# wwPDB EM Validation Summary Report (i)

Feb 13, 2024 – 04:50 PM EST

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|---|---|---|
| PDB ID | : | 3JAP |
| EMDB ID | : | EMD-3048 |
| Title | : | Structure of a partial yeast 48S preinitiation complex in closed conformation |
| Authors | : | Llacer, J.L.; Hussain, T.; Ramakrishnan, V. |
| Deposited on | : | 2015-06-18 |
| Resolution | : | 4.90 Å(reported) |
| Based on initial models | : | 4U1E, 2D74, 3CW2, 4U1D, 4U1C, 3J81 |

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

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

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

The following versions of software and data (see references (1)) were used in the production of this report:

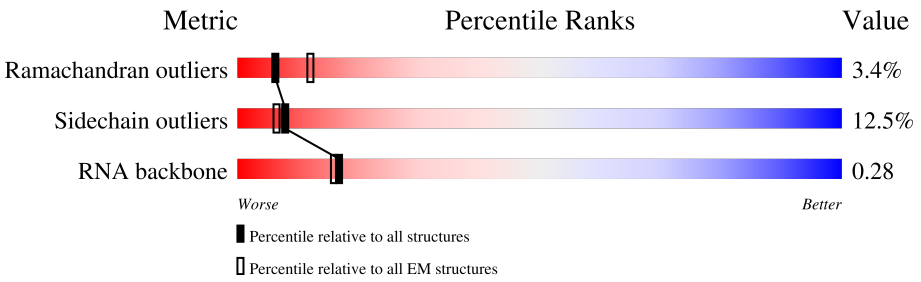
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev70 |
| Mogul | : | 1.8.5 (274361), CSD as541be (2020) |
| MolProbity | : | 4.02b-467 |
| buster-report | : | 1.1.7 (2018) |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| MapQ | : | 1.9.9 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.36 |

# 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 4.90 Å.

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




| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|---|---|---|
| Ramachandran outliers | 154571 | 4023 |
| Sidechain outliers | 154315 | 3826 |
| RNA backbone | 4643 | 859 |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% 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 | 1 | 75 | 28% 51% 49% |
| 2 | 2 | 1781 | 6% 49% 50% |
| 3 | 3 | 25 | 20% 12% 44% 44% |
| 4 | A | 254 | • 68% 13% • 18% |
| 5 | B | 255 | • 74% 13% 13% |
| 6 | C | 259 | • 73% 11% 16% |
| 7 | D | 237 | 5% 76% 18% 6% |
| 8 | E | 261 | • 84% 15% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 9 | F | 227 | 8% 73% 18% 9% |
| 10 | G | 236 | 86% 9% |
| 11 | H | 190 | 5% 78% 18% |
| 12 | I | 201 | 5% 83% 9% 6% |
| 13 | J | 188 | 84% 12% |
| 14 | K | 106 | 5% 69% 20% 9% |
| 15 | L | 156 | 11% 90% 8% |
| 16 | M | 134 | 22% 73% 14% 13% |
| 17 | N | 151 | 8% 87% 12% |
| 18 | O | 137 | 82% 9% 7% |
| 19 | P | 142 | 6% 67% 14% 18% |
| 20 | Q | 143 | 79% 19% |
| 21 | R | 136 | 6% 74% 14% 12% |
| 22 | S | 146 | 8% 77% 22% |
| 23 | T | 144 | 5% 85% 14% |
| 24 | U | 117 | 11% 78% 11% 9% |
| 25 | V | 87 | 89% 10% |
| 26 | W | 130 | 89% 9% |
| 27 | X | 145 | 80% 17% |
| 28 | Y | 135 | 89% 10% |
| 29 | Z | 108 | 13% 60% 35% |
| 30 | a | 119 | 70% 12% 18% |
| 31 | b | 82 | 90% 9% |
| 32 | c | 67 | 7% 81% 10% 7% |
| 33 | d | 56 | 5% 79% 14% 5% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 34 | e | 63 | 11% 71% 14% 14% |
| 35 | f | 150 | 9% 34% 11% • 54% |
| 36 | g | 326 | 9% 84% 13% • • |
| 37 | h | 25 | 56% 88% 12% |
| 38 | i | 153 | 7% 58% 14% 27% |
| 39 | j | 304 | 54% 67% 13% • 18% |
| 40 | k | 527 | 70% 69% 6% 25% |
| 41 | l | 285 | 42% 38% 7% 55% |
| 42 | m | 108 | 56% 69% 13% • 17% |
| 43 | o | 588 | 93% 85% 9% 6% |
| 44 | p | 652 | 93% 89% 8% • |
| 45 | q | 347 | 98% 93% 6% • |
| 46 | r | 31 | 100% 90% 10% |
| 47 | s | 52 | 100% 88% 12% |

# 2 Entry composition (i)

There are 51 unique types of molecules in this entry. The entry contains 98333 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 RNA chain called Met-tRNAi (U31:A39 variant).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 1 | 1 | 75 | 1607 | 716 | 296 | 520 | 75 | 0 | 0 |

- Molecule 2 is a RNA chain called 18S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 2 | 2 | 1780 | 37797 | 16892 | 6658 | 12467 | 1780 | 0 | 0 |

- Molecule 3 is a RNA chain called mRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | | |
| 3 | 3 | 14 | 287 | 129 | 42 | 102 | 14 | 0 | 0 |

- Molecule 4 is a protein called uS2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 4 | A | 208 | 1626 | 1040 | 286 | 298 | 2 | 0 | 0 |

- Molecule 5 is a protein called eS1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 5 | B | 222 | 1769 | 1117 | 324 | 325 | 3 | 0 | 0 |

- Molecule 6 is a protein called uS5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 6 | C | 217 | 1629 | 1041 | 287 | 297 | 4 | 0 | 0 |

- Molecule 7 is a protein called uS3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 7 | D | 223 | 1744 | 1108 | 313 | 318 | 5 | 0 | 0 |

- Molecule 8 is a protein called eS4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 8 | E | 260 | 2078 | 1322 | 393 | 359 | 4 | 0 | 0 |

- Molecule 9 is a protein called uS7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 9 | F | 206 | 1609 | 1008 | 298 | 300 | 3 | 0 | 0 |

- Molecule 10 is a protein called eS6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 10 | G | 226 | 1812 | 1134 | 348 | 326 | 4 | 0 | 0 |

- Molecule 11 is a protein called eS7.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 11 | H | 184 | 1483 | 950 | 270 | 263 | 0 | 0 |

- Molecule 12 is a protein called eS8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 12 | I | 188 | 1489 | 923 | 300 | 265 | 1 | 0 | 0 |

- Molecule 13 is a protein called uS4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 13 | J | 182 | 1471 | 929 | 287 | 254 | 1 | 0 | 0 |

- Molecule 14 is a protein called eS10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 14 | K | 96 | 809 | 533 | 129 | 146 | 1 | 0 | 0 |

- Molecule 15 is a protein called uS17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 15 | L | 155 | 1248 | 798 | 237 | 210 | 3 | 0 | 0 |

- Molecule 16 is a protein called eS12.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 16 | M | 117 | 885 | 553 | 161 | 171 | 0 | 0 |

- Molecule 17 is a protein called uS15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 17 | N | 150 | 1187 | 756 | 223 | 206 | 2 | 0 | 0 |

- Molecule 18 is a protein called uS11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 18 | O | 127 | 942 | 578 | 188 | 173 | 3 | 0 | 0 |

- Molecule 19 is a protein called uS19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 19 | P | 117 | 927 | 595 | 166 | 161 | 5 | 0 | 0 |

- Molecule 20 is a protein called uS9.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 20 | Q | 141 | 1105 | 709 | 204 | 192 | 0 | 0 |

- Molecule 21 is a protein called eS17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 21 | R | 120 | 959 | 598 | 178 | 180 | 3 | 0 | 0 |

- Molecule 22 is a protein called uS13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 22 | S | 145 | 1193 | 741 | 240 | 210 | 2 | 0 | 0 |

- Molecule 23 is a protein called eS19.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 23 | T | 143 | 1110 | 693 | 210 | 207 | 0 | 0 |

- Molecule 24 is a protein called uS10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 24 | U | 106 | 845 | 540 | 152 | 152 | 1 | 0 | 0 |

- Molecule 25 is a protein called eS21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 25 | V | 87 | 687 | 424 | 126 | 135 | 2 | 0 | 0 |

- Molecule 26 is a protein called uS8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 26 | W | 129 | 1021 | 651 | 187 | 180 | 3 | 0 | 0 |

- Molecule 27 is a protein called uS12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 27 | X | 144 | 1119 | 708 | 218 | 191 | 2 | 0 | 0 |

- Molecule 28 is a protein called eS24.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 28 | Y | 134 | 1061 | 665 | 207 | 189 | 0 | 0 |

- Molecule 29 is a protein called eS25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 29 | Z | 70 | 558 | 355 | 104 | 98 | 1 | 0 | 0 |

- Molecule 30 is a protein called eS26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 30 | a | 98 | 779 | 480 | 165 | 129 | 5 | 0 | 0 |

- Molecule 31 is a protein called eS27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 31 | b | 81 | 609 | 379 | 112 | 113 | 5 | 0 | 0 |

- Molecule 32 is a protein called eS28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 32 | c | 62 | 487 | 301 | 97 | 88 | 1 | 0 | 0 |

- Molecule 33 is a protein called uS14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 33 | d | 53 | 446 | 280 | 89 | 76 | 1 | 0 | 0 |

- Molecule 34 is a protein called eS30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 34 | e | 54 | 433 | 271 | 88 | 73 | 1 | 0 | 0 |

- Molecule 35 is a protein called eS31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 35 | f | 69 | 546 | 351 | 101 | 90 | 4 | 0 | 0 |

- Molecule 36 is a protein called RACK1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 36 | g | 318 | 2466 | 1561 | 430 | 470 | 5 | 0 | 0 |

- Molecule 37 is a protein called eL41.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 37 | h | 25 | 233 | 142 | 63 | 27 | 1 | 0 | 0 |

- Molecule 38 is a protein called eIF1A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 38 | i | 111 | 884 | 542 | 170 | 167 | 5 | 0 | 0 |

- Molecule 39 is a protein called eIF2 alpha.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 39 | j | 249 | 2006 | 1283 | 333 | 382 | 8 | 0 | 0 |

- Molecule 40 is a protein called eIF2 gamma.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 40 | k | 396 | 3034 | 1932 | 542 | 544 | 16 | 0 | 0 |

- Molecule 41 is a protein called eIF2 beta.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 41 | l | 128 | 1036 | 661 | 186 | 182 | 7 | 0 | 0 |

- Molecule 42 is a protein called eIF1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 42 | m | 90 | 716 | 452 | 132 | 128 | 4 | 0 | 0 |

- Molecule 43 is a protein called eIF3a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 43 | o | 550 | 4189 | 2667 | 721 | 794 | 7 | 0 | 0 |

- Molecule 44 is a protein called eIF3c.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 44 | p | 634 | 4899 | 3121 | 826 | 940 | 12 | 0 | 0 |

- Molecule 45 is a protein called eIF3i.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 45 | q | 342 | 2693 | 1711 | 443 | 530 | 9 | 0 | 0 |

- Molecule 46 is a protein called eIF3b.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | | |
| 46 | r | 31 | 277 | 177 | 48 | 50 | 2 | 0 | 0 |

- Molecule 47 is a protein called eIF3g.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | | |
| 47 | s | 52 | 418 | 257 | 82 | 79 | 0 | 0 |

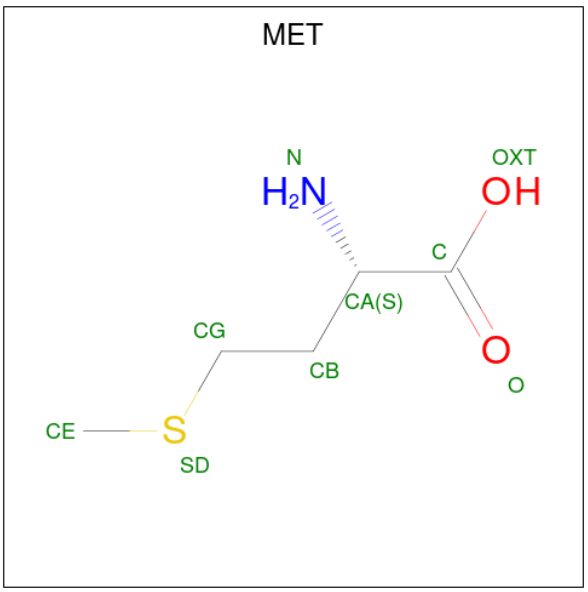
- Molecule 48 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| | | | Total | Mg | |
| 48 | 2 | 80 | 80 | 80 | 0 |
| 48 | k | 1 | 1 | 1 | 0 |

- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

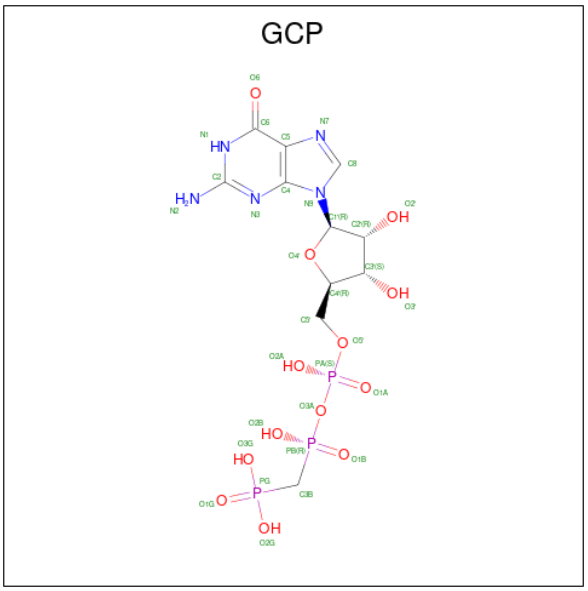
| Mol | Chain | Residues | Atoms | | AltConf |
|---|---|---|---|---|---|
| | | | Total | Zn | |
| 49 | a | 1 | 1 | 1 | 0 |
| 49 | b | 1 | 1 | 1 | 0 |
| 49 | f | 1 | 1 | 1 | 0 |
| 49 | l | 1 | 1 | 1 | 0 |

- Molecule 50 is METHIONINE (three-letter code: MET) (formula: $C_5H_{11}NO_2S$).




| Mol | Chain | Residues | Atoms | | | | | AltConf |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | S | |
| 50 | k | 1 | 8 | 5 | 1 | 1 | 1 | 0 |

- Molecule 51 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).



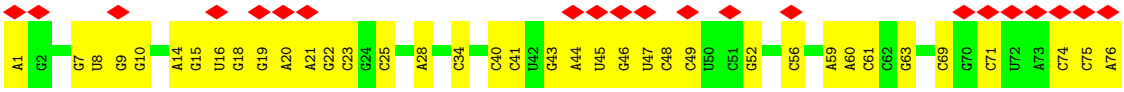

| Mol | Chain | Residues | Atoms | | | | | AltConf |
|---|---|---|---|---|---|---|---|---|
| | | | Total | C | N | O | P | |
| 51 | k | 1 | 32 | 11 | 5 | 13 | 3 | 0 |

# 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.

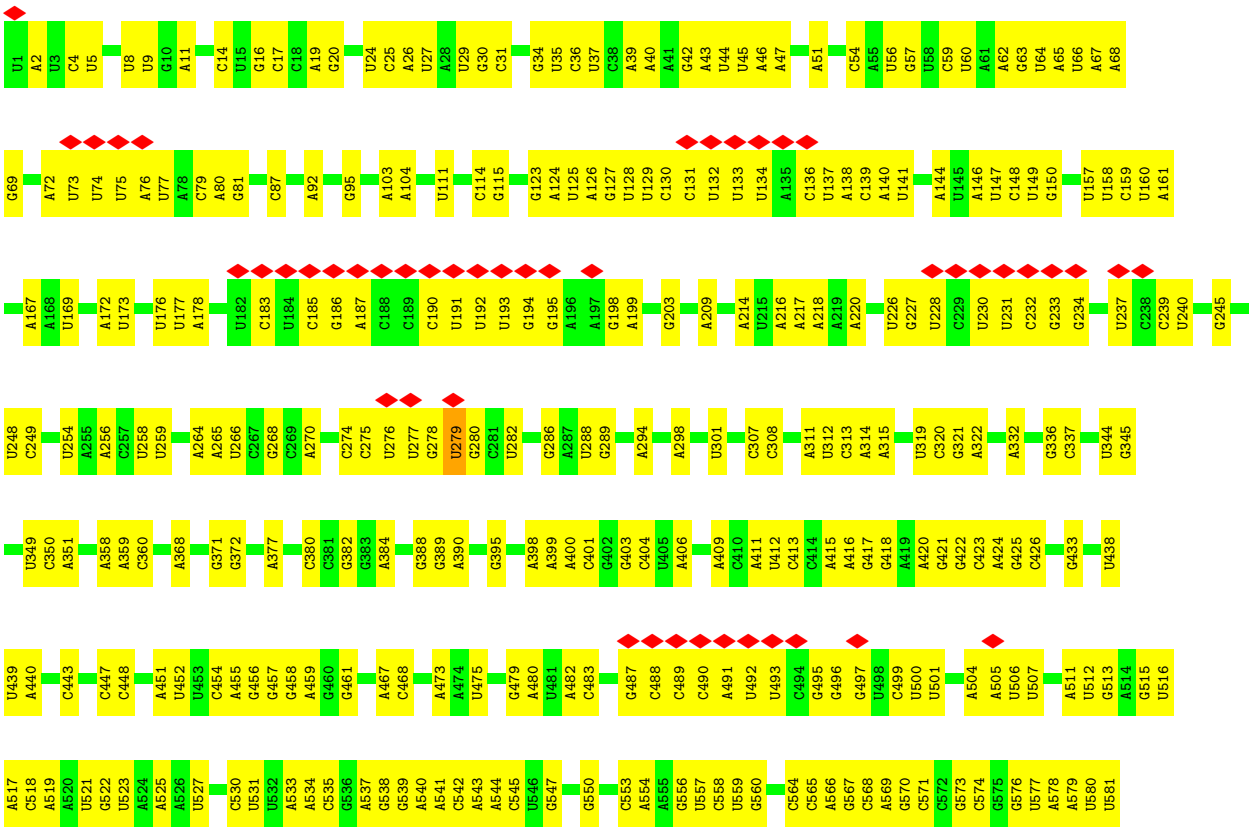
- Molecule 1: Met-tRNAi (U31:A39 variant)

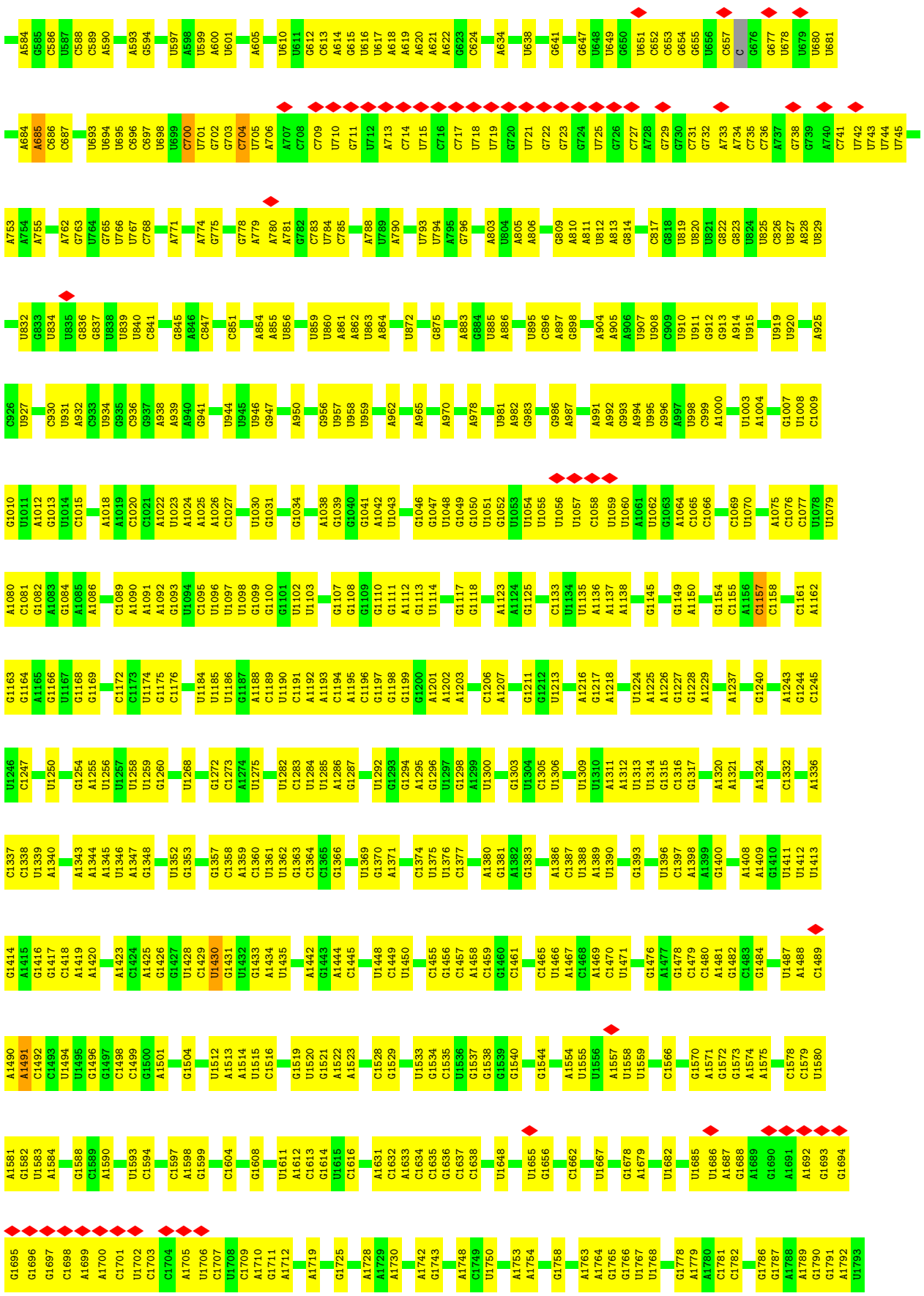
Chain 1:




- Molecule 2: 18S rRNA

Chain 2:




A584 G585 C586 U587 C588 C589 A590 A593 G594 U597 A598 U599 A600 U601 A605 U610 U611 G612 C613 A614 G615 U616 U617 A618 A619 A620 A621 A622 G623 C624 A634 U638 G641 G647 U648 U649 G650 U651 C652 C653 G654 G655 U656 C657 C G676 G677 U678 U679 U680 U681
A684 A685 C686 C687 U693 U694 U695 C696 C697 U698 U699 C700 U701 G702 G703 C704 U705 A706 A707 C708 C709 U710 G711 U712 A713 C714 U715 C716 C717 U718 U719 G720 U721 G722 G723 G724 U725 G726 C727 A728 G729 G730 C731 G732 A733 A734 C735 C736 A737 G738 G739 A740 C741 U742 U743 U744 U745
A753 A754 A755 A762 G763 U764 G765 U766 U767 C768 A771 A774 G775 G778 A779 A780 A781 G782 C783 U784 C785 A788 U789 A790 U793 U794 A795 G796 A803 U804 A805 A806 G809 A810 A811 U812 A813 G814 C817 G818 U819 U820 U821 G822 G823 U824 U825 C826 U827 A828 U829
U832 G833 U834 U835 G836 G837 U838 U839 U840 C841 G845 A846 C847 C851 A854 A855 U856 U859 U860 A861 A862 U863 A864 U872 G875 A883 G884 U885 A886 U895 C896 A897 G898 A904 A905 A906 U907 U908 C909 U910 U911 G912 G913 A914 U915 U919 U920 A925
C926 U927 C930 U931 A932 C933 U934 G935 C936 G937 A938 A939 A940 G941 U944 U945 U946 G947 A950 G956 U957 U958 U959 A962 A965 A970 A978 U981 A982 G983 G986 A987 A991 A992 G993 A994 U995 G996 A997 U998 C999 A1000 U1003 A1004 G1007 U1008 C1009
G1010 U1011 A1012 G1013 U1014 C1015 A1018 A1019 C1020 C1021 A1022 U1023 A1024 A1025 A1026 C1027 U1030 G1031 G1034 A1038 G1039 G1040 G1041 A1042 U1043 G1046 G1047 U1048 G1049 G1050 U1051 G1052 U1053 U1054 U1055 U1056 U1057 C1058 U1059 U1060 A1061 U1062 G1063 A1064 C1065 C1066 C1069 U1070 A1075 C1076 C1077 U1078 U1079
A1080 C1081 G1082 A1083 G1084 A1085 A1086 C1089 A1090 A1091 A1092 G1093 U1094 C1095 U1096 U1097 U1098 G1099 G1100 G1101 U1102 U1103 G1107 G1108 G1109 G1110 G1111 A1112 G1113 U1114 G1117 G1118 A1123 A1124 G1125 C1133 U1134 U1135 A1136 A1137 A1138 G1145 G1149 A1150 G1154 C1155 A1156 C1157 C1158 C1161 A1162
G1163 G1164 A1165 G1166 U1167 G1168 G1169 C1172 C1173 U1174 G1175 C1176 U1184 U1185 U1186 G1187 A1188 G1189 U1190 C1191 A1192 A1193 C1194 A1195 C1196 G1197 G1198 G1199 G1200 A1201 A1202 A1203 C1206 A1207 G1211 G1212 U1213 A1216 G1217 A1218 U1224 A1225 A1226 G1227 G1228 A1229 A1237 G1240 A1243 G1244 C1245
U1246 C1247 U1250 G1254 A1255 U1256 U1257 U1258 U1259 G1260 U1268 G1272 C1273 A1274 U1275 U1282 C1283 C1284 U1285 A1286 G1287 U1292 G1293 G1294 A1295 G1296 U1297 G1298 A1299 U1300 G1303 U1304 C1305 U1306 U1309 U1310 A1311 A1312 U1313 U1314 G1315 C1316 G1317 A1320 A1321 A1324 C1332 A1336
C1337 C1338 U1339 A1340 A1343 A1344 A1345 U1346 A1347 G1348 U1352 G1353 G1357 C1358 A1359 C1360 U1361 U1362 G1363 C1364 C1365 G1366 U1369 G1370 A1371 C1374 U1375 U1376 C1377 A1380 G1381 A1382 G1383 A1386 C1387 U1388 A1389 U1390 G1393 U1396 C1397 A1398 A1399 G1400 A1408 A1409 G1410 U1411 U1412 U1413
G1414 A1415 G1416 G1417 C1418 A1419 A1420 A1423 C1424 A1425 G1426 G1427 U1428 C1429 U1430 G1431 U1432 G1433 A1434 U1435 A1442 G1443 A1444 C1445 U1448 C1449 U1450 C1455 G1456 C1457 A1458 C1459 G1460 C1461 C1465 U1466 A1467 C1468 A1469 C1470 U1471 G1476 A1477 G1478 C1479 C1480 A1481 G1482 C1483 G1484 U1487 A1488 C1489
A1490 A1491 C1492 C1493 U1494 U1495 G1496 G1497 C1498 C1499 G1500 A1501 G1504 U1512 A1513 A1514 U1515 C1516 G1519 U1520 G1521 A1522 A1523 C1528 G1529 U1533 G1534 C1535 U1536 G1537 G1538 G1539 G1540 G1544 A1554 U1555 U1556 A1557 U1558 U1559 C1566 G1570 A1571 G1572 G1573 A1574 A1575 C1578 C1579 U1580
A1581 G1582 U1583 A1584 G1588 C1589 A1590 U1593 C1594 C1597 A1598 G1599 C1604 G1608 U1611 A1612 C1613 G1614 U1615 C1616 A1631 C1632 A1633 C1634 C1635 G1636 C1637 C1638 U1648 U1655 G1656 C1662 U1667 G1678 A1679 U1682 U1685 U1686 A1687 G1688 A1689 G1690 A1691 A1692 G1693 G1694
G1695 G1696 G1697 C1698 A1699 A1700 C1701 U1702 C1703 C1704 A1705 U1706 C1707 U1708 C1709 A1710 G1711 A1712 A1719 G1725 A1728 A1729 A1730 A1742 G1743 A1748 C1749 U1750 A1753 A1754 G1758 A1763 A1764 G1765 G1766 U1767 U1768 G1778 A1779 A1780 C1781 C1782 G1786 G1787 A1788 A1789 G1790 G1791 A1792 U1793

C1794 A1795 U1796 U1797 A1798

- Molecule 3: mRNA

Chain 3:

G G A A3 U4 C5 U6 C7 U8 C9 U10 C11 U12 A13 C16 U C U C U C U C

- Molecule 4: uS2

Chain A:

MET S2 R21 G25 E34 K39 A40 R41 P42 D43 V58 L59 I63 N69 P70 E71 R79 T80 R84 T93 G94 A95 T96 T103 T108 N109 T112 R113 R119 L120 V121 I122 E135 V143 V158 R165 G166 K167 I170 T192

Q193 P194 W195 A196 I197 M198 L201 Y202 R205 E209 ILE GLU GLN GLN THR ALA GLU GLU GLU ALA VAL ALA SER GLY GLU GLN THR GLU GLU ALA VAL ASP ALA THR GLU GLU GLN THR GLU ALA ALA GLU TRP ALA GLU GLU GLY GLN ALA GLN GLU GLU GLU TRP ASN

- Molecule 5: eS1

Chain B:

MET ALA V3 G4 L9 SER LYS GLY LYS LYS GLY LEU LYS LYS R19 D22 E28 L47 G53 L54 R64 V68 C69 L70 D78 R82 K83 V84 D104 R111 Q118 T119 V125 T126 V127 I140 N148 E170 Q177 L181 L184

I189 P190 E196 F205 P206 L207 Q208 R213 K214 K219 Q220 P221 D224 L228 G233 GLU ALA SER ALA GLU GLU LYS GLY LYS LYS VAL ALA GLY PHE LYS ASP GLU ILE LEU GLU THR VAL

- Molecule 6: uS5

Chain C:

MET SER ALA PRO GLN ALA GLN GLY GLY GLN GLN GLN ALA ALA PRO ARG ARG ARG GLY GLY PHE GLY GLY ALA ASN ARG GLY GLY GLY ARG GLY GLY ARG ARG ARG GLY GLY ARG ARG ASP GLN GLU GLU LYS G39 T44 I58 S65 F71 Q72 D75 L78 D83 M86 N87 I88 V91

Q92 K93 Q99 V109 N113 E125 R131 V141 R145 R146 Q155 K166 P187 K190 E199 I223 L234 W235 E236 L240 D246 T253 A254 S255 LYS LYS LYS LYS LEU

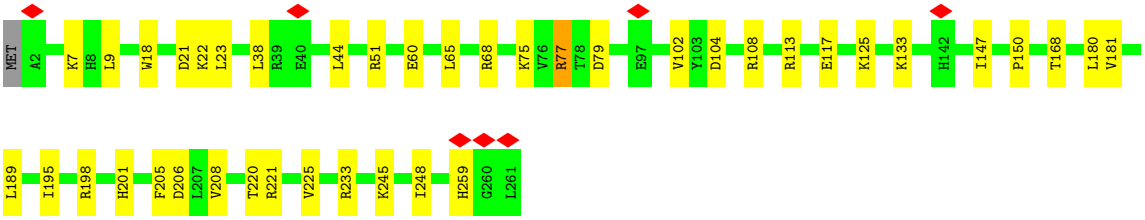
- Molecule 7: uS3

Chain D:

MET VAL A3 I4 I5 S6 V16 E20 E31 P43 R51 D57 G63 E68 L69 T70 K75 R76 D93 R94 E103 L109 L110 N111 G112 L113 R116 V122 E128 K132 L142 R143 A144 A145 R146 A147 K148 I158 P163 D166

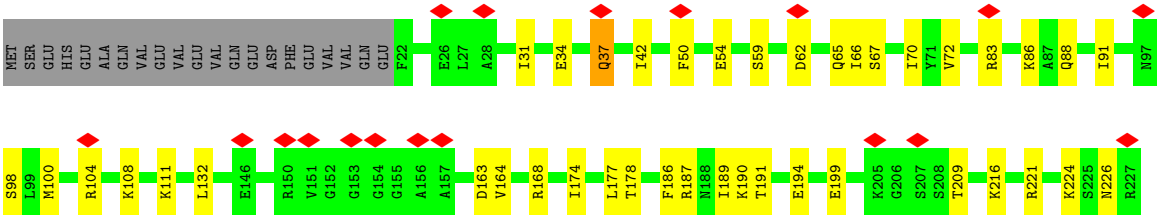
- Molecule 8: eS4

Chain E:



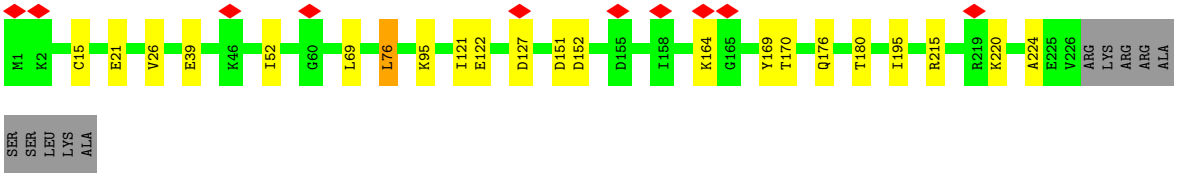

- Molecule 9: uS7

Chain F:



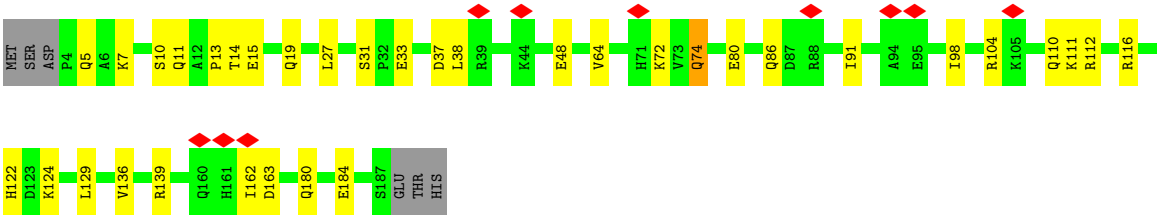

- Molecule 10: eS6

Chain G:



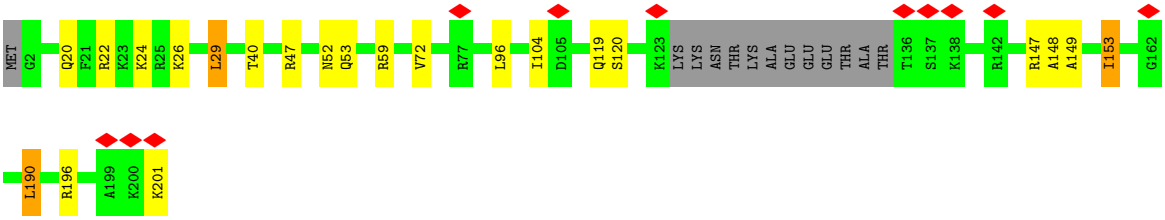

- Molecule 11: eS7

Chain H:



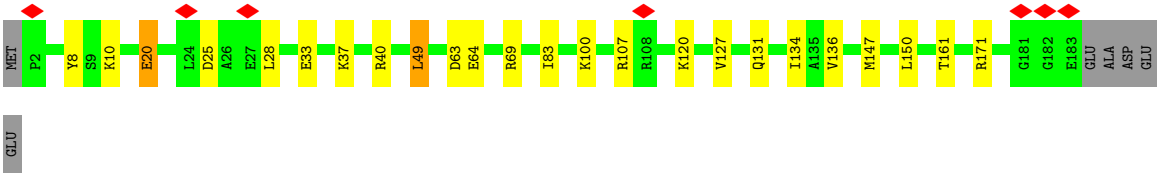

- Molecule 12: eS8

Chain I:



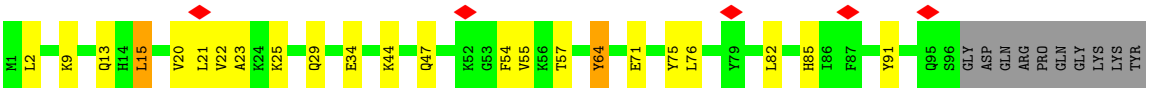

- Molecule 13: uS4

Chain J:



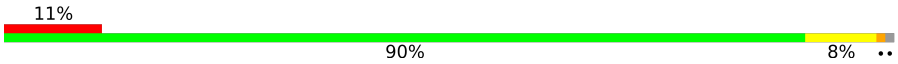

- Molecule 14: eS10

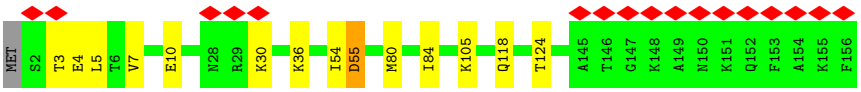
Chain K:




- Molecule 15: uS17

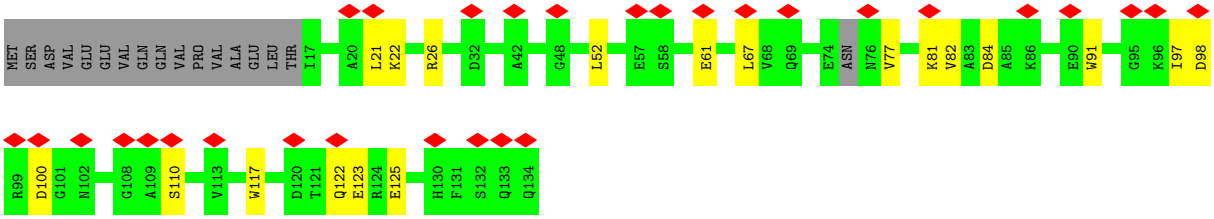
Chain L:



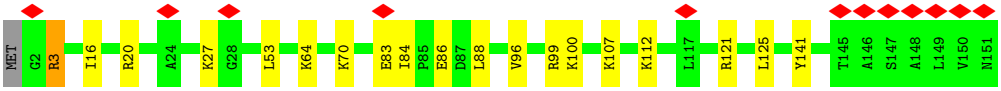

- Molecule 16: eS12

Chain M:



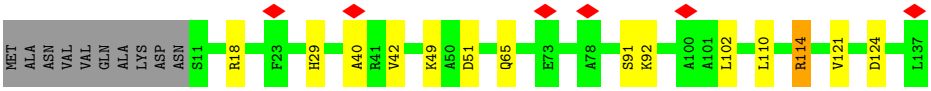

- Molecule 17: uS15

Chain N:



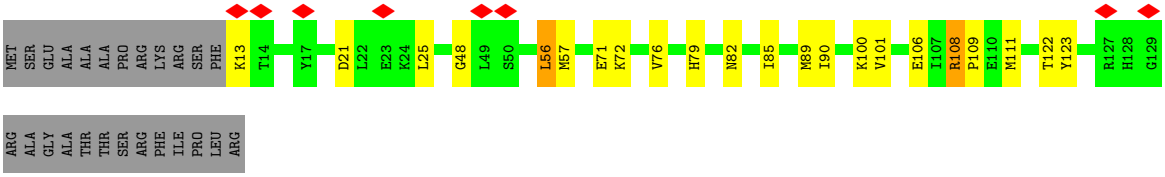
- Molecule 18: uS11

Chain O:



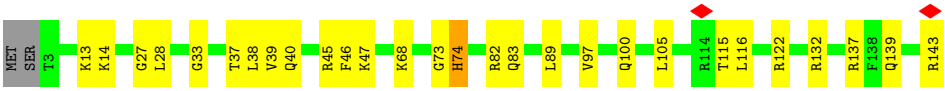

- Molecule 19: uS19

Chain P:



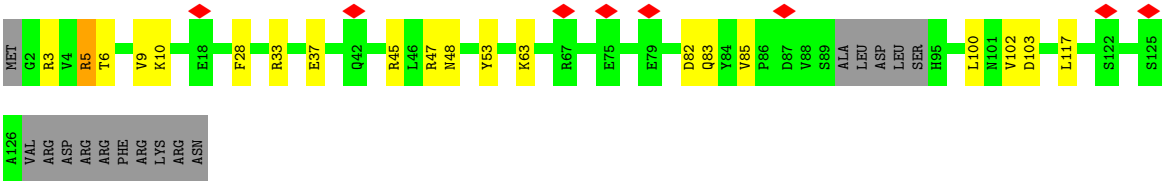

- Molecule 20: uS9

Chain Q:



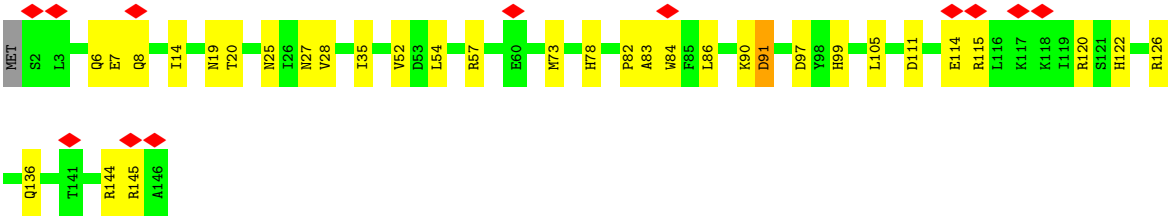

- Molecule 21: eS17

Chain R:



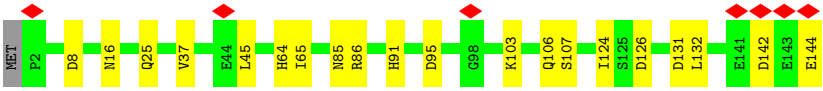

- Molecule 22: uS13

Chain S:

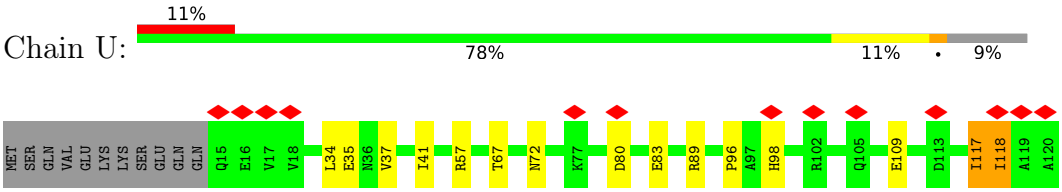



- Molecule 23: eS19

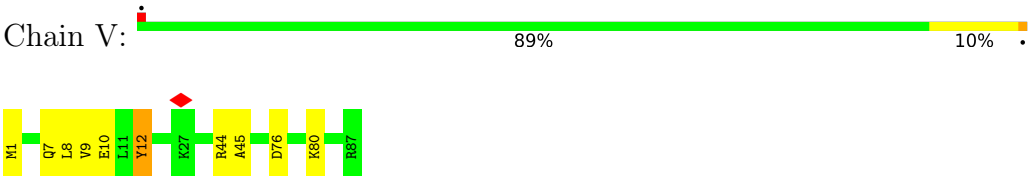
Chain T:



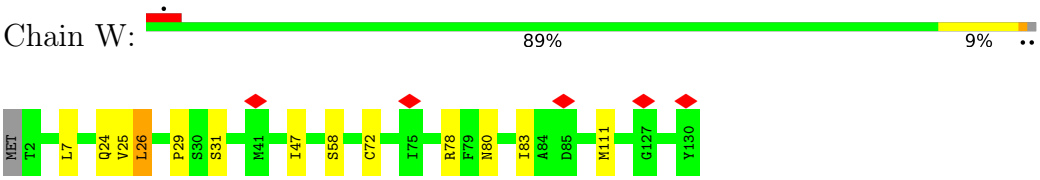

- Molecule 24: uS10



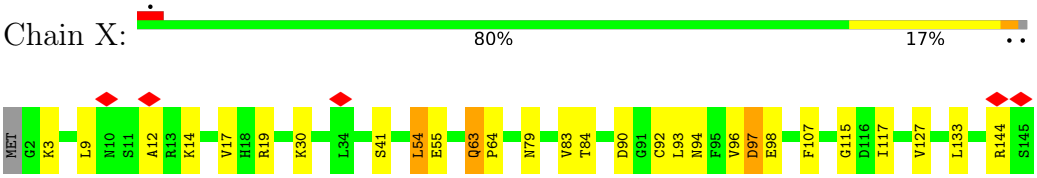

- Molecule 25: eS21



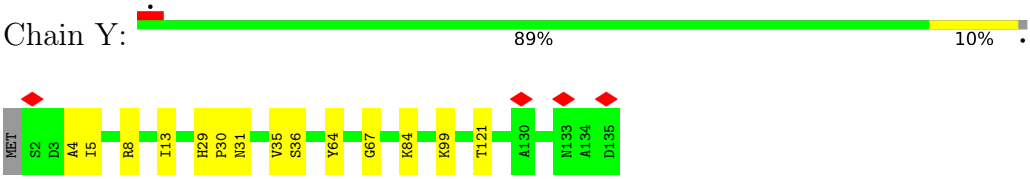

- Molecule 26: uS8



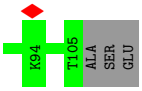

- Molecule 27: uS12




- Molecule 28: eS24

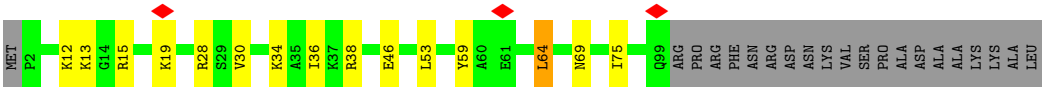



- Molecule 29: eS25



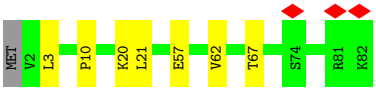

- Molecule 30: eS26

Chain a:



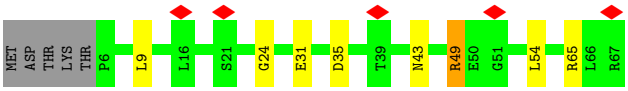

- Molecule 31: eS27

Chain b:



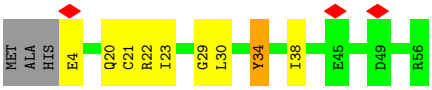

- Molecule 32: eS28

Chain c:



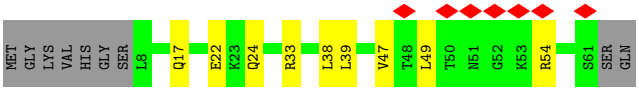

- Molecule 33: uS14

Chain d:



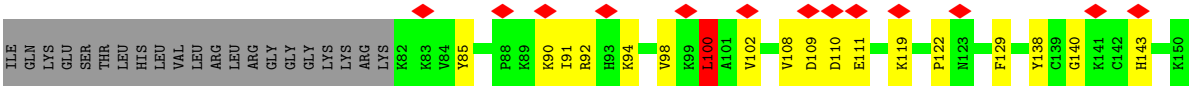

- Molecule 34: eS30

Chain e:



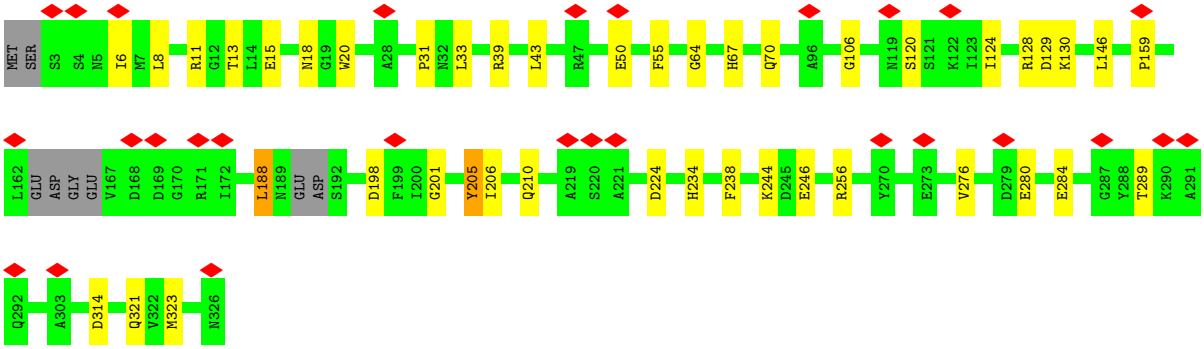

- Molecule 35: eS31

Chain f:



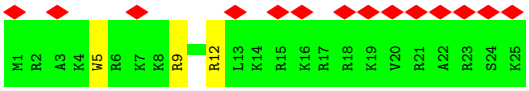
- Molecule 36: RACK1

Chain g:



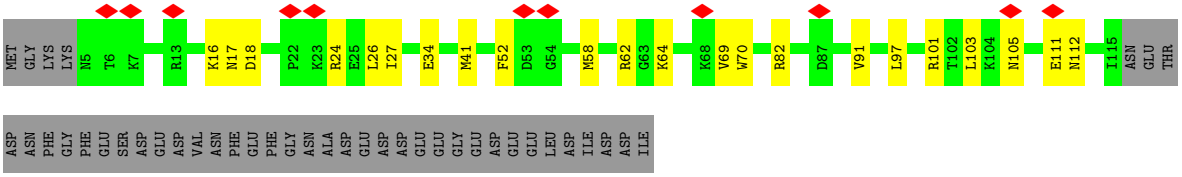

- Molecule 37: eL41

Chain h:



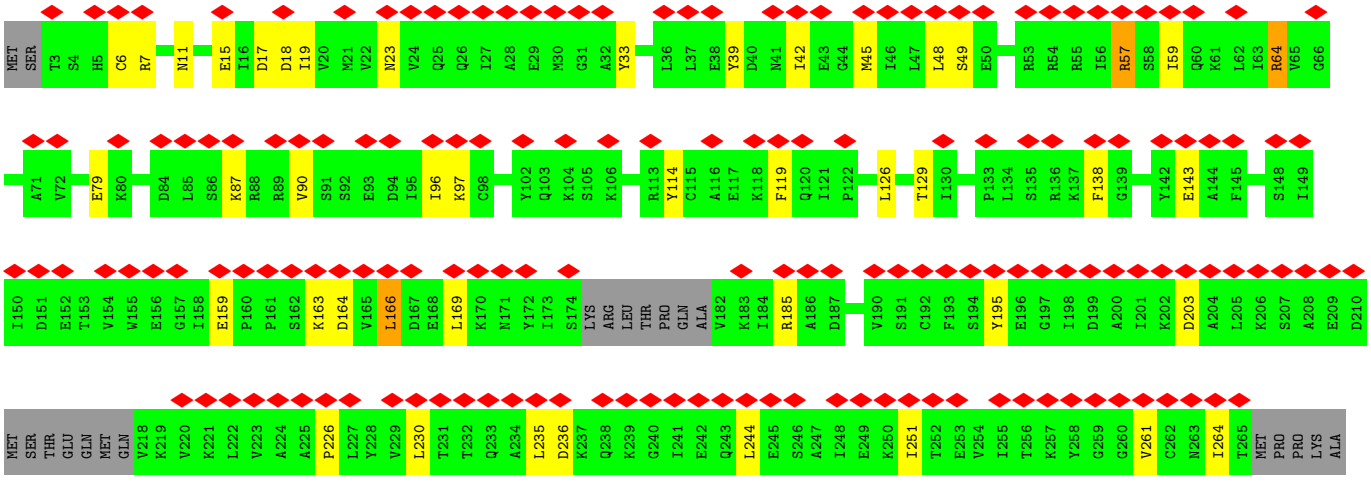

- Molecule 38: eIF1A

Chain i:




- Molecule 39: eIF2 alpha

Chain j:



VAL THR ALA THR GLU ASP ALA GLU LEU GLN ALA LEU LEU GLU SER LYS GLU LEU ASP ASN ARG SER ASP SER GLU ASP ASP GLU ASP GLU SER ASP ASP GLU

- Molecule 40: eIF2 gamma

Chain k: 70% 69% 6% 25%

MET SER ASP LEU GLN ASP GLN GLU PRO SER ILE ILE ILE ASN GLY ASN LEU GLU PRO VAL GLY GLU PRO ASP ILE VAL GLU GLU THR GLU VAL VAL ALA GLN GLU GLN THR GLN GLU THR GLN ASP ALA ASP LYS PRO LYS LYS LYS VAL ALA PHE THR GLY LEU GLU GLU ASP GLY GLU THR

GLU GLU GLU LYS ARG LYS ARG GLU PHE GLU GLU GLY GLY GLY LEU PRO GLU GLN PRO LEU ASN PRO ASP PHE SER LYS LEU ASN PRO LEU SER ALA GLU ILE ILE ASN ARG Q98 A99 T100 I101 N102 I103 G104 T105 I106 G107 H108 V109 A110 H111 S114 T115 V116 V117 R118 A119 I120 S121

G122 V123 Q124 T125 V126 R127 F128 K129 D130 E131 L132 E133 R134 N135 I136 T137 I138 K139 L140 G141 Y142 A143 N144 A145 K146 I147 Y148 K149 C150 Q151 E152 PRO THR CYS PRO GLU PRO ASP CYS TYR ARG SER PHE LYS SER ASP LYS E169 I170 S171 P172 K173 C174 Q175 R176 P177 G178 C179 P180 G181

R182 Y183 K184 L185 V186 R187 H188 V189 S190 F191 V192 D193 C194 P195 G196 H197 D198 I199 L200 M201 S202 T203 M204 L205 S206 G207 A208 A209 V210 M211 D212 A213 A214 L215 L216 L217 I218 A219 G220 N221 E222 S223 C224 P225 Q226 P227 Q228 E231 H232 L233 A234 A235 I236 E237 I238 M239 K240 L241 K242

H243 V244 I245 I246 L247 Q248 N249 K250 V251 D252 L253 M254 R255 E256 E257 S258 A259 L260 E261 H262 Q263 K264 S265 I266 L267 K268 F269 I270 R271 G272 T273 I274 A275 D276 G277 A278 P279 I280 V281 P282 I283 S284 A285 Q286 L287 K288 Y289 N290 I291 D292 A293 V294 N295 E296 F297 I298 V299 K300 T301 I302

P303 V304 P305 P306 R307 D308 F309 M310 I311 S312 P313 R314 I315 I316 V317 I318 R319 S320 F321 D322 V323 N324 K325 P326 G327 A328 E329 I330 E331 D332 I333 K334 G335 G336 V337 A338 G339 G340 S341 I342 I343 N344 F347 K348 L349 G350 D351 E352 I353 E354 I355 R356 P357 G358 I359 V360 T361 LYS ASP

ASP LYS GLY LYS I368 Q369 C370 K371 P372 I373 F374 S375 N376 I377 V378 S379 L380 F381 A382 E383 Q384 N385 D386 L387 K388 F389 A390 V391 P392 G393 G394 L395 I396 G397 V398 G399 T400 K401 V402 D403 P404 T405 L406 C407 R408 A409 D410 R411 L412 V413 G414 Q415 V416 V417 G418 A419 K420 G421 H422 L423

P424 N425 I426 Y427 T428 D429 I430 E431 I432 N433 Y434 F435 L436 L437 R438 R439 L440 L441 G442 V443 K444 THR ASP GLY GLN K449 Q450 A451 K452 V453 R454 K455 L456 E457 P458 N459 E460 V461 L462 M463 V464 N465 I466 G467 S468 T469 A470 T471 G472 A473 R474 V475 V476 A477 V478 K479 A480 D481 M482 A483

R484 L485 Q486 L487 T488 S489 P490 A491 C492 T493 E494 I495 N496 E497 K498 I499 A500 L501 S502 R503 R504 I505 E506 K507 H508 W509 R510 L511 I512 G513 W514 A515 T516 I517 K518 K519 GLY THR THR LEU GLU PRO ILE ALA

- Molecule 41: eIF2 beta

Chain l: 42% 38% 7% 55%

MET SER SER ASP LEU ALA ALA GLU LEU GLY PHE ASP PRO ALA LEU LYS LYS LYS LYS THR LYS LYS VAL ILE PRO ASP ASP PHE ASP ALA ALA VAL ASN GLY LYS GLU ASN GLY SER GLY ASP ASP LEU PHE ALA GLY LEU LYS LYS LYS LYS LYS LYS SER LYS SER VAL SER ALA

ASP ALA GLU ALA GLU LYS GLU PRO THR ASP ASP ILE ALA GLU ALA LEU LEU GLY GLU LEU SER LEU LYS LYS LYS LYS LYS LYS LYS THR LYS ASP SER SER VAL ASP ALA PHE GLU LYS GLU LEU ALA LYS ALA GLY LEU ASP ASN VAL ASP ALA GLU SER LYS GLU GLY THR PRO SER ALA ASN

SER SER ILE GLN GLN GLU V127 G128 L129 P130 Y131 S132 E133 L134 L135 S136 R137 F138 F139 N140 I141 L142 R143 THR ASN ASN PRO GLU LEU ALA GLY ASP ARG SER GLY PRO K157 F158 R159 I160 P161 P162 P163 V164 C165 L166 R167 D168 G169 K170 K171 T172 I173 N176 I177 Q178 D179 I180 A181

E182 K183 L184 H185 R186 S187 P188 E189 H190 L191 I192 Q193 Y194 L195 F196 A197 E198 L199 G200 T201 S202 G203 S204 V205 D206 G207 GLN K209 R210 L211 V212 I213 K214 G215 K216 F217 Q218 S219 K220 Q221 M222 E223 N224 V225 L226 R227 R228 Y229 I230 L231 E232 Y233 V234 T235 C236 K237 T238 C239 K240 S241

I242 N243 T244 E245 L246 K247 R248 E249 GLN SER N252 R253 L254 F255 F256 M257 V258 C259 K260 S261 C262 G263 S264 T265 R266 S267 V268 S269 S270 ILE LYS THR GLY PHE GLN ALA THR VAL GLY LYS ARG ARG ARG MET

- Molecule 42: eIF1

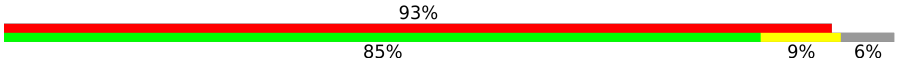
Chain m:

MET SER ILE GLU ASN LEU LYS SER PHE ASP PRO PHE ALA ASP THR GLY ASP ASP E19 T20 A21 T22 S23 N24 Y25 I26 H27 I28 R29 I30 R33 N34 G35 R36 K37 T38 L39 T40 T41 V42 Q43 G44 E48 I54 L55 K56 V57 L58 K59 K60 D61 F62 N65 G66 N67 I68

V69 K70 D71 P72 E73 M74 G75 E76 I77 T78 Q79 L80 Q81 G82 D83 Q84 R85 A86 K87 E90 F91 N92 I93 S94 Q95 L96 G97 L98 Q99 K100 K101 N102 I103 K104 I105 H106 G107 F108

- Molecule 43: eIF3a

Chain o:




MET ALA PRO PRO PRO F6 R7 P8 E9 N10 A11 I12 K13 R14 A15 D16 E17 L18 I19 S20 V21 G22 E23 K24 Q25 A26 A27 L28 Q29 S30 L31 H32 D33 F34 I35 T36 A37 R38 R39 I40 R41 W42 A43 T44 P45 S46 T47 V48 E49 P50 V51 V52 F53 K54 F55 L56 E57 I58 G59 V60

E61 L62 K63 K64 G65 K66 L67 L68 K69 D70 G71 L72 H73 Q74 Y75 K76 K77 L78 I79 Q80 G81 S82 T83 E84 G85 L86 V87 S88 V89 G90 A91 V92 A93 R94 K95 F96 I97 D98 L99 V100 E101 S102 K103 I104 A105 S106 E107 Q108 T109 R110 A111 D112 E113 L114 Q115 K116 Q117 E118 I119 D120

ASP ASP LEU GLU GLY GLY VAL THR PRO GLU ASN LEU LEU ILE SER VAL TYR GLU SER ASP GLN SER VAL ALA GLY PHE ASN ASP GLU A150 I151 T152 S153 W154 L155 R156 F157 T158 W159 E160 S161 Y162 R163 A164 V165 L166 D167 L168 L169 R170 N171 N172 A173 L174 L175 E176 I177 T178 Y179 S180

G181 V182 V183 K184 K185 T186 M187 H188 F189 C190 L191 K192 Y193 Q194 R195 K196 N197 E198 F199 K200 R201 L202 A203 E204 M205 L206 R207 Q208 H209 L210 D211 A212 A213 N214 Y215 Q216 Q217 S218 K219 S220 G221 N222 N223 LEU VAL ASP LEU S228 D229 A230 D231 T232 L233 Q234 R235 Y236 L237 D238 Q239 R240

F241 Q242 Q243 V244 D245 V246 S247 V248 K249 L250 E251 L252 W253 H254 E255 A256 Y257 R258 S259 I260 E261 D262 V263 F264 H265 L266 M267 K268 I269 S270 K271 R272 A273 P274 K275 P276 S277 T278 L279 A280 N281 Y282 Y283 E284 N285 L286 V287 K288 V289 F290 F291 V292 S293 G294 D295 P296 L297 L298 H299 T300

T301 A302 W303 K304 K305 F306 Y307 K308 L309 Y310 S311 T312 N313 P314 R315 A316 T317 E318 E319 E320 F321 K322 T323 Y324 S325 S326 T327 I328 F329 L330 S331 A332 I333 S334 T335 Q336 L337 D338 E339 I340 P341 S342 I343 G344 Y345 D346 P347 H348 L349 R350 M351 Y352 R353 L354 L355 N356 L357 D358 A359 K360

P361 T362 R363 K364 E365 M366 L367 Q368 S369 I370 I371 E372 D373 E374 S375 I376 Y377 G378 K379 V380 D381 E382 E383 L384 K385 E386 L387 Y388 D389 I390 I391 E392 V393 N394 F395 D396 V397 D398 T399 V400 K401 Q402 Q403 L404 E405 N406 L407 L408 V409 K410 L411 S412 S413 K414 T415 Y416 F417 S418 Q419 Y420

I421 A422 P423 L424 R425 D426 V427 I428 M429 R430 R431 V432 F433 V434 A435 A436 S437 Q438 K439 F440 T441 T442 V443 S444 Q445 S446 E447 L448 Y449 K450 L451 A452 T453 L454 P455 A456 P457 L458 D459 L460 S461 A462 W463 D464 I465 E466 K467 S468 L469 L470 Q471 A472 A473 V474 E475 D476 Y477 V478 S479 I480

T481 I482 D483 H484 E485 S486 A487 K488 V489 T490 F491 A492 K493 D494 P495 X753 X754 X755 X756 X757 X758 X759 X760 X761 X762 X763 X764 X765 X766 X767 X768 X769 X772 X773 X774 X775 X776 X777 X778 X779 X780 X781 X782 X783 X784 X785 X788 X789 X790 X791 X792 X793 X794 X795 X796 X797 X798 X799 X800 X801

X802 X806 X807 X808 X809 X810 X811 X812 X813 X814 X815 X816 X817 X818 X828 X829 X830 X831 X832 X833 X834 X837 X838 X839 X840 X841 X842 X843 X844 X845 X846 X850 X851 X852 X853 X854 X855 X856 X857 X858 X859 X860 X861 X862 X863 X864 X865 X866

- Molecule 44: eIF3c

Chain p: 93% 89% 8%

X20 X21 X22 X23 X24 X25 X26 X27 X28 X29 X30 X31 X32 X116 X117 X118 X119 X120 X121 X122 X123 X124 X125 X126 X127 X128 X129 X130 X131 X132 X133 X134 X135 X139 X140 X141 X144 X145 X146 X147 X148 X150 X151 X152 X153 X156 X157 X158 X170 X171 X172 X173 X174 X175 X176 X179 X180

X181 X182 X183 X184 X185 Y195 N196 T197 T198 K199 Q200 R201 V202 K203 K204 V205 S206 X211 X212 X213 X214 X215 X216 X217 X218 Q251 E252 D253 F254 F255 T256 R257 L258 Q259 T260 I261 I262 D263 S264 R265 G266 K267 K268 T269 V270 N271 Q272 Q273 S274 L275 I276 S277 T278 L279 E280 E281 L282 L283 T284

V285 A286 E287 K288 P289 Y290 E291 F292 I293 M294 A295 Y296 L297 T298 L299 I300 P301 S302 R303 F304 D305 A306 S307 A308 N309 L310 S311 Y312 Q313 P314 I315 D316 Q317 W318 K319 S320 S321 F322 N323 D324 I325 S326 K327 L328 L329 S330 I331 L332 D333 Q334 T335 I336 D337 T338 Y339 Q340 V341 N342 E343 F344

A345 D346 P347 I348 D349 F350 I351 E352 D353 E354 P355 K356 E357 D358 S359 D360 G361 V362 K363 R364 I365 L366 G367 S368 I369 F370 S371 F372 V373 E374 R375 L376 D377 D378 E379 F380 M381 K382 S383 L384 L385 N386 I387 D388 P389 H390 S391 S392 D393 Y394 L395 I396 R397 L398 R399 D400 E401 Q402 S403 I404

Y405 N406 L407 I408 L409 R410 T411 Q412 L413 Y414 F415 E416 A417 T418 L419 K420 D421 E422 H423 D424 L425 E426 R427 A428 L429 T430 R431 P432 F433 V434 K435 R436 L437 D438 H439 I440 Y441 Y442 K443 S444 E445 N446 L447 I448 K449 I450 M451 E452 T453 A454 A455 W456 N457 I458 I459 P460 A461 Q462 F463 K464

S465 K466 F467 T468 S469 K470 D471 Q472 L473 D474 S475 A476 D477 Y478 V479 D480 N481 L482 I483 D484 G485 L486 S487 T488 I489 L490 S491 K492 Q493 N494 N495 I496 A497 V498 Q499 K500 R501 A502 I503 L504 Y505 N506 I507 Y508 Y509 T510 A511 L512 N513 K514 D515 F516 Q517 T518 A519 K520 D521 M522 L523 L524

T525 S526 Q527 V528 Q529 T530 N531 I532 N533 Q534 F535 D536 S537 S538 L539 Q540 I541 L542 F543 N544 R545 V546 V547 V548 Q549 L550 G551 L552 S553 A554 F555 K556 L557 C558 L559 I560 E561 E562 C563 H564 Q565 I566 L567 N568 D569 L570 L571 S572 S573 S574 H575 L576 R577 E578 I579 L580 G581 Q582 Q583 S584

L585 H586 R587 I588 S589 L590 N591 S592 S593 N594 N595 A596 S597 A598 D599 E600 R601 A602 R603 Q604 C605 L606 P607 Y608 H609 Q610 H611 I612 N613 L614 D615 L616 I617 D618 V619 V620 F621 L622 T623 C624 S625 L626 L627 I628 E629 I630 P631 R632 M633 T634 A635 F636 Y637 S638 G639 I640 K641 V642 K643 R644

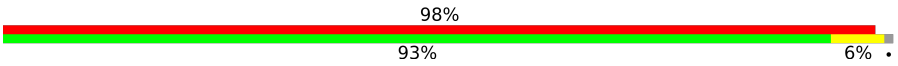
I645 P646 Y647 S648 P649 K650 S651 I652 R653 R654 S655 L656 E657 H658 Y659 D660 K661 L662 S663 F664 Q665 G666 P667 P668 E669 T670 L671 R672 D673 Y674 V675 L676 F677 A678 A679 K680 S681 M682 Q683 K684 G685 N686 W687 R688 D689 S690 V691 K692 Y693 L694 R695 E696 I697 K698 S699 W700 A701 L702 L703 P704

N705 M706 E707 T708 V709 L710 N711 S712 L713 T714 E715 R716 V717 Q718 V719 E720 S721 L722 K723 T724 Y725 F726 F727 S728 F729 K730 R731 F732 Y733 S734 S735 F736 S737 V738 A739 K740 L741 A742 E743 L744 F745 D746 L747 P748 E749 N750 K751 V752 V753 E754 V755 L756 Q757 S758 V759 I760 A761 E762 L763 E764

I765 P766 A767 K768 L769 N770 D771 E772 K773 T774 I775 F776 V777 V778 E779 K780 G781 D782 E783 I784 T785 K786 L787 E788 E789 A790 M791 V792 K793 L794 ASN LYS GLU TYR LYS ILE ALA LYS GLU ARG LEU ASN PRO PRO SER ASN ARG ARG

- Molecule 45: eIF3i

Chain q:




M1 K2 A3 I4 K5 L6 T7 G8 H9 E10 R11 P12 L13 T14 Q15 V16 K17 Y18 N19 K20 E21 G22 D23 L24 L25 F26 S27 C28 S29 K30 D31 S32 S33 A34 S35 V36 W37 Y38 S39 L40 N41 G42 E43 R44 L45 G46 T47 L48 D49 G50 H51 T52 G53 T54 I55 W56 S57 I58 D59 V60

D61 G62 F63 T64 K65 Y66 C67 V68 T69 G70 S71 A72 D73 Y74 S75 I76 K77 L78 W79 D80 Y81 S82 N83 G84 Q85 C86 V87 A88 T89 W90 K91 S92 P93 V94 P95 V96 K97 R98 V99 E100 F101 S102 P103 C104 G105 N106 Y107 F108 L109 A110 I111 L112 D113 N114 V115 M116 K117 N118 P119 G120

S121 I122 N123 I124 Y125 E126 I127 E128 R129 D130 S131 A132 T133 H134 E135 L136 T137 K138 V139 S140 E141 E142 P143 I144 H145 K146 I147 I148 T149 H150 E151 G152 L153 D154 A155 A156 T157 V158 A159 G160 W161 S162 T163 K164 G165 K166 Y167 I168 I169 A170 G171 H172 K173 D174 G175 K176 I177 S178 K179 Y180

D181 V182 S183 N184 N185 Y186 E187 Y188 V189 D190 S191 I192 D193 L194 H195 E196 K197 S198 I199 S200 D201 M202 Q203 F204 S205 P206 D207 L208 T209 Y210 F211 I212 T213 S214 S215 R216 D217 T218 N219 S220 F221 L222 V223 D224 V225 S226 T227 L228 Q229 V230 L231 K232 K233 Y234 E235 T236 D237 C238 P239 L240

N241 T242 A243 V244 I245 T246 P247 L248 K249 E250 F251 I252 I253 L254 G255 G256 G257 Q258 E259 A260 K261 D262 V263 T264 T265 T266 S267 A268 N269 E270 G271 K272 F273 E274 A275 R276 F277 Y278 H279 K280 I281 F282 E283 E284 E285 I286 G287 R288 V289 Q290 G291 H292 F293 G294 P295 L296 N297 T298 V299 A300

I301 S302 P303 Q304 G305 T306 S307 Y308 A309 S310 G311 G312 E313 D314 G315 F316 I317 R318 L319 H320 H321 F322 E323 K324 S325 Y326 F327 D328 F329 K330 Y331 D332 V333 E334 K335 A336 A337 E338 A339 K340 E341 H342 MET GLN GLU ALA ASN

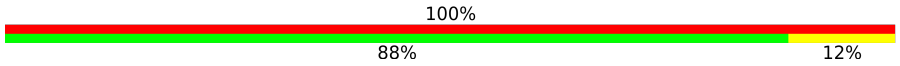
- Molecule 46: eIF3b

Chain r:

L704 H705 Q706 R707 E708 L709 L710 K711 Q712 W713 T714 E715 Y716 R717 E718 K719 I720 G721 Q722 E723 M724 E725 K726 S727 M728 N729 F730 K731 I732 F733 D734

- Molecule 47: eIF3g

Chain s:




V45 H46 K47 S48 V49 A50 E51 R52 K53 N54 W55 H56 K57 Y58 G59 S60 E61 K62 G63 S64 P65 A66 G67 P68 S69 A70 V71 T72 A73 R74 L75 G76 E77 E78 V79 E80 L81 R82 L83 S84 R85 N86 W87 K88 Q89 A90 E91 E92 E93 R94 I95 Q96

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 21401 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | Each particle | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/Å^2$) | 27 | Depositor |
| Minimum defocus (nm) | 1500 | Depositor |
| Maximum defocus (nm) | 4000 | Depositor |
| Magnification | 104478 | Depositor |
| Image detector | FEI FALCON II (4k x 4k) | Depositor |
| Maximum map value | 0.443 | Depositor |
| Minimum map value | -0.234 | Depositor |
| Average map value | 0.000 | Depositor |
| Map value standard deviation | 0.023 | Depositor |
| Recommended contour level | 0.07 | Depositor |
| Map size (Å) | 402.0, 402.0, 402.0 | wwPDB |
| Map dimensions | 300, 300, 300 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.34, 1.34, 1.34 | 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, GCP

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 | 1 | 0.38 | 1/1797 (0.1%) | 0.69 | 0/2799 |
| 2 | 2 | 0.27 | 0/42269 | 0.69 | 7/65862 (0.0%) |
| 3 | 3 | 0.30 | 0/317 | 0.69 | 0/489 |
| 4 | A | 0.42 | 0/1666 | 0.78 | 2/2279 (0.1%) |
| 5 | B | 0.40 | 0/1793 | 0.72 | 2/2414 (0.1%) |
| 6 | C | 0.39 | 0/1659 | 0.69 | 0/2252 |
| 7 | D | 0.42 | 0/1769 | 0.72 | 1/2378 (0.0%) |
| 8 | E | 0.38 | 0/2122 | 0.67 | 0/2861 |
| 9 | F | 0.41 | 0/1628 | 0.75 | 0/2198 |
| 10 | G | 0.41 | 0/1835 | 0.72 | 1/2451 (0.0%) |
| 11 | H | 0.42 | 0/1507 | 0.71 | 0/2028 |
| 12 | I | 0.41 | 0/1515 | 0.73 | 2/2029 (0.1%) |
| 13 | J | 0.40 | 0/1495 | 0.75 | 1/2001 (0.0%) |
| 14 | K | 0.48 | 0/831 | 0.77 | 1/1123 (0.1%) |
| 15 | L | 0.41 | 0/1276 | 0.63 | 0/1718 |
| 16 | M | 0.46 | 0/891 | 0.80 | 1/1201 (0.1%) |
| 17 | N | 0.41 | 0/1210 | 0.77 | 0/1628 |
| 18 | O | 0.38 | 0/953 | 0.68 | 0/1279 |
| 19 | P | 0.42 | 0/946 | 0.71 | 1/1273 (0.1%) |
| 20 | Q | 0.43 | 0/1125 | 0.71 | 0/1510 |
| 21 | R | 0.43 | 0/969 | 0.77 | 1/1299 (0.1%) |
| 22 | S | 0.43 | 0/1212 | 0.78 | 0/1629 |
| 23 | T | 0.40 | 0/1129 | 0.72 | 0/1520 |
| 24 | U | 0.40 | 0/857 | 0.73 | 0/1158 |
| 25 | V | 0.36 | 0/696 | 0.66 | 0/938 |
| 26 | W | 0.39 | 0/1039 | 0.74 | 1/1399 (0.1%) |
| 27 | X | 0.40 | 0/1137 | 0.75 | 2/1516 (0.1%) |
| 28 | Y | 0.40 | 0/1075 | 0.69 | 0/1433 |
| 29 | Z | 0.44 | 0/567 | 0.69 | 0/762 |
| 30 | a | 0.36 | 0/791 | 0.67 | 0/1059 |
| 31 | b | 0.38 | 0/619 | 0.65 | 0/837 |
| 32 | c | 0.38 | 0/489 | 0.71 | 0/655 |

| Mol | Chain | Bond lengths | | Bond angles | |
|---|---|---|---|---|---|
| | | RMSZ | #\|Z\| >5 | RMSZ | #\|Z\| >5 |
| 33 | d | 0.41 | 0/457 | 0.62 | 0/607 |
| 34 | e | 0.40 | 0/440 | 0.73 | 0/586 |
| 35 | f | 0.49 | 0/559 | 0.73 | 1/747 (0.1%) |
| 36 | g | 0.41 | 0/2521 | 0.64 | 1/3431 (0.0%) |
| 37 | h | 0.36 | 0/234 | 0.75 | 0/300 |
| 38 | i | 0.39 | 0/894 | 0.70 | 0/1188 |
| 39 | j | 0.47 | 0/2034 | 0.77 | 2/2737 (0.1%) |
| 40 | k | 0.47 | 0/3079 | 0.70 | 1/4157 (0.0%) |
| 41 | l | 0.47 | 0/1051 | 0.76 | 1/1402 (0.1%) |
| 42 | m | 0.41 | 0/724 | 0.75 | 1/968 (0.1%) |
| 43 | o | 0.49 | 0/3796 | 0.80 | 0/5128 |
| 44 | p | 0.49 | 0/4602 | 0.76 | 2/6226 (0.0%) |
| 45 | q | 0.50 | 0/2757 | 0.67 | 0/3733 |
| 46 | r | 0.49 | 0/282 | 0.74 | 0/373 |
| 47 | s | 0.47 | 0/426 | 0.64 | 0/571 |
| All | All | 0.38 | 1/103040 (0.0%) | 0.71 | 32/148132 (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 |
|---|---|---|---|
| 9 | F | 0 | 1 |
| 27 | X | 0 | 1 |
| 28 | Y | 0 | 1 |
| 41 | l | 0 | 1 |
| All | All | 0 | 4 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 1 | 1 | 1 | A | OP3-P | -9.88 | 1.49 | 1.61 |

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

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | 2 | 685 | A | C2'-C3'-O3' | 8.09 | 127.30 | 109.50 |
| 12 | I | 29 | LEU | CA-CB-CG | 7.26 | 132.00 | 115.30 |
| 39 | j | 166 | LEU | CA-CB-CG | 6.66 | 130.62 | 115.30 |
| 41 | l | 191 | LEU | CA-CB-CG | 6.50 | 130.25 | 115.30 |
| 26 | W | 26 | LEU | CA-CB-CG | 6.10 | 129.33 | 115.30 |

There are no chirality outliers.

All (4) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|---|---|---|---|---|
| 9 | F | 191 | THR | Peptide |
| 27 | X | 63 | GLN | Peptide |
| 28 | Y | 29 | HIS | Peptide |
| 41 | l | 158 | PHE | 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 | |
|---|---|---|---|---|---|---|---|
| 4 | A | 206/254 (81%) | 170 (82%) | 27 (13%) | 9 (4%) | 2 | 24 |
| 5 | B | 218/255 (86%) | 185 (85%) | 25 (12%) | 8 (4%) | 3 | 27 |
| 6 | C | 215/259 (83%) | 186 (86%) | 22 (10%) | 7 (3%) | 4 | 29 |
| 7 | D | 221/237 (93%) | 196 (89%) | 16 (7%) | 9 (4%) | 3 | 25 |
| 8 | E | 258/261 (99%) | 225 (87%) | 28 (11%) | 5 (2%) | 8 | 40 |
| 9 | F | 204/227 (90%) | 169 (83%) | 28 (14%) | 7 (3%) | 3 | 29 |
| 10 | G | 224/236 (95%) | 197 (88%) | 23 (10%) | 4 (2%) | 8 | 41 |
| 11 | H | 182/190 (96%) | 157 (86%) | 15 (8%) | 10 (6%) | 2 | 21 |
| 12 | I | 184/201 (92%) | 160 (87%) | 15 (8%) | 9 (5%) | 2 | 22 |
| 13 | J | 180/188 (96%) | 154 (86%) | 19 (11%) | 7 (4%) | 3 | 26 |
| 14 | K | 94/106 (89%) | 81 (86%) | 7 (7%) | 6 (6%) | 1 | 18 |
| 15 | L | 153/156 (98%) | 133 (87%) | 13 (8%) | 7 (5%) | 2 | 23 |
| 16 | M | 113/134 (84%) | 85 (75%) | 21 (19%) | 7 (6%) | 1 | 18 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|---|---|---|---|---|---|---|---|
| 17 | N | 148/151 (98%) | 134 (90%) | 13 (9%) | 1 (1%) | 22 | 62 |
| 18 | O | 125/137 (91%) | 102 (82%) | 16 (13%) | 7 (6%) | 2 | 20 |
| 19 | P | 115/142 (81%) | 96 (84%) | 13 (11%) | 6 (5%) | 2 | 21 |
| 20 | Q | 139/143 (97%) | 108 (78%) | 20 (14%) | 11 (8%) | 1 | 14 |
| 21 | R | 116/136 (85%) | 101 (87%) | 13 (11%) | 2 (2%) | 9 | 43 |
| 22 | S | 143/146 (98%) | 111 (78%) | 21 (15%) | 11 (8%) | 1 | 14 |
| 23 | T | 141/144 (98%) | 126 (89%) | 15 (11%) | 0 | 100 | 100 |
| 24 | U | 104/117 (89%) | 84 (81%) | 16 (15%) | 4 (4%) | 3 | 26 |
| 25 | V | 85/87 (98%) | 74 (87%) | 7 (8%) | 4 (5%) | 2 | 23 |
| 26 | W | 127/130 (98%) | 112 (88%) | 10 (8%) | 5 (4%) | 3 | 26 |
| 27 | X | 142/145 (98%) | 117 (82%) | 14 (10%) | 11 (8%) | 1 | 14 |
| 28 | Y | 132/135 (98%) | 118 (89%) | 7 (5%) | 7 (5%) | 2 | 21 |
| 29 | Z | 68/108 (63%) | 50 (74%) | 17 (25%) | 1 (2%) | 10 | 46 |
| 30 | a | 96/119 (81%) | 81 (84%) | 11 (12%) | 4 (4%) | 3 | 24 |
| 31 | b | 79/82 (96%) | 61 (77%) | 15 (19%) | 3 (4%) | 3 | 26 |
| 32 | c | 60/67 (90%) | 51 (85%) | 6 (10%) | 3 (5%) | 2 | 22 |
| 33 | d | 51/56 (91%) | 33 (65%) | 15 (29%) | 3 (6%) | 1 | 19 |
| 34 | e | 52/63 (82%) | 45 (86%) | 6 (12%) | 1 (2%) | 8 | 40 |
| 35 | f | 67/150 (45%) | 48 (72%) | 9 (13%) | 10 (15%) | 0 | 4 |
| 36 | g | 312/326 (96%) | 257 (82%) | 45 (14%) | 10 (3%) | 4 | 30 |
| 37 | h | 23/25 (92%) | 23 (100%) | 0 | 0 | 100 | 100 |
| 38 | i | 109/153 (71%) | 92 (84%) | 14 (13%) | 3 (3%) | 5 | 32 |
| 39 | j | 243/304 (80%) | 205 (84%) | 32 (13%) | 6 (2%) | 5 | 34 |
| 40 | k | 388/527 (74%) | 339 (87%) | 43 (11%) | 6 (2%) | 10 | 46 |
| 41 | l | 120/285 (42%) | 100 (83%) | 16 (13%) | 4 (3%) | 4 | 29 |
| 42 | m | 88/108 (82%) | 76 (86%) | 10 (11%) | 2 (2%) | 6 | 36 |
| 43 | o | 451/588 (77%) | 417 (92%) | 31 (7%) | 3 (1%) | 22 | 62 |
| 44 | p | 554/652 (85%) | 497 (90%) | 45 (8%) | 12 (2%) | 6 | 37 |
| 45 | q | 340/347 (98%) | 302 (89%) | 33 (10%) | 5 (2%) | 10 | 46 |
| 46 | r | 29/31 (94%) | 27 (93%) | 2 (7%) | 0 | 100 | 100 |
| 47 | s | 50/52 (96%) | 46 (92%) | 4 (8%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles |
|---|---|---|---|---|---|---|
| All | All | 7149/8360 (86%) | 6131 (86%) | 778 (11%) | 240 (3%) | 6 29 |

5 of 240 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 4 | A | 95 | ALA |
| 4 | A | 166 | GLY |
| 6 | C | 141 | VAL |
| 6 | C | 235 | TRP |
| 7 | D | 216 | 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 |
|---|---|---|---|---|---|
| 4 | A | 174/211 (82%) | 147 (84%) | 27 (16%) | 2 15 |
| 5 | B | 198/228 (87%) | 174 (88%) | 24 (12%) | 5 22 |
| 6 | C | 176/203 (87%) | 153 (87%) | 23 (13%) | 4 20 |
| 7 | D | 185/196 (94%) | 152 (82%) | 33 (18%) | 2 11 |
| 8 | E | 223/224 (100%) | 186 (83%) | 37 (17%) | 2 13 |
| 9 | F | 174/194 (90%) | 140 (80%) | 34 (20%) | 1 9 |
| 10 | G | 192/200 (96%) | 174 (91%) | 18 (9%) | 8 30 |
| 11 | H | 164/170 (96%) | 138 (84%) | 26 (16%) | 2 15 |
| 12 | I | 147/159 (92%) | 133 (90%) | 14 (10%) | 8 29 |
| 13 | J | 153/158 (97%) | 135 (88%) | 18 (12%) | 5 22 |
| 14 | K | 88/96 (92%) | 70 (80%) | 18 (20%) | 1 7 |
| 15 | L | 136/137 (99%) | 128 (94%) | 8 (6%) | 19 46 |
| 16 | M | 93/109 (85%) | 82 (88%) | 11 (12%) | 5 22 |
| 17 | N | 127/128 (99%) | 108 (85%) | 19 (15%) | 3 16 |
| 18 | O | 96/104 (92%) | 88 (92%) | 8 (8%) | 11 36 |
| 19 | P | 100/119 (84%) | 83 (83%) | 17 (17%) | 2 13 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|---|---|---|---|---|---|---|
| 20 | Q | 117/119 (98%) | 99 (85%) | 18 (15%) | 2 | 15 |
| 21 | R | 109/124 (88%) | 91 (84%) | 18 (16%) | 2 | 14 |
| 22 | S | 128/129 (99%) | 105 (82%) | 23 (18%) | 1 | 11 |
| 23 | T | 117/118 (99%) | 97 (83%) | 20 (17%) | 2 | 12 |
| 24 | U | 96/107 (90%) | 83 (86%) | 13 (14%) | 4 | 19 |
| 25 | V | 73/73 (100%) | 66 (90%) | 7 (10%) | 8 | 29 |
| 26 | W | 110/111 (99%) | 102 (93%) | 8 (7%) | 14 | 40 |
| 27 | X | 119/120 (99%) | 102 (86%) | 17 (14%) | 3 | 17 |
| 28 | Y | 108/109 (99%) | 102 (94%) | 6 (6%) | 21 | 48 |
| 29 | Z | 60/88 (68%) | 55 (92%) | 5 (8%) | 11 | 36 |
| 30 | a | 83/100 (83%) | 71 (86%) | 12 (14%) | 3 | 17 |
| 31 | b | 71/72 (99%) | 67 (94%) | 4 (6%) | 21 | 48 |
| 32 | c | 54/59 (92%) | 48 (89%) | 6 (11%) | 6 | 24 |
| 33 | d | 46/48 (96%) | 39 (85%) | 7 (15%) | 3 | 16 |
| 34 | e | 47/55 (86%) | 39 (83%) | 8 (17%) | 2 | 13 |
| 35 | f | 57/133 (43%) | 48 (84%) | 9 (16%) | 2 | 15 |
| 36 | g | 265/272 (97%) | 231 (87%) | 34 (13%) | 4 | 20 |
| 37 | h | 23/23 (100%) | 20 (87%) | 3 (13%) | 4 | 20 |
| 38 | i | 93/130 (72%) | 74 (80%) | 19 (20%) | 1 | 7 |
| 39 | j | 224/274 (82%) | 185 (83%) | 39 (17%) | 2 | 12 |
| 40 | k | 332/449 (74%) | 306 (92%) | 26 (8%) | 12 | 38 |
| 41 | l | 119/246 (48%) | 103 (87%) | 16 (13%) | 4 | 19 |
| 42 | m | 77/96 (80%) | 64 (83%) | 13 (17%) | 2 | 13 |
| 43 | o | 411/444 (93%) | 364 (89%) | 47 (11%) | 5 | 23 |
| 44 | p | 507/536 (95%) | 469 (92%) | 38 (8%) | 13 | 39 |
| 45 | q | 297/301 (99%) | 280 (94%) | 17 (6%) | 20 | 47 |
| 46 | r | 30/30 (100%) | 27 (90%) | 3 (10%) | 7 | 28 |
| 47 | s | 43/43 (100%) | 37 (86%) | 6 (14%) | 3 | 18 |
| All | All | 6242/7045 (89%) | 5465 (88%) | 777 (12%) | 8 | 21 |

5 of 777 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 28 | Y | 99 | LYS |
| 39 | j | 7 | ARG |
| 30 | a | 38 | ARG |
| 28 | Y | 84 | LYS |
| 36 | g | 18 | ASN |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 36 | g | 161 | ASN |
| 43 | o | 32 | HIS |
| 38 | i | 44 | ASN |
| 40 | k | 508 | HIS |
| 43 | o | 242 | GLN |

### 5.3.3 RNA (i)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 1 | 1 | 74/75 (98%) | 32 (43%) | 7 (9%) |
| 2 | 2 | 1778/1781 (99%) | 879 (49%) | 146 (8%) |
| 3 | 3 | 13/25 (52%) | 11 (84%) | 1 (7%) |
| All | All | 1865/1881 (99%) | 922 (49%) | 154 (8%) |

5 of 922 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | 1 | 8 | U |
| 1 | 1 | 9 | G |
| 1 | 1 | 10 | G |
| 1 | 1 | 14 | A |
| 1 | 1 | 15 | G |

5 of 154 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | 2 | 1315 | G |
| 2 | 2 | 1579 | C |
| 2 | 2 | 1360 | C |
| 2 | 2 | 1430 | U |
| 2 | 2 | 1765 | G |

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

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

## 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 87 ligands modelled in this entry, 85 are monoatomic - leaving 2 for Mogul analysis.

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

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\| > 2$ | Counts | RMSZ | $\#\|Z\| > 2$ |
| 51 | GCP | k | 603 | 48 | 27,34,34 | 1.96 | 8 (29%) | 34,54,54 | 1.98 | 8 (23%) |
| 50 | MET | k | 601 | - | 6,7,8 | 0.43 | 0 | 2,7,9 | 0.19 | 0 |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 51 | GCP | k | 603 | 48 | - | 2/15/38/38 | 0/3/3/3 |
| 50 | MET | k | 601 | - | - | 1/5/6/8 | - |

The worst 5 of 8 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 51 | k | 603 | GCP | PG-O1G | 5.43 | 1.61 | 1.50 |
| 51 | k | 603 | GCP | C5-C6 | 4.82 | 1.49 | 1.41 |
| 51 | k | 603 | GCP | PB-O3A | 3.15 | 1.61 | 1.58 |
| 51 | k | 603 | GCP | PG-O2G | 2.86 | 1.61 | 1.54 |
| 51 | k | 603 | GCP | C5-C4 | 2.82 | 1.48 | 1.40 |

The worst 5 of 8 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 51 | k | 603 | GCP | C2-N3-C4 | 5.46 | 121.60 | 115.36 |
| 51 | k | 603 | GCP | C2-N1-C6 | 4.11 | 122.46 | 115.93 |
| 51 | k | 603 | GCP | C5-C6-N1 | -3.86 | 118.16 | 123.43 |
| 51 | k | 603 | GCP | C4-C5-C6 | -3.77 | 117.20 | 120.80 |
| 51 | k | 603 | GCP | N3-C2-N1 | -3.63 | 122.38 | 127.22 |

There are no chirality outliers.

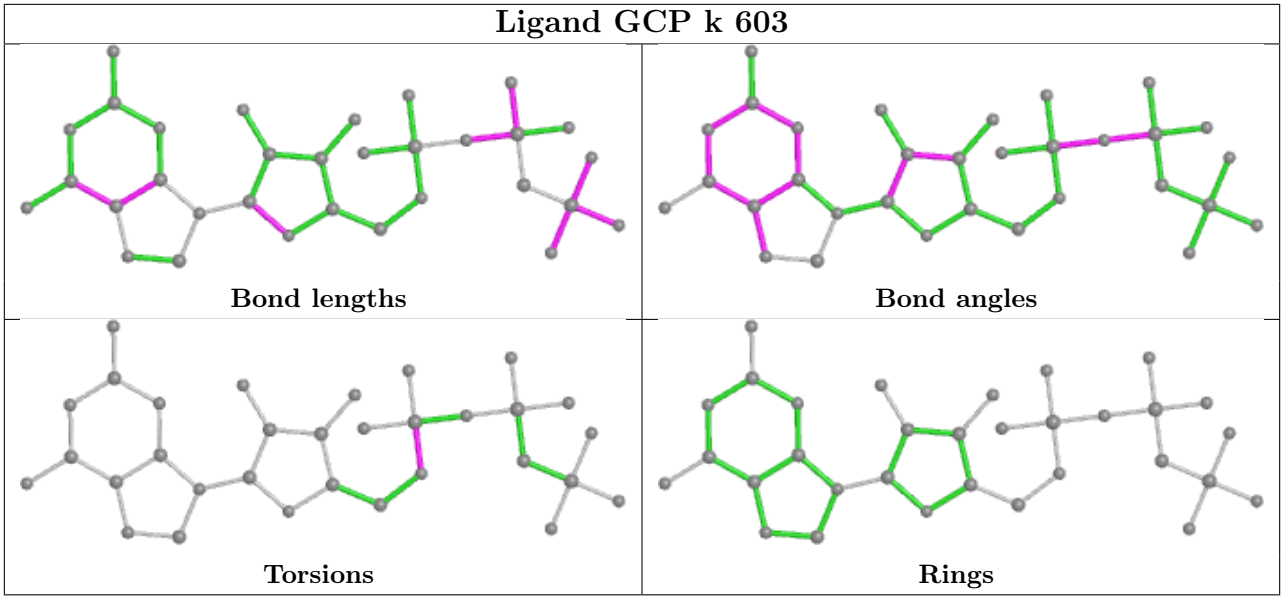
All (3) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 51 | k | 603 | GCP | C5'-O5'-PA-O3A |
| 50 | k | 601 | MET | CA-CB-CG-SD |
| 51 | k | 603 | GCP | C5'-O5'-PA-O1A |

There are no ring outliers.

No monomer is involved in short contacts.

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




## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|---|---|---|
| 43 | o | 7 |
| 44 | p | 7 |

The worst 5 of 14 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|---|---|---|---|---|---|---|
| 1 | o | 495:PRO | C | 753:UNK | N | 221.30 |
| 1 | p | 218:UNK | C | 251:GLN | N | 63.04 |
| 1 | p | 32:UNK | C | 116:UNK | N | 42.95 |
| 1 | p | 185:UNK | C | 193:ARG | N | 15.92 |
| 1 | o | 818:UNK | C | 828:UNK | N | 14.63 |

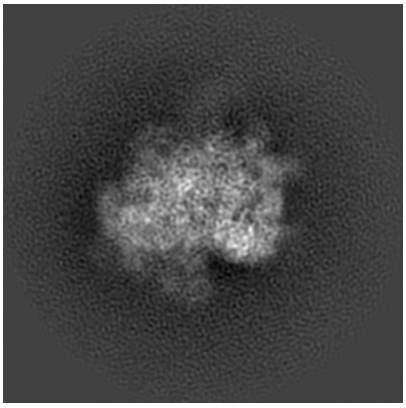
# 6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-3048. These allow visual inspection of the internal detail of the map and identification of artifacts.

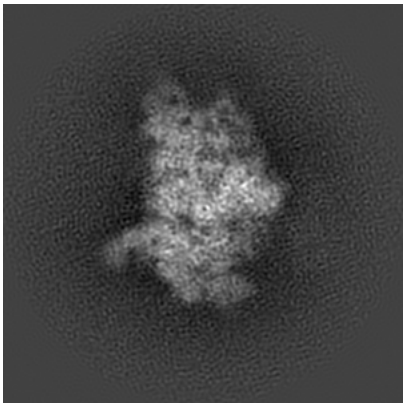
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

## 6.1 Orthogonal projections (i)

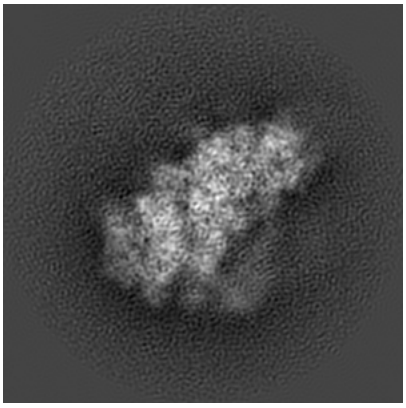
### 6.1.1 Primary map



X



Y

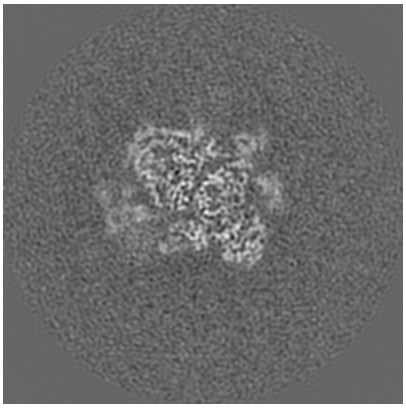


Z

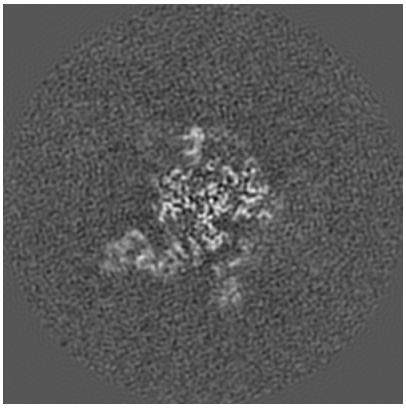
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices (i)

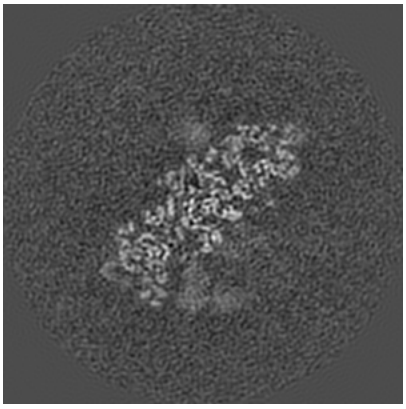
### 6.2.1 Primary map



X Index: 150



Y Index: 150

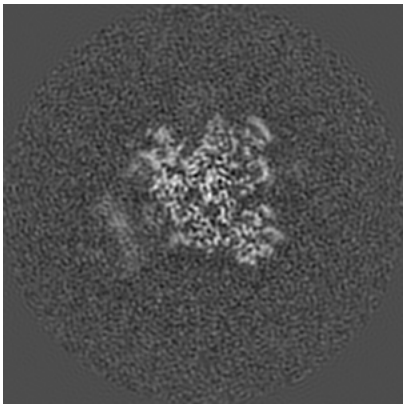


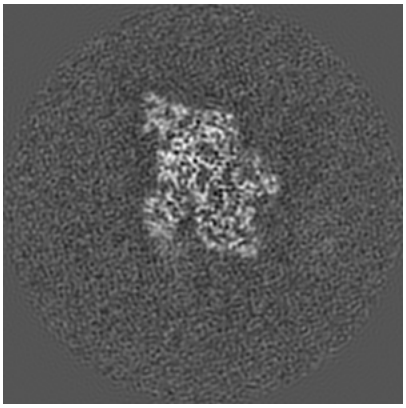
Z Index: 150

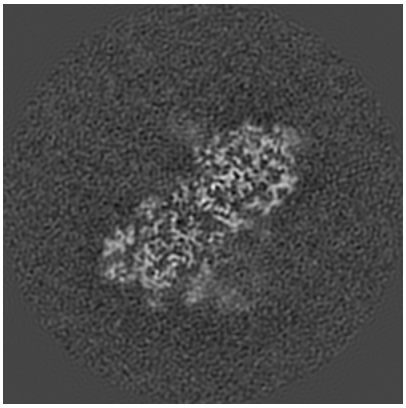
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

### 6.3.1 Primary map


X Index: 161

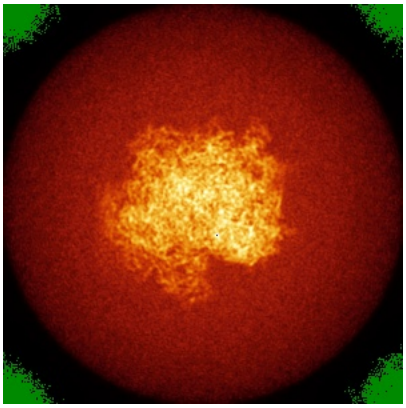

Y Index: 171

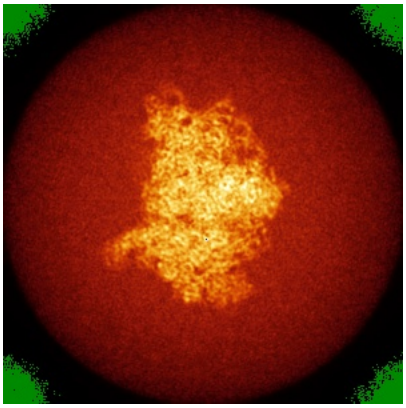

Z Index: 143

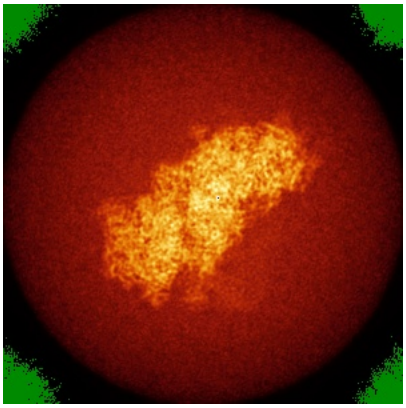
The images above show the largest variance slices of the map in three orthogonal directions.

## 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 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

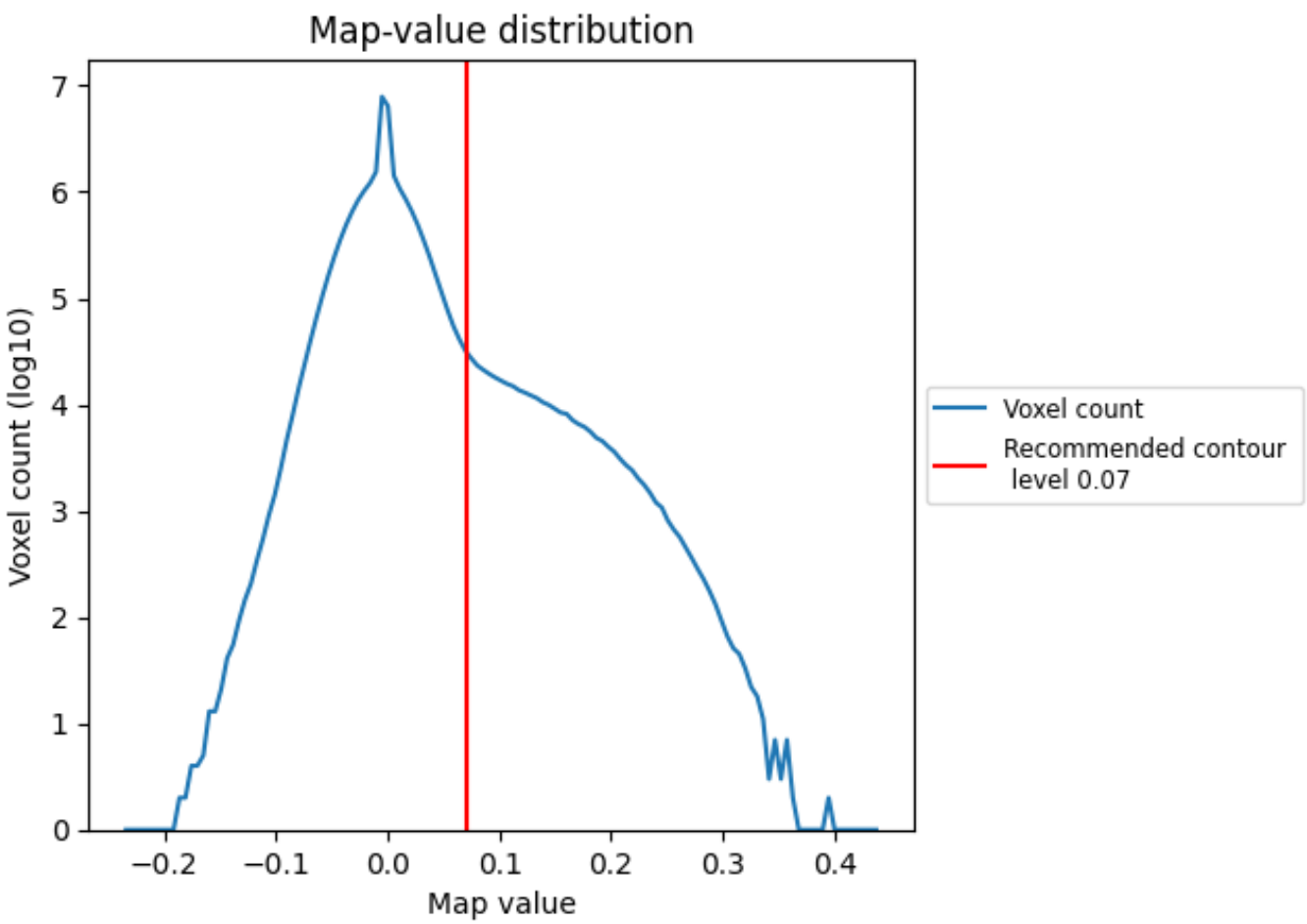
## 6.6 Mask visualisation (i)

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

# 7 Map analysis (i)

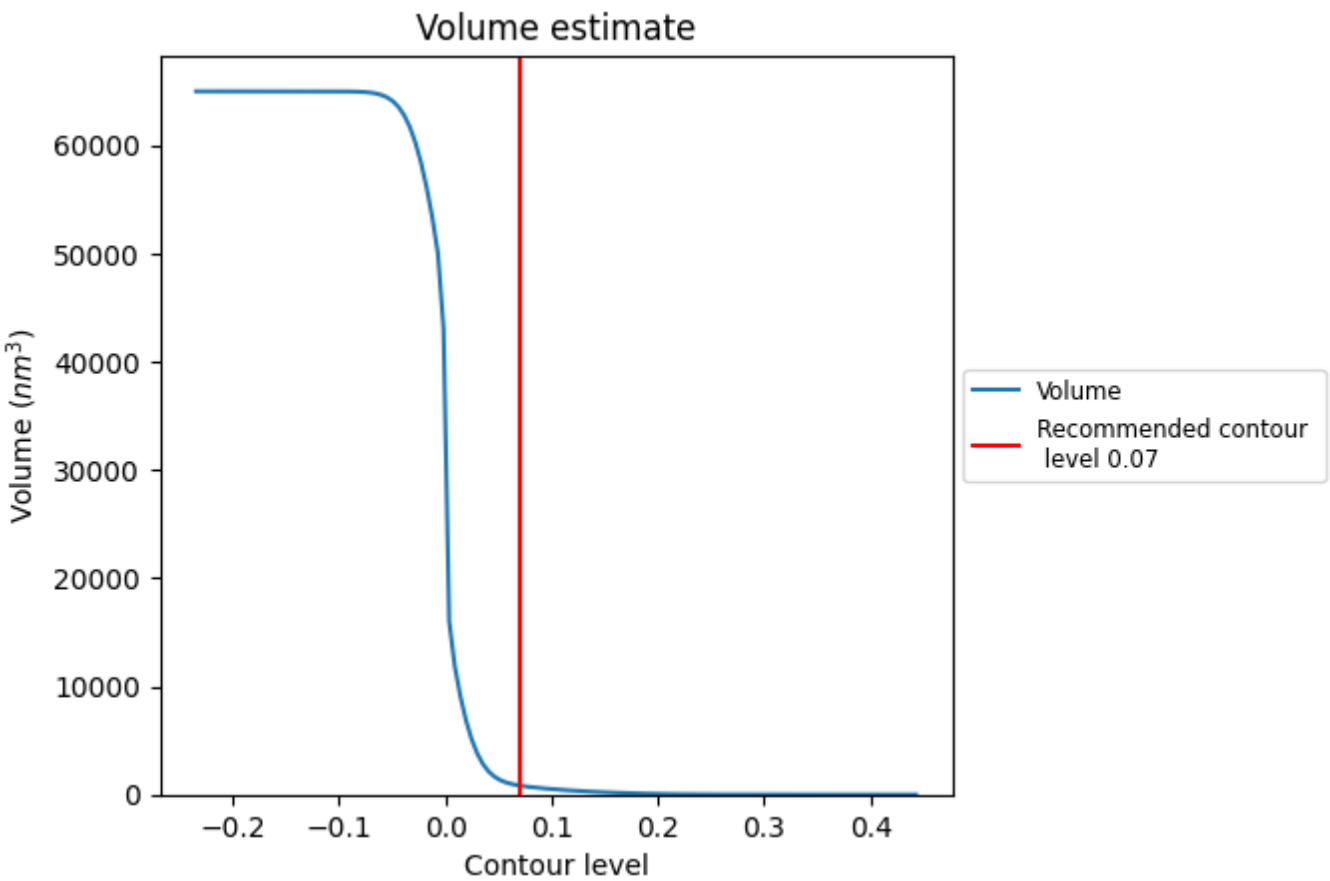
This section contains the results of statistical analysis of the map.

## 7.1 Map-value distribution (i)




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

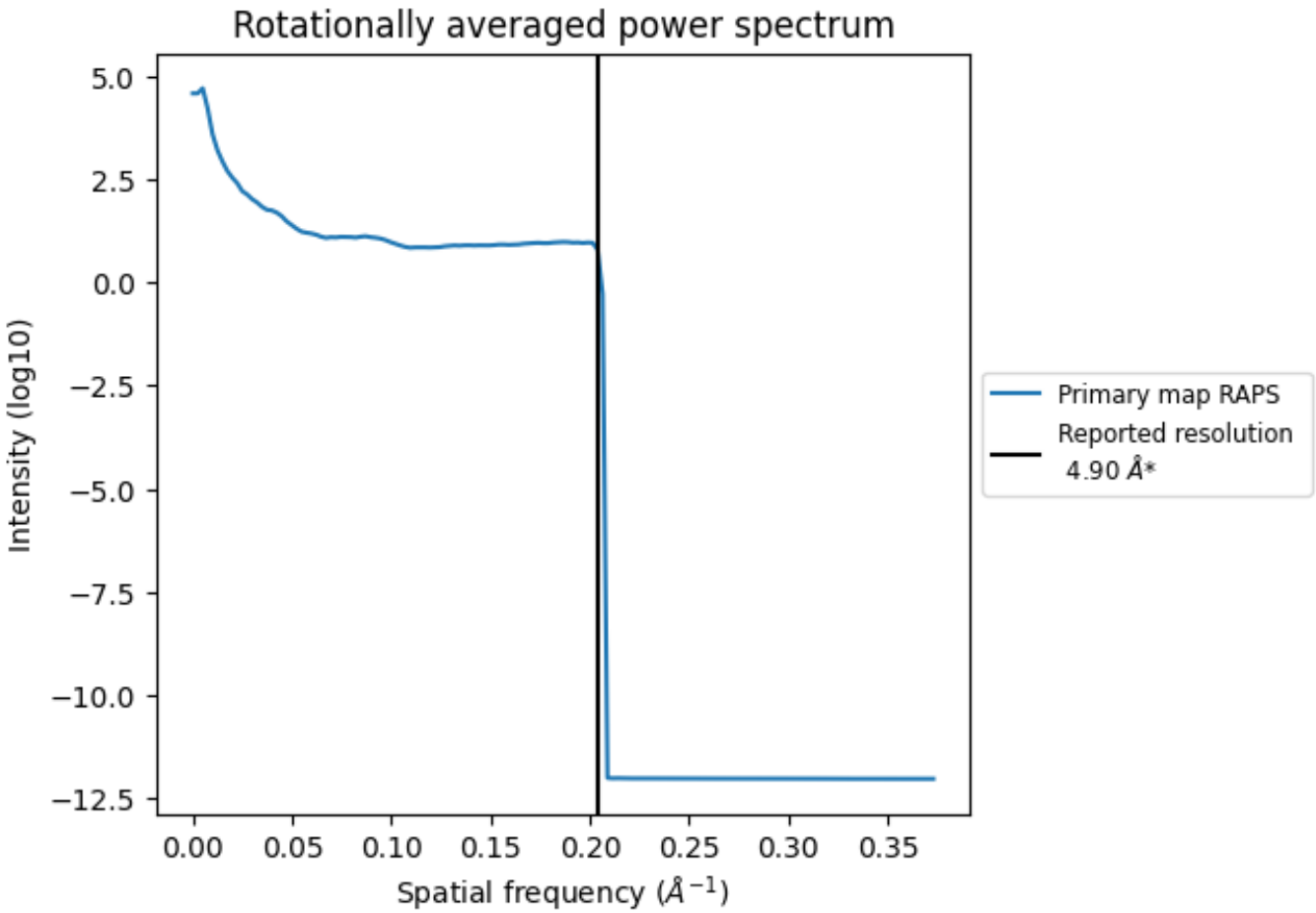
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 830 $nm^3$; this corresponds to an approximate mass of 750 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)

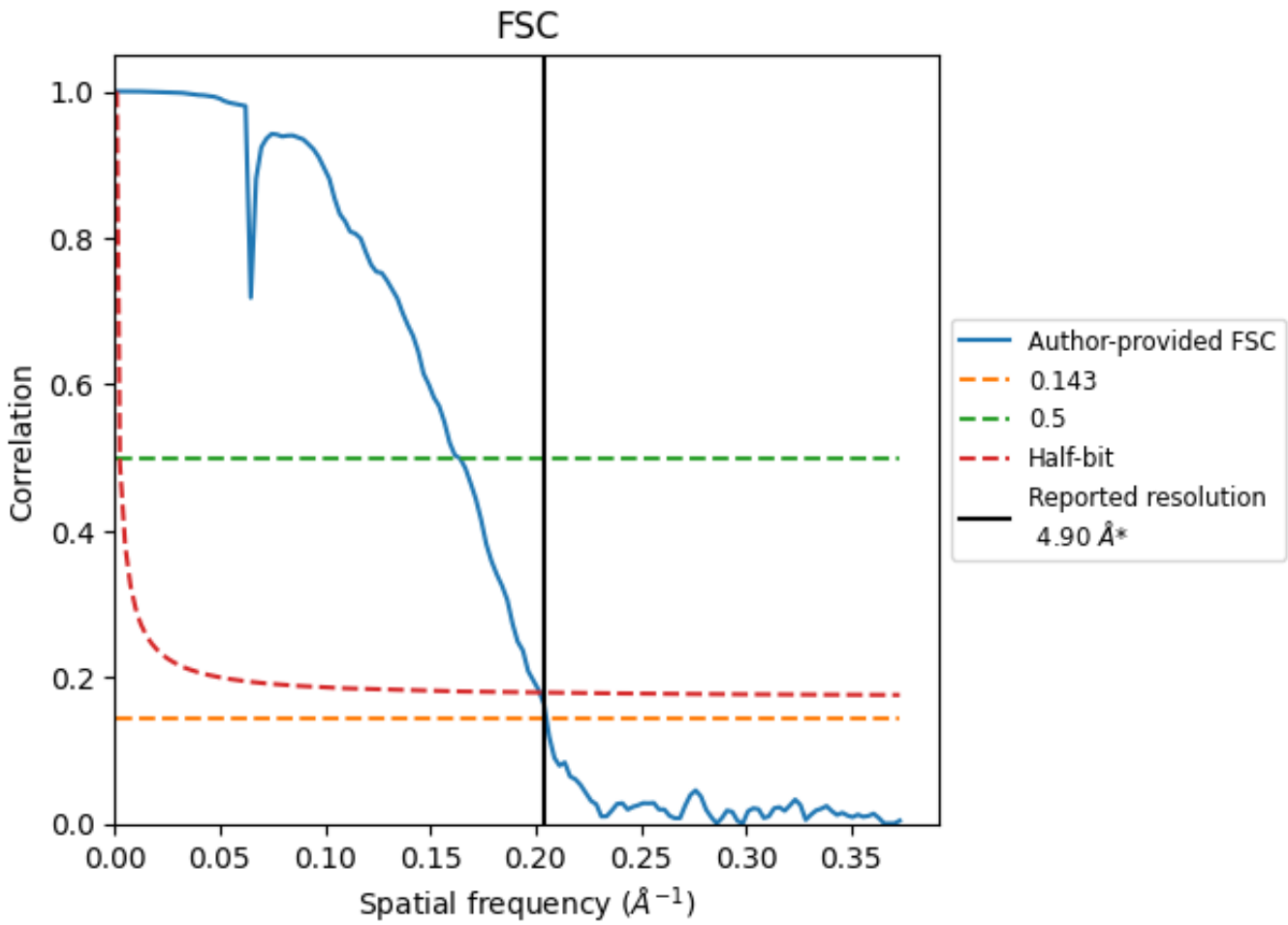



*Reported resolution corresponds to spatial frequency of 0.204 Å$^{-1}$

# 8 Fourier-Shell correlation (i)

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

## 8.1 FSC (i)




*Reported resolution corresponds to spatial frequency of 0.204 Å$^{-1}$

## 8.2 Resolution estimates (i)

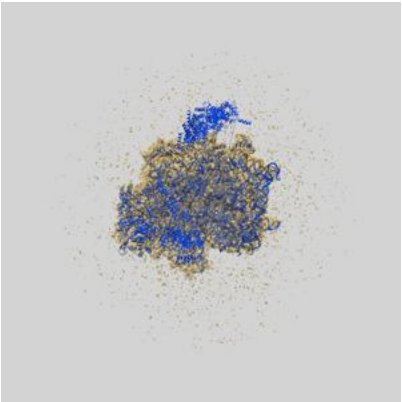
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---|---|---|---|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 4.90 | - | - |
| Author-provided FSC curve | 4.88 | 6.12 | 4.95 |
| Unmasked-calculated* | - | - | - |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

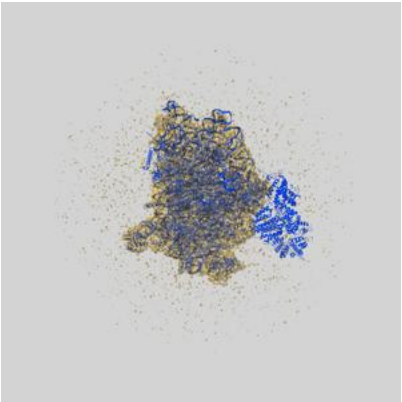
# 9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-3048 and PDB model 3JAP. Per-residue inclusion information can be found in section 3 on page 14.

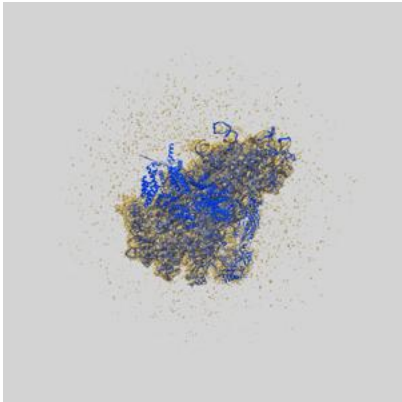
## 9.1 Map-model overlay (i)



X



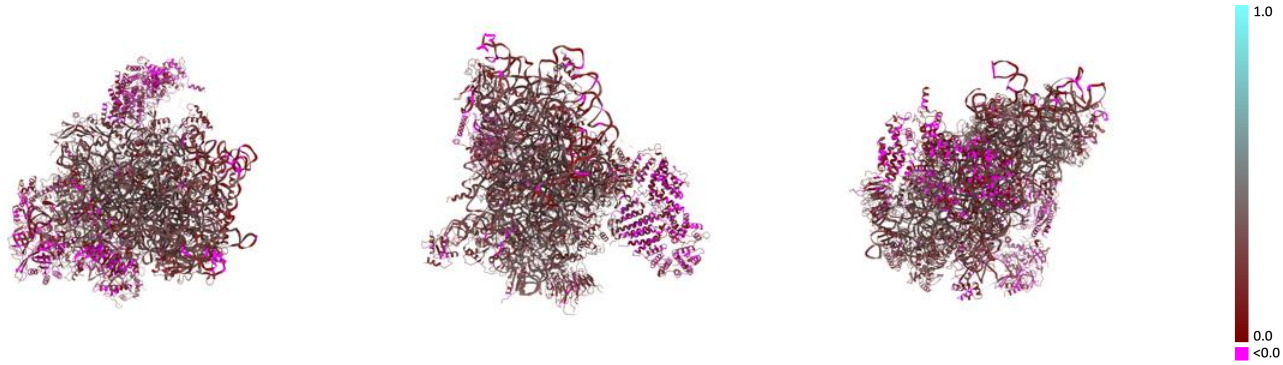
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.07 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.

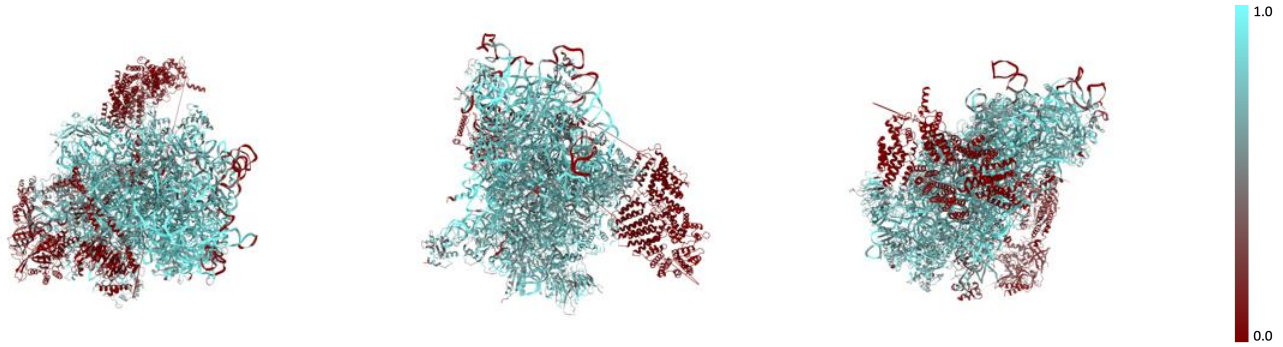
## 9.2 Q-score mapped to coordinate model (i)




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.

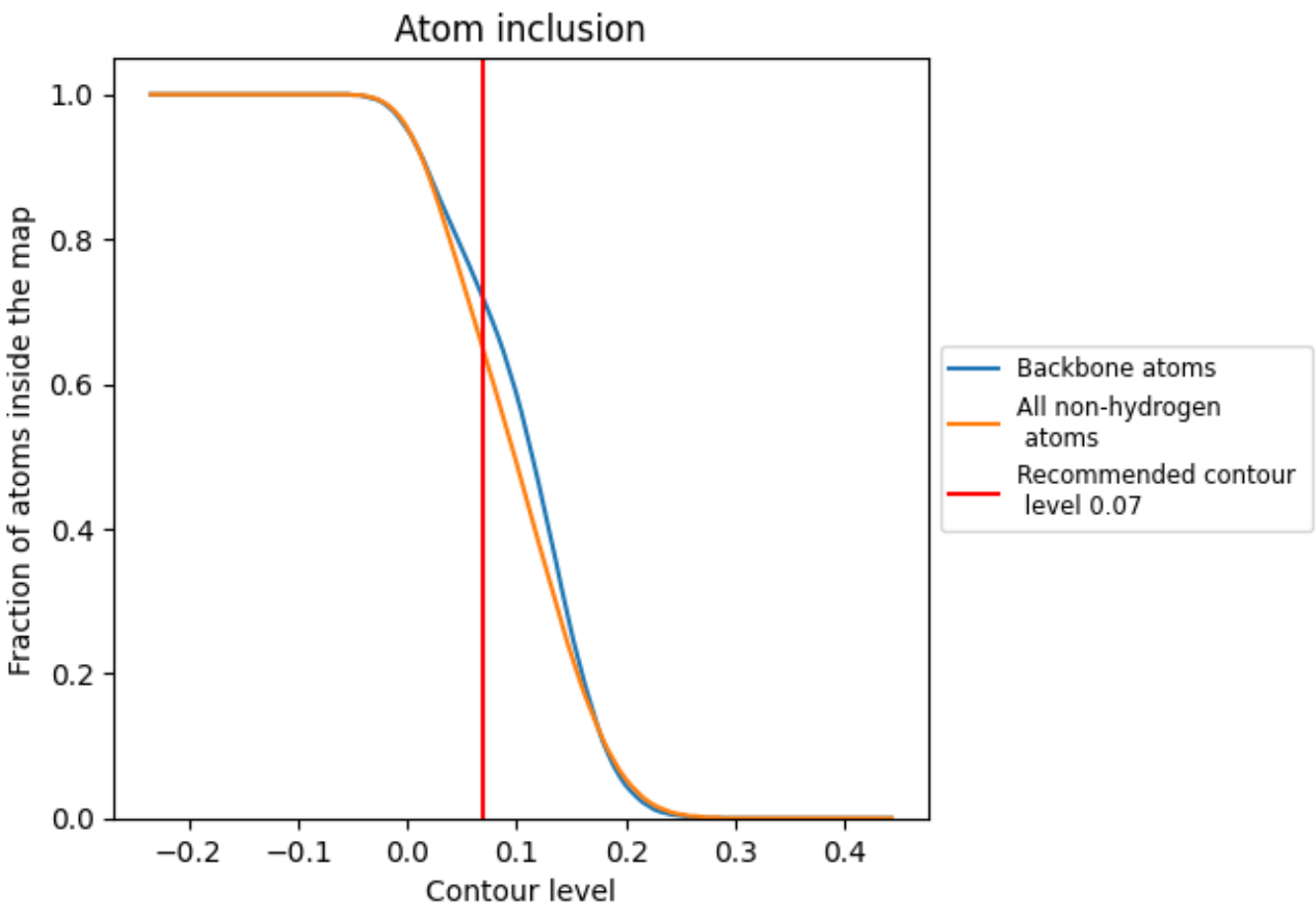
## 9.3 Atom inclusion mapped to coordinate model (i)




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 (0.07).

## 9.4 Atom inclusion (i)




At the recommended contour level, 72% of all backbone atoms, 64% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.6440 | 0.2440 |
| 1 | 0.5980 | 0.1680 |
| 2 | 0.8680 | 0.2900 |
| 3 | 0.5500 | 0.2110 |
| A | 0.7510 | 0.2890 |
| B | 0.7500 | 0.2810 |
| C | 0.7190 | 0.3090 |
| D | 0.6810 | 0.2810 |
| E | 0.7300 | 0.2980 |
| F | 0.6790 | 0.2580 |
| G | 0.7150 | 0.2460 |
| H | 0.6710 | 0.2540 |
| I | 0.7160 | 0.2620 |
| J | 0.7290 | 0.2960 |
| K | 0.7120 | 0.2710 |
| L | 0.6860 | 0.2970 |
| M | 0.5650 | 0.2000 |
| N | 0.7280 | 0.2870 |
| O | 0.7510 | 0.2800 |
| P | 0.7200 | 0.2620 |
| Q | 0.7090 | 0.2650 |
| R | 0.7170 | 0.2850 |
| S | 0.6780 | 0.2640 |
| T | 0.7290 | 0.2560 |
| U | 0.6470 | 0.2680 |
| V | 0.7320 | 0.3010 |
| W | 0.7130 | 0.2930 |
| X | 0.7190 | 0.3190 |
| Y | 0.7650 | 0.2910 |
| Z | 0.6190 | 0.2420 |
| a | 0.7430 | 0.3170 |
| b | 0.7180 | 0.2800 |
| c | 0.6940 | 0.2950 |
| d | 0.7590 | 0.3010 |
| e | 0.7160 | 0.3180 |

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| Chain | Atom inclusion | Q-score |
|---|---|---|
| f | 0.6550 | 0.2270 |
| g | 0.7090 | 0.2410 |
| h | 0.3730 | 0.2170 |
| i | 0.6400 | 0.2810 |
| j | 0.3060 | 0.1650 |
| k | 0.1170 | 0.1100 |
| l | 0.1040 | 0.1240 |
| m | 0.2760 | 0.2020 |
| o | 0.0130 | 0.0720 |
| p | 0.0310 | 0.0920 |
| q | 0.0260 | 0.0530 |
| r | 0.0180 | 0.0550 |
| s | 0.0030 | 0.0760 |