# wwPDB EM Validation Summary Report (i)

Nov 6, 2022 – 11:04 PM EST

| | | |
|---|---|---|
| PDB ID | : | 6NU2 |
| EMDB ID | : | EMD-0514 |
| Title | : | Structural insights into unique features of the human mitochondrial ribosome recycling |
| Authors | : | Sharma, M.R.; Koripella, R.K.; Agrawal, R.K. |
| Deposited on | : | 2019-01-30 |
| Resolution | : | 3.90 Å(reported) |
| Based on initial model | : | 3JD5 |

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

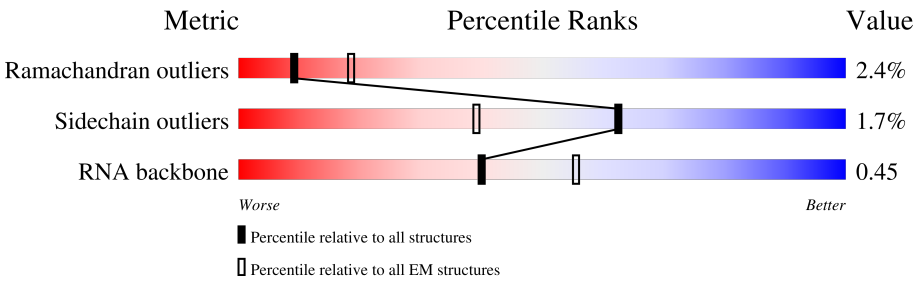
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev43 |
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| MapQ | : | FAILED |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.31.2 |

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.90 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 | 154571 | 4023 |
| Sidechain outliers | 154315 | 3826 |
| RNA backbone | 4643 | 859 |

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 <=5%

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 1472 | 73% 27% |
| 2 | B | 56 | 77% 23% |
| 3 | D | 236 | 96% • |
| 4 | E | 304 | 95% • • |
| 5 | F | 250 | 96% • • |
| 6 | H | 95 | 96% • |
| 7 | I | 168 | 92% • 6% |
| 8 | J | 140 | 96% • |
| 9 | K | 177 | 95% 5% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 10 | L | 115 | 95% 5% |
| 11 | M | 287 | 96% |
| 12 | N | 205 | 99% |
| 13 | O | 152 | 99% |
| 14 | P | 138 | 94% |
| 15 | Q | 219 | 97% |
| 16 | R | 140 | 98% |
| 17 | S | 156 | 97% |
| 18 | T | 166 | 98% |
| 19 | U | 111 | 96% |
| 20 | V | 202 | 87% 6% 6% |
| 21 | W | 115 | 96% |
| 22 | X | 243 | 94% 6% |
| 23 | Y | 176 | 98% |
| 24 | Z | 120 | 97% |
| 25 | 0 | 108 | 96% |
| 26 | 1 | 52 | 94% 6% |
| 27 | 2 | 46 | 100% |
| 28 | 3 | 95 | 98% |
| 29 | 4 | 36 | 100% |
| 30 | 5 | 392 | 92% |
| 31 | 6 | 354 | 88% 8% |
| 32 | 7 | 287 | 89% 7% |
| 33 | 8 | 99 | 97% |
| 34 | 9 | 123 | 84% 5% 11% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 35 | a | 108 | 73% 24% |
| 36 | b | 148 | 97% |
| 37 | c | 286 | 94% |
| 38 | d | 171 | 92% 5% |
| 39 | e | 237 | 88% 8% |
| 40 | f | 146 | 89% 10% |
| 41 | g | 129 | 95% 5% |
| 42 | h | 103 | 95% |
| 43 | i | 97 | 94% 6% |
| 44 | j | 85 | 98% |
| 45 | k | 84 | 93% 7% |
| 46 | l | 23 | 100% |
| 47 | m | 45 | 93% 7% |
| 48 | o | 94 | 96% |
| 49 | p | 156 | 79% 19% |
| 50 | q | 128 | 96% |
| 51 | r | 162 | 86% 10% |
| 52 | s | 390 | 93% 5% |
| 53 | t | 28 | 100% |
| 54 | u | 2 | 100% |
| 55 | z | 204 | 97% |
| 56 | AA | 923 | 66% 34% |
| 57 | AB | 217 | 99% |
| 58 | AC | 132 | 97% |
| 59 | AD | 343 | 88% 6% 6% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 60 | AE | 122 | 97% |
| 61 | AF | 208 | 95% |
| 62 | AG | 326 | 88% 5% 6% |
| 63 | AH | 122 | 94% 6% |
| 64 | AI | 136 | 96% |
| 65 | AJ | 108 | 95% 5% |
| 66 | AK | 101 | 92% 8% |
| 67 | AL | 164 | 99% |
| 68 | AM | 116 | 97% |
| 69 | AN | 107 | 93% 7% |
| 70 | AO | 185 | 94% 6% |
| 71 | AP | 96 | 98% |
| 72 | AQ | 86 | 97% |
| 73 | AR | 242 | 94% 6% |
| 74 | AS | 126 | 98% |
| 75 | AT | 162 | 98% |
| 76 | AU | 173 | 95% 5% |
| 77 | AV | 365 | 87% 10% |
| 78 | AW | 97 | 97% |
| 79 | AX | 348 | 84% 6% 9% |
| 80 | AY | 108 | 95% 5% |
| 81 | AZ | 87 | 94% 6% |
| 82 | A0 | 208 | 93% |
| 83 | A1 | 272 | 90% 6% |
| 84 | A2 | 116 | 95% 5% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 85 | A3 | 69 | 99% |
| 86 | A4 | 474 | 86% 13% |

# 2 Entry composition (i)

There are 88 unique types of molecules in this entry. The entry contains 294948 atoms, of which 134991 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 16S rRNA.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | P | | |
| 1 | A | 1472 | 47118 | 14025 | 15857 | 5642 | 10122 | 1472 | 0 | 0 |

- Molecule 2 is a RNA chain called mt-tRNAVal.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | P | | |
| 2 | B | 56 | 1794 | 534 | 603 | 214 | 387 | 56 | 0 | 0 |

- Molecule 3 is a protein called 39S ribosomal protein L2, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 3 | D | 236 | 3738 | 1145 | 1896 | 373 | 315 | 9 | 0 | 0 |

- Molecule 4 is a protein called 39S ribosomal protein L3, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 4 | E | 300 | 4743 | 1523 | 2378 | 410 | 422 | 10 | 0 | 0 |

- Molecule 5 is a protein called 39S ribosomal protein L4, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 5 | F | 250 | 4058 | 1294 | 2045 | 365 | 348 | 6 | 0 | 0 |

- Molecule 6 is a protein called 39S ribosomal protein L9, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | | |
| 6 | H | 95 | 1616 | 498 | 832 | 152 | 134 | 0 | 0 |

- Molecule 7 is a protein called 39S ribosomal protein L10, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 7 | I | 158 | 2652 | 828 | 1369 | 235 | 210 | 10 | 0 | 0 |

- Molecule 8 is a protein called 39S ribosomal protein L11, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 8 | J | 140 | 2202 | 680 | 1141 | 192 | 187 | 2 | 0 | 0 |

- Molecule 9 is a protein called 39S ribosomal protein L13, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 9 | K | 177 | 2899 | 934 | 1448 | 259 | 251 | 7 | 0 | 0 |

- Molecule 10 is a protein called 39S ribosomal protein L14, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 10 | L | 115 | 1830 | 559 | 941 | 171 | 154 | 5 | 0 | 0 |

- Molecule 11 is a protein called 39S ribosomal protein L15, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 11 | M | 287 | 4683 | 1472 | 2378 | 425 | 402 | 6 | 0 | 0 |

- Molecule 12 is a protein called 39S ribosomal protein L16, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 12 | N | 205 | 3334 | 1056 | 1680 | 308 | 280 | 10 | 0 | 0 |

- Molecule 13 is a protein called 39S ribosomal protein L17, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 13 | O | 152 | 2528 | 784 | 1283 | 239 | 215 | 7 | 0 | 0 |

- Molecule 14 is a protein called 39S ribosomal protein L18, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 14 | P | 133 | 2162 | 677 | 1082 | 209 | 189 | 5 | 0 | 0 |

- Molecule 15 is a protein called 39S ribosomal protein L19, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 15 | Q | 219 | 3681 | 1168 | 1859 | 322 | 323 | 9 | 0 | 0 |

- Molecule 16 is a protein called 39S ribosomal protein L20, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 16 | R | 140 | 2367 | 732 | 1214 | 231 | 186 | 4 | 0 | 0 |

- Molecule 17 is a protein called 39S ribosomal protein L21, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 17 | S | 156 | 2573 | 806 | 1322 | 222 | 219 | 4 | 0 | 0 |

- Molecule 18 is a protein called 39S ribosomal protein L22, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 18 | T | 166 | 2778 | 875 | 1410 | 254 | 232 | 7 | 0 | 0 |

- Molecule 19 is a protein called 39S ribosomal protein L23, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 19 | U | 111 | 1857 | 591 | 935 | 176 | 153 | 2 | 0 | 0 |

- Molecule 20 is a protein called 39S ribosomal protein L24, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 20 | V | 189 | 3109 | 987 | 1558 | 278 | 278 | 8 | 0 | 0 |

- Molecule 21 is a protein called 39S ribosomal protein L27, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 21 | W | 115 | 1816 | 571 | 922 | 169 | 151 | 3 | 0 | 0 |

- Molecule 22 is a protein called 39S ribosomal protein L28, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 22 | X | 243 | 4089 | 1317 | 2054 | 351 | 362 | 5 | 0 | 0 |

- Molecule 23 is a protein called 39S ribosomal protein L47, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 23 | Y | 176 | 3078 | 970 | 1561 | 291 | 252 | 4 | 0 | 0 |

- Molecule 24 is a protein called 39S ribosomal protein L30, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 24 | Z | 120 | 2008 | 626 | 1030 | 183 | 166 | 3 | 0 | 0 |

- Molecule 25 is a protein called 39S ribosomal protein L32, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 25 | 0 | 108 | 1782 | 545 | 902 | 172 | 157 | 6 | 0 | 0 |

- Molecule 26 is a protein called 39S ribosomal protein L33, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 26 | 1 | 52 | 908 | 278 | 475 | 83 | 70 | 2 | 0 | 0 |

- Molecule 27 is a protein called 39S ribosomal protein L34, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 27 | 2 | 46 | 782 | 233 | 406 | 83 | 59 | 1 | 0 | 0 |

- Molecule 28 is a protein called 39S ribosomal protein L35, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 28 | 3 | 95 | 1714 | 539 | 883 | 162 | 127 | 3 | 0 | 0 |

- Molecule 29 is a protein called 39S ribosomal protein L36, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 29 | 4 | 36 | 666 | 203 | 344 | 70 | 46 | 3 | 0 | 0 |

- Molecule 30 is a protein called 39S ribosomal protein L37, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 30 | 5 | 376 | 6123 | 1987 | 3059 | 529 | 538 | 10 | 0 | 0 |

- Molecule 31 is a protein called 39S ribosomal protein L38, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 31 | 6 | 325 | 5087 | 1692 | 2451 | 465 | 470 | 9 | 0 | 0 |

- Molecule 32 is a protein called 39S ribosomal protein L39, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 32 | 7 | 266 | 4331 | 1383 | 2173 | 371 | 388 | 16 | 0 | 0 |

- Molecule 33 is a protein called 39S ribosomal protein L40, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 33 | 8 | 99 | 1680 | 535 | 844 | 144 | 155 | 2 | 0 | 0 |

- Molecule 34 is a protein called 39S ribosomal protein L41, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 34 | 9 | 109 | 1751 | 565 | 878 | 152 | 154 | 2 | 0 | 0 |

- Molecule 35 is a protein called 39S ribosomal protein L42, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 35 | a | 82 | 1344 | 434 | 658 | 124 | 123 | 5 | 0 | 0 |

- Molecule 36 is a protein called 39S ribosomal protein L43, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 36 | b | 148 | 2358 | 733 | 1180 | 229 | 213 | 3 | 0 | 0 |

- Molecule 37 is a protein called 39S ribosomal protein L44, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 37 | c | 275 | 4437 | 1415 | 2220 | 383 | 410 | 9 | 0 | 0 |

- Molecule 38 is a protein called 39S ribosomal protein L45, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 38 | d | 162 | 2690 | 870 | 1343 | 234 | 235 | 8 | 0 | 0 |

- Molecule 39 is a protein called 39S ribosomal protein L46, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 39 | e | 217 | 3529 | 1124 | 1767 | 310 | 323 | 5 | 0 | 0 |

- Molecule 40 is a protein called 39S ribosomal protein L48, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 40 | f | 131 | 2083 | 663 | 1044 | 169 | 203 | 4 | 0 | 0 |

- Molecule 41 is a protein called 39S ribosomal protein L49, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 41 | g | 129 | 2123 | 690 | 1056 | 185 | 190 | 2 | 0 | 0 |

- Molecule 42 is a protein called 39S ribosomal protein L50, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 42 | h | 100 | 1633 | 524 | 806 | 146 | 155 | 2 | 0 | 0 |

- Molecule 43 is a protein called 39S ribosomal protein L51, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 43 | i | 97 | 1684 | 532 | 857 | 165 | 126 | 4 | 0 | 0 |

- Molecule 44 is a protein called 39S ribosomal protein L52, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 44 | j | 85 | 1357 | 423 | 673 | 133 | 126 | 2 | 0 | 0 |

- Molecule 45 is a protein called 39S ribosomal protein L53, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 45 | k | 84 | 1311 | 407 | 656 | 122 | 121 | 5 | 0 | 0 |

- Molecule 46 is a protein called 39S ribosomal protein L54, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | | |
| 46 | l | 23 | 448 | 137 | 227 | 52 | 32 | 0 | 0 |

- Molecule 47 is a protein called 39S ribosomal protein L55, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 47 | m | 45 | 759 | 232 | 387 | 76 | 62 | 2 | 0 | 0 |

- Molecule 48 is a protein called Ribosomal protein 63, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 48 | o | 94 | 1601 | 501 | 804 | 165 | 128 | 3 | 0 | 0 |

- Molecule 49 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 49 | p | 127 | 2141 | 661 | 1083 | 201 | 192 | 4 | 0 | 0 |

- Molecule 50 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 50 | q | 128 | 2125 | 671 | 1049 | 208 | 192 | 5 | 0 | 0 |

- Molecule 51 is a protein called 39S ribosomal protein S18a, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 51 | r | 146 | 2423 | 764 | 1220 | 232 | 199 | 8 | 0 | 0 |

- Molecule 52 is a protein called 39S ribosomal protein S30, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 52 | s | 370 | 6058 | 1946 | 3022 | 542 | 534 | 14 | 0 | 0 |

- Molecule 53 is a protein called Unknown protein/protein extension.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | | |
| 53 | t | 28 | 170 | 84 | 30 | 28 | 28 | 0 | 0 |

- Molecule 54 is a RNA chain called E-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | P | | |
| 54 | u | 2 | 65 | 19 | 23 | 8 | 13 | 2 | 0 | 0 |

- Molecule 55 is a protein called Ribosome-recycling factor, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 55 | z | 204 | 3240 | 974 | 1665 | 285 | 308 | 8 | 0 | 0 |

- Molecule 56 is a RNA chain called 12S rRNA.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | P | | |
| 56 | AA | 923 | 29552 | 8790 | 9946 | 3535 | 6358 | 923 | 0 | 0 |

- Molecule 57 is a protein called 28S ribosomal protein S2, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 57 | AB | 217 | 3533 | 1131 | 1765 | 321 | 306 | 10 | 0 | 0 |

- Molecule 58 is a protein called 28S ribosomal protein S24, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 58 | AC | 132 | 2170 | 699 | 1088 | 195 | 184 | 4 | 0 | 0 |

- Molecule 59 is a protein called 28S ribosomal protein S5, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 59 | AD | 322 | 5153 | 1611 | 2596 | 476 | 457 | 13 | 0 | 0 |

- Molecule 60 is a protein called 28S ribosomal protein S6, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 60 | AE | 122 | 1973 | 614 | 1001 | 177 | 177 | 4 | 0 | 0 |

- Molecule 61 is a protein called 28S ribosomal protein S7, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 61 | AF | 201 | 3385 | 1069 | 1717 | 305 | 283 | 11 | 0 | 0 |

- Molecule 62 is a protein called 28S ribosomal protein S9, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 62 | AG | 305 | 5019 | 1599 | 2503 | 448 | 455 | 14 | 0 | 0 |

- Molecule 63 is a protein called 28S ribosomal protein S10, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 63 | AH | 122 | 2023 | 643 | 1024 | 168 | 185 | 3 | 0 | 0 |

- Molecule 64 is a protein called 28S ribosomal protein S11, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 64 | AI | 136 | 2063 | 637 | 1052 | 192 | 178 | 4 | 0 | 0 |

- Molecule 65 is a protein called 28S ribosomal protein S12, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 65 | AJ | 108 | 1725 | 521 | 887 | 169 | 142 | 6 | 0 | 0 |

- Molecule 66 is a protein called 28S ribosomal protein S14, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 66 | AK | 101 | 1746 | 537 | 885 | 179 | 140 | 5 | 0 | 0 |

- Molecule 67 is a protein called 28S ribosomal protein S15, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 67 | AL | 164 | 2855 | 883 | 1473 | 257 | 235 | 7 | 0 | 0 |

- Molecule 68 is a protein called 28S ribosomal protein S16, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 68 | AM | 116 | 1870 | 582 | 950 | 182 | 150 | 6 | 0 | 0 |

- Molecule 69 is a protein called 28S ribosomal protein S17, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 69 | AN | 107 | 1754 | 549 | 908 | 153 | 141 | 3 | 0 | 0 |

- Molecule 70 is a protein called 28S ribosomal protein S18b, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 70 | AO | 185 | 3016 | 970 | 1488 | 285 | 267 | 6 | 0 | 0 |

- Molecule 71 is a protein called 28S ribosomal protein S18c, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 71 | AP | 96 | 1578 | 498 | 804 | 133 | 135 | 8 | 0 | 0 |

- Molecule 72 is a protein called 28S ribosomal protein S21, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 72 | AQ | 86 | 1481 | 455 | 746 | 147 | 124 | 9 | 0 | 0 |

- Molecule 73 is a protein called 28S ribosomal protein S22, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 73 | AR | 242 | 4039 | 1285 | 2031 | 343 | 372 | 8 | 0 | 0 |

- Molecule 74 is a protein called 28S ribosomal protein S23, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 74 | AS | 126 | 2079 | 673 | 1037 | 183 | 185 | 1 | 0 | 0 |

- Molecule 75 is a protein called 28S ribosomal protein S25, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 75 | AT | 162 | 2674 | 850 | 1344 | 231 | 238 | 11 | 0 | 0 |

- Molecule 76 is a protein called 28S ribosomal protein S26, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 76 | AU | 173 | 2932 | 900 | 1471 | 294 | 263 | 4 | 0 | 0 |

- Molecule 77 is a protein called 28S ribosomal protein S27, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 77 | AV | 328 | 5392 | 1737 | 2690 | 452 | 502 | 11 | 0 | 0 |

- Molecule 78 is a protein called 28S ribosomal protein S28, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 78 | AW | 97 | 1551 | 486 | 785 | 137 | 139 | 4 | 0 | 0 |

- Molecule 79 is a protein called 28S ribosomal protein S29, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 79 | AX | 316 | 5051 | 1625 | 2520 | 440 | 455 | 11 | 0 | 0 |

- Molecule 80 is a protein called 28S ribosomal protein S31, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 80 | AY | 108 | 1773 | 593 | 859 | 150 | 169 | 2 | 0 | 0 |

- Molecule 81 is a protein called 28S ribosomal protein S33, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 81 | AZ | 87 | 1487 | 473 | 747 | 133 | 130 | 4 | 0 | 0 |

- Molecule 82 is a protein called 28S ribosomal protein S34, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 82 | A0 | 201 | 3369 | 1065 | 1685 | 322 | 292 | 5 | 0 | 0 |

- Molecule 83 is a protein called 28S ribosomal protein S35, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 83 | A1 | 256 | 4173 | 1321 | 2097 | 350 | 395 | 10 | 0 | 0 |

- Molecule 84 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 84 | A2 | 116 | 1887 | 574 | 962 | 181 | 162 | 8 | 0 | 0 |

- Molecule 85 is a protein called Aurora kinase A-interacting protein.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 85 | A3 | 69 | 1292 | 393 | 682 | 130 | 86 | 1 | 0 | 0 |

- Molecule 86 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | H | N | O | S | | |
| 86 | A4 | 414 | 5103 | 1805 | 2265 | 490 | 529 | 14 | 0 | 0 |

- Molecule 87 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| | | | Total | Mg | |
| 87 | A | 97 | 97 | 97 | 0 |
| 87 | M | 1 | 1 | 1 | 0 |
| 87 | g | 1 | 1 | 1 | 0 |
| 87 | AA | 28 | 28 | 28 | 0 |

- Molecule 88 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| | | | Total | Zn | |
| 88 | 0 | 1 | 1 | 1 | 0 |
| 88 | 4 | 1 | 1 | 1 | 0 |
| 88 | r | 1 | 1 | 1 | 0 |
| 88 | AB | 1 | 1 | 1 | 0 |
| 88 | AO | 1 | 1 | 1 | 0 |
| 88 | AP | 1 | 1 | 1 | 0 |

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*Continued from previous page...*

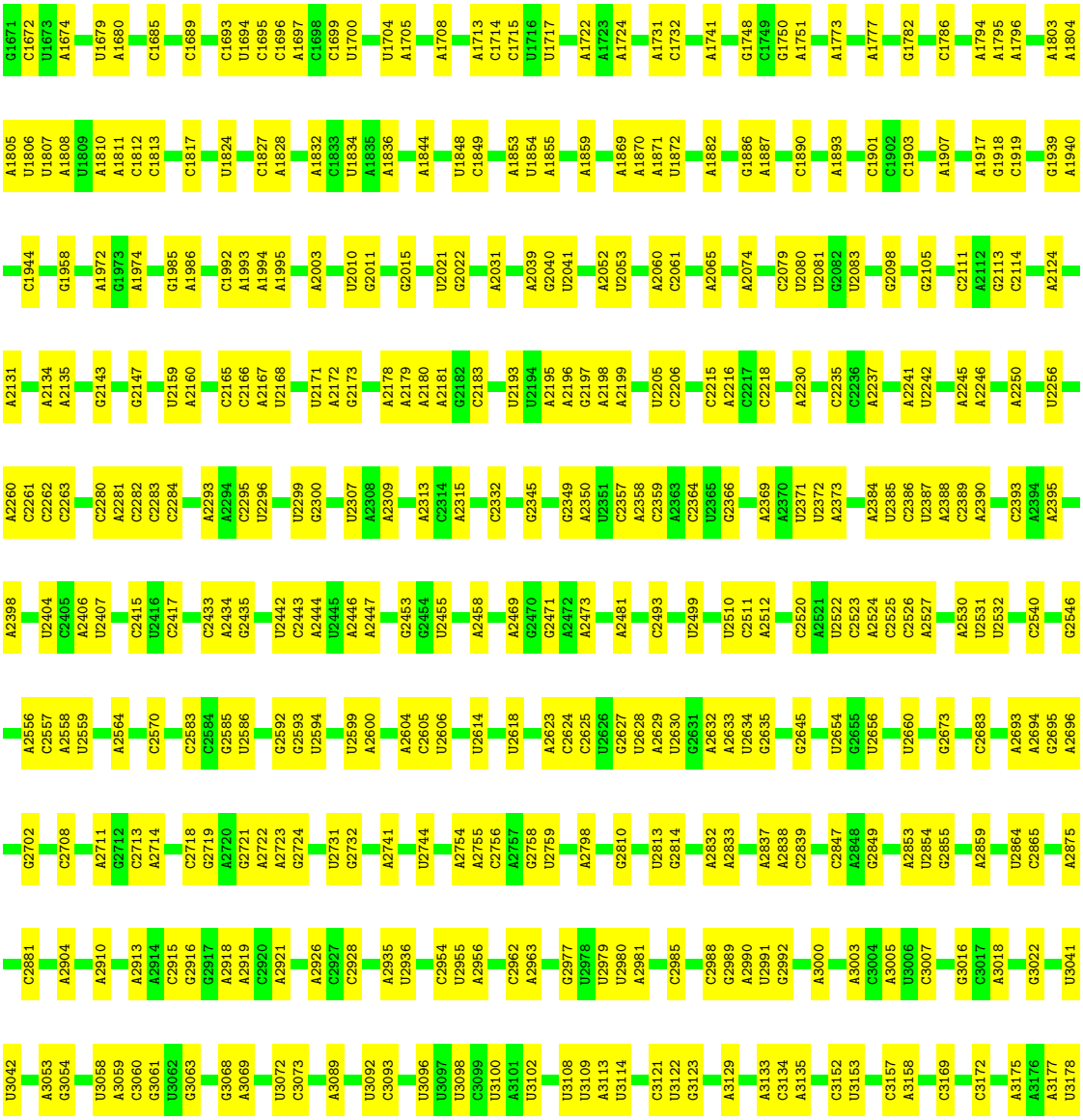
| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| | | | Total | Zn | |
| 88 | AT | 1 | 1 | 1 | 0 |

# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: 16S rRNA

Chain A: 73% 27%



• Molecule 2: mt-tRNAVal

Chain B: 77% 23%

• Molecule 3: 39S ribosomal protein L2, mitochondrial

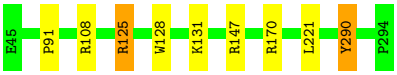
Chain D: 96%

• Molecule 4: 39S ribosomal protein L3, mitochondrial

Chain E: 95%

• Molecule 5: 39S ribosomal protein L4, mitochondrial

Chain F: 96%




• Molecule 6: 39S ribosomal protein L9, mitochondrial

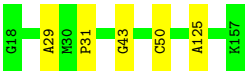
Chain H: 96%

• Molecule 7: 39S ribosomal protein L10, mitochondrial

Chain I: 92% 6%

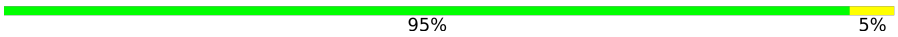
• Molecule 8: 39S ribosomal protein L11, mitochondrial

Chain J: 96%



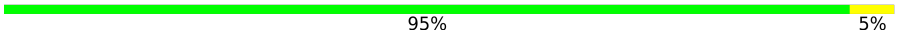

• Molecule 9: 39S ribosomal protein L13, mitochondrial

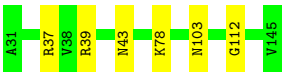
Chain K:



• Molecule 10: 39S ribosomal protein L14, mitochondrial

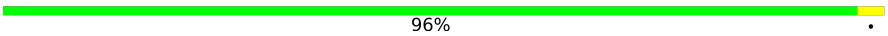
Chain L:



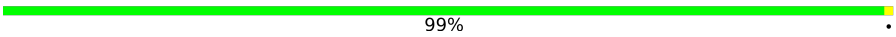

• Molecule 11: 39S ribosomal protein L15, mitochondrial

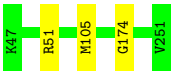
Chain M:



• Molecule 12: 39S ribosomal protein L16, mitochondrial

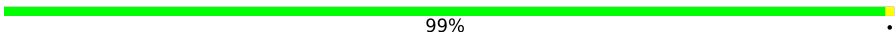
Chain N:



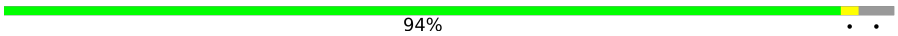

• Molecule 13: 39S ribosomal protein L17, mitochondrial

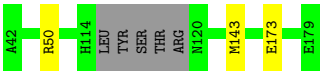
Chain O:



• Molecule 14: 39S ribosomal protein L18, mitochondrial

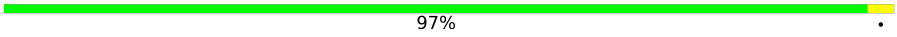
Chain P:



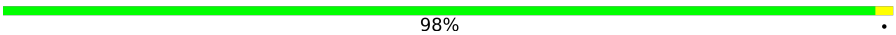

• Molecule 15: 39S ribosomal protein L19, mitochondrial

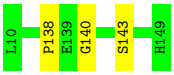
Chain Q:



• Molecule 16: 39S ribosomal protein L20, mitochondrial

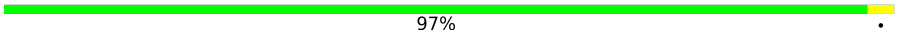
Chain R:

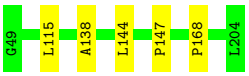



• Molecule 17: 39S ribosomal protein L21, mitochondrial

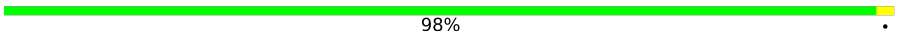
Chain S:



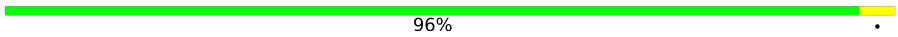

• Molecule 18: 39S ribosomal protein L22, mitochondrial

Chain T:



• Molecule 19: 39S ribosomal protein L23, mitochondrial

Chain U:

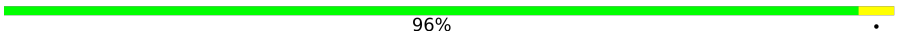


• Molecule 20: 39S ribosomal protein L24, mitochondrial

Chain V:

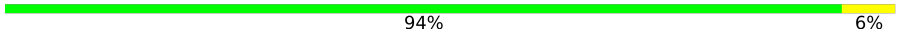
• Molecule 21: 39S ribosomal protein L27, mitochondrial

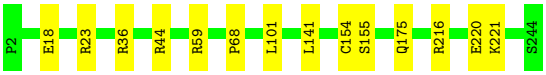
Chain W:



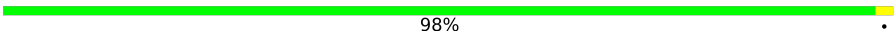
• Molecule 22: 39S ribosomal protein L28, mitochondrial

Chain X:

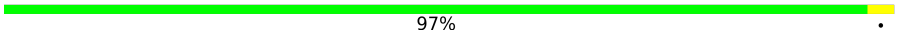


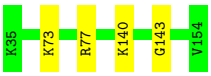



• Molecule 23: 39S ribosomal protein L47, mitochondrial

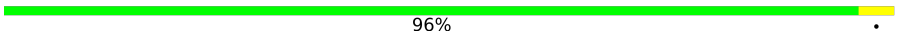
Chain Y: 

• Molecule 24: 39S ribosomal protein L30, mitochondrial

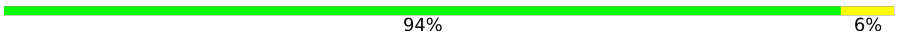
Chain Z: 


• Molecule 25: 39S ribosomal protein L32, mitochondrial

Chain 0: 

• Molecule 26: 39S ribosomal protein L33, mitochondrial

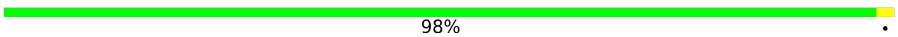
Chain 1: 

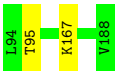
• Molecule 27: 39S ribosomal protein L34, mitochondrial

Chain 2:

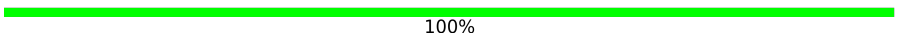

There are no outlier residues recorded for this chain.

• Molecule 28: 39S ribosomal protein L35, mitochondrial

Chain 3: 


• Molecule 29: 39S ribosomal protein L36, mitochondrial

Chain 4: 


There are no outlier residues recorded for this chain.

• Molecule 30: 39S ribosomal protein L37, mitochondrial

Chain 5: 92%

Y31 L70 D141 ASP PRO ARG ASN HIS ILE GLU ASN Q150 P171 R215 R229 D272 T277 P286 L294 D295 K296 A297 D348 D365 CYS ASN GLU G369 L373 L381 L382 Y383 I392 LYS LYS ARG VAL VAL V398 L415 A422

• Molecule 31: 39S ribosomal protein L38, mitochondrial

Chain 6: 88% 8%

R27 K50 H69 G79 GLU LYS THR ASP PRO LYS GLU LYS ILE ASP ILE GLY LEU PRO PRO PRO LYS VAL SER R99 E118 GLU E120 R124 LEU ARG T127 R159 L173 C189 E209 GLU GLY SER L213 L225 Q277 S282 GLU ASP ALA ARG P287

A314 L334 H351 H359 G378 I379 Y380

• Molecule 32: 39S ribosomal protein L39, mitochondrial

Chain 7: 89% 7%

S36 K64 K121 R156 A157 F158 LYS ASP GLU TYR MET VAL N165 L185 ASP SER LYS LEU ASP GLU TRP M193 D213 R256 P270 S281 N285 LEU GLN PRO THR GLN PRO SER LEU I294 A308 R319 S320 R321 K322

• Molecule 33: 39S ribosomal protein L40, mitochondrial

Chain 8: 97%

I83 P91 D96 R101 P181

• Molecule 34: 39S ribosomal protein L41, mitochondrial

Chain 9: 84% 5% 11%

A15 R25 K34 G37 A38 K39 S46 D103 PHE LYS ASP GLY THR PHE ASP PRO ASP ASN LEU GLU LYS TYR G118 R133 R137

• Molecule 35: 39S ribosomal protein L42, mitochondrial

Chain a: 73% 24%

T35 N44 R77 PRO ASP PRO VAL HIS ASN ASN GLU GLU THR HIS ASP GLN VAL LEU LYS THR ARG LEU GLU GLU LYS VAL GLU HIS LEU E104 Q111 R122 R142

• Molecule 36: 39S ribosomal protein L43, mitochondrial

Chain b: 97%

T2 L15 E50 R74 R116 R144 Q149

• Molecule 37: 39S ribosomal protein L44, mitochondrial

Chain c: 94%

V31 R52 P64 Q107 LEU GLY ILE GLU LYS GLU ALA VAL LEU LEU ASN L119 G162 E183 S206 P313 Y316

• Molecule 38: 39S ribosomal protein L45, mitochondrial

Chain d: 92% 5%

A117 E190 G199 SER SER MET MET ASN GLN GLY N207 R227 R230 L231 L252 THR ASN P255 L287

• Molecule 39: 39S ribosomal protein L46, mitochondrial

Chain e: 88% 8%

S43 R55 D104 LEU HIS ASP GLU GLU ASP GLU GLN ASP ILE LEU L116 A135 R151 K152 W171 P174 F217 PRO GLN ALA MET ARG THR GLU SER ASN L227 H251 L264 R273 L279

• Molecule 40: 39S ribosomal protein L48, mitochondrial

Chain f: 89% 10%

Y48 E66 GLU PRO LYS LYS LYS LYS GLY LYS VAL GLU V77 Q138 ASP GLN GLY SER LYS M144 R155 D193

• Molecule 41: 39S ribosomal protein L49, mitochondrial

Chain g: 95% 5%

F38 T55 P69 S70 N81 Q121 V143 T144 G145 F166

• Molecule 42: 39S ribosomal protein L50, mitochondrial

Chain h: 95%

R56 F78 GLY SER SER L82 R137 N147 Y158

• Molecule 43: 39S ribosomal protein L51, mitochondrial

Chain i: 94% 6%

I32 R35 F66 R101 L107 R113 F127 R128

• Molecule 44: 39S ribosomal protein L52, mitochondrial

Chain j: 98%

G24 G25 A34 A108

• Molecule 45: 39S ribosomal protein L53, mitochondrial

Chain k: 93% 7%

V13 T36 S39 N46 D58 P62 C63 V64 A96

• Molecule 46: 39S ribosomal protein L54, mitochondrial

Chain l: 100%

There are no outlier residues recorded for this chain.

• Molecule 47: 39S ribosomal protein L55, mitochondrial

Chain m: 93% 7%

D34 R42 E70 P71 P78

• Molecule 48: Ribosomal protein 63, mitochondrial

Chain o: 96%

R9 R15 G61 K81 S102

• Molecule 49: Peptidyl-tRNA hydrolase ICT1, mitochondrial

Chain p: 79% 19%

E38 V61 PRO ASN GLY ALA LYS GLN ALA ASP SER D70 S83 SER GLY PRO GLY GLY GLN ASN VAL ASN LYS V95 A108 T122 R129 Q163 THR PRO LYS GLU PRO THR LYS GLU ASP VAL K174 K191 R192 I193

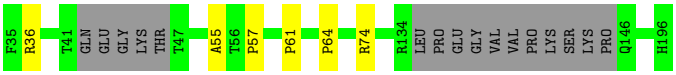
• Molecule 50: Growth arrest and DNA damage-inducible proteins-interacting protein 1

Chain q: 96%

Y25 R28 P42 L52 S78 R114 R152

• Molecule 51: 39S ribosomal protein S18a, mitochondrial

Chain r: 86% 10%




• Molecule 52: 39S ribosomal protein S30, mitochondrial

Chain s: 93% • 5%

• Molecule 53: Unknown protein/protein extension

Chain t: 100%

There are no outlier residues recorded for this chain.

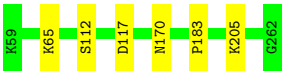
• Molecule 54: E-site tRNA

Chain u: 100%

There are no outlier residues recorded for this chain.

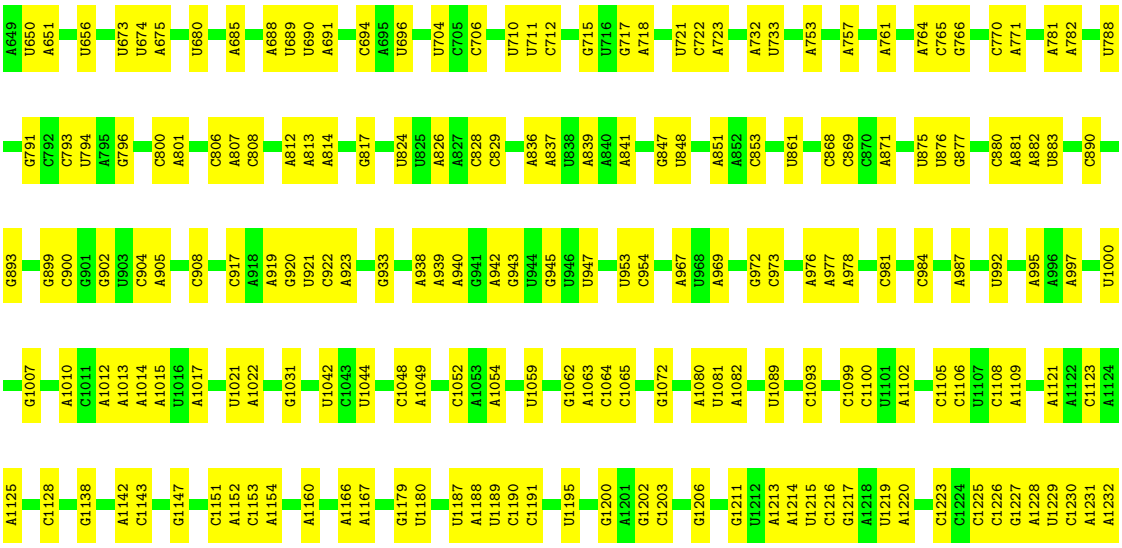
• Molecule 55: Ribosome-recycling factor, mitochondrial

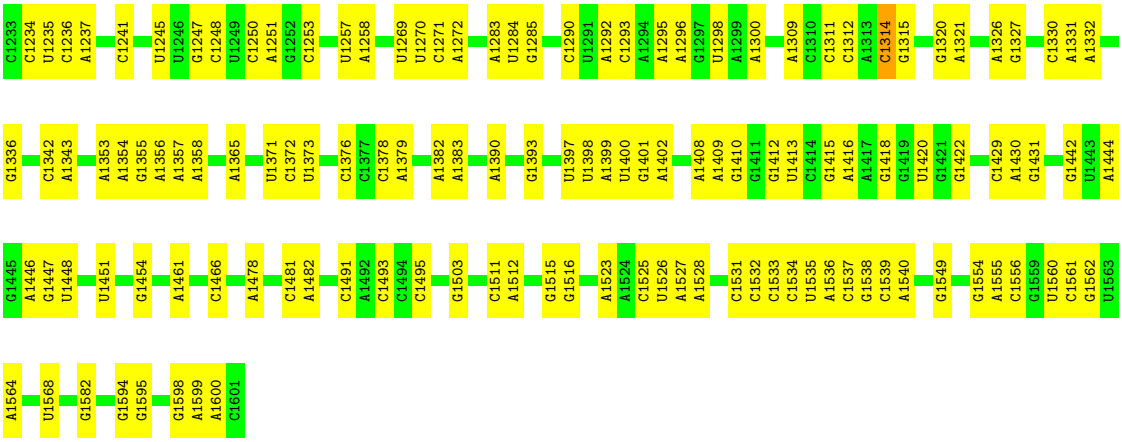
Chain z: 97% •




• Molecule 56: 12S rRNA

Chain AA: 66% 34%






- Molecule 57: 28S ribosomal protein S2, mitochondrial

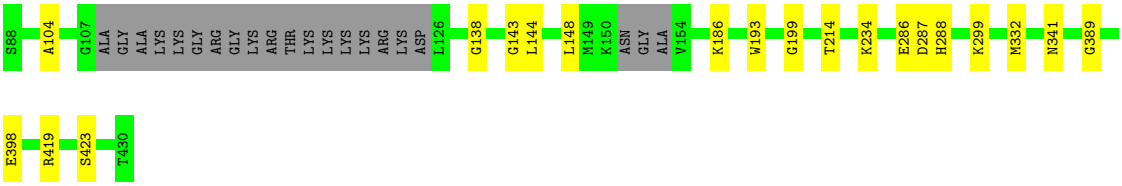
Chain AB: 99%

- Molecule 58: 28S ribosomal protein S24, mitochondrial

Chain AC: 97%

- Molecule 59: 28S ribosomal protein S5, mitochondrial

Chain AD: 88% 6% 6%




- Molecule 60: 28S ribosomal protein S6, mitochondrial

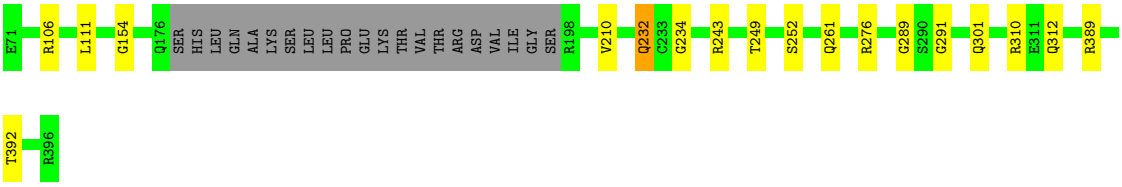
Chain AE: 97%

- Molecule 61: 28S ribosomal protein S7, mitochondrial

Chain AF: 95%

• Molecule 62: 28S ribosomal protein S9, mitochondrial

Chain AG: 88% 5% 6%

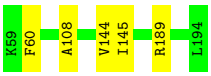



• Molecule 63: 28S ribosomal protein S10, mitochondrial

Chain AH: 94% 6%

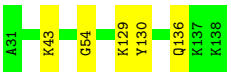
• Molecule 64: 28S ribosomal protein S11, mitochondrial

Chain AI: 96%




• Molecule 65: 28S ribosomal protein S12, mitochondrial

Chain AJ: 95% 5%

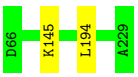



• Molecule 66: 28S ribosomal protein S14, mitochondrial

Chain AK: 92% 8%

• Molecule 67: 28S ribosomal protein S15, mitochondrial

Chain AL: 99%




• Molecule 68: 28S ribosomal protein S16, mitochondrial

Chain AM: 97% •

K10 G15 P56 G62 E63 K64 T125

• Molecule 69: 28S ribosomal protein S17, mitochondrial

Chain AN: 93% 7%

R5 L65 R73 K78 G97 C100 A101 G102 P109 L110 S111

• Molecule 70: 28S ribosomal protein S18b, mitochondrial

Chain AO: 94% 6%

K52 D53 C94 I95 R96 R109 C128 Y136 C143 K148 L163 R173 Q221 P236

• Molecule 71: 28S ribosomal protein S18c, mitochondrial

Chain AP: 98% •

N47 M54 K131 E142

• Molecule 72: 28S ribosomal protein S21, mitochondrial

Chain AQ: 97% •

A2 K6 R10 A81 C87

• Molecule 73: 28S ribosomal protein S22, mitochondrial

Chain AR: 94% 6%

K67 I95 K99 R116 K127 R135 E144 T153 T154 K155 G179 R256 G257 K258 Y267 R291 D292 H308

• Molecule 74: 28S ribosomal protein S23, mitochondrial

Chain AS: 98% •

A2 R42 G54 V77 A127

• Molecule 75: 28S ribosomal protein S25, mitochondrial

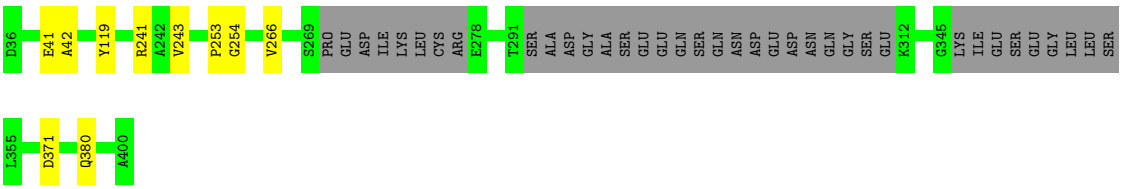
Chain AT: 98%

• Molecule 76: 28S ribosomal protein S26, mitochondrial

Chain AU: 95% 5%

• Molecule 77: 28S ribosomal protein S27, mitochondrial

Chain AV: 87% 10%

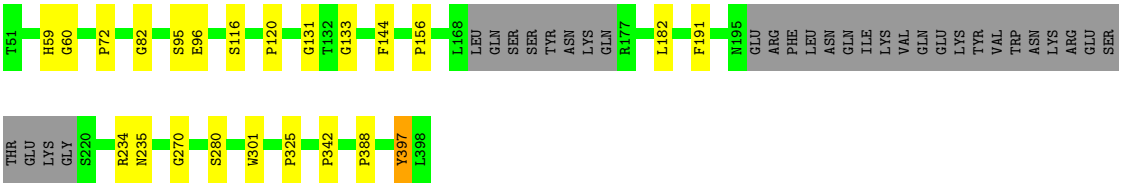



• Molecule 78: 28S ribosomal protein S28, mitochondrial

Chain AW: 97%

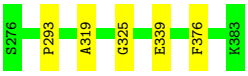
• Molecule 79: 28S ribosomal protein S29, mitochondrial

Chain AX: 84% 6% 9%



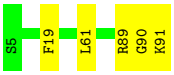

• Molecule 80: 28S ribosomal protein S31, mitochondrial

Chain AY: 95% 5%



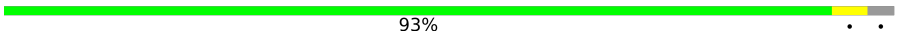

• Molecule 81: 28S ribosomal protein S33, mitochondrial

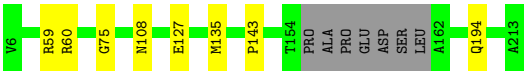
Chain AZ: 94% 6%




• Molecule 82: 28S ribosomal protein S34, mitochondrial

Chain A0:



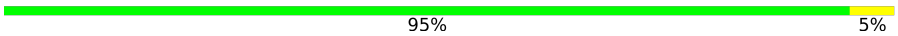



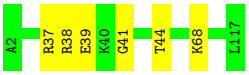

• Molecule 83: 28S ribosomal protein S35, mitochondrial

Chain A1:

• Molecule 84: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1

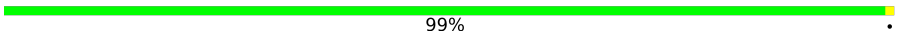
Chain A2:

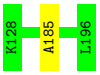



• Molecule 85: Aurora kinase A-interacting protein

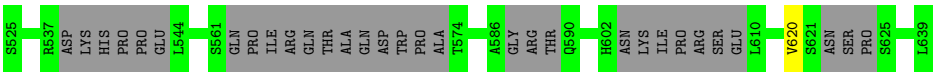
Chain A3:




• Molecule 86: Pentatricopeptide repeat domain-containing protein 3, mitochondrial

Chain A4:



# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 67116 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | NONE | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose $(e^-/\text{Å}^2)$ | 70 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |

# 5 Model quality (i)

## 5.1 Standard geometry (i)

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

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

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | $\#\|Z\|>5$ | RMSZ | $\#\|Z\|>5$ |
| 1 | A | 0.14 | 0/34967 | 0.71 | 4/54407 (0.0%) |
| 2 | B | 0.13 | 0/1328 | 0.69 | 0/2056 |
| 3 | D | 0.23 | 0/1879 | 0.40 | 0/2527 |
| 4 | E | 0.23 | 0/2433 | 0.39 | 0/3299 |
| 5 | F | 0.23 | 0/2071 | 0.37 | 0/2817 |
| 6 | H | 0.22 | 0/798 | 0.40 | 0/1073 |
| 7 | I | 0.23 | 0/1308 | 0.37 | 0/1761 |
| 8 | J | 0.23 | 0/1077 | 0.38 | 0/1452 |
| 9 | K | 0.23 | 0/1495 | 0.36 | 0/2029 |
| 10 | L | 0.22 | 0/904 | 0.40 | 0/1218 |
| 11 | M | 0.24 | 0/2359 | 0.38 | 0/3185 |
| 12 | N | 0.23 | 0/1697 | 0.38 | 0/2281 |
| 13 | O | 0.22 | 0/1269 | 0.36 | 0/1708 |
| 14 | P | 0.23 | 0/1103 | 0.38 | 0/1491 |
| 15 | Q | 0.23 | 0/1863 | 0.38 | 0/2509 |
| 16 | R | 0.23 | 0/1174 | 0.35 | 0/1572 |
| 17 | S | 0.23 | 0/1276 | 0.40 | 0/1729 |
| 18 | T | 0.23 | 0/1402 | 0.36 | 0/1886 |
| 19 | U | 0.24 | 0/946 | 0.39 | 0/1283 |
| 20 | V | 0.22 | 0/1590 | 0.39 | 0/2151 |
| 21 | W | 0.23 | 0/916 | 0.39 | 0/1233 |
| 22 | X | 0.23 | 0/2090 | 0.35 | 0/2825 |
| 23 | Y | 0.23 | 0/1552 | 0.34 | 0/2079 |
| 24 | Z | 0.22 | 0/1003 | 0.38 | 0/1354 |
| 25 | 0 | 0.23 | 0/895 | 0.39 | 0/1201 |
| 26 | 1 | 0.23 | 0/438 | 0.41 | 0/583 |
| 27 | 2 | 0.23 | 0/382 | 0.40 | 0/507 |
| 28 | 3 | 0.23 | 0/852 | 0.38 | 0/1136 |
| 29 | 4 | 0.21 | 0/329 | 0.40 | 0/435 |
| 30 | 5 | 0.23 | 0/3154 | 0.39 | 0/4295 |
| 31 | 6 | 0.23 | 0/2722 | 0.37 | 0/3709 |
| 32 | 7 | 0.23 | 0/2207 | 0.36 | 0/2978 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 33 | 8 | 0.23 | 0/855 | 0.36 | 0/1152 |
| 34 | 9 | 0.24 | 0/896 | 0.37 | 0/1205 |
| 35 | a | 0.22 | 0/709 | 0.37 | 0/963 |
| 36 | b | 0.23 | 0/1202 | 0.39 | 0/1626 |
| 37 | c | 0.24 | 0/2264 | 0.35 | 0/3059 |
| 38 | d | 0.22 | 0/1385 | 0.38 | 0/1877 |
| 39 | e | 0.23 | 0/1797 | 0.37 | 0/2422 |
| 40 | f | 0.23 | 0/1055 | 0.39 | 0/1427 |
| 41 | g | 0.24 | 0/1102 | 0.38 | 0/1503 |
| 42 | h | 0.23 | 0/847 | 0.35 | 0/1150 |
| 43 | i | 0.23 | 0/849 | 0.35 | 0/1135 |
| 44 | j | 0.23 | 0/698 | 0.33 | 0/940 |
| 45 | k | 0.22 | 0/665 | 0.38 | 0/897 |
| 46 | l | 0.20 | 0/226 | 0.29 | 0/299 |
| 47 | m | 0.22 | 0/379 | 0.40 | 0/510 |
| 48 | o | 0.22 | 0/818 | 0.35 | 0/1097 |
| 49 | p | 0.22 | 0/1071 | 0.37 | 0/1433 |
| 50 | q | 0.23 | 0/1107 | 0.33 | 0/1498 |
| 51 | r | 0.22 | 0/1238 | 0.36 | 0/1676 |
| 52 | s | 0.23 | 0/3114 | 0.38 | 0/4225 |
| 54 | u | 0.06 | 0/46 | 0.62 | 0/69 |
| 55 | z | 0.23 | 0/1584 | 0.37 | 0/2126 |
| 56 | AA | 0.15 | 0/21926 | 0.74 | 7/34121 (0.0%) |
| 57 | AB | 0.24 | 0/1811 | 0.37 | 0/2451 |
| 58 | AC | 0.23 | 0/1112 | 0.37 | 0/1505 |
| 59 | AD | 0.23 | 0/2607 | 0.38 | 0/3498 |
| 60 | AE | 0.23 | 0/989 | 0.39 | 0/1335 |
| 61 | AF | 0.23 | 0/1708 | 0.36 | 0/2291 |
| 62 | AG | 0.23 | 0/2570 | 0.37 | 0/3443 |
| 63 | AH | 0.22 | 0/1019 | 0.38 | 0/1379 |
| 64 | AI | 0.23 | 0/1031 | 0.40 | 0/1390 |
| 65 | AJ | 0.23 | 0/854 | 0.41 | 0/1148 |
| 66 | AK | 0.21 | 0/879 | 0.36 | 0/1182 |
| 67 | AL | 0.23 | 0/1406 | 0.34 | 0/1878 |
| 68 | AM | 0.23 | 0/941 | 0.37 | 0/1265 |
| 69 | AN | 0.23 | 0/864 | 0.40 | 0/1169 |
| 70 | AO | 0.23 | 0/1580 | 0.38 | 0/2150 |
| 71 | AP | 0.23 | 0/791 | 0.38 | 0/1062 |
| 72 | AQ | 0.22 | 0/747 | 0.37 | 0/995 |
| 73 | AR | 0.23 | 0/2050 | 0.36 | 0/2770 |
| 74 | AS | 0.23 | 0/1069 | 0.35 | 0/1441 |
| 75 | AT | 0.24 | 0/1361 | 0.38 | 0/1829 |
| 76 | AU | 0.23 | 0/1482 | 0.34 | 0/1987 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 77 | AV | 0.23 | 0/2758 | 0.34 | 0/3724 |
| 78 | AW | 0.23 | 0/778 | 0.40 | 0/1048 |
| 79 | AX | 0.23 | 0/2596 | 0.37 | 0/3519 |
| 80 | AY | 0.23 | 0/943 | 0.32 | 0/1274 |
| 81 | AZ | 0.23 | 0/757 | 0.36 | 0/1011 |
| 82 | A0 | 0.22 | 0/1727 | 0.38 | 0/2338 |
| 83 | A1 | 0.23 | 0/2121 | 0.37 | 0/2873 |
| 84 | A2 | 0.23 | 0/939 | 0.37 | 0/1256 |
| 85 | A3 | 0.22 | 0/621 | 0.35 | 0/820 |
| 86 | A4 | 0.23 | 0/2137 | 0.31 | 0/2872 |
| All | All | 0.20 | 0/167560 | 0.53 | 11/238082 (0.0%) |

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | A | 3206 | C | C2-N1-C1' | 6.09 | 125.50 | 118.80 |
| 1 | A | 1890 | C | N3-C2-O2 | -6.02 | 117.68 | 121.90 |
| 56 | AA | 984 | C | N3-C2-O2 | -5.93 | 117.75 | 121.90 |
| 56 | AA | 765 | C | C2-N1-C1' | 5.86 | 125.24 | 118.80 |
| 1 | A | 1786 | C | N1-C2-O2 | 5.79 | 122.37 | 118.90 |

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 | |
|---|---|---|---|---|---|---|---|
| 3 | D | 234/236 (99%) | 200 (86%) | 29 (12%) | 5 (2%) | 7 | 39 |
| 4 | E | 296/304 (97%) | 245 (83%) | 43 (14%) | 8 (3%) | 5 | 35 |
| 5 | F | 248/250 (99%) | 206 (83%) | 38 (15%) | 4 (2%) | 9 | 44 |
| 6 | H | 93/95 (98%) | 79 (85%) | 11 (12%) | 3 (3%) | 4 | 32 |
| 7 | I | 154/168 (92%) | 133 (86%) | 17 (11%) | 4 (3%) | 5 | 35 |
| 8 | J | 138/140 (99%) | 115 (83%) | 19 (14%) | 4 (3%) | 4 | 33 |
| 9 | K | 175/177 (99%) | 155 (89%) | 16 (9%) | 4 (2%) | 6 | 38 |
| 10 | L | 113/115 (98%) | 93 (82%) | 17 (15%) | 3 (3%) | 5 | 35 |
| 11 | M | 285/287 (99%) | 238 (84%) | 40 (14%) | 7 (2%) | 5 | 36 |
| 12 | N | 203/205 (99%) | 177 (87%) | 25 (12%) | 1 (0%) | 29 | 67 |
| 13 | O | 150/152 (99%) | 133 (89%) | 16 (11%) | 1 (1%) | 22 | 60 |
| 14 | P | 129/138 (94%) | 114 (88%) | 14 (11%) | 1 (1%) | 19 | 57 |
| 15 | Q | 217/219 (99%) | 180 (83%) | 31 (14%) | 6 (3%) | 5 | 34 |
| 16 | R | 138/140 (99%) | 124 (90%) | 11 (8%) | 3 (2%) | 6 | 38 |
| 17 | S | 154/156 (99%) | 134 (87%) | 17 (11%) | 3 (2%) | 8 | 41 |
| 18 | T | 164/166 (99%) | 145 (88%) | 16 (10%) | 3 (2%) | 8 | 42 |
| 19 | U | 109/111 (98%) | 90 (83%) | 17 (16%) | 2 (2%) | 8 | 42 |
| 20 | V | 183/202 (91%) | 151 (82%) | 24 (13%) | 8 (4%) | 2 | 25 |
| 21 | W | 113/115 (98%) | 97 (86%) | 13 (12%) | 3 (3%) | 5 | 35 |
| 22 | X | 241/243 (99%) | 207 (86%) | 27 (11%) | 7 (3%) | 4 | 33 |
| 23 | Y | 174/176 (99%) | 154 (88%) | 17 (10%) | 3 (2%) | 9 | 43 |
| 24 | Z | 118/120 (98%) | 106 (90%) | 10 (8%) | 2 (2%) | 9 | 43 |
| 25 | 0 | 106/108 (98%) | 91 (86%) | 13 (12%) | 2 (2%) | 8 | 41 |
| 26 | 1 | 50/52 (96%) | 41 (82%) | 8 (16%) | 1 (2%) | 7 | 40 |
| 27 | 2 | 44/46 (96%) | 42 (96%) | 2 (4%) | 0 | 100 | 100 |
| 28 | 3 | 93/95 (98%) | 85 (91%) | 7 (8%) | 1 (1%) | 14 | 51 |
| 29 | 4 | 34/36 (94%) | 29 (85%) | 5 (15%) | 0 | 100 | 100 |
| 30 | 5 | 368/392 (94%) | 308 (84%) | 49 (13%) | 11 (3%) | 4 | 33 |
| 31 | 6 | 313/354 (88%) | 266 (85%) | 39 (12%) | 8 (3%) | 5 | 35 |
| 32 | 7 | 258/287 (90%) | 227 (88%) | 26 (10%) | 5 (2%) | 8 | 41 |
| 33 | 8 | 97/99 (98%) | 88 (91%) | 7 (7%) | 2 (2%) | 7 | 39 |
| 34 | 9 | 105/123 (85%) | 89 (85%) | 10 (10%) | 6 (6%) | 1 | 21 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 35 | a | 78/108 (72%) | 75 (96%) | 3 (4%) | 0 | 100 | 100 |
| 36 | b | 146/148 (99%) | 126 (86%) | 18 (12%) | 2 (1%) | 11 | 46 |
| 37 | c | 271/286 (95%) | 240 (89%) | 25 (9%) | 6 (2%) | 6 | 38 |
| 38 | d | 156/171 (91%) | 127 (81%) | 26 (17%) | 3 (2%) | 8 | 41 |
| 39 | e | 211/237 (89%) | 177 (84%) | 30 (14%) | 4 (2%) | 8 | 41 |
| 40 | f | 125/146 (86%) | 106 (85%) | 19 (15%) | 0 | 100 | 100 |
| 41 | g | 127/129 (98%) | 109 (86%) | 12 (9%) | 6 (5%) | 2 | 24 |
| 42 | h | 96/103 (93%) | 78 (81%) | 16 (17%) | 2 (2%) | 7 | 39 |
| 43 | i | 95/97 (98%) | 84 (88%) | 9 (10%) | 2 (2%) | 7 | 39 |
| 44 | j | 83/85 (98%) | 77 (93%) | 4 (5%) | 2 (2%) | 6 | 37 |
| 45 | k | 82/84 (98%) | 62 (76%) | 15 (18%) | 5 (6%) | 1 | 20 |
| 46 | l | 21/23 (91%) | 20 (95%) | 1 (5%) | 0 | 100 | 100 |
| 47 | m | 43/45 (96%) | 33 (77%) | 8 (19%) | 2 (5%) | 2 | 24 |
| 48 | o | 92/94 (98%) | 80 (87%) | 9 (10%) | 3 (3%) | 4 | 31 |
| 49 | p | 119/156 (76%) | 109 (92%) | 8 (7%) | 2 (2%) | 9 | 43 |
| 50 | q | 126/128 (98%) | 120 (95%) | 4 (3%) | 2 (2%) | 9 | 44 |
| 51 | r | 140/162 (86%) | 119 (85%) | 17 (12%) | 4 (3%) | 4 | 33 |
| 52 | s | 366/390 (94%) | 318 (87%) | 42 (12%) | 6 (2%) | 9 | 44 |
| 55 | z | 202/204 (99%) | 176 (87%) | 23 (11%) | 3 (2%) | 10 | 45 |
| 57 | AB | 215/217 (99%) | 186 (86%) | 27 (13%) | 2 (1%) | 17 | 54 |
| 58 | AC | 130/132 (98%) | 101 (78%) | 27 (21%) | 2 (2%) | 10 | 45 |
| 59 | AD | 316/343 (92%) | 261 (83%) | 41 (13%) | 14 (4%) | 2 | 25 |
| 60 | AE | 120/122 (98%) | 96 (80%) | 22 (18%) | 2 (2%) | 9 | 43 |
| 61 | AF | 197/208 (95%) | 168 (85%) | 26 (13%) | 3 (2%) | 10 | 45 |
| 62 | AG | 301/326 (92%) | 248 (82%) | 43 (14%) | 10 (3%) | 4 | 31 |
| 63 | AH | 120/122 (98%) | 97 (81%) | 20 (17%) | 3 (2%) | 5 | 36 |
| 64 | AI | 134/136 (98%) | 102 (76%) | 28 (21%) | 4 (3%) | 4 | 33 |
| 65 | AJ | 106/108 (98%) | 88 (83%) | 15 (14%) | 3 (3%) | 5 | 34 |
| 66 | AK | 99/101 (98%) | 73 (74%) | 20 (20%) | 6 (6%) | 1 | 20 |
| 67 | AL | 162/164 (99%) | 146 (90%) | 15 (9%) | 1 (1%) | 25 | 63 |
| 68 | AM | 114/116 (98%) | 100 (88%) | 10 (9%) | 4 (4%) | 3 | 30 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 69 | AN | 105/107 (98%) | 89 (85%) | 13 (12%) | 3 (3%) | 4 | 33 |
| 70 | AO | 183/185 (99%) | 153 (84%) | 27 (15%) | 3 (2%) | 9 | 44 |
| 71 | AP | 94/96 (98%) | 77 (82%) | 16 (17%) | 1 (1%) | 14 | 51 |
| 72 | AQ | 84/86 (98%) | 72 (86%) | 10 (12%) | 2 (2%) | 6 | 37 |
| 73 | AR | 240/242 (99%) | 204 (85%) | 27 (11%) | 9 (4%) | 3 | 28 |
| 74 | AS | 124/126 (98%) | 105 (85%) | 17 (14%) | 2 (2%) | 9 | 44 |
| 75 | AT | 160/162 (99%) | 136 (85%) | 21 (13%) | 3 (2%) | 8 | 41 |
| 76 | AU | 171/173 (99%) | 154 (90%) | 12 (7%) | 5 (3%) | 4 | 33 |
| 77 | AV | 320/365 (88%) | 273 (85%) | 40 (12%) | 7 (2%) | 6 | 38 |
| 78 | AW | 95/97 (98%) | 76 (80%) | 16 (17%) | 3 (3%) | 4 | 32 |
| 79 | AX | 310/348 (89%) | 233 (75%) | 56 (18%) | 21 (7%) | 1 | 18 |
| 80 | AY | 106/108 (98%) | 92 (87%) | 10 (9%) | 4 (4%) | 3 | 28 |
| 81 | AZ | 85/87 (98%) | 75 (88%) | 9 (11%) | 1 (1%) | 13 | 49 |
| 82 | A0 | 197/208 (95%) | 162 (82%) | 30 (15%) | 5 (2%) | 5 | 36 |
| 83 | A1 | 252/272 (93%) | 197 (78%) | 48 (19%) | 7 (3%) | 5 | 34 |
| 84 | A2 | 114/116 (98%) | 95 (83%) | 16 (14%) | 3 (3%) | 5 | 35 |
| 85 | A3 | 67/69 (97%) | 61 (91%) | 5 (8%) | 1 (2%) | 10 | 45 |
| 86 | A4 | 237/474 (50%) | 215 (91%) | 20 (8%) | 2 (1%) | 19 | 57 |
| All | All | 12834/13719 (94%) | 10913 (85%) | 1610 (12%) | 311 (2%) | 9 | 37 |

5 of 311 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 11 | M | 134 | ARG |
| 20 | V | 101 | THR |
| 20 | V | 177 | THR |
| 30 | 5 | 381 | LEU |
| 30 | 5 | 383 | TYR |

### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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 | |
|---|---|---|---|---|---|---|
| 3 | D | 190/190 (100%) | 185 (97%) | 5 (3%) | 46 | 68 |
| 4 | E | 255/259 (98%) | 253 (99%) | 2 (1%) | 81 | 89 |
| 5 | F | 217/217 (100%) | 210 (97%) | 7 (3%) | 39 | 63 |
| 6 | H | 86/86 (100%) | 85 (99%) | 1 (1%) | 71 | 83 |
| 7 | I | 145/155 (94%) | 145 (100%) | 0 | 100 | 100 |
| 8 | J | 113/113 (100%) | 112 (99%) | 1 (1%) | 78 | 87 |
| 9 | K | 155/155 (100%) | 151 (97%) | 4 (3%) | 46 | 68 |
| 10 | L | 98/98 (100%) | 95 (97%) | 3 (3%) | 40 | 64 |
| 11 | M | 245/245 (100%) | 240 (98%) | 5 (2%) | 55 | 74 |
| 12 | N | 172/172 (100%) | 170 (99%) | 2 (1%) | 71 | 83 |
| 13 | O | 133/133 (100%) | 132 (99%) | 1 (1%) | 81 | 89 |
| 14 | P | 115/120 (96%) | 113 (98%) | 2 (2%) | 60 | 78 |
| 15 | Q | 201/201 (100%) | 200 (100%) | 1 (0%) | 88 | 93 |
| 16 | R | 118/118 (100%) | 118 (100%) | 0 | 100 | 100 |
| 17 | S | 141/141 (100%) | 139 (99%) | 2 (1%) | 67 | 81 |
| 18 | T | 146/146 (100%) | 145 (99%) | 1 (1%) | 84 | 90 |
| 19 | U | 99/99 (100%) | 97 (98%) | 2 (2%) | 55 | 74 |
| 20 | V | 169/180 (94%) | 164 (97%) | 5 (3%) | 41 | 64 |
| 21 | W | 93/93 (100%) | 91 (98%) | 2 (2%) | 52 | 71 |
| 22 | X | 219/219 (100%) | 212 (97%) | 7 (3%) | 39 | 63 |
| 23 | Y | 159/159 (100%) | 158 (99%) | 1 (1%) | 86 | 91 |
| 24 | Z | 111/111 (100%) | 109 (98%) | 2 (2%) | 59 | 77 |
| 25 | 0 | 97/97 (100%) | 95 (98%) | 2 (2%) | 53 | 73 |
| 26 | 1 | 49/49 (100%) | 47 (96%) | 2 (4%) | 30 | 58 |
| 27 | 2 | 40/40 (100%) | 40 (100%) | 0 | 100 | 100 |
| 28 | 3 | 88/88 (100%) | 87 (99%) | 1 (1%) | 73 | 84 |
| 29 | 4 | 35/35 (100%) | 35 (100%) | 0 | 100 | 100 |
| 30 | 5 | 337/353 (96%) | 333 (99%) | 4 (1%) | 71 | 83 |
| 31 | 6 | 266/313 (85%) | 262 (98%) | 4 (2%) | 65 | 80 |
| 32 | 7 | 242/263 (92%) | 237 (98%) | 5 (2%) | 53 | 73 |
| 33 | 8 | 91/91 (100%) | 90 (99%) | 1 (1%) | 73 | 84 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 34 | 9 | 91/104 (88%) | 91 (100%) | 0 | 100 | 100 |
| 35 | a | 78/104 (75%) | 75 (96%) | 3 (4%) | 33 | 59 |
| 36 | b | 130/130 (100%) | 127 (98%) | 3 (2%) | 50 | 71 |
| 37 | c | 241/250 (96%) | 241 (100%) | 0 | 100 | 100 |
| 38 | d | 151/159 (95%) | 149 (99%) | 2 (1%) | 69 | 82 |
| 39 | e | 188/207 (91%) | 183 (97%) | 5 (3%) | 44 | 67 |
| 40 | f | 117/130 (90%) | 116 (99%) | 1 (1%) | 78 | 87 |
| 41 | g | 119/119 (100%) | 118 (99%) | 1 (1%) | 81 | 89 |
| 42 | h | 95/97 (98%) | 95 (100%) | 0 | 100 | 100 |
| 43 | i | 86/86 (100%) | 82 (95%) | 4 (5%) | 26 | 55 |
| 44 | j | 68/68 (100%) | 68 (100%) | 0 | 100 | 100 |
| 45 | k | 74/74 (100%) | 73 (99%) | 1 (1%) | 67 | 81 |
| 46 | l | 23/23 (100%) | 23 (100%) | 0 | 100 | 100 |
| 47 | m | 40/40 (100%) | 39 (98%) | 1 (2%) | 47 | 69 |
| 48 | o | 80/80 (100%) | 79 (99%) | 1 (1%) | 69 | 82 |
| 49 | p | 117/140 (84%) | 115 (98%) | 2 (2%) | 60 | 78 |
| 50 | q | 110/110 (100%) | 107 (97%) | 3 (3%) | 44 | 67 |
| 51 | r | 133/147 (90%) | 131 (98%) | 2 (2%) | 65 | 80 |
| 52 | s | 326/344 (95%) | 323 (99%) | 3 (1%) | 78 | 87 |
| 55 | z | 179/179 (100%) | 176 (98%) | 3 (2%) | 60 | 78 |
| 57 | AB | 191/191 (100%) | 190 (100%) | 1 (0%) | 88 | 93 |
| 58 | AC | 115/115 (100%) | 113 (98%) | 2 (2%) | 60 | 78 |
| 59 | AD | 269/286 (94%) | 263 (98%) | 6 (2%) | 52 | 71 |
| 60 | AE | 104/104 (100%) | 102 (98%) | 2 (2%) | 57 | 75 |
| 61 | AF | 178/185 (96%) | 176 (99%) | 2 (1%) | 73 | 84 |
| 62 | AG | 265/284 (93%) | 256 (97%) | 9 (3%) | 37 | 62 |
| 63 | AH | 112/112 (100%) | 108 (96%) | 4 (4%) | 35 | 61 |
| 64 | AI | 104/104 (100%) | 103 (99%) | 1 (1%) | 76 | 86 |
| 65 | AJ | 93/93 (100%) | 91 (98%) | 2 (2%) | 52 | 71 |
| 66 | AK | 91/91 (100%) | 89 (98%) | 2 (2%) | 52 | 71 |
| 67 | AL | 152/152 (100%) | 151 (99%) | 1 (1%) | 84 | 90 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 68 | AM | 95/95 (100%) | 95 (100%) | 0 | 100 | 100 |
| 69 | AN | 93/93 (100%) | 89 (96%) | 4 (4%) | 29 | 57 |
| 70 | AO | 166/166 (100%) | 158 (95%) | 8 (5%) | 25 | 54 |
| 71 | AP | 87/87 (100%) | 86 (99%) | 1 (1%) | 73 | 84 |
| 72 | AQ | 78/78 (100%) | 77 (99%) | 1 (1%) | 69 | 82 |
| 73 | AR | 224/224 (100%) | 219 (98%) | 5 (2%) | 52 | 71 |
| 74 | AS | 109/109 (100%) | 108 (99%) | 1 (1%) | 78 | 87 |
| 75 | AT | 150/150 (100%) | 149 (99%) | 1 (1%) | 84 | 90 |
| 76 | AU | 149/149 (100%) | 146 (98%) | 3 (2%) | 55 | 74 |
| 77 | AV | 295/327 (90%) | 292 (99%) | 3 (1%) | 76 | 86 |
| 78 | AW | 84/84 (100%) | 84 (100%) | 0 | 100 | 100 |
| 79 | AX | 275/308 (89%) | 272 (99%) | 3 (1%) | 73 | 84 |
| 80 | AY | 99/99 (100%) | 98 (99%) | 1 (1%) | 76 | 86 |
| 81 | AZ | 80/80 (100%) | 76 (95%) | 4 (5%) | 24 | 53 |
| 82 | A0 | 176/182 (97%) | 173 (98%) | 3 (2%) | 60 | 78 |
| 83 | A1 | 237/250 (95%) | 233 (98%) | 4 (2%) | 60 | 78 |
| 84 | A2 | 99/99 (100%) | 96 (97%) | 3 (3%) | 41 | 64 |
| 85 | A3 | 63/64 (98%) | 63 (100%) | 0 | 100 | 100 |
| 86 | A4 | 226/291 (78%) | 222 (98%) | 4 (2%) | 59 | 77 |
| All | All | 11530/11982 (96%) | 11339 (98%) | 191 (2%) | 62 | 78 |

5 of 191 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 59 | AD | 234 | LYS |
| 69 | AN | 73 | ARG |
| 60 | AE | 15 | ARG |
| 62 | AG | 312 | GLN |
| 70 | AO | 143 | CYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 57 | AB | 226 | ASN |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 72 | AQ | 53 | GLN |
| 59 | AD | 341 | ASN |
| 61 | AF | 147 | GLN |
| 74 | AS | 91 | ASN |

### 5.3.3 RNA (i)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 1 | A | 1460/1472 (99%) | 373 (25%) | 46 (3%) |
| 2 | B | 52/56 (92%) | 12 (23%) | 2 (3%) |
| 54 | u | 1/2 (50%) | 0 | 0 |
| 56 | AA | 914/923 (99%) | 301 (32%) | 22 (2%) |
| All | All | 2427/2453 (98%) | 686 (28%) | 70 (2%) |

5 of 686 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | A | 1672 | C |
| 1 | A | 1674 | A |
| 1 | A | 1679 | U |
| 1 | A | 1680 | A |
| 1 | A | 1685 | C |

5 of 70 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 56 | AA | 1021 | U |
| 56 | AA | 1099 | C |
| 56 | AA | 1429 | C |
| 1 | A | 2442 | U |
| 1 | A | 2387 | U |

## 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 monosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 134 ligands modelled in this entry, 134 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|---|---|---|
| 1 | A | 14 |
| 86 | A4 | 13 |
| 56 | AA | 8 |
| 2 | B | 4 |

The worst 5 of 39 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|---|---|---|---|---|---|---|
| 1 | A | 2218:C | O3' | 2228:A | P | 35.95 |
| 1 | AA | 955:A | O3' | 965:C | P | 34.65 |
| 1 | A | 2760:A | O3' | 2792:A | P | 26.71 |
| 1 | A | 2881:C | O3' | 2889:C | P | 26.07 |
| 1 | A | 1760:G | O3' | 1766:U | P | 25.62 |

# 6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-0514. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

## 6.1 Orthogonal projections (i)

This section was not generated.

## 6.2 Central slices (i)

This section was not generated.

## 6.3 Largest variance slices (i)

This section was not generated.

## 6.4 Orthogonal surface views (i)

This section was not generated.

## 6.5 Mask visualisation (i)

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

# 7 Map analysis (i)

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

## 7.1 Map-value distribution (i)

This section was not generated.

## 7.2 Volume estimate versus contour level (i)

This section was not generated.

## 7.3 Rotationally averaged power spectrum (i)

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

# 8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

# 9 Map-model fit (i)

This section was not generated.