



wwPDB EM Validation Summary Report ⓘ

Oct 15, 2024 – 09:52 am BST

PDB ID : 8S8I
EMDB ID : EMD-19806
Title : Structure of a yeast 48S-AUC preinitiation complex in closed conformation (model py48S-AUC-eIF1)
Authors : Villamayor-Belinchon, L.; Sharma, P.; Llacer, J.L.; Hussain, T.
Deposited on : 2024-03-06
Resolution : 4.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

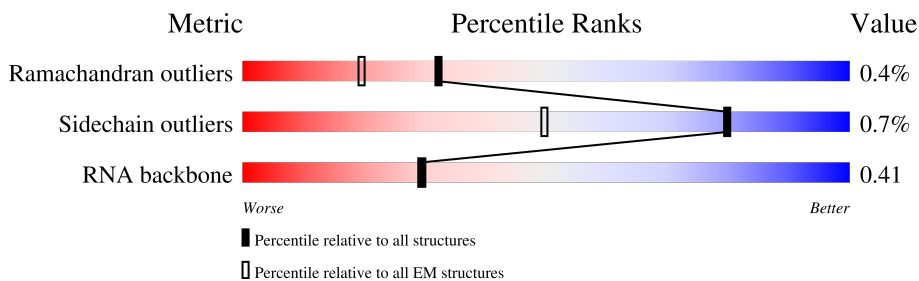
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 Å.

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



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

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

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | 2 | 1798 | |
| 2 | A | 254 | |
| 3 | B | 255 | |
| 4 | C | 259 | |
| 5 | E | 261 | |
| 6 | G | 236 | |
| 7 | H | 190 | |
| 8 | I | 201 | |

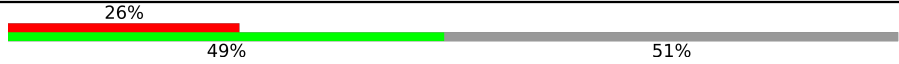
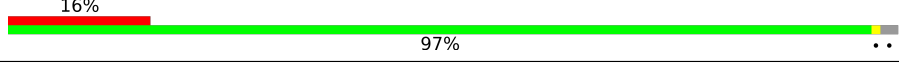


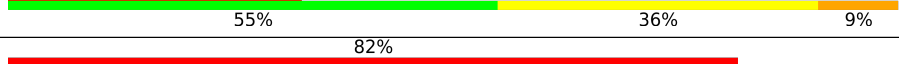

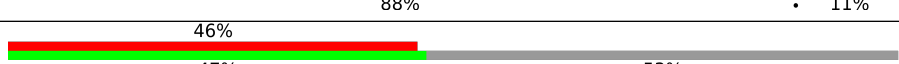


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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 9 | J | 188 | 5% 93% |
| 10 | L | 156 | 12% 97% |
| 11 | N | 151 | 5% 100% |
| 12 | O | 137 | 11% 93% 6% |
| 13 | V | 87 | 100% |
| 14 | W | 130 | 98% |
| 15 | X | 145 | 99% |
| 16 | Y | 135 | 98% |
| 17 | a | 119 | 6% 85% 14% |
| 18 | b | 82 | 6% 98% |
| 19 | e | 63 | 24% 95% 5% |
| 20 | h | 25 | 100% 100% |
| 21 | D | 237 | 10% 95% |
| 22 | F | 227 | 17% 89% 9% |
| 23 | K | 106 | 12% 91% 9% |
| 24 | M | 134 | 73% 84% 13% |
| 25 | P | 142 | 13% 82% 18% |
| 26 | Q | 143 | 97% |
| 27 | R | 136 | 19% 93% |
| 28 | S | 146 | 13% 99% |
| 29 | T | 144 | 7% 99% |
| 30 | U | 117 | 17% 90% 9% |
| 31 | Z | 108 | 34% 72% 28% |
| 32 | c | 67 | 19% 94% |
| 33 | d | 56 | 5% 96% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 34 | f | 150 |  |
| 35 | g | 326 |  |
| 36 | i | 153 |  |
| 37 | 3 | 49 |  |
| 38 | 1 | 75 |  |
| 39 | j | 304 |  |
| 40 | k | 527 |  |
| 41 | l | 285 |  |
| 42 | m | 108 |  |

2 Entry composition [i](#)

There are 47 unique types of molecules in this entry. The entry contains 87328 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 18S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| | | | Total | C | N | O | P | | |
| 1 | 2 | 1789 | 38003 | 16989 | 6694 | 12531 | 1789 | 0 | 0 |

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 2 | A | 219 | 1702 | 1085 | 299 | 316 | 2 | 0 | 0 |

- Molecule 3 is a protein called Small ribosomal subunit protein eS1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 3 | B | 225 | 1796 | 1135 | 330 | 328 | 3 | 0 | 0 |

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 4 | C | 220 | 1648 | 1053 | 291 | 300 | 4 | 0 | 0 |

- Molecule 5 is a protein called 40S ribosomal protein S4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 5 | E | 260 | 2078 | 1322 | 393 | 359 | 4 | 0 | 0 |

- Molecule 6 is a protein called Small ribosomal subunit protein eS6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 6 | G | 230 | 1832 | 1146 | 352 | 330 | 4 | 0 | 0 |

- Molecule 7 is a protein called 40S ribosomal protein S7.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| | | | Total | C | N | O | | |
| 7 | H | 184 | 1483 | 950 | 270 | 263 | 0 | 0 |

- Molecule 8 is a protein called 40S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 8 | I | 188 | 1489 | 923 | 300 | 265 | 1 | 0 | 0 |

- Molecule 9 is a protein called KLLA0E23673p.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 9 | J | 182 | 1471 | 929 | 287 | 254 | 1 | 0 | 0 |

- Molecule 10 is a protein called KLLA0A10483p.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 10 | L | 155 | 1248 | 798 | 237 | 210 | 3 | 0 | 0 |

- Molecule 11 is a protein called KLLA0F18040p.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 11 | N | 151 | 1195 | 761 | 224 | 207 | 3 | 0 | 0 |

- Molecule 12 is a protein called Small ribosomal subunit protein uS11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 12 | O | 129 | 955 | 585 | 191 | 176 | 3 | 0 | 0 |

- Molecule 13 is a protein called 40S ribosomal protein S21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 13 | V | 87 | 687 | 424 | 126 | 135 | 2 | 0 | 0 |

- Molecule 14 is a protein called Small ribosomal subunit protein uS8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 14 | W | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1021 | 651 | 187 | 180 | 3 | | |

- Molecule 15 is a protein called KLLA0B11231p.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15 | X | 144 | Total | C | N | O | S | 0 | 0 |
| | | | 1119 | 708 | 218 | 191 | 2 | | |

- Molecule 16 is a protein called 40S ribosomal protein S24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16 | Y | 134 | Total | C | N | O | S | 0 | 0 |
| | | | 1061 | 665 | 207 | 189 | | | |

- Molecule 17 is a protein called 40S ribosomal protein S26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17 | a | 102 | Total | C | N | O | S | 0 | 0 |
| | | | 797 | 492 | 168 | 132 | 5 | | |

- Molecule 18 is a protein called 40S ribosomal protein S27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 18 | b | 81 | Total | C | N | O | S | 0 | 0 |
| | | | 609 | 379 | 112 | 113 | 5 | | |

- Molecule 19 is a protein called 40S ribosomal protein S30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 19 | e | 60 | Total | C | N | O | S | 0 | 0 |
| | | | 472 | 295 | 96 | 80 | 1 | | |

- Molecule 20 is a protein called 40S ribosomal protein L41-A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 20 | h | 25 | Total | C | N | O | S | 0 | 0 |
| | | | 233 | 142 | 63 | 27 | 1 | | |

- Molecule 21 is a protein called 40S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 21 | D | 227 | Total | C | N | O | S | 0 | 0 |
| | | | 1774 | 1126 | 320 | 323 | 5 | | |

- Molecule 22 is a protein called KLLA0D10659p.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 22 | F | 206 | Total | C | N | O | S | 0 | 0 |
| | | | 1609 | 1008 | 298 | 300 | 3 | | |

- Molecule 23 is a protein called KLLA0B08173p.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23 | K | 96 | Total | C | N | O | S | 0 | 0 |
| | | | 809 | 533 | 129 | 146 | 1 | | |

- Molecule 24 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 24 | M | 117 | Total | C | N | O | 0 | 0 |
| | | | 885 | 553 | 161 | 171 | | |

- Molecule 25 is a protein called KLLA0F07843p.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25 | P | 117 | Total | C | N | O | S | 0 | 0 |
| | | | 923 | 592 | 165 | 161 | 5 | | |

- Molecule 26 is a protein called Small ribosomal subunit protein uS9.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 26 | Q | 141 | Total | C | N | O | 0 | 0 |
| | | | 1105 | 709 | 204 | 192 | | |

- Molecule 27 is a protein called KLLA0B01474p.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27 | R | 130 | Total | C | N | O | S | 0 | 0 |
| | | | 1033 | 643 | 194 | 193 | 3 | | |

- Molecule 28 is a protein called KLLA0B01562p.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 28 | S | 145 | 1189 | 739 | 239 | 209 | 2 | 0 | 0 |

- Molecule 29 is a protein called KLLA0A07194p.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 29 | T | 143 | 1110 | 693 | 210 | 207 | | 0 | 0 |

- Molecule 30 is a protein called Small ribosomal subunit protein uS10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 30 | U | 106 | 845 | 540 | 152 | 152 | 1 | 0 | 0 |

- Molecule 31 is a protein called 40S ribosomal protein S25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 31 | Z | 78 | 594 | 376 | 111 | 106 | 1 | 0 | 0 |

- Molecule 32 is a protein called Small ribosomal subunit protein eS28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 32 | c | 64 | 499 | 308 | 99 | 91 | 1 | 0 | 0 |

- Molecule 33 is a protein called Small ribosomal subunit protein uS14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 33 | d | 55 | 461 | 289 | 93 | 78 | 1 | 0 | 0 |

- Molecule 34 is a protein called Small ribosomal subunit protein eS31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| | | | Total | C | N | O | S | | |
| 34 | f | 74 | 584 | 374 | 111 | 95 | 4 | 0 | 0 |

- Molecule 35 is a protein called KLLA0E12277p.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 35 | g | 320 | Total | C | N | O | S | 0 | 0 |
| | | | 2469 | 1561 | 432 | 471 | 5 | | |

- Molecule 36 is a protein called Eukaryotic translation initiation factor 1A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 36 | i | 95 | Total | C | N | O | S | 0 | 0 |
| | | | 764 | 474 | 142 | 143 | 5 | | |

- Molecule 37 is a RNA chain called mRNA (5'-R(P*AP*AP*U)-3').

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|----|---------|-------|
| 37 | 3 | 26 | Total | C | N | O | P | 0 | 0 |
| | | | 536 | 242 | 84 | 184 | 26 | | |

- Molecule 38 is a RNA chain called Met-tRNAi.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 38 | 1 | 75 | Total | C | N | O | P | 0 | 0 |
| | | | 1639 | 734 | 298 | 531 | 76 | | |

- Molecule 39 is a protein called Eukaryotic translation initiation factor 2 subunit alpha.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 39 | j | 267 | Total | C | N | O | S | 0 | 0 |
| | | | 2139 | 1366 | 355 | 407 | 11 | | |

- Molecule 40 is a protein called Eukaryotic translation initiation factor 2 subunit gamma.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 40 | k | 470 | Total | C | N | O | S | 0 | 0 |
| | | | 3596 | 2279 | 633 | 666 | 18 | | |

- Molecule 41 is a protein called Eukaryotic translation initiation factor 2 subunit beta.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 41 | l | 134 | Total | C | N | O | S | 0 | 0 |
| | | | 1083 | 689 | 194 | 193 | 7 | | |

- Molecule 42 is a protein called Eukaryotic translation initiation factor eIF-1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42 | m | 77 | Total | C | N | O | S | 0 | 0 |
| | | | 619 | 395 | 109 | 111 | 4 | | |

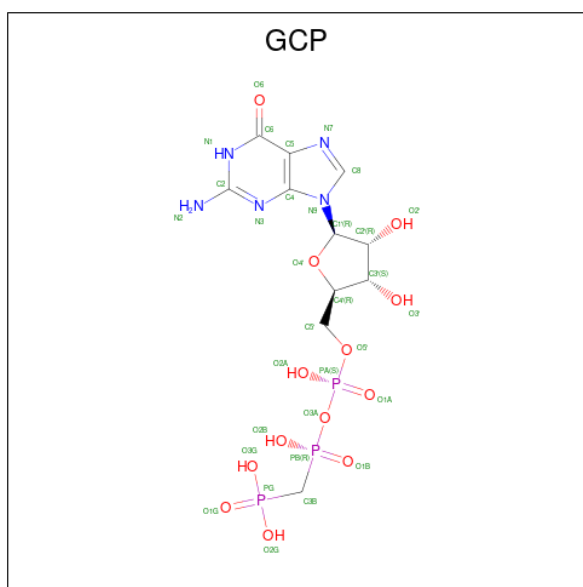
- Molecule 43 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|-----|---------|
| 43 | 2 | 114 | Total | Mg | 0 |
| | | | 114 | 114 | |
| 43 | S | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 43 | i | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 43 | k | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |

- Molecule 44 is ZINC ION (three-letter code: ZN) (formula: Zn).

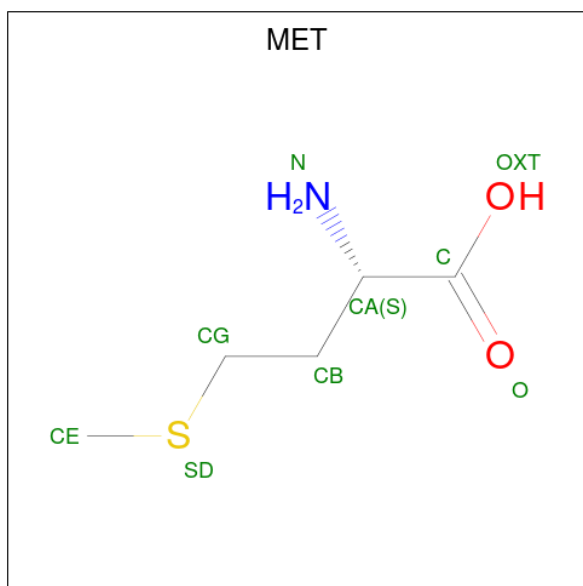
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 44 | a | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 44 | b | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 44 | f | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 44 | l | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |

- Molecule 45 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).



| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|----|---|---------|
| | | | Total | C | N | O | P | |
| 45 | k | 1 | 32 | 11 | 5 | 13 | 3 | 0 |

- Molecule 46 is METHIONINE (three-letter code: MET) (formula: $C_5H_{11}NO_2S$).



| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|---|---|---|---|---------|
| | | | Total | C | N | O | S | |
| 46 | k | 1 | 8 | 5 | 1 | 1 | 1 | 0 |

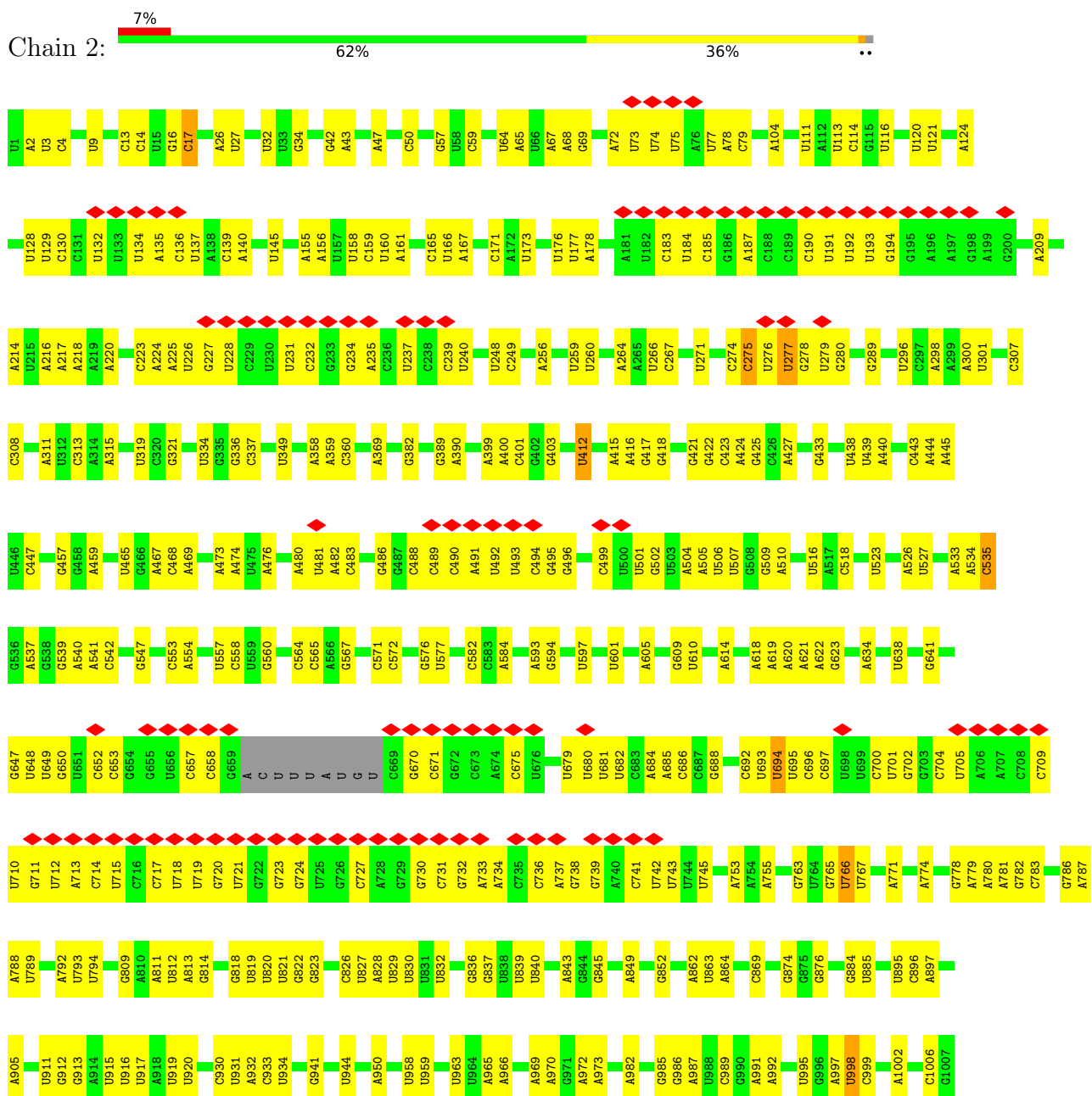
- Molecule 47 is water.

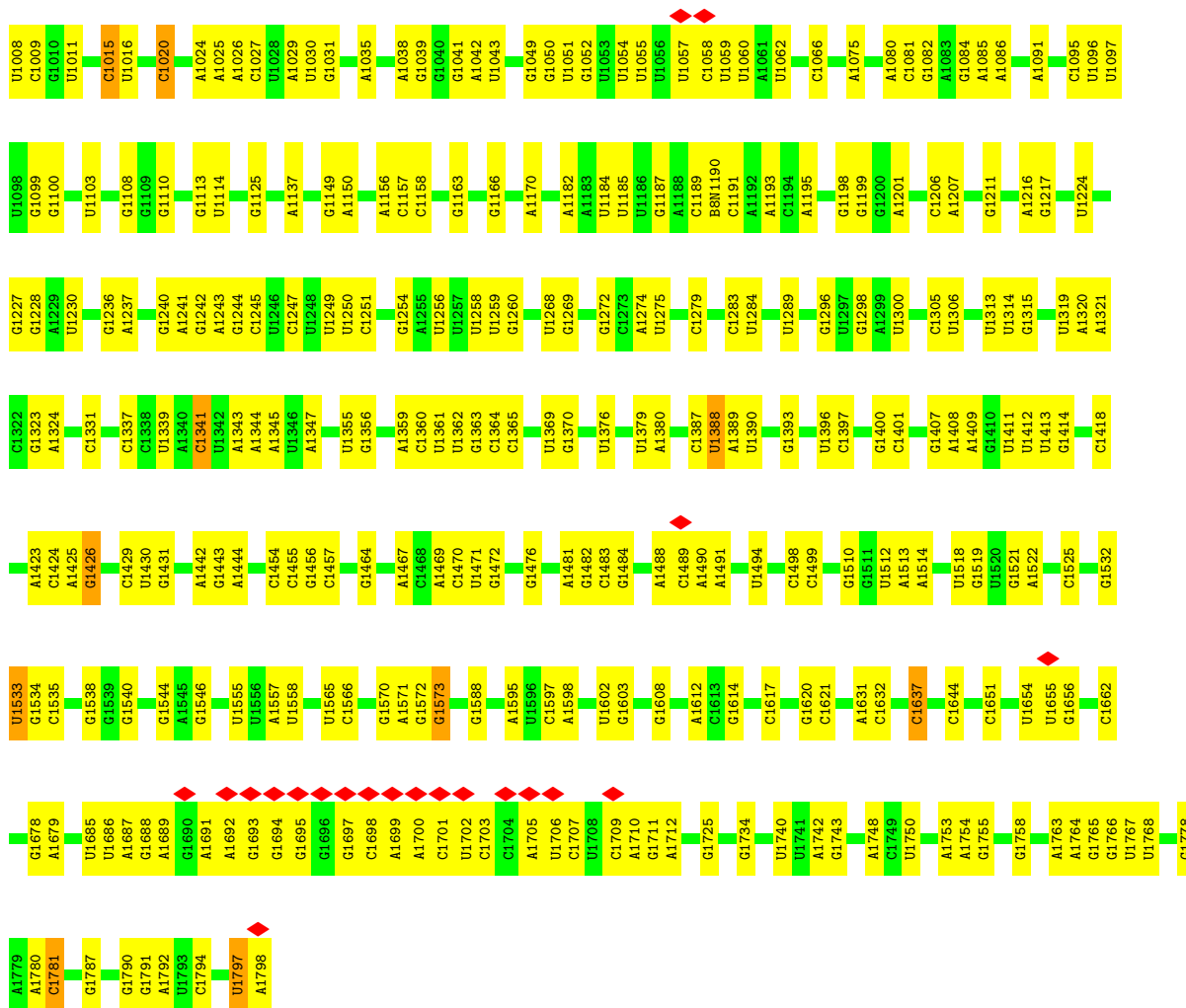
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|--------|---------|
| 47 | 2 | 3 | Total 3 | O 3 | 0 |

3 Residue-property plots

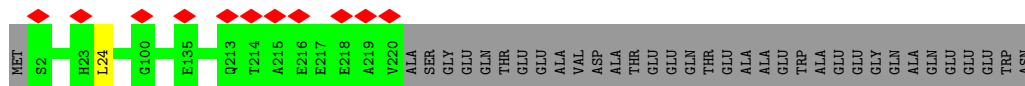
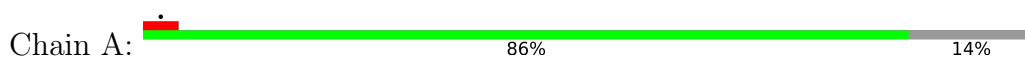
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 18S ribosomal RNA

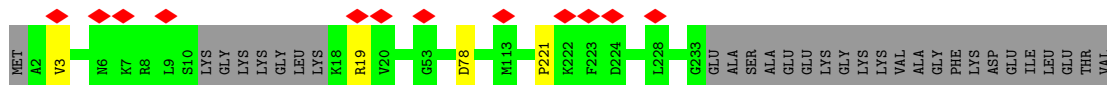
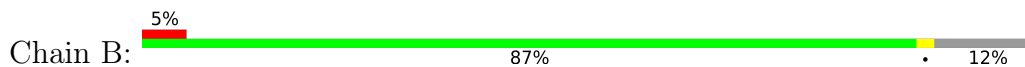




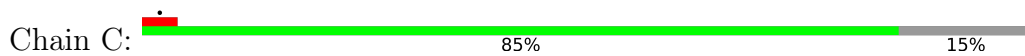
• Molecule 2: Small ribosomal subunit protein uS2

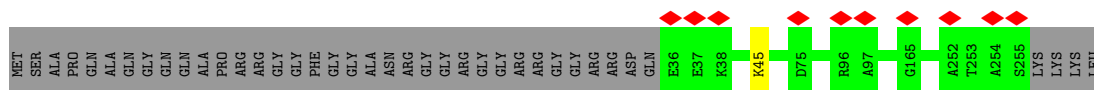


• Molecule 3: Small ribosomal subunit protein eS1

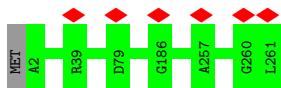


• Molecule 4: Small ribosomal subunit protein uS5

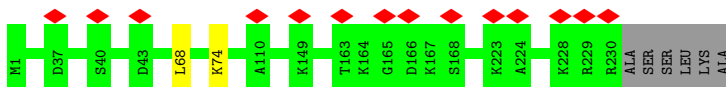




- Molecule 5: 40S ribosomal protein S4



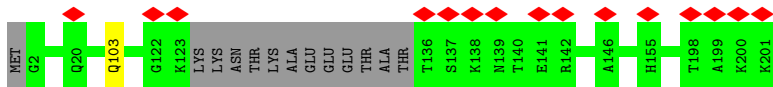
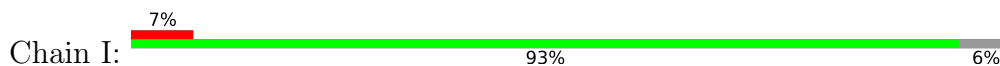
- Molecule 6: Small ribosomal subunit protein eS6



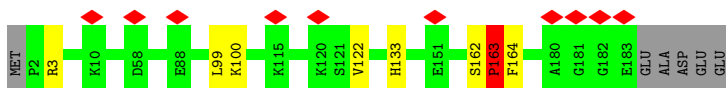
- Molecule 7: 40S ribosomal protein S7



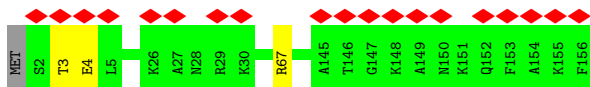
- Molecule 8: 40S ribosomal protein S8



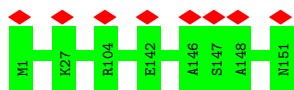
- Molecule 9: KLLA0E23673p



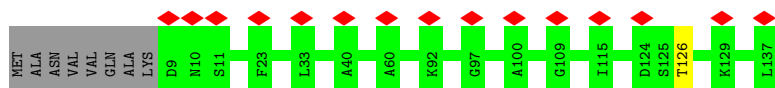
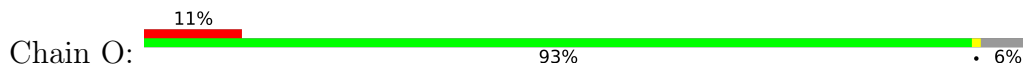
- Molecule 10: KLLA0A10483p



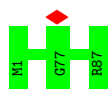
- Molecule 11: KLLA0F18040p



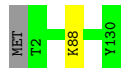
- Molecule 12: Small ribosomal subunit protein uS11



- Molecule 13: 40S ribosomal protein S21



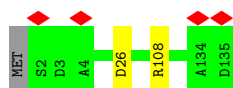
- Molecule 14: Small ribosomal subunit protein uS8



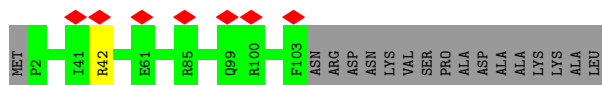
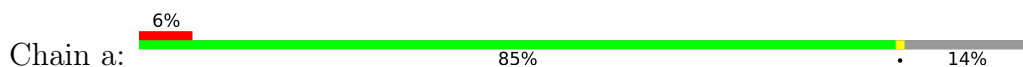
- Molecule 15: KLLA0B11231p



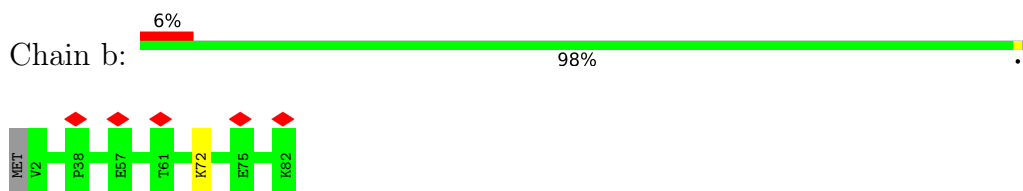
- Molecule 16: 40S ribosomal protein S24



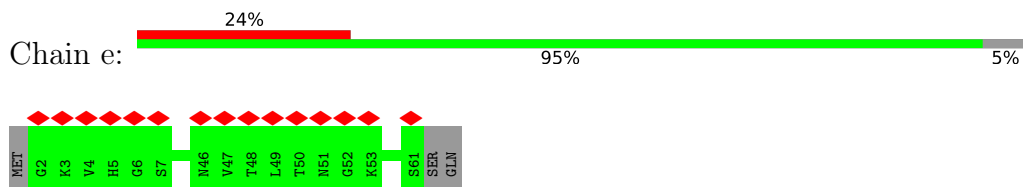
- Molecule 17: 40S ribosomal protein S26



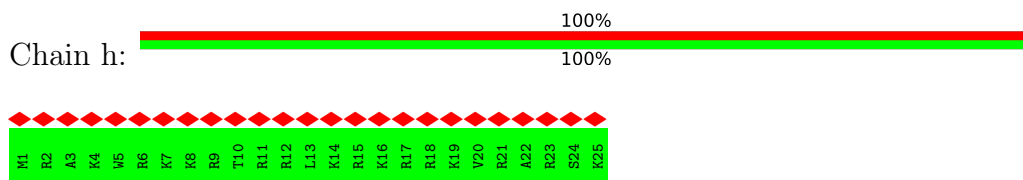
- Molecule 18: 40S ribosomal protein S27



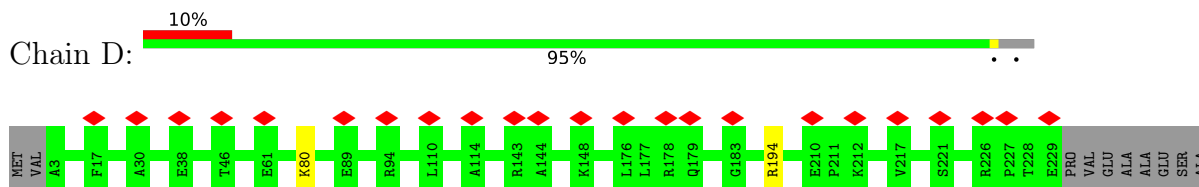
- Molecule 19: 40S ribosomal protein S30



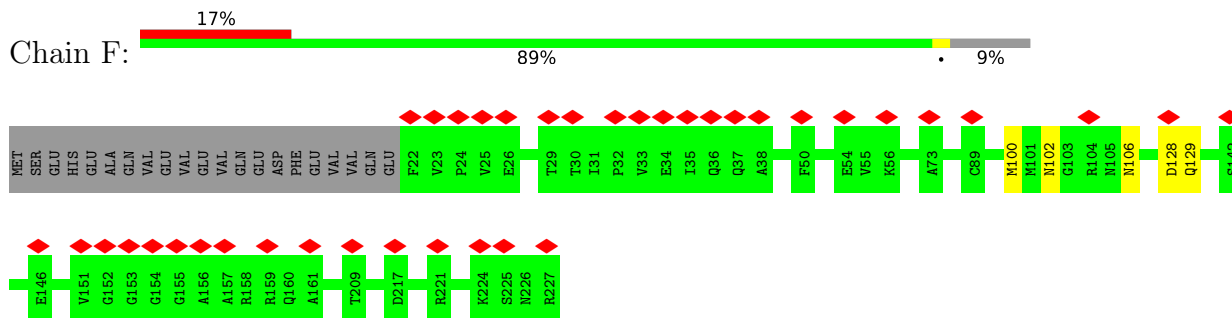
- Molecule 20: 40S ribosomal protein L41-A



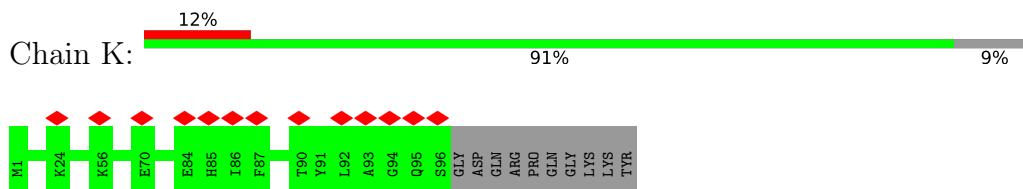
- Molecule 21: 40S ribosomal protein S3



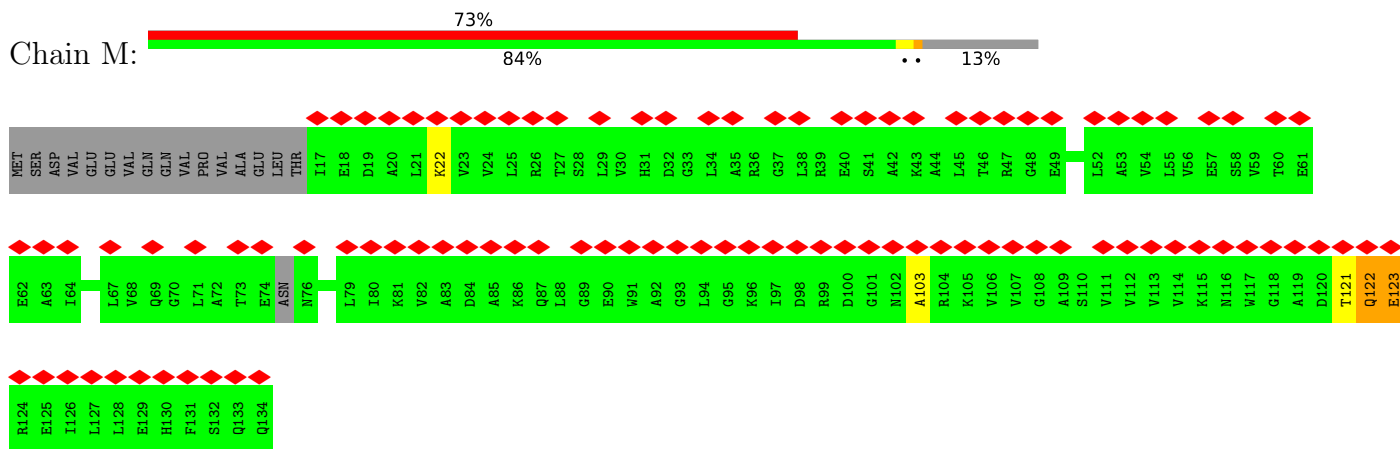
- Molecule 22: KLLA0D10659p



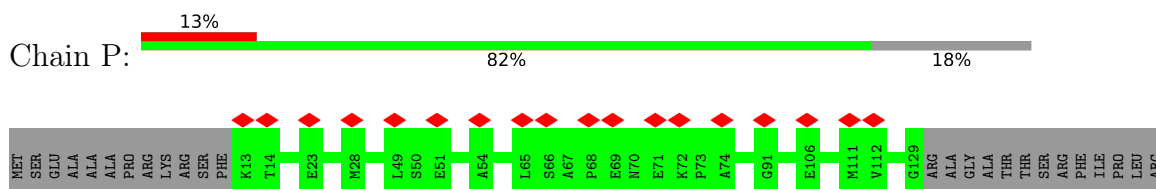
- Molecule 23: KLLA0B08173p



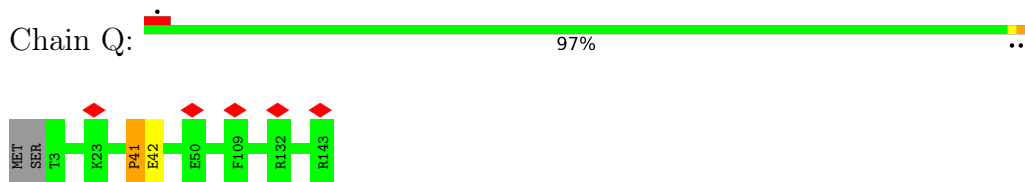
- Molecule 24: 40S ribosomal protein S12



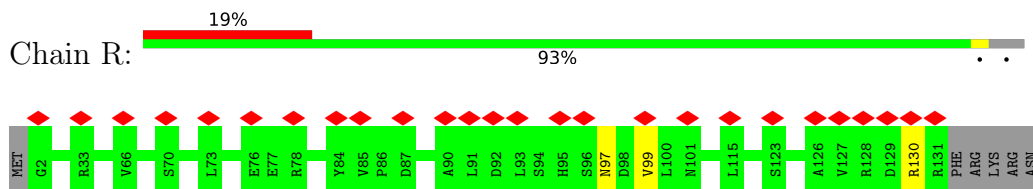
• Molecule 25: KLLA0F07843p



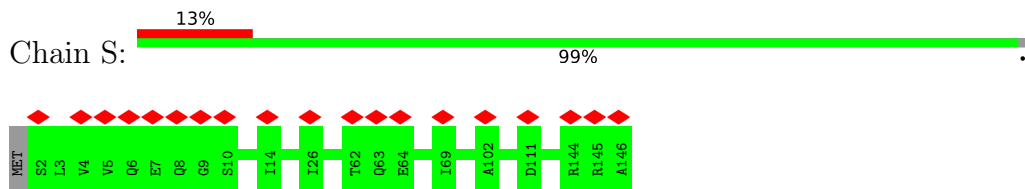
• Molecule 26: Small ribosomal subunit protein uS9



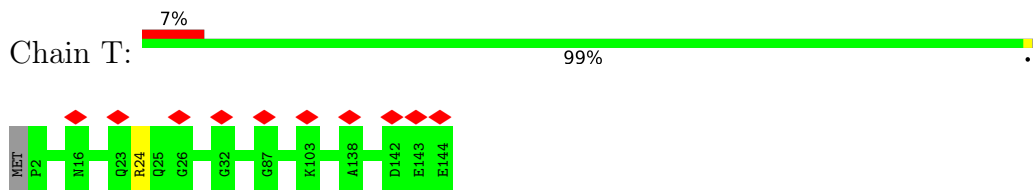
• Molecule 27: KLLA0B01474p



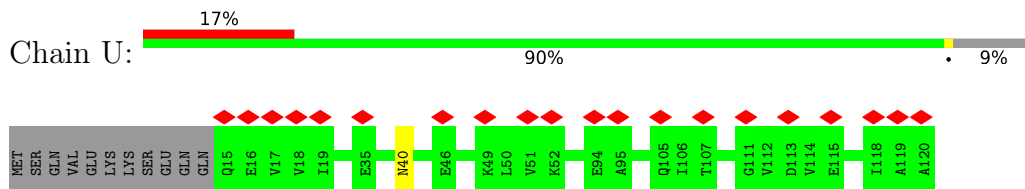
• Molecule 28: KLLA0B01562p



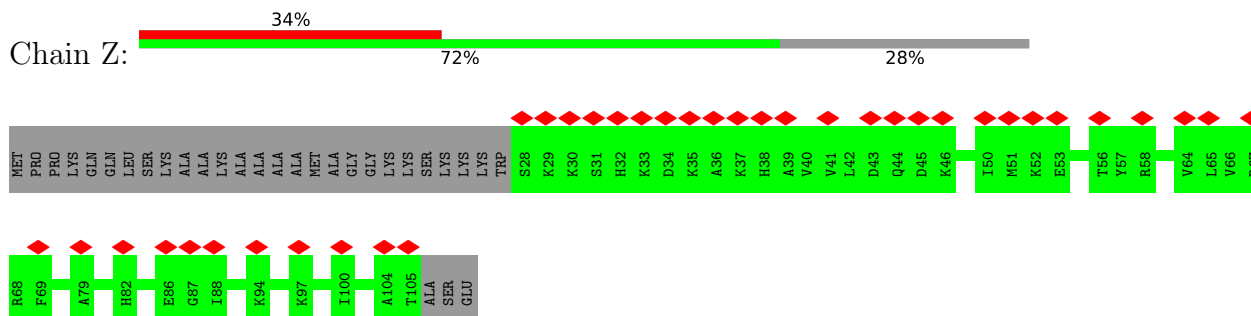
• Molecule 29: KLLA0A07194p



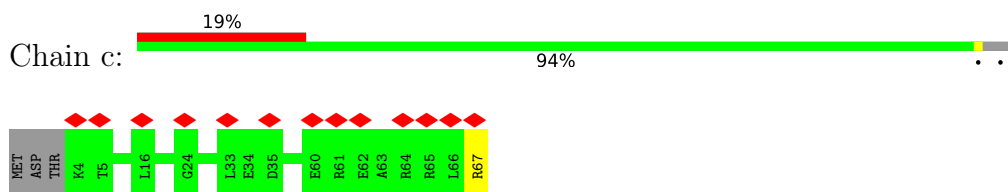
- Molecule 30: Small ribosomal subunit protein uS10



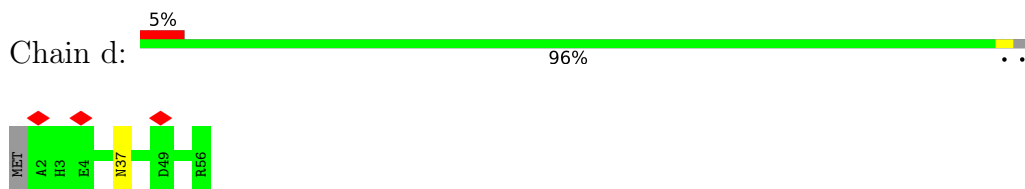
- Molecule 31: 40S ribosomal protein S25



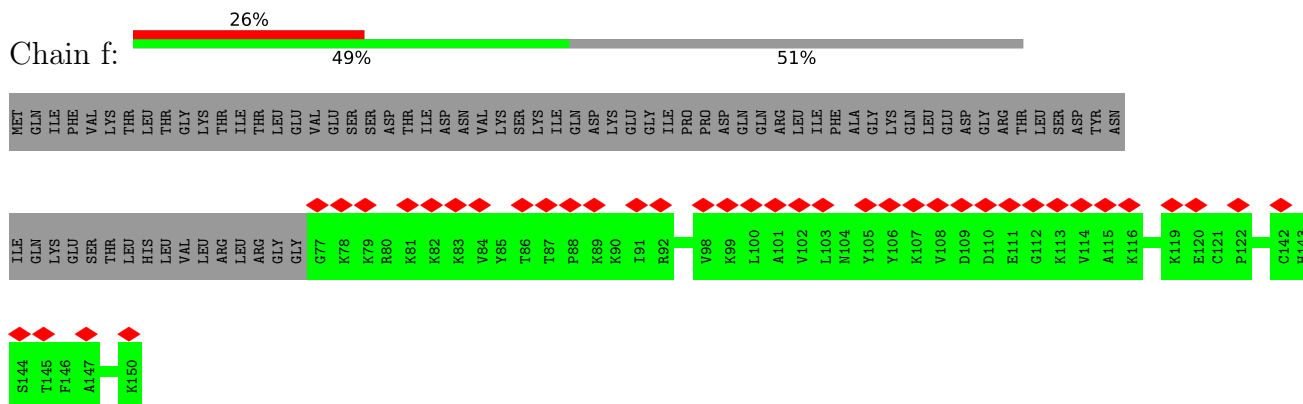
- Molecule 32: Small ribosomal subunit protein eS28



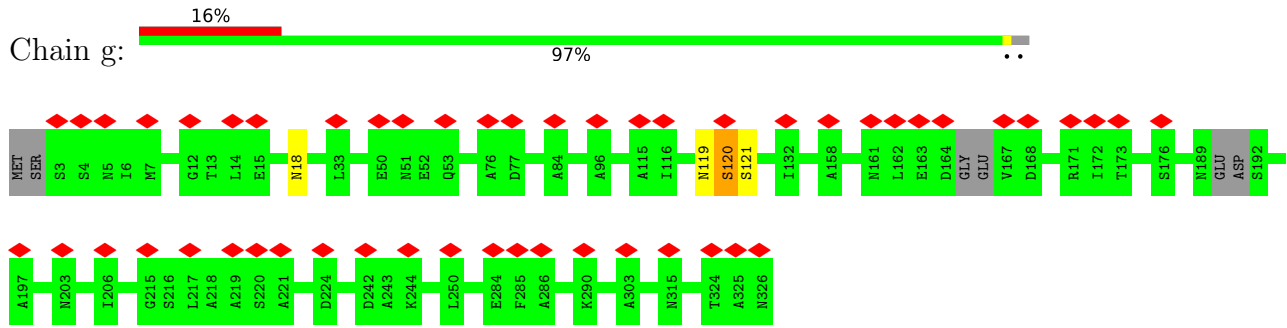
- Molecule 33: Small ribosomal subunit protein uS14



- Molecule 34: Small ribosomal subunit protein eS31



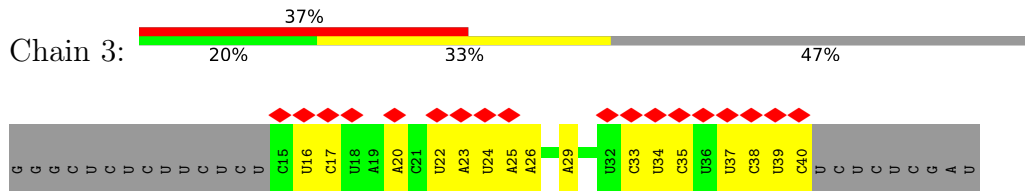
- Molecule 35: KLLA0E12277p



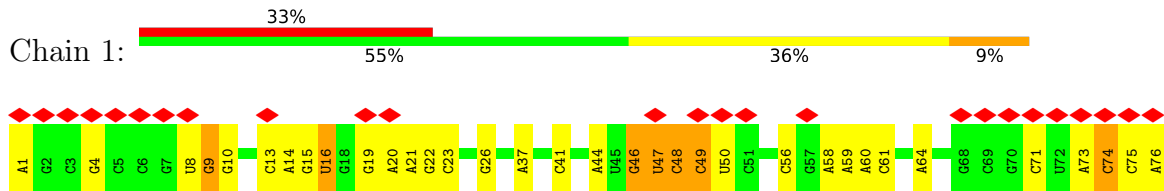
• Molecule 36: Eukaryotic translation initiation factor 1A



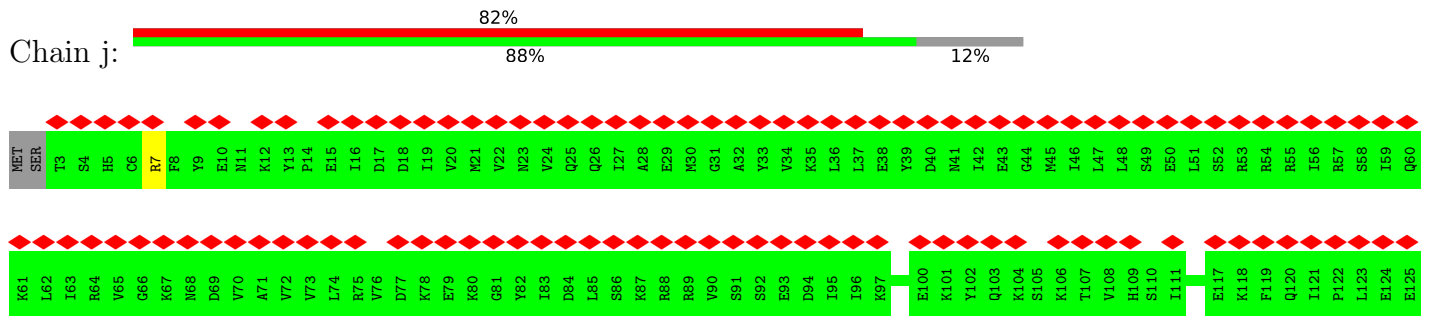
• Molecule 37: mRNA (5'-R(P*AP*AP*U)-3')

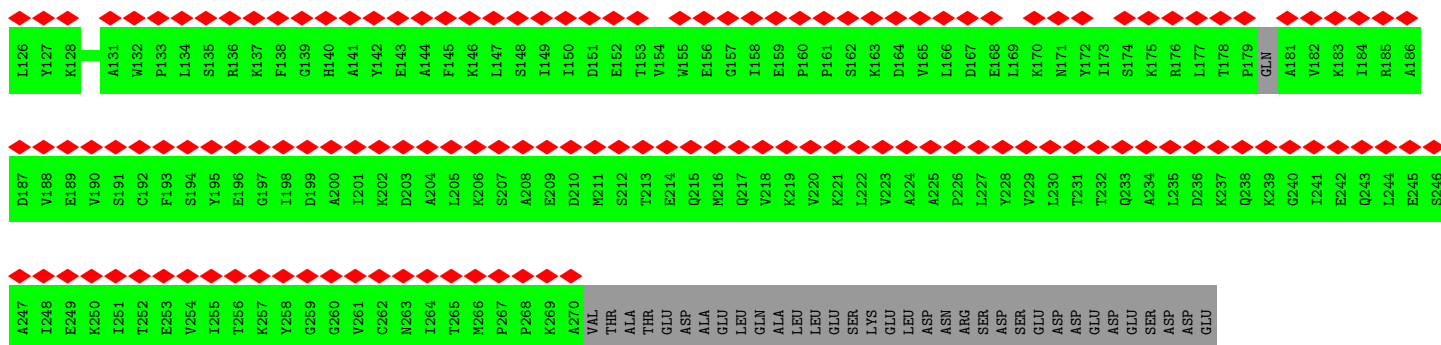


• Molecule 38: Met-tRNAi

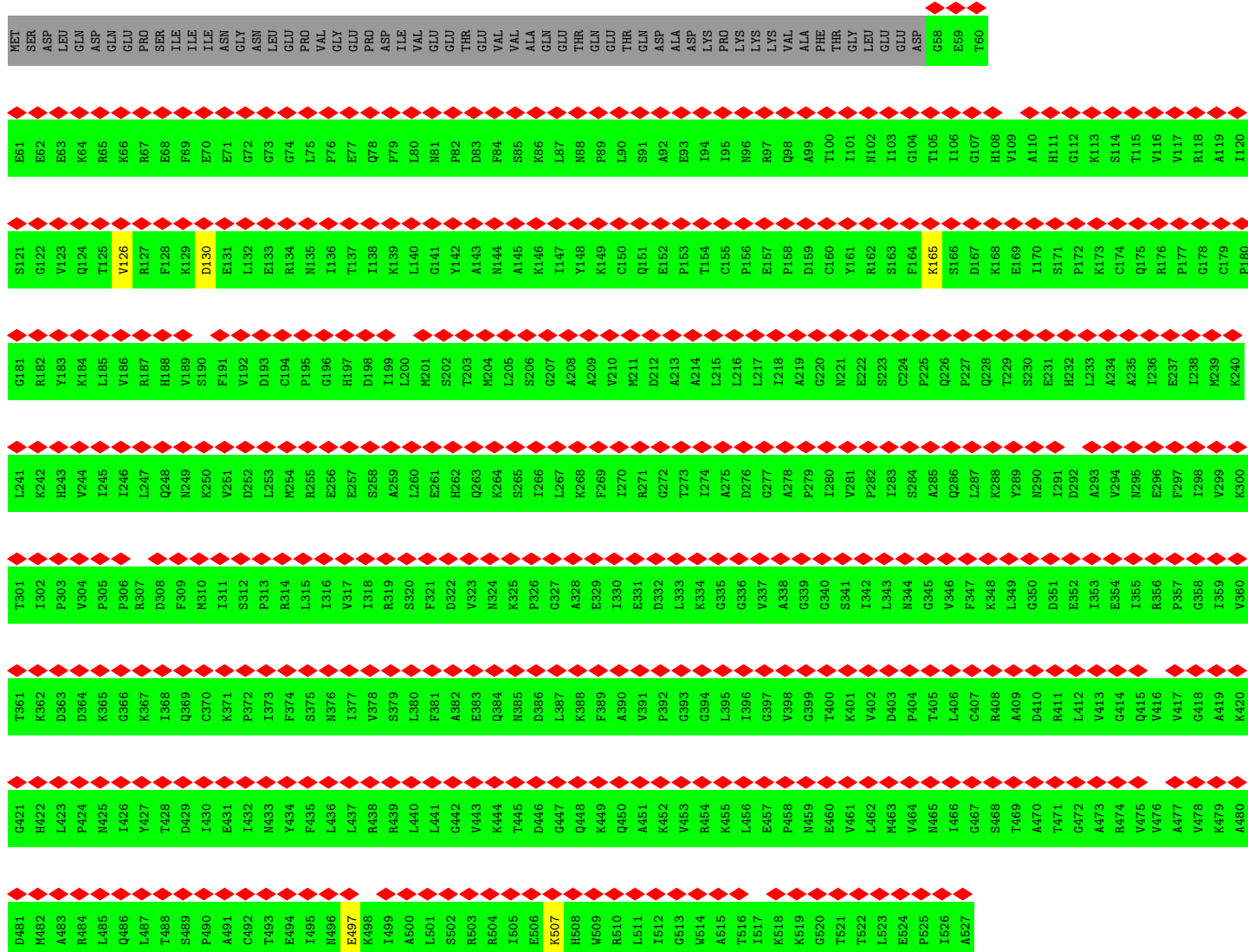
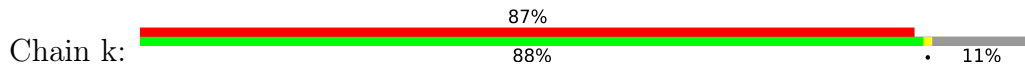


• Molecule 39: Eukaryotic translation initiation factor 2 subunit alpha



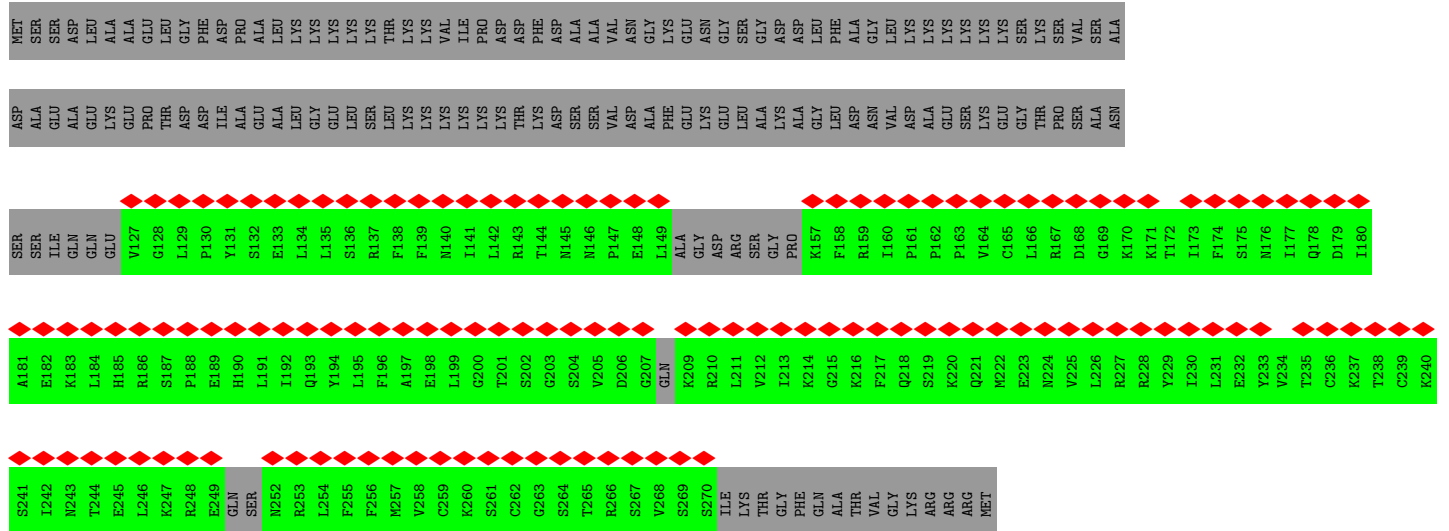


• Molecule 40: Eukaryotic translation initiation factor 2 subunit gamma

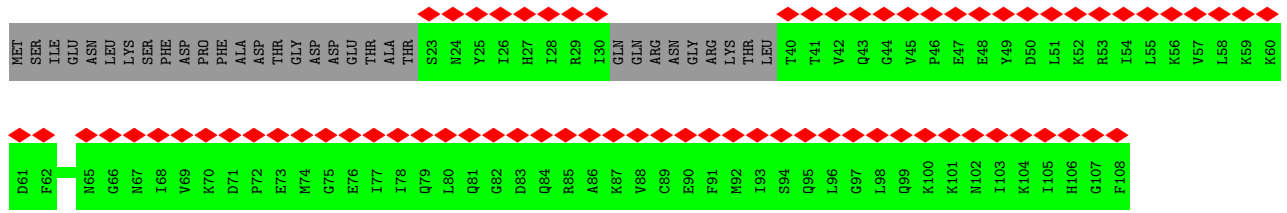


• Molecule 41: Eukaryotic translation initiation factor 2 subunit beta





● Molecule 42: Eukaryotic translation initiation factor eIF-1



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 26818 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 30 | Depositor |
| Minimum defocus (nm) | 1000 | Depositor |
| Maximum defocus (nm) | 3500 | Depositor |
| Magnification | 59000 | Depositor |
| Image detector | FEI FALCON III (4k x 4k) | Depositor |
| Maximum map value | 0.330 | Depositor |
| Minimum map value | -0.169 | Depositor |
| Average map value | -0.000 | Depositor |
| Map value standard deviation | 0.018 | Depositor |
| Recommended contour level | 0.06 | 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: 2MG, ZN, MA6, PSU, 5MC, MG, B8N, M2G, 1MG, T6A, H2U, 7MG, 1MA, RIA, 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 | 2 | 0.44 | 0/42201 | 0.89 | 40/65752 (0.1%) |
| 2 | A | 0.32 | 0/1742 | 0.59 | 1/2383 (0.0%) |
| 3 | B | 0.30 | 0/1820 | 0.61 | 1/2448 (0.0%) |
| 4 | C | 0.33 | 0/1678 | 0.56 | 0/2277 |
| 5 | E | 0.33 | 0/2122 | 0.62 | 0/2861 |
| 6 | G | 0.29 | 0/1855 | 0.57 | 1/2479 (0.0%) |
| 7 | H | 0.30 | 0/1507 | 0.61 | 0/2028 |
| 8 | I | 0.31 | 0/1515 | 0.61 | 0/2029 |
| 9 | J | 0.34 | 0/1495 | 0.68 | 1/2001 (0.0%) |
| 10 | L | 0.36 | 0/1276 | 0.58 | 0/1718 |
| 11 | N | 0.29 | 0/1218 | 0.54 | 0/1638 |
| 12 | O | 0.29 | 0/966 | 0.64 | 0/1297 |
| 13 | V | 0.32 | 0/696 | 0.59 | 0/938 |
| 14 | W | 0.35 | 0/1039 | 0.61 | 0/1399 |
| 15 | X | 0.34 | 0/1137 | 0.60 | 0/1516 |
| 16 | Y | 0.31 | 0/1075 | 0.62 | 1/1433 (0.1%) |
| 17 | a | 0.31 | 0/810 | 0.65 | 0/1087 |
| 18 | b | 0.27 | 0/619 | 0.56 | 0/837 |
| 19 | e | 0.29 | 0/480 | 0.56 | 0/640 |
| 20 | h | 0.25 | 0/234 | 0.75 | 0/300 |
| 21 | D | 0.29 | 0/1800 | 0.58 | 0/2421 |
| 22 | F | 0.31 | 0/1628 | 0.58 | 0/2198 |
| 23 | K | 0.32 | 0/831 | 0.53 | 0/1123 |
| 24 | M | 0.29 | 0/891 | 0.63 | 0/1201 |
| 25 | P | 0.30 | 0/942 | 0.59 | 0/1269 |
| 26 | Q | 0.33 | 0/1125 | 0.62 | 0/1510 |
| 27 | R | 0.34 | 0/1044 | 0.64 | 0/1402 |
| 28 | S | 0.28 | 0/1208 | 0.60 | 0/1624 |
| 29 | T | 0.29 | 0/1129 | 0.56 | 0/1520 |
| 30 | U | 0.30 | 0/857 | 0.59 | 0/1158 |
| 31 | Z | 0.29 | 0/603 | 0.59 | 0/814 |
| 32 | c | 0.31 | 0/501 | 0.65 | 0/673 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|----------------|-------------|------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 33 | d | 0.32 | 0/473 | 0.62 | 0/629 |
| 34 | f | 0.27 | 0/597 | 0.54 | 0/795 |
| 35 | g | 0.30 | 0/2523 | 0.56 | 0/3434 |
| 36 | i | 0.27 | 0/773 | 0.59 | 0/1031 |
| 37 | 3 | 0.25 | 0/595 | 0.75 | 0/920 |
| 38 | 1 | 0.41 | 1/1529 (0.1%) | 0.89 | 2/2376 (0.1%) |
| 39 | j | 0.26 | 0/2171 | 0.53 | 0/2924 |
| 40 | k | 0.25 | 0/3657 | 0.51 | 0/4946 |
| 41 | l | 0.25 | 0/1099 | 0.52 | 0/1469 |
| 42 | m | 0.26 | 0/626 | 0.54 | 0/835 |
| All | All | 0.38 | 1/92087 (0.0%) | 0.76 | 47/133333 (0.0%) |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|--------|-------------|----------|
| 38 | 1 | 1 | A | OP3-P | -10.66 | 1.48 | 1.61 |

The worst 5 of 47 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-----------|-------|-------------|----------|
| 1 | 2 | 1020 | C | N3-C2-O2 | -8.03 | 116.28 | 121.90 |
| 1 | 2 | 572 | C | N3-C2-O2 | -7.90 | 116.37 | 121.90 |
| 1 | 2 | 1020 | C | N1-C2-O2 | 7.22 | 123.23 | 118.90 |
| 1 | 2 | 933 | C | N1-C2-O2 | 7.10 | 123.16 | 118.90 |
| 1 | 2 | 694 | U | C2-N1-C1' | 7.08 | 126.19 | 117.70 |

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 2 | A | 217/254 (85%) | 193 (89%) | 24 (11%) | 0 | 100 | 100 |
| 3 | B | 221/255 (87%) | 189 (86%) | 31 (14%) | 1 (0%) | 25 | 63 |
| 4 | C | 218/259 (84%) | 197 (90%) | 20 (9%) | 1 (0%) | 25 | 63 |
| 5 | E | 258/261 (99%) | 224 (87%) | 34 (13%) | 0 | 100 | 100 |
| 6 | G | 228/236 (97%) | 211 (92%) | 17 (8%) | 0 | 100 | 100 |
| 7 | H | 182/190 (96%) | 157 (86%) | 23 (13%) | 2 (1%) | 12 | 46 |
| 8 | I | 184/201 (92%) | 162 (88%) | 22 (12%) | 0 | 100 | 100 |
| 9 | J | 180/188 (96%) | 151 (84%) | 24 (13%) | 5 (3%) | 4 | 25 |
| 10 | L | 153/156 (98%) | 135 (88%) | 16 (10%) | 2 (1%) | 10 | 42 |
| 11 | N | 149/151 (99%) | 137 (92%) | 12 (8%) | 0 | 100 | 100 |
| 12 | O | 127/137 (93%) | 108 (85%) | 19 (15%) | 0 | 100 | 100 |
| 13 | V | 85/87 (98%) | 77 (91%) | 8 (9%) | 0 | 100 | 100 |
| 14 | W | 127/130 (98%) | 112 (88%) | 15 (12%) | 0 | 100 | 100 |
| 15 | X | 142/145 (98%) | 114 (80%) | 28 (20%) | 0 | 100 | 100 |
| 16 | Y | 132/135 (98%) | 123 (93%) | 9 (7%) | 0 | 100 | 100 |
| 17 | a | 100/119 (84%) | 81 (81%) | 19 (19%) | 0 | 100 | 100 |
| 18 | b | 79/82 (96%) | 66 (84%) | 13 (16%) | 0 | 100 | 100 |
| 19 | e | 58/63 (92%) | 50 (86%) | 8 (14%) | 0 | 100 | 100 |
| 20 | h | 23/25 (92%) | 23 (100%) | 0 | 0 | 100 | 100 |
| 21 | D | 225/237 (95%) | 208 (92%) | 17 (8%) | 0 | 100 | 100 |
| 22 | F | 204/227 (90%) | 182 (89%) | 21 (10%) | 1 (0%) | 25 | 63 |
| 23 | K | 94/106 (89%) | 82 (87%) | 12 (13%) | 0 | 100 | 100 |
| 24 | M | 113/134 (84%) | 92 (81%) | 17 (15%) | 4 (4%) | 3 | 21 |
| 25 | P | 115/142 (81%) | 97 (84%) | 18 (16%) | 0 | 100 | 100 |
| 26 | Q | 139/143 (97%) | 120 (86%) | 17 (12%) | 2 (1%) | 9 | 40 |
| 27 | R | 128/136 (94%) | 106 (83%) | 21 (16%) | 1 (1%) | 16 | 53 |
| 28 | S | 143/146 (98%) | 124 (87%) | 19 (13%) | 0 | 100 | 100 |
| 29 | T | 141/144 (98%) | 128 (91%) | 13 (9%) | 0 | 100 | 100 |
| 30 | U | 104/117 (89%) | 97 (93%) | 7 (7%) | 0 | 100 | 100 |
| 31 | Z | 76/108 (70%) | 68 (90%) | 8 (10%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|-----------|----------|-------------|-----|
| 32 | c | 62/67 (92%) | 57 (92%) | 5 (8%) | 0 | 100 | 100 |
| 33 | d | 53/56 (95%) | 51 (96%) | 2 (4%) | 0 | 100 | 100 |
| 34 | f | 72/150 (48%) | 52 (72%) | 20 (28%) | 0 | 100 | 100 |
| 35 | g | 314/326 (96%) | 280 (89%) | 33 (10%) | 1 (0%) | 37 | 72 |
| 36 | i | 93/153 (61%) | 81 (87%) | 12 (13%) | 0 | 100 | 100 |
| 39 | j | 263/304 (86%) | 238 (90%) | 25 (10%) | 0 | 100 | 100 |
| 40 | k | 468/527 (89%) | 431 (92%) | 33 (7%) | 4 (1%) | 14 | 50 |
| 41 | l | 126/285 (44%) | 122 (97%) | 4 (3%) | 0 | 100 | 100 |
| 42 | m | 73/108 (68%) | 64 (88%) | 9 (12%) | 0 | 100 | 100 |
| All | All | 5869/6690 (88%) | 5190 (88%) | 655 (11%) | 24 (0%) | 32 | 67 |

5 of 24 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 7 | H | 66 | SER |
| 9 | J | 163 | PRO |
| 9 | J | 164 | PHE |
| 22 | F | 106 | ASN |
| 24 | M | 123 | GLU |

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 | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 2 | A | 180/211 (85%) | 180 (100%) | 0 | 100 | 100 |
| 3 | B | 202/228 (89%) | 200 (99%) | 2 (1%) | 73 | 82 |
| 4 | C | 177/203 (87%) | 177 (100%) | 0 | 100 | 100 |
| 5 | E | 223/224 (100%) | 223 (100%) | 0 | 100 | 100 |
| 6 | G | 192/200 (96%) | 191 (100%) | 1 (0%) | 86 | 90 |
| 7 | H | 164/170 (96%) | 164 (100%) | 0 | 100 | 100 |
| 8 | I | 147/159 (92%) | 146 (99%) | 1 (1%) | 81 | 87 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 9 | J | 153/158 (97%) | 149 (97%) | 4 (3%) | 41 | 61 |
| 10 | L | 136/137 (99%) | 135 (99%) | 1 (1%) | 81 | 87 |
| 11 | N | 128/128 (100%) | 128 (100%) | 0 | 100 | 100 |
| 12 | O | 97/104 (93%) | 96 (99%) | 1 (1%) | 73 | 82 |
| 13 | V | 73/73 (100%) | 73 (100%) | 0 | 100 | 100 |
| 14 | W | 110/111 (99%) | 109 (99%) | 1 (1%) | 75 | 83 |
| 15 | X | 119/120 (99%) | 118 (99%) | 1 (1%) | 79 | 85 |
| 16 | Y | 108/109 (99%) | 107 (99%) | 1 (1%) | 75 | 83 |
| 17 | a | 83/100 (83%) | 82 (99%) | 1 (1%) | 67 | 79 |
| 18 | b | 71/72 (99%) | 70 (99%) | 1 (1%) | 62 | 76 |
| 19 | e | 51/55 (93%) | 51 (100%) | 0 | 100 | 100 |
| 20 | h | 23/23 (100%) | 23 (100%) | 0 | 100 | 100 |
| 21 | D | 188/196 (96%) | 186 (99%) | 2 (1%) | 70 | 80 |
| 22 | F | 174/194 (90%) | 170 (98%) | 4 (2%) | 45 | 65 |
| 23 | K | 88/96 (92%) | 88 (100%) | 0 | 100 | 100 |
| 24 | M | 93/109 (85%) | 90 (97%) | 3 (3%) | 34 | 55 |
| 25 | P | 99/119 (83%) | 99 (100%) | 0 | 100 | 100 |
| 26 | Q | 117/119 (98%) | 116 (99%) | 1 (1%) | 75 | 83 |
| 27 | R | 116/124 (94%) | 114 (98%) | 2 (2%) | 56 | 73 |
| 28 | S | 127/129 (98%) | 127 (100%) | 0 | 100 | 100 |
| 29 | T | 117/118 (99%) | 116 (99%) | 1 (1%) | 75 | 83 |
| 30 | U | 96/107 (90%) | 95 (99%) | 1 (1%) | 73 | 82 |
| 31 | Z | 59/88 (67%) | 59 (100%) | 0 | 100 | 100 |
| 32 | c | 55/59 (93%) | 54 (98%) | 1 (2%) | 54 | 72 |
| 33 | d | 47/48 (98%) | 46 (98%) | 1 (2%) | 48 | 67 |
| 34 | f | 60/133 (45%) | 60 (100%) | 0 | 100 | 100 |
| 35 | g | 264/272 (97%) | 260 (98%) | 4 (2%) | 60 | 75 |
| 36 | i | 80/130 (62%) | 80 (100%) | 0 | 100 | 100 |
| 39 | j | 239/274 (87%) | 238 (100%) | 1 (0%) | 89 | 91 |
| 40 | k | 393/449 (88%) | 392 (100%) | 1 (0%) | 91 | 92 |
| 41 | l | 125/246 (51%) | 125 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|-------------|-----|
| 42 | m | 69/96 (72%) | 69 (100%) | 0 | 100 | 100 |
| All | All | 5043/5691 (89%) | 5006 (99%) | 37 (1%) | 80 | 87 |

5 of 37 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 30 | U | 40 | ASN |
| 39 | j | 7 | ARG |
| 32 | c | 67 | ARG |
| 35 | g | 119 | ASN |
| 16 | Y | 108 | ARG |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 30 | U | 44 | ASN |
| 42 | m | 81 | GLN |
| 30 | U | 72 | ASN |
| 35 | g | 107 | HIS |
| 11 | N | 49 | GLN |

5.3.3 RNA [i](#)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 1 | 2 | 1785/1798 (99%) | 645 (36%) | 26 (1%) |
| 37 | 3 | 25/49 (51%) | 16 (64%) | 0 |
| 38 | 1 | 71/75 (94%) | 28 (39%) | 3 (4%) |
| All | All | 1881/1922 (97%) | 689 (36%) | 29 (1%) |

5 of 689 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | 2 | 2 | A |
| 1 | 2 | 3 | U |
| 1 | 2 | 4 | C |
| 1 | 2 | 9 | U |
| 1 | 2 | 13 | C |

5 of 29 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 1 | 2 | 930 | C |
| 38 | 1 | 48 | 5MC |
| 1 | 2 | 1198 | G |
| 1 | 2 | 1765 | G |
| 1 | 2 | 1080 | A |

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

23 non-standard protein/DNA/RNA residues are modelled in this entry.

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$ |
| 1 | 2MG | 2 | 1570 | 1 | 18,26,27 | 2.45 | 7 (38%) | 16,38,41 | 1.49 | 4 (25%) |
| 1 | 7MG | 2 | 1573 | 1 | 22,26,27 | 3.72 | 10 (45%) | 29,39,42 | 2.03 | 9 (31%) |
| 1 | MA6 | 2 | 1780 | 1 | 18,26,27 | 1.04 | 2 (11%) | 19,38,41 | 3.52 | 2 (10%) |
| 1 | PSU | 2 | 120 | 1 | 18,21,22 | 4.28 | 7 (38%) | 22,30,33 | 1.88 | 5 (22%) |
| 1 | PSU | 2 | 998 | 1 | 18,21,22 | 4.18 | 8 (44%) | 22,30,33 | 1.86 | 5 (22%) |
| 38 | H2U | 1 | 47 | 38 | 18,21,22 | 3.10 | 4 (22%) | 21,30,33 | 1.88 | 4 (19%) |
| 38 | 2MG | 1 | 10 | 38 | 18,26,27 | 2.50 | 7 (38%) | 16,38,41 | 1.30 | 3 (18%) |
| 38 | 5MC | 1 | 48 | 38 | 18,22,23 | 3.58 | 7 (38%) | 26,32,35 | 1.11 | 1 (3%) |
| 38 | RIA | 1 | 64 | 38 | 31,38,39 | 5.07 | 12 (38%) | 39,57,60 | 1.99 | 5 (12%) |
| 1 | PSU | 2 | 465 | 1 | 18,21,22 | 4.19 | 7 (38%) | 22,30,33 | 1.78 | 5 (22%) |
| 38 | T6A | 1 | 37 | 38 | 27,34,35 | 2.05 | 7 (25%) | 29,49,52 | 2.14 | 8 (27%) |
| 1 | 5MC | 2 | 1637 | 1 | 18,22,23 | 3.50 | 7 (38%) | 26,32,35 | 1.15 | 2 (7%) |
| 38 | H2U | 1 | 16 | 38 | 18,21,22 | 3.01 | 4 (22%) | 21,30,33 | 1.93 | 5 (23%) |
| 1 | 5MC | 2 | 1006 | 1 | 18,22,23 | 3.53 | 7 (38%) | 26,32,35 | 1.03 | 3 (11%) |
| 38 | 1MG | 1 | 9 | 38 | 18,26,27 | 2.99 | 6 (33%) | 19,39,42 | 1.53 | 3 (15%) |
| 1 | PSU | 2 | 766 | 1 | 18,21,22 | 4.19 | 8 (44%) | 22,30,33 | 1.99 | 6 (27%) |
| 38 | 1MA | 1 | 58 | 38 | 16,25,26 | 4.40 | 4 (25%) | 18,37,40 | 1.70 | 3 (16%) |
| 1 | 2MG | 2 | 1426 | 43,1 | 18,26,27 | 2.48 | 7 (38%) | 16,38,41 | 1.40 | 3 (18%) |
| 1 | B8N | 2 | 1190 | 1 | 24,29,30 | 3.03 | 7 (29%) | 29,42,45 | 1.77 | 6 (20%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|------|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 1 | PSU | 2 | 1289 | 1 | 18,21,22 | 4.26 | 7 (38%) | 22,30,33 | 1.70 | 3 (13%) |
| 38 | 5MC | 1 | 49 | 38 | 18,22,23 | 3.63 | 7 (38%) | 26,32,35 | 1.04 | 1 (3%) |
| 38 | 7MG | 1 | 46 | 38 | 22,26,27 | 3.87 | 10 (45%) | 29,39,42 | 2.03 | 9 (31%) |
| 38 | M2G | 1 | 26 | 38 | 20,27,28 | 3.81 | 8 (40%) | 22,40,43 | 1.35 | 5 (22%) |

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 |
|-----|------|-------|------|------|---------|------------|---------|
| 1 | 2MG | 2 | 1570 | 1 | - | 1/5/27/28 | 0/3/3/3 |
| 1 | 7MG | 2 | 1573 | 1 | - | 2/7/37/38 | 0/3/3/3 |
| 1 | MA6 | 2 | 1780 | 1 | - | 2/7/29/30 | 0/3/3/3 |
| 1 | PSU | 2 | 120 | 1 | - | 0/7/25/26 | 0/2/2/2 |
| 1 | PSU | 2 | 998 | 1 | - | 4/7/25/26 | 0/2/2/2 |
| 38 | H2U | 1 | 47 | 38 | - | 5/7/38/39 | 0/2/2/2 |
| 38 | 2MG | 1 | 10 | 38 | - | 0/5/27/28 | 0/3/3/3 |
| 38 | 5MC | 1 | 48 | 38 | - | 3/7/25/26 | 0/2/2/2 |
| 38 | RIA | 1 | 64 | 38 | - | 8/13/51/52 | 0/4/4/4 |
| 1 | PSU | 2 | 465 | 1 | - | 0/7/25/26 | 0/2/2/2 |
| 38 | T6A | 1 | 37 | 38 | - | 2/19/41/42 | 0/3/3/3 |
| 1 | 5MC | 2 | 1637 | 1 | - | 3/7/25/26 | 0/2/2/2 |
| 38 | H2U | 1 | 16 | 38 | - | 7/7/38/39 | 0/2/2/2 |
| 1 | 5MC | 2 | 1006 | 1 | - | 0/7/25/26 | 0/2/2/2 |
| 38 | 1MG | 1 | 9 | 38 | - | 2/3/25/26 | 0/3/3/3 |
| 1 | PSU | 2 | 766 | 1 | - | 2/7/25/26 | 0/2/2/2 |
| 38 | 1MA | 1 | 58 | 38 | - | 2/3/25/26 | 0/3/3/3 |
| 1 | 2MG | 2 | 1426 | 43,1 | - | 0/5/27/28 | 0/3/3/3 |
| 1 | B8N | 2 | 1190 | 1 | - | 2/16/34/35 | 0/2/2/2 |
| 1 | PSU | 2 | 1289 | 1 | - | 0/7/25/26 | 0/2/2/2 |
| 38 | 5MC | 1 | 49 | 38 | - | 2/7/25/26 | 0/2/2/2 |
| 38 | 7MG | 1 | 46 | 38 | - | 1/7/37/38 | 0/3/3/3 |
| 38 | M2G | 1 | 26 | 38 | - | 2/7/29/30 | 0/3/3/3 |

The worst 5 of 160 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|---------|--------|-------------|----------|
| 38 | 1 | 64 | RIA | C1'-C2' | -16.25 | 1.32 | 1.52 |
| 38 | 1 | 58 | 1MA | C2-N3 | 15.88 | 1.48 | 1.29 |
| 38 | 1 | 64 | RIA | O4'-C1A | 15.56 | 1.62 | 1.41 |
| 38 | 1 | 26 | M2G | C2-N3 | 13.27 | 1.46 | 1.30 |
| 1 | 2 | 1289 | PSU | C6-C5 | 11.05 | 1.48 | 1.35 |

The worst 5 of 100 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|----------|--------|-------------|----------|
| 1 | 2 | 1780 | MA6 | N1-C6-N6 | -14.08 | 102.23 | 117.06 |
| 38 | 1 | 64 | RIA | C5-C6-N6 | 7.61 | 131.92 | 120.35 |
| 38 | 1 | 16 | H2U | C4-N3-C2 | -6.56 | 120.35 | 125.79 |
| 38 | 1 | 47 | H2U | C4-N3-C2 | -6.40 | 120.48 | 125.79 |
| 38 | 1 | 37 | T6A | N3-C2-N1 | -5.94 | 119.39 | 128.68 |

There are no chirality outliers.

5 of 50 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|------|------|-----------------|
| 1 | 2 | 766 | PSU | C3'-C4'-C5'-O5' |
| 1 | 2 | 1190 | B8N | O4'-C4'-C5'-O5' |
| 1 | 2 | 1190 | B8N | C3'-C4'-C5'-O5' |
| 1 | 2 | 1637 | 5MC | O4'-C4'-C5'-O5' |
| 38 | 1 | 9 | 1MG | O4'-C4'-C5'-O5' |

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 123 ligands modelled in this entry, 121 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 | $\# Z > 2$ |
| 46 | MET | k | 602 | - | 6,7,8 | 0.52 | 0 | 2,7,9 | 0.10 | 0 |
| 45 | GCP | k | 601 | - | 27,34,34 | 1.53 | 6 (22%) | 34,54,54 | 1.95 | 8 (23%) |

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 |
|-----|------|-------|-----|------|---------|------------|---------|
| 46 | MET | k | 602 | - | - | 1/5/6/8 | - |
| 45 | GCP | k | 601 | - | - | 0/15/38/38 | 0/3/3/3 |

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

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|--------|------|-------------|----------|
| 45 | k | 601 | GCP | C5-C6 | 4.24 | 1.48 | 1.41 |
| 45 | k | 601 | GCP | PG-O3G | 2.87 | 1.61 | 1.54 |
| 45 | k | 601 | GCP | PG-O2G | 2.83 | 1.61 | 1.54 |
| 45 | k | 601 | GCP | PB-O3A | 2.81 | 1.61 | 1.58 |
| 45 | k | 601 | GCP | C5-C4 | 2.49 | 1.47 | 1.40 |

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

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|-------|-------------|----------|
| 45 | k | 601 | GCP | C2-N3-C4 | 4.98 | 121.04 | 115.36 |
| 45 | k | 601 | GCP | C2-N1-C6 | 4.04 | 122.35 | 115.93 |
| 45 | k | 601 | GCP | C5-C6-N1 | -3.99 | 117.98 | 123.43 |
| 45 | k | 601 | GCP | PB-O3A-PA | -3.80 | 120.50 | 132.56 |
| 45 | k | 601 | GCP | C4-C5-C6 | -3.70 | 117.26 | 120.80 |

There are no chirality outliers.

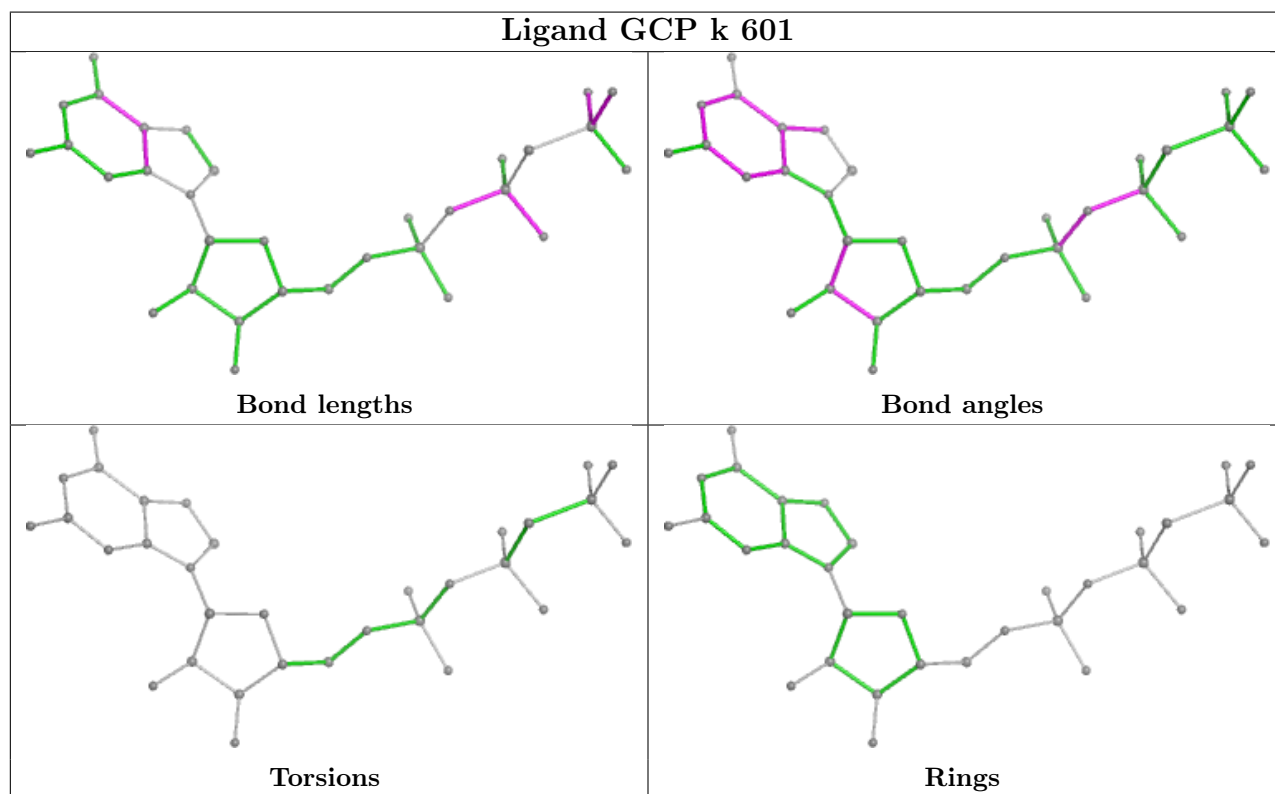
All (1) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|-------------|
| 46 | k | 602 | MET | CB-CG-SD-CE |

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [\(i\)](#)

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 |
|-----|-------|------------------|
| 38 | 1 | 3 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | 1 | 64:RIA | O3' | 65:G | P | 7.03 |
| 1 | 1 | 63:G | O3' | 64:RIA | P | 5.87 |
| 1 | 1 | 16:H2U | O3' | 18:G | P | 4.04 |

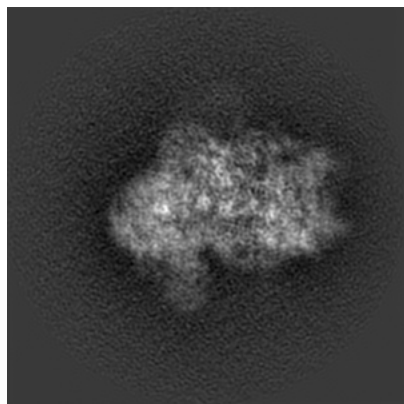
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19806. These allow visual inspection of the internal detail of the map and identification of artifacts.

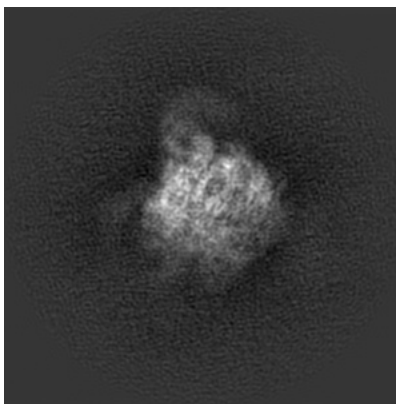
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

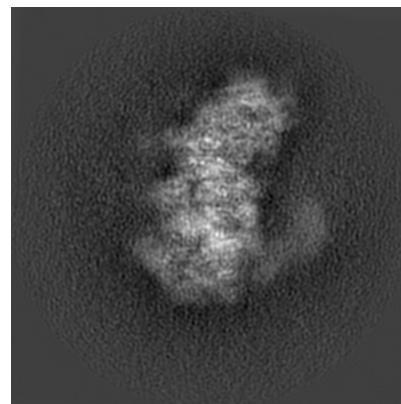
6.1.1 Primary map



X

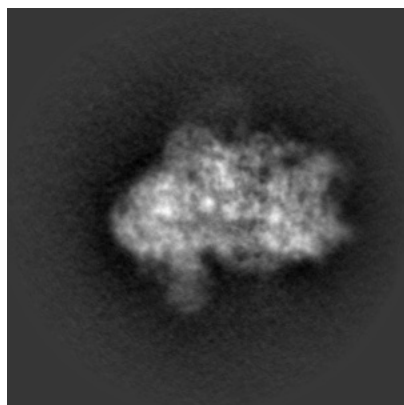


Y

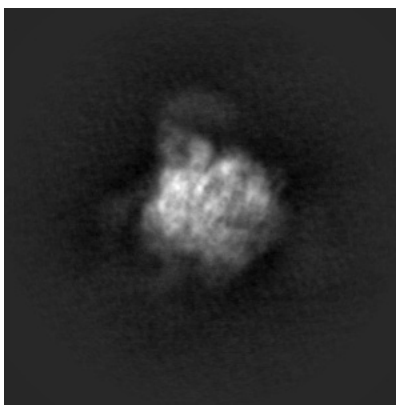


Z

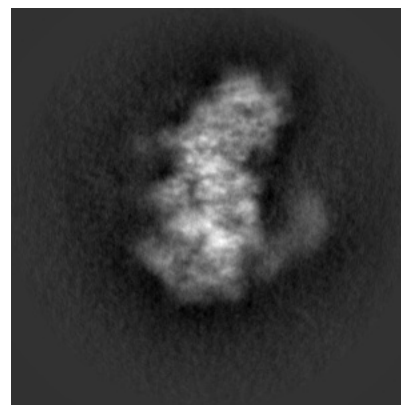
6.1.2 Raw map



X



Y

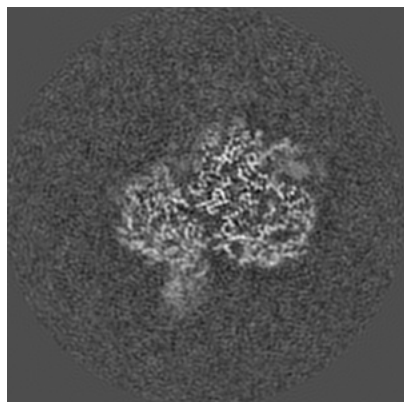


Z

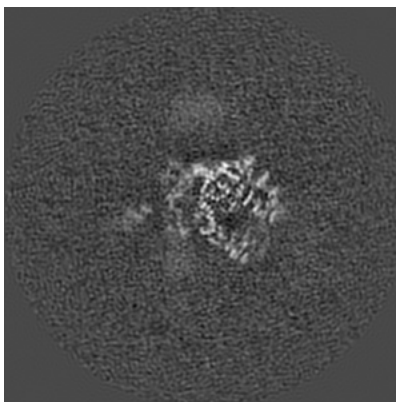
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

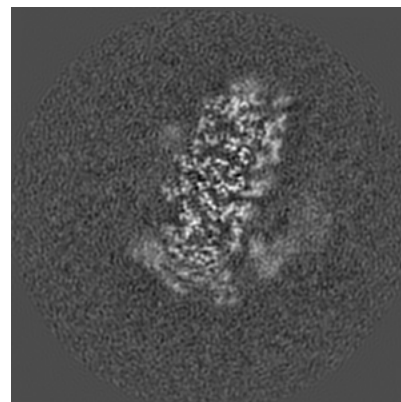
6.2.1 Primary map



X Index: 150

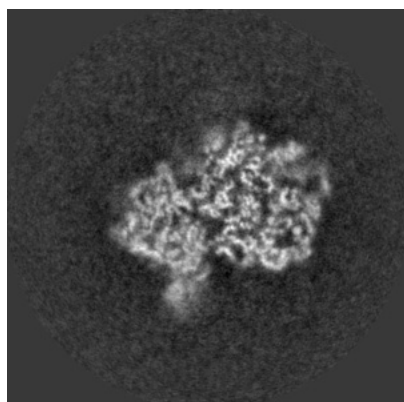


Y Index: 150

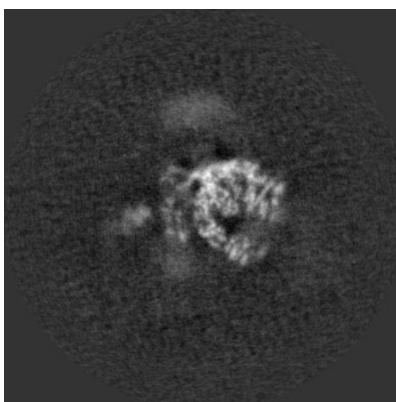


Z Index: 150

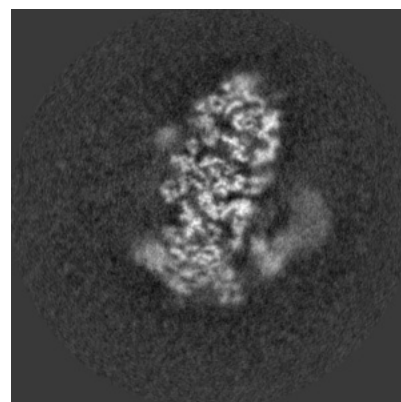
6.2.2 Raw map



X Index: 150



Y Index: 150

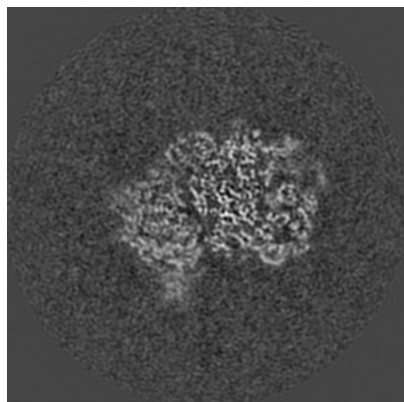


Z Index: 150

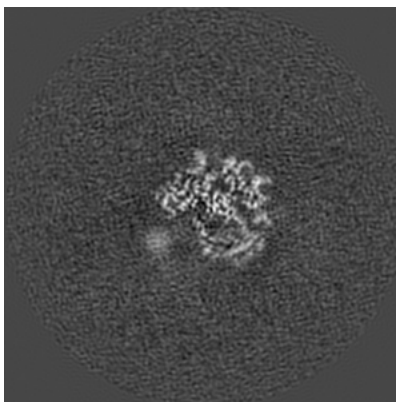
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

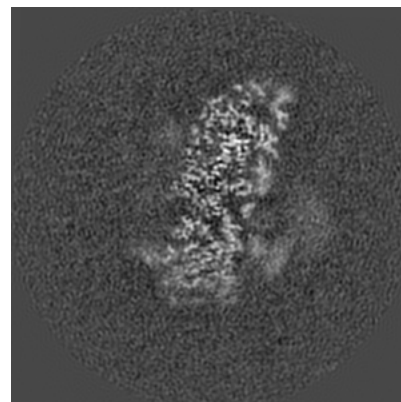
6.3.1 Primary map



X Index: 154

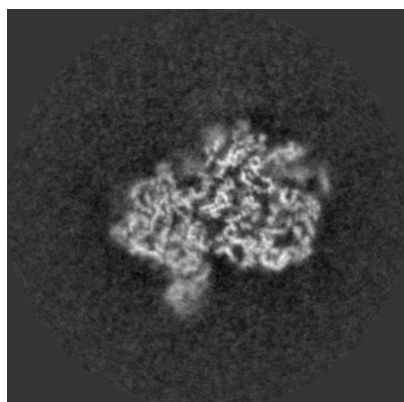


Y Index: 162

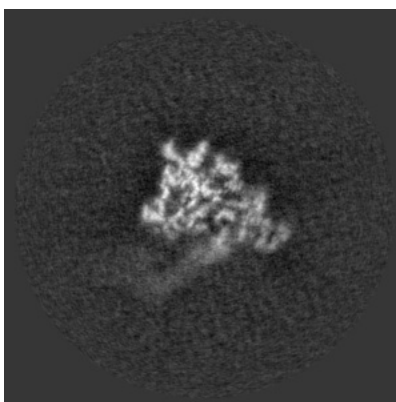


Z Index: 146

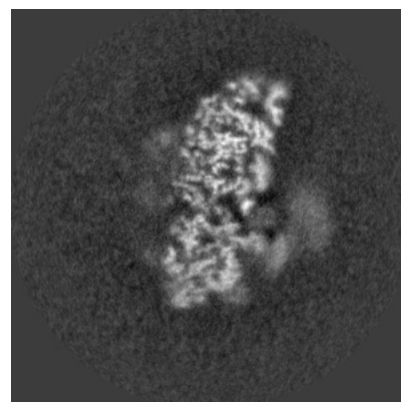
6.3.2 Raw map



X Index: 149



Y Index: 201

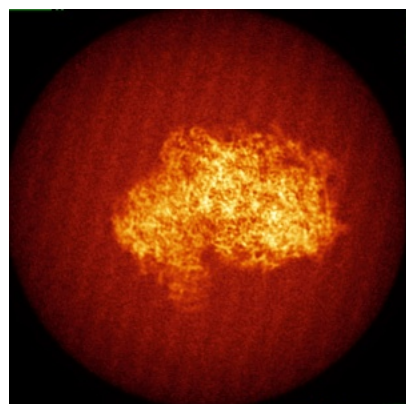


Z Index: 143

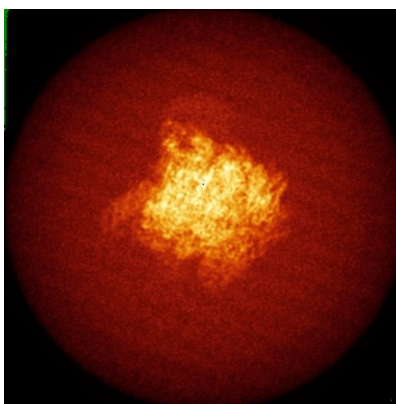
The images above show the largest variance slices of the map in three orthogonal directions.

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

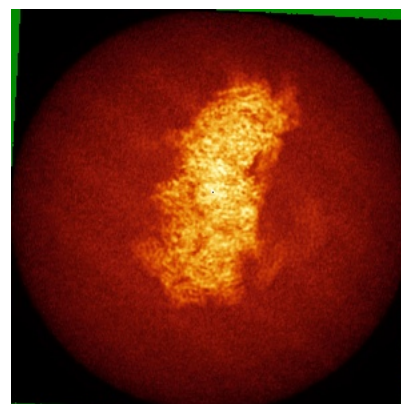
6.4.1 Primary map



X

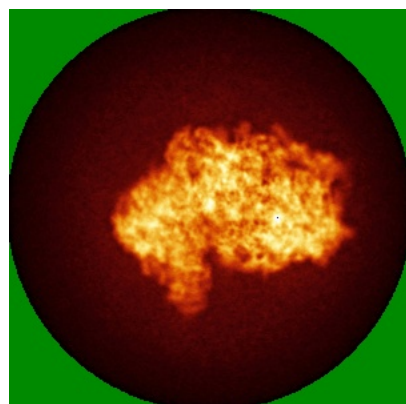


Y

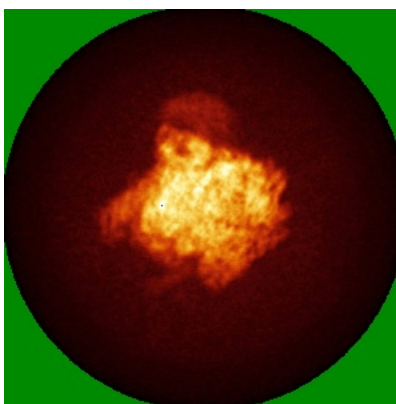


Z

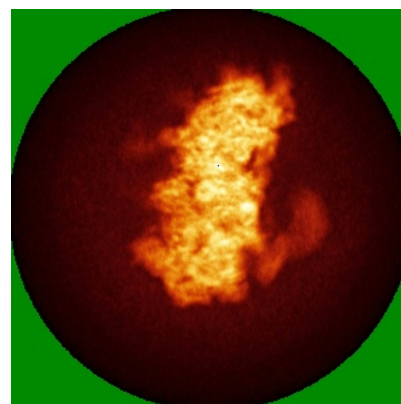
6.4.2 Raw map



X



Y

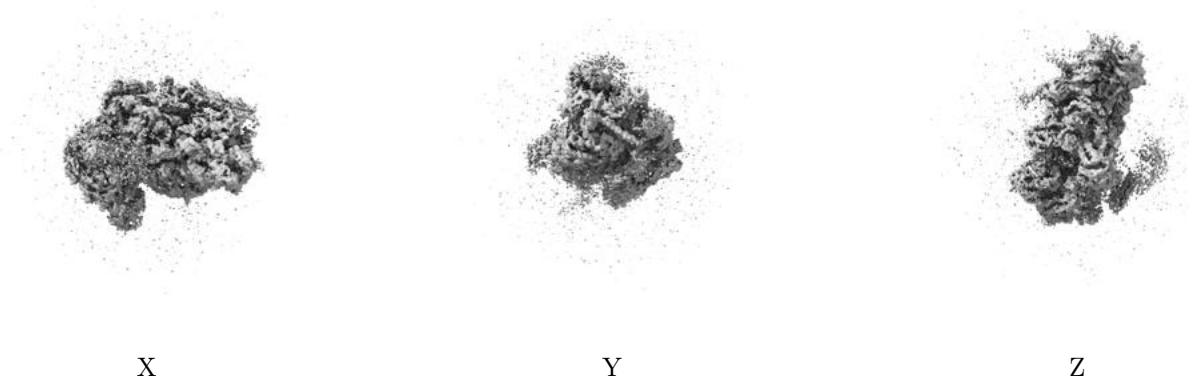


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

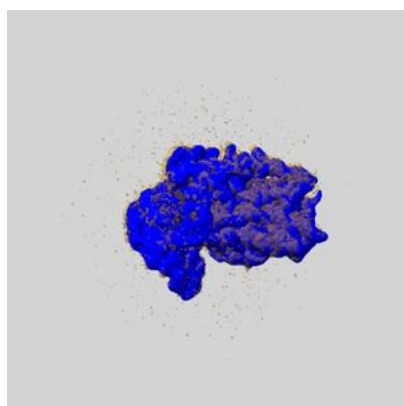
6.6 Mask visualisation [i](#)

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

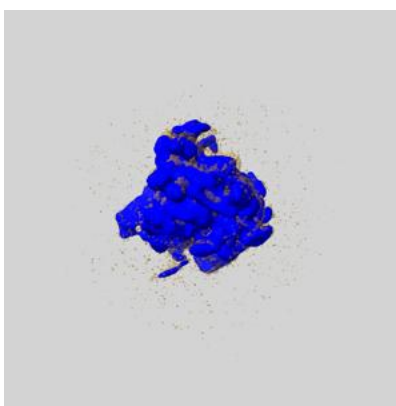
A mask typically either:

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

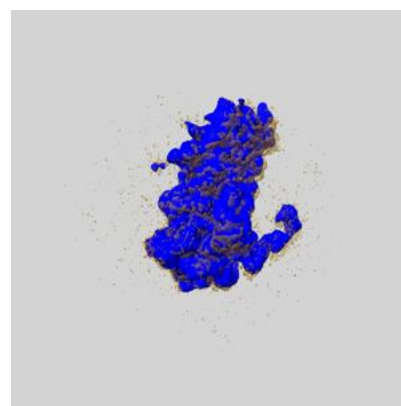
6.6.1 emd_19806_msk_1.map [i](#)



X



Y

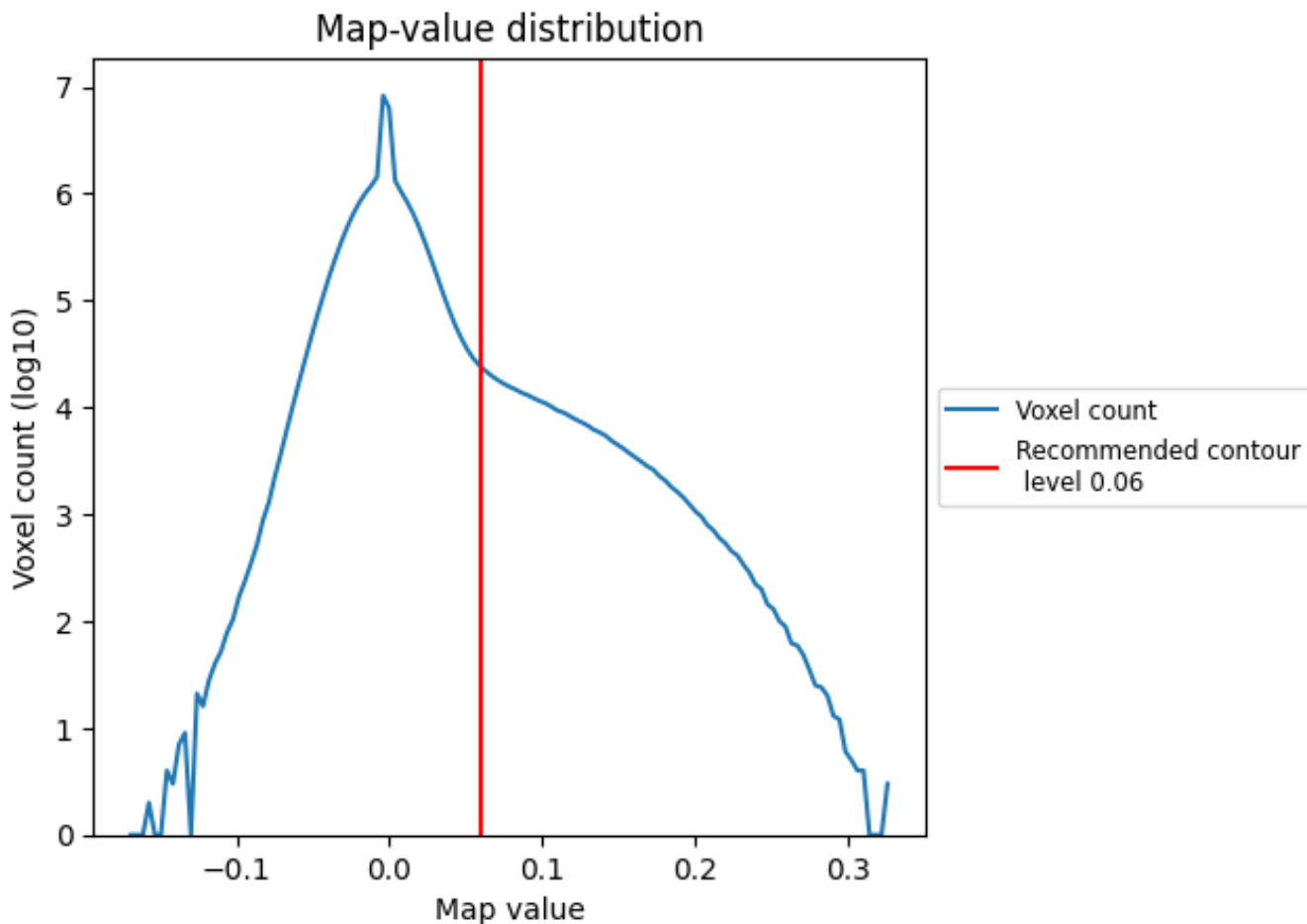


Z

7 Map analysis [i](#)

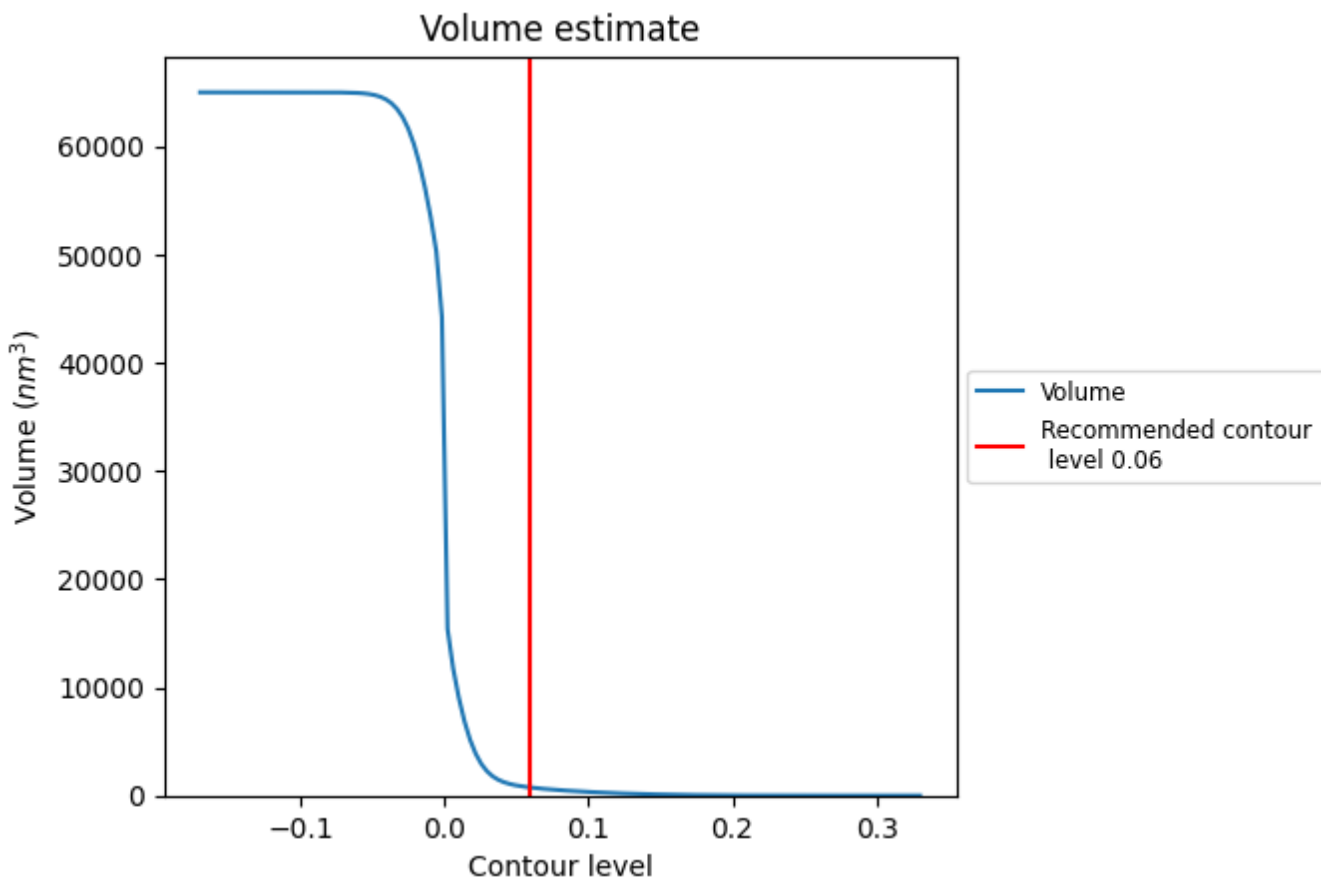
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

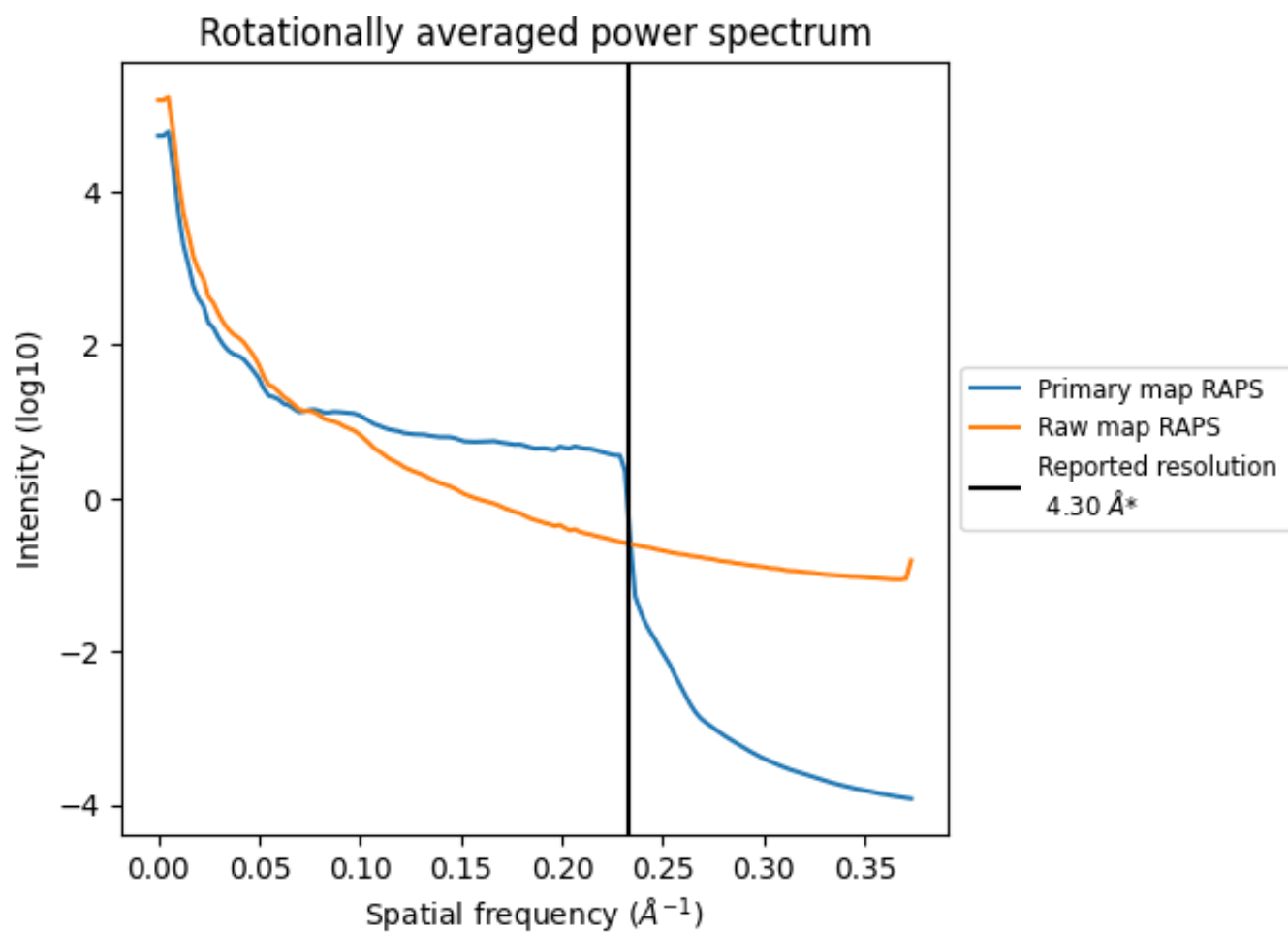
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 744 nm³; this corresponds to an approximate mass of 672 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](#)

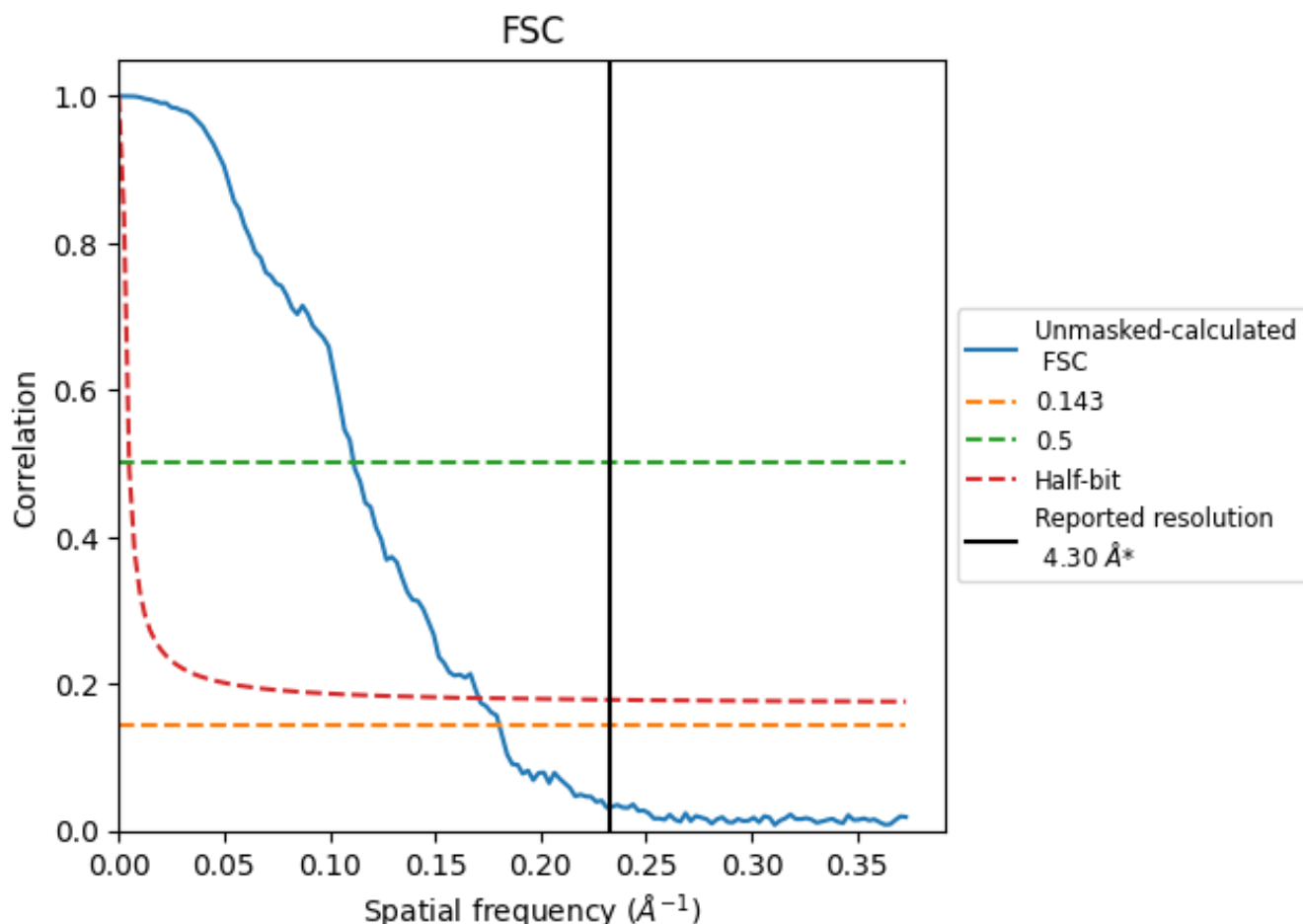


*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

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 0.233 Å⁻¹

8.2 Resolution estimates [i](#)

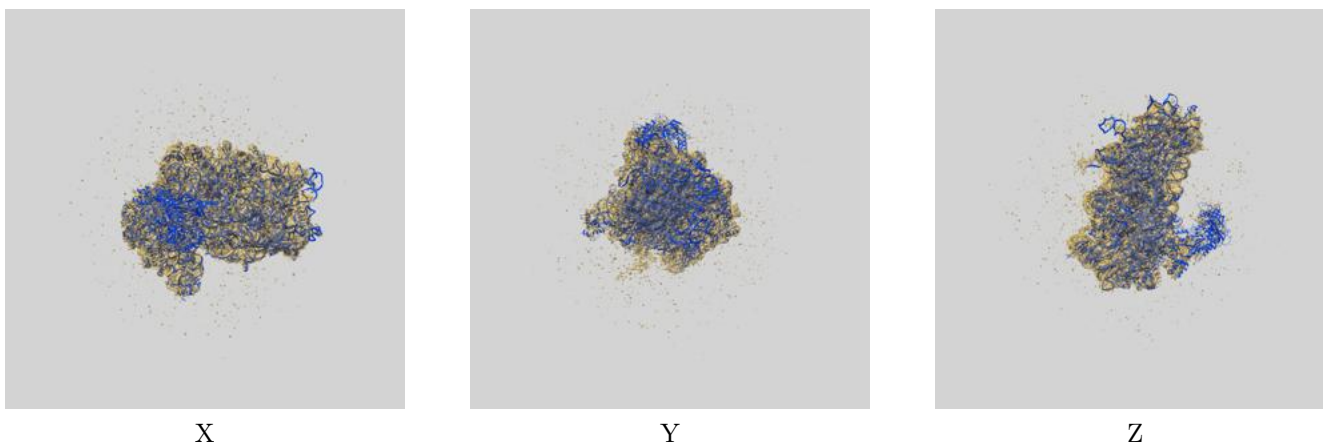
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 4.30 | - | - |
| Author-provided FSC curve | - | - | - |
| Unmasked-calculated* | 5.54 | 8.97 | 5.86 |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.54 differs from the reported value 4.3 by more than 10 %

9 Map-model fit [i](#)

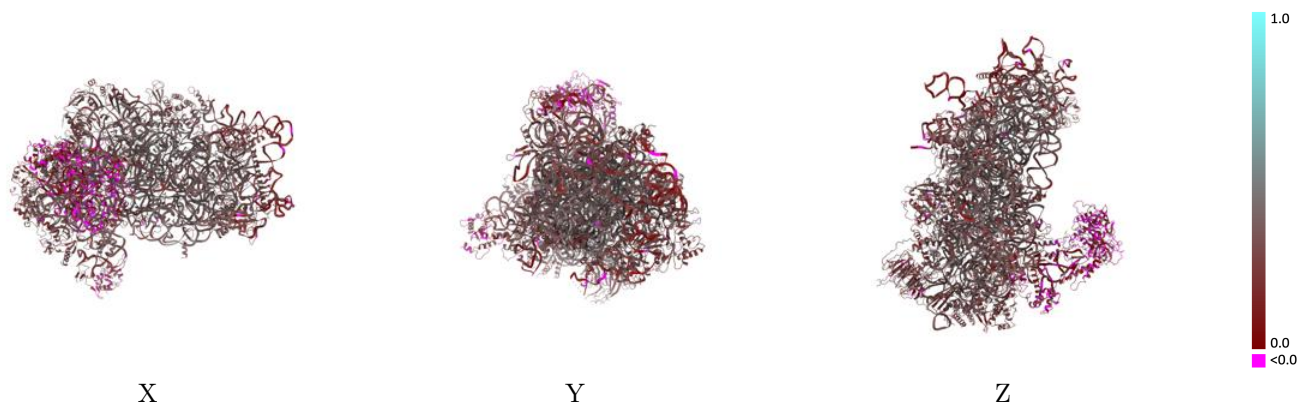
This section contains information regarding the fit between EMDB map EMD-19806 and PDB model 8S8I. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



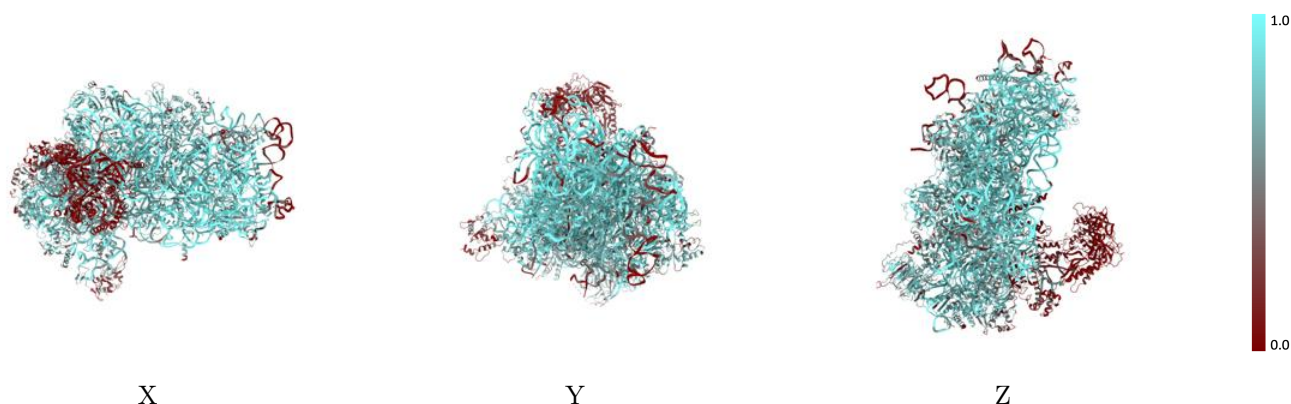
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



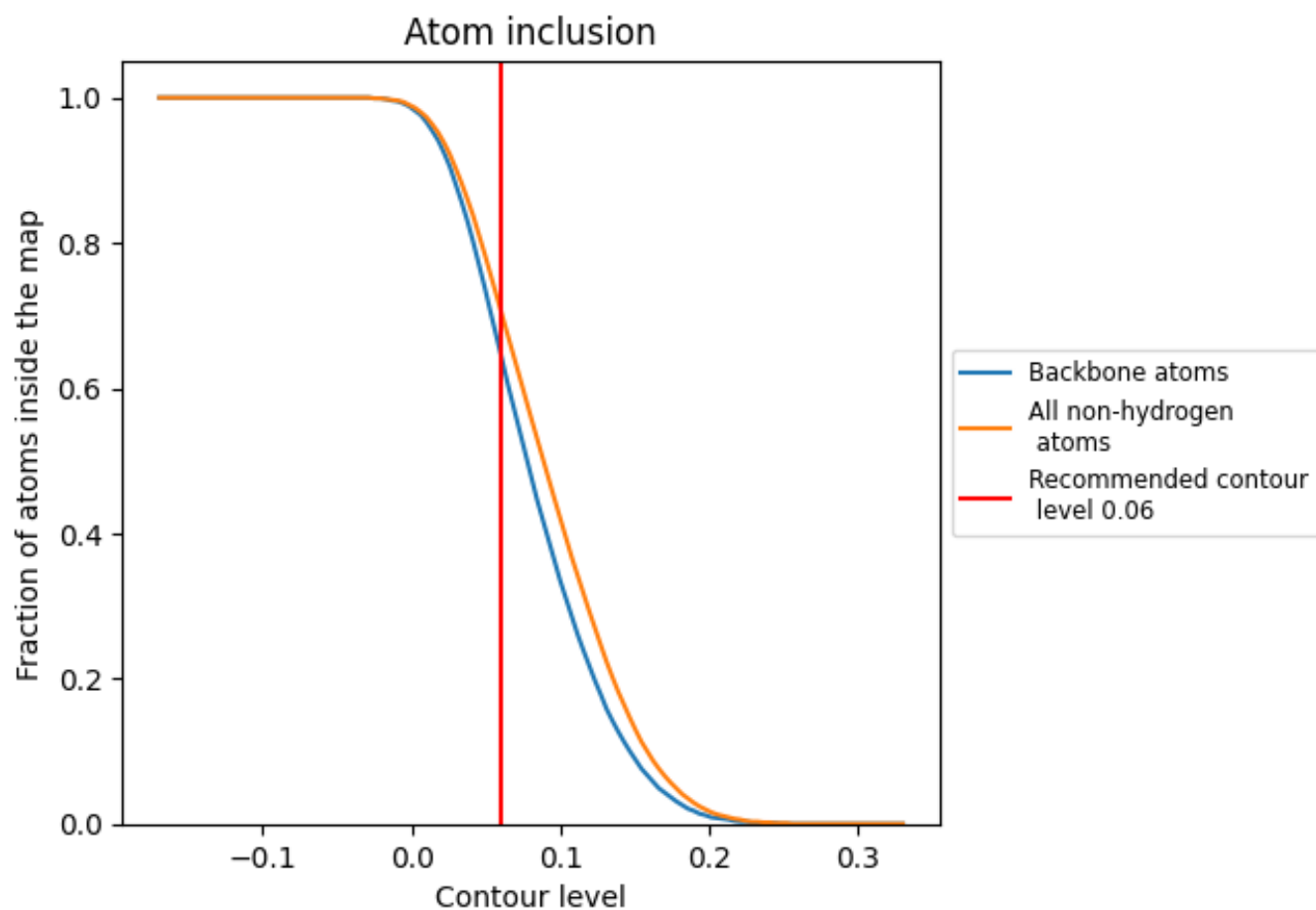
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.06).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 71% 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 (0.06) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.7080 |  0.3090 |
| 1 |  0.5620 |  0.1870 |
| 2 |  0.8790 |  0.3360 |
| 3 |  0.2980 |  0.3010 |
| A |  0.7530 |  0.3390 |
| B |  0.7380 |  0.3180 |
| C |  0.7530 |  0.3700 |
| D |  0.6640 |  0.3330 |
| E |  0.7750 |  0.3730 |
| F |  0.6600 |  0.3260 |
| G |  0.7680 |  0.3060 |
| H |  0.6180 |  0.3050 |
| I |  0.7490 |  0.3440 |
| J |  0.7440 |  0.3490 |
| K |  0.6830 |  0.2770 |
| L |  0.7150 |  0.3660 |
| M |  0.1900 |  0.1540 |
| N |  0.7710 |  0.3480 |
| O |  0.7290 |  0.3390 |
| P |  0.6820 |  0.2860 |
| Q |  0.7520 |  0.3260 |
| R |  0.6280 |  0.2980 |
| S |  0.6880 |  0.2880 |
| T |  0.7740 |  0.3000 |
| U |  0.5950 |  0.3060 |
| V |  0.8040 |  0.3590 |
| W |  0.7760 |  0.3790 |
| X |  0.7580 |  0.3830 |
| Y |  0.7980 |  0.3370 |
| Z |  0.4060 |  0.2540 |
| a |  0.7200 |  0.3750 |
| b |  0.7390 |  0.3590 |
| c |  0.6160 |  0.3460 |
| d |  0.7850 |  0.3390 |
| e |  0.6550 |  0.3690 |



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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| f |  0.4120 |  0.1930 |
| g |  0.6530 |  0.2820 |
| h |  0.0660 |  0.2370 |
| i |  0.3830 |  0.2990 |
| j |  0.1040 |  0.1350 |
| k |  0.0370 |  0.0900 |
| l |  0.0290 |  0.1370 |
| m |  0.0640 |  0.2100 |