# wwPDB EM Validation Summary Report ⓘ

May 20, 2024 – 01:08 AM JST

| | | |
|---|---|---|
| PDB ID | : | 7CPU |
| EMDB ID | : | EMD-30432 |
| Title | : | Cryo-EM structure of 80S ribosome from mouse kidney |
| Authors | : | Huo, Y.G.; He, X.; Jiang, T.; Qin, Y.; Guo, X.J.; Sha, J.H. |
| Deposited on | : | 2020-08-08 |
| Resolution | : | 2.82 Å(reported) |
| Based on initial model | : | 6EK0 |

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

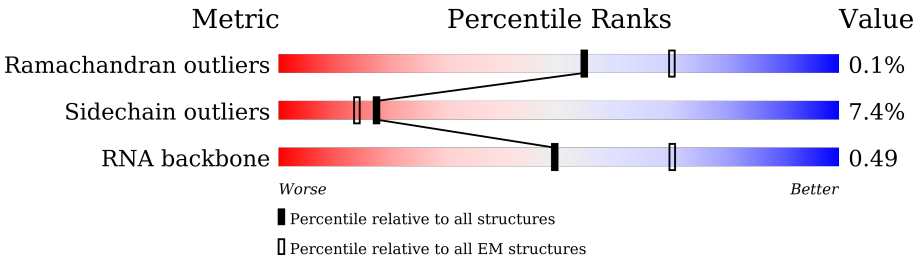
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev92 |
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| MapQ | : | 1.9.13 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.36.2 |

# 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 2.82 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% 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 | LA | 257 | 93% |
| 2 | SA | 295 | 7% 65% 5% 30% |
| 3 | LB | 403 | 95% |
| 4 | SB | 264 | 5% 77% 19% |
| 5 | LC | 419 | 80% 6% 14% |
| 6 | LD | 297 | 94% 5% |
| 7 | LE | 296 | 7% 73% 5% 22% |
| 8 | LF | 270 | 77% 21% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 9 | LG | 266 | 5% 80% 6% 14% |
| 10 | LH | 192 | 92% 7% |
| 11 | LI | 214 | 90% 6% |
| 12 | LJ | 178 | 89% 7% |
| 13 | LL | 211 | 90% 8% |
| 14 | LM | 217 | 60% 37% |
| 15 | LN | 204 | 97% |
| 16 | LO | 203 | 94% 5% |
| 17 | LP | 184 | 78% 6% 16% |
| 18 | LQ | 188 | 97% |
| 19 | LR | 196 | 84% 5% 11% |
| 20 | LS | 176 | 93% 6% |
| 21 | LT | 160 | 95% 5% |
| 22 | LU | 128 | 73% 5% 22% |
| 23 | LV | 140 | 89% 7% |
| 24 | LW | 157 | 39% 61% |
| 25 | LX | 156 | 72% 24% |
| 26 | LY | 145 | 84% 7% 9% |
| 27 | LZ | 136 | 95% |
| 28 | La | 148 | 94% 5% |
| 29 | Lb | 160 | 57% 5% 38% |
| 30 | Lc | 115 | 78% 18% |
| 31 | Ld | 125 | 5% 84% 14% |
| 32 | Le | 135 | 93% 5% |
| 33 | Lf | 110 | 94% 5% |

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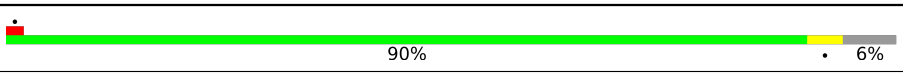
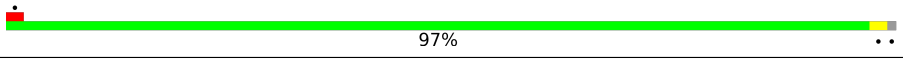
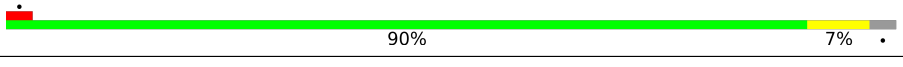
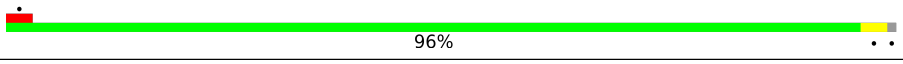
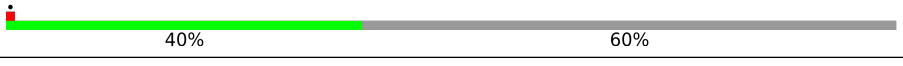
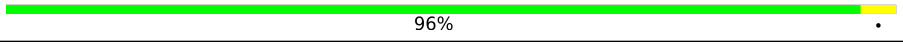
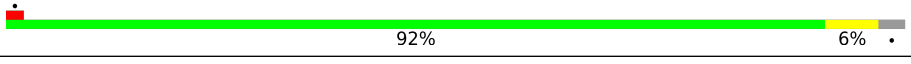
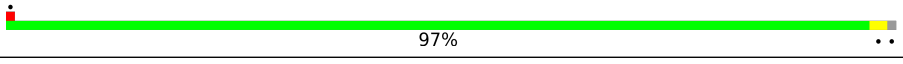
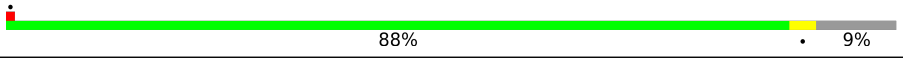
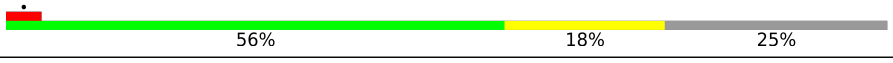
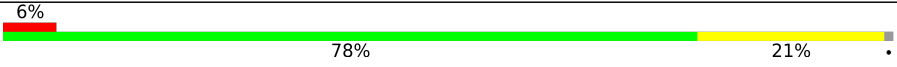
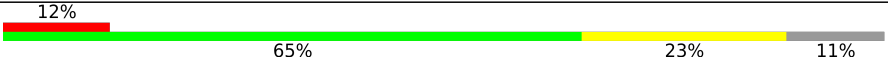
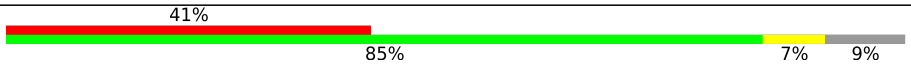
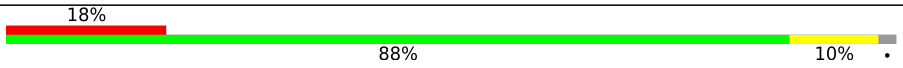
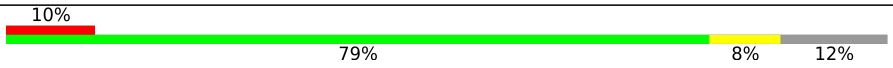
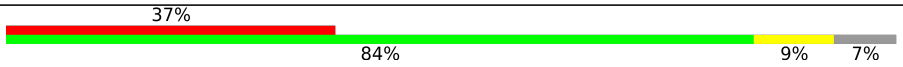
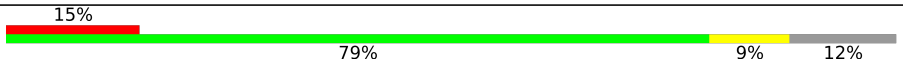
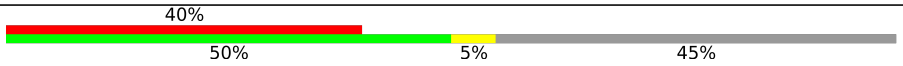
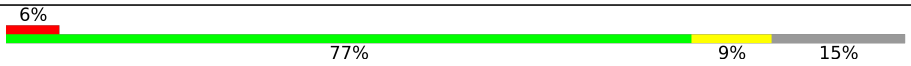
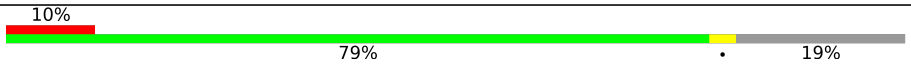
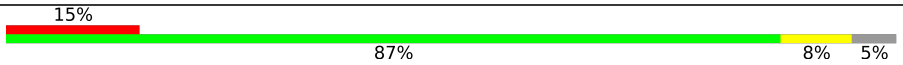
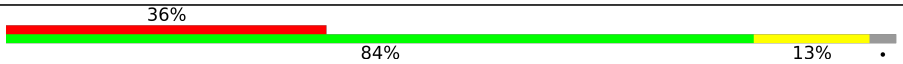
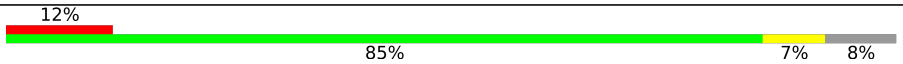
| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 34 | Lg | 117 |   |
| 35 | Lh | 123 |   |
| 36 | Li | 105 |   |
| 37 | Lj | 97 |   |
| 38 | Lk | 70 |   |
| 39 | Lm | 128 |   |
| 40 | Ln | 25 |   |
| 41 | Lo | 106 |   |
| 42 | Lp | 92 |   |
| 43 | Lr | 137 |   |
| 44 | L5 | 4731 |   |
| 45 | L7 | 120 |   |
| 46 | L8 | 158 |   |
| 47 | S2 | 1870 |   |
| 48 | SD | 243 |   |
| 49 | SE | 263 |   |
| 50 | SF | 204 |   |
| 51 | SH | 194 |   |
| 52 | SI | 208 |   |
| 53 | SK | 165 |   |
| 54 | SL | 158 |   |
| 55 | SP | 145 |   |
| 56 | SQ | 146 |   |
| 57 | SR | 135 |   |
| 58 | SS | 152 |   |

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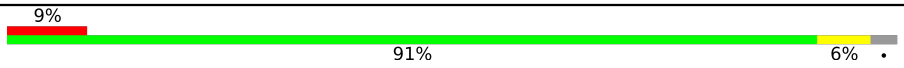
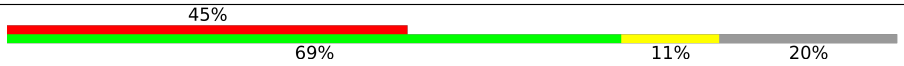
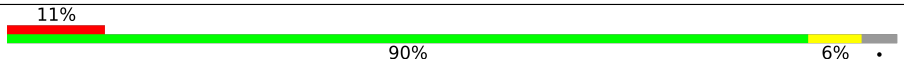
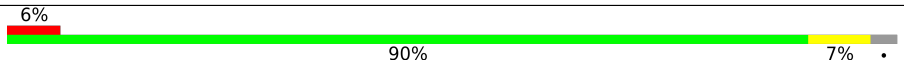
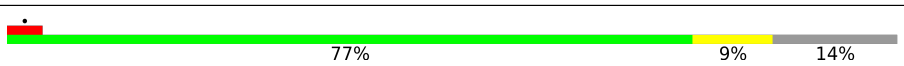
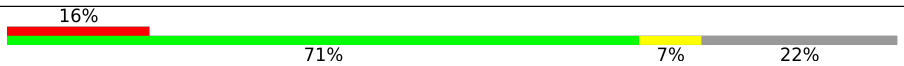
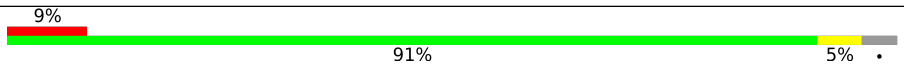
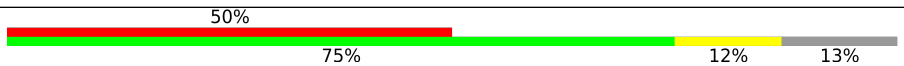
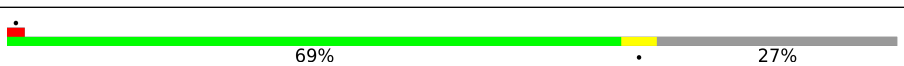
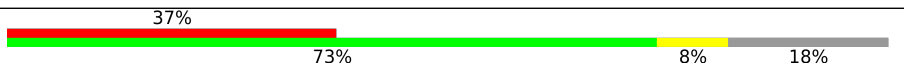
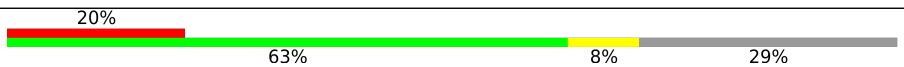
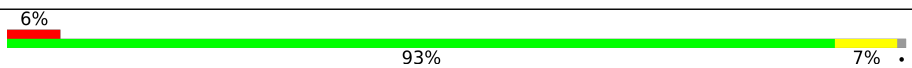
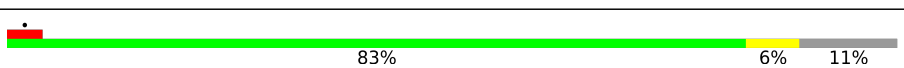
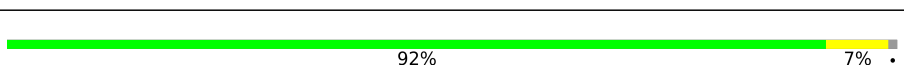
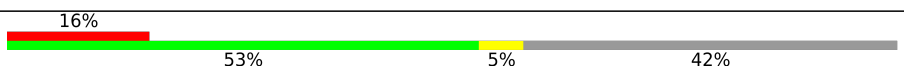
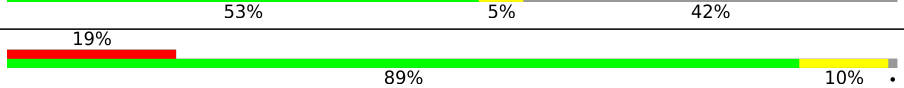
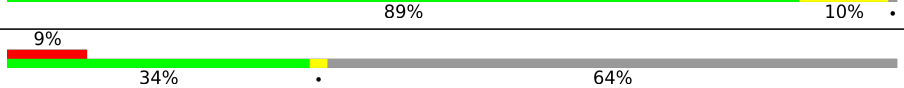
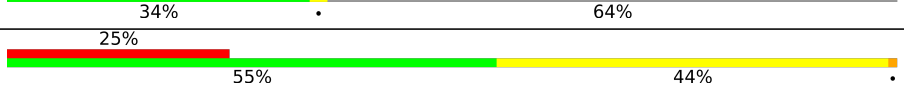
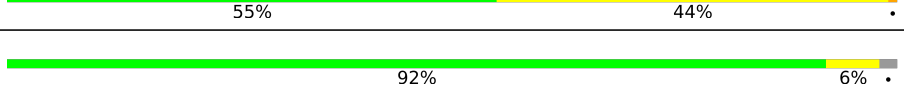
| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 59 | ST | 145 |   |
| 60 | SU | 119 |   |
| 61 | SV | 83 |   |
| 62 | SX | 143 |   |
| 63 | Sa | 115 |   |
| 64 | Sc | 69 |   |
| 65 | Sd | 56 |   |
| 66 | Sg | 317 |   |
| 67 | SC | 293 |   |
| 68 | SG | 249 |   |
| 69 | SJ | 194 |   |
| 70 | SN | 151 |   |
| 71 | SO | 151 |   |
| 72 | SW | 130 |   |
| 73 | SY | 133 |   |
| 74 | SZ | 125 |   |
| 75 | Sb | 84 |   |
| 76 | Se | 133 |   |
| 77 | S6 | 75 |   |
| 78 | Ll | 51 |   |

# 2 Entry composition (i)

There are 81 unique types of molecules in this entry. The entry contains 206288 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 1 | LA | 248 | 1898 | 1189 | 389 | 314 | 6 | 0 | 0 |

- Molecule 2 is a protein called 40S ribosomal protein SA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 2 | SA | 207 | 1636 | 1042 | 288 | 298 | 8 | 0 | 0 |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 3 | LB | 397 | 3202 | 2039 | 603 | 546 | 14 | 0 | 0 |

- Molecule 4 is a protein called 40S ribosomal protein S3a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 4 | SB | 213 | 1729 | 1098 | 309 | 308 | 14 | 0 | 0 |

- Molecule 5 is a protein called 60S ribosomal protein L4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 5 | LC | 362 | 2891 | 1819 | 577 | 480 | 15 | 0 | 0 |

- Molecule 6 is a protein called 60S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 6 | LD | 293 | 2385 | 1506 | 440 | 425 | 14 | 0 | 0 |

- Molecule 7 is a protein called 60S ribosomal protein L6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 7 | LE | 231 | Total | C | N | O | S | 0 | 0 |
| | | | 1874 | 1195 | 358 | 317 | 4 | | |

- Molecule 8 is a protein called 60S ribosomal protein L7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 8 | LF | 214 | Total | C | N | O | S | 0 | 0 |
| | | | 1771 | 1139 | 337 | 287 | 8 | | |

- Molecule 9 is a protein called 60S ribosomal protein L7a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 9 | LG | 229 | Total | C | N | O | S | 0 | 0 |
| | | | 1848 | 1179 | 354 | 311 | 4 | | |

- Molecule 10 is a protein called 60S ribosomal protein L9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 10 | LH | 190 | Total | C | N | O | S | 0 | 0 |
| | | | 1519 | 956 | 284 | 273 | 6 | | |

- Molecule 11 is a protein called 60S ribosomal protein L10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 11 | LI | 201 | Total | C | N | O | S | 0 | 0 |
| | | | 1633 | 1037 | 316 | 268 | 12 | | |

- Molecule 12 is a protein called 60S ribosomal protein L11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 12 | LJ | 171 | Total | C | N | O | S | 0 | 0 |
| | | | 1371 | 866 | 255 | 244 | 6 | | |

- Molecule 13 is a protein called 60S ribosomal protein L13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 13 | LL | 206 | Total | C | N | O | S | 0 | 0 |
| | | | 1667 | 1043 | 343 | 277 | 4 | | |

- Molecule 14 is a protein called 60S ribosomal protein L14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 14 | LM | 136 | Total | C | N | O | S | 0 | 0 |
| | | | 1125 | 721 | 218 | 179 | 7 | | |

- Molecule 15 is a protein called 60S ribosomal protein L15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 15 | LN | 203 | Total | C | N | O | S | 0 | 0 |
| | | | 1701 | 1072 | 359 | 266 | 4 | | |

- Molecule 16 is a protein called 60S ribosomal protein L13a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 16 | LO | 201 | Total | C | N | O | S | 0 | 0 |
| | | | 1640 | 1055 | 320 | 259 | 6 | | |

- Molecule 17 is a protein called 60S ribosomal protein L17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 17 | LP | 154 | Total | C | N | O | S | 0 | 0 |
| | | | 1251 | 782 | 243 | 217 | 9 | | |

- Molecule 18 is a protein called 60S ribosomal protein L18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 18 | LQ | 187 | Total | C | N | O | S | 0 | 0 |
| | | | 1515 | 948 | 314 | 249 | 4 | | |

- Molecule 19 is a protein called 60S ribosomal protein L19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 19 | LR | 174 | Total | C | N | O | S | 0 | 0 |
| | | | 1457 | 901 | 316 | 231 | 9 | | |

- Molecule 20 is a protein called 60S ribosomal protein L18a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 20 | LS | 175 | Total | C | N | O | S | 0 | 0 |
| | | | 1451 | 924 | 283 | 234 | 10 | | |

- Molecule 21 is a protein called 60S ribosomal protein L21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 21 | LT | 160 | Total | C | N | O | S | 0 | 0 |
| | | | 1307 | 829 | 253 | 218 | 7 | | |

- Molecule 22 is a protein called 60S ribosomal protein L22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 22 | LU | 100 | Total | C | N | O | S | 0 | 0 |
| | | | 817 | 523 | 143 | 149 | 2 | | |

- Molecule 23 is a protein called 60S ribosomal protein L23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 23 | LV | 130 | Total | C | N | O | S | 0 | 0 |
| | | | 973 | 615 | 183 | 170 | 5 | | |

- Molecule 24 is a protein called 60S ribosomal protein L24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 24 | LW | 62 | Total | C | N | O | S | 0 | 0 |
| | | | 519 | 332 | 101 | 83 | 3 | | |

- Molecule 25 is a protein called 60S ribosomal protein L23a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 25 | LX | 118 | Total | C | N | O | S | 0 | 0 |
| | | | 967 | 618 | 181 | 167 | 1 | | |

- Molecule 26 is a protein called 60S ribosomal protein L26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 26 | LY | 132 | Total | C | N | O | S | 0 | 0 |
| | | | 1102 | 692 | 223 | 184 | 3 | | |

- Molecule 27 is a protein called 60S ribosomal protein L27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 27 | LZ | 135 | Total | C | N | O | S | 0 | 0 |
| | | | 1107 | 714 | 208 | 182 | 3 | | |

- Molecule 28 is a protein called 60S ribosomal protein L27a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 28 | La | 147 | Total | C | N | O | S | 0 | 0 |
| | | | 1164 | 736 | 239 | 185 | 4 | | |

- Molecule 29 is a protein called 60S ribosomal protein L29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 29 | Lb | 99 | Total | C | N | O | S | 0 | 0 |
| | | | 807 | 505 | 174 | 124 | 4 | | |

- Molecule 30 is a protein called 60S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 30 | Lc | 94 | Total | C | N | O | S | 0 | 0 |
| | | | 732 | 465 | 130 | 131 | 6 | | |

- Molecule 31 is a protein called 60S ribosomal protein L31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 31 | Ld | 108 | Total | C | N | O | S | 0 | 0 |
| | | | 896 | 566 | 172 | 156 | 2 | | |

- Molecule 32 is a protein called 60S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 32 | Le | 128 | Total | C | N | O | S | 0 | 0 |
| | | | 1053 | 667 | 216 | 165 | 5 | | |

- Molecule 33 is a protein called 60S ribosomal protein L35a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 33 | Lf | 109 | Total | C | N | O | S | 0 | 0 |
| | | | 876 | 555 | 174 | 143 | 4 | | |

- Molecule 34 is a protein called 60S ribosomal protein L34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 34 | Lg | 110 | Total | C | N | O | S | 0 | 0 |
| | | | 873 | 546 | 180 | 141 | 6 | | |

- Molecule 35 is a protein called 60S ribosomal protein L35.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 35 | Lh | 122 | Total | C | N | O | S | 0 | 0 |
| | | | 1015 | 643 | 204 | 167 | 1 | | |

- Molecule 36 is a protein called 60S ribosomal protein L36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 36 | Li | 102 | Total | C | N | O | S | 0 | 0 |
| | | | 832 | 521 | 177 | 129 | 5 | | |

- Molecule 37 is a protein called 60S ribosomal protein L37.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 37 | Lj | 86 | Total | C | N | O | S | 0 | 0 |
| | | | 705 | 434 | 155 | 111 | 5 | | |

- Molecule 38 is a protein called 60S ribosomal protein L38.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 38 | Lk | 69 | Total | C | N | O | S | 0 | 0 |
| | | | 568 | 365 | 103 | 99 | 1 | | |

- Molecule 39 is a protein called Ubiquitin-60S ribosomal protein L40.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 39 | Lm | 51 | Total | C | N | O | S | 0 | 0 |
| | | | 419 | 260 | 88 | 65 | 6 | | |

- Molecule 40 is a protein called 60S ribosomal protein L41.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 40 | Ln | 25 | Total | C | N | O | S | 0 | 0 |
| | | | 239 | 145 | 64 | 27 | 3 | | |

- Molecule 41 is a protein called 60S ribosomal protein L36a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 41 | Lo | 103 | Total | C | N | O | S | 0 | 0 |
| | | | 842 | 528 | 172 | 136 | 6 | | |

- Molecule 42 is a protein called 60S ribosomal protein L37a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 42 | Lp | 91 | Total | C | N | O | S | 0 | 0 |
| | | | 708 | 445 | 136 | 120 | 7 | | |

- Molecule 43 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 43 | Lr | 124 | Total | C | N | O | S | 0 | 0 |
| | | | 994 | 616 | 206 | 167 | 5 | | |

- Molecule 44 is a RNA chain called Mus musculus 28S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 44 | L5 | 3539 | Total | C | N | O | P | 0 | 0 |
| | | | 75867 | 33789 | 13863 | 24677 | 3538 | | |

- Molecule 45 is a RNA chain called Mus musculus 5S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 45 | L7 | 120 | Total | C | N | O | P | 0 | 0 |
| | | | 2558 | 1141 | 456 | 842 | 119 | | |

- Molecule 46 is a RNA chain called Mus musculus 5.8S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 46 | L8 | 156 | Total | C | N | O | P | 0 | 0 |
| | | | 3314 | 1480 | 585 | 1094 | 155 | | |

- Molecule 47 is a RNA chain called Mus musculus 18S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 47 | S2 | 1656 | Total | C | N | O | P | 0 | 0 |
| | | | 35228 | 15723 | 6313 | 11537 | 1655 | | |

- Molecule 48 is a protein called 40S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 48 | SD | 222 | Total | C | N | O | S | 0 | 0 |
| | | | 1726 | 1100 | 310 | 309 | 7 | | |

- Molecule 49 is a protein called 40S ribosomal protein S4, X isoform.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 49 | SE | 258 | Total | C | N | O | S | 0 | 0 |
| | | | 2050 | 1311 | 381 | 350 | 8 | | |

- Molecule 50 is a protein called 40S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 50 | SF | 179 | Total | C | N | O | S | 0 | 0 |
| | | | 1416 | 888 | 262 | 259 | 7 | | |

- Molecule 51 is a protein called 40S ribosomal protein S7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 51 | SH | 180 | Total | C | N | O | S | 0 | 0 |
| | | | 1449 | 924 | 266 | 258 | 1 | | |

- Molecule 52 is a protein called 40S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 52 | SI | 183 | Total | C | N | O | S | 0 | 0 |
| | | | 1499 | 943 | 293 | 258 | 5 | | |

- Molecule 53 is a protein called 40S ribosomal protein S10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 53 | SK | 90 | Total | C | N | O | S | 0 | 0 |
| | | | 760 | 495 | 135 | 124 | 6 | | |

- Molecule 54 is a protein called 40S ribosomal protein S11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 54 | SL | 135 | Total | C | N | O | S | 0 | 0 |
| | | | 1110 | 708 | 207 | 189 | 6 | | |

- Molecule 55 is a protein called 40S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 55 | SP | 118 | Total | C | N | O | S | 0 | 0 |
| | | | 981 | 625 | 183 | 166 | 7 | | |

- Molecule 56 is a protein called 40S ribosomal protein S16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 56 | SQ | 139 | Total | C | N | O | S | 0 | 0 |
| | | | 1109 | 704 | 210 | 192 | 3 | | |

- Molecule 57 is a protein called 40S ribosomal protein S17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 57 | SR | 131 | Total | C | N | O | S | 0 | 0 |
| | | | 1064 | 668 | 198 | 194 | 4 | | |

- Molecule 58 is a protein called 40S ribosomal protein S18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 58 | SS | 140 | Total | C | N | O | S | 0 | 0 |
| | | | 1157 | 728 | 231 | 197 | 1 | | |

- Molecule 59 is a protein called 40S ribosomal protein S19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 59 | ST | 140 | Total | C | N | O | S | 0 | 0 |
| | | | 1090 | 681 | 212 | 195 | 2 | | |

- Molecule 60 is a protein called 40S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 60 | SU | 95 | Total | C | N | O | S | 0 | 0 |
| | | | 753 | 471 | 142 | 136 | 4 | | |

- Molecule 61 is a protein called 40S ribosomal protein S21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 61 | SV | 80 | Total | C | N | O | S | 0 | 0 |
| | | | 610 | 373 | 114 | 118 | 5 | | |

- Molecule 62 is a protein called 40S ribosomal protein S23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 62 | SX | 139 | Total | C | N | O | S | 0 | 0 |
| | | | 1080 | 682 | 214 | 181 | 3 | | |

- Molecule 63 is a protein called 40S ribosomal protein S26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 63 | Sa | 99 | Total | C | N | O | S | 1 | 0 |
| | | | 800 | 497 | 168 | 130 | 5 | | |

- Molecule 64 is a protein called 40S ribosomal protein S28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 64 | Sc | 54 | Total | C | N | O | S | 0 | 0 |
| | | | 416 | 257 | 80 | 77 | 2 | | |

- Molecule 65 is a protein called 40S ribosomal protein S29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 65 | Sd | 54 | Total | C | N | O | S | 0 | 0 |
| | | | 455 | 284 | 93 | 73 | 5 | | |

- Molecule 66 is a protein called Receptor of activated protein C kinase 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 66 | Sg | 276 | Total | C | N | O | S | 0 | 0 |
| | | | 2148 | 1357 | 378 | 401 | 12 | | |

- Molecule 67 is a protein called 40S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 67 | SC | 215 | Total | C | N | O | S | 1 | 0 |
| | | | 1673 | 1085 | 288 | 291 | 9 | | |

- Molecule 68 is a protein called 40S ribosomal protein S6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 68 | SG | 204 | Total | C | N | O | S | 0 | 0 |
| | | | 1645 | 1029 | 330 | 280 | 6 | | |

- Molecule 69 is a protein called 40S ribosomal protein S9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 69 | SJ | 138 | Total | C | N | O | S | 0 | 0 |
| | | | 1162 | 743 | 230 | 187 | 2 | | |

- Molecule 70 is a protein called 40S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 70 | SN | 150 | Total | C | N | O | S | 0 | 0 |
| | | | 1208 | 773 | 229 | 205 | 1 | | |

- Molecule 71 is a protein called 40S ribosomal protein S14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 71 | SO | 134 | Total | C | N | O | S | 0 | 0 |
| | | | 1002 | 612 | 197 | 187 | 6 | | |

- Molecule 72 is a protein called 40S ribosomal protein S15a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 72 | SW | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1034 | 659 | 193 | 176 | 6 | | |

- Molecule 73 is a protein called 40S ribosomal protein S24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 73 | SY | 110 | Total | C | N | O | S | 0 | 0 |
| | | | 891 | 565 | 173 | 149 | 4 | | |

- Molecule 74 is a protein called 40S ribosomal protein S25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 74 | SZ | 72 | Total | C | N | O | S | 0 | 0 |
| | | | 574 | 368 | 104 | 101 | 1 | | |

- Molecule 75 is a protein called 40S ribosomal protein S27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 75 | Sb | 83 | Total | C | N | O | S | 0 | 0 |
| | | | 651 | 408 | 121 | 115 | 7 | | |

- Molecule 76 is a protein called 40S ribosomal protein S30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 76 | Se | 48 | Total | C | N | O | S | 0 | 0 |
| | | | 384 | 234 | 86 | 63 | 1 | | |

- Molecule 77 is a RNA chain called tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 77 | S6 | 75 | Total | C | N | O | P | 0 | 0 |
| | | | 1604 | 717 | 298 | 515 | 74 | | |

- Molecule 78 is a protein called Ribosomal protein L39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 78 | Ll | 50 | Total | C | N | O | S | 0 | 0 |
| | | | 444 | 281 | 98 | 64 | 1 | | |

- Molecule 79 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 79 | LN | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 79 | LP | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 79 | LT | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 79 | LV | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 79 | Le | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 79 | Lf | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 79 | L5 | 173 | Total | Mg | 0 |
| | | | 173 | 173 | |
| 79 | L7 | 3 | Total | Mg | 0 |
| | | | 3 | 3 | |
| 79 | L8 | 5 | Total | Mg | 0 |
| | | | 5 | 5 | |
| 79 | S2 | 82 | Total | Mg | 0 |
| | | | 82 | 82 | |
| 79 | SF | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 79 | Sd | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |

- Molecule 80 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| 80 | Lg | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |

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| Mol | Chain | Residues | Atoms | AltConf |
|---|---|---|---|---|
| 80 | Lj | 1 | Total Zn<br>1 1 | 0 |
| 80 | Lm | 1 | Total Zn<br>1 1 | 0 |
| 80 | Lo | 1 | Total Zn<br>1 1 | 0 |
| 80 | Lp | 1 | Total Zn<br>1 1 | 0 |
| 80 | Sa | 1 | Total Zn<br>1 1 | 0 |
| 80 | Sd | 1 | Total Zn<br>1 1 | 0 |

- Molecule 81 is water.

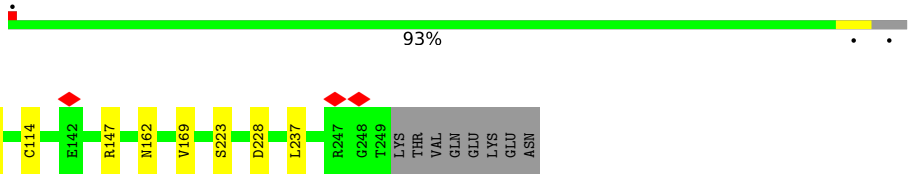
| Mol | Chain | Residues | Atoms | AltConf |
|---|---|---|---|---|
| 81 | LB | 1 | Total O<br>1 1 | 0 |
| 81 | LH | 1 | Total O<br>1 1 | 0 |
| 81 | LI | 2 | Total O<br>2 2 | 0 |
| 81 | La | 2 | Total O<br>2 2 | 0 |
| 81 | L5 | 9 | Total O<br>9 9 | 0 |
| 81 | S2 | 3 | Total O<br>3 3 | 0 |
| 81 | SV | 1 | Total O<br>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 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.

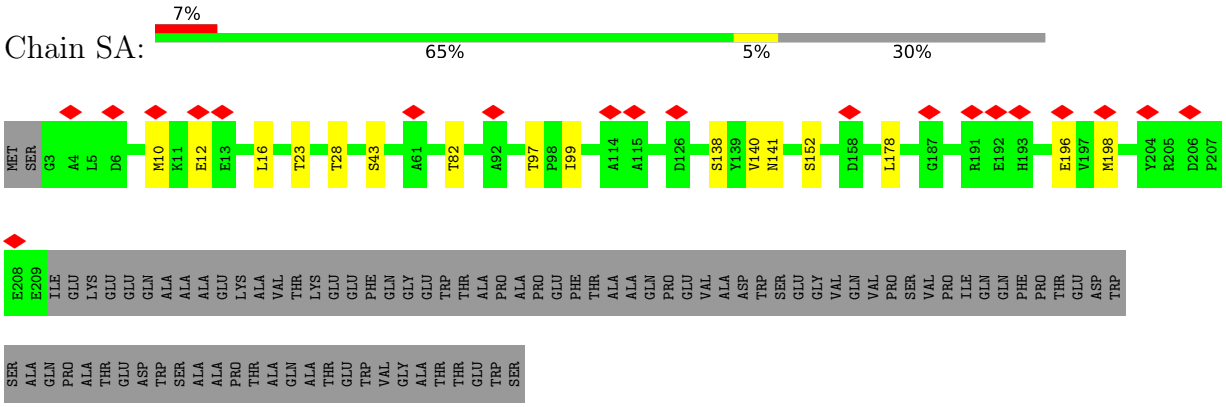
• Molecule 1: 60S ribosomal protein L8

Chain LA:



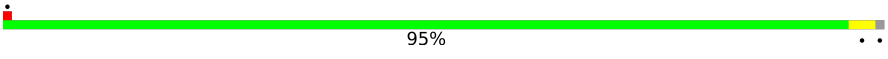

• Molecule 2: 40S ribosomal protein SA

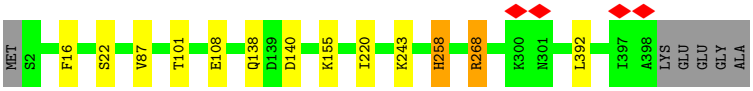
Chain SA:




• Molecule 3: 60S ribosomal protein L3

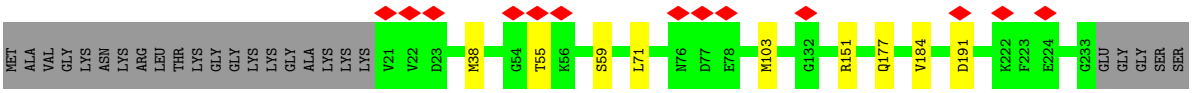
Chain LB:



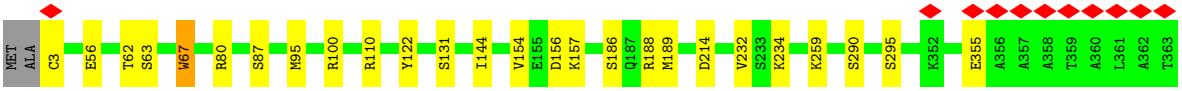

• Molecule 4: 40S ribosomal protein S3a

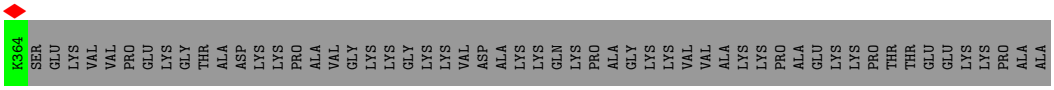
Chain SB:


• Molecule 5: 60S ribosomal protein L4

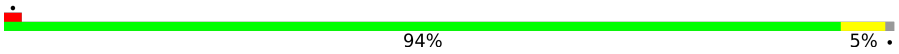
Chain LC:

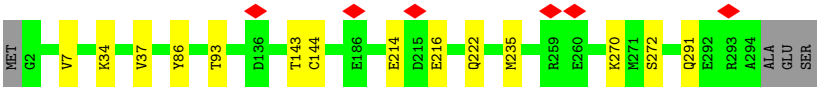




• Molecule 6: 60S ribosomal protein L5

Chain LD:

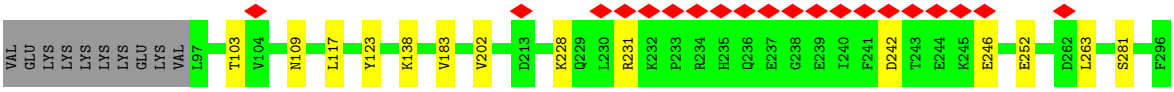



• Molecule 7: 60S ribosomal protein L6

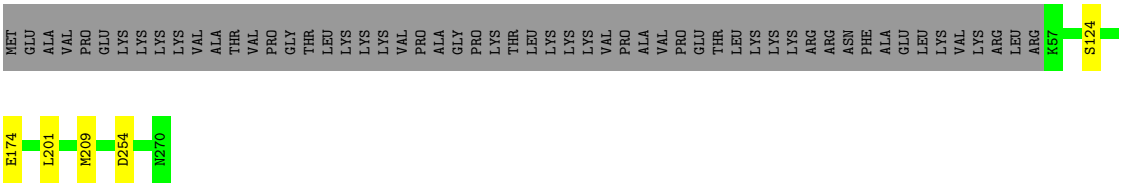
Chain LE:





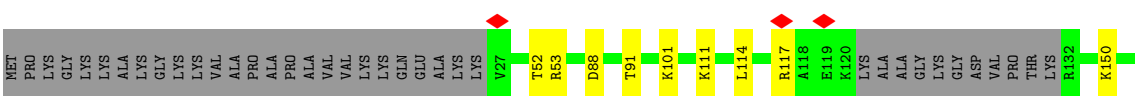

• Molecule 8: 60S ribosomal protein L7

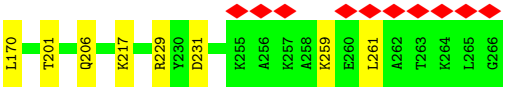
Chain LF:


• Molecule 9: 60S ribosomal protein L7a

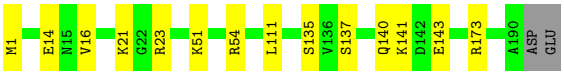
Chain LG:




• Molecule 10: 60S ribosomal protein L9

Chain LH:

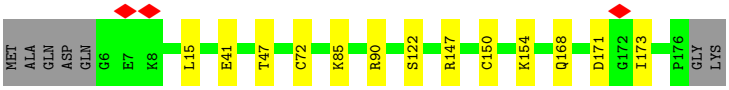

• Molecule 11: 60S ribosomal protein L10

Chain LI:



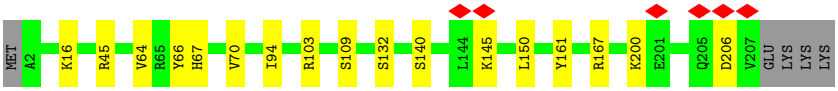
• Molecule 12: 60S ribosomal protein L11

Chain LJ:


• Molecule 13: 60S ribosomal protein L13

Chain LL:

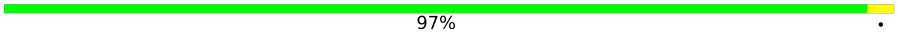

• Molecule 14: 60S ribosomal protein L14

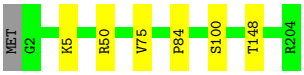
Chain LM:



• Molecule 15: 60S ribosomal protein L15

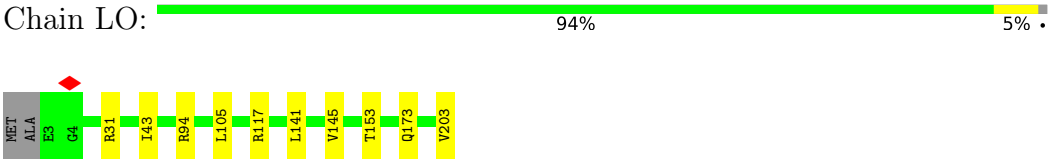
Chain LN:



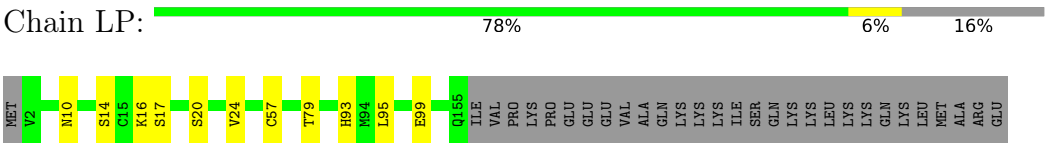
• Molecule 16: 60S ribosomal protein L13a

Chain LO:



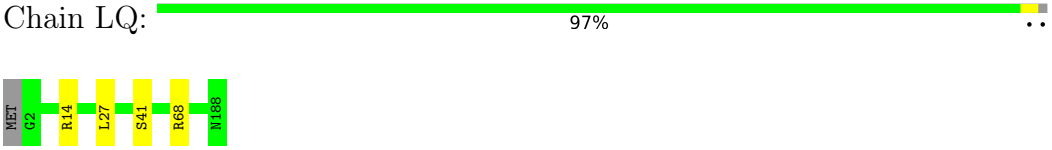

• Molecule 17: 60S ribosomal protein L17

Chain LP:



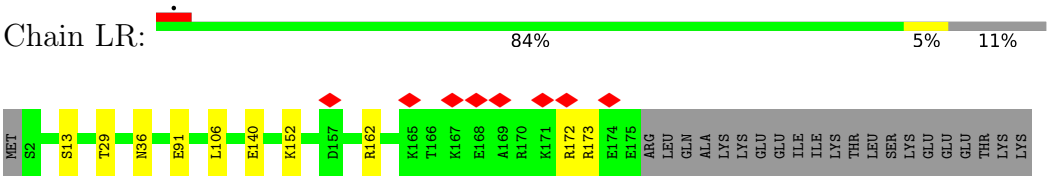

• Molecule 18: 60S ribosomal protein L18

Chain LQ:



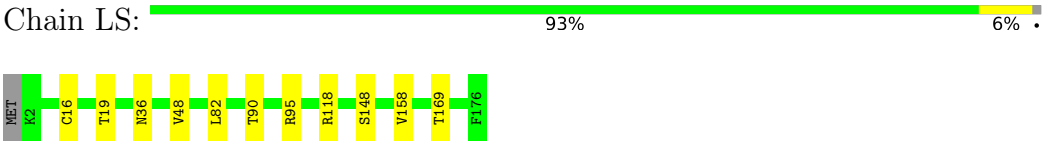

• Molecule 19: 60S ribosomal protein L19

Chain LR:



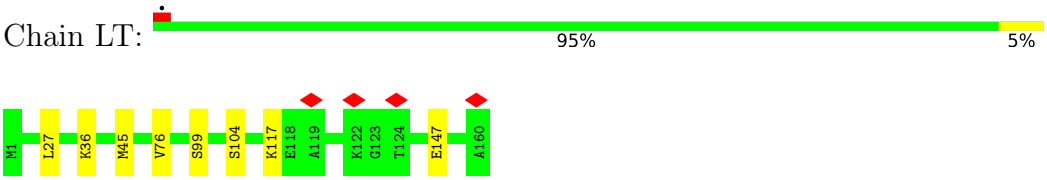

• Molecule 20: 60S ribosomal protein L18a

Chain LS:



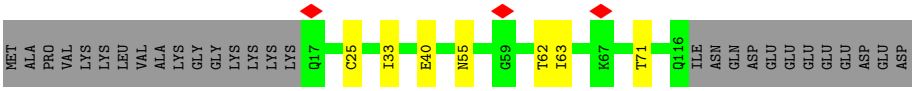

• Molecule 21: 60S ribosomal protein L21

Chain LT:



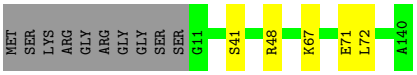

• Molecule 22: 60S ribosomal protein L22

Chain LU:



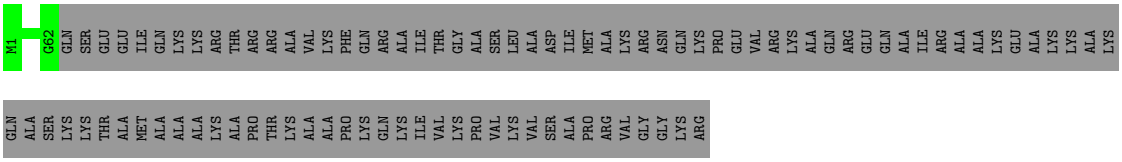

• Molecule 23: 60S ribosomal protein L23

Chain LV:

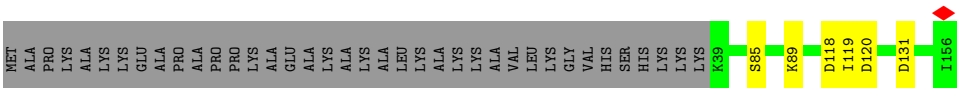

• Molecule 24: 60S ribosomal protein L24

Chain LW:


• Molecule 25: 60S ribosomal protein L23a

Chain LX:

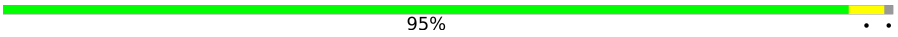

• Molecule 26: 60S ribosomal protein L26

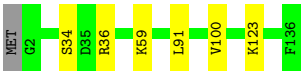
Chain LY:



• Molecule 27: 60S ribosomal protein L27

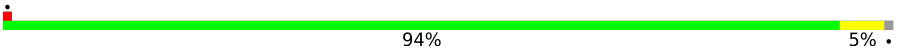
Chain LZ:

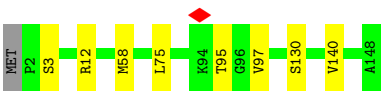



• Molecule 28: 60S ribosomal protein L27a

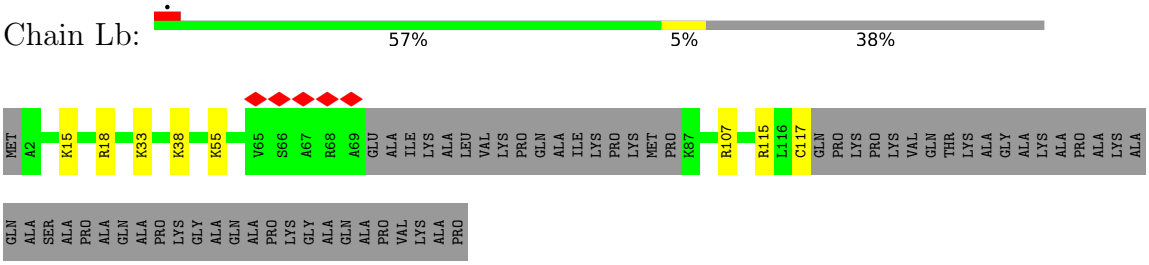
Chain La:



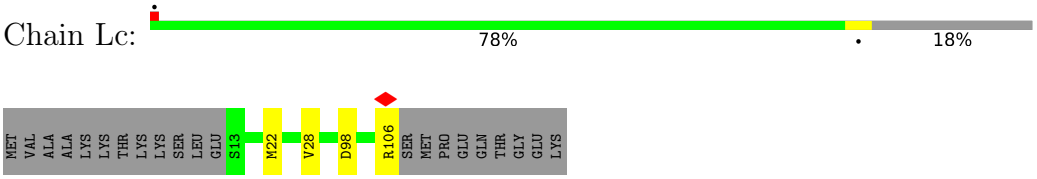

• Molecule 29: 60S ribosomal protein L29

Chain Lb:



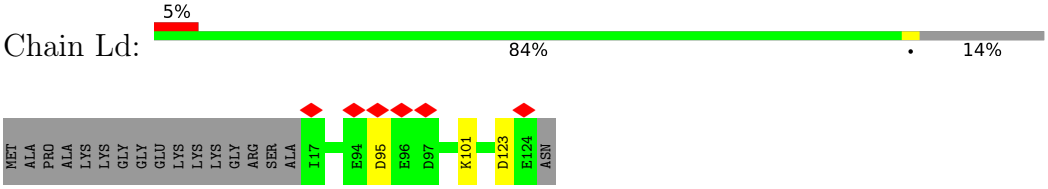

• Molecule 30: 60S ribosomal protein L30

Chain Lc:



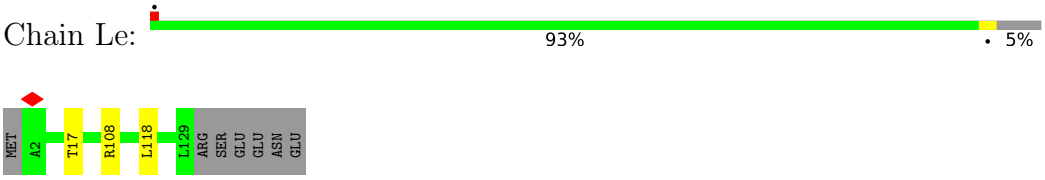

• Molecule 31: 60S ribosomal protein L31

Chain Ld:



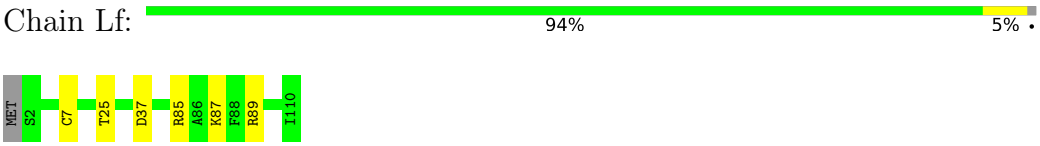

• Molecule 32: 60S ribosomal protein L32

Chain Le:



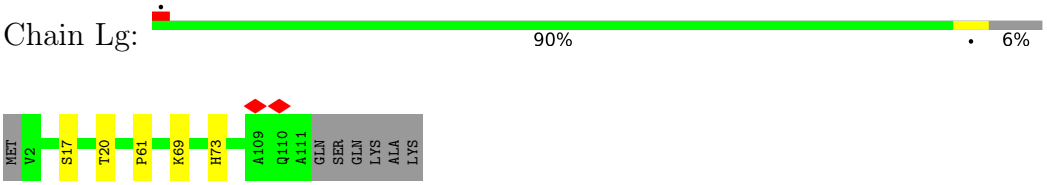

• Molecule 33: 60S ribosomal protein L35a

Chain Lf:



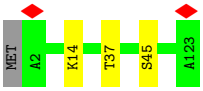

• Molecule 34: 60S ribosomal protein L34

Chain Lg:



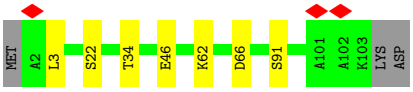

• Molecule 35: 60S ribosomal protein L35

Chain Lh:



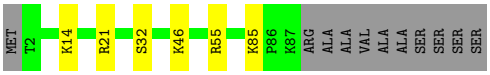

• Molecule 36: 60S ribosomal protein L36

Chain Li:

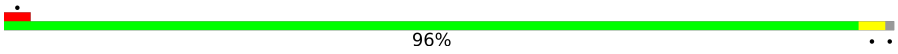

• Molecule 37: 60S ribosomal protein L37

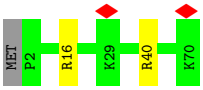
Chain Lj:


• Molecule 38: 60S ribosomal protein L38

Chain Lk:

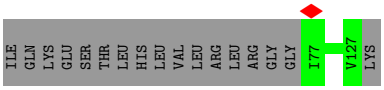



• Molecule 39: Ubiquitin-60S ribosomal protein L40

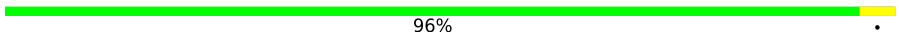
Chain Lm:






• Molecule 40: 60S ribosomal protein L41

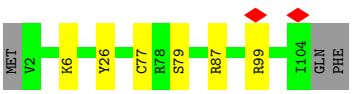
Chain Ln:





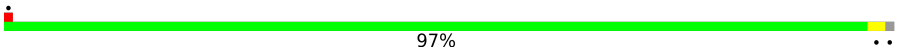
• Molecule 41: 60S ribosomal protein L36a

Chain Lo:

• Molecule 42: 60S ribosomal protein L37a

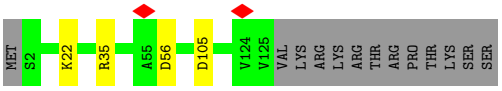
Chain Lp:





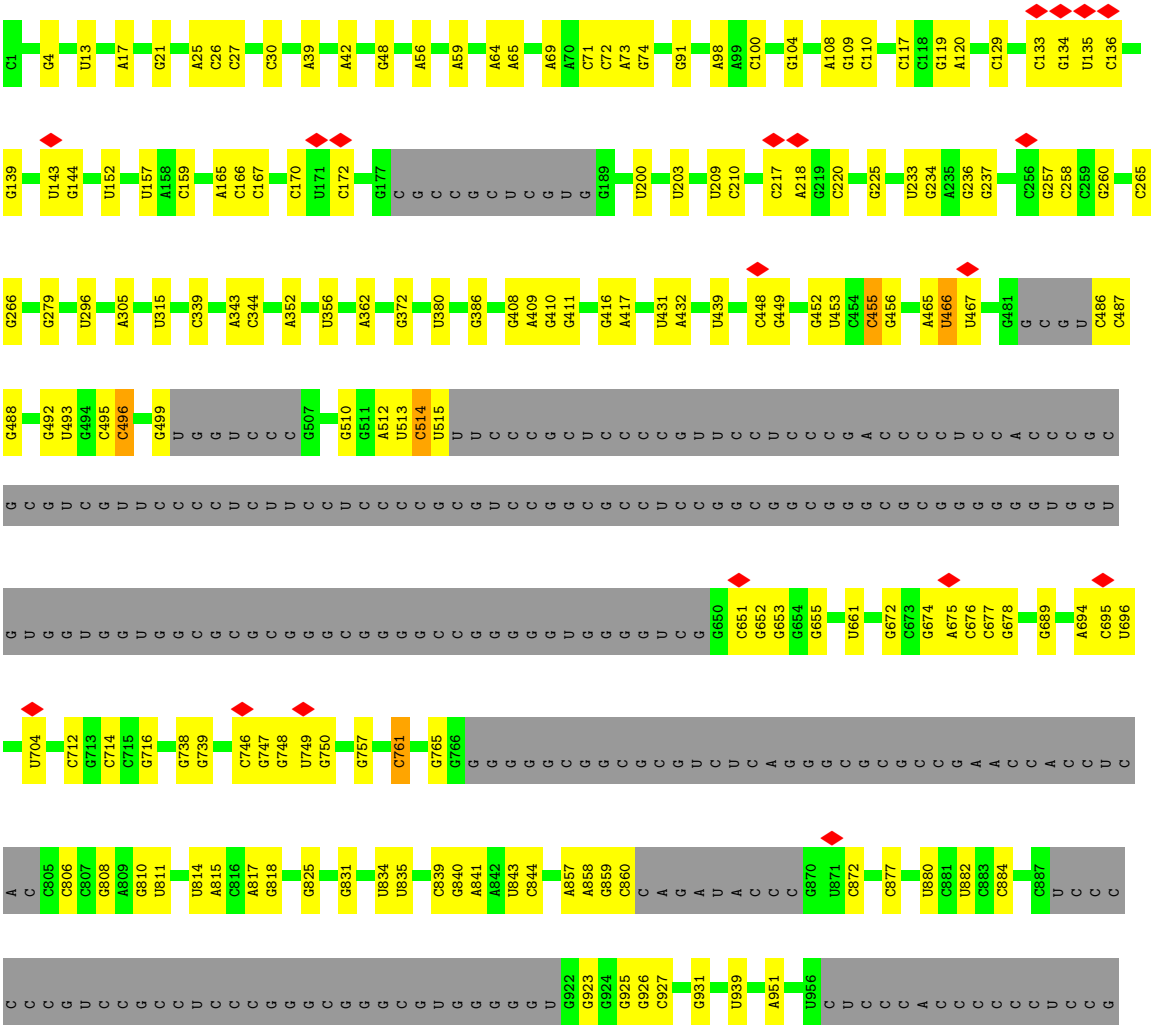
• Molecule 43: 60S ribosomal protein L28

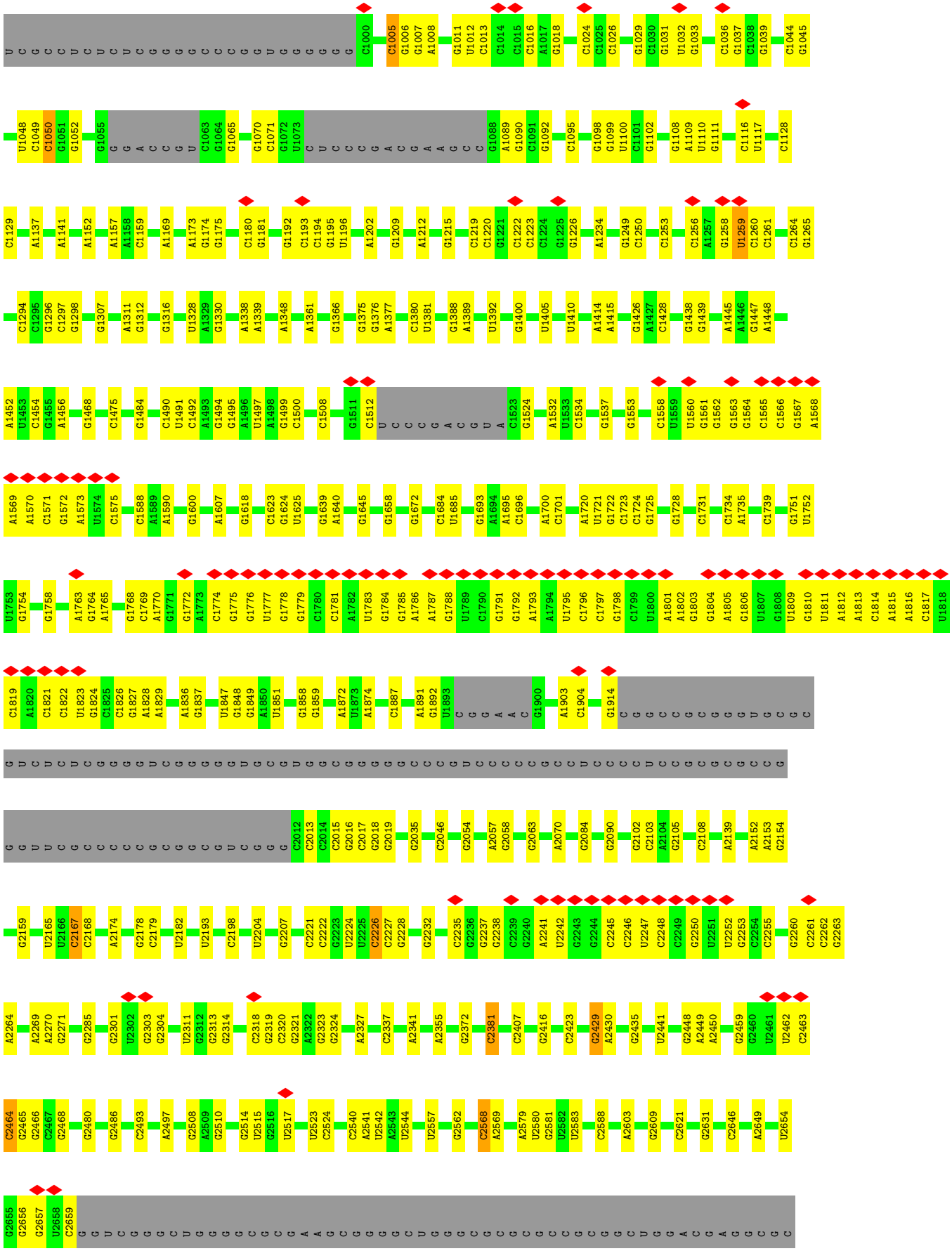
Chain Lr:

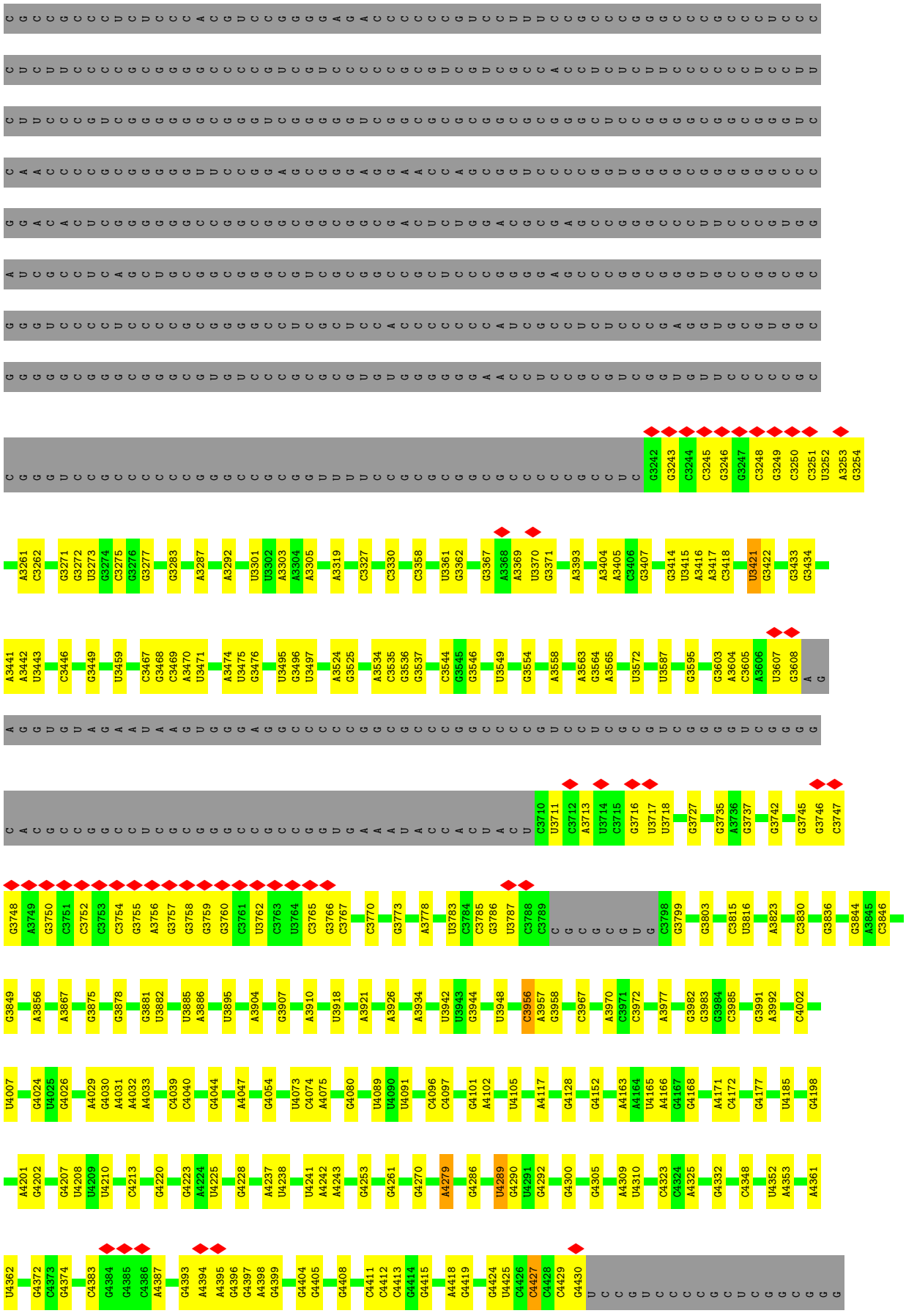



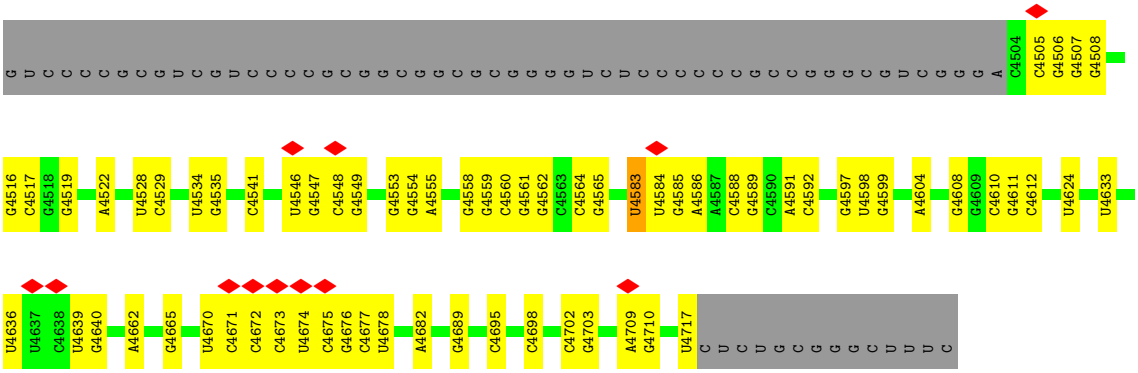

• Molecule 44: Mus musculus 28S ribosomal RNA

Chain L5:

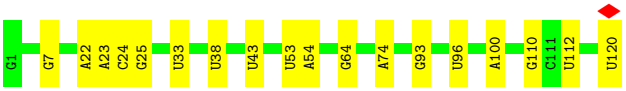






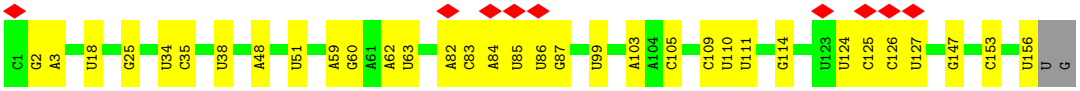
• Molecule 45: Mus musculus 5S ribosomal RNA

Chain L7:

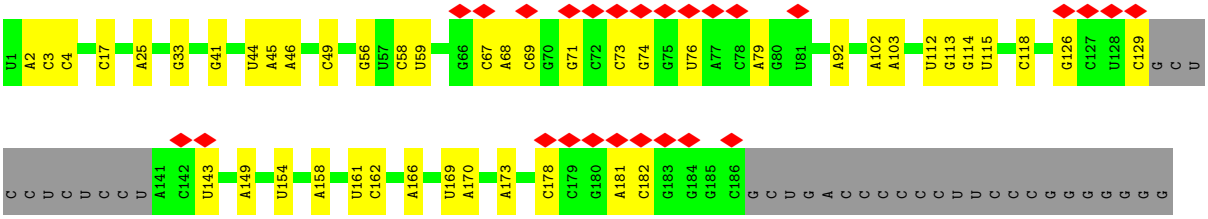
• Molecule 46: Mus musculus 5.8S ribosomal RNA

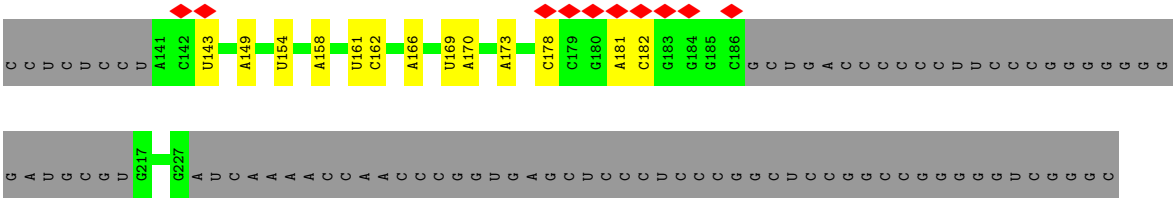
Chain L8:

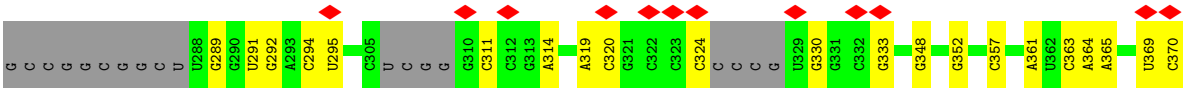
• Molecule 47: Mus musculus 18S ribosomal RNA

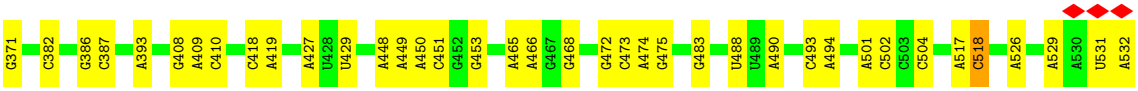
Chain S2:

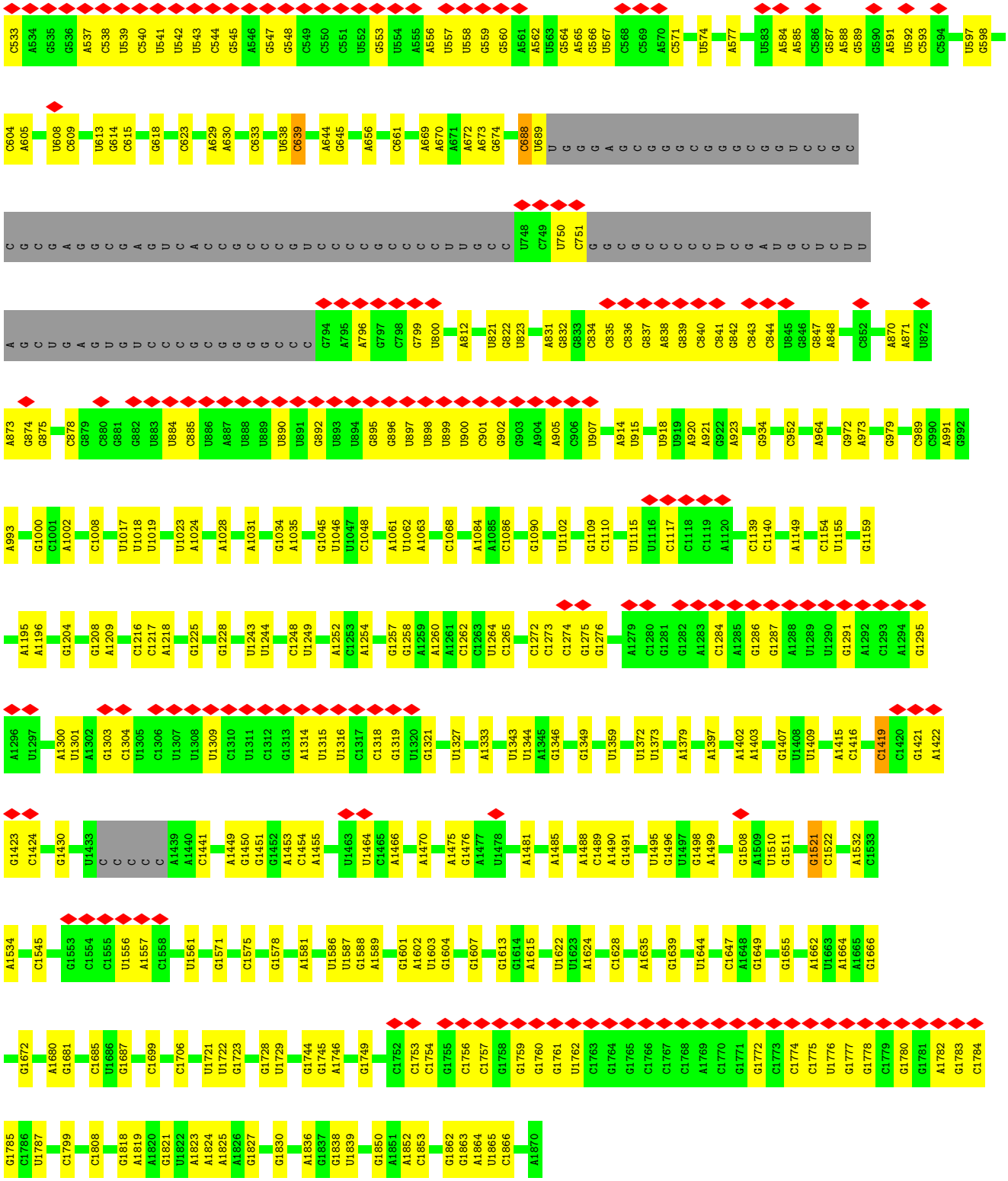







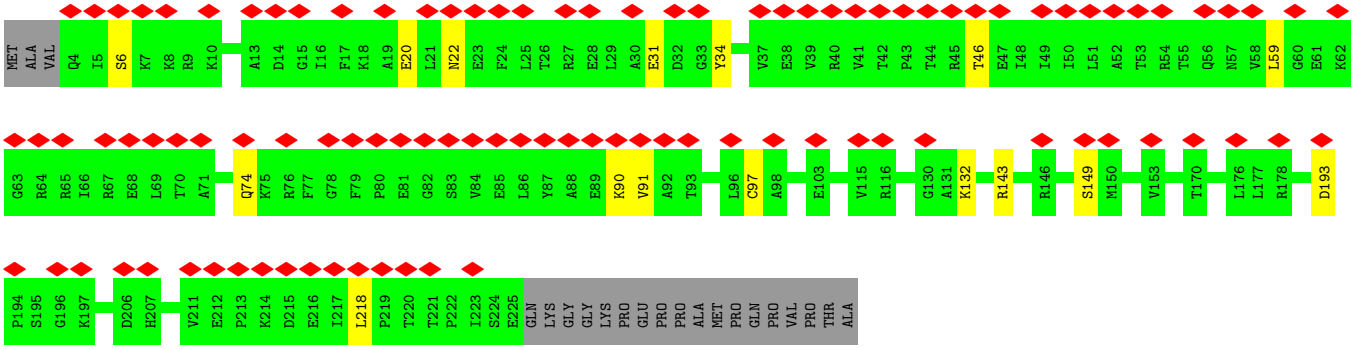




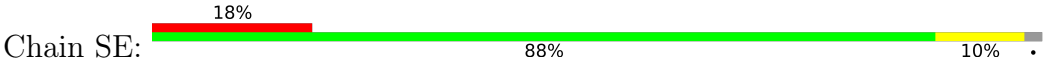


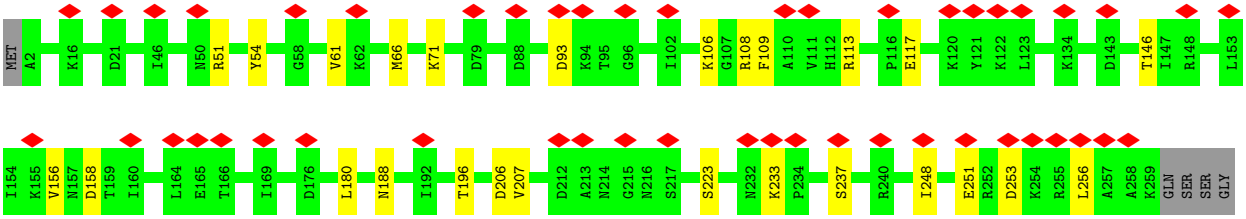
• Molecule 48: 40S ribosomal protein S3

Chain SD:

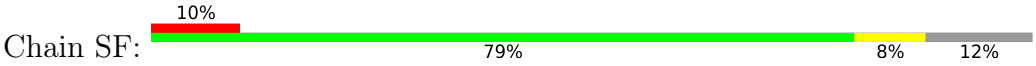


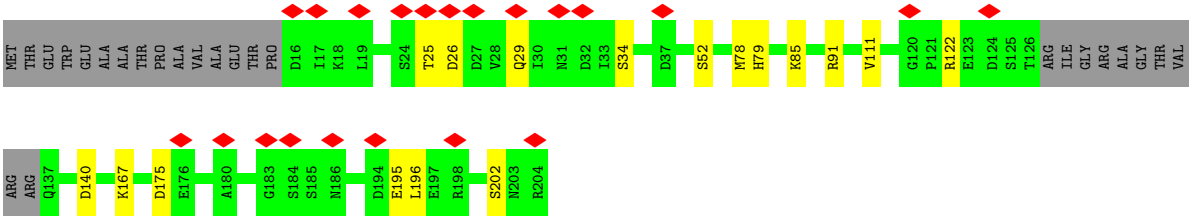

• Molecule 49: 40S ribosomal protein S4, X isoform



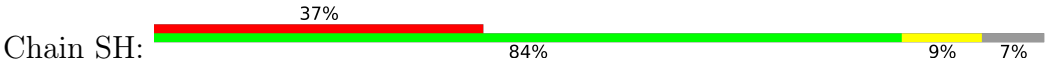



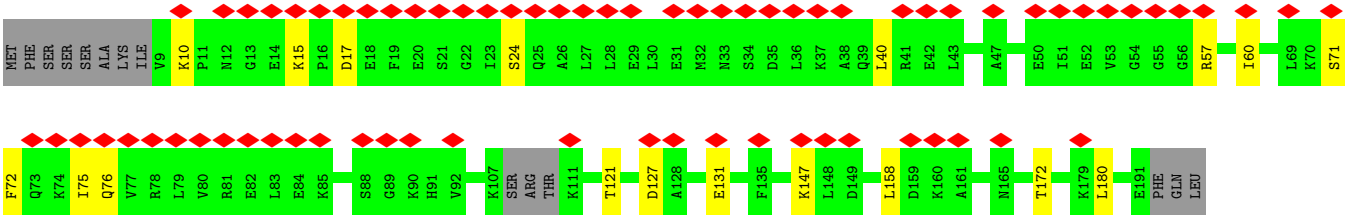

• Molecule 50: 40S ribosomal protein S5



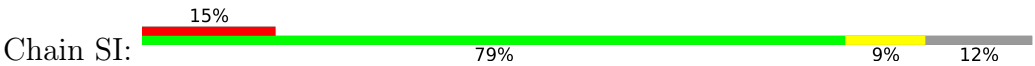



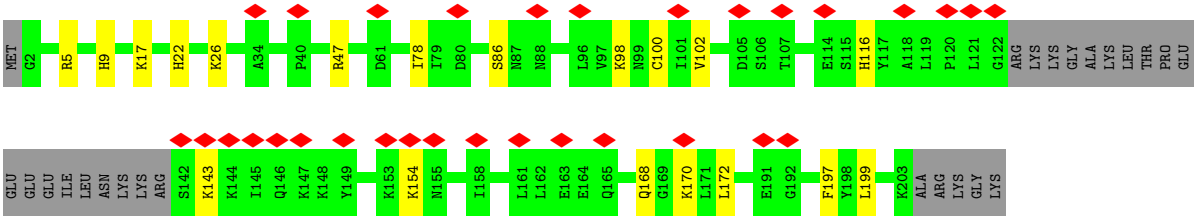

• Molecule 51: 40S ribosomal protein S7



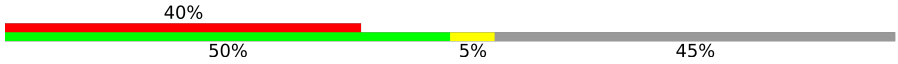

• Molecule 52: 40S ribosomal protein S8

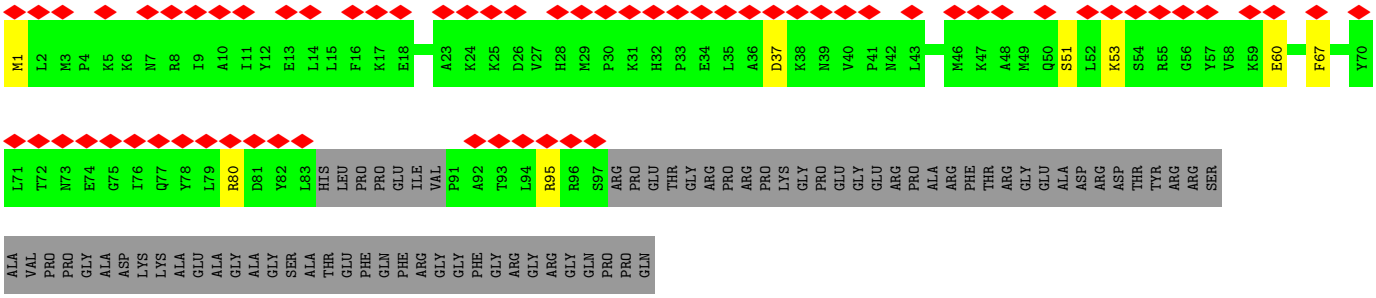




• Molecule 53: 40S ribosomal protein S10

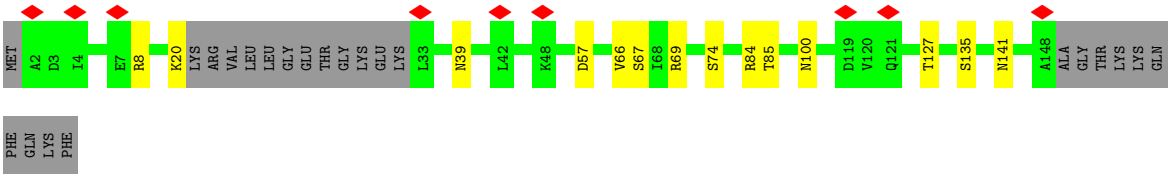
Chain SK:



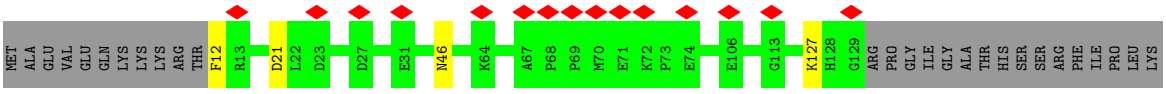
• Molecule 54: 40S ribosomal protein S11

Chain SL:

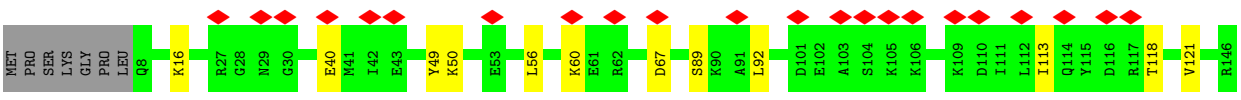
• Molecule 55: 40S ribosomal protein S15

Chain SP:

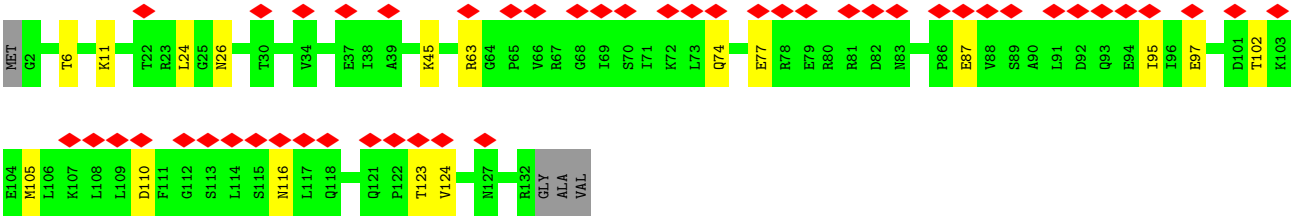
• Molecule 56: 40S ribosomal protein S16

Chain SQ:

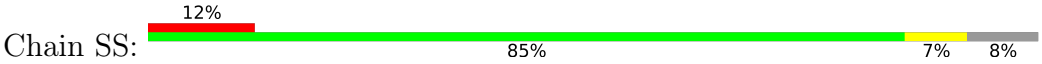



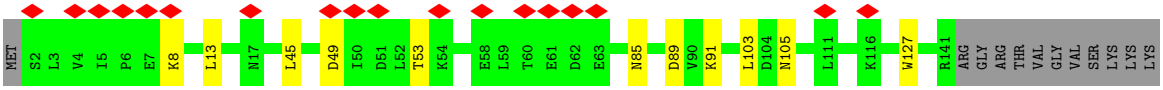
• Molecule 57: 40S ribosomal protein S17

Chain SR:

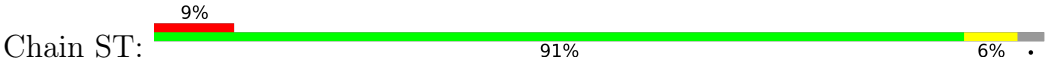


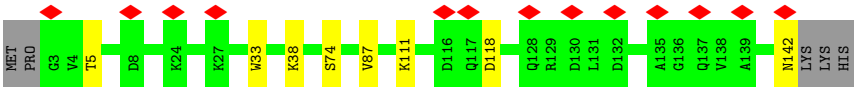

• Molecule 58: 40S ribosomal protein S18



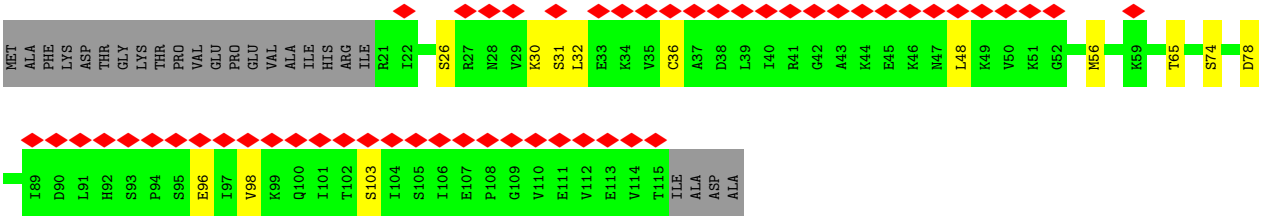




• Molecule 59: 40S ribosomal protein S19

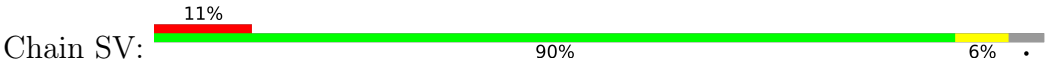


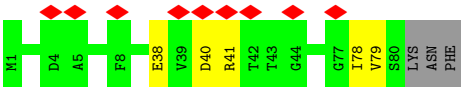




• Molecule 60: 40S ribosomal protein S20

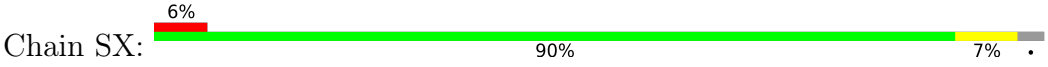



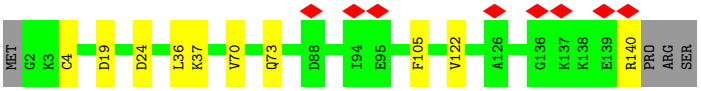

• Molecule 61: 40S ribosomal protein S21



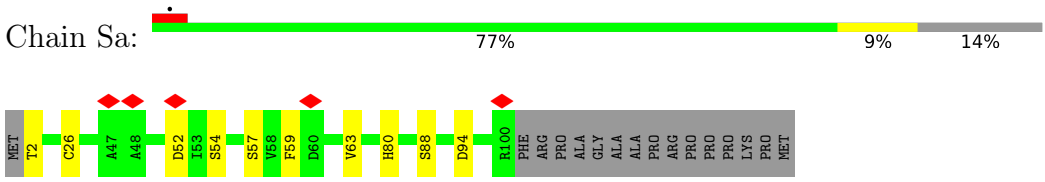

• Molecule 62: 40S ribosomal protein S23



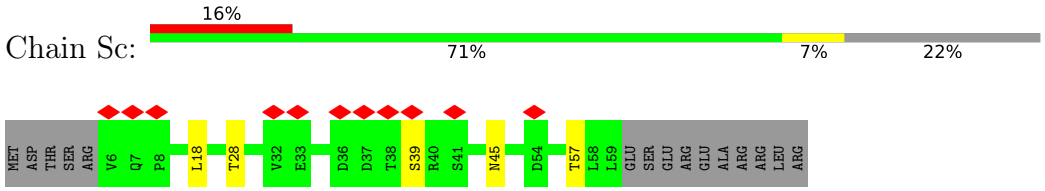

• Molecule 63: 40S ribosomal protein S26

Chain Sa:



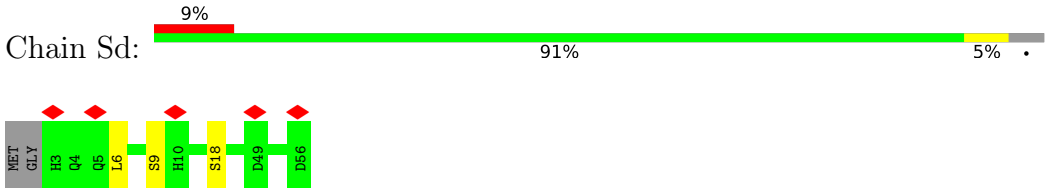

• Molecule 64: 40S ribosomal protein S28

Chain Sc:



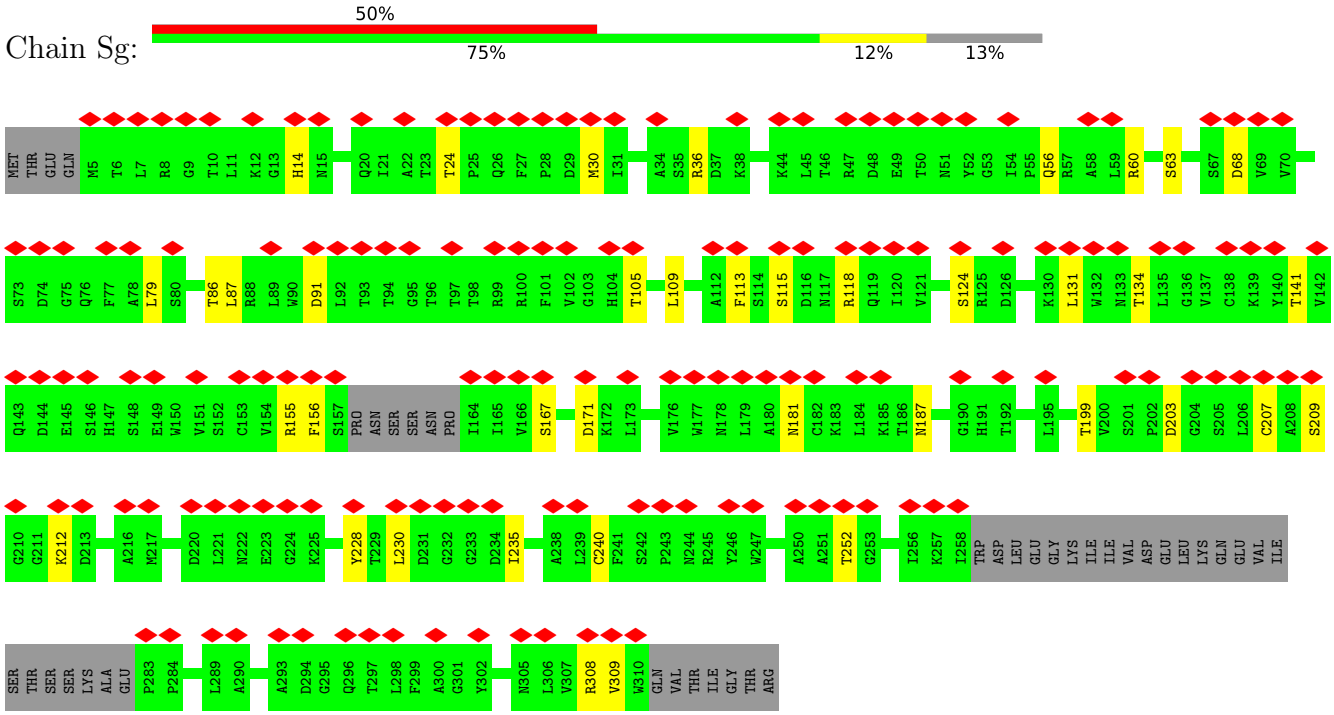

• Molecule 65: 40S ribosomal protein S29

Chain Sd:



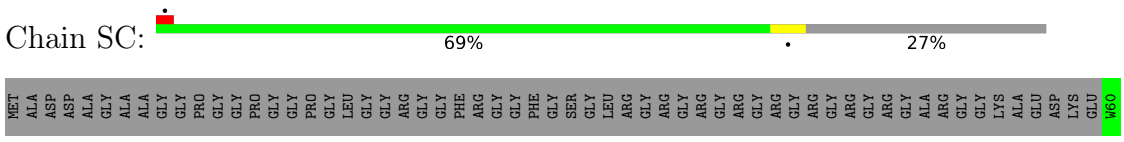

• Molecule 66: Receptor of activated protein C kinase 1

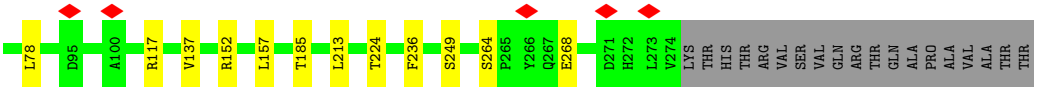
Chain Sg:




• Molecule 67: 40S ribosomal protein S2

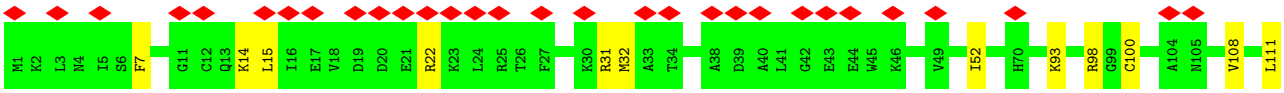
Chain SC:

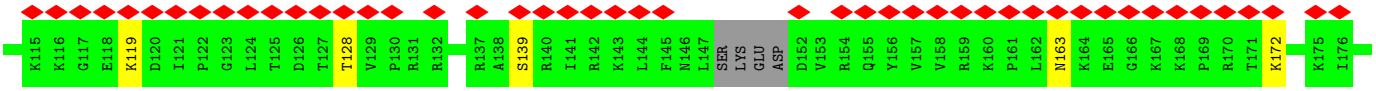


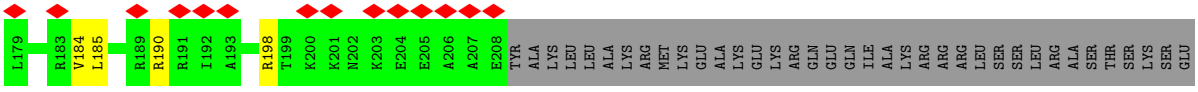



• Molecule 68: 40S ribosomal protein S6

Chain SG:

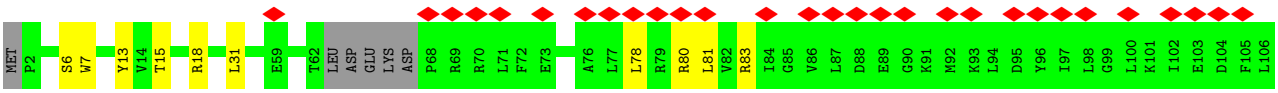



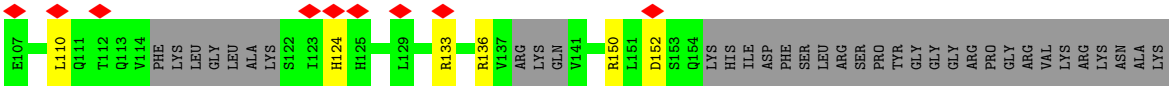



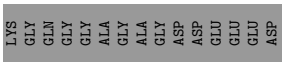


• Molecule 69: 40S ribosomal protein S9

Chain SJ:

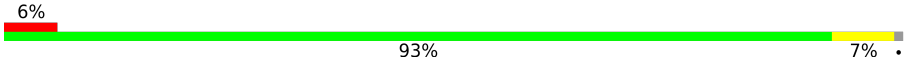



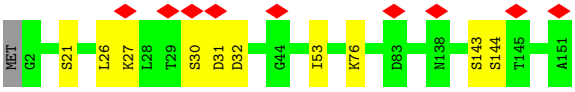




• Molecule 70: 40S ribosomal protein S13

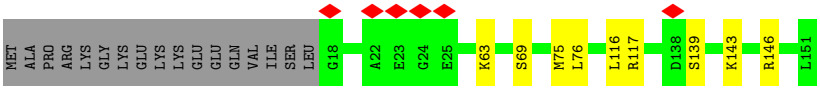
Chain SN:



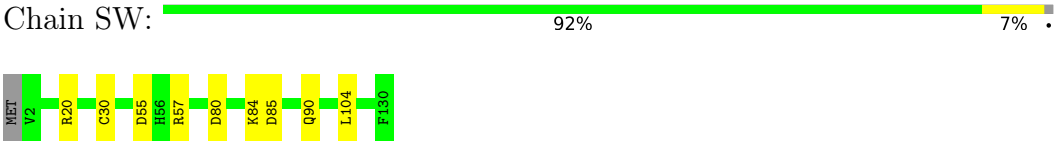

• Molecule 71: 40S ribosomal protein S14

Chain SO:

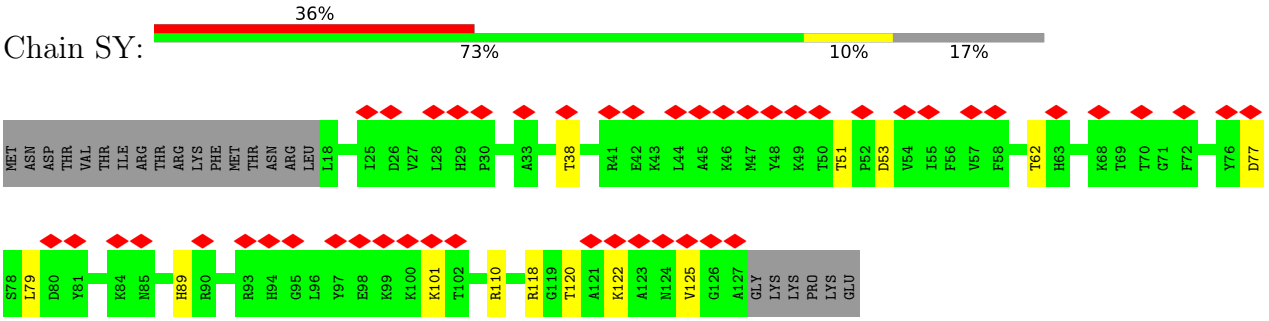
• Molecule 72: 40S ribosomal protein S15a

Chain SW:



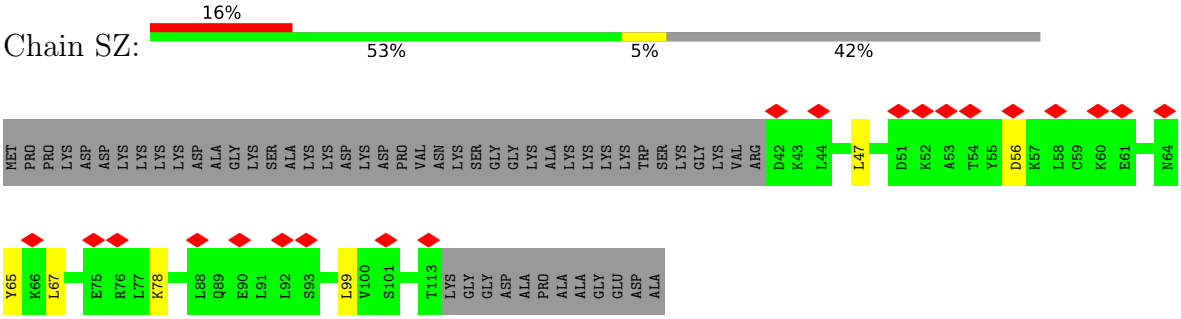

• Molecule 73: 40S ribosomal protein S24

Chain SY:



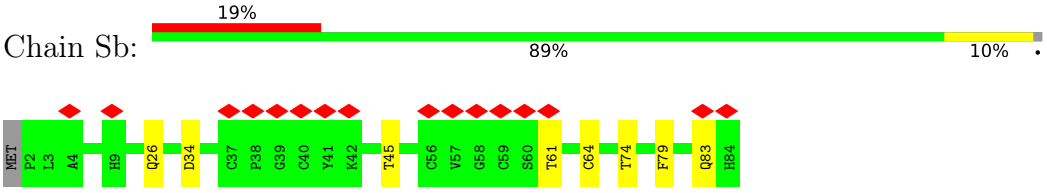

• Molecule 74: 40S ribosomal protein S25

Chain SZ:



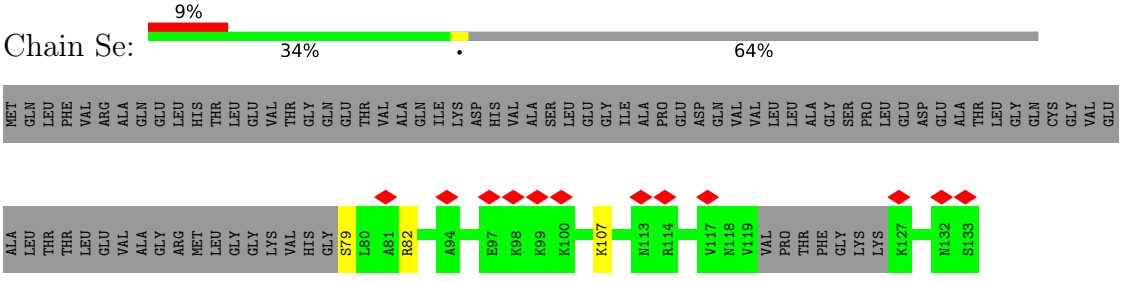

• Molecule 75: 40S ribosomal protein S27

Chain Sb:



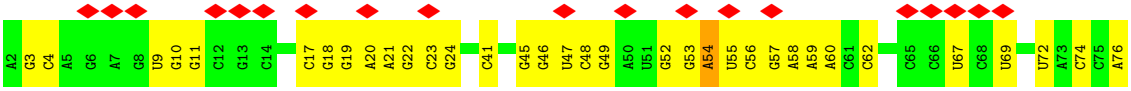

• Molecule 76: 40S ribosomal protein S30

Chain Se:




• Molecule 77: tRNA

Chain S6:




• Molecule 78: Ribosomal protein L39

Chain Ll:


# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 280287 | 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 ($e^-/Å^2$) | 60 | Depositor |
| Minimum defocus (nm) | 1000 | Depositor |
| Maximum defocus (nm) | 1500 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |
| Maximum map value | 0.326 | Depositor |
| Minimum map value | -0.162 | Depositor |
| Average map value | 0.000 | Depositor |
| Map value standard deviation | 0.012 | Depositor |
| Recommended contour level | 0.026 | Depositor |
| Map size (Å) | 416.0, 416.0, 416.0 | wwPDB |
| Map dimensions | 400, 400, 400 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.04, 1.04, 1.04 | 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 | LA | 0.42 | 0/1936 | 0.54 | 0/2596 |
| 2 | SA | 0.29 | 0/1673 | 0.48 | 0/2275 |
| 3 | LB | 0.39 | 0/3269 | 0.54 | 2/4375 (0.0%) |
| 4 | SB | 0.29 | 0/1756 | 0.48 | 0/2350 |
| 5 | LC | 0.37 | 0/2945 | 0.52 | 1/3953 (0.0%) |
| 6 | LD | 0.38 | 0/2431 | 0.48 | 0/3256 |
| 7 | LE | 0.34 | 0/1910 | 0.50 | 0/2562 |
| 8 | LF | 0.40 | 0/1805 | 0.48 | 0/2408 |
| 9 | LG | 0.34 | 0/1880 | 0.46 | 0/2531 |
| 10 | LH | 0.35 | 0/1537 | 0.51 | 0/2065 |
| 11 | LI | 0.37 | 0/1671 | 0.46 | 0/2230 |
| 12 | LJ | 0.33 | 0/1394 | 0.50 | 0/1864 |
| 13 | LL | 0.36 | 0/1698 | 0.48 | 0/2274 |
| 14 | LM | 0.37 | 0/1146 | 0.46 | 0/1531 |
| 15 | LN | 0.42 | 0/1746 | 0.50 | 0/2338 |
| 16 | LO | 0.39 | 0/1670 | 0.48 | 0/2232 |
| 17 | LP | 0.38 | 0/1277 | 0.49 | 0/1712 |
| 18 | LQ | 0.40 | 0/1539 | 0.51 | 0/2053 |
| 19 | LR | 0.32 | 0/1473 | 0.43 | 0/1947 |
| 20 | LS | 0.41 | 0/1491 | 0.50 | 1/2000 (0.1%) |
| 21 | LT | 0.39 | 0/1335 | 0.47 | 0/1781 |
| 22 | LU | 0.33 | 0/831 | 0.48 | 0/1115 |
| 23 | LV | 0.38 | 0/987 | 0.50 | 0/1324 |
| 24 | LW | 0.39 | 0/532 | 0.46 | 0/708 |
| 25 | LX | 0.36 | 0/984 | 0.45 | 0/1323 |
| 26 | LY | 0.36 | 0/1119 | 0.46 | 0/1488 |
| 27 | LZ | 0.38 | 0/1130 | 0.47 | 0/1507 |
| 28 | La | 0.41 | 0/1193 | 0.48 | 0/1593 |
| 29 | Lb | 0.32 | 0/821 | 0.43 | 0/1082 |
| 30 | Lc | 0.38 | 0/742 | 0.51 | 0/996 |
| 31 | Ld | 0.37 | 0/911 | 0.49 | 0/1227 |
| 32 | Le | 0.40 | 0/1071 | 0.48 | 0/1429 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 33 | Lf | 0.41 | 0/895 | 0.54 | 0/1198 |
| 34 | Lg | 0.37 | 0/883 | 0.51 | 0/1178 |
| 35 | Lh | 0.33 | 0/1023 | 0.44 | 0/1350 |
| 36 | Li | 0.32 | 0/843 | 0.45 | 0/1115 |
| 37 | Lj | 0.40 | 0/720 | 0.50 | 0/952 |
| 38 | Lk | 0.34 | 0/574 | 0.44 | 0/760 |
| 39 | Lm | 0.35 | 0/425 | 0.45 | 0/564 |
| 40 | Ln | 0.30 | 0/240 | 0.44 | 0/305 |
| 41 | Lo | 0.37 | 0/855 | 0.49 | 0/1128 |
| 42 | Lp | 0.38 | 0/718 | 0.49 | 0/953 |
| 43 | Lr | 0.37 | 0/1009 | 0.48 | 0/1353 |
| 44 | L5 | 0.71 | 1/84865 (0.0%) | 0.87 | 62/132368 (0.0%) |
| 45 | L7 | 0.70 | 0/2858 | 0.82 | 0/4455 |
| 46 | L8 | 0.69 | 0/3701 | 0.82 | 2/5766 (0.0%) |
| 47 | S2 | 0.43 | 0/39386 | 0.83 | 36/61368 (0.1%) |
| 48 | SD | 0.28 | 0/1754 | 0.52 | 0/2362 |
| 49 | SE | 0.27 | 0/2092 | 0.50 | 0/2816 |
| 50 | SF | 0.27 | 0/1436 | 0.45 | 0/1930 |
| 51 | SH | 0.27 | 0/1470 | 0.48 | 0/1968 |
| 52 | SI | 0.28 | 0/1526 | 0.48 | 0/2038 |
| 53 | SK | 0.28 | 0/780 | 0.48 | 0/1046 |
| 54 | SL | 0.31 | 0/1130 | 0.49 | 0/1514 |
| 55 | SP | 0.29 | 0/1000 | 0.48 | 0/1335 |
| 56 | SQ | 0.30 | 0/1126 | 0.51 | 0/1506 |
| 57 | SR | 0.28 | 0/1078 | 0.48 | 0/1447 |
| 58 | SS | 0.28 | 0/1175 | 0.45 | 0/1575 |
| 59 | ST | 0.27 | 0/1108 | 0.45 | 0/1486 |
| 60 | SU | 0.27 | 0/762 | 0.50 | 0/1023 |
| 61 | SV | 0.28 | 0/616 | 0.49 | 0/825 |
| 62 | SX | 0.30 | 0/1097 | 0.50 | 0/1464 |
| 63 | Sa | 0.32 | 0/816 | 0.47 | 0/1093 |
| 64 | Sc | 0.28 | 0/418 | 0.57 | 0/562 |
| 65 | Sd | 0.29 | 0/466 | 0.42 | 0/618 |
| 66 | Sg | 0.26 | 0/2199 | 0.55 | 0/2989 |
| 67 | SC | 0.30 | 0/1712 | 0.48 | 0/2314 |
| 68 | SG | 0.27 | 0/1666 | 0.50 | 0/2222 |
| 69 | SJ | 0.26 | 0/1178 | 0.51 | 0/1574 |
| 70 | SN | 0.29 | 0/1232 | 0.43 | 0/1656 |
| 71 | SO | 0.29 | 0/1015 | 0.51 | 0/1361 |
| 72 | SW | 0.30 | 0/1051 | 0.49 | 0/1406 |
| 73 | SY | 0.27 | 0/907 | 0.46 | 0/1204 |
| 74 | SZ | 0.29 | 0/580 | 0.49 | 0/780 |
| 75 | Sb | 0.27 | 0/665 | 0.46 | 0/891 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 76 | Se | 0.26 | 0/386 | 0.50 | 0/504 |
| 77 | S6 | 0.38 | 0/1795 | 0.96 | 4/2798 (0.1%) |
| 78 | Ll | 0.65 | 0/454 | 0.60 | 0/599 |
| All | All | 0.54 | 1/221588 (0.0%) | 0.74 | 108/325844 (0.0%) |

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

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|---|---|---|---|
| 1 | LA | 0 | 1 |
| 3 | LB | 0 | 2 |
| 10 | LH | 0 | 1 |
| 12 | LJ | 0 | 1 |
| 14 | LM | 0 | 1 |
| 50 | SF | 0 | 1 |
| 59 | ST | 0 | 1 |
| 61 | SV | 0 | 1 |
| 68 | SG | 0 | 1 |
| All | All | 0 | 10 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 44 | L5 | 1338 | A | N9-C4 | -5.93 | 1.34 | 1.37 |

The worst 5 of 108 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 44 | L5 | 486 | C | C2-N1-C1' | 9.59 | 129.35 | 118.80 |
| 47 | S2 | 1454 | C | N1-C2-O2 | 8.86 | 124.22 | 118.90 |
| 47 | S2 | 1419 | C | N1-C2-O2 | 8.82 | 124.19 | 118.90 |
| 47 | S2 | 1454 | C | C2-N1-C1' | 8.63 | 128.30 | 118.80 |
| 44 | L5 | 2464 | C | N1-C2-O2 | 8.56 | 124.04 | 118.90 |

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 1 | LA | 13 | GLY | Peptide |

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| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 3 | LB | 16 | PHE | Peptide |
| 3 | LB | 258 | HIS | Peptide |
| 10 | LH | 173 | ARG | Peptide |
| 12 | LJ | 173 | ILE | Peptide |

## 5.2 Too-close contacts (i)

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

## 5.3 Torsion angles (i)

### 5.3.1 Protein backbone (i)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 1 | LA | 246/257 (96%) | 220 (89%) | 26 (11%) | 0 | 100 | 100 |
| 2 | SA | 205/295 (70%) | 183 (89%) | 22 (11%) | 0 | 100 | 100 |
| 3 | LB | 395/403 (98%) | 374 (95%) | 21 (5%) | 0 | 100 | 100 |
| 4 | SB | 211/264 (80%) | 194 (92%) | 17 (8%) | 0 | 100 | 100 |
| 5 | LC | 360/419 (86%) | 323 (90%) | 36 (10%) | 1 (0%) | 41 | 70 |
| 6 | LD | 291/297 (98%) | 271 (93%) | 20 (7%) | 0 | 100 | 100 |
| 7 | LE | 227/296 (77%) | 201 (88%) | 26 (12%) | 0 | 100 | 100 |
| 8 | LF | 212/270 (78%) | 200 (94%) | 12 (6%) | 0 | 100 | 100 |
| 9 | LG | 225/266 (85%) | 207 (92%) | 18 (8%) | 0 | 100 | 100 |
| 10 | LH | 188/192 (98%) | 172 (92%) | 16 (8%) | 0 | 100 | 100 |
| 11 | LI | 197/214 (92%) | 193 (98%) | 4 (2%) | 0 | 100 | 100 |
| 12 | LJ | 169/178 (95%) | 153 (90%) | 16 (10%) | 0 | 100 | 100 |
| 13 | LL | 204/211 (97%) | 187 (92%) | 17 (8%) | 0 | 100 | 100 |
| 14 | LM | 134/217 (62%) | 125 (93%) | 9 (7%) | 0 | 100 | 100 |
| 15 | LN | 201/204 (98%) | 190 (94%) | 10 (5%) | 1 (0%) | 29 | 59 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 16 | LO | 199/203 (98%) | 192 (96%) | 7 (4%) | 0 | 100 | 100 |
| 17 | LP | 152/184 (83%) | 142 (93%) | 10 (7%) | 0 | 100 | 100 |
| 18 | LQ | 185/188 (98%) | 174 (94%) | 11 (6%) | 0 | 100 | 100 |
| 19 | LR | 172/196 (88%) | 166 (96%) | 6 (4%) | 0 | 100 | 100 |
| 20 | LS | 173/176 (98%) | 164 (95%) | 9 (5%) | 0 | 100 | 100 |
| 21 | LT | 158/160 (99%) | 153 (97%) | 5 (3%) | 0 | 100 | 100 |
| 22 | LU | 98/128 (77%) | 86 (88%) | 12 (12%) | 0 | 100 | 100 |
| 23 | LV | 128/140 (91%) | 118 (92%) | 10 (8%) | 0 | 100 | 100 |
| 24 | LW | 60/157 (38%) | 56 (93%) | 4 (7%) | 0 | 100 | 100 |
| 25 | LX | 116/156 (74%) | 110 (95%) | 6 (5%) | 0 | 100 | 100 |
| 26 | LY | 130/145 (90%) | 124 (95%) | 6 (5%) | 0 | 100 | 100 |
| 27 | LZ | 133/136 (98%) | 123 (92%) | 10 (8%) | 0 | 100 | 100 |
| 28 | La | 145/148 (98%) | 132 (91%) | 13 (9%) | 0 | 100 | 100 |
| 29 | Lb | 95/160 (59%) | 88 (93%) | 7 (7%) | 0 | 100 | 100 |
| 30 | Lc | 92/115 (80%) | 85 (92%) | 7 (8%) | 0 | 100 | 100 |
| 31 | Ld | 106/125 (85%) | 98 (92%) | 8 (8%) | 0 | 100 | 100 |
| 32 | Le | 126/135 (93%) | 115 (91%) | 11 (9%) | 0 | 100 | 100 |
| 33 | Lf | 107/110 (97%) | 102 (95%) | 5 (5%) | 0 | 100 | 100 |
| 34 | Lg | 108/117 (92%) | 107 (99%) | 1 (1%) | 0 | 100 | 100 |
| 35 | Lh | 120/123 (98%) | 118 (98%) | 2 (2%) | 0 | 100 | 100 |
| 36 | Li | 100/105 (95%) | 93 (93%) | 7 (7%) | 0 | 100 | 100 |
| 37 | Lj | 84/97 (87%) | 78 (93%) | 5 (6%) | 1 (1%) | 13 | 37 |
| 38 | Lk | 67/70 (96%) | 64 (96%) | 3 (4%) | 0 | 100 | 100 |
| 39 | Lm | 49/128 (38%) | 49 (100%) | 0 | 0 | 100 | 100 |
| 40 | Ln | 23/25 (92%) | 23 (100%) | 0 | 0 | 100 | 100 |
| 41 | Lo | 101/106 (95%) | 94 (93%) | 7 (7%) | 0 | 100 | 100 |
| 42 | Lp | 89/92 (97%) | 85 (96%) | 4 (4%) | 0 | 100 | 100 |
| 43 | Lr | 122/137 (89%) | 116 (95%) | 6 (5%) | 0 | 100 | 100 |
| 48 | SD | 220/243 (90%) | 192 (87%) | 28 (13%) | 0 | 100 | 100 |
| 49 | SE | 256/263 (97%) | 222 (87%) | 33 (13%) | 1 (0%) | 34 | 64 |
| 50 | SF | 175/204 (86%) | 158 (90%) | 17 (10%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 51 | SH | 176/194 (91%) | 148 (84%) | 28 (16%) | 0 | 100 | 100 |
| 52 | SI | 179/208 (86%) | 167 (93%) | 12 (7%) | 0 | 100 | 100 |
| 53 | SK | 86/165 (52%) | 75 (87%) | 11 (13%) | 0 | 100 | 100 |
| 54 | SL | 131/158 (83%) | 118 (90%) | 13 (10%) | 0 | 100 | 100 |
| 55 | SP | 116/145 (80%) | 106 (91%) | 10 (9%) | 0 | 100 | 100 |
| 56 | SQ | 137/146 (94%) | 117 (85%) | 20 (15%) | 0 | 100 | 100 |
| 57 | SR | 129/135 (96%) | 117 (91%) | 12 (9%) | 0 | 100 | 100 |
| 58 | SS | 138/152 (91%) | 120 (87%) | 18 (13%) | 0 | 100 | 100 |
| 59 | ST | 138/145 (95%) | 126 (91%) | 12 (9%) | 0 | 100 | 100 |
| 60 | SU | 93/119 (78%) | 84 (90%) | 9 (10%) | 0 | 100 | 100 |
| 61 | SV | 78/83 (94%) | 71 (91%) | 6 (8%) | 1 (1%) | 12 | 34 |
| 62 | SX | 137/143 (96%) | 125 (91%) | 12 (9%) | 0 | 100 | 100 |
| 63 | Sa | 98/115 (85%) | 90 (92%) | 8 (8%) | 0 | 100 | 100 |
| 64 | Sc | 52/69 (75%) | 41 (79%) | 11 (21%) | 0 | 100 | 100 |
| 65 | Sd | 52/56 (93%) | 47 (90%) | 5 (10%) | 0 | 100 | 100 |
| 66 | Sg | 270/317 (85%) | 213 (79%) | 57 (21%) | 0 | 100 | 100 |
| 67 | SC | 214/293 (73%) | 199 (93%) | 14 (6%) | 1 (0%) | 29 | 59 |
| 68 | SG | 200/249 (80%) | 180 (90%) | 20 (10%) | 0 | 100 | 100 |
| 69 | SJ | 130/194 (67%) | 115 (88%) | 15 (12%) | 0 | 100 | 100 |
| 70 | SN | 148/151 (98%) | 142 (96%) | 6 (4%) | 0 | 100 | 100 |
| 71 | SO | 132/151 (87%) | 116 (88%) | 16 (12%) | 0 | 100 | 100 |
| 72 | SW | 127/130 (98%) | 118 (93%) | 9 (7%) | 0 | 100 | 100 |
| 73 | SY | 108/133 (81%) | 93 (86%) | 15 (14%) | 0 | 100 | 100 |
| 74 | SZ | 70/125 (56%) | 59 (84%) | 11 (16%) | 0 | 100 | 100 |
| 75 | Sb | 81/84 (96%) | 74 (91%) | 7 (9%) | 0 | 100 | 100 |
| 76 | Se | 44/133 (33%) | 38 (86%) | 6 (14%) | 0 | 100 | 100 |
| 78 | Ll | 48/51 (94%) | 46 (96%) | 2 (4%) | 0 | 100 | 100 |
| All | All | 10666/12499 (85%) | 9765 (92%) | 895 (8%) | 6 (0%) | 54 | 80 |

5 of 6 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 61 | SV | 79 | VAL |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 37 | Lj | 21 | ARG |
| 49 | SE | 248 | ILE |
| 67 | SC | 78 | LEU |
| 15 | LN | 84 | PRO |

### 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 |
|---|---|---|---|---|---|
| 1 | LA | 190/199 (96%) | 181 (95%) | 9 (5%) | 26 57 |
| 2 | SA | 173/242 (72%) | 157 (91%) | 16 (9%) | 9 26 |
| 3 | LB | 344/348 (99%) | 332 (96%) | 12 (4%) | 36 68 |
| 4 | SB | 194/229 (85%) | 185 (95%) | 9 (5%) | 27 58 |
| 5 | LC | 304/348 (87%) | 279 (92%) | 25 (8%) | 11 31 |
| 6 | LD | 245/249 (98%) | 231 (94%) | 14 (6%) | 20 49 |
| 7 | LE | 208/256 (81%) | 193 (93%) | 15 (7%) | 14 37 |
| 8 | LF | 185/234 (79%) | 180 (97%) | 5 (3%) | 44 77 |
| 9 | LG | 197/223 (88%) | 180 (91%) | 17 (9%) | 10 29 |
| 10 | LH | 169/171 (99%) | 156 (92%) | 13 (8%) | 13 34 |
| 11 | LI | 171/181 (94%) | 162 (95%) | 9 (5%) | 22 52 |
| 12 | LJ | 144/149 (97%) | 132 (92%) | 12 (8%) | 11 31 |
| 13 | LL | 173/178 (97%) | 156 (90%) | 17 (10%) | 8 23 |
| 14 | LM | 116/157 (74%) | 112 (97%) | 4 (3%) | 37 69 |
| 15 | LN | 171/172 (99%) | 166 (97%) | 5 (3%) | 42 74 |
| 16 | LO | 172/173 (99%) | 162 (94%) | 10 (6%) | 20 48 |
| 17 | LP | 135/163 (83%) | 124 (92%) | 11 (8%) | 11 32 |
| 18 | LQ | 164/165 (99%) | 160 (98%) | 4 (2%) | 49 80 |
| 19 | LR | 154/175 (88%) | 144 (94%) | 10 (6%) | 17 43 |
| 20 | LS | 155/156 (99%) | 145 (94%) | 10 (6%) | 17 43 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles |
|---|---|---|---|---|---|
| 21 | LT | 140/140 (100%) | 132 (94%) | 8 (6%) | 20 49 |
| 22 | LU | 90/114 (79%) | 83 (92%) | 7 (8%) | 12 33 |
| 23 | LV | 100/107 (94%) | 95 (95%) | 5 (5%) | 24 55 |
| 24 | LW | 54/126 (43%) | 54 (100%) | 0 | 100 100 |
| 25 | LX | 106/133 (80%) | 100 (94%) | 6 (6%) | 20 49 |
| 26 | LY | 123/135 (91%) | 113 (92%) | 10 (8%) | 11 32 |
| 27 | LZ | 117/118 (99%) | 111 (95%) | 6 (5%) | 24 54 |
| 28 | La | 120/121 (99%) | 112 (93%) | 8 (7%) | 16 41 |
| 29 | Lb | 83/124 (67%) | 75 (90%) | 8 (10%) | 8 24 |
| 30 | Lc | 79/97 (81%) | 75 (95%) | 4 (5%) | 24 54 |
| 31 | Ld | 99/110 (90%) | 96 (97%) | 3 (3%) | 41 73 |
| 32 | Le | 114/121 (94%) | 111 (97%) | 3 (3%) | 46 78 |
| 33 | Lf | 88/89 (99%) | 82 (93%) | 6 (7%) | 16 40 |
| 34 | Lg | 94/100 (94%) | 89 (95%) | 5 (5%) | 22 52 |
| 35 | Lh | 109/110 (99%) | 106 (97%) | 3 (3%) | 43 76 |
| 36 | Li | 86/89 (97%) | 79 (92%) | 7 (8%) | 11 32 |
| 37 | Lj | 73/80 (91%) | 68 (93%) | 5 (7%) | 16 40 |
| 38 | Lk | 64/65 (98%) | 62 (97%) | 2 (3%) | 40 72 |
| 39 | Lm | 47/116 (40%) | 47 (100%) | 0 | 100 100 |
| 40 | Ln | 24/24 (100%) | 23 (96%) | 1 (4%) | 30 62 |
| 41 | Lo | 91/94 (97%) | 85 (93%) | 6 (7%) | 16 42 |
| 42 | Lp | 74/75 (99%) | 72 (97%) | 2 (3%) | 44 77 |
| 43 | Lr | 108/121 (89%) | 104 (96%) | 4 (4%) | 34 66 |
| 48 | SD | 186/202 (92%) | 170 (91%) | 16 (9%) | 10 29 |
| 49 | SE | 221/225 (98%) | 196 (89%) | 25 (11%) | 6 17 |
| 50 | SF | 152/170 (89%) | 136 (90%) | 16 (10%) | 7 20 |
| 51 | SH | 161/174 (92%) | 143 (89%) | 18 (11%) | 6 18 |
| 52 | SI | 159/180 (88%) | 140 (88%) | 19 (12%) | 5 15 |
| 53 | SK | 81/136 (60%) | 73 (90%) | 8 (10%) | 8 22 |
| 54 | SL | 123/142 (87%) | 109 (89%) | 14 (11%) | 5 17 |
| 55 | SP | 107/130 (82%) | 103 (96%) | 4 (4%) | 34 66 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles |
|---|---|---|---|---|---|
| 56 | SQ | 115/121 (95%) | 103 (90%) | 12 (10%) | 7 20 |
| 57 | SR | 119/121 (98%) | 102 (86%) | 17 (14%) | 3 9 |
| 58 | SS | 122/132 (92%) | 111 (91%) | 11 (9%) | 9 27 |
| 59 | ST | 110/115 (96%) | 103 (94%) | 7 (6%) | 17 44 |
| 60 | SU | 88/107 (82%) | 75 (85%) | 13 (15%) | 3 9 |
| 61 | SV | 64/67 (96%) | 61 (95%) | 3 (5%) | 26 57 |
| 62 | SX | 111/115 (96%) | 101 (91%) | 10 (9%) | 9 27 |
| 63 | Sa | 87/98 (89%) | 77 (88%) | 10 (12%) | 5 17 |
| 64 | Sc | 48/62 (77%) | 43 (90%) | 5 (10%) | 7 20 |
| 65 | Sd | 48/49 (98%) | 45 (94%) | 3 (6%) | 18 44 |
| 66 | Sg | 237/275 (86%) | 198 (84%) | 39 (16%) | 2 6 |
| 67 | SC | 182/224 (81%) | 171 (94%) | 11 (6%) | 19 47 |
| 68 | SG | 178/218 (82%) | 158 (89%) | 20 (11%) | 6 18 |
| 69 | SJ | 126/168 (75%) | 110 (87%) | 16 (13%) | 4 13 |
| 70 | SN | 130/131 (99%) | 120 (92%) | 10 (8%) | 13 34 |
| 71 | SO | 104/119 (87%) | 95 (91%) | 9 (9%) | 10 28 |
| 72 | SW | 112/113 (99%) | 103 (92%) | 9 (8%) | 12 32 |
| 73 | SY | 93/115 (81%) | 80 (86%) | 13 (14%) | 3 10 |
| 74 | SZ | 64/103 (62%) | 58 (91%) | 6 (9%) | 8 25 |
| 75 | Sb | 75/76 (99%) | 67 (89%) | 8 (11%) | 6 19 |
| 76 | Se | 39/106 (37%) | 36 (92%) | 3 (8%) | 13 34 |
| 78 | Ll | 47/48 (98%) | 44 (94%) | 3 (6%) | 17 44 |
| All | All | 9336/10619 (88%) | 8642 (93%) | 694 (7%) | 17 36 |

5 of 694 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 56 | SQ | 89 | SER |
| 66 | Sg | 187 | ASN |
| 57 | SR | 87 | GLU |
| 56 | SQ | 67 | ASP |
| 62 | SX | 19 | ASP |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 156 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 55 | SP | 41 | GLN |
| 68 | SG | 197 | GLN |
| 56 | SQ | 77 | HIS |
| 62 | SX | 61 | GLN |
| 73 | SY | 85 | ASN |

### 5.3.3 RNA

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 44 | L5 | 3521/4731 (74%) | 853 (24%) | 19 (0%) |
| 45 | L7 | 119/120 (99%) | 18 (15%) | 0 |
| 46 | L8 | 155/158 (98%) | 32 (20%) | 0 |
| 47 | S2 | 1638/1870 (87%) | 425 (25%) | 9 (0%) |
| 77 | S6 | 74/75 (98%) | 32 (43%) | 4 (5%) |
| All | All | 5507/6954 (79%) | 1360 (24%) | 32 (0%) |

5 of 1360 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 44 | L5 | 4 | G |
| 44 | L5 | 13 | U |
| 44 | L5 | 17 | A |
| 44 | L5 | 21 | G |
| 44 | L5 | 25 | A |

5 of 32 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 77 | S6 | 19 | G |
| 77 | S6 | 53 | G |
| 44 | L5 | 3271 | G |
| 44 | L5 | 2540 | C |
| 77 | S6 | 54 | A |

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

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

## 5.5 Carbohydrates

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 278 ligands modelled in this entry, 278 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)

There are no chain breaks in this entry.

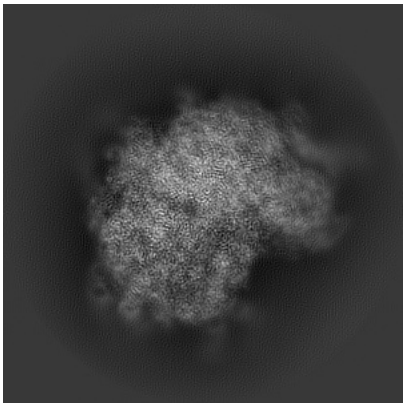
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-30432. These allow visual inspection of the internal detail of the map and identification of artifacts.

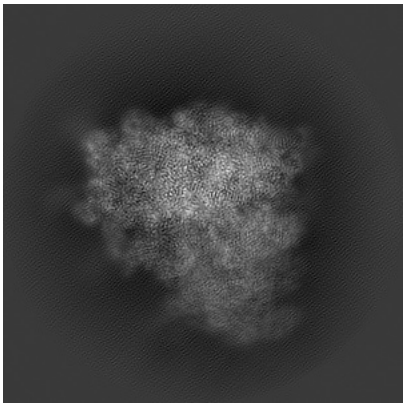
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

## 6.1 Orthogonal projections

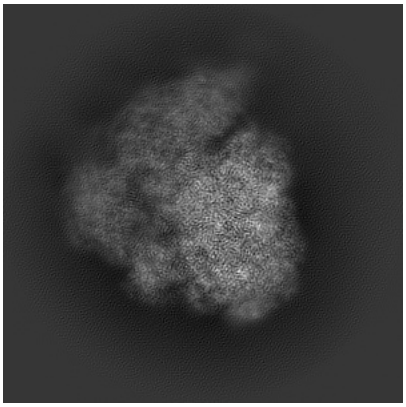
### 6.1.1 Primary map



X



Y

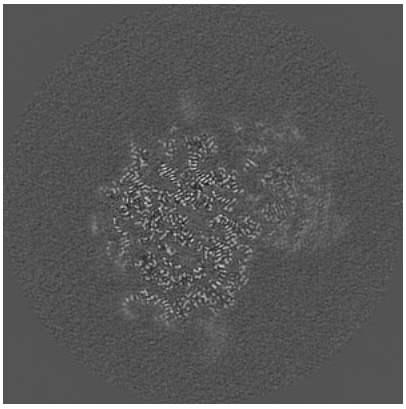


Z

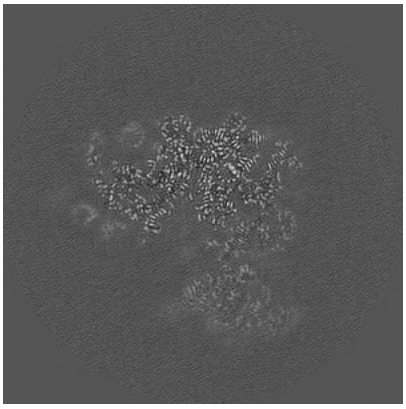
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices

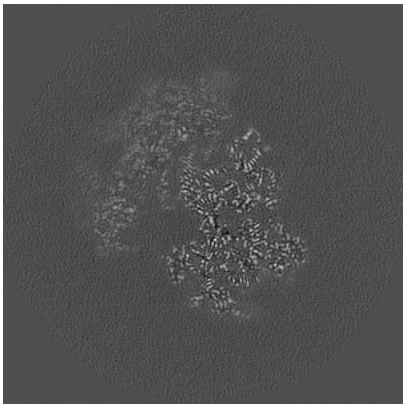
### 6.2.1 Primary map



X Index: 200



Y Index: 200

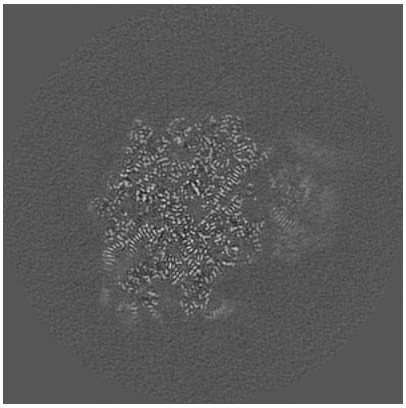


Z Index: 200

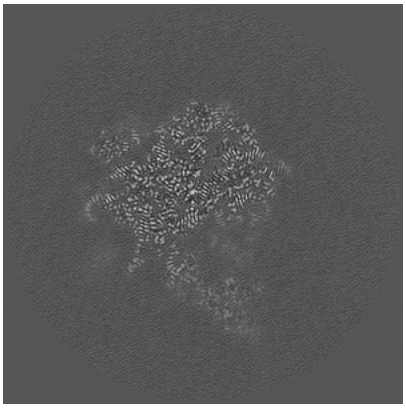
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

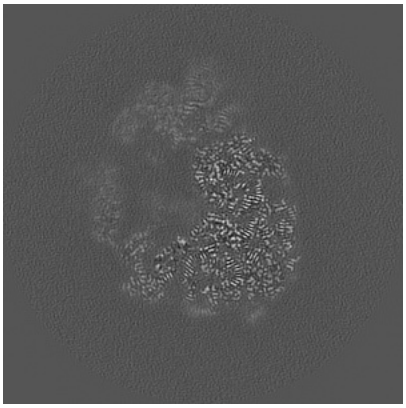
### 6.3.1 Primary map



X Index: 219



Y Index: 159

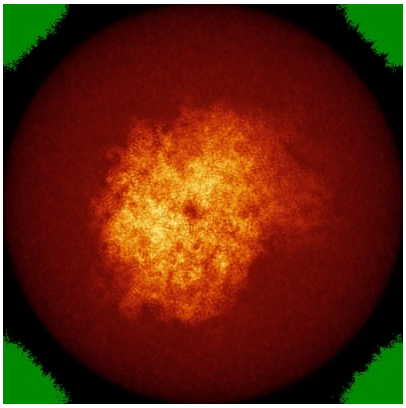


Z Index: 181

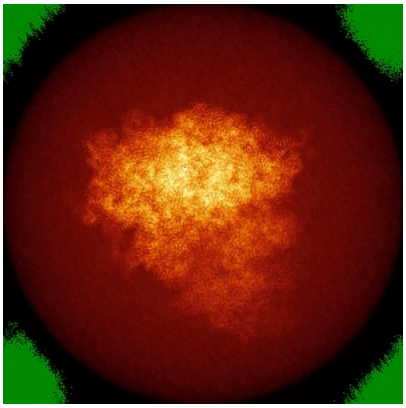
The images above show the largest variance slices of the map in three orthogonal directions.

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

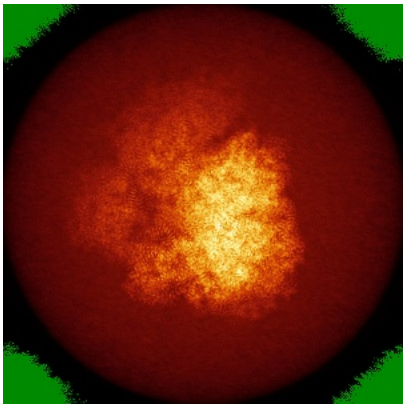
### 6.4.1 Primary map



X



Y

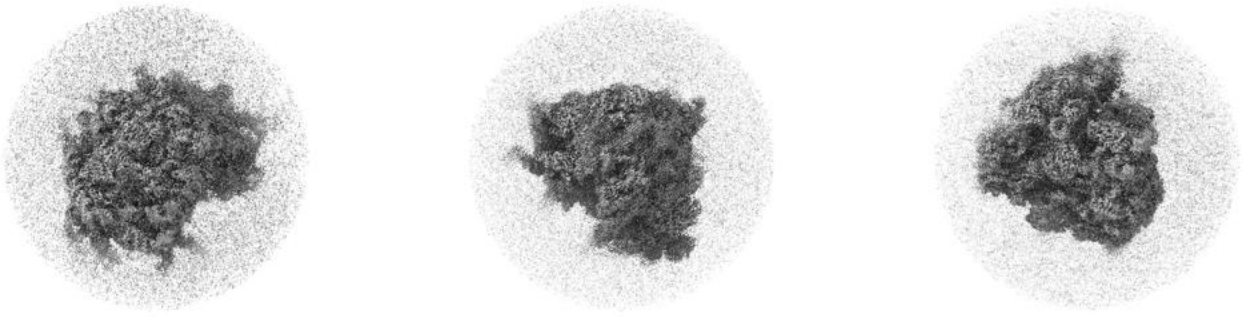


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

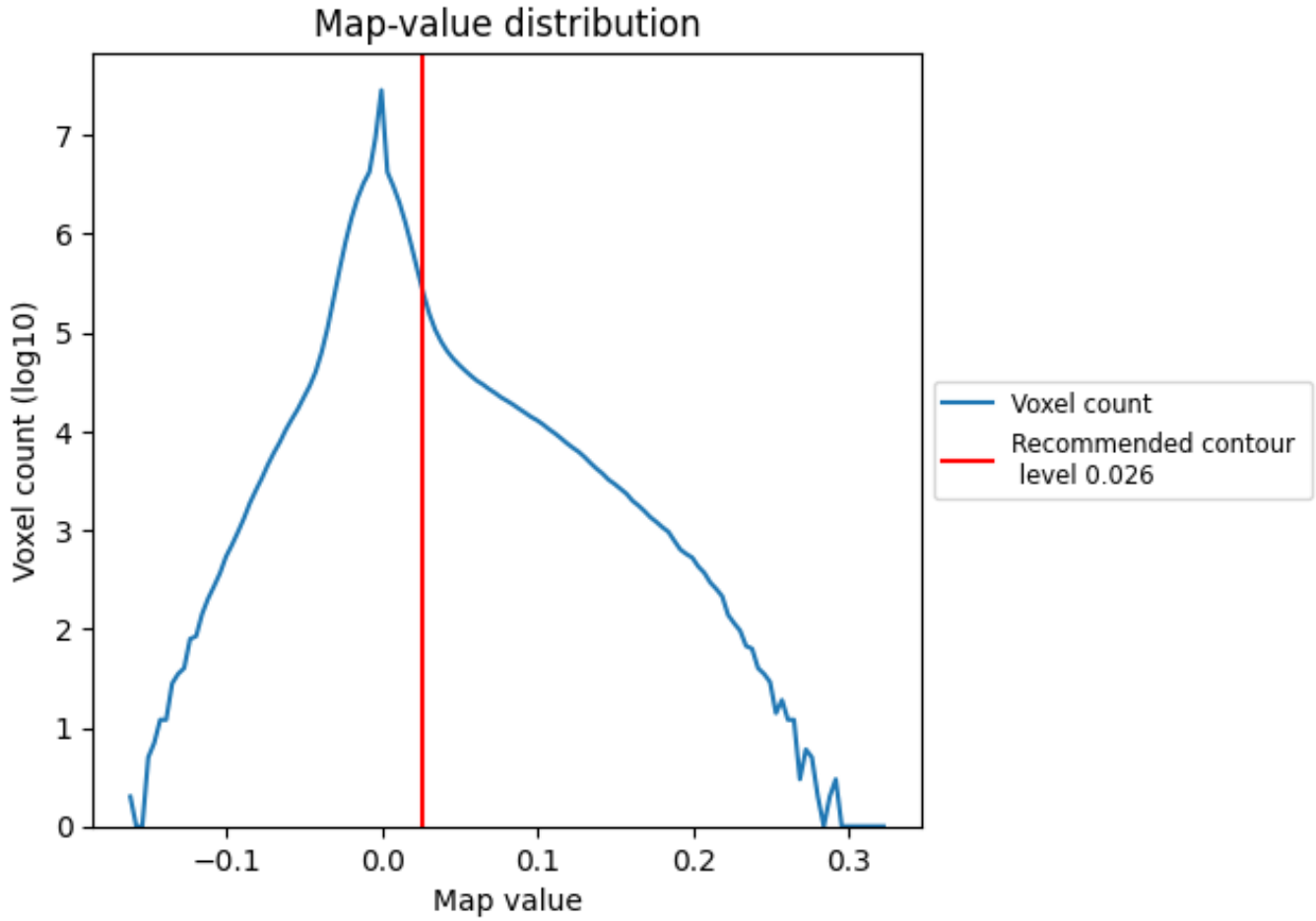
## 6.6 Mask visualisation (i)

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

# 7 Map analysis

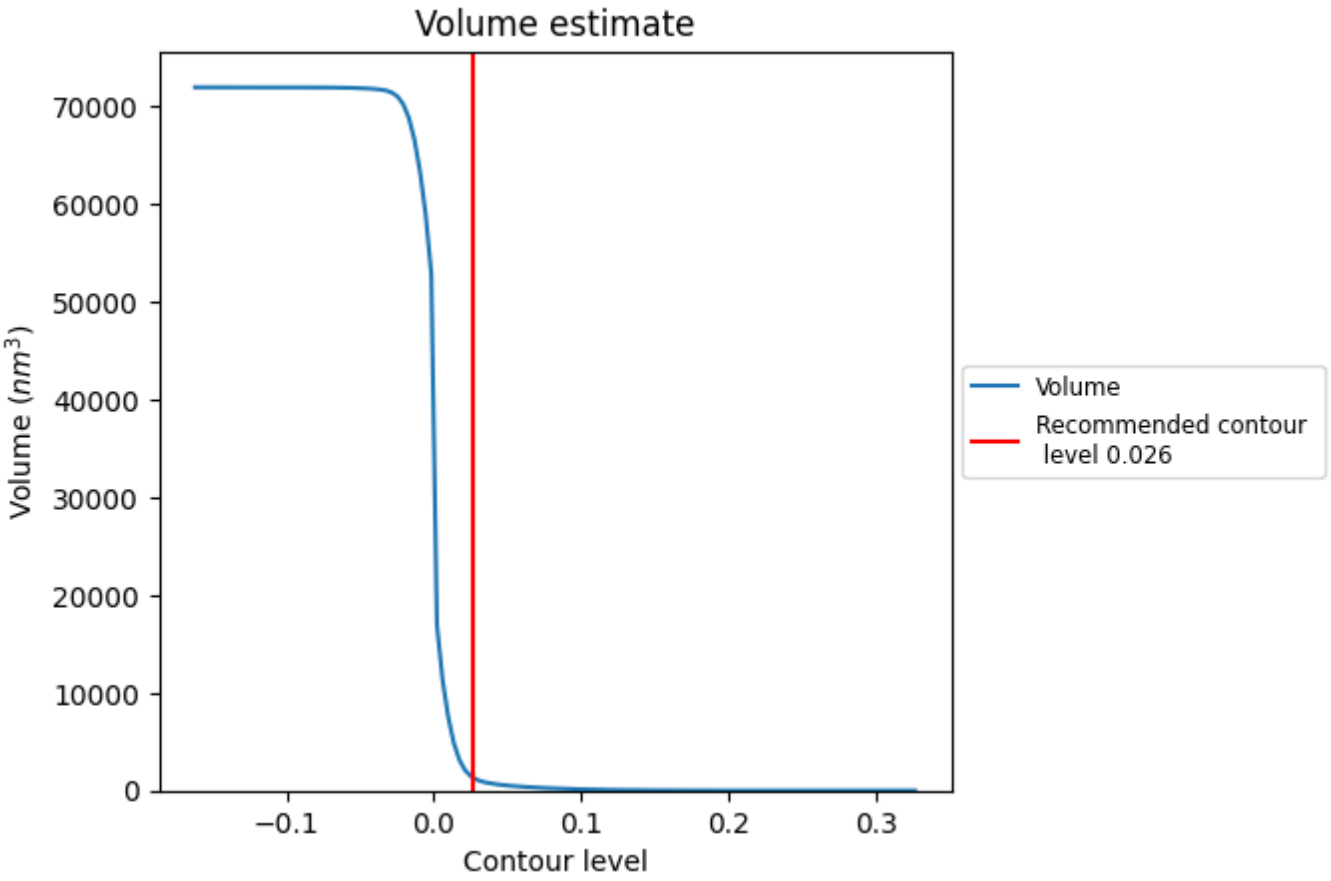
This section contains the results of statistical analysis of the map.

## 7.1 Map-value distribution




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.

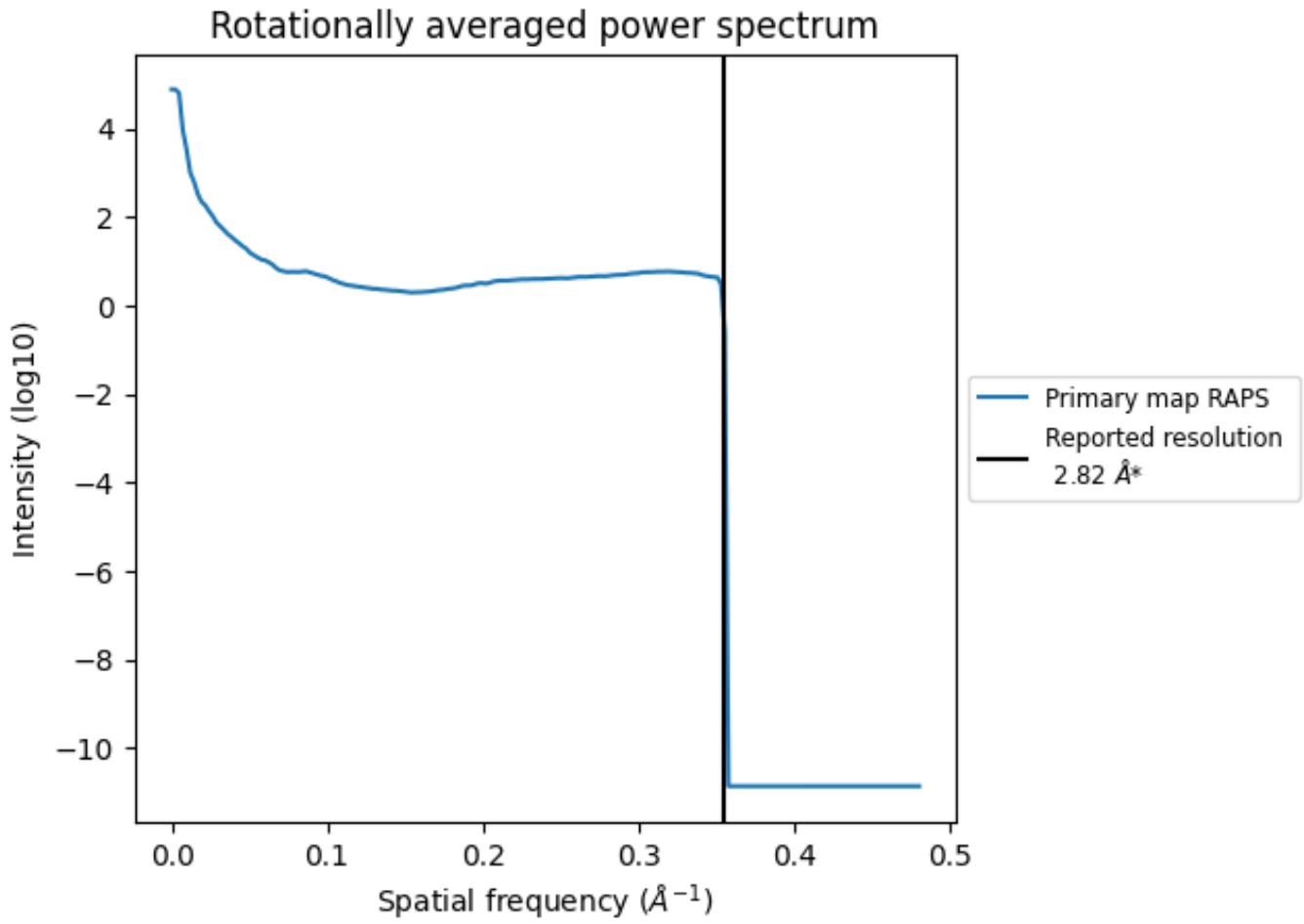
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 1382 $nm^3$; this corresponds to an approximate mass of 1248 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 (i)




*Reported resolution corresponds to spatial frequency of 0.355 Å$^{-1}$

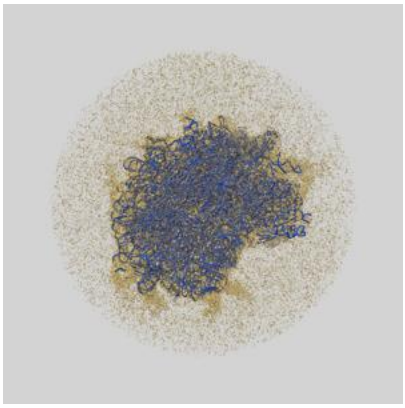
# 8 Fourier-Shell correlation (i)

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

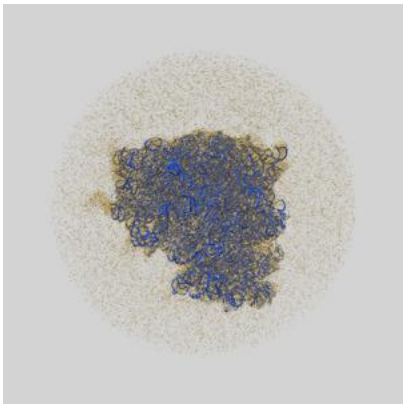
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-30432 and PDB model 7CPU. Per-residue inclusion information can be found in section 3 on page 19.

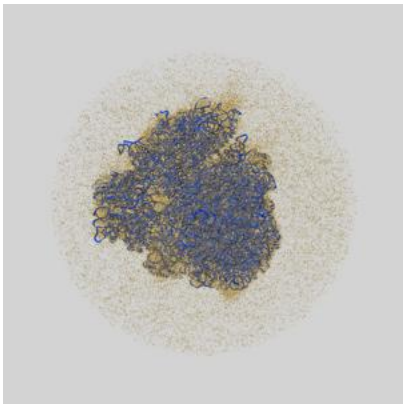
## 9.1 Map-model overlay



X



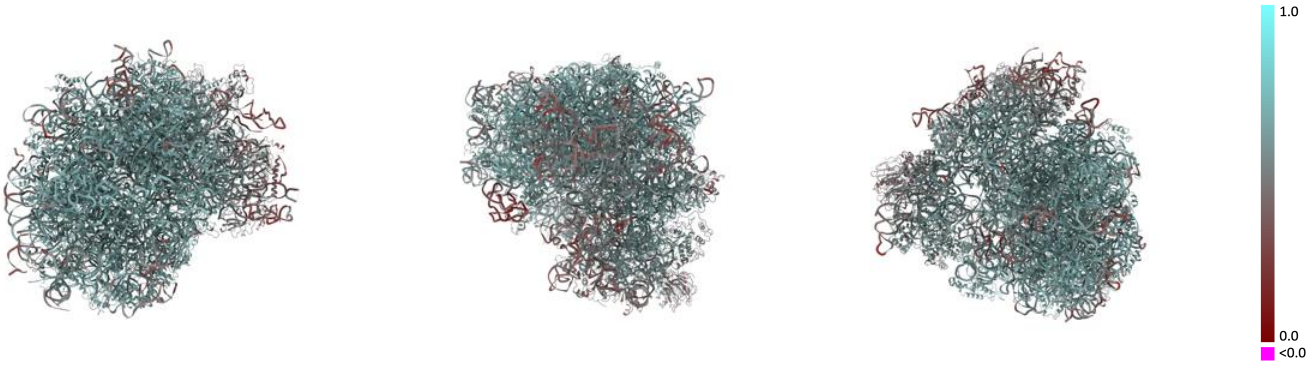
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.026 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.

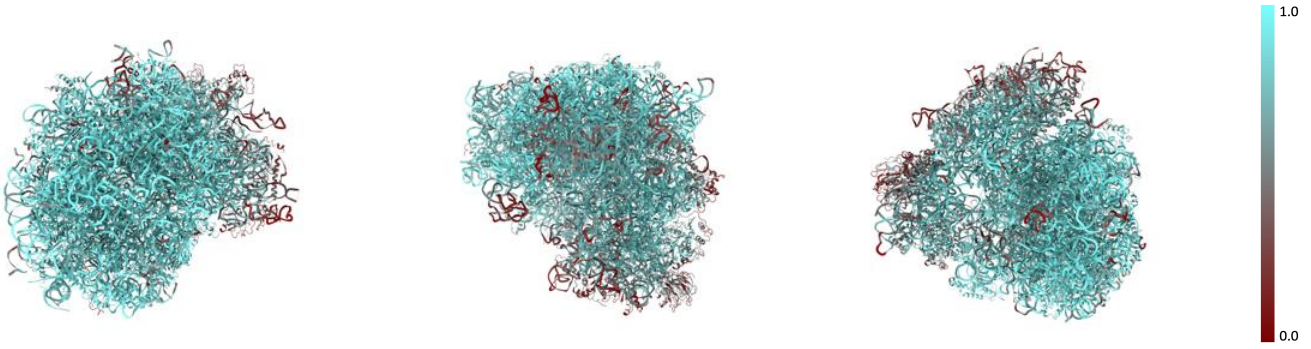
## 9.2 Q-score mapped to coordinate model (i)




X Y Z

The images above show the model with each residue coloured according 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.

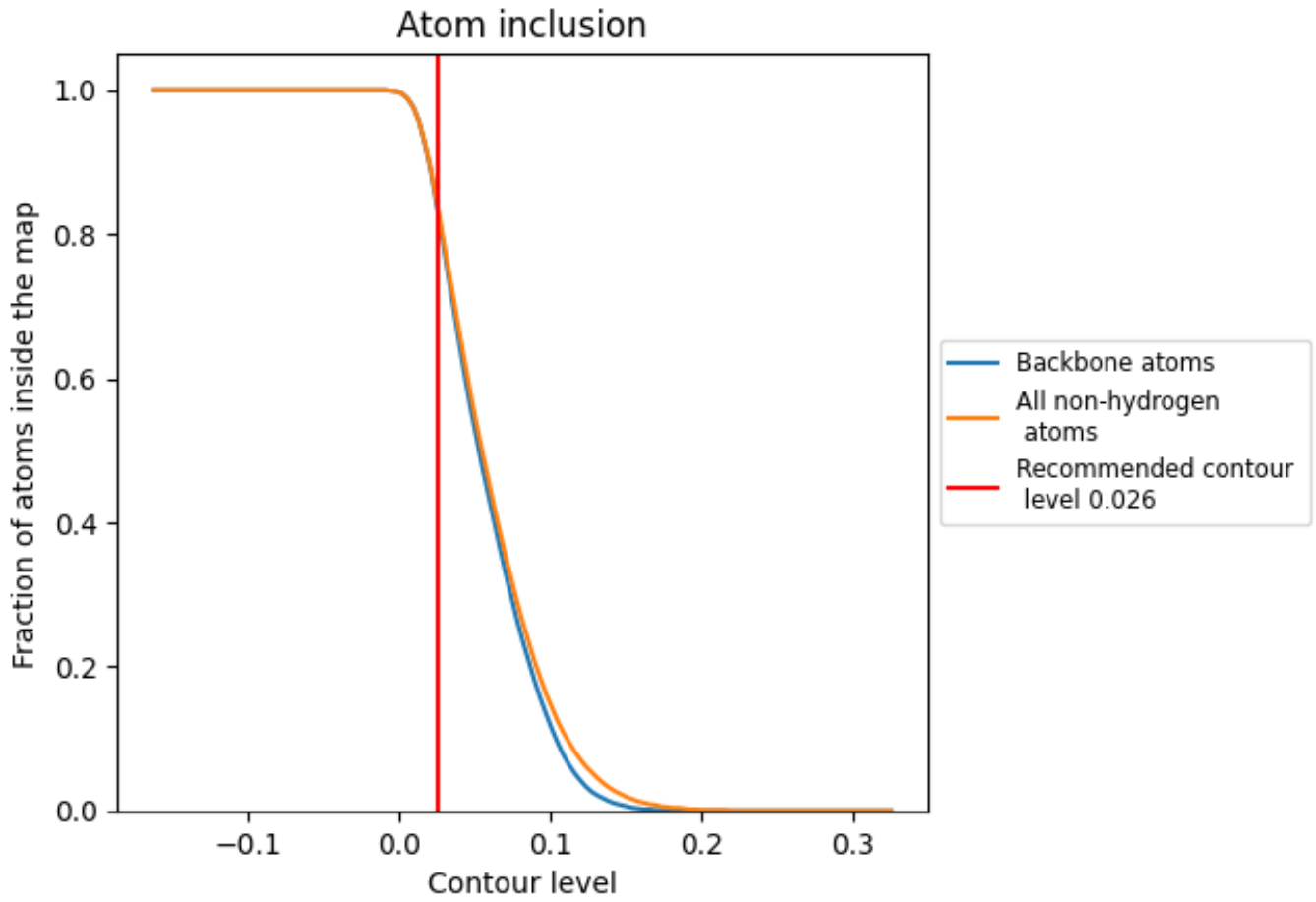
## 9.3 Atom inclusion mapped to coordinate model (i)




X Y Z

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 (0.026).

## 9.4 Atom inclusion (i)




At the recommended contour level, 83% of all backbone atoms, 83% 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 (0.026) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.8340 | 0.5800 |
| L5 | 0.9050 | 0.5950 |
| L7 | 0.9810 | 0.6350 |
| L8 | 0.9240 | 0.6160 |
| LA | 0.9410 | 0.6470 |
| LB | 0.9260 | 0.6370 |
| LC | 0.9170 | 0.6310 |
| LD | 0.9020 | 0.6180 |
| LE | 0.8350 | 0.5930 |
| LF | 0.9460 | 0.6470 |
| LG | 0.8500 | 0.6060 |
| LH | 0.9080 | 0.6220 |
| LI | 0.9240 | 0.6350 |
| LJ | 0.8410 | 0.5920 |
| LL | 0.8980 | 0.6180 |
| LM | 0.9370 | 0.6330 |
| LN | 0.9690 | 0.6540 |
| LO | 0.9370 | 0.6420 |
| LP | 0.9240 | 0.6410 |
| LQ | 0.9410 | 0.6510 |
| LR | 0.8490 | 0.6110 |
| LS | 0.9500 | 0.6510 |
| LT | 0.9030 | 0.6240 |
| LU | 0.8010 | 0.5750 |
| LV | 0.9220 | 0.6380 |
| LW | 0.9220 | 0.6360 |
| LX | 0.9020 | 0.6350 |
| LY | 0.9060 | 0.6300 |
| LZ | 0.8820 | 0.6120 |
| La | 0.9580 | 0.6520 |
| Lb | 0.8680 | 0.6130 |
| Lc | 0.8890 | 0.6130 |
| Ld | 0.8770 | 0.6240 |
| Le | 0.9450 | 0.6480 |
| Lf | 0.9600 | 0.6560 |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| Chain | Atom inclusion | Q-score |
|---|---|---|
| Lg | 0.9200 | 0.6350 |
| Lh | 0.8930 | 0.6290 |
| Li | 0.8680 | 0.6110 |
| Lj | 0.9550 | 0.6430 |
| Lk | 0.7910 | 0.6040 |
| Ll | 0.9310 | 0.6430 |
| Lm | 0.9290 | 0.6360 |
| Ln | 0.8170 | 0.6030 |
| Lo | 0.9010 | 0.6360 |
| Lp | 0.8940 | 0.6370 |
| Lr | 0.9360 | 0.6330 |
| S2 | 0.7820 | 0.5320 |
| S6 | 0.5950 | 0.4350 |
| SA | 0.6800 | 0.5450 |
| SB | 0.7620 | 0.5780 |
| SC | 0.7790 | 0.5800 |
| SD | 0.4550 | 0.4910 |
| SE | 0.5970 | 0.4910 |
| SF | 0.6650 | 0.5500 |
| SG | 0.4530 | 0.4760 |
| SH | 0.4940 | 0.4990 |
| SI | 0.6350 | 0.5060 |
| SJ | 0.5540 | 0.4460 |
| SK | 0.3160 | 0.4500 |
| SL | 0.7610 | 0.5690 |
| SN | 0.7530 | 0.5840 |
| SO | 0.7900 | 0.5810 |
| SP | 0.7020 | 0.5480 |
| SQ | 0.6520 | 0.5310 |
| SR | 0.5190 | 0.5050 |
| SS | 0.6940 | 0.5600 |
| ST | 0.6980 | 0.5500 |
| SU | 0.4130 | 0.4550 |
| SV | 0.6820 | 0.5480 |
| SW | 0.8430 | 0.6000 |
| SX | 0.7500 | 0.5810 |
| SY | 0.4430 | 0.4160 |
| SZ | 0.5720 | 0.5180 |
| Sa | 0.8150 | 0.5910 |
| Sb | 0.6540 | 0.5470 |
| Sc | 0.6020 | 0.5180 |
| Sd | 0.7520 | 0.5660 |

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| Chain | Atom inclusion | Q-score |
|---|---|---|
| Se | 0.5180 | 0.4890 |
| Sg | 0.3740 | 0.4500 |