



Full wwPDB EM Validation Report ⓘ

Oct 13, 2024 – 02:44 pm BST

PDB ID : 6YWX
EMDB ID : EMD-10978
Title : The structure of the mitoribosome from *Neurospora crassa* with tRNA bound to the E-site
Authors : Amunts, A.; Itoh, Y.; Naschberger, A.
Deposited on : 2020-04-30
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

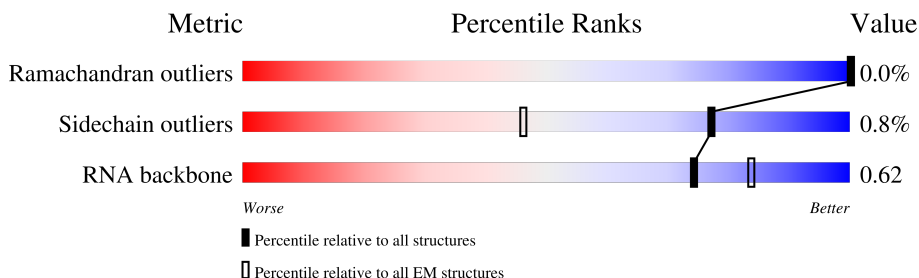
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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.



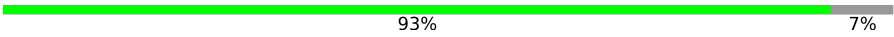
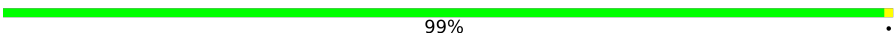



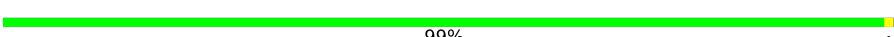




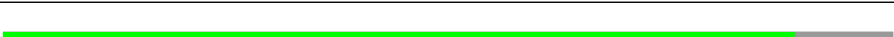


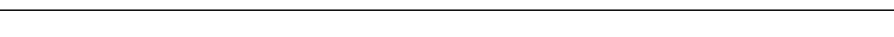
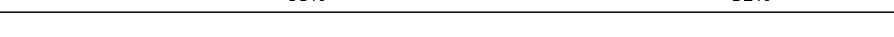
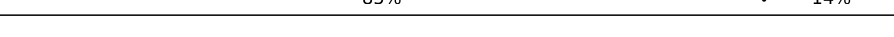



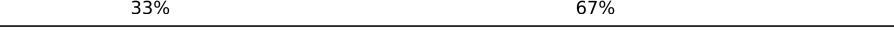




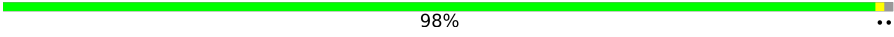
| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Ramachandran outliers | 207382 | 16835 |
| Sidechain outliers | 206894 | 16415 |
| RNA backbone | 6643 | 2191 |

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 | A | 3464 | |
| 2 | B | 383 | |
| 3 | C | 384 | |
| 4 | D | 325 | |
| 5 | E | 352 | |
| 6 | F | 255 | |
| 7 | G | 300 | |
| 8 | f | 347 | |








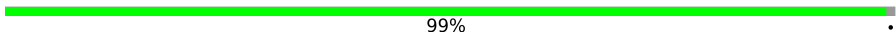







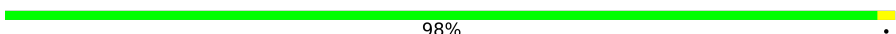

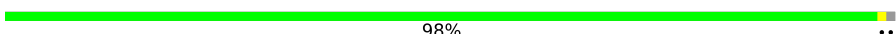




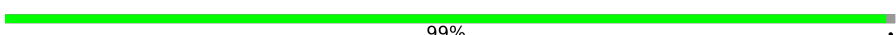
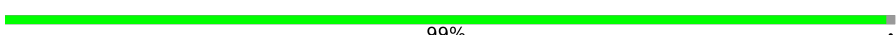

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 9 | g | 158 |  |
| 10 | H | 183 |  |
| 11 | I | 131 |  |
| 12 | J | 312 |  |
| 13 | K | 249 |  |
| 14 | L | 193 |  |
| 15 | M | 258 |  |
| 16 | N | 217 |  |
| 17 | O | 364 |  |
| 18 | P | 228 |  |
| 19 | Q | 396 |  |
| 20 | R | 447 |  |
| 21 | S | 274 |  |
| 22 | T | 263 |  |
| 23 | U | 161 |  |
| 24 | V | 219 |  |
| 25 | W | 129 |  |
| 26 | X | 59 |  |
| 27 | Y | 140 |  |
| 28 | 0 | 124 |  |
| 29 | 1 | 449 |  |
| 30 | 2 | 370 |  |
| 31 | 3 | 103 |  |
| 32 | 4 | 138 |  |
| 33 | 5 | 439 |  |


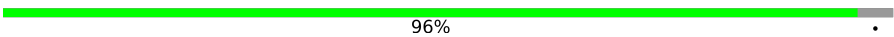








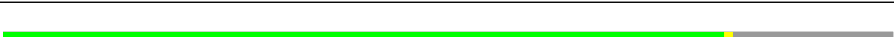


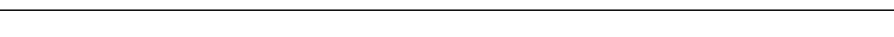
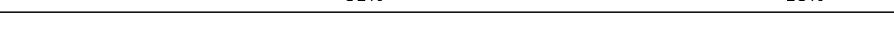
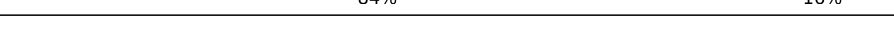



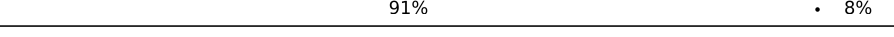





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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 34 | 6 | 368 |  |
| 35 | 7 | 165 |  |
| 36 | 8 | 443 |  |
| 37 | h | 98 |  |
| 38 | i | 218 |  |
| 39 | 9 | 267 |  |
| 40 | a | 225 |  |
| 41 | b | 162 |  |
| 42 | c | 110 |  |
| 43 | d | 292 |  |
| 44 | AA | 470 |  |
| 45 | BB | 428 |  |
| 46 | CC | 508 |  |
| 47 | DD | 453 |  |
| 48 | EE | 477 |  |
| 49 | FF | 117 |  |
| 50 | GG | 309 |  |
| 51 | HH | 161 |  |
| 52 | II | 315 |  |
| 53 | JJ | 268 |  |
| 54 | KK | 376 |  |
| 55 | LL | 174 |  |
| 56 | MM | 119 |  |
| 57 | NN | 113 |  |
| 58 | OO | 320 |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 59 | PP | 107 |  |
| 60 | QQ | 165 |  |
| 61 | RR | 256 |  |
| 62 | SS | 91 |  |
| 63 | TT | 236 |  |
| 64 | UU | 253 |  |
| 65 | VV | 316 |  |
| 66 | WW | 396 |  |
| 67 | XX | 469 |  |
| 68 | YY | 108 |  |
| 69 | ZZ | 382 |  |
| 70 | 11 | 90 |  |
| 71 | 22 | 344 |  |
| 72 | 33 | 236 |  |
| 73 | 44 | 310 |  |
| 73 | 55 | 310 |  |
| 74 | 66 | 348 |  |
| 75 | 77 | 414 |  |
| 76 | 88 | 508 |  |
| 77 | 00 | 95 |  |
| 77 | 99 | 95 |  |
| 78 | aa | 1864 |  |
| 79 | bb | 61 |  |
| 80 | e | 303 |  |
| 81 | j | 201 |  |

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 390774 atoms, of which 173664 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 RNA chain called 23S rRNA.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|-------|------|---------|-------|
| 1 | A | 2838 | Total | C | H | N | O | P | 0 | 0 |
| | | | 90895 | 27142 | 30363 | 10859 | 19693 | 2838 | | |

- Molecule 2 is a protein called 60S ribosomal protein L2.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 2 | B | 317 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4996 | 1537 | 2523 | 502 | 419 | 15 | | |

- Molecule 3 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 3 | C | 307 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4757 | 1468 | 2421 | 447 | 413 | 8 | | |

- Molecule 4 is a protein called 60S ribosomal protein L4, variant.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 4 | D | 254 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4068 | 1280 | 2040 | 372 | 371 | 5 | | |

- Molecule 5 is a protein called 50S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 5 | E | 309 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4910 | 1558 | 2461 | 436 | 443 | 12 | | |

- Molecule 6 is a protein called 60S ribosomal protein L6.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 6 | F | 201 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3253 | 1022 | 1645 | 290 | 288 | 8 | | |

- Molecule 7 is a protein called RIBOSOMAL_L9 domain-containing protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| 7 | G | 74 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1245 | 390 | 627 | 121 | 104 | 3 | | |

- Molecule 8 is a protein called uL10m.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 8 | f | 245 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3801 | 1202 | 1925 | 325 | 346 | 3 | | |

- Molecule 9 is a protein called 60S ribosomal protein L19.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 9 | g | 147 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2257 | 700 | 1154 | 203 | 196 | 4 | | |

- Molecule 10 is a protein called Ribosomal protein L13.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 10 | H | 183 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2885 | 899 | 1459 | 268 | 251 | 8 | | |

- Molecule 11 is a protein called 50S ribosomal protein L14.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| 11 | I | 119 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1898 | 564 | 985 | 182 | 159 | 8 | | |

- Molecule 12 is a protein called 50S ribosomal subunit protein L15.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 12 | J | 243 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3827 | 1198 | 1939 | 346 | 343 | 1 | | |

- Molecule 13 is a protein called 60S ribosomal protein L16.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 13 | K | 168 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2751 | 850 | 1401 | 263 | 231 | 6 | | |

- Molecule 14 is a protein called 50S ribosomal protein L17.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 14 | L | 192 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3135 | 960 | 1590 | 294 | 285 | 6 | | |

- Molecule 15 is a protein called Mitochondrial ribosomal protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|----|---------|-------|
| 15 | M | 194 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3164 | 981 | 1628 | 292 | 253 | 10 | | |

- Molecule 16 is a protein called Aconitate hydratase.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 16 | N | 133 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2176 | 673 | 1120 | 195 | 182 | 6 | | |

- Molecule 17 is a protein called Mitochondrial large ribosomal subunit.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 17 | O | 272 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4532 | 1392 | 2323 | 424 | 387 | 6 | | |

- Molecule 18 is a protein called Mitochondrial ribosomal protein subunit L23.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 18 | P | 180 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2975 | 953 | 1494 | 270 | 254 | 4 | | |

- Molecule 19 is a protein called KOW domain-containing protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 19 | Q | 353 | Total | C | H | N | O | S | 0 | 0 |
| | | | 5829 | 1786 | 2961 | 547 | 524 | 11 | | |

- Molecule 20 is a protein called bL27m.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 20 | R | 249 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4195 | 1283 | 2149 | 412 | 347 | 4 | | |

- Molecule 21 is a protein called 50S ribosomal protein L24.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 21 | S | 179 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2979 | 937 | 1507 | 281 | 252 | 2 | | |

- Molecule 22 is a protein called 54S ribosomal protein L4, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 22 | T | 180 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2950 | 937 | 1453 | 279 | 278 | 3 | | |

- Molecule 23 is a protein called 50S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 23 | U | 138 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2263 | 698 | 1164 | 213 | 185 | 3 | | |

- Molecule 24 is a protein called bL31m.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---|---------|-------|
| 24 | V | 56 | Total | C | H | N | O | S | 0 | 0 |
| | | | 921 | 291 | 462 | 85 | 82 | 1 | | |

- Molecule 25 is a protein called Mitochondrial ribosomal protein subunit L32.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---|---------|-------|
| 25 | W | 59 | Total | C | H | N | O | S | 0 | 0 |
| | | | 949 | 282 | 489 | 98 | 72 | 8 | | |

- Molecule 26 is a protein called bL33m.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---|---------|-------|
| 26 | X | 48 | Total | C | H | N | O | S | 0 | 0 |
| | | | 836 | 263 | 433 | 71 | 65 | 4 | | |

- Molecule 27 is a protein called Related to ribosomal protein L34, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---|---------|-------|
| 27 | Y | 46 | Total | C | H | N | O | S | 0 | 0 |
| | | | 777 | 224 | 412 | 84 | 56 | 1 | | |

- Molecule 28 is a protein called Ribosomal protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---|---------|-------|
| 28 | 0 | 46 | Total | C | H | N | O | S | 0 | 0 |
| | | | 797 | 240 | 409 | 86 | 58 | 4 | | |

- Molecule 29 is a protein called Mitochondrial large ribosomal subunit YmL35.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 29 | 1 | 367 | Total | C | H | N | O | S | 0 | 0 |
| | | | 6014 | 1899 | 3029 | 547 | 531 | 8 | | |

- Molecule 30 is a protein called mL40.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 30 | 2 | 123 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2101 | 660 | 1055 | 211 | 171 | 4 | | |

- Molecule 31 is a protein called mL41.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| 31 | 3 | 95 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1536 | 489 | 773 | 135 | 137 | 2 | | |

- Molecule 32 is a protein called Mitochondrial ribosomal protein L43.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 32 | 4 | 137 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2139 | 671 | 1087 | 192 | 183 | 6 | | |

- Molecule 33 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 33 | 5 | 350 | Total | C | H | N | O | S | 0 | 0 |
| | | | 5429 | 1740 | 2710 | 477 | 493 | 9 | | |

- Molecule 34 is a protein called 50S ribosomal subunit L30.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 34 | 6 | 273 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4474 | 1418 | 2248 | 399 | 401 | 8 | | |

- Molecule 35 is a protein called mL49.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|
| 35 | 7 | 84 | Total | C | H | N | O | 0 | 0 |
| | | | 1383 | 431 | 709 | 130 | 113 | | |

- Molecule 36 is a protein called mL50.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 36 | 8 | 331 | Total | C | H | N | O | S | 0 | 0 |
| | | | 5374 | 1683 | 2714 | 480 | 489 | 8 | | |

- Molecule 37 is a protein called Mitochondrial ribosomal protein L44.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| 37 | h | 98 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1577 | 490 | 798 | 139 | 146 | 4 | | |

- Molecule 38 is a protein called mL54.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 38 | i | 124 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1999 | 613 | 1022 | 181 | 178 | 5 | | |

- Molecule 39 is a protein called RNase III domain-containing protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 39 | 9 | 206 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3341 | 1051 | 1698 | 295 | 290 | 7 | | |

- Molecule 40 is a protein called 60S ribosomal protein L20.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 40 | a | 161 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2671 | 837 | 1340 | 253 | 235 | 6 | | |

- Molecule 41 is a protein called Mitochondrial 60S ribosomal protein L25.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 41 | b | 161 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2693 | 840 | 1379 | 249 | 221 | 4 | | |

- Molecule 42 is a protein called 54S ribosomal protein L31, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| 42 | c | 98 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1700 | 528 | 873 | 162 | 134 | 3 | | |

- Molecule 43 is a protein called mL67.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 43 | d | 235 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3797 | 1180 | 1909 | 363 | 339 | 6 | | |

- Molecule 44 is a protein called bS1m.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 44 | AA | 372 | Total | C | H | N | O | S | 0 | 0 |
| | | | 5790 | 1827 | 2907 | 507 | 543 | 6 | | |

- Molecule 45 is a protein called Mito ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 45 | BB | 290 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4570 | 1426 | 2301 | 423 | 414 | 6 | | |

- Molecule 46 is a protein called Ribosomal protein S5, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 46 | CC | 438 | Total | C | H | N | O | S | 0 | 0 |
| | | | 7538 | 2388 | 3897 | 636 | 612 | 5 | | |

- Molecule 47 is a protein called Mito ribosomal protein S4.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 47 | DD | 290 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4716 | 1501 | 2373 | 430 | 401 | 11 | | |

- Molecule 48 is a protein called 37S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 48 | EE | 367 | Total | C | H | N | O | S | 0 | 0 |
| | | | 5798 | 1799 | 2918 | 526 | 543 | 12 | | |

- Molecule 49 is a protein called Mito ribosomal protein S6.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| 49 | FF | 117 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1901 | 591 | 966 | 176 | 165 | 3 | | |

- Molecule 50 is a protein called Ribosomal_S7 domain-containing protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 50 | GG | 217 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3409 | 1063 | 1737 | 307 | 296 | 6 | | |

- Molecule 51 is a protein called 40S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 51 | HH | 160 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2521 | 783 | 1286 | 226 | 220 | 6 | | |

- Molecule 52 is a protein called 37S ribosomal protein S9, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 52 | II | 247 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3995 | 1253 | 2026 | 366 | 345 | 5 | | |

- Molecule 53 is a protein called 37S ribosomal protein S10, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 53 | JJ | 188 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3105 | 998 | 1554 | 273 | 272 | 8 | | |

- Molecule 54 is a protein called Mitochondrial ribosomal protein subunit S18.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 54 | KK | 124 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2020 | 625 | 1025 | 195 | 170 | 5 | | |

- Molecule 55 is a protein called Mitochondrial 30S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 55 | LL | 128 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1992 | 591 | 1033 | 198 | 165 | 5 | | |

- Molecule 56 is a protein called 40S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| 56 | MM | 118 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1923 | 586 | 986 | 186 | 161 | 4 | | |

- Molecule 57 is a protein called Mitochondrial 40S ribosomal protein MRP2.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| 57 | NN | 112 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1875 | 573 | 961 | 184 | 150 | 7 | | |

- Molecule 58 is a protein called Ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 58 | OO | 276 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4428 | 1361 | 2230 | 431 | 401 | 5 | | |

- Molecule 59 is a protein called Ribosomal protein S16, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| 59 | PP | 98 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1612 | 510 | 826 | 141 | 135 | | | |

- Molecule 60 is a protein called Mitochondrial 37S ribosomal protein S17.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 60 | QQ | 158 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2561 | 789 | 1314 | 234 | 219 | 5 | | |

- Molecule 61 is a protein called Mito ribosomal protein S18.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 61 | RR | 134 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2169 | 679 | 1089 | 206 | 190 | 5 | | |

- Molecule 62 is a protein called Mitochondrial ribosomal protein S19.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| 62 | SS | 81 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1325 | 422 | 677 | 118 | 107 | 1 | | |

- Molecule 63 is a protein called Mito ribosomal protein S21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|
| 63 | TT | 88 | Total | C | H | N | O | 0 | 0 |
| | | | 1518 | 470 | 772 | 157 | 119 | | |

- Molecule 64 is a protein called 37S ribosomal protein S25, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 64 | UU | 218 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3600 | 1139 | 1801 | 334 | 319 | 7 | | |

- Molecule 65 is a protein called mS26.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 65 | VV | 261 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4192 | 1300 | 2112 | 390 | 387 | 3 | | |

- Molecule 66 is a protein called mS27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| 66 | WW | 353 | Total | C | H | N | O | S | 0 | 0 |
| | | | 5744 | 1804 | 2901 | 514 | 515 | 10 | | |

- Molecule 67 is a protein called Mitochondrial ribosomal protein DAP3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| 67 | XX | 408 | Total | C | H | N | O | S | 0 | 0 |
| | | | 6446 | 2010 | 3271 | 562 | 587 | 16 | | |

- Molecule 68 is a protein called mS33.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| 68 | YY | 99 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1609 | 491 | 823 | 152 | 142 | 1 | | |

- Molecule 69 is a protein called 37S ribosomal protein S24, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 69 | ZZ | 312 | Total | C | H | N | O | S | 0 | 0 |
| | | | 5114 | 1631 | 2528 | 450 | 495 | 10 | | |

- Molecule 70 is a protein called 37S ribosomal protein mrp10, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|---|---------|-------|
| 70 | 11 | 88 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1358 | 417 | 686 | 128 | 121 | 6 | | |

- Molecule 71 is a protein called DUF1713 domain-containing protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---|---------|-------|
| 71 | 22 | 33 | Total | C | H | N | O | S | 0 | 0 |
| | | | 660 | 187 | 359 | 70 | 43 | 1 | | |

- Molecule 72 is a protein called IGR domain-containing protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 72 | 33 | 193 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3161 | 989 | 1607 | 295 | 268 | 2 | | |

- Molecule 73 is a protein called Fe superoxide dismutase.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 73 | 44 | 260 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4045 | 1318 | 1983 | 355 | 378 | 11 | | |
| 73 | 55 | 232 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3652 | 1195 | 1794 | 316 | 337 | 10 | | |

- Molecule 74 is a protein called mS45.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|---|---------|-------|
| 74 | 66 | 283 | Total | C | H | N | O | S | 0 | 0 |
| | | | 4628 | 1455 | 2330 | 425 | 414 | 4 | | |

- Molecule 75 is a protein called mS46.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 75 | 77 | 179 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2796 | 893 | 1396 | 227 | 277 | 3 | | |

- Molecule 76 is a protein called 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|----|---------|-------|
| 76 | 88 | 467 | Total | C | H | N | O | S | 0 | 0 |
| | | | 7327 | 2340 | 3650 | 634 | 691 | 12 | | |

- Molecule 77 is a protein called IF1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|
| 77 | 00 | 48 | Total | C | H | N | O | 0 | 0 |
| | | | 823 | 252 | 417 | 77 | 77 | | |
| 77 | 99 | 36 | Total | C | H | N | O | 0 | 0 |
| | | | 639 | 191 | 333 | 59 | 56 | | |

- Molecule 78 is a RNA chain called 16S rRNA.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|------|------|------|---------|-------|
| 78 | aa | 1435 | Total | C | H | N | O | P | 0 | 0 |
| | | | 45981 | 13712 | 15373 | 5486 | 9975 | 1435 | | |

- Molecule 79 is a RNA chain called tRNA E-site.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|-----|----|---------|-------|
| 79 | bb | 61 | Total | C | H | N | O | P | 0 | 0 |
| | | | 1957 | 581 | 658 | 233 | 424 | 61 | | |

- Molecule 80 is a protein called 60S ribosomal protein L1.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 80 | e | 150 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2435 | 762 | 1234 | 212 | 220 | 7 | | |

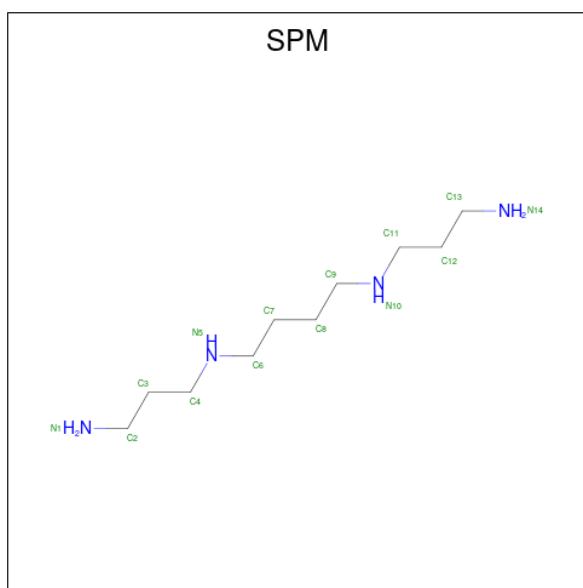
- Molecule 81 is a protein called L51_S25_CI-B8 domain-containing protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| 81 | j | 195 | Total | C | H | N | O | S | 0 | 0 |
| | | | 3139 | 971 | 1586 | 290 | 284 | 8 | | |

- Molecule 82 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|-----|---------|
| 82 | A | 150 | Total | Mg | 0 |
| | | | 150 | 150 | |
| 82 | BB | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 82 | XX | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 82 | 00 | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 82 | aa | 96 | Total | Mg | 0 |
| | | | 96 | 96 | |

- Molecule 83 is SPERMINE (three-letter code: SPM) (formula: $C_{10}H_{26}N_4$).

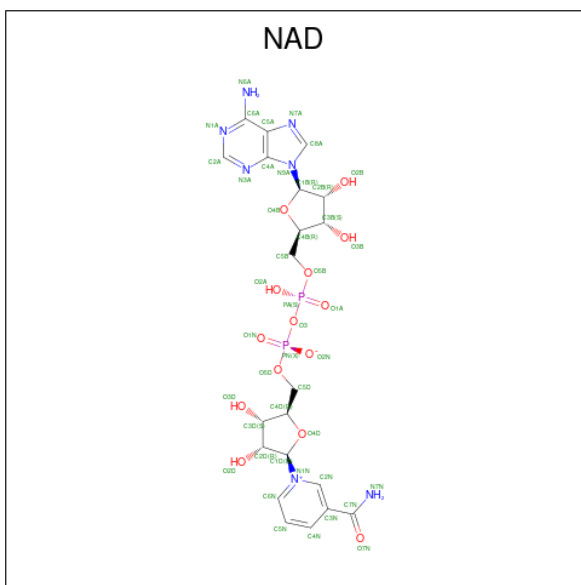


| Mol | Chain | Residues | Atoms | | | | AltConf |
|-----|-------|----------|-------|----|----|---|---------|
| 83 | A | 1 | Total | C | H | N | 0 |
| | | | 40 | 10 | 26 | 4 | |

- Molecule 84 is POTASSIUM ION (three-letter code: K) (formula: K).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 84 | A | 28 | Total | K | 0 |
| | | | 28 | 28 | |
| 84 | K | 1 | Total | K | 0 |
| | | | 1 | 1 | |
| 84 | 2 | 1 | Total | K | 0 |
| | | | 1 | 1 | |
| 84 | 3 | 1 | Total | K | 0 |
| | | | 1 | 1 | |
| 84 | 77 | 1 | Total | K | 0 |
| | | | 1 | 1 | |
| 84 | 88 | 1 | Total | K | 0 |
| | | | 1 | 1 | |
| 84 | aa | 17 | Total | K | 0 |
| | | | 17 | 17 | |

- Molecule 85 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



| Mol | Chain | Residues | Atoms | | | | | | AltConf |
|-----|-------|----------|-------|----|----|---|----|---|---------|
| 85 | E | 1 | Total | C | H | N | O | P | 0 |
| | | | 69 | 21 | 25 | 7 | 14 | 2 | |

- Molecule 86 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | AltConf |
|-----|-------|----------|-----------------|---------|
| 86 | W | 1 | Total Zn 1 1 | 0 |
| 86 | 0 | 1 | Total Zn 1 1 | 0 |

- Molecule 87 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{13}\text{P}_3$) (labeled as "Ligand of Interest" by depositor).

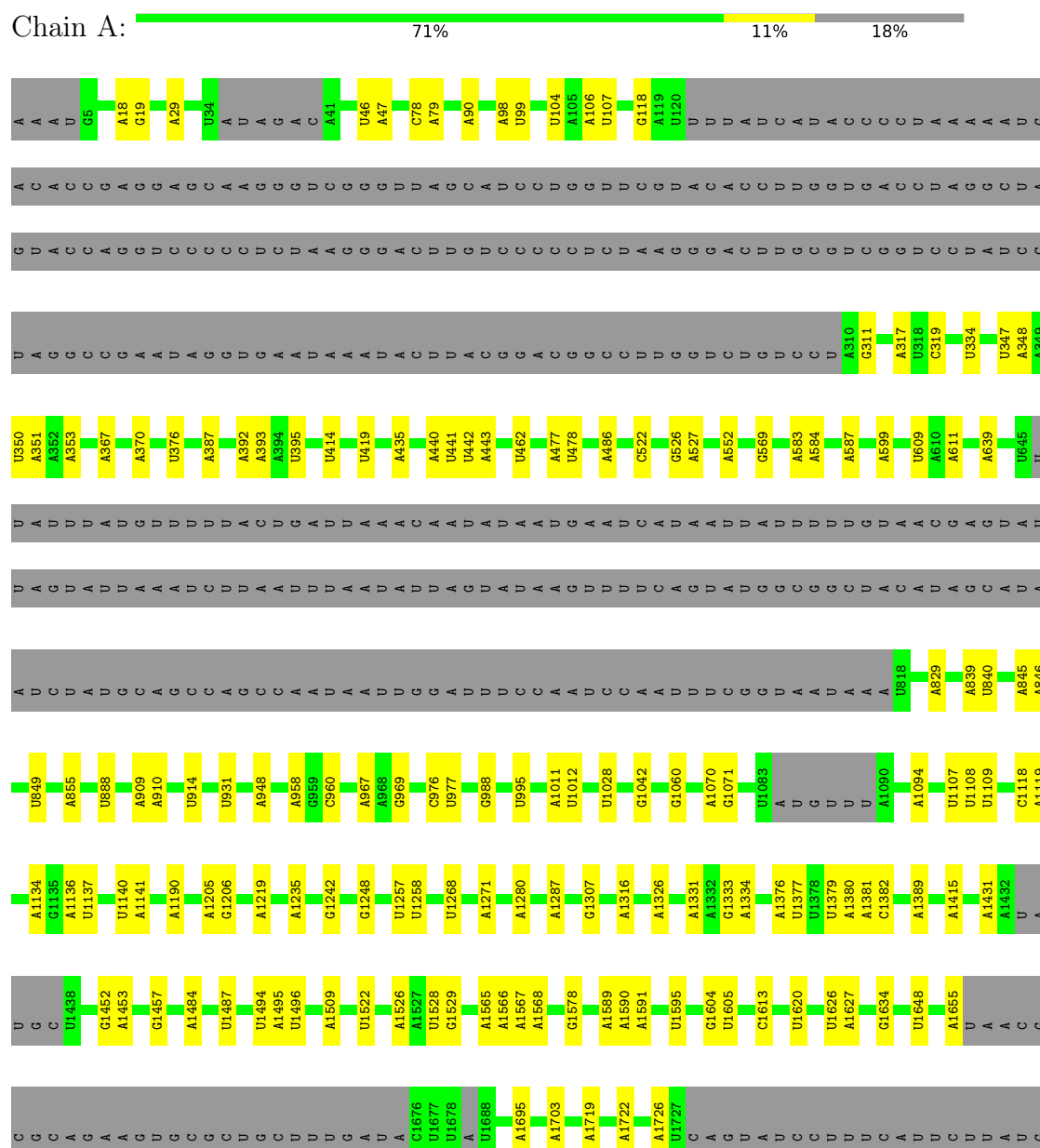


| Mol | Chain | Residues | Atoms | | | | | AltConf | |
|-----|-------|----------|-------|----|----|---|----|---------|---|
| 87 | XX | 1 | Total | C | H | N | O | P | 0 |
| | | | 43 | 10 | 12 | 5 | 13 | 3 | |


3 Residue-property plots

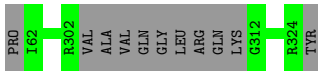
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 23S rRNA



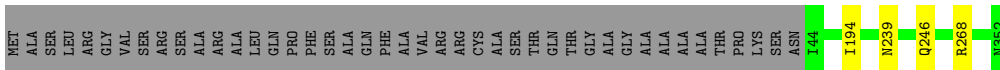
- Molecule 4: 60S ribosomal protein L4, variant

Chain D:  78% 22%

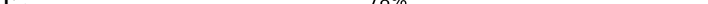


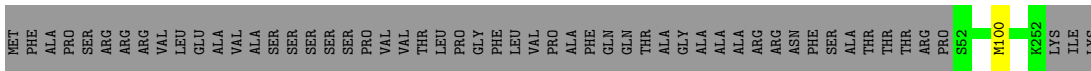
- Molecule 5: 50S ribosomal protein L5

Chain E:  87% . 12%



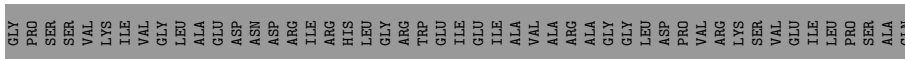
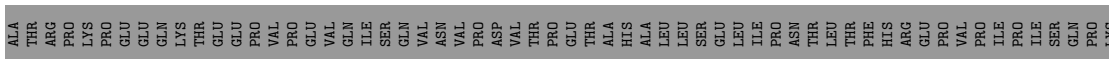
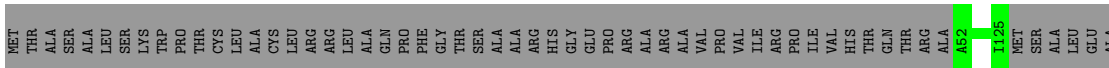
- Molecule 6: 60S ribosomal protein L6

Chain F:  78% 21%



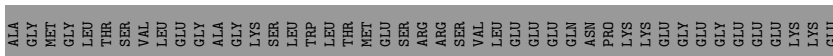
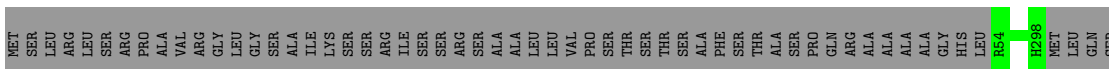
- Molecule 7: RIBOSOMAL_L9 domain-containing protein

Chain G: 25% 75%



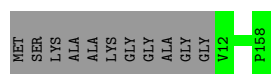
- Molecule 8: uL10m

Chain f: 71% 29%



- Molecule 9: 60S ribosomal protein L19

Chain g:  93% 7%



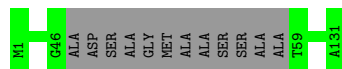
- Molecule 10: Ribosomal protein L13

Chain H:  99% .




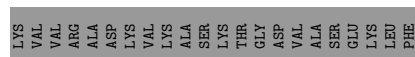
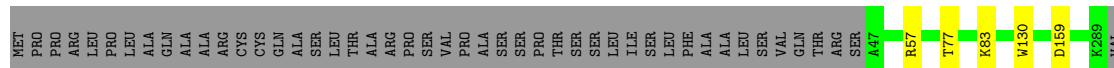
- Molecule 11: 50S ribosomal protein L14

Chain I:  91% 9%



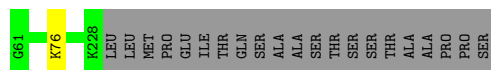
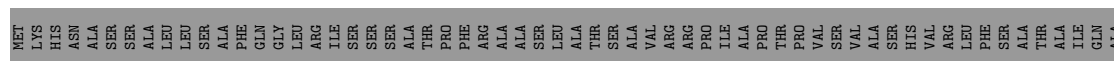
- Molecule 12: 50S ribosomal subunit protein L15

Chain J:  76% 22%



- Molecule 13: 60S ribosomal protein L16

Chain K:  67% 33%



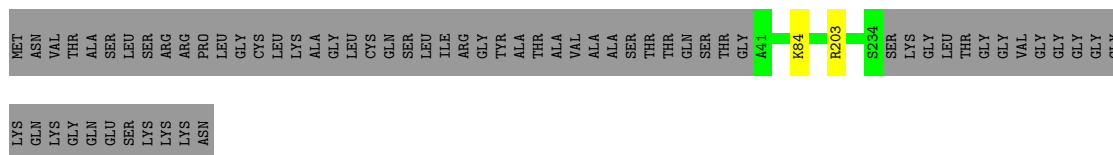
- Molecule 14: 50S ribosomal protein L17

Chain L:  99% ..

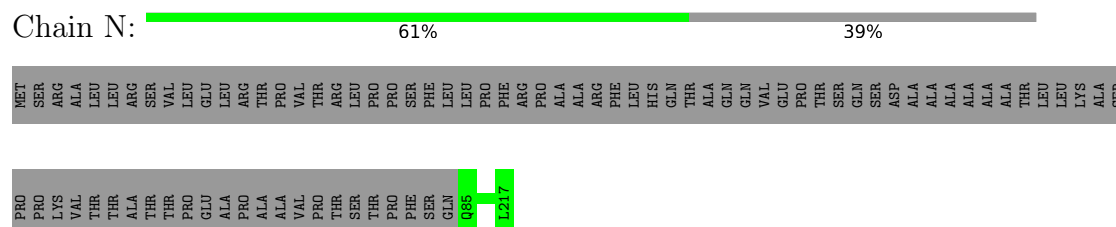


- Molecule 15: Mitochondrial ribosomal protein

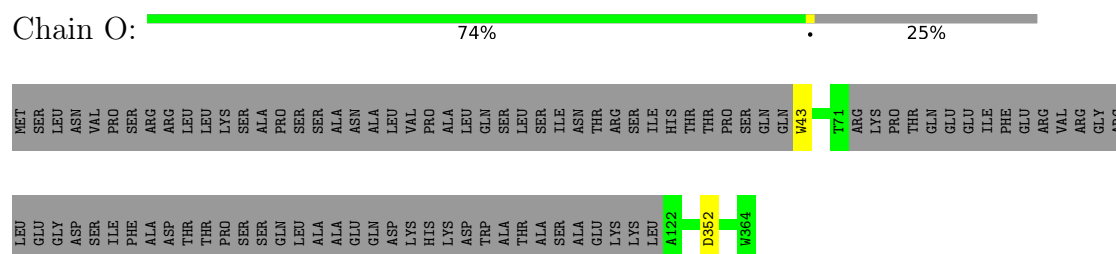
Chain M:  74% 25%



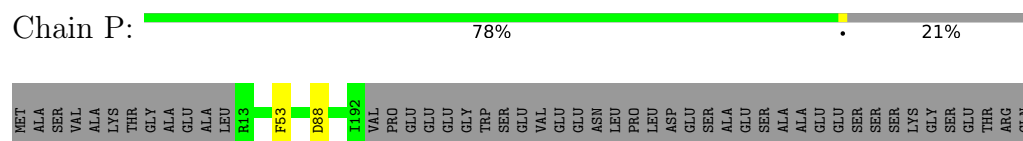
• Molecule 16: Aconitate hydratase



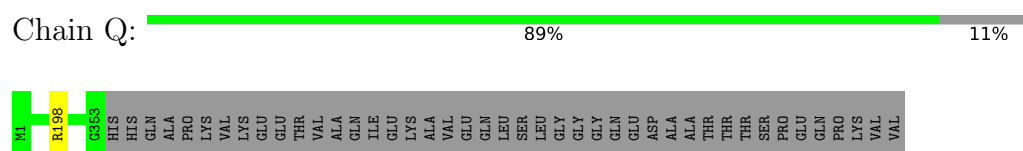
• Molecule 17: Mitochondrial large ribosomal subunit



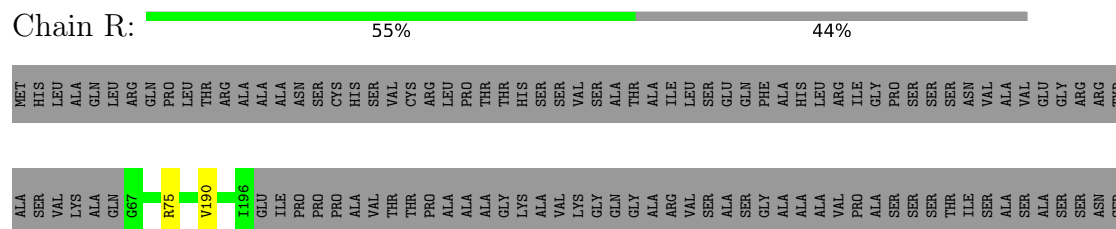
• Molecule 18: Mitochondrial ribosomal protein subunit L23

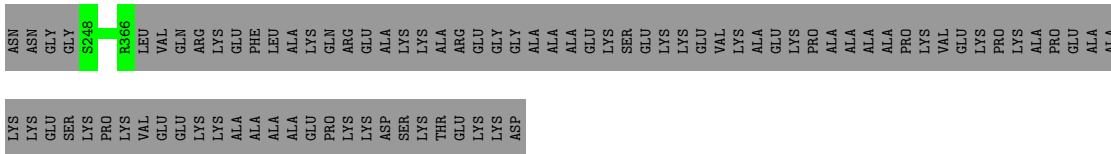


• Molecule 19: KOW domain-containing protein

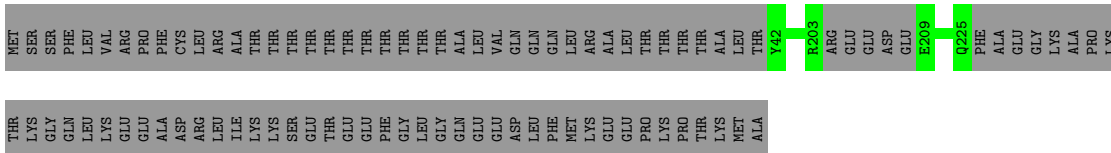


• Molecule 20: bL27m

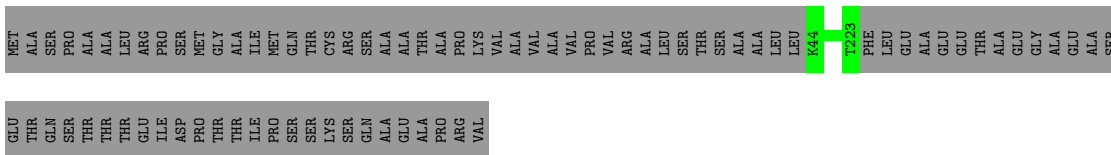




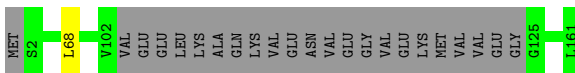
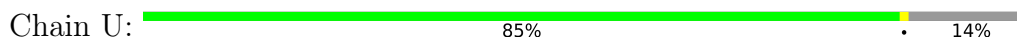
- Molecule 21: 50S ribosomal protein L24



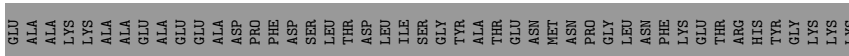
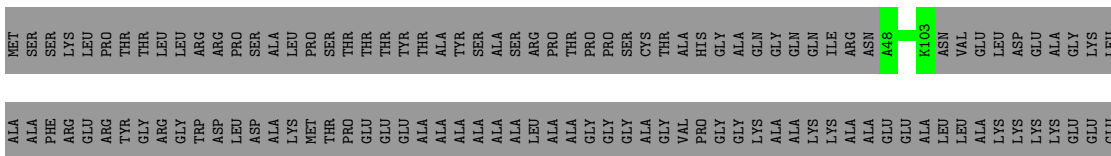
- Molecule 22: 54S ribosomal protein L4, mitochondrial



- Molecule 23: 50S ribosomal protein L30



- Molecule 24: bL31m



- Molecule 25: Mitochondrial ribosomal protein subunit L32



THR ARG
LEU PHE
ALA
GLY
GLY
ARG
ARG
PRO
SER
PRO
SER
SER
LEU
LEU
LEU
PRO
ASN
LYS
PRO
ALA
THR
ALA
ALA
LEU
PRO
THR
THR
ALA
ILE
ILE
GLN
HIS
GLN
GLN
THR
SER
ALA
SER
TYR
ALA
SER
LYS
LYS
GLY
GLY
PRO
PRO
ALA
ALA
GLY
MET
PHE
SER
GLY
GLN
LYS
ALA
GLY
LYS

SER
LYS
GLY
PRO
LYS
GLN
VAL
D248
R265
R325
R370

- Molecule 31: mL41

Chain 3: 90% 8%

MET
GLN
PRO
THR
ARG
ILE
LEU
GLN
G9
R31
Y41
D103

- Molecule 32: Mitochondrial ribosomal protein L43

Chain 4: 98% ..

MET
T2
E91
S123
Y138

- Molecule 33: 60S ribosomal protein L3

Chain 5: 79% 20%

MET
LYS
ILE
ALA
THR
PRO
SER
LEU
THR
SER
ARG
LEU
LEU
VAL
ALA
SER
ARG
GLY
VAL
SER
PRO
ALA
THR
ALA
ALA
ILE
ILE
ARG
GLN
ASP
ARG
SER
GLN
SER
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THR
ALA
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LEU
ALA
GLN
HIS
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ALA
SER
HIS
ASP
LEU
ASN
N65
S237
ASP
PRO
LYS

VAL
ALA
ASP
LEU
LYS
ALA
MET
GLU
GLN
ASP
GLN
THR
PRO
GLU
GLU
ALA
MET
VAL
ALA
ASN
GLN
GLU
ASP
GLN
D273
E289
L419
R439

- Molecule 34: 50S ribosomal subunit L30

Chain 6: 73% 26%

MET
SER
ALA
SER
SER
ARG
GLY
ALA
ALA
LEU
LEU
SER
ARG
SER
GLN
GLN
ARG
ILE
CYS
LEU
GLN
CYS
ASN
GLN
THR
ARG
VAL
LEU
ALA
PRO
ALA
GLY
VAL
THR
SER
ALA
PRO
ARG
PHE
TYR
SER
ALA
GLU
ALA
SER
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THR
LEU
PRO
PRO
HIS
PRO
PRO
VAL
THR
THR
SER
THR
GLY
HIS
ALA
ALA
SER
THR
THR
S82
R181
Y245
ALA
ASP
LYS
GLY
GLY
GLU
GLU
A253
F303
GLY
GLN
LYS
ASP
GLY
ALA
LEU
L311
N334
L349
R368

- Molecule 35: mL49

Chain 7: 51% 49%

MET
PHE
ARG
SER
THR
PHE
PHE
GLY
LEU
SER
THR
ARG
ALA
ILE
VAL
GLN
PRO
ALA
SER
THR
PRO
LEU
THR
VAL
ARG
ALA
ALA
PHE
GLN
SER
SER
PHE
PHE
TYR
SER
ALA
ALA
ALA
ALA
SER
GLN
PRO
THR
THR
THR
ALA
THR
THR
THR
PRO
LEU
GLN
GLN
GLN
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GLN
GLN
PRO
THR
THR


GLN
PRO
THR
THR
ILE
GLN
THR
GLN
THR
ALA
ALA
PRO
THR
GLU
SER
THR
PRO
VAL
A82
F165

- Molecule 36: mL50

MET PHE GLY ALA PHE ARG PHE THR ASN PRO LEU SER G13 K57 S102 Y110

- Chain d: 79% 20%

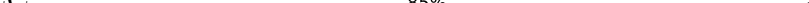
[illegible]

- Chain AA:  77% 1% 21%

| | | |
|-----|------|------|
| SER | ASP | MET |
| PRO | S288 | ALA |
| THR | | PHE |
| MET | R337 | SER |
| SER | GLY | ARG |
| GLY | LEU | 66 |
| SER | | |
| SER | G341 | T55 |
| GLY | | |
| TYR | G358 | I124 |
| GLY | THR | SER |
| LEU | SER | ASP |
| ARG | HIS | PRO |
| | SER | SER |
| | ASN | ARG |
| | LEU | LEU |
| | ARG | PHE |
| | GLY | R132 |
| | ASN | |
| | S368 | D151 |
| | | E152 |
| | K372 | Q153 |
| | | |
| | V385 | E215 |
| | | THR |
| | K414 | ALA |
| | E415 | ALA |
| | | LEU |
| | D419 | ARG |
| | A420 | GLY |
| | R421 | ASP |
| | | ALA |
| | K430 | VAL |
| | ARG | ALA |
| | GLN | GLU |
| | GLU | THR |
| | LYS | GLN |
| | THR | GLU |
| | PHE | PRO |
| | LYS | PHE |
| | LYS | K230 |
| | ILE | |
| | PRO | P269 |
| | MET | GLN |
| | THR | ALA |
| | ALA | ALA |
| | ALA | GLU |
| | ARG | ALA |
| | LEU | ARG |
| | ARG | GLN |
| | GLY | HIS |
| | ARG | SER |
| | TYR | LEU |
| | GLU | LEU |
| | ASN | VAL |
| | SER | ASN |
| | ASP | LEU |
| | SER | ARG |
| | PRO | ALA |

- Chain BB:  67% 32%

[illegible]

- Chain CC:  85% 14%

[illegible]

ALA
PRO
ALA
LEU
SER
ILE
ASP
ASN
F69
N216
R315

- Molecule 53: 37S ribosomal protein S10, mitochondrial



| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | ILE | ILE | ARG | PRO | VAL | ARG | SER | GLN | GLY | ARG | ALA | PRO | LEU | ALA | THR | LEU | ARG | SER | GLN | SER | VAL | PHE | GLN | PRO | PRO | PRO | GLN | LEU | ARG | ASN | ALA | SER | VAL | THR | THR | GLY | PRO | ASP | ALA | ALA | SER | LYS | ALA | SER | THR | THR | THR | THR | THR | THR |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|
| GLU | ALA | PRO | LYS | ASP | GLN | LYS | LYS | ALA | LYS | ALA | ALA | ALA | ALA | ALA | ALA | GLU | PRO | GLU | E81 | I121 | R122 | R268 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|

- Molecule 54: Mitochondrial ribosomal protein subunit S18



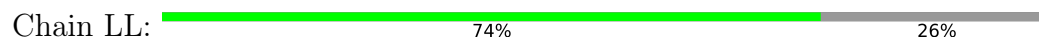
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | ALA | GLY | GLN | ILE | ASP | PRO | ILE | ARG | ALA | GLU | LEU | VAL | GLY | THR | PRO | ARG | VAL | PRO | ARG | ASN | LEU | LEU | ALA | ALA | SER | LEU | PRO | PRO | PRO | GLY | LYS | ARG | GLN | ASN | THR | PRO | ALA | PRO | LYS | LEU | PRO | PRO | PRO | GLN | ILE | SER | SER | PHE | SER | SER | PRO | PRO | PRO | PRO | CYS | TYR | GLN | GLN | GLU | LYS | CYS |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

LEU PRO PRO HIS ARG ARG VAL SER TRP SER PRO LEU LEU ILE LEU GLN ARG CYS CYS PRO PRO GLY HIS PRO LEU LYS ILE SER ARG ARG ASP GLY SER PHE THR PHU LEU THR ALA PHE ALA ARG PRO ARG THR THR GLU PRO PRO

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| SER | LEU | HIS | TYR | LEU | ASP | SER | PRO | THR | PRO | ALA | CYS | GLN | LEU | LEU | PHE | HIS | GLN | ILE | GLN | GLY | HIS | PHE | SER | PHE | VAL | VAL | HIS | THR | THR | VAL | ARG | SER | ILE | TRP | PRO | ALA | LYS | NET | SER | ARG | PHE | THR | GLY | LEU | LEU | ALA | ASN |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|
| LYS | LEU | ALA | THR | ASN | ILE | GLY | LEU | ARG | ASP | THR | GLU | D253 | G376 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|

- Molecule 55: Mitochondrial 30S ribosomal protein S12



| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|
| MET | ALA | THR | THR | PHE | LEU | ARG | ASN | LEU | PHE | SER | GLN | ALA | GLN | PRO | SER | LEU | ARG | PRO | LEU | MET | PRO | SER | SER | SER | SER | ILE | LEU | PRO | ALA | ALA | ALA | ARG | LEU | PHE | SER | SER | THR | PRO | ALA | GLN | ASN | A45 | S172 | VAL | GLY |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|

- Molecule 56: 40S ribosomal protein S13



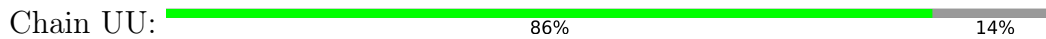
MET
V2
G119

- Molecule 57: Mitochondrial 40S ribosomal protein MRP2

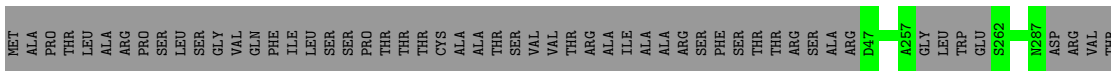
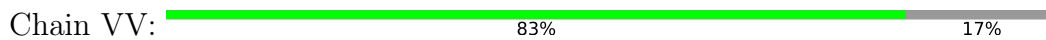




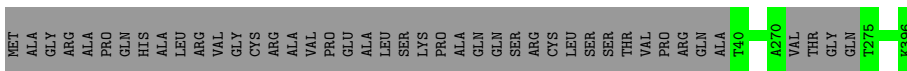
- Molecule 64: 37S ribosomal protein S25, mitochondrial



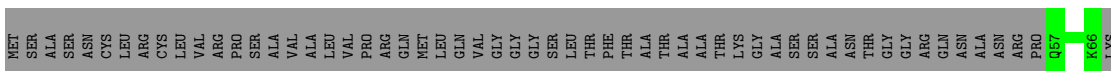
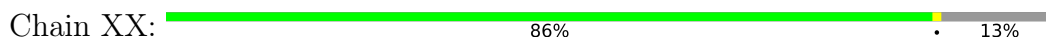
- Molecule 65: mS26



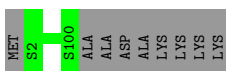
- Molecule 66: mS27



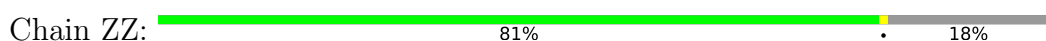
- Molecule 67: Mitochondrial ribosomal protein DAP3



- Molecule 68: mS33



- Molecule 69: 37S ribosomal protein S24, mitochondrial



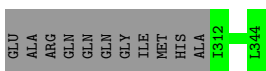
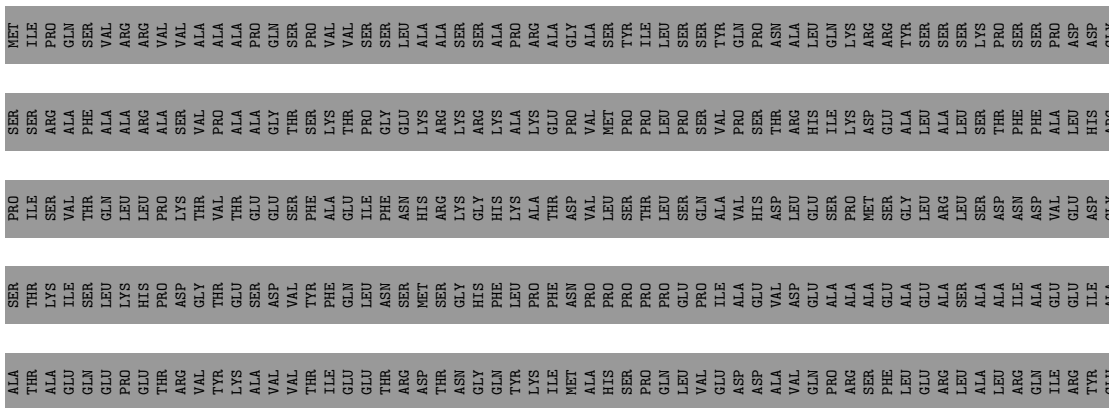
- Molecule 70: 37S ribosomal protein mrp10, mitochondrial

Chain 11:  98%



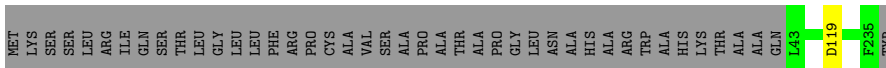
- Molecule 71: DUF1713 domain-containing protein

Chain 22: 10% 90%



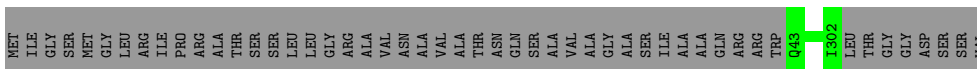
- Molecule 72: IGR domain-containing protein

Chain 33: 81% 18%




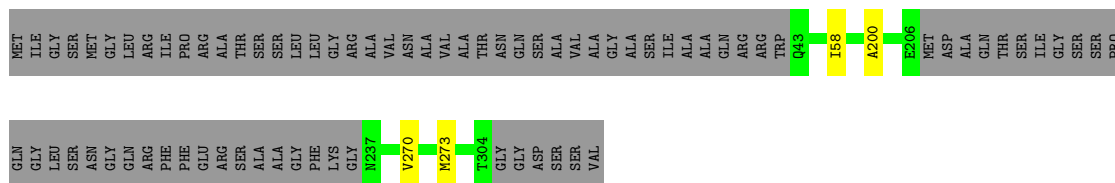
- Molecule 73: Fe superoxide dismutase

Chain 44: 84% 16%

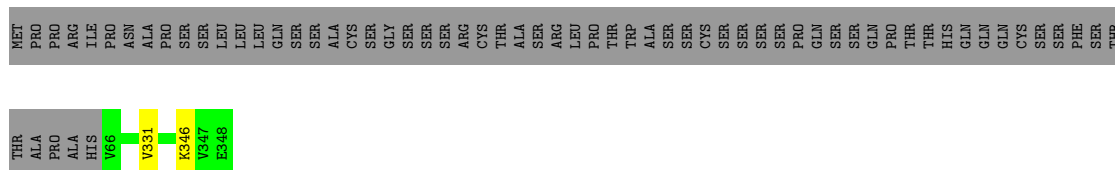
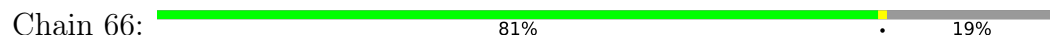


- Molecule 73: Fe superoxide dismutase

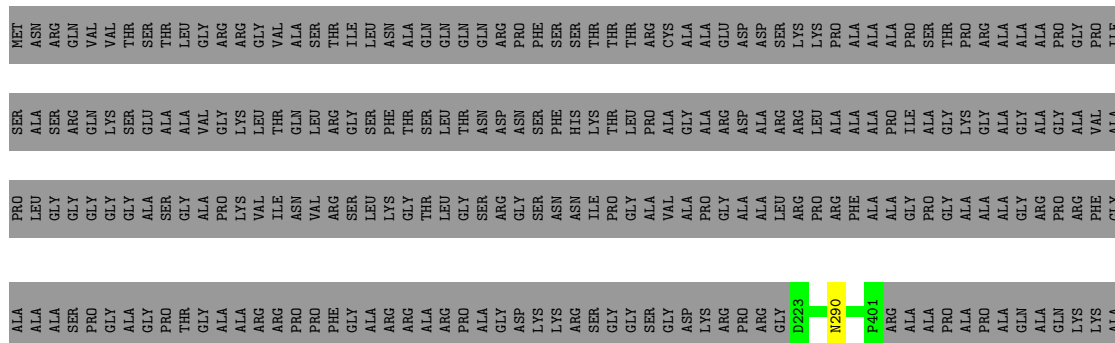
Chain 55:  74% . 25%



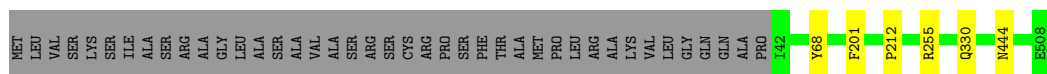
- Molecule 74: mS45



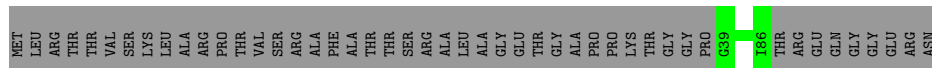
- Molecule 75: mS46



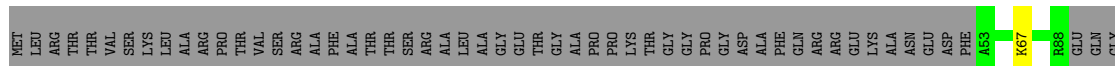
- Molecule 76: 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial



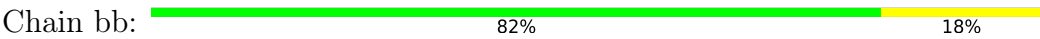
- Molecule 77: IF1



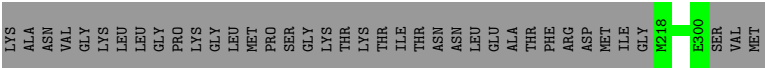
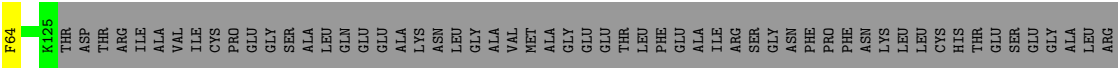
- Molecule 77: IF1



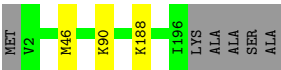
- Molecule 79: tRNA E-site



• Molecule 80: 60S ribosomal protein L1



• Molecule 81: L51_S25_CI-B8 domain-containing protein



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 23802 | 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 ($e^-/\text{\AA}^2$) | 35 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | 130000 | Depositor |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |
| Maximum map value | 37.985 | Depositor |
| Minimum map value | -23.213 | Depositor |
| Average map value | 0.006 | Depositor |
| Map value standard deviation | 1.342 | Depositor |
| Recommended contour level | 0.0295 | Depositor |
| Map size (Å) | 423.99997, 423.99997, 423.99997 | wwPDB |
| Map dimensions | 400, 400, 400 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.06, 1.06, 1.06 | Depositor |

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ATP, NAD, K, SPM, ZN

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

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-------------|-------------|-------------|
| | | RMSZ | $\# Z > 5$ | RMSZ | $\# Z > 5$ |
| 1 | A | 0.24 | 0/67790 | 0.68 | 0/105564 |
| 2 | B | 0.26 | 0/2531 | 0.45 | 0/3410 |
| 3 | C | 0.27 | 0/2380 | 0.46 | 0/3209 |
| 4 | D | 0.25 | 0/2072 | 0.40 | 0/2794 |
| 5 | E | 0.28 | 0/2518 | 0.41 | 0/3427 |
| 6 | F | 0.25 | 0/1644 | 0.41 | 0/2218 |
| 7 | G | 0.25 | 0/630 | 0.46 | 0/842 |
| 8 | f | 0.24 | 0/1923 | 0.40 | 0/2631 |
| 9 | g | 0.25 | 0/1126 | 0.42 | 0/1525 |
| 10 | H | 0.27 | 0/1460 | 0.43 | 0/1975 |
| 11 | I | 0.26 | 0/918 | 0.46 | 0/1225 |
| 12 | J | 0.26 | 0/1931 | 0.43 | 0/2597 |
| 13 | K | 0.25 | 0/1376 | 0.42 | 0/1842 |
| 14 | L | 0.25 | 0/1569 | 0.41 | 0/2106 |
| 15 | M | 0.25 | 0/1572 | 0.42 | 0/2117 |
| 16 | N | 0.26 | 0/1077 | 0.44 | 0/1452 |
| 17 | O | 0.25 | 0/2248 | 0.40 | 0/3015 |
| 18 | P | 0.26 | 0/1523 | 0.40 | 0/2058 |
| 19 | Q | 0.25 | 0/2916 | 0.40 | 0/3927 |
| 20 | R | 0.25 | 0/2083 | 0.42 | 0/2789 |
| 21 | S | 0.25 | 0/1510 | 0.40 | 0/2042 |
| 22 | T | 0.24 | 0/1538 | 0.39 | 0/2086 |
| 23 | U | 0.25 | 0/1117 | 0.43 | 0/1496 |
| 24 | V | 0.29 | 0/471 | 0.43 | 0/638 |
| 25 | W | 0.25 | 0/467 | 0.43 | 0/616 |
| 26 | X | 0.27 | 0/411 | 0.42 | 0/551 |
| 27 | Y | 0.26 | 0/368 | 0.44 | 0/485 |
| 28 | 0 | 0.27 | 0/395 | 0.46 | 0/523 |
| 29 | 1 | 0.27 | 0/3053 | 0.42 | 0/4108 |
| 30 | 2 | 0.28 | 0/1074 | 0.39 | 0/1449 |
| 31 | 3 | 0.27 | 0/783 | 0.43 | 0/1056 |
| 32 | 4 | 0.27 | 0/1077 | 0.42 | 0/1453 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|---------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 33 | 5 | 0.26 | 0/2790 | 0.40 | 0/3794 |
| 34 | 6 | 0.29 | 0/2274 | 0.43 | 0/3062 |
| 35 | 7 | 0.25 | 0/686 | 0.42 | 0/919 |
| 36 | 8 | 0.24 | 0/2714 | 0.39 | 0/3657 |
| 37 | h | 0.25 | 0/791 | 0.38 | 0/1065 |
| 38 | i | 0.24 | 0/990 | 0.40 | 0/1324 |
| 39 | 9 | 0.24 | 0/1678 | 0.39 | 0/2267 |
| 40 | a | 0.25 | 0/1364 | 0.41 | 0/1842 |
| 41 | b | 0.24 | 0/1348 | 0.37 | 0/1816 |
| 42 | c | 0.26 | 0/846 | 0.41 | 0/1134 |
| 43 | d | 0.24 | 0/1930 | 0.41 | 0/2597 |
| 44 | AA | 0.26 | 0/2948 | 0.40 | 0/3995 |
| 45 | BB | 0.26 | 0/2314 | 0.41 | 0/3142 |
| 46 | CC | 0.28 | 0/3712 | 0.41 | 0/4978 |
| 47 | DD | 0.27 | 0/2409 | 0.39 | 0/3255 |
| 48 | EE | 0.26 | 0/2928 | 0.41 | 0/3947 |
| 49 | FF | 0.26 | 0/952 | 0.42 | 0/1285 |
| 50 | GG | 0.26 | 0/1712 | 0.40 | 0/2324 |
| 51 | HH | 0.27 | 0/1259 | 0.43 | 0/1707 |
| 52 | II | 0.26 | 0/2013 | 0.40 | 0/2720 |
| 53 | JJ | 0.28 | 0/1590 | 0.41 | 0/2140 |
| 54 | KK | 0.25 | 0/1015 | 0.43 | 0/1357 |
| 55 | LL | 0.27 | 0/973 | 0.44 | 0/1305 |
| 56 | MM | 0.25 | 0/950 | 0.40 | 0/1274 |
| 57 | NN | 0.27 | 0/929 | 0.40 | 0/1243 |
| 58 | OO | 0.24 | 0/2242 | 0.39 | 0/3016 |
| 59 | PP | 0.29 | 0/806 | 0.42 | 0/1096 |
| 60 | QQ | 0.25 | 0/1268 | 0.39 | 0/1701 |
| 61 | RR | 0.25 | 0/1105 | 0.38 | 0/1491 |
| 62 | SS | 0.27 | 0/667 | 0.42 | 0/902 |
| 63 | TT | 0.25 | 0/761 | 0.37 | 0/1015 |
| 64 | UU | 0.26 | 0/1845 | 0.37 | 0/2491 |
| 65 | VV | 0.25 | 0/2120 | 0.38 | 0/2851 |
| 66 | WW | 0.24 | 0/2897 | 0.37 | 0/3911 |
| 67 | XX | 0.26 | 0/3234 | 0.41 | 0/4374 |
| 68 | YY | 0.26 | 0/797 | 0.40 | 0/1070 |
| 69 | ZZ | 0.26 | 0/2645 | 0.39 | 0/3566 |
| 70 | 11 | 0.24 | 0/686 | 0.38 | 0/929 |
| 71 | 22 | 0.24 | 0/301 | 0.39 | 0/388 |
| 72 | 33 | 0.26 | 0/1589 | 0.43 | 0/2140 |
| 73 | 44 | 0.24 | 0/2121 | 0.38 | 0/2879 |
| 73 | 55 | 0.25 | 0/1912 | 0.40 | 0/2600 |
| 74 | 66 | 0.26 | 0/2348 | 0.39 | 0/3163 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|----------|-------------|----------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 75 | 77 | 0.28 | 0/1431 | 0.39 | 0/1934 |
| 76 | 88 | 0.26 | 0/3760 | 0.40 | 0/5085 |
| 77 | 00 | 0.23 | 0/409 | 0.36 | 0/540 |
| 77 | 99 | 0.22 | 0/307 | 0.32 | 0/405 |
| 78 | aa | 0.24 | 0/34270 | 0.68 | 0/53383 |
| 79 | bb | 0.12 | 0/1449 | 0.65 | 0/2248 |
| 80 | e | 0.24 | 0/1223 | 0.40 | 0/1645 |
| 81 | j | 0.24 | 0/1583 | 0.42 | 0/2130 |
| All | All | 0.25 | 0/230442 | 0.56 | 0/332328 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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 | |
|-----|-------|---------------|------------|---------|----------|-------------|-----|
| 2 | B | 313/383 (82%) | 307 (98%) | 6 (2%) | 0 | 100 | 100 |
| 3 | C | 305/384 (79%) | 301 (99%) | 4 (1%) | 0 | 100 | 100 |
| 4 | D | 250/325 (77%) | 247 (99%) | 3 (1%) | 0 | 100 | 100 |
| 5 | E | 307/352 (87%) | 304 (99%) | 3 (1%) | 0 | 100 | 100 |
| 6 | F | 199/255 (78%) | 198 (100%) | 1 (0%) | 0 | 100 | 100 |
| 7 | G | 72/300 (24%) | 68 (94%) | 4 (6%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|------------|---------|----------|-------------|-----|
| 8 | f | 243/347 (70%) | 240 (99%) | 3 (1%) | 0 | 100 | 100 |
| 9 | g | 145/158 (92%) | 142 (98%) | 3 (2%) | 0 | 100 | 100 |
| 10 | H | 181/183 (99%) | 176 (97%) | 5 (3%) | 0 | 100 | 100 |
| 11 | I | 115/131 (88%) | 114 (99%) | 1 (1%) | 0 | 100 | 100 |
| 12 | J | 241/312 (77%) | 236 (98%) | 4 (2%) | 1 (0%) | 30 | 63 |
| 13 | K | 166/249 (67%) | 166 (100%) | 0 | 0 | 100 | 100 |
| 14 | L | 190/193 (98%) | 186 (98%) | 4 (2%) | 0 | 100 | 100 |
| 15 | M | 192/258 (74%) | 187 (97%) | 5 (3%) | 0 | 100 | 100 |
| 16 | N | 131/217 (60%) | 124 (95%) | 7 (5%) | 0 | 100 | 100 |
| 17 | O | 268/364 (74%) | 266 (99%) | 2 (1%) | 0 | 100 | 100 |
| 18 | P | 178/228 (78%) | 178 (100%) | 0 | 0 | 100 | 100 |
| 19 | Q | 351/396 (89%) | 350 (100%) | 1 (0%) | 0 | 100 | 100 |
| 20 | R | 245/447 (55%) | 241 (98%) | 4 (2%) | 0 | 100 | 100 |
| 21 | S | 175/274 (64%) | 173 (99%) | 2 (1%) | 0 | 100 | 100 |
| 22 | T | 178/263 (68%) | 177 (99%) | 1 (1%) | 0 | 100 | 100 |
| 23 | U | 134/161 (83%) | 133 (99%) | 1 (1%) | 0 | 100 | 100 |
| 24 | V | 54/219 (25%) | 54 (100%) | 0 | 0 | 100 | 100 |
| 25 | W | 57/129 (44%) | 54 (95%) | 3 (5%) | 0 | 100 | 100 |
| 26 | X | 46/59 (78%) | 44 (96%) | 2 (4%) | 0 | 100 | 100 |
| 27 | Y | 44/140 (31%) | 44 (100%) | 0 | 0 | 100 | 100 |
| 28 | 0 | 44/124 (36%) | 44 (100%) | 0 | 0 | 100 | 100 |
| 29 | 1 | 365/449 (81%) | 358 (98%) | 6 (2%) | 1 (0%) | 37 | 68 |
| 30 | 2 | 121/370 (33%) | 120 (99%) | 1 (1%) | 0 | 100 | 100 |
| 31 | 3 | 93/103 (90%) | 90 (97%) | 3 (3%) | 0 | 100 | 100 |
| 32 | 4 | 135/138 (98%) | 132 (98%) | 3 (2%) | 0 | 100 | 100 |
| 33 | 5 | 346/439 (79%) | 344 (99%) | 2 (1%) | 0 | 100 | 100 |
| 34 | 6 | 267/368 (73%) | 267 (100%) | 0 | 0 | 100 | 100 |
| 35 | 7 | 82/165 (50%) | 81 (99%) | 1 (1%) | 0 | 100 | 100 |
| 36 | 8 | 329/443 (74%) | 328 (100%) | 1 (0%) | 0 | 100 | 100 |
| 37 | h | 96/98 (98%) | 95 (99%) | 1 (1%) | 0 | 100 | 100 |
| 38 | i | 120/218 (55%) | 114 (95%) | 6 (5%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 39 | 9 | 204/267 (76%) | 199 (98%) | 5 (2%) | 0 | 100 | 100 |
| 40 | a | 157/225 (70%) | 156 (99%) | 1 (1%) | 0 | 100 | 100 |
| 41 | b | 159/162 (98%) | 158 (99%) | 1 (1%) | 0 | 100 | 100 |
| 42 | c | 96/110 (87%) | 95 (99%) | 1 (1%) | 0 | 100 | 100 |
| 43 | d | 231/292 (79%) | 229 (99%) | 2 (1%) | 0 | 100 | 100 |
| 44 | AA | 360/470 (77%) | 351 (98%) | 9 (2%) | 0 | 100 | 100 |
| 45 | BB | 288/428 (67%) | 279 (97%) | 9 (3%) | 0 | 100 | 100 |
| 46 | CC | 432/508 (85%) | 426 (99%) | 6 (1%) | 0 | 100 | 100 |
| 47 | DD | 286/453 (63%) | 280 (98%) | 6 (2%) | 0 | 100 | 100 |
| 48 | EE | 363/477 (76%) | 352 (97%) | 11 (3%) | 0 | 100 | 100 |
| 49 | FF | 115/117 (98%) | 113 (98%) | 2 (2%) | 0 | 100 | 100 |
| 50 | GG | 215/309 (70%) | 213 (99%) | 2 (1%) | 0 | 100 | 100 |
| 51 | HH | 158/161 (98%) | 155 (98%) | 3 (2%) | 0 | 100 | 100 |
| 52 | II | 245/315 (78%) | 239 (98%) | 6 (2%) | 0 | 100 | 100 |
| 53 | JJ | 186/268 (69%) | 180 (97%) | 6 (3%) | 0 | 100 | 100 |
| 54 | KK | 122/376 (32%) | 118 (97%) | 4 (3%) | 0 | 100 | 100 |
| 55 | LL | 126/174 (72%) | 118 (94%) | 8 (6%) | 0 | 100 | 100 |
| 56 | MM | 116/119 (98%) | 111 (96%) | 5 (4%) | 0 | 100 | 100 |
| 57 | NN | 110/113 (97%) | 109 (99%) | 1 (1%) | 0 | 100 | 100 |
| 58 | OO | 272/320 (85%) | 268 (98%) | 4 (2%) | 0 | 100 | 100 |
| 59 | PP | 96/107 (90%) | 94 (98%) | 2 (2%) | 0 | 100 | 100 |
| 60 | QQ | 156/165 (94%) | 154 (99%) | 2 (1%) | 0 | 100 | 100 |
| 61 | RR | 132/256 (52%) | 128 (97%) | 4 (3%) | 0 | 100 | 100 |
| 62 | SS | 79/91 (87%) | 77 (98%) | 2 (2%) | 0 | 100 | 100 |
| 63 | TT | 86/236 (36%) | 86 (100%) | 0 | 0 | 100 | 100 |
| 64 | UU | 216/253 (85%) | 212 (98%) | 4 (2%) | 0 | 100 | 100 |
| 65 | VV | 255/316 (81%) | 249 (98%) | 6 (2%) | 0 | 100 | 100 |
| 66 | WW | 349/396 (88%) | 346 (99%) | 3 (1%) | 0 | 100 | 100 |
| 67 | XX | 404/469 (86%) | 396 (98%) | 8 (2%) | 0 | 100 | 100 |
| 68 | YY | 97/108 (90%) | 97 (100%) | 0 | 0 | 100 | 100 |
| 69 | ZZ | 310/382 (81%) | 303 (98%) | 7 (2%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 70 | 11 | 86/90 (96%) | 84 (98%) | 2 (2%) | 0 | 100 | 100 |
| 71 | 22 | 31/344 (9%) | 31 (100%) | 0 | 0 | 100 | 100 |
| 72 | 33 | 191/236 (81%) | 182 (95%) | 9 (5%) | 0 | 100 | 100 |
| 73 | 44 | 258/310 (83%) | 254 (98%) | 4 (2%) | 0 | 100 | 100 |
| 73 | 55 | 228/310 (74%) | 223 (98%) | 4 (2%) | 1 (0%) | 30 | 63 |
| 74 | 66 | 281/348 (81%) | 279 (99%) | 2 (1%) | 0 | 100 | 100 |
| 75 | 77 | 177/414 (43%) | 176 (99%) | 1 (1%) | 0 | 100 | 100 |
| 76 | 88 | 465/508 (92%) | 447 (96%) | 18 (4%) | 0 | 100 | 100 |
| 77 | 00 | 46/95 (48%) | 45 (98%) | 1 (2%) | 0 | 100 | 100 |
| 77 | 99 | 34/95 (36%) | 34 (100%) | 0 | 0 | 100 | 100 |
| 80 | e | 146/303 (48%) | 141 (97%) | 5 (3%) | 0 | 100 | 100 |
| 81 | j | 193/201 (96%) | 188 (97%) | 5 (3%) | 0 | 100 | 100 |
| All | All | 15335/21339 (72%) | 15058 (98%) | 274 (2%) | 3 (0%) | 100 | 100 |

All (3) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 73 | 55 | 200 | ALA |
| 12 | J | 83 | LYS |
| 29 | 1 | 410 | VAL |

5.3.2 Protein sidechains ⓘ

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|---------------|------------|----------|-------------|-----|
| 2 | B | 259/312 (83%) | 257 (99%) | 2 (1%) | 79 | 89 |
| 3 | C | 242/303 (80%) | 241 (100%) | 1 (0%) | 89 | 94 |
| 4 | D | 216/274 (79%) | 216 (100%) | 0 | 100 | 100 |
| 5 | E | 267/296 (90%) | 263 (98%) | 4 (2%) | 60 | 80 |
| 6 | F | 173/216 (80%) | 172 (99%) | 1 (1%) | 84 | 91 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 7 | G | 64/254 (25%) | 64 (100%) | 0 | 100 | 100 |
| 8 | f | 206/287 (72%) | 206 (100%) | 0 | 100 | 100 |
| 9 | g | 120/124 (97%) | 120 (100%) | 0 | 100 | 100 |
| 10 | H | 149/149 (100%) | 148 (99%) | 1 (1%) | 81 | 90 |
| 11 | I | 100/105 (95%) | 100 (100%) | 0 | 100 | 100 |
| 12 | J | 198/255 (78%) | 194 (98%) | 4 (2%) | 50 | 74 |
| 13 | K | 142/205 (69%) | 141 (99%) | 1 (1%) | 81 | 90 |
| 14 | L | 164/165 (99%) | 163 (99%) | 1 (1%) | 84 | 91 |
| 15 | M | 164/209 (78%) | 162 (99%) | 2 (1%) | 67 | 83 |
| 16 | N | 119/188 (63%) | 119 (100%) | 0 | 100 | 100 |
| 17 | O | 235/315 (75%) | 233 (99%) | 2 (1%) | 75 | 88 |
| 18 | P | 158/196 (81%) | 156 (99%) | 2 (1%) | 65 | 82 |
| 19 | Q | 312/347 (90%) | 311 (100%) | 1 (0%) | 91 | 95 |
| 20 | R | 212/359 (59%) | 210 (99%) | 2 (1%) | 75 | 88 |
| 21 | S | 159/242 (66%) | 159 (100%) | 0 | 100 | 100 |
| 22 | T | 161/224 (72%) | 161 (100%) | 0 | 100 | 100 |
| 23 | U | 118/138 (86%) | 117 (99%) | 1 (1%) | 79 | 89 |
| 24 | V | 52/170 (31%) | 52 (100%) | 0 | 100 | 100 |
| 25 | W | 50/102 (49%) | 50 (100%) | 0 | 100 | 100 |
| 26 | X | 46/54 (85%) | 46 (100%) | 0 | 100 | 100 |
| 27 | Y | 38/116 (33%) | 38 (100%) | 0 | 100 | 100 |
| 28 | 0 | 41/108 (38%) | 40 (98%) | 1 (2%) | 44 | 70 |
| 29 | 1 | 316/384 (82%) | 310 (98%) | 6 (2%) | 52 | 75 |
| 30 | 2 | 109/317 (34%) | 107 (98%) | 2 (2%) | 54 | 76 |
| 31 | 3 | 83/91 (91%) | 81 (98%) | 2 (2%) | 44 | 70 |
| 32 | 4 | 113/114 (99%) | 111 (98%) | 2 (2%) | 54 | 76 |
| 33 | 5 | 279/351 (80%) | 277 (99%) | 2 (1%) | 81 | 90 |
| 34 | 6 | 238/310 (77%) | 234 (98%) | 4 (2%) | 56 | 78 |
| 35 | 7 | 69/136 (51%) | 69 (100%) | 0 | 100 | 100 |
| 36 | 8 | 285/378 (75%) | 283 (99%) | 2 (1%) | 81 | 90 |
| 37 | h | 88/88 (100%) | 88 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 38 | i | 101/162 (62%) | 101 (100%) | 0 | 100 | 100 |
| 39 | 9 | 176/225 (78%) | 173 (98%) | 3 (2%) | 56 | 78 |
| 40 | a | 146/196 (74%) | 146 (100%) | 0 | 100 | 100 |
| 41 | b | 141/141 (100%) | 141 (100%) | 0 | 100 | 100 |
| 42 | c | 86/96 (90%) | 84 (98%) | 2 (2%) | 45 | 70 |
| 43 | d | 201/243 (83%) | 198 (98%) | 3 (2%) | 60 | 80 |
| 44 | AA | 314/393 (80%) | 305 (97%) | 9 (3%) | 37 | 65 |
| 45 | BB | 237/347 (68%) | 235 (99%) | 2 (1%) | 79 | 89 |
| 46 | CC | 405/461 (88%) | 401 (99%) | 4 (1%) | 73 | 86 |
| 47 | DD | 242/377 (64%) | 239 (99%) | 3 (1%) | 67 | 83 |
| 48 | EE | 308/392 (79%) | 307 (100%) | 1 (0%) | 91 | 95 |
| 49 | FF | 99/99 (100%) | 97 (98%) | 2 (2%) | 50 | 74 |
| 50 | GG | 181/260 (70%) | 179 (99%) | 2 (1%) | 70 | 84 |
| 51 | HH | 134/135 (99%) | 132 (98%) | 2 (2%) | 60 | 80 |
| 52 | II | 206/263 (78%) | 205 (100%) | 1 (0%) | 86 | 92 |
| 53 | JJ | 166/227 (73%) | 164 (99%) | 2 (1%) | 67 | 83 |
| 54 | KK | 108/324 (33%) | 108 (100%) | 0 | 100 | 100 |
| 55 | LL | 103/142 (72%) | 103 (100%) | 0 | 100 | 100 |
| 56 | MM | 98/99 (99%) | 98 (100%) | 0 | 100 | 100 |
| 57 | NN | 96/97 (99%) | 96 (100%) | 0 | 100 | 100 |
| 58 | OO | 230/265 (87%) | 229 (100%) | 1 (0%) | 89 | 94 |
| 59 | PP | 85/92 (92%) | 85 (100%) | 0 | 100 | 100 |
| 60 | QQ | 132/138 (96%) | 132 (100%) | 0 | 100 | 100 |
| 61 | RR | 118/218 (54%) | 118 (100%) | 0 | 100 | 100 |
| 62 | SS | 70/80 (88%) | 70 (100%) | 0 | 100 | 100 |
| 63 | TT | 75/191 (39%) | 75 (100%) | 0 | 100 | 100 |
| 64 | UU | 187/218 (86%) | 187 (100%) | 0 | 100 | 100 |
| 65 | VV | 224/268 (84%) | 224 (100%) | 0 | 100 | 100 |
| 66 | WW | 300/333 (90%) | 300 (100%) | 0 | 100 | 100 |
| 67 | XX | 345/391 (88%) | 340 (99%) | 5 (1%) | 62 | 81 |
| 68 | YY | 83/89 (93%) | 83 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|-------------|-----|
| 69 | ZZ | 278/328 (85%) | 275 (99%) | 3 (1%) | 70 | 84 |
| 70 | 11 | 73/75 (97%) | 73 (100%) | 0 | 100 | 100 |
| 71 | 22 | 33/293 (11%) | 33 (100%) | 0 | 100 | 100 |
| 72 | 33 | 163/195 (84%) | 162 (99%) | 1 (1%) | 84 | 91 |
| 73 | 44 | 215/250 (86%) | 215 (100%) | 0 | 100 | 100 |
| 73 | 55 | 195/250 (78%) | 192 (98%) | 3 (2%) | 60 | 80 |
| 74 | 66 | 245/303 (81%) | 243 (99%) | 2 (1%) | 79 | 89 |
| 75 | 77 | 153/304 (50%) | 152 (99%) | 1 (1%) | 81 | 90 |
| 76 | 88 | 388/419 (93%) | 382 (98%) | 6 (2%) | 60 | 80 |
| 77 | 00 | 43/78 (55%) | 43 (100%) | 0 | 100 | 100 |
| 77 | 99 | 34/78 (44%) | 33 (97%) | 1 (3%) | 37 | 65 |
| 80 | e | 134/256 (52%) | 133 (99%) | 1 (1%) | 81 | 90 |
| 81 | j | 168/171 (98%) | 165 (98%) | 3 (2%) | 54 | 76 |
| All | All | 13264/17844 (74%) | 13155 (99%) | 109 (1%) | 77 | 89 |

All (109) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | B | 109 | HIS |
| 2 | B | 298 | HIS |
| 3 | C | 160 | GLU |
| 5 | E | 194 | ILE |
| 5 | E | 239 | ASN |
| 5 | E | 246 | GLN |
| 5 | E | 268 | ARG |
| 6 | F | 100 | MET |
| 10 | H | 2 | SER |
| 12 | J | 57 | ARG |
| 12 | J | 77 | THR |
| 12 | J | 130 | TRP |
| 12 | J | 159 | ASP |
| 13 | K | 76 | LYS |
| 14 | L | 8 | TYR |
| 15 | M | 84 | LYS |
| 15 | M | 203 | ARG |
| 17 | O | 43 | TRP |
| 17 | O | 352 | ASP |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 18 | P | 53 | PHE |
| 18 | P | 88 | ASP |
| 19 | Q | 198 | ARG |
| 20 | R | 75 | ARG |
| 20 | R | 190 | VAL |
| 23 | U | 68 | LEU |
| 28 | 0 | 106 | TYR |
| 29 | 1 | 211 | ILE |
| 29 | 1 | 271 | ARG |
| 29 | 1 | 402 | ARG |
| 29 | 1 | 405 | ILE |
| 29 | 1 | 409 | GLU |
| 29 | 1 | 430 | GLU |
| 30 | 2 | 265 | ARG |
| 30 | 2 | 325 | ARG |
| 31 | 3 | 31 | ARG |
| 31 | 3 | 41 | TYR |
| 32 | 4 | 91 | GLU |
| 32 | 4 | 123 | SER |
| 33 | 5 | 289 | GLU |
| 33 | 5 | 419 | LEU |
| 34 | 6 | 181 | ARG |
| 34 | 6 | 311 | LEU |
| 34 | 6 | 334 | ASN |
| 34 | 6 | 349 | LEU |
| 36 | 8 | 218 | ASN |
| 36 | 8 | 322 | TRP |
| 39 | 9 | 72 | ARG |
| 39 | 9 | 123 | LEU |
| 39 | 9 | 220 | MET |
| 42 | c | 57 | LYS |
| 42 | c | 102 | SER |
| 43 | d | 69 | LEU |
| 43 | d | 192 | LYS |
| 43 | d | 212 | MET |
| 44 | AA | 55 | THR |
| 44 | AA | 151 | ASP |
| 44 | AA | 153 | GLN |
| 44 | AA | 372 | LYS |
| 44 | AA | 385 | VAL |
| 44 | AA | 414 | LYS |
| 44 | AA | 415 | GLU |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 44 | AA | 419 | ASP |
| 44 | AA | 421 | ARG |
| 45 | BB | 133 | GLN |
| 45 | BB | 177 | TRP |
| 46 | CC | 66 | ASN |
| 46 | CC | 360 | GLN |
| 46 | CC | 361 | LYS |
| 46 | CC | 363 | VAL |
| 47 | DD | 123 | ASN |
| 47 | DD | 143 | ARG |
| 47 | DD | 170 | THR |
| 48 | EE | 338 | MET |
| 49 | FF | 84 | ASP |
| 49 | FF | 92 | ASN |
| 50 | GG | 190 | HIS |
| 50 | GG | 198 | TYR |
| 51 | HH | 31 | TYR |
| 51 | HH | 78 | ARG |
| 52 | II | 216 | ASN |
| 53 | JJ | 121 | ILE |
| 53 | JJ | 122 | ARG |
| 58 | OO | 271 | ASN |
| 67 | XX | 181 | VAL |
| 67 | XX | 182 | THR |
| 67 | XX | 186 | LEU |
| 67 | XX | 218 | TYR |
| 67 | XX | 307 | PHE |
| 69 | ZZ | 93 | GLN |
| 69 | ZZ | 200 | TYR |
| 69 | ZZ | 338 | ASP |
| 72 | 33 | 119 | ASP |
| 73 | 55 | 58 | ILE |
| 73 | 55 | 270 | VAL |
| 73 | 55 | 273 | MET |
| 74 | 66 | 331 | VAL |
| 74 | 66 | 346 | LYS |
| 75 | 77 | 290 | ASN |
| 76 | 88 | 68 | TYR |
| 76 | 88 | 201 | PHE |
| 76 | 88 | 212 | PRO |
| 76 | 88 | 255 | ARG |
| 76 | 88 | 330 | GLN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 76 | 88 | 444 | ASN |
| 77 | 99 | 67 | LYS |
| 80 | e | 64 | PHE |
| 81 | j | 46 | MET |
| 81 | j | 90 | LYS |
| 81 | j | 188 | LYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 6 | F | 205 | GLN |
| 18 | P | 142 | GLN |
| 29 | 1 | 342 | ASN |
| 46 | CC | 58 | ASN |
| 46 | CC | 121 | HIS |
| 49 | FF | 74 | HIS |
| 57 | NN | 23 | HIS |
| 74 | 66 | 195 | GLN |

5.3.3 RNA [i](#)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 1 | A | 2820/3464 (81%) | 370 (13%) | 11 (0%) |
| 78 | aa | 1430/1864 (76%) | 201 (14%) | 0 |
| 79 | bb | 57/61 (93%) | 11 (19%) | 0 |
| All | All | 4307/5389 (79%) | 582 (13%) | 11 (0%) |

All (582) RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 18 | A |
| 1 | A | 19 | G |
| 1 | A | 29 | A |
| 1 | A | 46 | U |
| 1 | A | 47 | A |
| 1 | A | 78 | C |
| 1 | A | 79 | A |
| 1 | A | 90 | A |
| 1 | A | 98 | A |
| 1 | A | 99 | U |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 104 | U |
| 1 | A | 106 | A |
| 1 | A | 107 | U |
| 1 | A | 118 | G |
| 1 | A | 311 | G |
| 1 | A | 317 | A |
| 1 | A | 319 | C |
| 1 | A | 334 | U |
| 1 | A | 347 | U |
| 1 | A | 348 | A |
| 1 | A | 350 | U |
| 1 | A | 351 | A |
| 1 | A | 353 | A |
| 1 | A | 367 | A |
| 1 | A | 370 | A |
| 1 | A | 376 | U |
| 1 | A | 387 | A |
| 1 | A | 392 | A |
| 1 | A | 393 | A |
| 1 | A | 395 | U |
| 1 | A | 414 | U |
| 1 | A | 419 | U |
| 1 | A | 435 | A |
| 1 | A | 440 | A |
| 1 | A | 441 | U |
| 1 | A | 442 | U |
| 1 | A | 443 | A |
| 1 | A | 462 | U |
| 1 | A | 477 | A |
| 1 | A | 478 | U |
| 1 | A | 486 | A |
| 1 | A | 522 | C |
| 1 | A | 526 | G |
| 1 | A | 527 | A |
| 1 | A | 552 | A |
| 1 | A | 569 | G |
| 1 | A | 583 | A |
| 1 | A | 584 | A |
| 1 | A | 587 | A |
| 1 | A | 599 | A |
| 1 | A | 609 | U |
| 1 | A | 611 | A |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | A | 639 | A |
| 1 | A | 829 | A |
| 1 | A | 839 | A |
| 1 | A | 840 | U |
| 1 | A | 845 | A |
| 1 | A | 846 | A |
| 1 | A | 849 | U |
| 1 | A | 855 | A |
| 1 | A | 888 | U |
| 1 | A | 910 | A |
| 1 | A | 914 | U |
| 1 | A | 931 | U |
| 1 | A | 948 | A |
| 1 | A | 958 | A |
| 1 | A | 960 | C |
| 1 | A | 967 | A |
| 1 | A | 969 | G |
| 1 | A | 976 | C |
| 1 | A | 977 | U |
| 1 | A | 988 | G |
| 1 | A | 995 | U |
| 1 | A | 1011 | A |
| 1 | A | 1012 | U |
| 1 | A | 1028 | U |
| 1 | A | 1042 | G |
| 1 | A | 1060 | G |
| 1 | A | 1070 | A |
| 1 | A | 1071 | G |
| 1 | A | 1094 | A |
| 1 | A | 1107 | U |
| 1 | A | 1108 | U |
| 1 | A | 1109 | U |
| 1 | A | 1118 | C |
| 1 | A | 1119 | A |
| 1 | A | 1134 | A |
| 1 | A | 1136 | A |
| 1 | A | 1137 | U |
| 1 | A | 1140 | U |
| 1 | A | 1141 | A |
| 1 | A | 1190 | A |
| 1 | A | 1206 | G |
| 1 | A | 1219 | A |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | A | 1235 | A |
| 1 | A | 1242 | G |
| 1 | A | 1248 | G |
| 1 | A | 1257 | U |
| 1 | A | 1258 | U |
| 1 | A | 1268 | U |
| 1 | A | 1271 | A |
| 1 | A | 1280 | A |
| 1 | A | 1287 | A |
| 1 | A | 1307 | G |
| 1 | A | 1316 | A |
| 1 | A | 1326 | A |
| 1 | A | 1331 | A |
| 1 | A | 1333 | G |
| 1 | A | 1334 | A |
| 1 | A | 1376 | A |
| 1 | A | 1377 | U |
| 1 | A | 1379 | U |
| 1 | A | 1380 | A |
| 1 | A | 1381 | A |
| 1 | A | 1382 | C |
| 1 | A | 1389 | A |
| 1 | A | 1415 | A |
| 1 | A | 1431 | A |
| 1 | A | 1452 | G |
| 1 | A | 1453 | A |
| 1 | A | 1457 | G |
| 1 | A | 1484 | A |
| 1 | A | 1487 | U |
| 1 | A | 1494 | U |
| 1 | A | 1495 | A |
| 1 | A | 1496 | U |
| 1 | A | 1509 | A |
| 1 | A | 1522 | U |
| 1 | A | 1526 | A |
| 1 | A | 1528 | U |
| 1 | A | 1529 | G |
| 1 | A | 1565 | A |
| 1 | A | 1566 | A |
| 1 | A | 1567 | A |
| 1 | A | 1568 | A |
| 1 | A | 1578 | G |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | A | 1589 | A |
| 1 | A | 1590 | A |
| 1 | A | 1591 | A |
| 1 | A | 1595 | U |
| 1 | A | 1604 | G |
| 1 | A | 1605 | U |
| 1 | A | 1613 | C |
| 1 | A | 1620 | U |
| 1 | A | 1626 | U |
| 1 | A | 1627 | A |
| 1 | A | 1634 | G |
| 1 | A | 1648 | U |
| 1 | A | 1655 | A |
| 1 | A | 1695 | A |
| 1 | A | 1703 | A |
| 1 | A | 1719 | A |
| 1 | A | 1722 | A |
| 1 | A | 1726 | A |
| 1 | A | 1835 | U |
| 1 | A | 1836 | A |
| 1 | A | 1842 | A |
| 1 | A | 1843 | A |
| 1 | A | 1844 | U |
| 1 | A | 1850 | A |
| 1 | A | 1866 | A |
| 1 | A | 1880 | U |
| 1 | A | 1881 | G |
| 1 | A | 1882 | A |
| 1 | A | 1884 | U |
| 1 | A | 1896 | C |
| 1 | A | 1910 | G |
| 1 | A | 1921 | A |
| 1 | A | 1922 | C |
| 1 | A | 1951 | A |
| 1 | A | 1970 | A |
| 1 | A | 1971 | A |
| 1 | A | 1973 | A |
| 1 | A | 1985 | U |
| 1 | A | 1988 | A |
| 1 | A | 1991 | A |
| 1 | A | 1993 | U |
| 1 | A | 2002 | A |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | A | 2029 | C |
| 1 | A | 2030 | A |
| 1 | A | 2039 | A |
| 1 | A | 2041 | A |
| 1 | A | 2048 | A |
| 1 | A | 2051 | A |
| 1 | A | 2052 | U |
| 1 | A | 2105 | A |
| 1 | A | 2136 | A |
| 1 | A | 2142 | G |
| 1 | A | 2145 | C |
| 1 | A | 2147 | U |
| 1 | A | 2148 | A |
| 1 | A | 2149 | G |
| 1 | A | 2150 | C |
| 1 | A | 2153 | G |
| 1 | A | 2154 | A |
| 1 | A | 2163 | A |
| 1 | A | 2164 | G |
| 1 | A | 2165 | G |
| 1 | A | 2172 | A |
| 1 | A | 2173 | A |
| 1 | A | 2190 | U |
| 1 | A | 2198 | U |
| 1 | A | 2199 | G |
| 1 | A | 2202 | U |
| 1 | A | 2205 | A |
| 1 | A | 2206 | U |
| 1 | A | 2207 | G |
| 1 | A | 2226 | U |
| 1 | A | 2228 | U |
| 1 | A | 2256 | A |
| 1 | A | 2258 | A |
| 1 | A | 2265 | C |
| 1 | A | 2266 | A |
| 1 | A | 2268 | A |
| 1 | A | 2278 | C |
| 1 | A | 2287 | A |
| 1 | A | 2290 | C |
| 1 | A | 2291 | G |
| 1 | A | 2295 | A |
| 1 | A | 2304 | G |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | A | 2328 | G |
| 1 | A | 2329 | A |
| 1 | A | 2331 | U |
| 1 | A | 2332 | A |
| 1 | A | 2333 | C |
| 1 | A | 2334 | G |
| 1 | A | 2337 | U |
| 1 | A | 2347 | U |
| 1 | A | 2367 | A |
| 1 | A | 2370 | A |
| 1 | A | 2371 | G |
| 1 | A | 2384 | C |
| 1 | A | 2406 | U |
| 1 | A | 2409 | U |
| 1 | A | 2411 | A |
| 1 | A | 2418 | A |
| 1 | A | 2419 | A |
| 1 | A | 2420 | U |
| 1 | A | 2421 | U |
| 1 | A | 2427 | A |
| 1 | A | 2439 | A |
| 1 | A | 2440 | G |
| 1 | A | 2441 | A |
| 1 | A | 2477 | A |
| 1 | A | 2481 | G |
| 1 | A | 2482 | U |
| 1 | A | 2483 | G |
| 1 | A | 2486 | U |
| 1 | A | 2506 | G |
| 1 | A | 2509 | U |
| 1 | A | 2511 | C |
| 1 | A | 2512 | A |
| 1 | A | 2541 | A |
| 1 | A | 2543 | C |
| 1 | A | 2547 | A |
| 1 | A | 2548 | U |
| 1 | A | 2558 | A |
| 1 | A | 2559 | G |
| 1 | A | 2578 | C |
| 1 | A | 2581 | G |
| 1 | A | 2582 | G |
| 1 | A | 2583 | G |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | A | 2592 | A |
| 1 | A | 2595 | A |
| 1 | A | 2596 | A |
| 1 | A | 2611 | A |
| 1 | A | 2612 | U |
| 1 | A | 2613 | U |
| 1 | A | 2621 | A |
| 1 | A | 2623 | U |
| 1 | A | 2626 | U |
| 1 | A | 2628 | C |
| 1 | A | 2638 | A |
| 1 | A | 2658 | A |
| 1 | A | 2659 | G |
| 1 | A | 2663 | U |
| 1 | A | 2666 | G |
| 1 | A | 2675 | A |
| 1 | A | 2685 | A |
| 1 | A | 2686 | U |
| 1 | A | 2689 | G |
| 1 | A | 2690 | G |
| 1 | A | 2694 | G |
| 1 | A | 2705 | U |
| 1 | A | 2706 | C |
| 1 | A | 2710 | U |
| 1 | A | 2711 | U |
| 1 | A | 2719 | U |
| 1 | A | 2720 | U |
| 1 | A | 2721 | U |
| 1 | A | 2722 | U |
| 1 | A | 2758 | U |
| 1 | A | 2759 | U |
| 1 | A | 2775 | U |
| 1 | A | 2784 | U |
| 1 | A | 2786 | A |
| 1 | A | 2795 | U |
| 1 | A | 2797 | C |
| 1 | A | 2806 | U |
| 1 | A | 2808 | A |
| 1 | A | 2810 | A |
| 1 | A | 2811 | A |
| 1 | A | 2836 | G |
| 1 | A | 2838 | C |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | A | 2842 | G |
| 1 | A | 2843 | G |
| 1 | A | 2852 | A |
| 1 | A | 2875 | U |
| 1 | A | 2878 | U |
| 1 | A | 2881 | G |
| 1 | A | 2882 | A |
| 1 | A | 2883 | A |
| 1 | A | 2884 | A |
| 1 | A | 2891 | G |
| 1 | A | 2897 | G |
| 1 | A | 2898 | A |
| 1 | A | 2899 | U |
| 1 | A | 2900 | A |
| 1 | A | 2909 | A |
| 1 | A | 2912 | U |
| 1 | A | 2927 | A |
| 1 | A | 2942 | U |
| 1 | A | 2945 | G |
| 1 | A | 2949 | C |
| 1 | A | 2964 | G |
| 1 | A | 2969 | A |
| 1 | A | 2971 | C |
| 1 | A | 2980 | U |
| 1 | A | 2981 | G |
| 1 | A | 3018 | A |
| 1 | A | 3019 | A |
| 1 | A | 3025 | C |
| 1 | A | 3030 | G |
| 1 | A | 3034 | G |
| 1 | A | 3053 | C |
| 1 | A | 3054 | A |
| 1 | A | 3055 | G |
| 1 | A | 3061 | U |
| 1 | A | 3062 | U |
| 1 | A | 3065 | U |
| 1 | A | 3081 | U |
| 1 | A | 3082 | U |
| 1 | A | 3124 | G |
| 1 | A | 3125 | G |
| 1 | A | 3156 | U |
| 1 | A | 3166 | U |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | A | 3259 | A |
| 1 | A | 3260 | C |
| 1 | A | 3262 | A |
| 1 | A | 3263 | U |
| 1 | A | 3276 | G |
| 1 | A | 3288 | A |
| 1 | A | 3296 | A |
| 1 | A | 3310 | A |
| 1 | A | 3349 | A |
| 1 | A | 3359 | A |
| 1 | A | 3391 | A |
| 1 | A | 3399 | A |
| 1 | A | 3407 | U |
| 1 | A | 3408 | A |
| 1 | A | 3413 | A |
| 1 | A | 3420 | A |
| 1 | A | 3424 | A |
| 1 | A | 3425 | U |
| 1 | A | 3428 | U |
| 1 | A | 3429 | A |
| 1 | A | 3447 | A |
| 1 | A | 3448 | A |
| 1 | A | 3449 | U |
| 1 | A | 3455 | U |
| 78 | aa | 49 | U |
| 78 | aa | 51 | G |
| 78 | aa | 52 | A |
| 78 | aa | 54 | G |
| 78 | aa | 67 | G |
| 78 | aa | 77 | A |
| 78 | aa | 84 | U |
| 78 | aa | 90 | U |
| 78 | aa | 92 | C |
| 78 | aa | 93 | U |
| 78 | aa | 96 | A |
| 78 | aa | 106 | A |
| 78 | aa | 113 | G |
| 78 | aa | 115 | U |
| 78 | aa | 117 | A |
| 78 | aa | 118 | A |
| 78 | aa | 121 | U |
| 78 | aa | 125 | C |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 78 | aa | 238 | C |
| 78 | aa | 242 | A |
| 78 | aa | 249 | G |
| 78 | aa | 256 | A |
| 78 | aa | 266 | A |
| 78 | aa | 268 | A |
| 78 | aa | 269 | A |
| 78 | aa | 270 | U |
| 78 | aa | 271 | A |
| 78 | aa | 273 | U |
| 78 | aa | 278 | C |
| 78 | aa | 282 | U |
| 78 | aa | 302 | U |
| 78 | aa | 311 | U |
| 78 | aa | 314 | C |
| 78 | aa | 318 | A |
| 78 | aa | 376 | A |
| 78 | aa | 380 | G |
| 78 | aa | 388 | U |
| 78 | aa | 389 | C |
| 78 | aa | 390 | A |
| 78 | aa | 401 | G |
| 78 | aa | 416 | G |
| 78 | aa | 417 | C |
| 78 | aa | 430 | U |
| 78 | aa | 431 | A |
| 78 | aa | 441 | G |
| 78 | aa | 445 | A |
| 78 | aa | 446 | A |
| 78 | aa | 454 | A |
| 78 | aa | 455 | G |
| 78 | aa | 482 | A |
| 78 | aa | 483 | A |
| 78 | aa | 496 | A |
| 78 | aa | 497 | U |
| 78 | aa | 499 | G |
| 78 | aa | 518 | U |
| 78 | aa | 523 | C |
| 78 | aa | 540 | A |
| 78 | aa | 556 | G |
| 78 | aa | 561 | A |
| 78 | aa | 669 | C |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 78 | aa | 670 | G |
| 78 | aa | 674 | A |
| 78 | aa | 676 | U |
| 78 | aa | 677 | U |
| 78 | aa | 679 | U |
| 78 | aa | 684 | U |
| 78 | aa | 722 | A |
| 78 | aa | 725 | U |
| 78 | aa | 737 | U |
| 78 | aa | 744 | C |
| 78 | aa | 756 | G |
| 78 | aa | 759 | A |
| 78 | aa | 773 | A |
| 78 | aa | 786 | A |
| 78 | aa | 790 | A |
| 78 | aa | 799 | A |
| 78 | aa | 802 | G |
| 78 | aa | 803 | G |
| 78 | aa | 828 | A |
| 78 | aa | 830 | U |
| 78 | aa | 838 | A |
| 78 | aa | 849 | A |
| 78 | aa | 856 | U |
| 78 | aa | 861 | A |
| 78 | aa | 862 | A |
| 78 | aa | 867 | G |
| 78 | aa | 871 | U |
| 78 | aa | 879 | A |
| 78 | aa | 880 | G |
| 78 | aa | 911 | G |
| 78 | aa | 913 | C |
| 78 | aa | 921 | G |
| 78 | aa | 945 | A |
| 78 | aa | 952 | G |
| 78 | aa | 974 | A |
| 78 | aa | 978 | A |
| 78 | aa | 990 | U |
| 78 | aa | 991 | A |
| 78 | aa | 1012 | A |
| 78 | aa | 1014 | U |
| 78 | aa | 1024 | C |
| 78 | aa | 1038 | U |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 78 | aa | 1039 | U |
| 78 | aa | 1040 | A |
| 78 | aa | 1063 | U |
| 78 | aa | 1064 | A |
| 78 | aa | 1106 | A |
| 78 | aa | 1118 | G |
| 78 | aa | 1119 | U |
| 78 | aa | 1122 | C |
| 78 | aa | 1126 | C |
| 78 | aa | 1127 | A |
| 78 | aa | 1138 | A |
| 78 | aa | 1152 | U |
| 78 | aa | 1158 | G |
| 78 | aa | 1161 | C |
| 78 | aa | 1164 | C |
| 78 | aa | 1167 | A |
| 78 | aa | 1168 | A |
| 78 | aa | 1169 | A |
| 78 | aa | 1184 | U |
| 78 | aa | 1185 | G |
| 78 | aa | 1192 | A |
| 78 | aa | 1345 | G |
| 78 | aa | 1357 | U |
| 78 | aa | 1358 | C |
| 78 | aa | 1385 | U |
| 78 | aa | 1386 | U |
| 78 | aa | 1392 | G |
| 78 | aa | 1417 | U |
| 78 | aa | 1425 | A |
| 78 | aa | 1426 | U |
| 78 | aa | 1437 | U |
| 78 | aa | 1438 | U |
| 78 | aa | 1445 | U |
| 78 | aa | 1446 | A |
| 78 | aa | 1450 | A |
| 78 | aa | 1457 | G |
| 78 | aa | 1475 | A |
| 78 | aa | 1476 | A |
| 78 | aa | 1480 | A |
| 78 | aa | 1481 | U |
| 78 | aa | 1492 | A |
| 78 | aa | 1493 | U |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 78 | aa | 1504 | A |
| 78 | aa | 1505 | U |
| 78 | aa | 1511 | U |
| 78 | aa | 1518 | U |
| 78 | aa | 1526 | A |
| 78 | aa | 1527 | A |
| 78 | aa | 1529 | A |
| 78 | aa | 1537 | G |
| 78 | aa | 1539 | A |
| 78 | aa | 1553 | U |
| 78 | aa | 1559 | A |
| 78 | aa | 1566 | A |
| 78 | aa | 1579 | A |
| 78 | aa | 1580 | A |
| 78 | aa | 1581 | U |
| 78 | aa | 1582 | A |
| 78 | aa | 1583 | U |
| 78 | aa | 1584 | A |
| 78 | aa | 1585 | C |
| 78 | aa | 1601 | A |
| 78 | aa | 1619 | A |
| 78 | aa | 1620 | A |
| 78 | aa | 1630 | A |
| 78 | aa | 1643 | C |
| 78 | aa | 1647 | A |
| 78 | aa | 1654 | G |
| 78 | aa | 1655 | G |
| 78 | aa | 1658 | A |
| 78 | aa | 1664 | C |
| 78 | aa | 1677 | A |
| 78 | aa | 1680 | A |
| 78 | aa | 1707 | G |
| 78 | aa | 1723 | C |
| 78 | aa | 1724 | U |
| 78 | aa | 1725 | U |
| 78 | aa | 1731 | U |
| 78 | aa | 1735 | A |
| 78 | aa | 1738 | U |
| 78 | aa | 1751 | A |
| 78 | aa | 1753 | G |
| 78 | aa | 1758 | G |
| 78 | aa | 1803 | A |

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| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 78 | aa | 1805 | G |
| 78 | aa | 1814 | C |
| 78 | aa | 1817 | U |
| 78 | aa | 1818 | U |
| 78 | aa | 1828 | G |
| 78 | aa | 1840 | G |
| 78 | aa | 1841 | A |
| 78 | aa | 1843 | U |
| 78 | aa | 1844 | U |
| 78 | aa | 1847 | C |
| 78 | aa | 1848 | A |
| 78 | aa | 1849 | A |
| 78 | aa | 1853 | U |
| 78 | aa | 1854 | G |
| 78 | aa | 1864 | A |
| 79 | bb | 9 | A |
| 79 | bb | 13 | C |
| 79 | bb | 19 | G |
| 79 | bb | 20 | U |
| 79 | bb | 21 | A |
| 79 | bb | 44 | A |
| 79 | bb | 49 | C |
| 79 | bb | 66 | C |
| 79 | bb | 69 | A |
| 79 | bb | 75 | C |
| 79 | bb | 76 | A |

All (11) RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | A | 442 | U |
| 1 | A | 526 | G |
| 1 | A | 909 | A |
| 1 | A | 1107 | U |
| 1 | A | 1205 | A |
| 1 | A | 2051 | A |
| 1 | A | 2481 | G |
| 1 | A | 2720 | U |
| 1 | A | 2758 | U |
| 1 | A | 2883 | A |
| 1 | A | 3054 | A |

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

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 304 ligands modelled in this entry, 301 are monoatomic - leaving 3 for Mogul analysis.

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

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|------|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 87 | ATP | XX | 501 | 82 | 26,33,33 | 3.49 | 1 (3%) | 31,52,52 | 0.94 | 1 (3%) |
| 83 | SPM | A | 3651 | - | 13,13,13 | 0.32 | 0 | 12,12,12 | 0.76 | 0 |
| 85 | NAD | E | 4301 | 84 | 42,48,48 | 0.75 | 1 (2%) | 50,73,73 | 1.10 | 3 (6%) |

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 |
|-----|------|-------|------|------|---------|------------|---------|
| 87 | ATP | XX | 501 | 82 | - | 3/18/38/38 | 0/3/3/3 |
| 83 | SPM | A | 3651 | - | - | 2/11/11/11 | - |
| 85 | NAD | E | 4301 | 84 | - | 7/26/62/62 | 0/5/5/5 |

All (2) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|---------|--------|-------------|----------|
| 87 | XX | 501 | ATP | C2'-C1' | -17.14 | 1.27 | 1.53 |
| 85 | E | 4301 | NAD | C2N-N1N | -2.39 | 1.32 | 1.35 |

All (4) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-------------|-------|-------------|----------|
| 85 | E | 4301 | NAD | O4D-C1D-C2D | -4.42 | 100.47 | 106.93 |
| 87 | XX | 501 | ATP | C3'-C2'-C1' | 3.57 | 106.35 | 100.98 |
| 85 | E | 4301 | NAD | N3A-C2A-N1A | -2.63 | 124.56 | 128.68 |
| 85 | E | 4301 | NAD | O4B-C1B-C2B | -2.62 | 103.09 | 106.93 |

There are no chirality outliers.

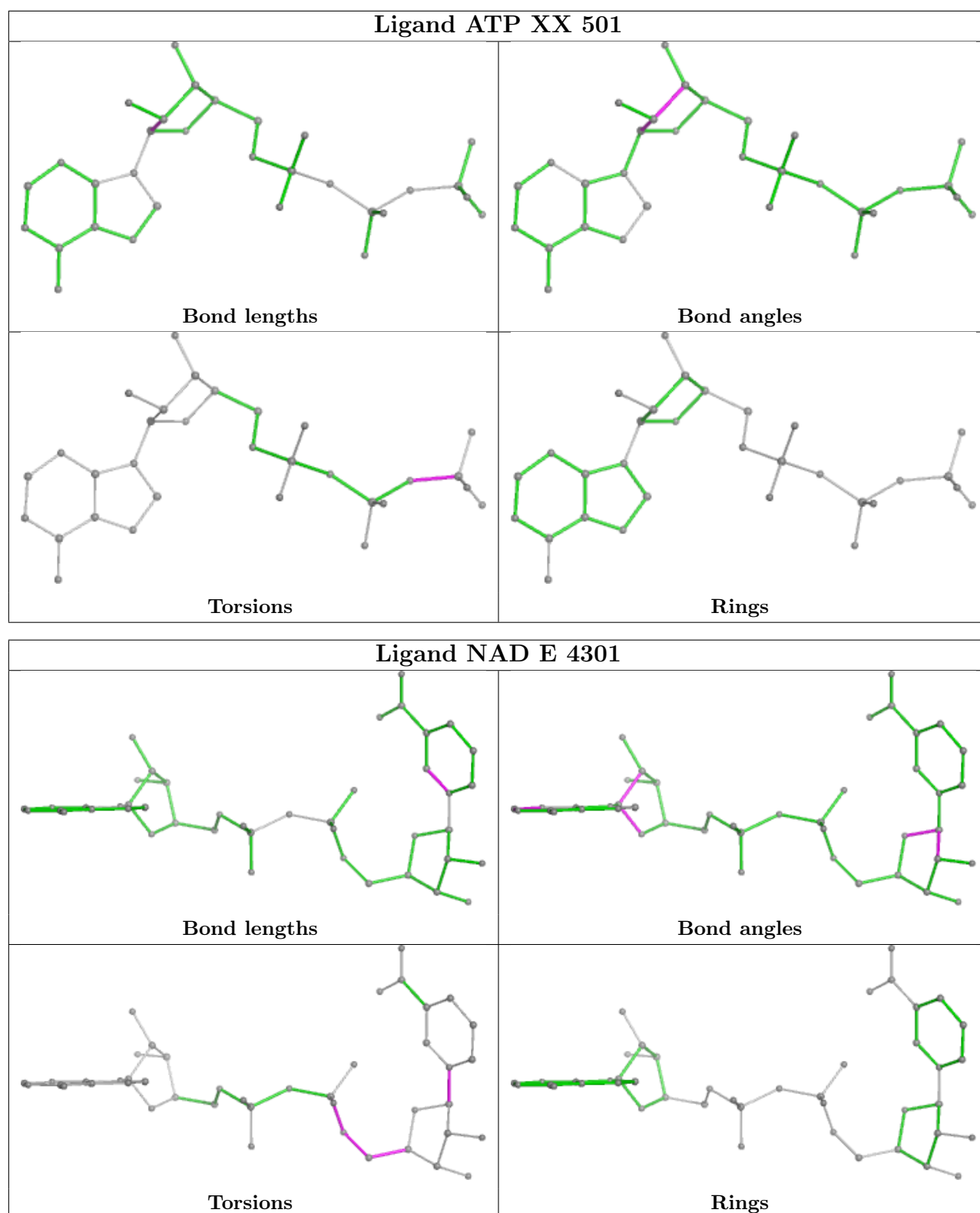
All (12) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|------|------|-----------------|
| 85 | E | 4301 | NAD | C5D-O5D-PN-O3 |
| 87 | XX | 501 | ATP | PB-O3B-PG-O2G |
| 87 | XX | 501 | ATP | PB-O3B-PG-O3G |
| 83 | A | 3651 | SPM | C12-C11-N10-C9 |
| 83 | A | 3651 | SPM | N5-C6-C7-C8 |
| 85 | E | 4301 | NAD | C4D-C5D-O5D-PN |
| 85 | E | 4301 | NAD | C5D-O5D-PN-O1N |
| 85 | E | 4301 | NAD | C3D-C4D-C5D-O5D |
| 85 | E | 4301 | NAD | C2D-C1D-N1N-C2N |
| 85 | E | 4301 | NAD | C2D-C1D-N1N-C6N |
| 85 | E | 4301 | NAD | O4D-C4D-C5D-O5D |
| 87 | XX | 501 | ATP | PB-O3B-PG-O1G |

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 79 | bb | 3 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | bb | 28:A | O3' | 41:G | P | 18.21 |
| 1 | bb | 15:A | O3' | 18:A | P | 8.73 |
| 1 | bb | 46:G | O3' | 48:U | P | 3.74 |

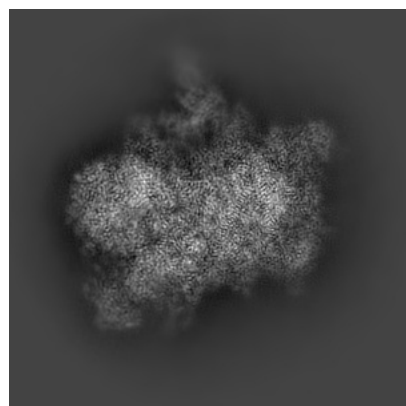
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10978. These allow visual inspection of the internal detail of the map and identification of artifacts.

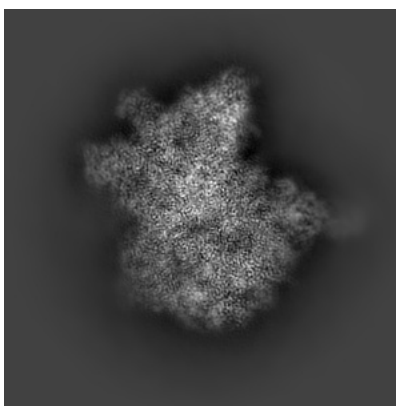
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

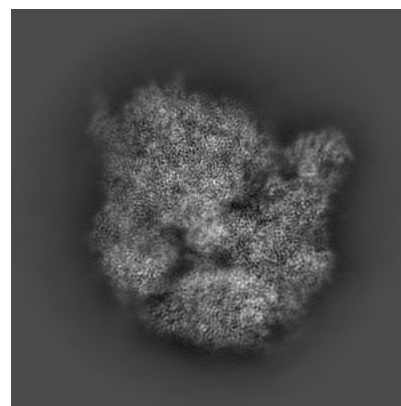
6.1.1 Primary map



X

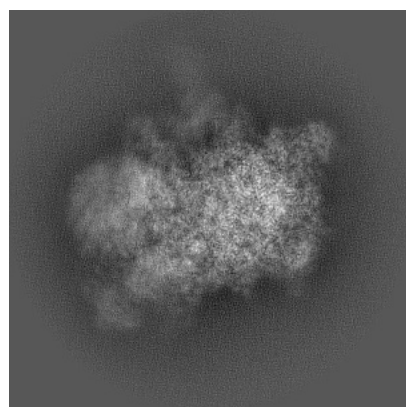


Y

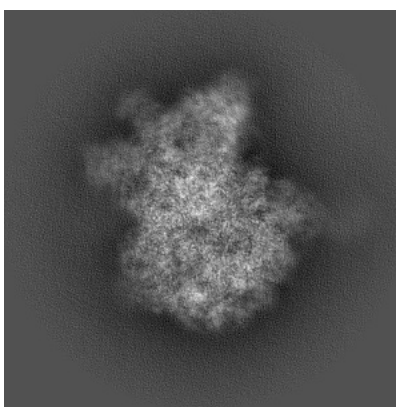


Z

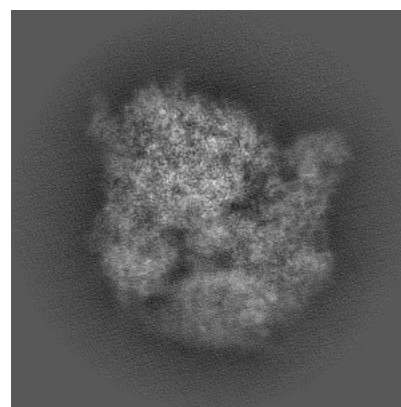
6.1.2 Raw map



X



Y

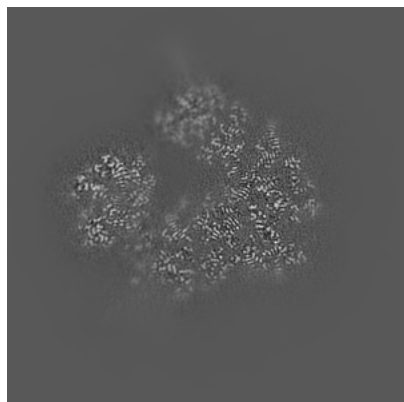


Z

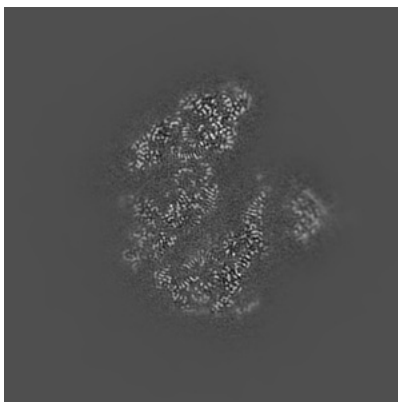
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

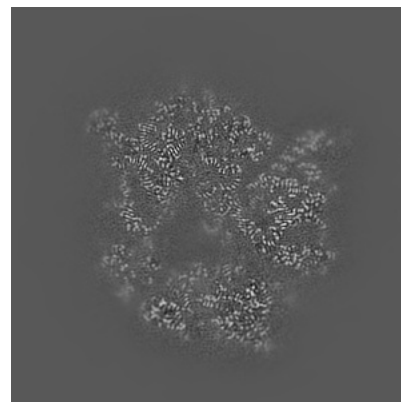
6.2.1 Primary map



X Index: 200

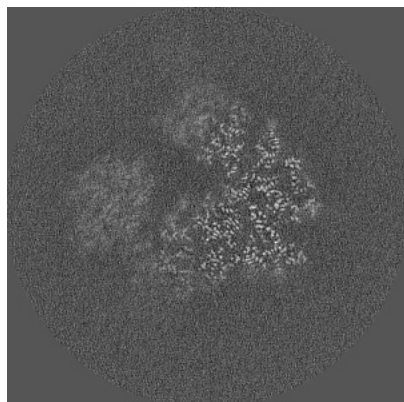


Y Index: 200

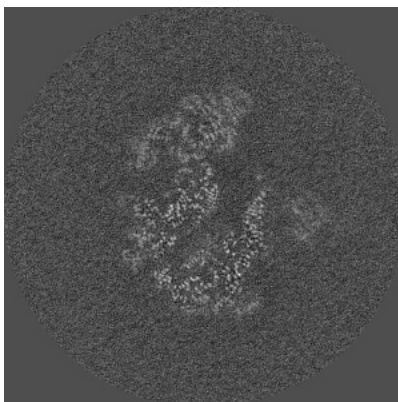


Z Index: 200

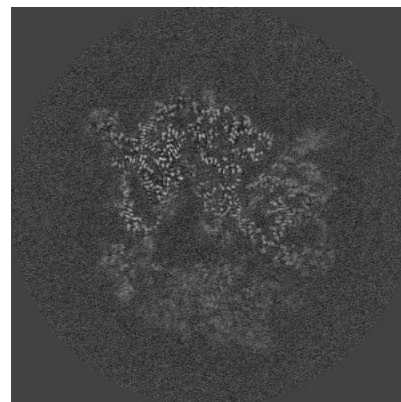
6.2.2 Raw map



X Index: 200



Y Index: 200

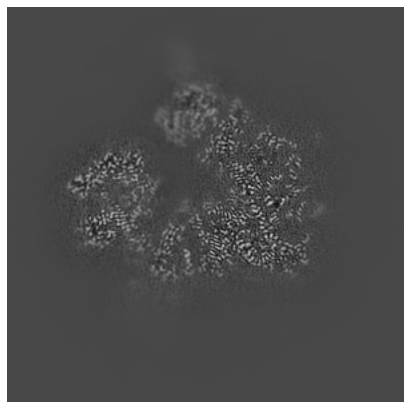


Z Index: 200

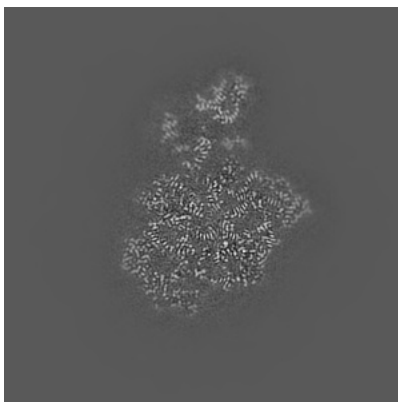
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

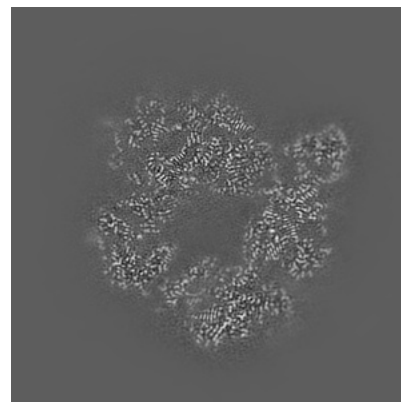
6.3.1 Primary map



X Index: 195

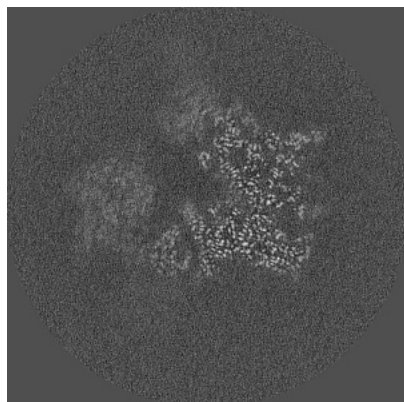


Y Index: 228

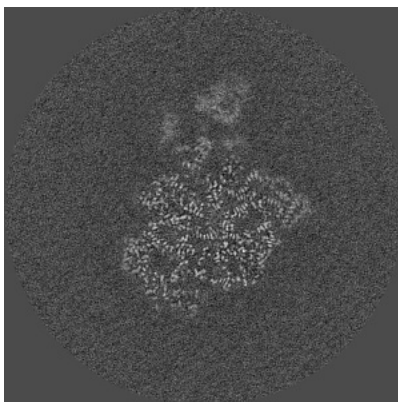


Z Index: 219

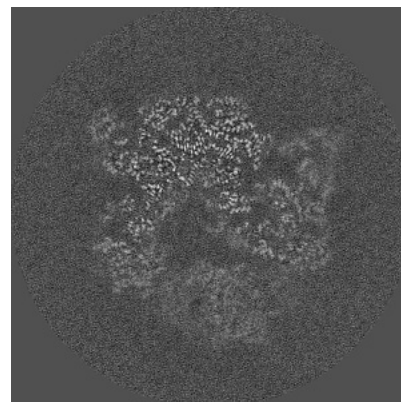
6.3.2 Raw map



X Index: 192



Y Index: 228

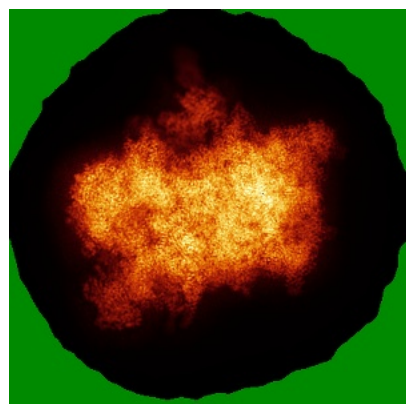


Z Index: 207

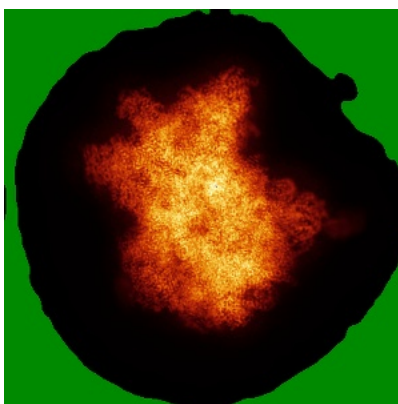
The images above show the largest variance slices of the map in three orthogonal directions.

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

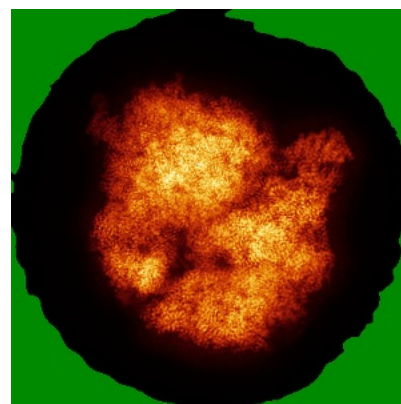
6.4.1 Primary map



X

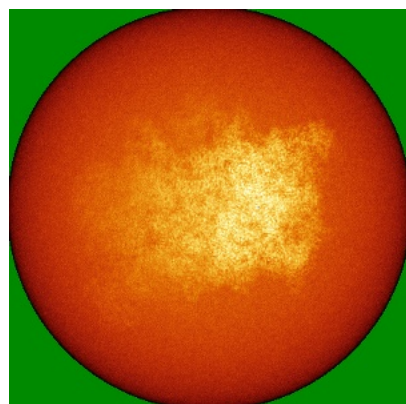


Y

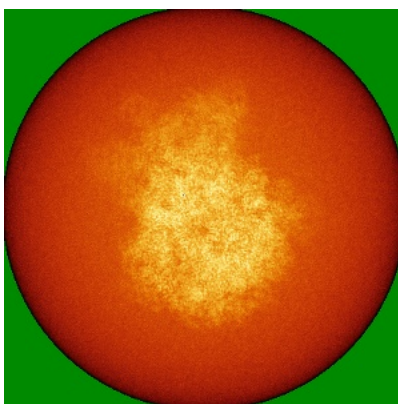


Z

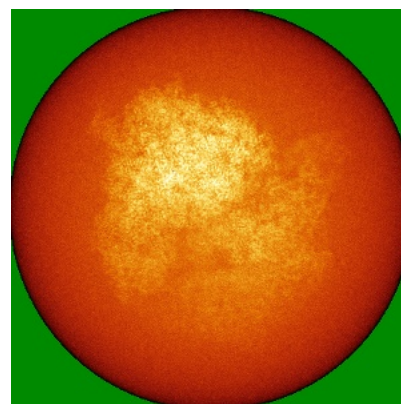
6.4.2 Raw map



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.

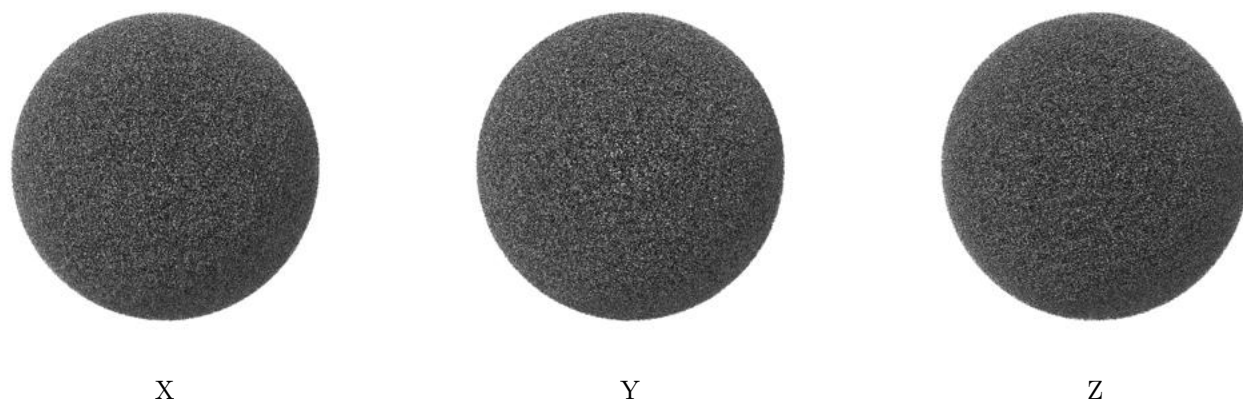
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0295. 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.

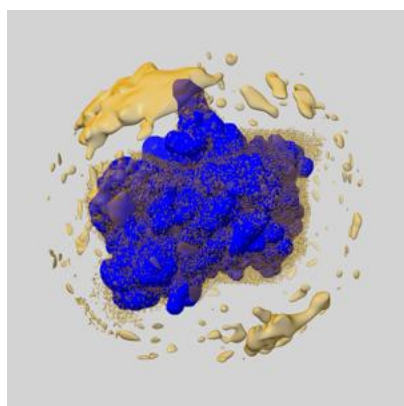
6.6 Mask visualisation [i](#)

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

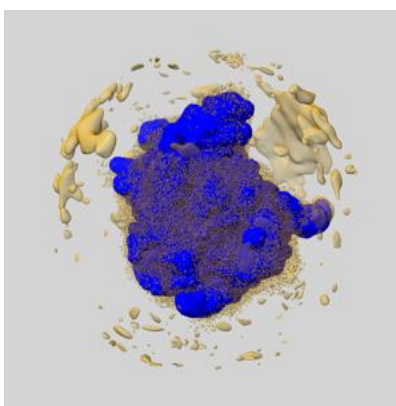
A mask typically either:

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

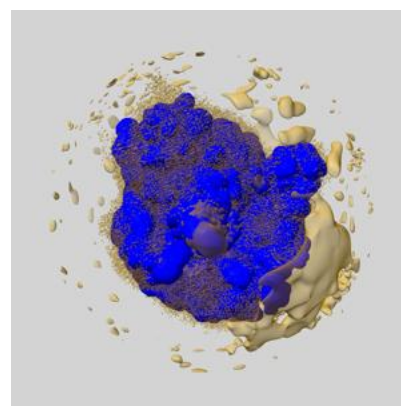
6.6.1 emd_10978_msk_1.map [i](#)



X



Y

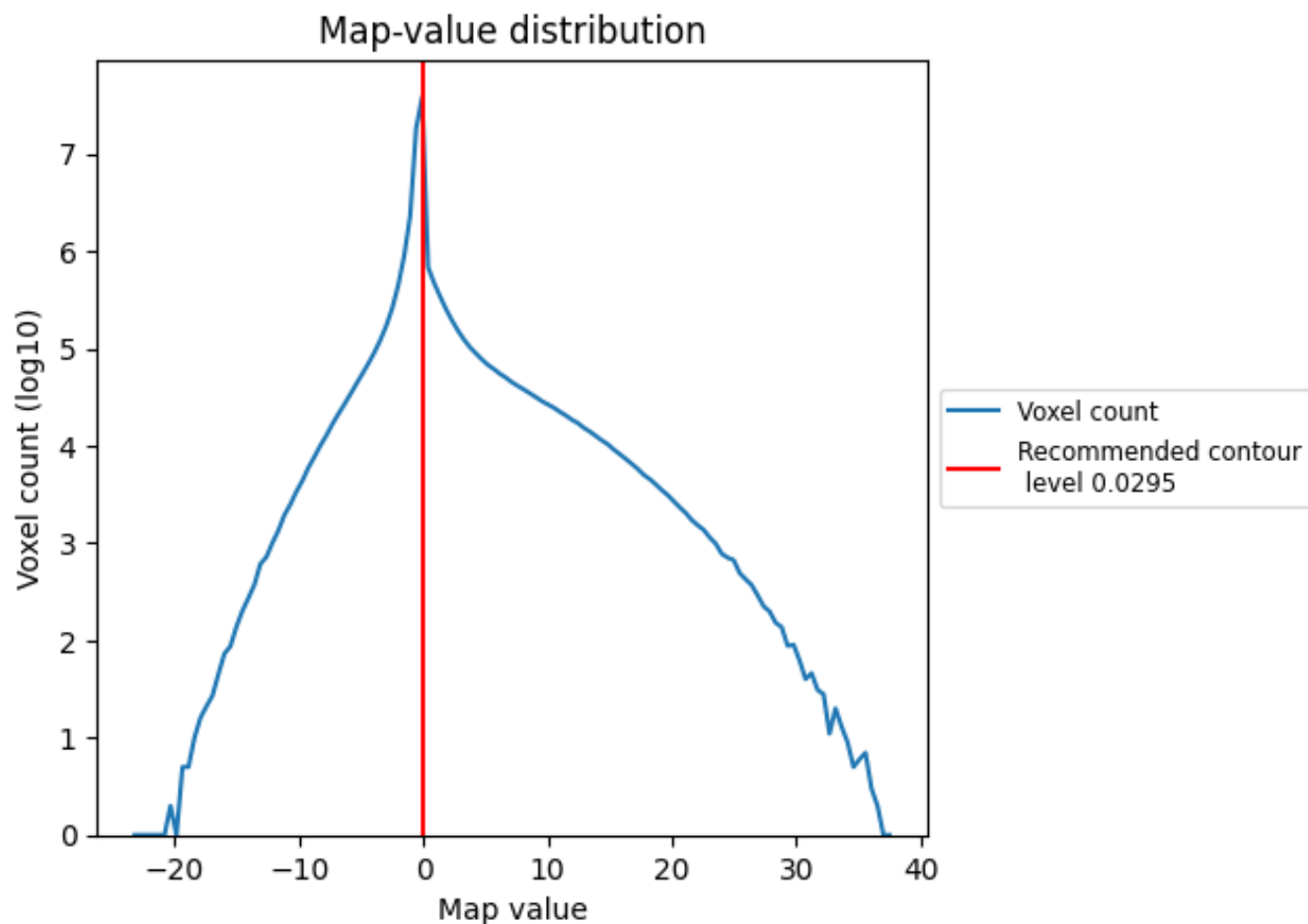


Z

7 Map analysis [i](#)

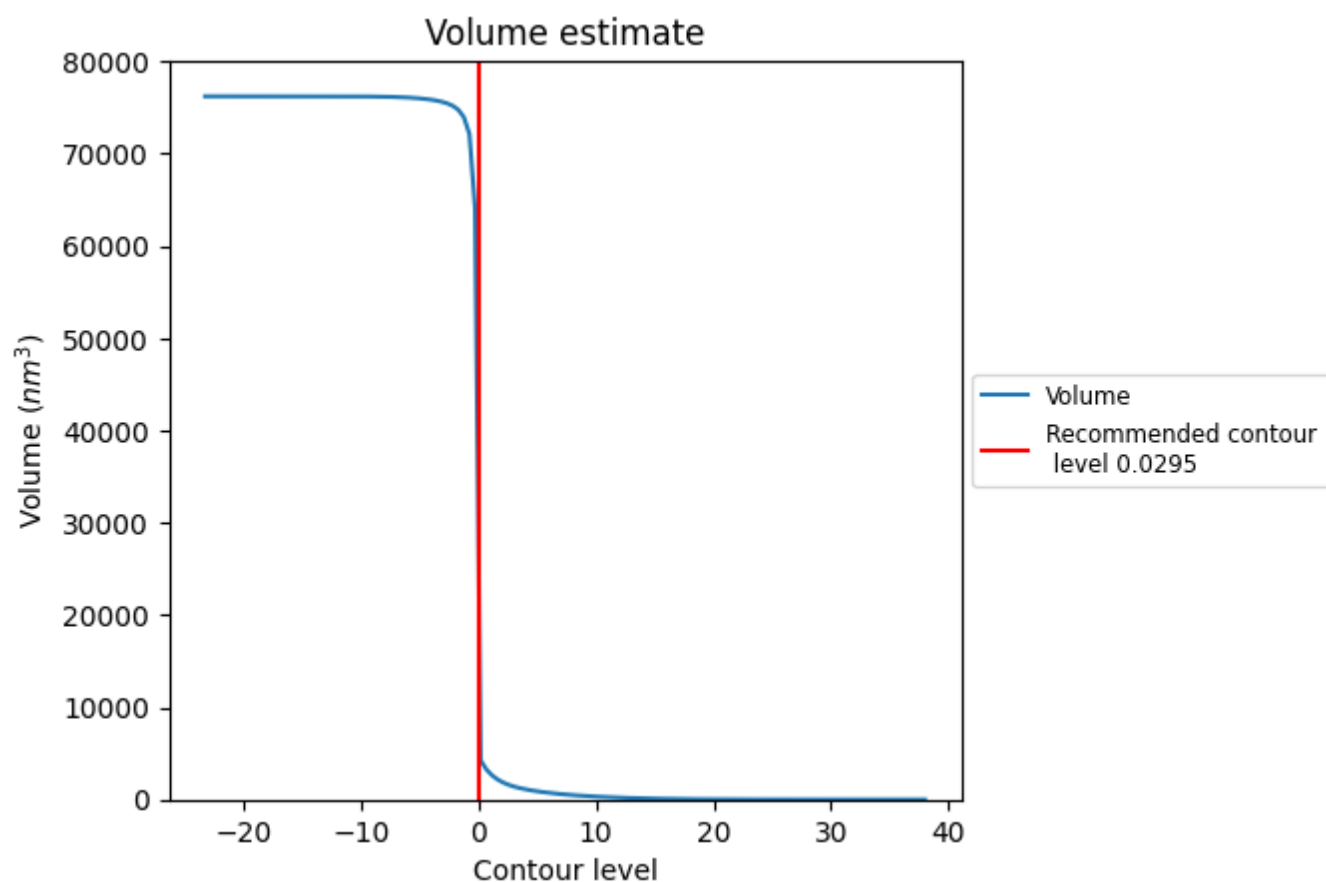
This section contains the results of statistical analysis of the map.

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.

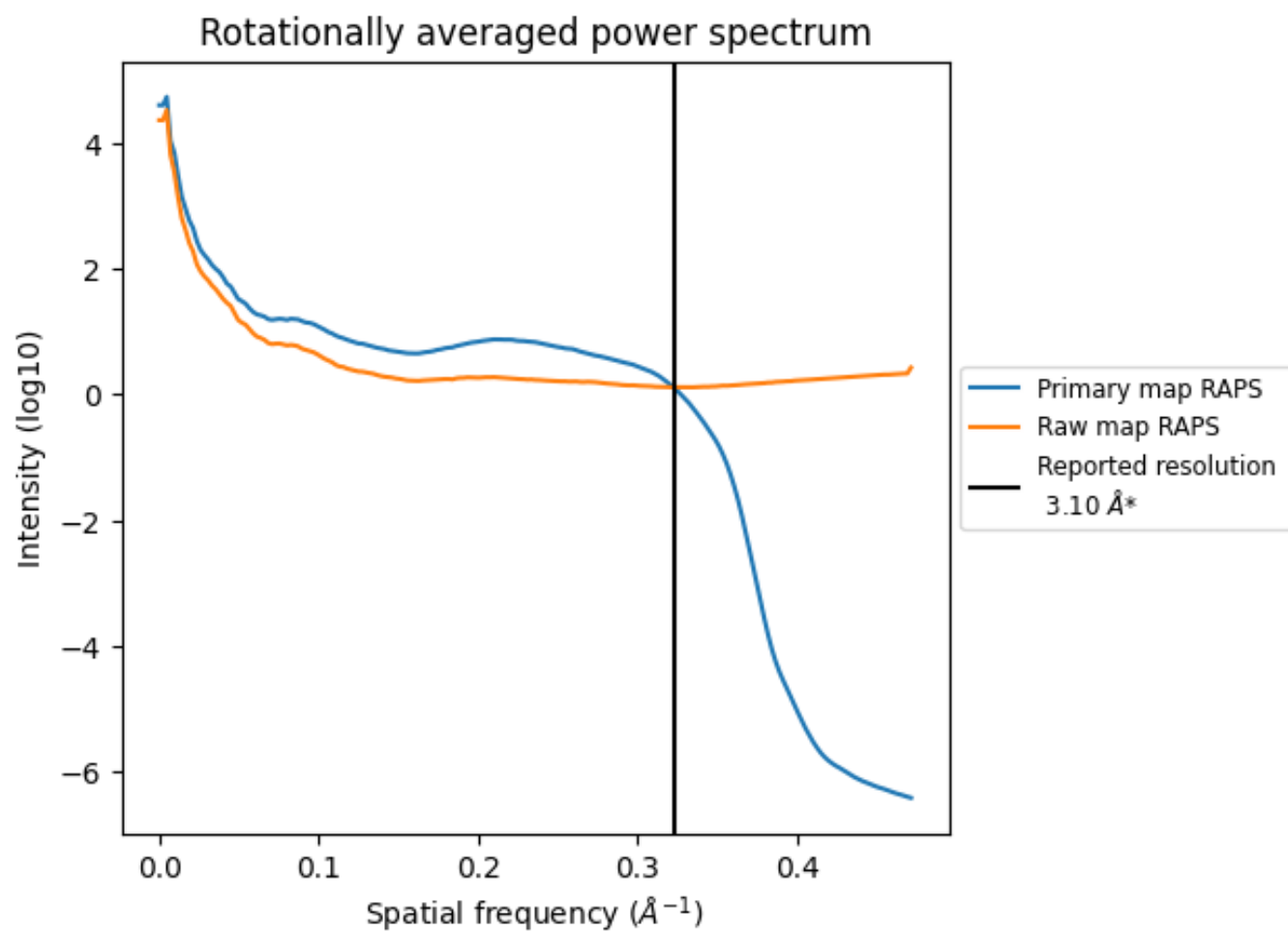
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 27404 nm³; this corresponds to an approximate mass of 24754 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 ⓘ

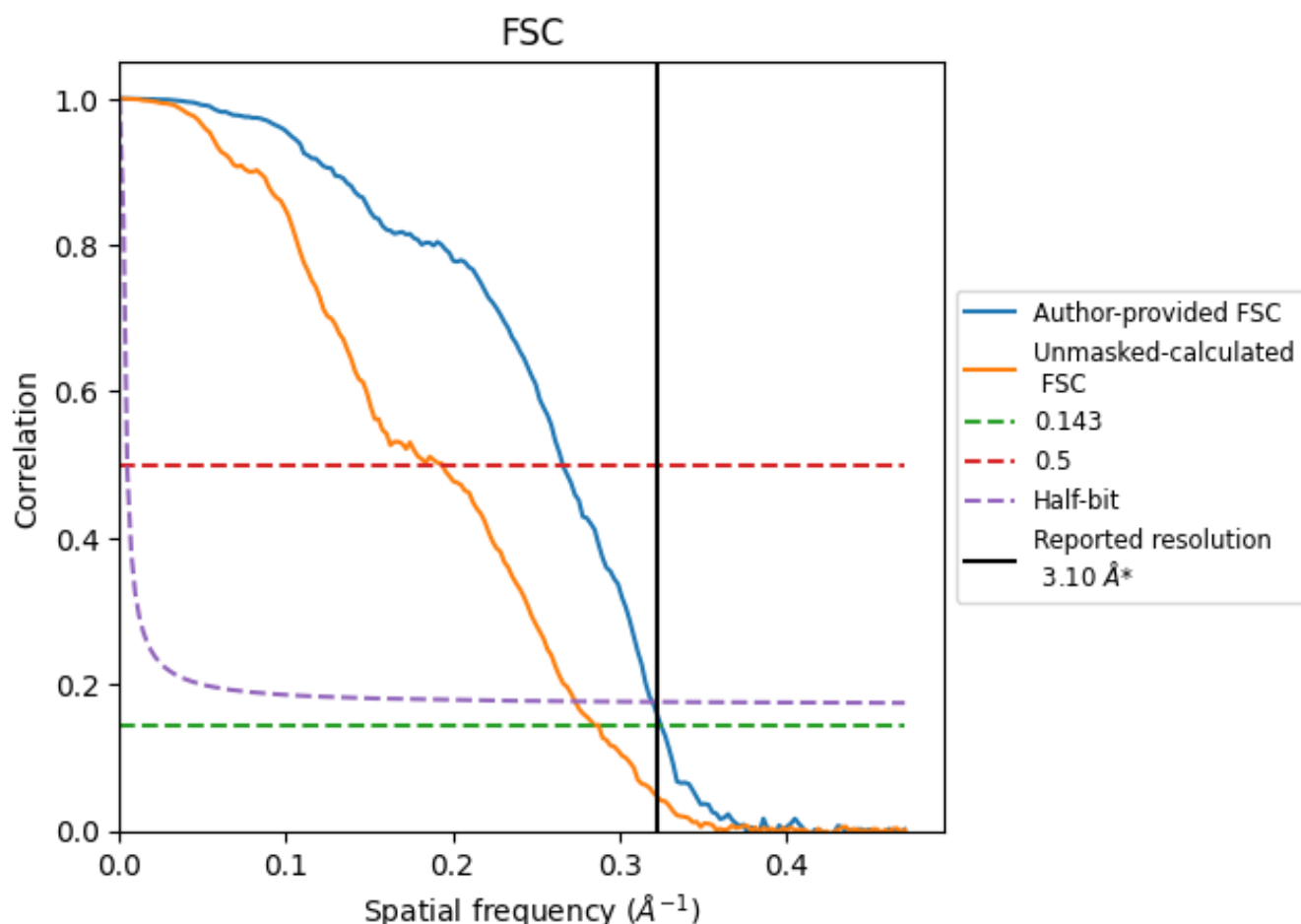


*Reported resolution corresponds to spatial frequency of 0.323 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

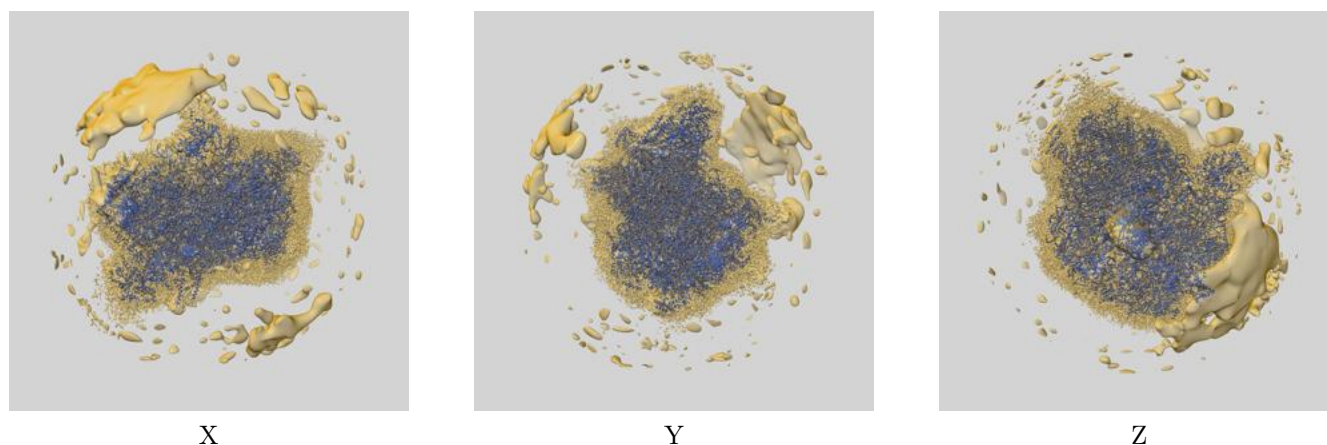
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.10 | - | - |
| Author-provided FSC curve | 3.07 | 3.76 | 3.12 |
| Unmasked-calculated* | 3.47 | 5.16 | 3.65 |

*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 3.47 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

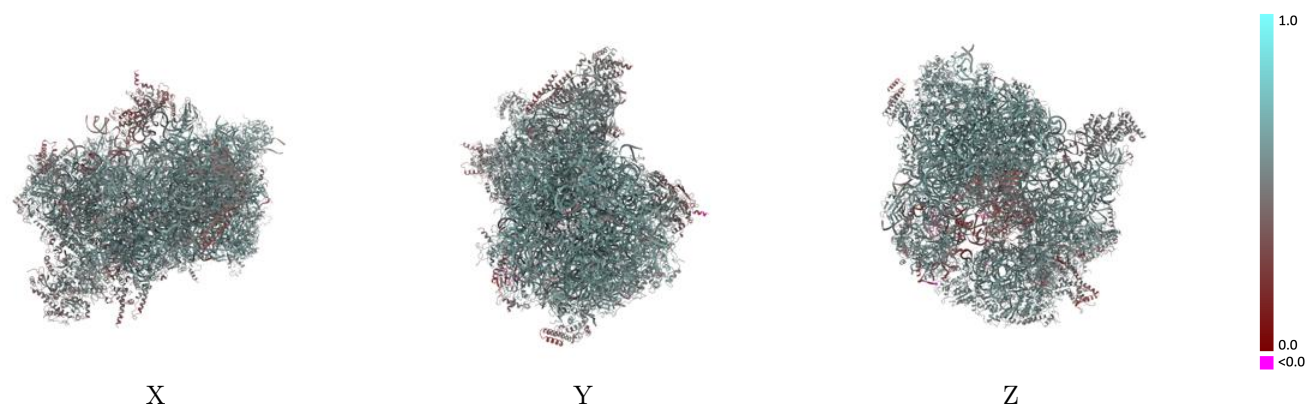
This section contains information regarding the fit between EMDB map EMD-10978 and PDB model 6YWX. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



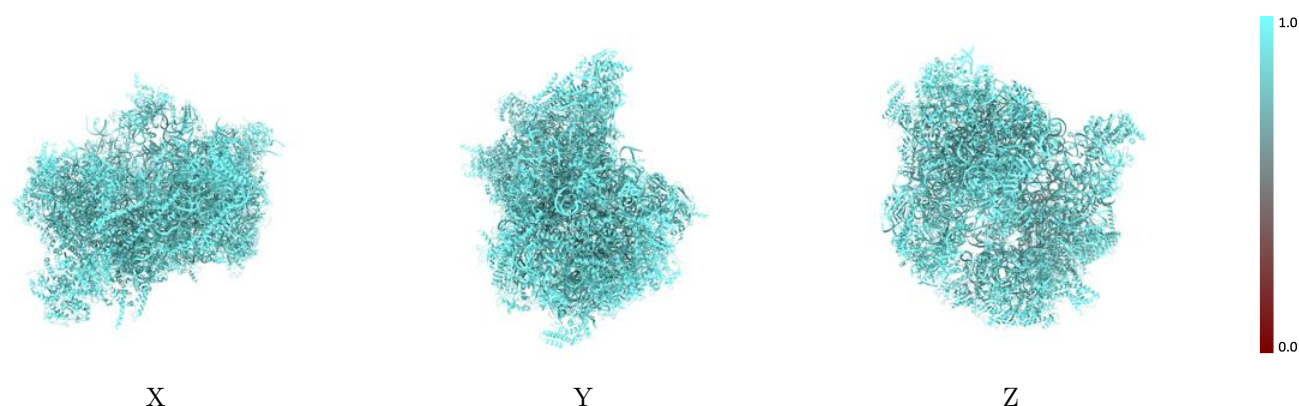
The images above show the 3D surface view of the map at the recommended contour level 0.0295 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



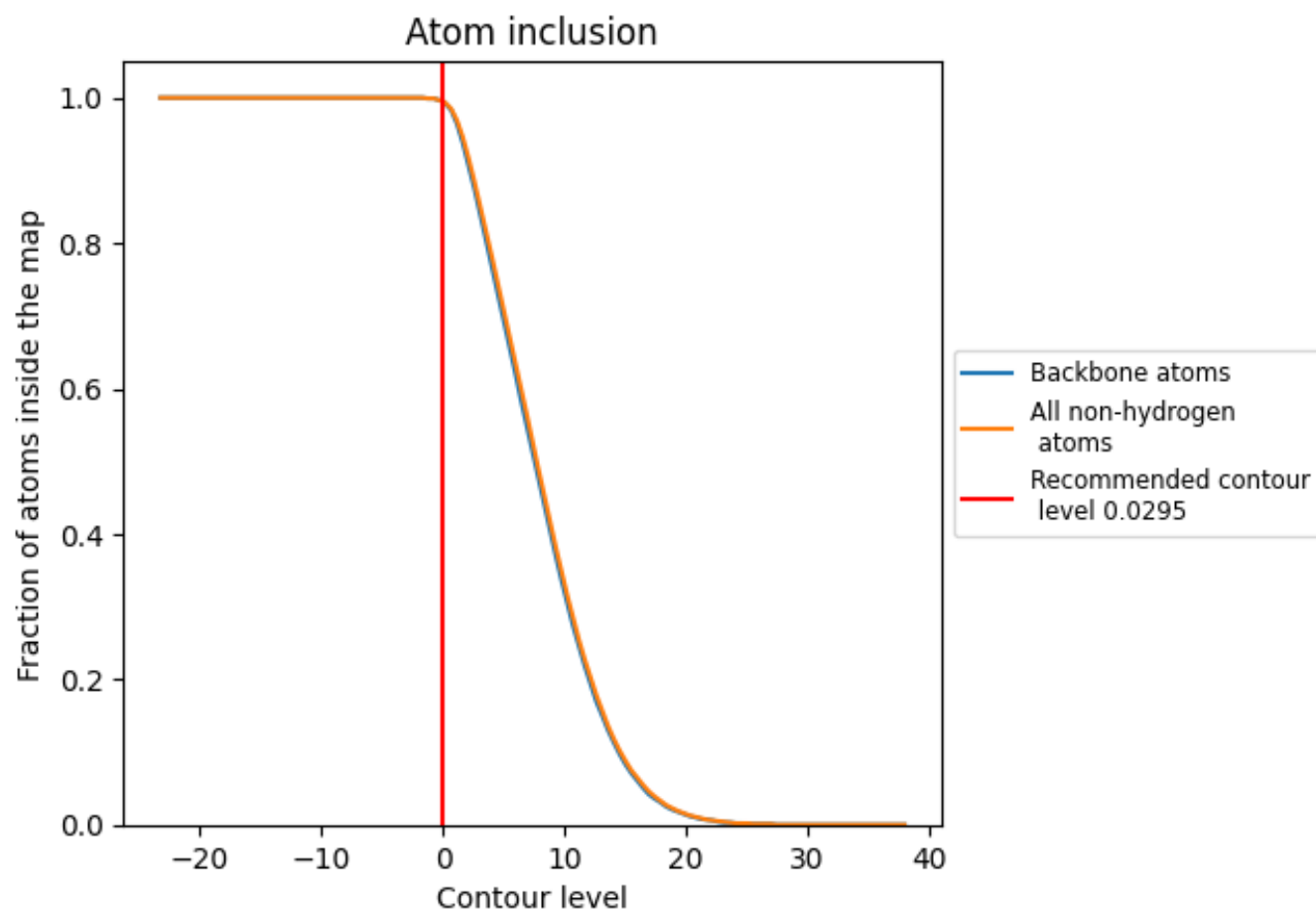
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0295).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.0295) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.9950 |  0.5460 |
| 0 |  0.9950 |  0.6210 |
| 00 |  0.9850 |  0.3820 |
| 1 |  0.9940 |  0.5640 |
| 11 |  0.9860 |  0.4900 |
| 2 |  0.9830 |  0.5810 |
| 22 |  0.9790 |  0.5730 |
| 3 |  0.9930 |  0.5840 |
| 33 |  0.9870 |  0.5100 |
| 4 |  0.9960 |  0.6080 |
| 44 |  0.9940 |  0.4670 |
| 5 |  0.9910 |  0.5650 |
| 55 |  0.9920 |  0.4480 |
| 6 |  0.9910 |  0.5620 |
| 66 |  0.9910 |  0.5310 |
| 7 |  0.9920 |  0.5750 |
| 77 |  0.9910 |  0.5260 |
| 8 |  0.9940 |  0.4800 |
| 88 |  0.9930 |  0.5130 |
| 9 |  0.9970 |  0.5290 |
| 99 |  0.9930 |  0.3150 |
| A |  0.9980 |  0.5770 |
| AA |  0.9900 |  0.4750 |
| B |  0.9980 |  0.5960 |
| BB |  0.9940 |  0.5460 |
| C |  0.9930 |  0.6130 |
| CC |  0.9890 |  0.5160 |
| D |  0.9950 |  0.5750 |
| DD |  0.9960 |  0.5510 |
| E |  0.9900 |  0.5720 |
| EE |  0.9950 |  0.5480 |
| F |  0.9920 |  0.5320 |
| FF |  0.9930 |  0.5500 |
| G |  0.9970 |  0.5410 |
| GG |  0.9890 |  0.5240 |

















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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| H |  0.9930 |  0.6130 |
| HH |  0.9860 |  0.5830 |
| I |  0.9980 |  0.5960 |
| II |  0.9930 |  0.5240 |
| J |  0.9940 |  0.5850 |
| JJ |  0.9930 |  0.5660 |
| K |  0.9950 |  0.5860 |
| KK |  0.9970 |  0.5560 |
| L |  0.9940 |  0.5960 |
| LL |  0.9870 |  0.5620 |
| M |  0.9950 |  0.5650 |
| MM |  0.9930 |  0.5430 |
| N |  0.9980 |  0.5980 |
| NN |  0.9880 |  0.5860 |
| O |  0.9950 |  0.5860 |
| OO |  0.9910 |  0.5340 |
| P |  0.9890 |  0.5870 |
| PP |  0.9940 |  0.5670 |
| Q |  0.9950 |  0.5600 |
| QQ |  0.9940 |  0.5230 |
| R |  0.9960 |  0.5190 |
| RR |  0.9950 |  0.5210 |
| S |  0.9970 |  0.5710 |
| SS |  0.9870 |  0.5320 |
| T |  0.9960 |  0.5750 |
| TT |  0.9940 |  0.5700 |
| U |  0.9940 |  0.5830 |
| UU |  0.9900 |  0.5300 |
| V |  0.9980 |  0.5850 |
| VV |  0.9870 |  0.5020 |
| W |  0.9890 |  0.6120 |
| WW |  0.9870 |  0.4710 |
| X |  0.9950 |  0.5860 |
| XX |  0.9910 |  0.5260 |
| Y |  0.9890 |  0.6290 |
| YY |  0.9840 |  0.5570 |
| ZZ |  0.9920 |  0.4950 |
| a |  0.9930 |  0.5600 |
| aa |  0.9980 |  0.5700 |
| b |  0.9950 |  0.5540 |
| bb |  0.9680 |  0.1900 |
| c |  0.9940 |  0.6140 |

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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| d |  0.9950 |  0.5830 |
| e |  0.9800 |  0.1300 |
| f |  0.9920 |  0.3740 |
| g |  0.9950 |  0.3400 |
| h |  0.9800 |  0.3400 |
| i |  0.9860 |  0.3080 |
| j |  0.9930 |  0.1450 |