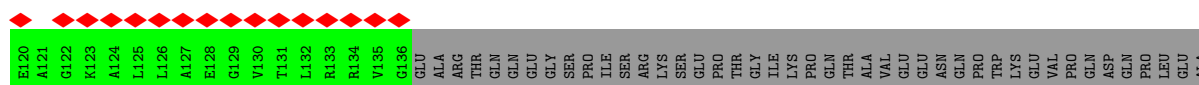
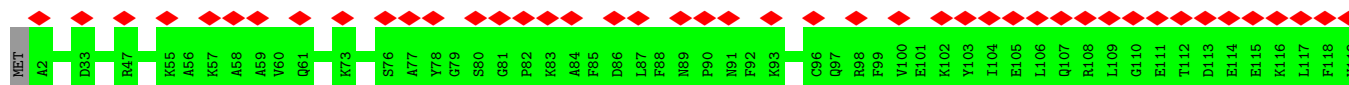
- Molecule 67: Mitochondrial ribosomal protein S22

Chain Aa:  40% 76% 24%



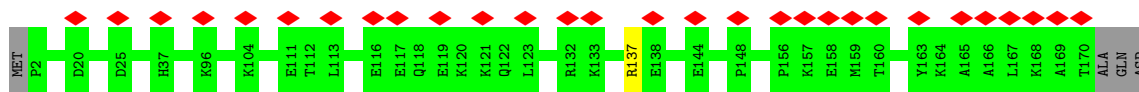
- Molecule 68: mS23

Chain Ab:  32% 71% 29%

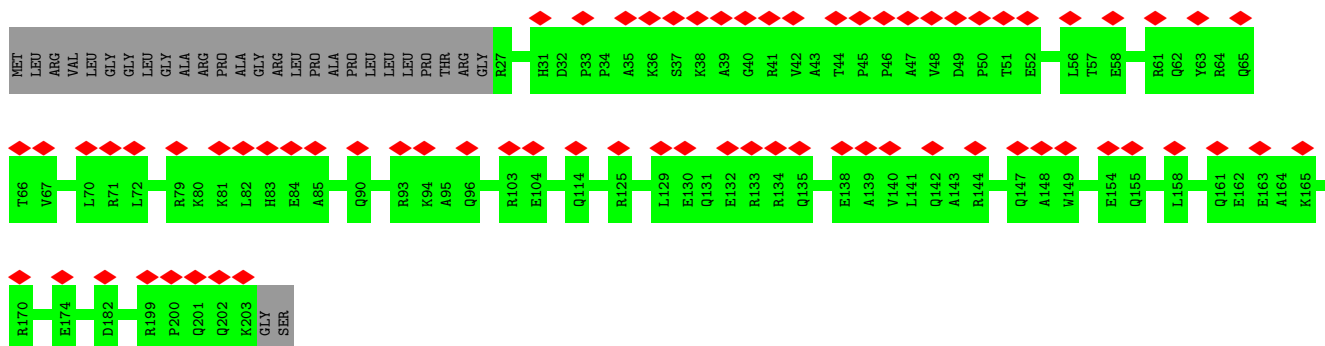
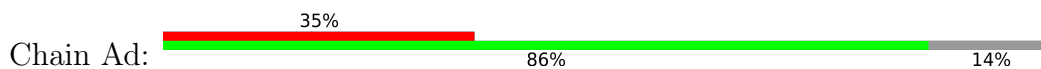


- Molecule 69: Mitochondrial ribosomal protein S25

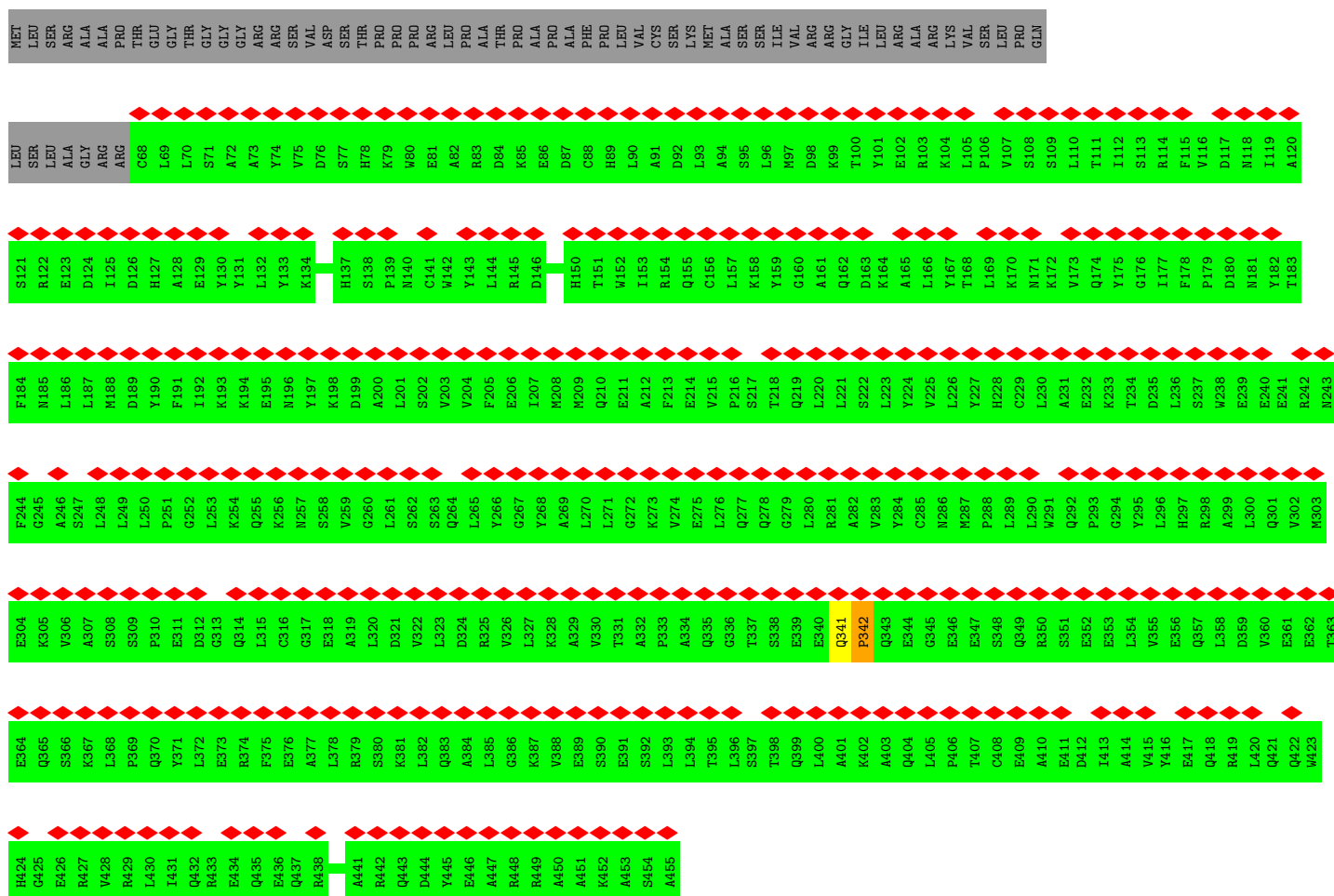
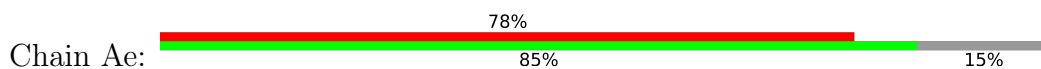
Chain Ac:  17% 97%



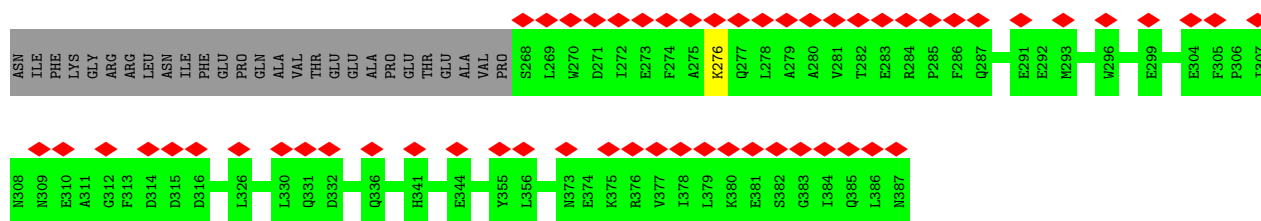
- Molecule 70: Mitochondrial ribosomal protein S26



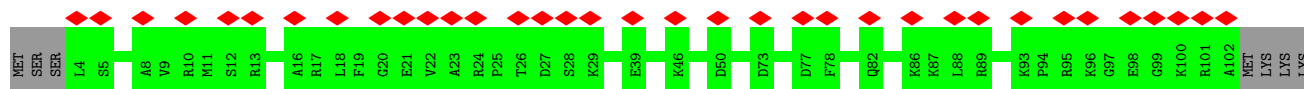
- Molecule 71: Mitochondrial ribosomal protein S27



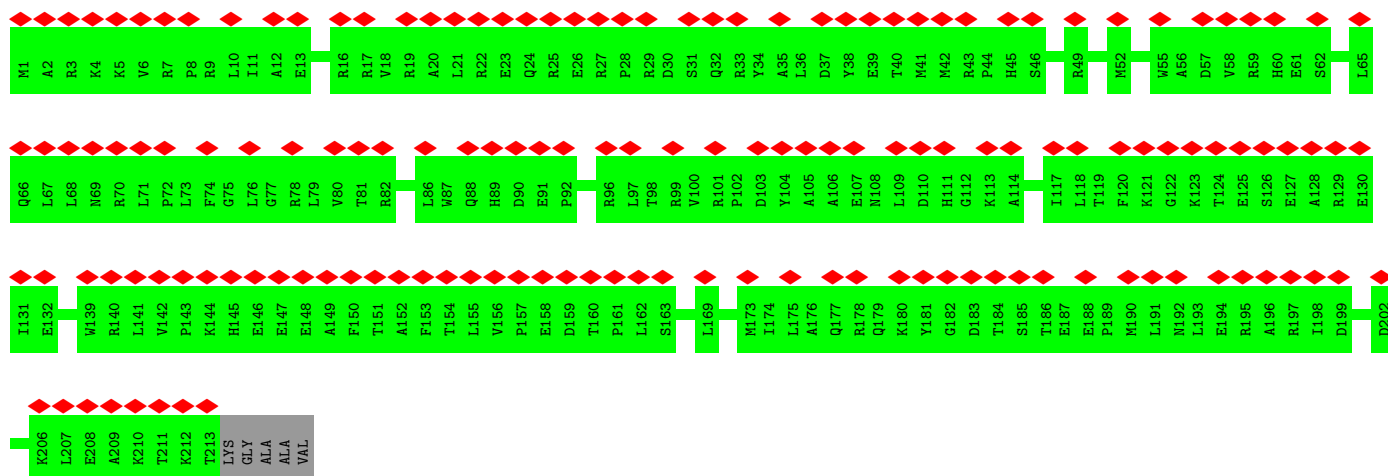
[illegible]



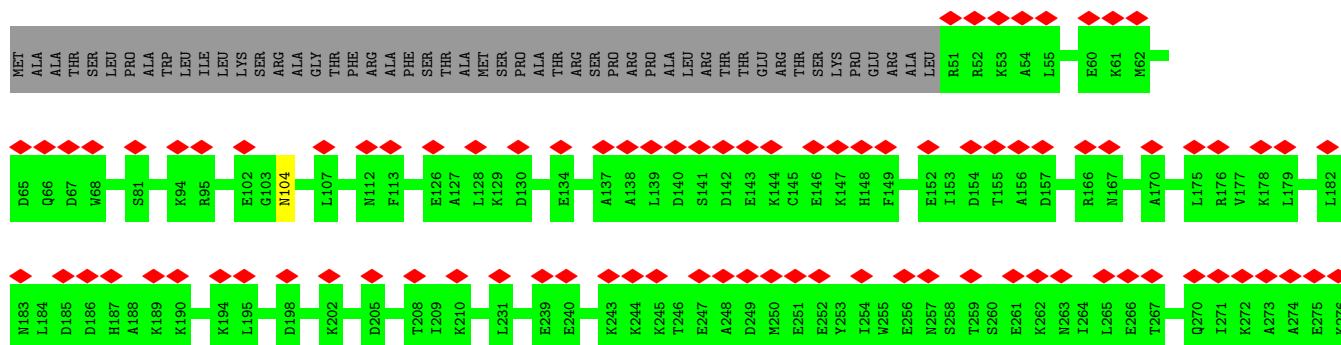
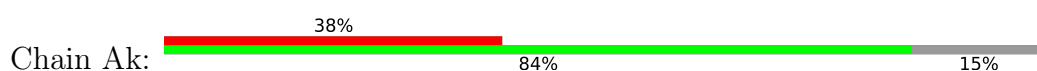
• Molecule 75: mS33

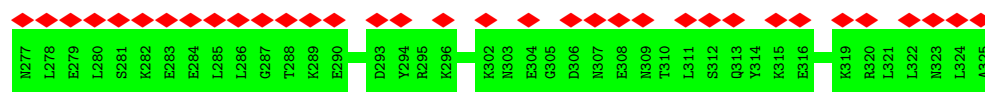


• Molecule 76: mS34

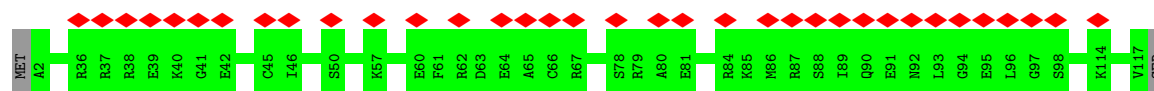


• Molecule 77: Mitochondrial ribosomal protein S35

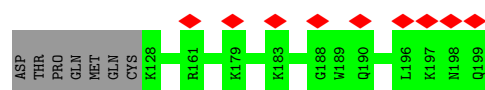
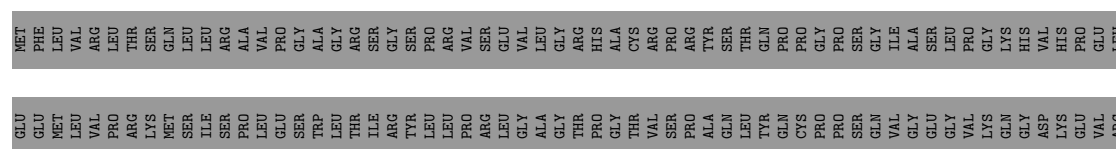




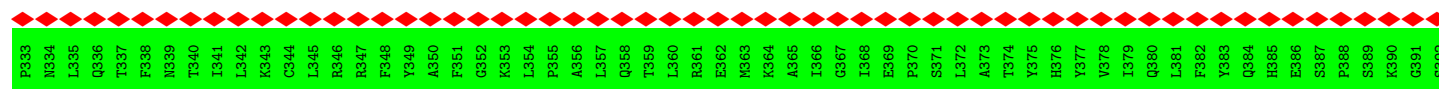
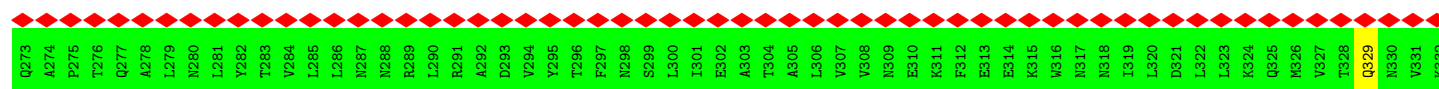
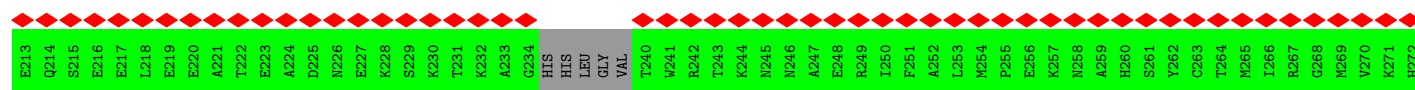
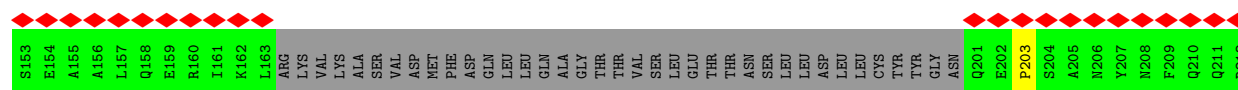
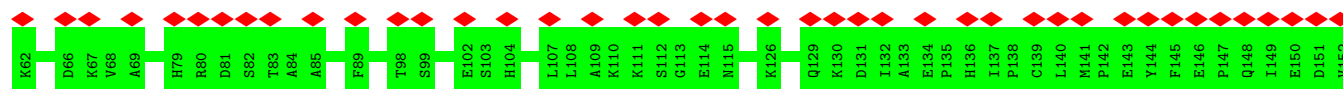
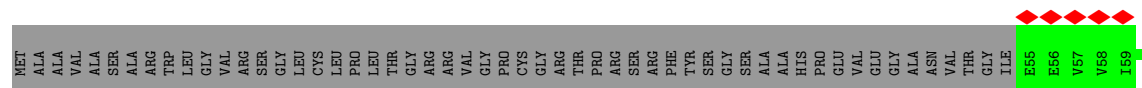
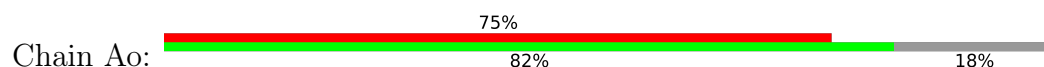
• Molecule 78: mS37



• Molecule 79: Aurora kinase A interacting protein 1

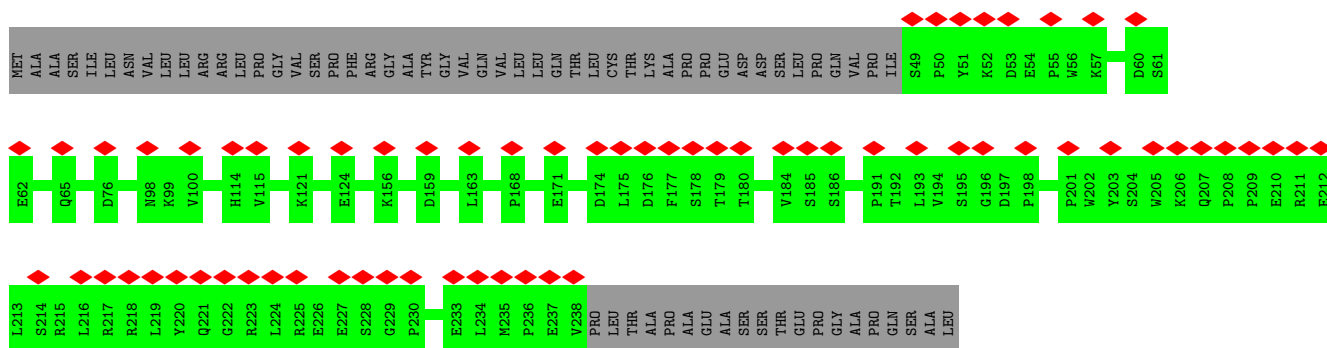
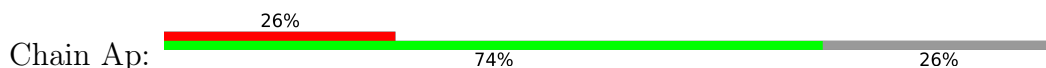


• Molecule 80: Pentatricopeptide repeat domain 3

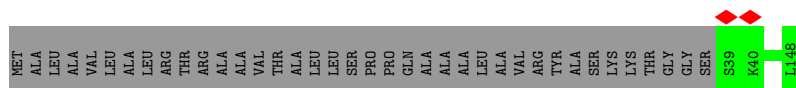
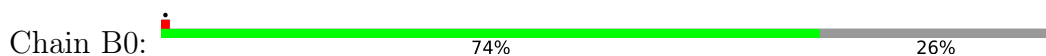




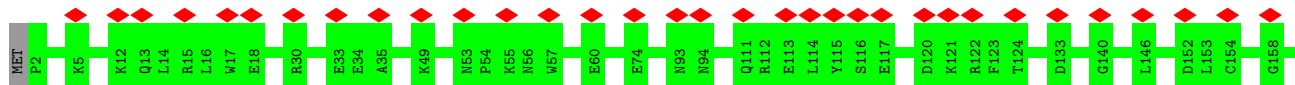
- Molecule 81: 28S ribosomal protein S18b, mitochondrial

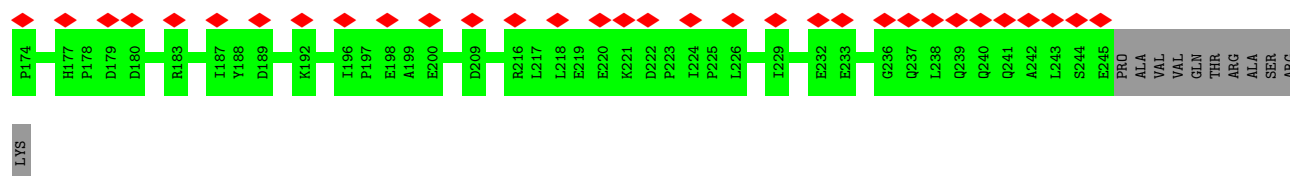


- Molecule 82: Mitochondrial ribosomal protein L27

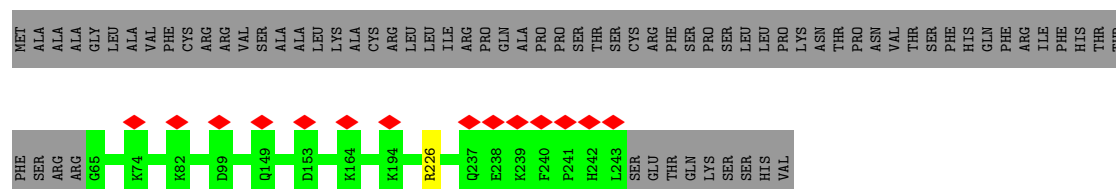


- Molecule 83: Mitochondrial ribosomal protein L28

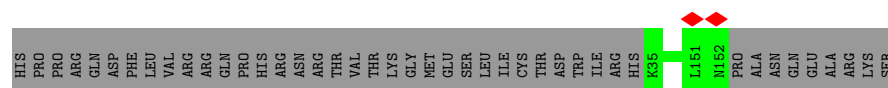
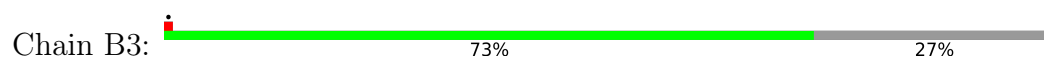




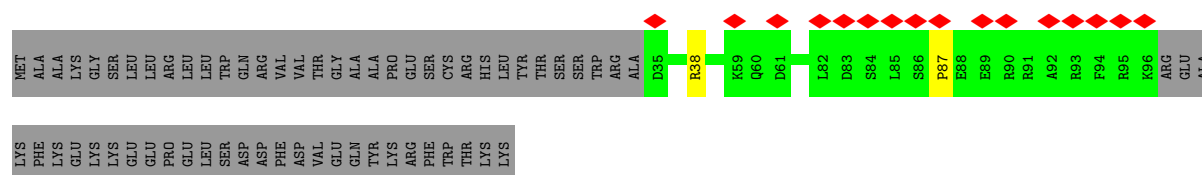
- Molecule 84: Mitochondrial ribosomal protein L47



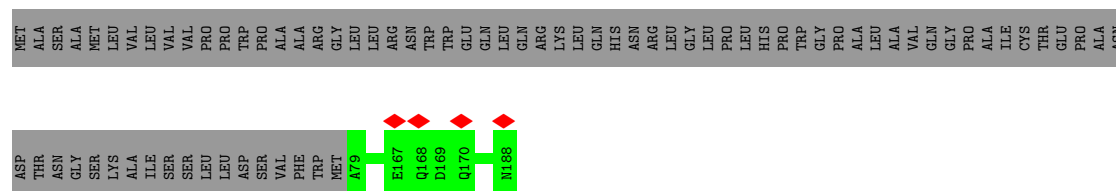
- Molecule 85: uL30m



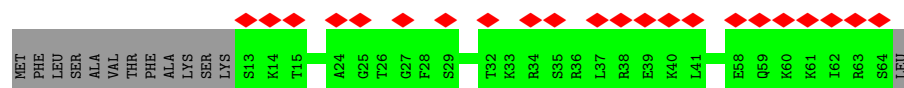
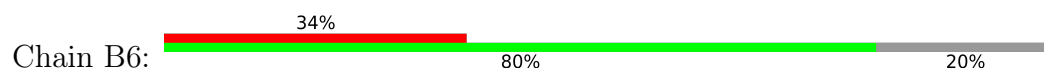
- Molecule 86: bL31m



- Molecule 87: bL32m



- Molecule 88: bL33m



4 Experimental information

| Property | Value | Source |
|--------------------------------------|-----------------------------------------|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 93623 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 40 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | FEI FALCON III (4k x 4k) | Depositor |
| Maximum map value | 1.037 | Depositor |
| Minimum map value | -0.651 | Depositor |
| Average map value | 0.001 | Depositor |
| Map value standard deviation | 0.046 | Depositor |
| Recommended contour level | 0.13 | Depositor |
| Map size (Å) | 444.8, 444.8, 444.8 | wwPDB |
| Map dimensions | 320, 320, 320 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.39, 1.39, 1.39 | Depositor |

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SPM, 5GP, MG, GTP

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 | B7 | 0.23 | 0/395 | 0.56 | 0/524 |
| 2 | B8 | 0.23 | 0/853 | 0.52 | 0/1136 |
| 3 | B9 | 0.24 | 0/342 | 0.55 | 0/450 |
| 4 | BA | 0.20 | 0/36784 | 0.78 | 14/57270 (0.0%) |
| 5 | BB | 0.31 | 1/1595 (0.1%) | 0.76 | 0/2475 |
| 6 | BD | 0.25 | 0/1898 | 0.54 | 0/2555 |
| 7 | BE | 0.26 | 0/2493 | 0.46 | 0/3387 |
| 8 | BF | 0.24 | 0/2069 | 0.51 | 0/2816 |
| 9 | BI | 0.23 | 0/819 | 0.55 | 0/1101 |
| 10 | BJ | 0.25 | 0/1742 | 0.51 | 0/2358 |
| 11 | BK | 0.25 | 0/1323 | 0.49 | 0/1785 |
| 12 | BL | 0.23 | 0/1127 | 0.51 | 0/1512 |
| 13 | BN | 0.24 | 0/1487 | 0.46 | 0/2017 |
| 14 | BO | 0.29 | 0/912 | 0.58 | 0/1231 |
| 15 | BP | 0.25 | 0/2368 | 0.53 | 0/3198 |
| 16 | BQ | 0.25 | 0/1850 | 0.51 | 0/2491 |
| 17 | BR | 0.24 | 0/1262 | 0.54 | 0/1700 |
| 18 | BS | 0.24 | 0/1197 | 0.56 | 0/1624 |
| 19 | BT | 0.27 | 0/2002 | 0.50 | 1/2708 (0.0%) |
| 20 | BU | 0.25 | 0/1179 | 0.55 | 0/1578 |
| 21 | BV | 0.24 | 0/1256 | 0.49 | 0/1706 |
| 22 | BW | 0.25 | 0/1407 | 0.53 | 0/1891 |
| 23 | BX | 0.26 | 0/1211 | 0.52 | 0/1646 |
| 24 | BY | 0.24 | 0/1719 | 0.53 | 0/2329 |
| 25 | Ba | 0.25 | 0/3267 | 0.48 | 0/4455 |
| 26 | Bb | 0.25 | 0/3047 | 0.51 | 0/4139 |
| 27 | Bc | 0.26 | 0/2464 | 0.49 | 0/3330 |
| 28 | Bd | 0.25 | 0/1183 | 0.54 | 0/1594 |
| 29 | Be | 0.26 | 0/1000 | 0.48 | 0/1345 |
| 30 | Bf | 0.25 | 0/851 | 0.58 | 2/1159 (0.2%) |
| 31 | Bg | 0.27 | 0/1191 | 0.56 | 0/1614 |
| 32 | Bh | 0.25 | 0/2372 | 0.49 | 1/3211 (0.0%) |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|----------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 33 | Bi | 0.25 | 0/2199 | 0.50 | 0/2980 |
| 34 | Bj | 0.24 | 0/1811 | 0.51 | 0/2436 |
| 35 | Bk | 0.27 | 0/1270 | 0.52 | 0/1714 |
| 36 | Bl | 0.26 | 0/1135 | 0.50 | 0/1549 |
| 37 | Bm | 0.24 | 0/917 | 0.48 | 0/1248 |
| 38 | Bn | 0.24 | 0/860 | 0.53 | 0/1150 |
| 39 | Bo | 0.25 | 0/787 | 0.47 | 0/1056 |
| 40 | Bp | 0.25 | 0/752 | 0.55 | 0/1013 |
| 41 | Bq | 0.25 | 0/490 | 0.51 | 0/662 |
| 42 | Bt | 0.24 | 0/798 | 0.55 | 0/1073 |
| 43 | Bu | 0.24 | 0/1214 | 0.54 | 1/1630 (0.1%) |
| 44 | Bv | 0.24 | 0/1157 | 0.50 | 0/1560 |
| 45 | Bw | 0.25 | 0/3206 | 0.48 | 0/4354 |
| 46 | Bx | 0.27 | 0/1364 | 0.53 | 0/1849 |
| 47 | AA | 0.17 | 0/22852 | 0.75 | 6/35580 (0.0%) |
| 48 | CL | 0.23 | 0/319 | 0.42 | 0/435 |
| 48 | DL | 0.22 | 0/212 | 0.41 | 0/286 |
| 48 | EL | 0.22 | 0/221 | 0.40 | 0/297 |
| 48 | FL | 0.22 | 0/212 | 0.40 | 0/286 |
| 48 | GL | 0.22 | 0/212 | 0.40 | 0/286 |
| 48 | HL | 0.22 | 0/204 | 0.41 | 0/275 |
| 49 | AB | 0.26 | 0/1804 | 0.53 | 0/2445 |
| 50 | AC | 0.26 | 0/1105 | 0.52 | 0/1496 |
| 51 | AE | 0.27 | 0/2785 | 0.56 | 2/3735 (0.1%) |
| 52 | AF | 0.26 | 0/999 | 0.57 | 0/1347 |
| 53 | AG | 0.25 | 0/1763 | 0.49 | 0/2368 |
| 54 | AI | 0.26 | 0/2707 | 0.50 | 0/3636 |
| 55 | AJ | 0.25 | 0/1181 | 0.51 | 0/1597 |
| 56 | AK | 0.25 | 0/1027 | 0.52 | 0/1389 |
| 57 | AL | 0.25 | 0/858 | 0.54 | 0/1152 |
| 58 | AN | 0.23 | 0/874 | 0.56 | 0/1171 |
| 59 | AO | 0.24 | 0/1473 | 0.47 | 0/1970 |
| 60 | AP | 0.25 | 0/954 | 0.58 | 0/1284 |
| 61 | AQ | 0.24 | 0/894 | 0.48 | 0/1213 |
| 62 | AR | 0.25 | 0/802 | 0.49 | 0/1079 |
| 63 | AU | 0.24 | 0/745 | 0.54 | 0/993 |
| 64 | AV | 0.21 | 0/1673 | 0.87 | 1/2602 (0.0%) |
| 65 | AX | 0.24 | 0/147 | 0.80 | 0/227 |
| 66 | AZ | 0.26 | 0/89 | 0.35 | 0/123 |
| 67 | Aa | 0.25 | 0/2428 | 0.50 | 1/3279 (0.0%) |
| 68 | Ab | 0.25 | 0/1126 | 0.52 | 0/1514 |
| 69 | Ac | 0.26 | 0/1399 | 0.50 | 0/1881 |
| 70 | Ad | 0.25 | 0/1490 | 0.55 | 0/2005 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-----------------|-------------|------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 71 | Ae | 0.25 | 0/3171 | 0.50 | 1/4292 (0.0%) |
| 72 | Af | 0.24 | 0/790 | 0.53 | 0/1064 |
| 73 | Ag | 0.25 | 0/2945 | 0.49 | 0/3984 |
| 74 | Ah | 0.25 | 0/1045 | 0.45 | 0/1409 |
| 75 | Ai | 0.26 | 0/841 | 0.55 | 0/1121 |
| 76 | Aj | 0.24 | 0/1835 | 0.56 | 0/2484 |
| 77 | Ak | 0.25 | 0/2268 | 0.47 | 0/3069 |
| 78 | Am | 0.24 | 0/947 | 0.53 | 0/1268 |
| 79 | An | 0.23 | 0/650 | 0.54 | 0/858 |
| 80 | Ao | 0.25 | 0/4626 | 0.49 | 1/6269 (0.0%) |
| 81 | Ap | 0.27 | 0/1616 | 0.53 | 0/2195 |
| 82 | B0 | 0.26 | 0/880 | 0.48 | 0/1189 |
| 83 | B1 | 0.24 | 0/2093 | 0.49 | 0/2835 |
| 84 | B2 | 0.24 | 0/1586 | 0.51 | 0/2123 |
| 85 | B3 | 0.24 | 0/993 | 0.49 | 0/1341 |
| 86 | B4 | 0.23 | 0/481 | 0.63 | 1/653 (0.2%) |
| 87 | B5 | 0.24 | 0/917 | 0.52 | 0/1227 |
| 88 | B6 | 0.25 | 0/430 | 0.55 | 0/570 |
| All | All | 0.23 | 1/183294 (0.0%) | 0.62 | 32/260511 (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 |
|-----|-------|---------------------|---------------------|
| 6 | BD | 0 | 1 |
| 10 | BJ | 0 | 1 |
| 38 | Bn | 0 | 1 |
| 73 | Ag | 0 | 1 |
| All | All | 0 | 4 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|--------|-------------|----------|
| 5 | BB | 1 | G | OP3-P | -10.58 | 1.48 | 1.61 |

The worst 5 of 32 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|-------|-------------|----------|
| 51 | AE | 395 | PRO | CA-N-CD | -8.95 | 98.97 | 111.50 |
| 47 | AA | 119 | C | C2-N1-C1' | 8.22 | 127.84 | 118.80 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|-------|-------------|----------|
| 64 | AV | 57 | C | N3-C2-O2 | -7.76 | 116.47 | 121.90 |
| 4 | BA | 848 | C | C2-N1-C1' | 6.95 | 126.44 | 118.80 |
| 51 | AE | 395 | PRO | N-CD-CG | -6.91 | 92.83 | 103.20 |

There are no chirality outliers.

All (4) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 73 | Ag | 337 | ASP | Peptide |
| 6 | BD | 207 | TYR | Peptide |
| 10 | BJ | 64 | CYS | Peptide |
| 38 | Bn | 65 | ASN | Peptide |

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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 | B7 | 44/95 (46%) | 44 (100%) | 0 | 0 | 100 | 100 |
| 2 | B8 | 93/188 (50%) | 93 (100%) | 0 | 0 | 100 | 100 |
| 3 | B9 | 36/100 (36%) | 36 (100%) | 0 | 0 | 100 | 100 |
| 6 | BD | 238/306 (78%) | 231 (97%) | 7 (3%) | 0 | 100 | 100 |
| 7 | BE | 305/399 (76%) | 291 (95%) | 14 (5%) | 0 | 100 | 100 |
| 8 | BF | 248/294 (84%) | 242 (98%) | 6 (2%) | 0 | 100 | 100 |
| 9 | BI | 96/268 (36%) | 95 (99%) | 1 (1%) | 0 | 100 | 100 |
| 10 | BJ | 210/262 (80%) | 199 (95%) | 11 (5%) | 0 | 100 | 100 |
| 11 | BK | 174/192 (91%) | 172 (99%) | 2 (1%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|------------|---------|----------|-------------|-----|
| 12 | BL | 135/184 (73%) | 133 (98%) | 2 (2%) | 0 | 100 | 100 |
| 13 | BN | 175/178 (98%) | 171 (98%) | 4 (2%) | 0 | 100 | 100 |
| 14 | BO | 113/145 (78%) | 110 (97%) | 3 (3%) | 0 | 100 | 100 |
| 15 | BP | 286/296 (97%) | 276 (96%) | 10 (4%) | 0 | 100 | 100 |
| 16 | BQ | 220/251 (88%) | 217 (99%) | 3 (1%) | 0 | 100 | 100 |
| 17 | BR | 151/169 (89%) | 146 (97%) | 5 (3%) | 0 | 100 | 100 |
| 18 | BS | 141/180 (78%) | 131 (93%) | 10 (7%) | 0 | 100 | 100 |
| 19 | BT | 238/292 (82%) | 233 (98%) | 4 (2%) | 1 (0%) | 30 | 60 |
| 20 | BU | 138/149 (93%) | 138 (100%) | 0 | 0 | 100 | 100 |
| 21 | BV | 153/209 (73%) | 149 (97%) | 4 (3%) | 0 | 100 | 100 |
| 22 | BW | 164/210 (78%) | 158 (96%) | 6 (4%) | 0 | 100 | 100 |
| 23 | BX | 147/150 (98%) | 145 (99%) | 2 (1%) | 0 | 100 | 100 |
| 24 | BY | 204/216 (94%) | 197 (97%) | 7 (3%) | 0 | 100 | 100 |
| 25 | Ba | 391/423 (92%) | 378 (97%) | 13 (3%) | 0 | 100 | 100 |
| 26 | Bb | 352/380 (93%) | 333 (95%) | 19 (5%) | 0 | 100 | 100 |
| 27 | Bc | 293/334 (88%) | 281 (96%) | 11 (4%) | 1 (0%) | 37 | 66 |
| 28 | Bd | 136/206 (66%) | 129 (95%) | 7 (5%) | 0 | 100 | 100 |
| 29 | Be | 120/135 (89%) | 112 (93%) | 8 (7%) | 0 | 100 | 100 |
| 30 | Bf | 106/142 (75%) | 102 (96%) | 2 (2%) | 2 (2%) | 6 | 26 |
| 31 | Bg | 146/159 (92%) | 137 (94%) | 9 (6%) | 0 | 100 | 100 |
| 32 | Bh | 287/332 (86%) | 274 (96%) | 13 (4%) | 0 | 100 | 100 |
| 33 | Bi | 258/306 (84%) | 244 (95%) | 14 (5%) | 0 | 100 | 100 |
| 34 | Bj | 211/279 (76%) | 200 (95%) | 11 (5%) | 0 | 100 | 100 |
| 35 | Bk | 151/269 (56%) | 144 (95%) | 7 (5%) | 0 | 100 | 100 |
| 36 | Bl | 131/166 (79%) | 128 (98%) | 3 (2%) | 0 | 100 | 100 |
| 37 | Bm | 107/198 (54%) | 106 (99%) | 1 (1%) | 0 | 100 | 100 |
| 38 | Bn | 95/128 (74%) | 90 (95%) | 5 (5%) | 0 | 100 | 100 |
| 39 | Bo | 95/124 (77%) | 94 (99%) | 1 (1%) | 0 | 100 | 100 |
| 40 | Bp | 95/112 (85%) | 90 (95%) | 5 (5%) | 0 | 100 | 100 |
| 41 | Bq | 52/138 (38%) | 49 (94%) | 3 (6%) | 0 | 100 | 100 |
| 42 | Bt | 92/102 (90%) | 86 (94%) | 6 (6%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|------------|---------|----------|-------------|-----|
| 43 | Bu | 147/205 (72%) | 139 (95%) | 7 (5%) | 1 (1%) | 19 | 47 |
| 44 | Bv | 133/222 (60%) | 133 (100%) | 0 | 0 | 100 | 100 |
| 45 | Bw | 385/433 (89%) | 365 (95%) | 20 (5%) | 0 | 100 | 100 |
| 46 | Bx | 160/196 (82%) | 152 (95%) | 8 (5%) | 0 | 100 | 100 |
| 48 | CL | 43/198 (22%) | 43 (100%) | 0 | 0 | 100 | 100 |
| 48 | DL | 25/198 (13%) | 25 (100%) | 0 | 0 | 100 | 100 |
| 48 | EL | 26/198 (13%) | 26 (100%) | 0 | 0 | 100 | 100 |
| 48 | FL | 25/198 (13%) | 25 (100%) | 0 | 0 | 100 | 100 |
| 48 | GL | 25/198 (13%) | 25 (100%) | 0 | 0 | 100 | 100 |
| 48 | HL | 24/198 (12%) | 24 (100%) | 0 | 0 | 100 | 100 |
| 49 | AB | 218/289 (75%) | 211 (97%) | 7 (3%) | 0 | 100 | 100 |
| 50 | AC | 130/167 (78%) | 123 (95%) | 7 (5%) | 0 | 100 | 100 |
| 51 | AE | 341/430 (79%) | 329 (96%) | 12 (4%) | 0 | 100 | 100 |
| 52 | AF | 120/276 (44%) | 119 (99%) | 1 (1%) | 0 | 100 | 100 |
| 53 | AG | 206/242 (85%) | 204 (99%) | 2 (1%) | 0 | 100 | 100 |
| 54 | AI | 326/397 (82%) | 320 (98%) | 6 (2%) | 0 | 100 | 100 |
| 55 | AJ | 138/200 (69%) | 125 (91%) | 13 (9%) | 0 | 100 | 100 |
| 56 | AK | 135/196 (69%) | 130 (96%) | 5 (4%) | 0 | 100 | 100 |
| 57 | AL | 107/139 (77%) | 99 (92%) | 8 (8%) | 0 | 100 | 100 |
| 58 | AN | 99/128 (77%) | 98 (99%) | 1 (1%) | 0 | 100 | 100 |
| 59 | AO | 173/239 (72%) | 169 (98%) | 4 (2%) | 0 | 100 | 100 |
| 60 | AP | 115/135 (85%) | 112 (97%) | 3 (3%) | 0 | 100 | 100 |
| 61 | AQ | 110/130 (85%) | 108 (98%) | 2 (2%) | 0 | 100 | 100 |
| 62 | AR | 95/143 (66%) | 95 (100%) | 0 | 0 | 100 | 100 |
| 63 | AU | 84/87 (97%) | 82 (98%) | 2 (2%) | 0 | 100 | 100 |
| 66 | AZ | 16/18 (89%) | 15 (94%) | 1 (6%) | 0 | 100 | 100 |
| 67 | Aa | 290/382 (76%) | 284 (98%) | 6 (2%) | 0 | 100 | 100 |
| 68 | Ab | 133/190 (70%) | 131 (98%) | 2 (2%) | 0 | 100 | 100 |
| 69 | Ac | 167/173 (96%) | 166 (99%) | 1 (1%) | 0 | 100 | 100 |
| 70 | Ad | 175/205 (85%) | 175 (100%) | 0 | 0 | 100 | 100 |
| 71 | Ae | 386/455 (85%) | 361 (94%) | 23 (6%) | 2 (0%) | 25 | 54 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 72 | Af | 97/188 (52%) | 95 (98%) | 2 (2%) | 0 | 100 | 100 |
| 73 | Ag | 351/410 (86%) | 337 (96%) | 14 (4%) | 0 | 100 | 100 |
| 74 | Ah | 118/387 (30%) | 117 (99%) | 1 (1%) | 0 | 100 | 100 |
| 75 | Ai | 97/106 (92%) | 95 (98%) | 2 (2%) | 0 | 100 | 100 |
| 76 | Aj | 211/218 (97%) | 205 (97%) | 6 (3%) | 0 | 100 | 100 |
| 77 | Ak | 273/325 (84%) | 266 (97%) | 7 (3%) | 0 | 100 | 100 |
| 78 | Am | 114/118 (97%) | 109 (96%) | 5 (4%) | 0 | 100 | 100 |
| 79 | An | 70/199 (35%) | 69 (99%) | 1 (1%) | 0 | 100 | 100 |
| 80 | Ao | 564/699 (81%) | 548 (97%) | 16 (3%) | 0 | 100 | 100 |
| 81 | Ap | 188/258 (73%) | 182 (97%) | 6 (3%) | 0 | 100 | 100 |
| 82 | B0 | 108/148 (73%) | 107 (99%) | 1 (1%) | 0 | 100 | 100 |
| 83 | B1 | 242/256 (94%) | 241 (100%) | 1 (0%) | 0 | 100 | 100 |
| 84 | B2 | 177/252 (70%) | 172 (97%) | 5 (3%) | 0 | 100 | 100 |
| 85 | B3 | 116/161 (72%) | 113 (97%) | 3 (3%) | 0 | 100 | 100 |
| 86 | B4 | 60/126 (48%) | 55 (92%) | 5 (8%) | 0 | 100 | 100 |
| 87 | B5 | 108/188 (57%) | 107 (99%) | 1 (1%) | 0 | 100 | 100 |
| 88 | B6 | 50/65 (77%) | 49 (98%) | 1 (2%) | 0 | 100 | 100 |
| All | All | 14328/19635 (73%) | 13864 (97%) | 457 (3%) | 7 (0%) | 100 | 100 |

5 of 7 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 19 | BT | 68 | PRO |
| 30 | Bf | 80 | PRO |
| 43 | Bu | 167 | PRO |
| 30 | Bf | 78 | PRO |
| 71 | Ae | 342 | 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 | B7 | 41/78 (53%) | 41 (100%) | 0 | 100 | 100 |
| 2 | B8 | 87/162 (54%) | 86 (99%) | 1 (1%) | 70 | 81 |
| 3 | B9 | 36/77 (47%) | 36 (100%) | 0 | 100 | 100 |
| 6 | BD | 193/248 (78%) | 193 (100%) | 0 | 100 | 100 |
| 7 | BE | 263/320 (82%) | 263 (100%) | 0 | 100 | 100 |
| 8 | BF | 217/251 (86%) | 217 (100%) | 0 | 100 | 100 |
| 9 | BI | 88/228 (39%) | 87 (99%) | 1 (1%) | 70 | 81 |
| 10 | BJ | 192/230 (84%) | 191 (100%) | 1 (0%) | 86 | 91 |
| 11 | BK | 129/151 (85%) | 128 (99%) | 1 (1%) | 79 | 87 |
| 12 | BL | 125/162 (77%) | 125 (100%) | 0 | 100 | 100 |
| 13 | BN | 156/157 (99%) | 156 (100%) | 0 | 100 | 100 |
| 14 | BO | 99/123 (80%) | 99 (100%) | 0 | 100 | 100 |
| 15 | BP | 245/249 (98%) | 244 (100%) | 1 (0%) | 89 | 93 |
| 16 | BQ | 190/210 (90%) | 190 (100%) | 0 | 100 | 100 |
| 17 | BR | 132/143 (92%) | 132 (100%) | 0 | 100 | 100 |
| 18 | BS | 123/153 (80%) | 122 (99%) | 1 (1%) | 79 | 87 |
| 19 | BT | 212/258 (82%) | 212 (100%) | 0 | 100 | 100 |
| 20 | BU | 118/127 (93%) | 118 (100%) | 0 | 100 | 100 |
| 21 | BV | 136/178 (76%) | 136 (100%) | 0 | 100 | 100 |
| 22 | BW | 144/180 (80%) | 144 (100%) | 0 | 100 | 100 |
| 23 | BX | 116/134 (87%) | 116 (100%) | 0 | 100 | 100 |
| 24 | BY | 185/192 (96%) | 182 (98%) | 3 (2%) | 58 | 75 |
| 25 | Ba | 348/365 (95%) | 348 (100%) | 0 | 100 | 100 |
| 26 | Bb | 310/328 (94%) | 306 (99%) | 4 (1%) | 65 | 78 |
| 27 | Bc | 271/299 (91%) | 270 (100%) | 1 (0%) | 89 | 93 |
| 28 | Bd | 127/181 (70%) | 127 (100%) | 0 | 100 | 100 |
| 29 | Be | 100/108 (93%) | 100 (100%) | 0 | 100 | 100 |
| 30 | Bf | 80/133 (60%) | 80 (100%) | 0 | 100 | 100 |
| 31 | Bg | 128/136 (94%) | 128 (100%) | 0 | 100 | 100 |
| 32 | Bh | 251/284 (88%) | 251 (100%) | 0 | 100 | 100 |
| 33 | Bi | 236/275 (86%) | 234 (99%) | 2 (1%) | 79 | 87 |
| 34 | Bj | 190/242 (78%) | 190 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|---------------|------------|----------|-------------|-----|
| 35 | Bk | 135/226 (60%) | 135 (100%) | 0 | 100 | 100 |
| 36 | Bl | 122/147 (83%) | 122 (100%) | 0 | 100 | 100 |
| 37 | Bm | 103/178 (58%) | 103 (100%) | 0 | 100 | 100 |
| 38 | Bn | 88/113 (78%) | 88 (100%) | 0 | 100 | 100 |
| 39 | Bo | 77/97 (79%) | 77 (100%) | 0 | 100 | 100 |
| 40 | Bp | 79/88 (90%) | 79 (100%) | 0 | 100 | 100 |
| 41 | Bq | 50/114 (44%) | 50 (100%) | 0 | 100 | 100 |
| 42 | Bt | 75/82 (92%) | 75 (100%) | 0 | 100 | 100 |
| 43 | Bu | 126/177 (71%) | 126 (100%) | 0 | 100 | 100 |
| 44 | Bv | 115/183 (63%) | 115 (100%) | 0 | 100 | 100 |
| 45 | Bw | 340/373 (91%) | 340 (100%) | 0 | 100 | 100 |
| 46 | Bx | 149/173 (86%) | 147 (99%) | 2 (1%) | 65 | 78 |
| 48 | CL | 30/157 (19%) | 30 (100%) | 0 | 100 | 100 |
| 48 | DL | 26/157 (17%) | 25 (96%) | 1 (4%) | 28 | 54 |
| 48 | EL | 27/157 (17%) | 27 (100%) | 0 | 100 | 100 |
| 48 | FL | 26/157 (17%) | 26 (100%) | 0 | 100 | 100 |
| 48 | GL | 26/157 (17%) | 26 (100%) | 0 | 100 | 100 |
| 48 | HL | 25/157 (16%) | 24 (96%) | 1 (4%) | 27 | 52 |
| 49 | AB | 187/233 (80%) | 186 (100%) | 1 (0%) | 86 | 91 |
| 50 | AC | 115/142 (81%) | 115 (100%) | 0 | 100 | 100 |
| 51 | AE | 282/351 (80%) | 278 (99%) | 4 (1%) | 62 | 77 |
| 52 | AF | 107/210 (51%) | 107 (100%) | 0 | 100 | 100 |
| 53 | AG | 181/205 (88%) | 181 (100%) | 0 | 100 | 100 |
| 54 | AI | 273/333 (82%) | 270 (99%) | 3 (1%) | 70 | 81 |
| 55 | AJ | 130/180 (72%) | 129 (99%) | 1 (1%) | 79 | 87 |
| 56 | AK | 103/151 (68%) | 102 (99%) | 1 (1%) | 73 | 83 |
| 57 | AL | 92/116 (79%) | 92 (100%) | 0 | 100 | 100 |
| 58 | AN | 92/114 (81%) | 92 (100%) | 0 | 100 | 100 |
| 59 | AO | 159/205 (78%) | 159 (100%) | 0 | 100 | 100 |
| 60 | AP | 97/113 (86%) | 97 (100%) | 0 | 100 | 100 |
| 61 | AQ | 97/114 (85%) | 97 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-------------------|--------------|----------|-------------|-----|
| 62 | AR | 89/127 (70%) | 89 (100%) | 0 | 100 | 100 |
| 63 | AU | 77/78 (99%) | 76 (99%) | 1 (1%) | 65 | 78 |
| 67 | Aa | 258/330 (78%) | 258 (100%) | 0 | 100 | 100 |
| 68 | Ab | 113/162 (70%) | 113 (100%) | 0 | 100 | 100 |
| 69 | Ac | 152/155 (98%) | 151 (99%) | 1 (1%) | 81 | 88 |
| 70 | Ad | 149/168 (89%) | 149 (100%) | 0 | 100 | 100 |
| 71 | Ae | 325/393 (83%) | 325 (100%) | 0 | 100 | 100 |
| 72 | Af | 86/160 (54%) | 86 (100%) | 0 | 100 | 100 |
| 73 | Ag | 312/361 (86%) | 309 (99%) | 3 (1%) | 73 | 83 |
| 74 | Ah | 109/346 (32%) | 108 (99%) | 1 (1%) | 75 | 86 |
| 75 | Ai | 86/93 (92%) | 86 (100%) | 0 | 100 | 100 |
| 76 | Aj | 188/190 (99%) | 188 (100%) | 0 | 100 | 100 |
| 77 | Ak | 249/289 (86%) | 248 (100%) | 1 (0%) | 89 | 93 |
| 78 | Am | 100/102 (98%) | 100 (100%) | 0 | 100 | 100 |
| 79 | An | 66/174 (38%) | 66 (100%) | 0 | 100 | 100 |
| 80 | Ao | 478/611 (78%) | 477 (100%) | 1 (0%) | 92 | 96 |
| 81 | Ap | 170/225 (76%) | 170 (100%) | 0 | 100 | 100 |
| 82 | B0 | 90/115 (78%) | 90 (100%) | 0 | 100 | 100 |
| 83 | B1 | 219/229 (96%) | 219 (100%) | 0 | 100 | 100 |
| 84 | B2 | 164/228 (72%) | 163 (99%) | 1 (1%) | 84 | 90 |
| 85 | B3 | 110/150 (73%) | 110 (100%) | 0 | 100 | 100 |
| 86 | B4 | 45/114 (40%) | 44 (98%) | 1 (2%) | 47 | 68 |
| 87 | B5 | 99/163 (61%) | 99 (100%) | 0 | 100 | 100 |
| 88 | B6 | 49/60 (82%) | 49 (100%) | 0 | 100 | 100 |
| All | All | 12585/16745 (75%) | 12545 (100%) | 40 (0%) | 90 | 95 |

5 of 40 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 56 | AK | 191 | ARG |
| 77 | Ak | 104 | ASN |
| 63 | AU | 52 | ARG |
| 73 | Ag | 212 | ARG |
| 48 | HL | 83 | ASN |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 50 | AC | 156 | GLN |
| 71 | Ae | 155 | GLN |
| 54 | AI | 148 | HIS |
| 62 | AR | 83 | GLN |
| 73 | Ag | 62 | HIS |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 4 | BA | 1542/1571 (98%) | 410 (26%) | 2 (0%) |
| 47 | AA | 959/962 (99%) | 178 (18%) | 0 |
| 5 | BB | 64/73 (87%) | 15 (23%) | 0 |
| 64 | AV | 70/71 (98%) | 22 (31%) | 0 |
| 65 | AX | 5/6 (83%) | 1 (20%) | 1 (20%) |
| All | All | 2640/2683 (98%) | 626 (23%) | 3 (0%) |

5 of 626 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 4 | BA | 4 | A |
| 4 | BA | 7 | G |
| 4 | BA | 11 | G |
| 4 | BA | 19 | U |
| 4 | BA | 20 | A |

All (3) RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 4 | BA | 48 | U |
| 4 | BA | 1241 | U |
| 65 | AX | 2 | A |

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 347 ligands modelled in this entry, 341 are monoatomic - leaving 6 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 |
| 92 | SPM | AA | 3001 | - | 13,13,13 | 0.34 | 0 | 12,12,12 | 0.79 | 0 |
| 91 | 5GP | BA | 3211 | - | 22,26,26 | 1.23 | 2 (9%) | 26,40,40 | 1.26 | 4 (15%) |
| 92 | SPM | BA | 3213 | - | 13,13,13 | 0.33 | 0 | 12,12,12 | 0.79 | 0 |
| 91 | 5GP | BA | 3212 | 90 | 22,26,26 | 1.24 | 2 (9%) | 26,40,40 | 1.25 | 4 (15%) |
| 92 | SPM | BA | 3214 | - | 13,13,13 | 0.35 | 0 | 12,12,12 | 0.77 | 0 |
| 93 | GTP | Ag | 500 | 90 | 26,34,34 | 1.12 | 2 (7%) | 32,54,54 | 1.59 | 7 (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 |
|-----|------|-------|------|------|---------|------------|---------|
| 92 | SPM | AA | 3001 | - | - | 2/11/11/11 | - |
| 91 | 5GP | BA | 3211 | - | - | 1/6/26/26 | 0/3/3/3 |
| 92 | SPM | BA | 3213 | - | - | 3/11/11/11 | - |
| 91 | 5GP | BA | 3212 | 90 | - | 1/6/26/26 | 0/3/3/3 |
| 92 | SPM | BA | 3214 | - | - | 3/11/11/11 | - |
| 93 | GTP | Ag | 500 | 90 | - | 2/18/38/38 | 0/3/3/3 |

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

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|-------|-------------|----------|
| 91 | BA | 3212 | 5GP | C5-C6 | -4.09 | 1.39 | 1.47 |
| 91 | BA | 3211 | 5GP | C5-C6 | -4.03 | 1.39 | 1.47 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|-------|-------------|----------|
| 93 | Ag | 500 | GTP | C5-C6 | -3.95 | 1.39 | 1.47 |
| 91 | BA | 3211 | 5GP | C6-N1 | -2.53 | 1.34 | 1.37 |
| 91 | BA | 3212 | 5GP | C6-N1 | -2.47 | 1.34 | 1.37 |

The worst 5 of 15 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-------------|-------|-------------|----------|
| 93 | Ag | 500 | GTP | PA-O3A-PB | -3.98 | 119.16 | 132.83 |
| 93 | Ag | 500 | GTP | C5-C6-N1 | 3.25 | 119.69 | 113.95 |
| 93 | Ag | 500 | GTP | C3'-C2'-C1' | 3.21 | 105.81 | 100.98 |
| 91 | BA | 3211 | 5GP | C5-C6-N1 | 3.14 | 119.50 | 113.95 |
| 91 | BA | 3212 | 5GP | C5-C6-N1 | 3.13 | 119.47 | 113.95 |

There are no chirality outliers.

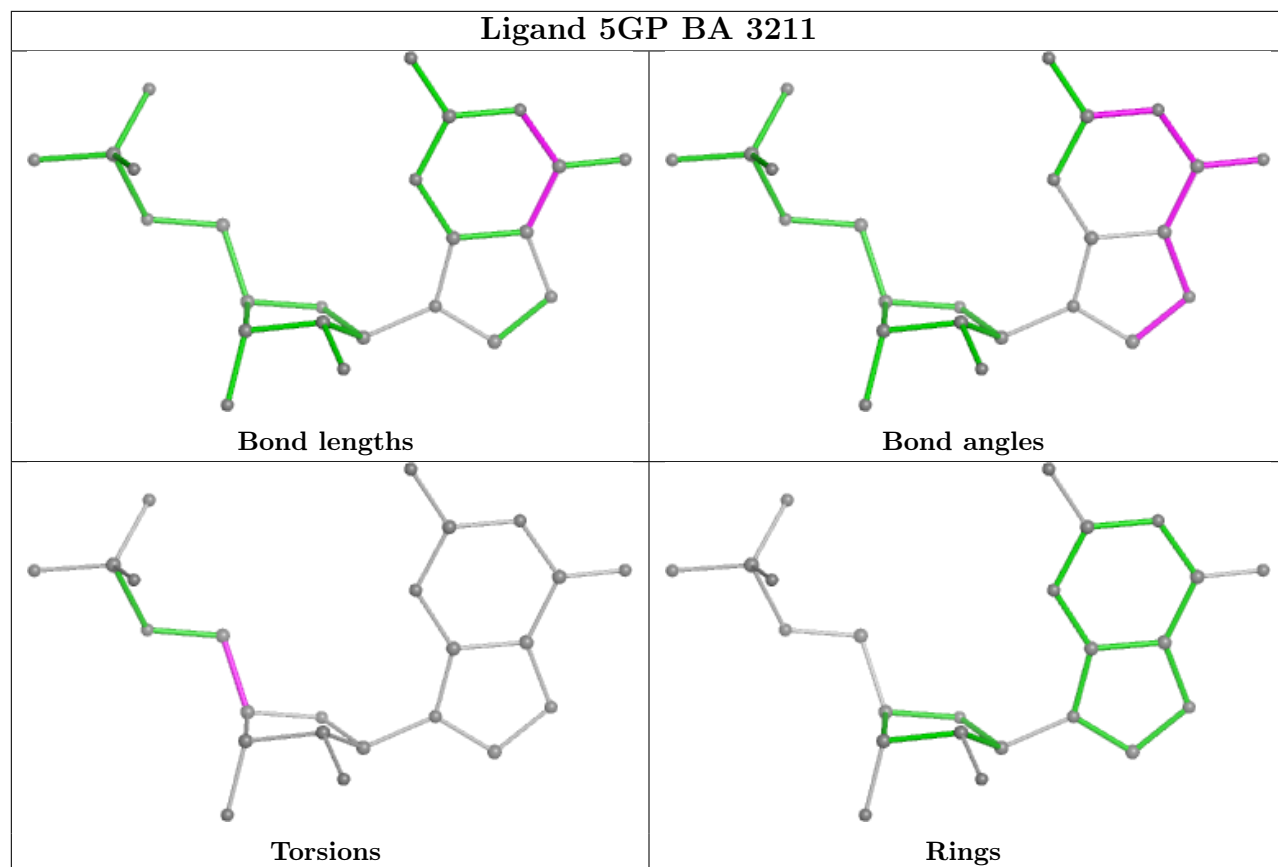
5 of 12 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|------|------|-----------------|
| 92 | BA | 3213 | SPM | C7-C8-C9-N10 |
| 92 | BA | 3214 | SPM | N5-C6-C7-C8 |
| 93 | Ag | 500 | GTP | O4'-C4'-C5'-O5' |
| 93 | Ag | 500 | GTP | C3'-C4'-C5'-O5' |
| 92 | AA | 3001 | SPM | C6-C7-C8-C9 |

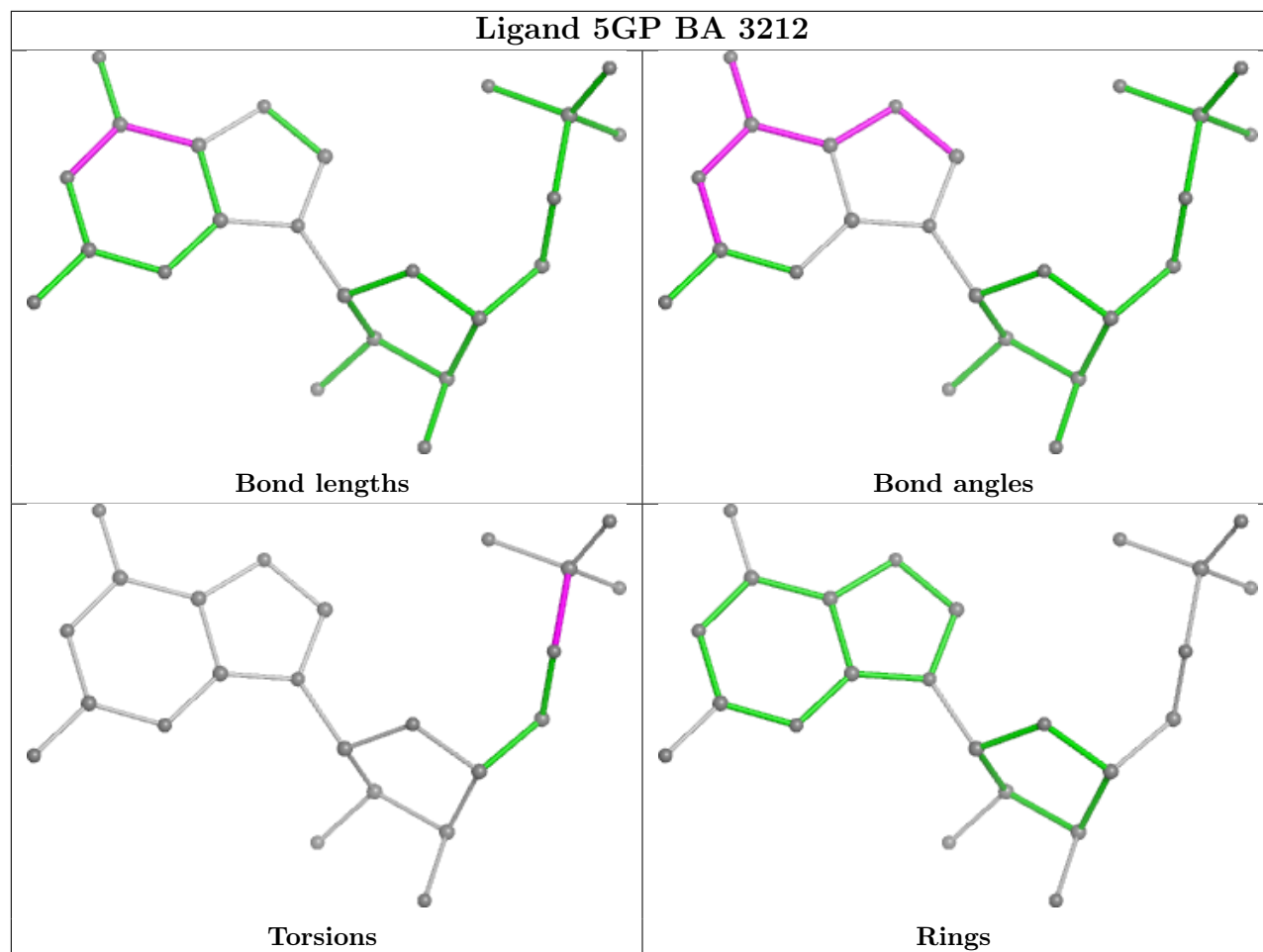
There are no ring outliers.

No monomer is involved in short contacts.

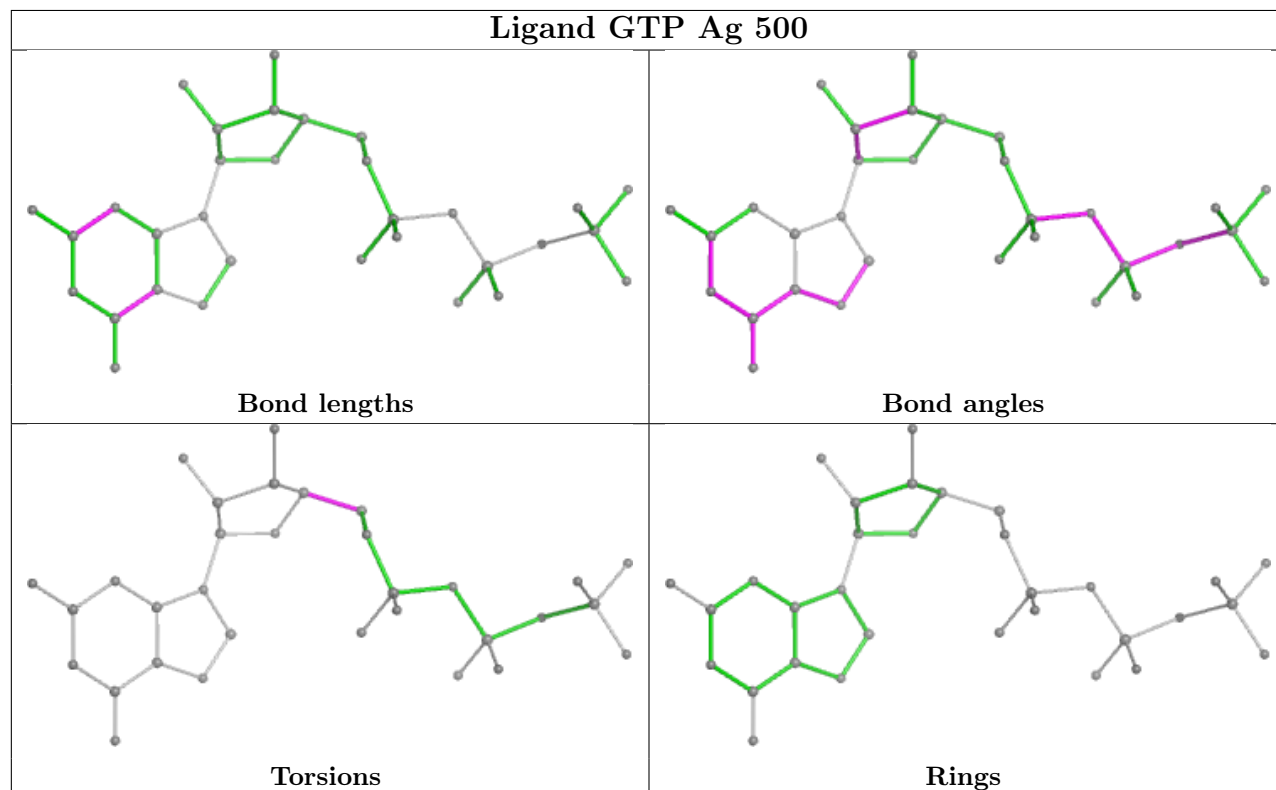
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



Ligand 5GP BA 3212



Ligand GTP Ag 500



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

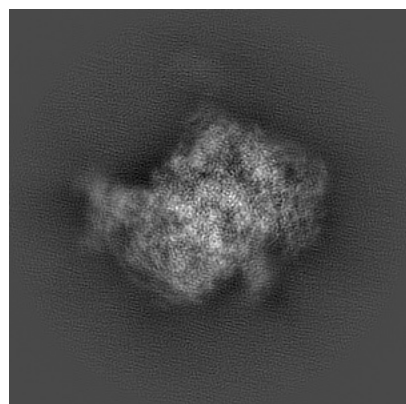
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12529. These allow visual inspection of the internal detail of the map and identification of artifacts.

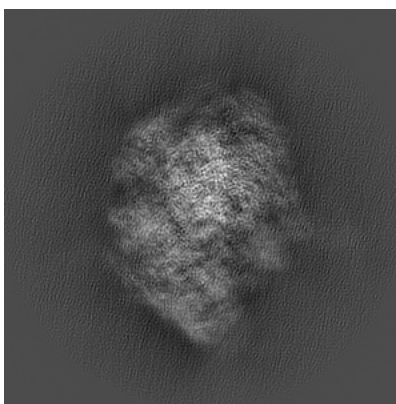
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

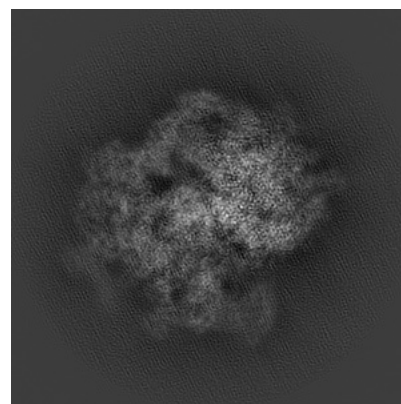
6.1.1 Primary map



X

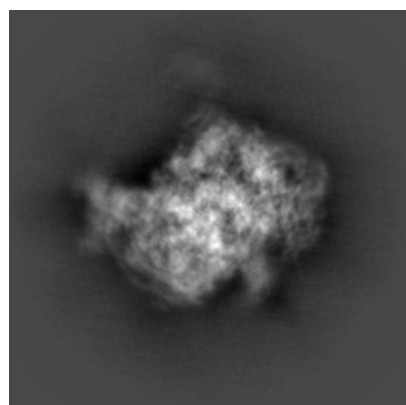


Y

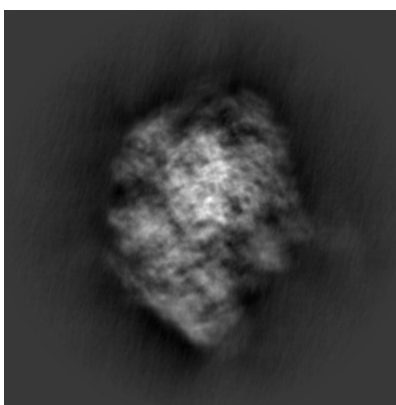


Z

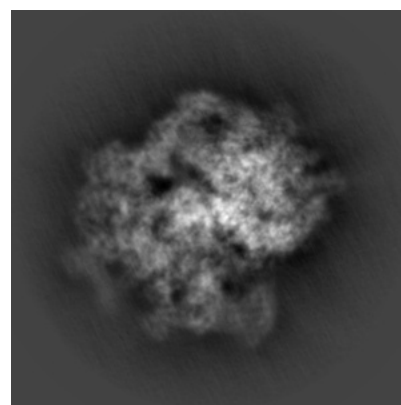
6.1.2 Raw map



X



Y

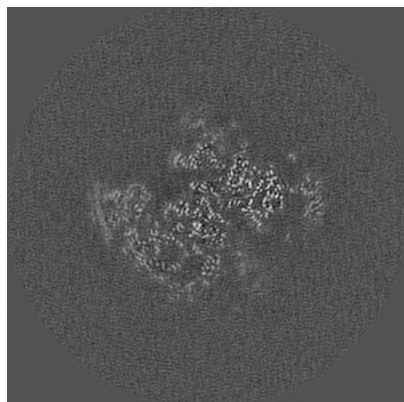


Z

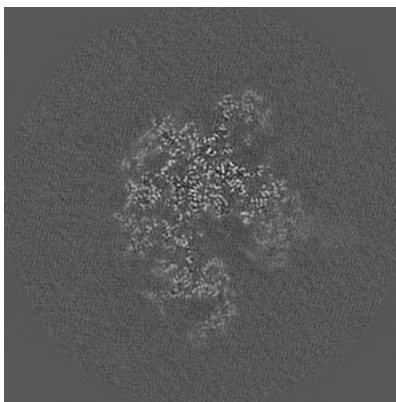
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

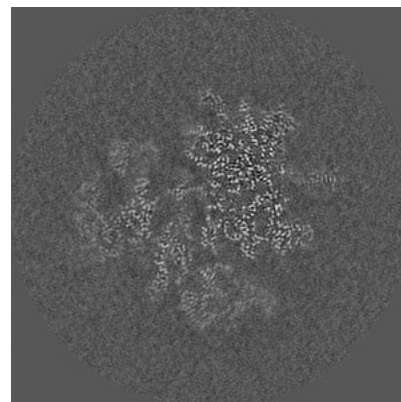
6.2.1 Primary map



X Index: 160

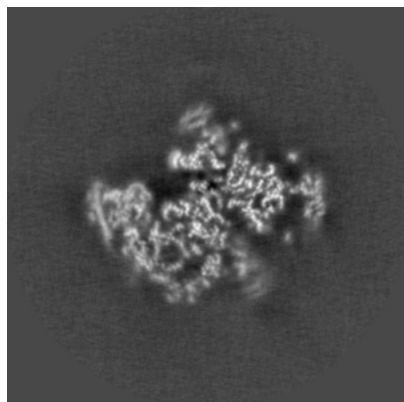


Y Index: 160

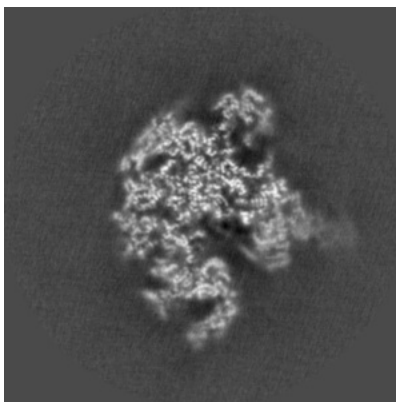


Z Index: 160

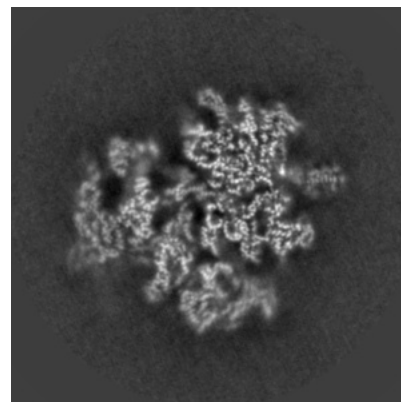
6.2.2 Raw map



X Index: 160



Y Index: 160

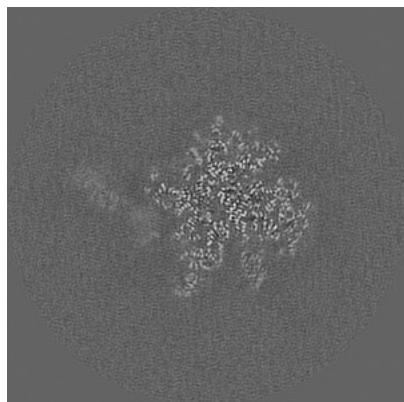


Z Index: 160

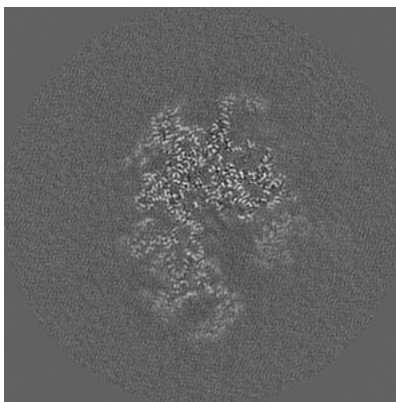
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

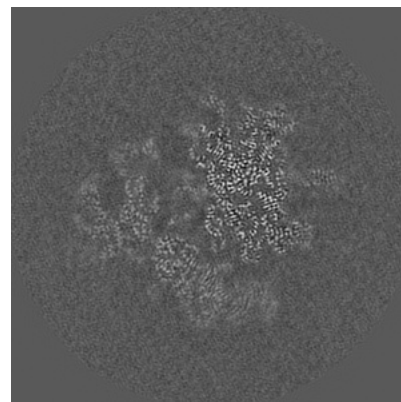
6.3.1 Primary map



X Index: 184

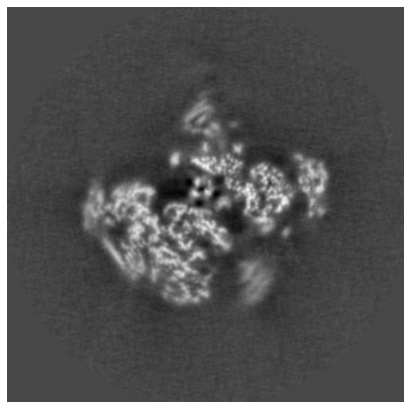


Y Index: 164

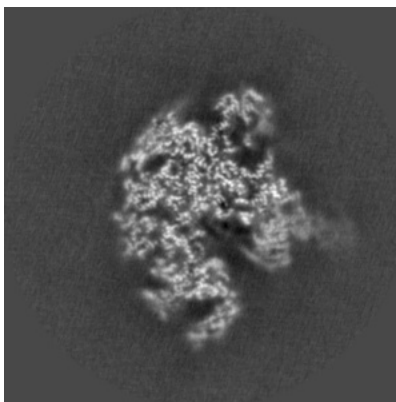


Z Index: 163

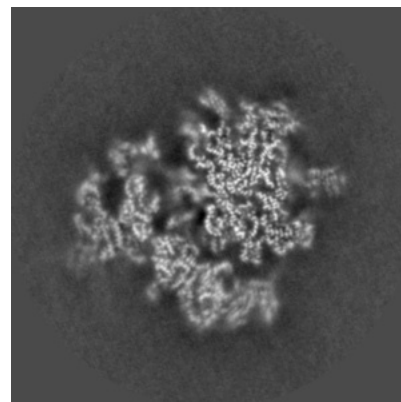
6.3.2 Raw map



X Index: 154



Y Index: 161

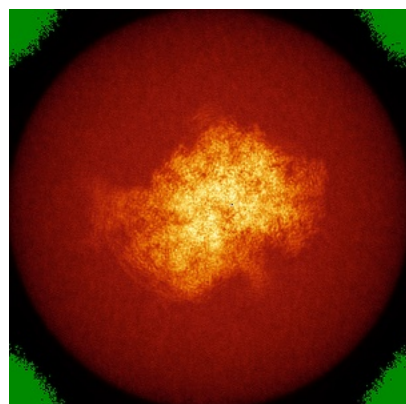


Z Index: 163

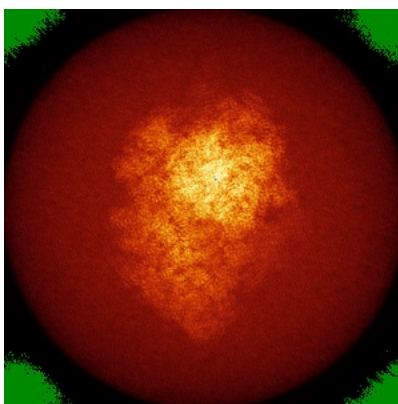
The images above show the largest variance slices of the map in three orthogonal directions.

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

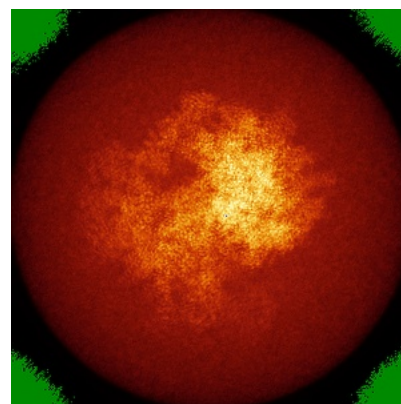
6.4.1 Primary map



X

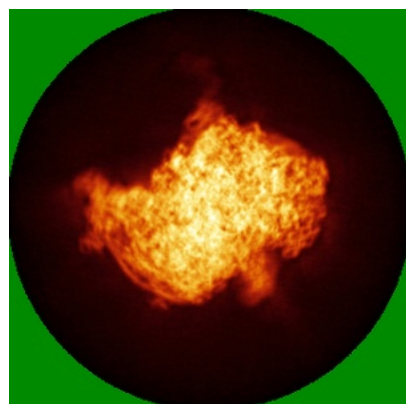


Y

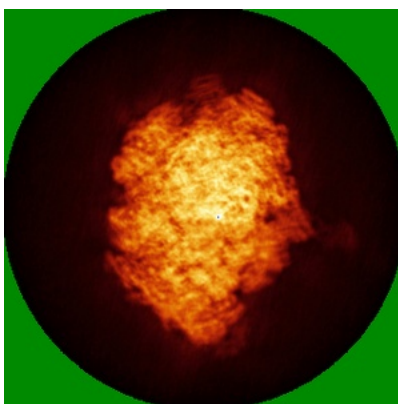


Z

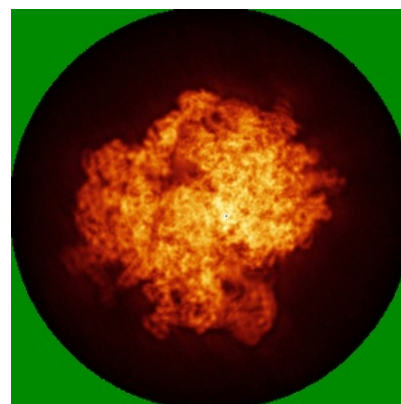
6.4.2 Raw map



X



Y

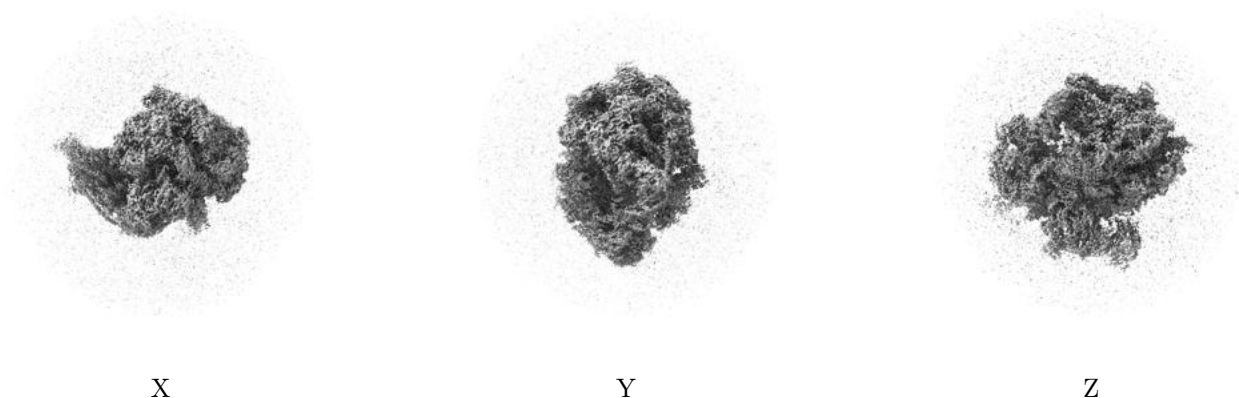


Z

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 0.13. 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.

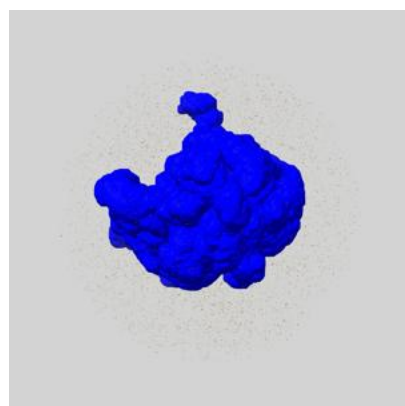
6.6 Mask visualisation [i](#)

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

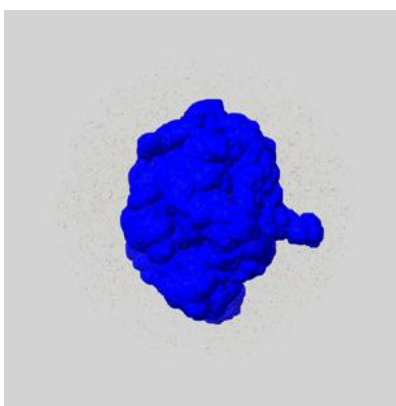
A mask typically either:

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

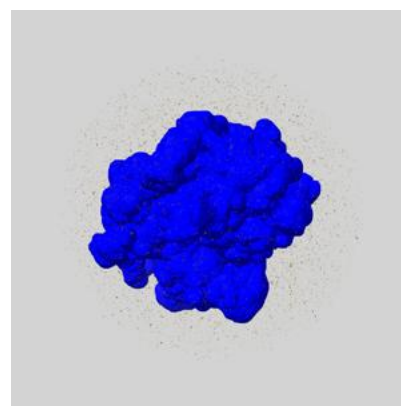
6.6.1 emd_12529_msk_1.map [i](#)



X



Y

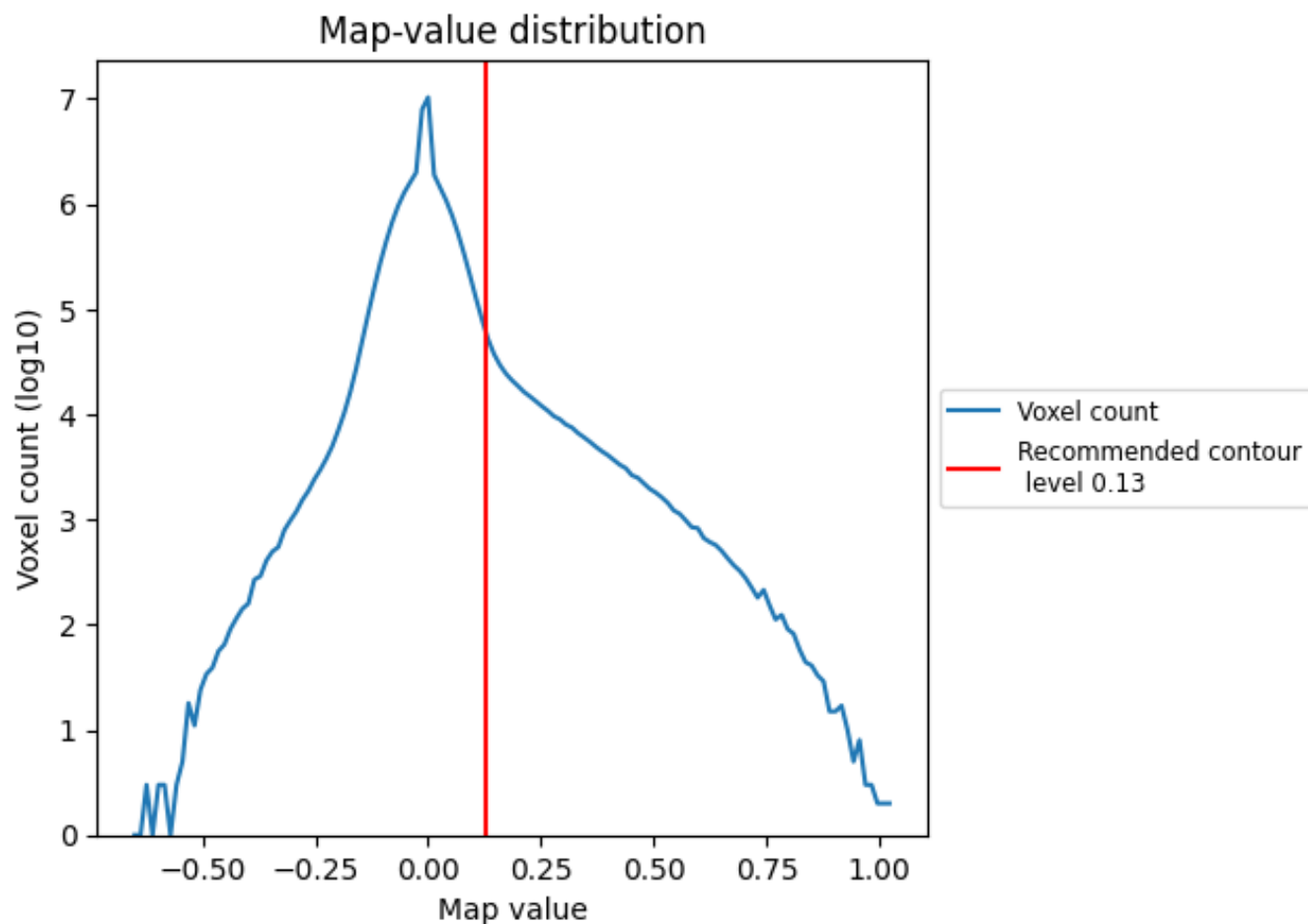


Z

7 Map analysis [i](#)

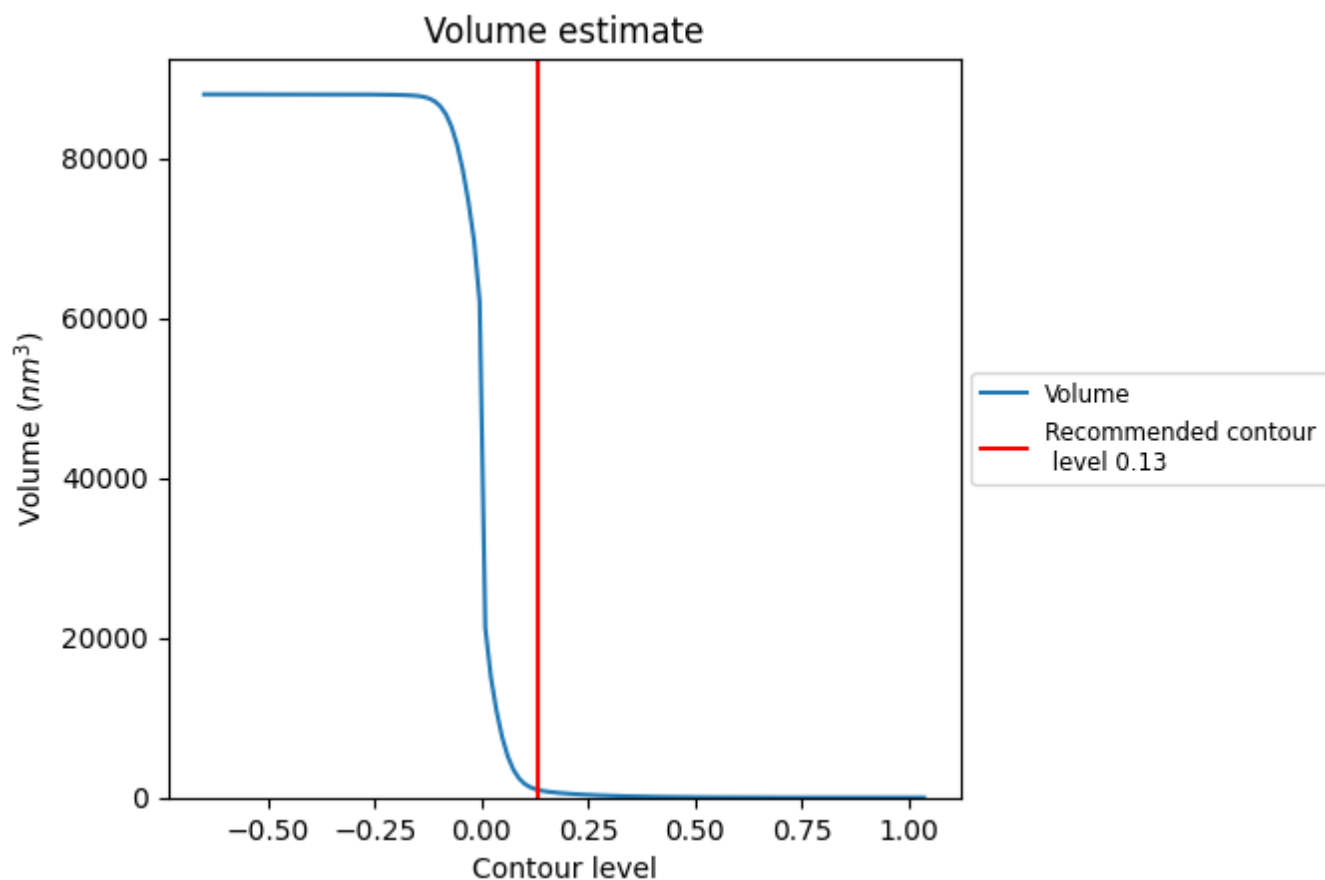
This section contains the results of statistical analysis of the map.

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.

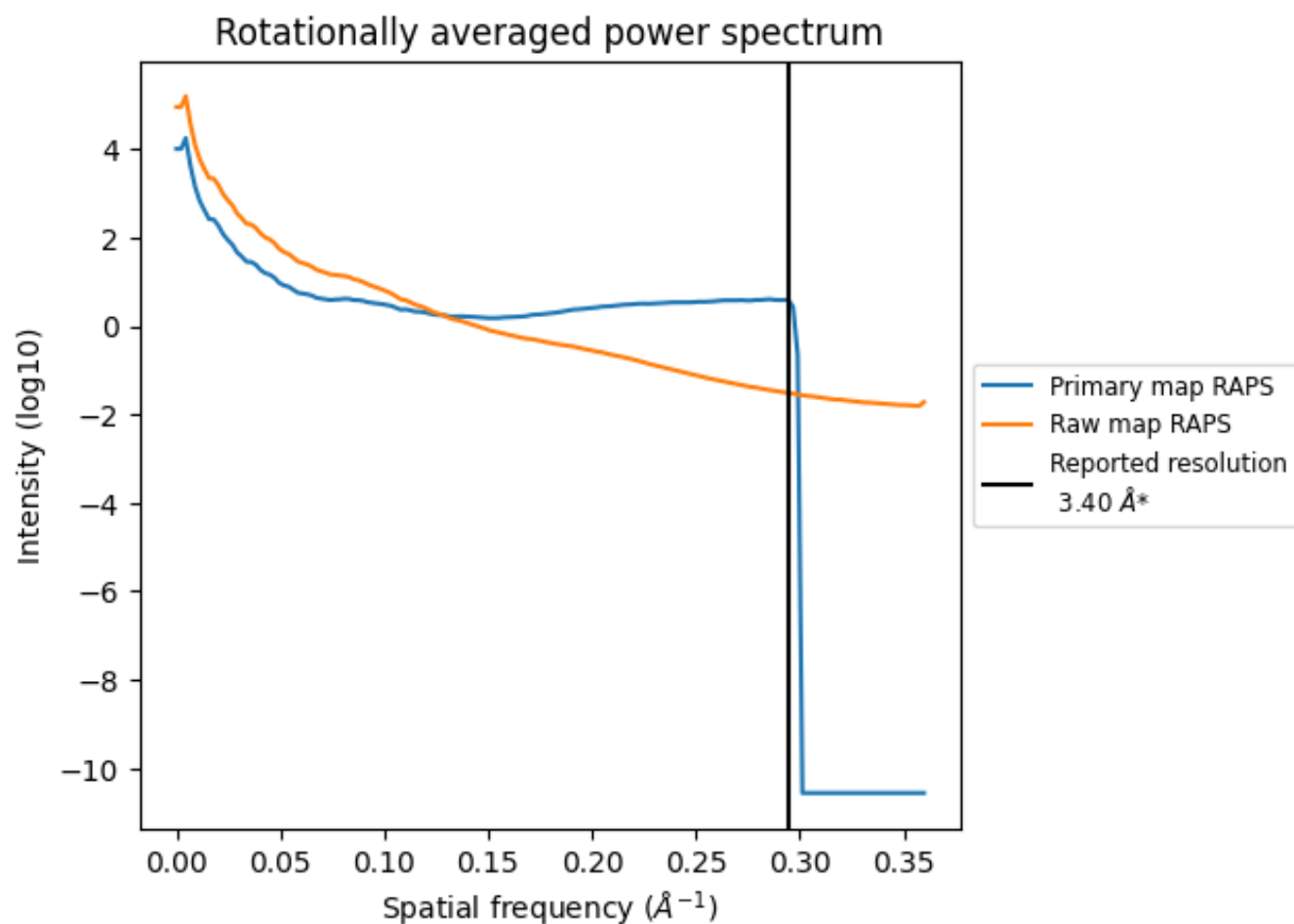
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 992 nm³; this corresponds to an approximate mass of 897 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 ⓘ

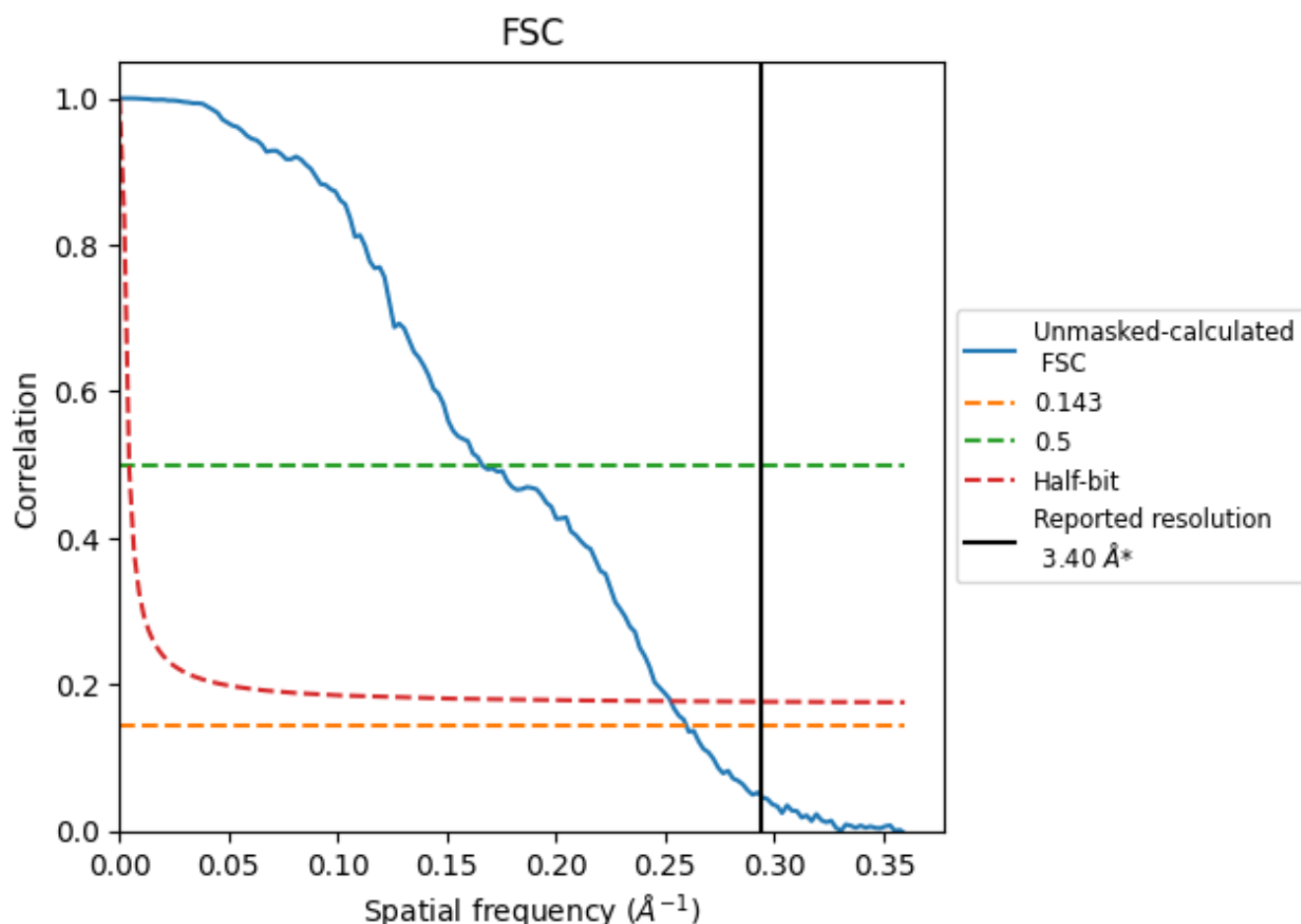


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

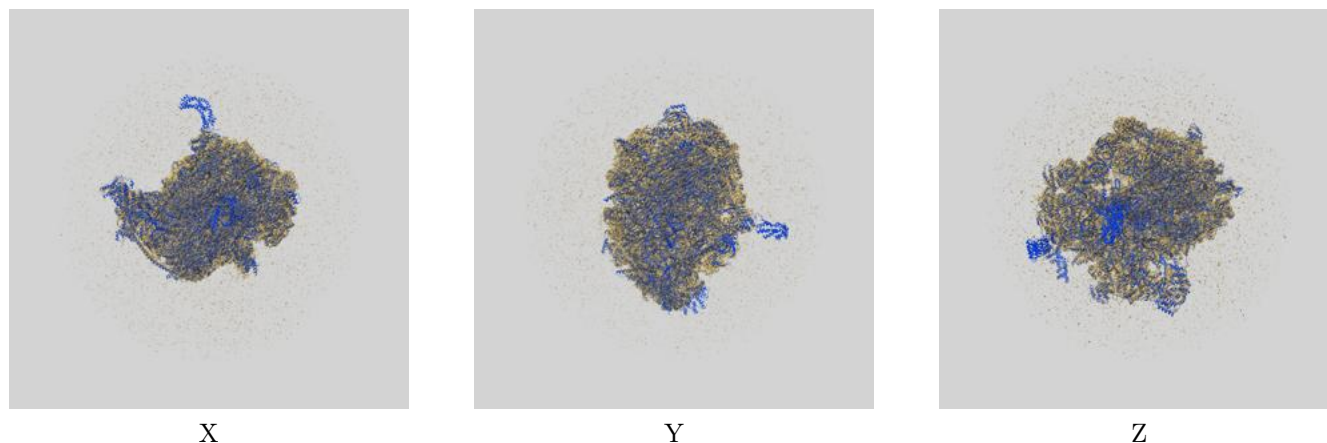
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.40 | - | - |
| Author-provided FSC curve | - | - | - |
| Unmasked-calculated* | 3.85 | 6.02 | 3.96 |

*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 3.85 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

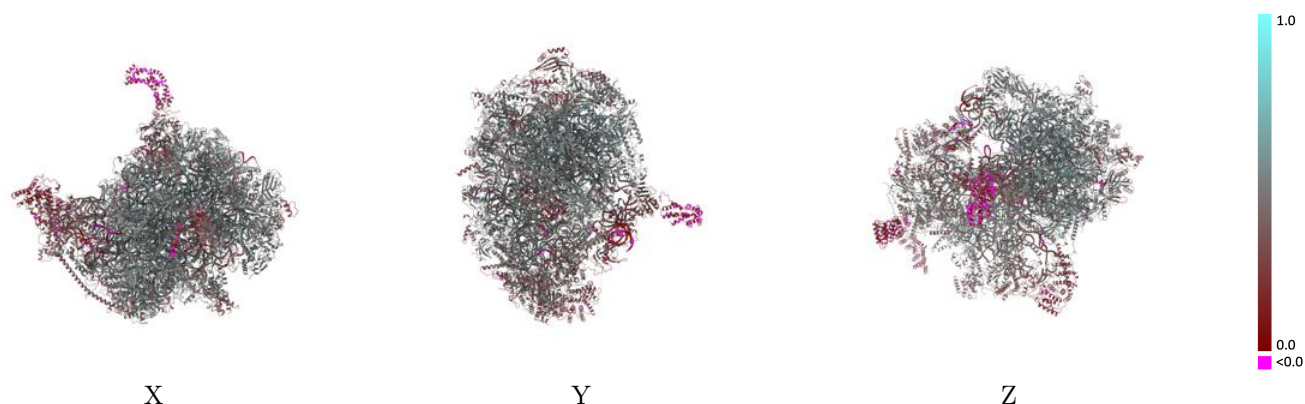
This section contains information regarding the fit between EMDB map EMD-12529 and PDB model 7NQL. Per-residue inclusion information can be found in section 3 on page 25.

9.1 Map-model overlay [i](#)



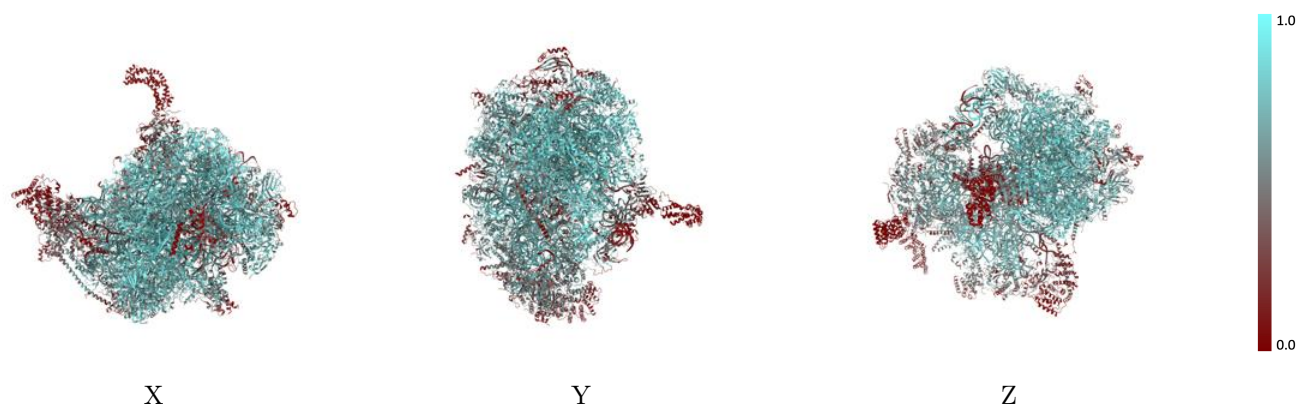
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



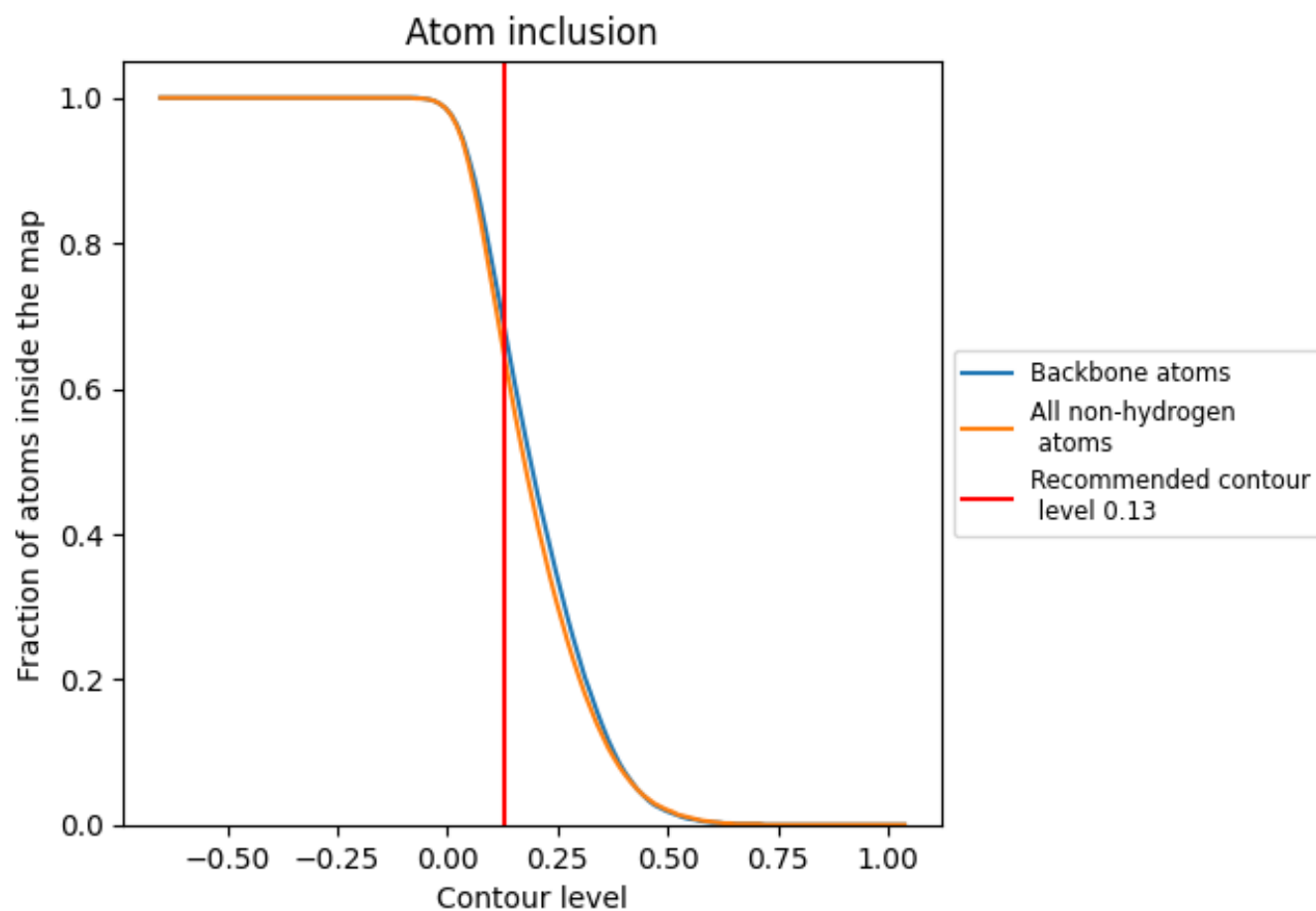
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 64% 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 (0.13) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| All |  0.6420 |  0.4370 |
| AA |  0.7650 |  0.4380 |
| AB |  0.6840 |  0.4670 |
| AC |  0.6190 |  0.4730 |
| AE |  0.5570 |  0.4510 |
| AF |  0.6700 |  0.4750 |
| AG |  0.5490 |  0.4250 |
| AI |  0.5230 |  0.4100 |
| AJ |  0.5500 |  0.4190 |
| AK |  0.6700 |  0.4770 |
| AL |  0.6400 |  0.4840 |
| AN |  0.6800 |  0.4640 |
| AO |  0.5520 |  0.4330 |
| AP |  0.5010 |  0.3880 |
| AQ |  0.6410 |  0.4620 |
| AR |  0.6560 |  0.4760 |
| AU |  0.7080 |  0.4840 |
| AV |  0.6020 |  0.3620 |
| AX |  0.7580 |  0.4820 |
| AZ |  0.3330 |  0.2130 |
| Aa |  0.3800 |  0.3680 |
| Ab |  0.4600 |  0.4010 |
| Ac |  0.6090 |  0.4400 |
| Ad |  0.4730 |  0.3740 |
| Ae |  0.1410 |  0.2260 |
| Af |  0.5650 |  0.4550 |
| Ag |  0.4680 |  0.3730 |
| Ah |  0.4130 |  0.3570 |
| Ai |  0.4960 |  0.4080 |
| Aj |  0.3000 |  0.3350 |
| Ak |  0.4400 |  0.3790 |
| Am |  0.5490 |  0.4370 |
| An |  0.6750 |  0.5050 |
| Ao |  0.0780 |  0.2060 |
| Ap |  0.5070 |  0.3980 |





































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| Chain | Atom inclusion | Q-score |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| B0 |  0.8310 |  0.5370 |
| B1 |  0.5990 |  0.4580 |
| B2 |  0.7020 |  0.4790 |
| B3 |  0.8130 |  0.5250 |
| B4 |  0.6220 |  0.4240 |
| B5 |  0.7420 |  0.5020 |
| B6 |  0.4350 |  0.4340 |
| B7 |  0.8540 |  0.5460 |
| B8 |  0.8430 |  0.5460 |
| B9 |  0.8720 |  0.5440 |
| BA |  0.8320 |  0.4810 |
| BB |  0.5350 |  0.2780 |
| BD |  0.7830 |  0.5180 |
| BE |  0.7900 |  0.5160 |
| BF |  0.7670 |  0.5020 |
| BI |  0.4470 |  0.4260 |
| BJ |  0.2770 |  0.3110 |
| BK |  0.1230 |  0.2410 |
| BL |  0.7030 |  0.4940 |
| BN |  0.8280 |  0.5350 |
| BO |  0.7450 |  0.5080 |
| BP |  0.7560 |  0.4990 |
| BQ |  0.7740 |  0.5150 |
| BR |  0.7770 |  0.5200 |
| BS |  0.7680 |  0.5040 |
| BT |  0.6900 |  0.4910 |
| BU |  0.8020 |  0.5210 |
| BV |  0.7890 |  0.5190 |
| BW |  0.7590 |  0.5210 |
| BX |  0.6480 |  0.4650 |
| BY |  0.3520 |  0.3860 |
| Ba |  0.7320 |  0.4820 |
| Bb |  0.7320 |  0.4660 |
| Bc |  0.6420 |  0.4460 |
| Bd |  0.5270 |  0.3800 |
| Be |  0.5600 |  0.4430 |
| Bf |  0.6880 |  0.4540 |
| Bg |  0.7870 |  0.5140 |
| Bh |  0.6970 |  0.4720 |
| Bi |  0.2860 |  0.3600 |
| Bj |  0.4720 |  0.3200 |
| Bk |  0.5550 |  0.4230 |

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| Chain | Atom inclusion | Q-score |
|-------|------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------|
| Bl |  0.7750 |  0.5020 |
| Bm |  0.2760 |  0.3810 |
| Bn |  0.7940 |  0.5190 |
| Bo |  0.7340 |  0.4900 |
| Bp |  0.3290 |  0.3560 |
| Bq |  0.3680 |  0.3810 |
| Bt |  0.7990 |  0.5180 |
| Bu |  0.4600 |  0.3940 |
| Bv |  0.4510 |  0.4080 |
| Bw |  0.7320 |  0.4860 |
| Bx |  0.7240 |  0.4710 |
| CL |  0.0090 |  0.1130 |
| DL |  0.0050 |  0.1040 |
| EL |  0.0000 |  0.0740 |
| FL |  0.0000 |  0.0320 |
| GL |  0.0000 |  0.0010 |
| HL |  0.0000 |  0.0060 |