



wwPDB EM Validation Summary Report ⓘ

Jul 23, 2025 – 12:39 PM JST

PDB ID : 9IOT / pdb_00009iot
EMDB ID : EMD-60747
Title : Cryo-EM structure of Escherichia coli hibernating ribosome with RNase I mutant
Authors : Tanzawa, T.; Minami, A.; Yoshida, H.; Kato, T.; Ogawa, T.
Deposited on : 2024-07-09
Resolution : 2.70 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.dev118
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
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) : 2.44

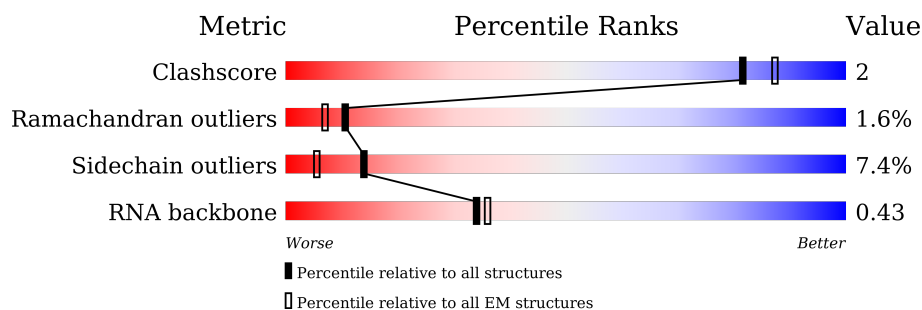
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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.




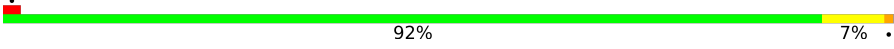
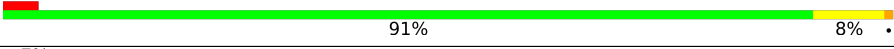
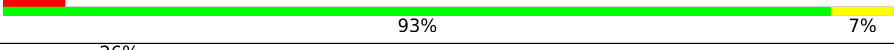


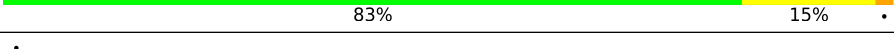
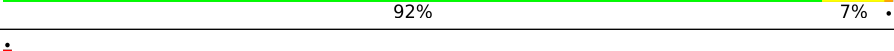
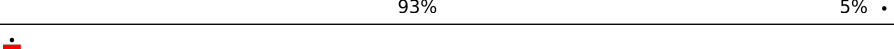
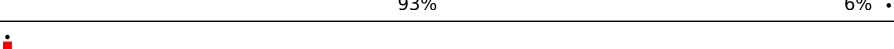
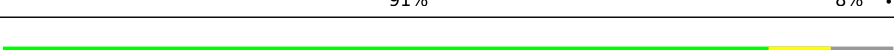

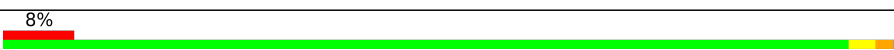
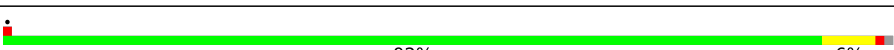
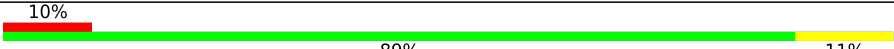
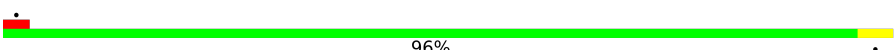




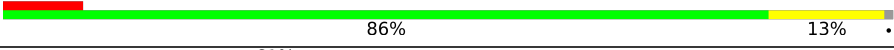




| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Clashscore | 210492 | 15764 |
| Ramachandran outliers | 207382 | 16835 |
| Sidechain outliers | 206894 | 16415 |
| RNA backbone | 6643 | 2191 |

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 | 0 | 63 | <div> <div>17%</div> <div>76%</div> <div>19%</div> <div>..</div> </div> |
| 2 | 1 | 59 | <div> <div>5%</div> <div>95%</div> <div>..</div> </div> |
| 3 | 3 | 57 | <div> <div>5%</div> <div>79%</div> <div>11%</div> <div>7%</div> <div>.</div> </div> |
| 4 | 4 | 55 | <div> <div>11%</div> <div>85%</div> <div>7%</div> <div>7%</div> </div> |
| 5 | 5 | 46 | <div> <div>91%</div> <div>9%</div> </div> |
| 6 | 6 | 65 | <div> <div>88%</div> <div>11%</div> <div>.</div> </div> |
| 7 | 7 | 38 | <div> <div>5%</div> <div>79%</div> <div>21%</div> </div> |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 8 | B | 120 |  |
| 9 | D | 273 |  |
| 10 | E | 209 |  |
| 11 | F | 201 |  |
| 12 | G | 179 |  |
| 13 | H | 177 |  |
| 14 | I | 41 |  |
| 15 | L | 142 |  |
| 16 | M | 123 |  |
| 17 | N | 144 |  |
| 18 | O | 136 |  |
| 19 | P | 127 |  |
| 20 | Q | 117 |  |
| 21 | R | 115 |  |
| 22 | S | 118 |  |
| 23 | T | 103 |  |
| 24 | U | 110 |  |
| 25 | V | 100 |  |
| 26 | W | 103 |  |
| 27 | X | 94 |  |
| 28 | Y | 85 |  |
| 29 | Z | 78 |  |
| 30 | 2 | 67 |  |
| 31 | A | 2904 |  |
| 32 | a | 1542 |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 33 | b | 241 | |
| 34 | c | 233 | |
| 35 | d | 206 | |
| 36 | e | 167 | |
| 37 | f | 102 | |
| 38 | g | 179 | |
| 39 | h | 130 | |
| 40 | i | 130 | |
| 41 | j | 103 | |
| 42 | k | 129 | |
| 43 | l | 124 | |
| 44 | m | 118 | |
| 45 | n | 101 | |
| 46 | o | 89 | |
| 47 | p | 82 | |
| 48 | q | 84 | |
| 49 | r | 75 | |
| 50 | s | 92 | |
| 51 | t | 87 | |
| 52 | u | 71 | |
| 53 | v | 95 | |
| 54 | y | 55 | |
| 55 | z | 268 | |
| 56 | 8 | 557 | |

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 143360 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein uL29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 1 | 0 | 61 | Total | C | N | O | S | 0 | 0 |
| | | | 495 | 305 | 97 | 92 | 1 | | |
| | | | | | | | | | |

- Molecule 2 is a protein called Large ribosomal subunit protein uL30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 2 | 1 | 58 | Total | C | N | O | S | 0 | 0 |
| | | | 449 | 281 | 87 | 79 | 2 | | |
| | | | | | | | | | |

- Molecule 3 is a protein called Large ribosomal subunit protein bL32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 3 | 3 | 55 | Total | C | N | O | S | 0 | 0 |
| | | | 434 | 263 | 92 | 78 | 1 | | |
| | | | | | | | | | |

- Molecule 4 is a protein called Large ribosomal subunit protein bL33.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 4 | 4 | 51 | Total | C | N | O | 0 | 0 |
| | | | 410 | 263 | 75 | 72 | | |
| | | | | | | | | |

- Molecule 5 is a protein called 50S ribosomal protein L34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 5 | 5 | 46 | Total | C | N | O | S | 0 | 0 |
| | | | 377 | 228 | 90 | 57 | 2 | | |
| | | | | | | | | | |

- Molecule 6 is a protein called Large ribosomal subunit protein bL35.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 6 | 6 | 64 | Total | C | N | O | S | 0 | 0 |
| | | | 504 | 323 | 105 | 74 | 2 | | |
| | | | | | | | | | |

- Molecule 7 is a protein called 50S ribosomal protein L36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 7 | 7 | 38 | Total | C | N | O | S | 0 | 0 |
| | | | 302 | 185 | 65 | 48 | 4 | | |

- Molecule 8 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 8 | B | 120 | Total | C | N | O | P | 0 | 0 |
| | | | 2572 | 1145 | 470 | 837 | 120 | | |

- Molecule 9 is a protein called Large ribosomal subunit protein uL2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 9 | D | 271 | Total | C | N | O | S | 0 | 0 |
| | | | 2075 | 1286 | 423 | 359 | 7 | | |

- Molecule 10 is a protein called 50S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10 | E | 209 | Total | C | N | O | S | 0 | 0 |
| | | | 1556 | 975 | 288 | 290 | 3 | | |

- Molecule 11 is a protein called 50S ribosomal protein L4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 11 | F | 201 | Total | C | N | O | S | 0 | 0 |
| | | | 1536 | 966 | 280 | 285 | 5 | | |

- Molecule 12 is a protein called Large ribosomal subunit protein uL5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12 | G | 177 | Total | C | N | O | S | 0 | 0 |
| | | | 1385 | 888 | 239 | 252 | 6 | | |

- Molecule 13 is a protein called Large ribosomal subunit protein uL6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 13 | H | 166 | Total | C | N | O | S | 0 | 0 |
| | | | 1226 | 774 | 224 | 226 | 2 | | |

- Molecule 14 is a protein called Large ribosomal subunit protein bL9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 14 | I | 41 | Total | C | N | O | S | 0 | 0 |
| | | | 303 | 194 | 54 | 54 | 1 | | |

- Molecule 15 is a protein called 50S ribosomal protein L13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15 | L | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1119 | 710 | 208 | 197 | 4 | | |

- Molecule 16 is a protein called 50S ribosomal protein L14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16 | M | 123 | Total | C | N | O | S | 0 | 0 |
| | | | 939 | 590 | 179 | 164 | 6 | | |

- Molecule 17 is a protein called Large ribosomal subunit protein uL15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17 | N | 144 | Total | C | N | O | S | 0 | 0 |
| | | | 1045 | 650 | 207 | 186 | 2 | | |

- Molecule 18 is a protein called Large ribosomal subunit protein uL16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 18 | O | 136 | Total | C | N | O | S | 0 | 0 |
| | | | 1070 | 684 | 205 | 175 | 6 | | |

- Molecule 19 is a protein called Large ribosomal subunit protein bL17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19 | P | 118 | Total | C | N | O | S | 0 | 0 |
| | | | 939 | 585 | 194 | 155 | 5 | | |

- Molecule 20 is a protein called Large ribosomal subunit protein uL18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20 | Q | 116 | Total | C | N | O | S | 0 | 0 |
| | | | 873 | 538 | 175 | 160 | | | |

- Molecule 21 is a protein called Large ribosomal subunit protein bL19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21 | R | 114 | Total | C | N | O | S | 0 | 0 |
| | | | 913 | 573 | 178 | 161 | 1 | | |

- Molecule 22 is a protein called Large ribosomal subunit protein bL20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 22 | S | 117 | Total | C | N | O | | 0 | 0 |
| | | | 944 | 603 | 192 | 149 | | | |

- Molecule 23 is a protein called 50S ribosomal protein L21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23 | T | 103 | Total | C | N | O | S | 0 | 0 |
| | | | 812 | 514 | 153 | 143 | 2 | | |

- Molecule 24 is a protein called 50S ribosomal protein L22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24 | U | 110 | Total | C | N | O | S | 0 | 0 |
| | | | 850 | 529 | 163 | 155 | 3 | | |

- Molecule 25 is a protein called Large ribosomal subunit protein uL23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25 | V | 93 | Total | C | N | O | S | 0 | 0 |
| | | | 738 | 466 | 139 | 131 | 2 | | |

- Molecule 26 is a protein called Large ribosomal subunit protein uL24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 26 | W | 102 | Total | C | N | O | | 0 | 0 |
| | | | 769 | 486 | 144 | 139 | | | |

- Molecule 27 is a protein called 50S ribosomal protein L25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27 | X | 94 | Total | C | N | O | S | 0 | 0 |
| | | | 746 | 474 | 136 | 134 | 2 | | |

- Molecule 28 is a protein called Large ribosomal subunit protein bL27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 28 | Y | 76 | Total | C | N | O | S | 0 | 0 |
| | | | 582 | 360 | 117 | 104 | 1 | | |

- Molecule 29 is a protein called Large ribosomal subunit protein bL28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29 | Z | 77 | Total | C | N | O | S | 0 | 0 |
| | | | 625 | 388 | 129 | 106 | 2 | | |

- Molecule 30 is a protein called Large ribosomal subunit protein bL31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 30 | 2 | 67 | Total | C | N | O | S | 0 | 0 |
| | | | 504 | 313 | 95 | 90 | 6 | | |

- Molecule 31 is a RNA chain called 23S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 31 | A | 2841 | Total | C | N | O | P | 0 | 0 |
| | | | 61011 | 27223 | 11229 | 19718 | 2841 | | |

- Molecule 32 is a RNA chain called 16S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 32 | a | 1534 | Total | C | N | O | P | 0 | 0 |
| | | | 32925 | 14692 | 6038 | 10661 | 1534 | | |

- Molecule 33 is a protein called Small ribosomal subunit protein uS2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33 | b | 224 | Total | C | N | O | S | 0 | 0 |
| | | | 1527 | 972 | 283 | 267 | 5 | | |

- Molecule 34 is a protein called Small ribosomal subunit protein uS3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 34 | c | 210 | Total | C | N | O | S | 0 | 0 |
| | | | 1636 | 1037 | 309 | 286 | 4 | | |

- Molecule 35 is a protein called Small ribosomal subunit protein uS4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 35 | d | 205 | Total | C | N | O | S | 0 | 0 |
| | | | 1619 | 1012 | 307 | 296 | 4 | | |

- Molecule 36 is a protein called Small ribosomal subunit protein uS5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 36 | e | 158 | Total | C | N | O | S | 0 | 0 |
| | | | 1129 | 702 | 216 | 205 | 6 | | |

- Molecule 37 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 37 | f | 102 | Total | C | N | O | S | 0 | 0 |
| | | | 770 | 491 | 138 | 137 | 4 | | |

- Molecule 38 is a protein called Small ribosomal subunit protein uS7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 38 | g | 155 | Total | C | N | O | S | 1 | 0 |
| | | | 1183 | 742 | 233 | 204 | 4 | | |

- Molecule 39 is a protein called Small ribosomal subunit protein uS8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 39 | h | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 966 | 612 | 169 | 179 | 6 | | |

- Molecule 40 is a protein called Small ribosomal subunit protein uS9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 40 | i | 127 | Total | C | N | O | S | 0 | 0 |
| | | | 955 | 594 | 194 | 166 | 1 | | |

- Molecule 41 is a protein called Small ribosomal subunit protein uS10.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 41 | j | 97 | Total | C | N | O | 0 | 0 |
| | | | 668 | 423 | 130 | 115 | | |

- Molecule 42 is a protein called Small ribosomal subunit protein uS11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42 | k | 117 | Total | C | N | O | S | 0 | 0 |
| | | | 853 | 527 | 167 | 156 | 3 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| k | 119 | IAS | ASN | conflict | UNP P0A7R9 |

- Molecule 43 is a protein called Small ribosomal subunit protein uS12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 43 | l | 122 | Total | C | N | O | S | 0 | 0 |
| | | | 933 | 576 | 189 | 163 | 5 | | |

- Molecule 44 is a protein called Small ribosomal subunit protein uS13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 44 | m | 116 | Total | C | N | O | S | 0 | 0 |
| | | | 845 | 527 | 171 | 145 | 2 | | |

- Molecule 45 is a protein called Small ribosomal subunit protein uS14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 45 | n | 100 | Total | C | N | O | S | 0 | 0 |
| | | | 794 | 493 | 163 | 135 | 3 | | |

- Molecule 46 is a protein called Small ribosomal subunit protein uS15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 46 | o | 88 | Total | C | N | O | S | 0 | 0 |
| | | | 696 | 430 | 140 | 125 | 1 | | |

- Molecule 47 is a protein called Small ribosomal subunit protein bS16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 47 | p | 80 | Total | C | N | O | S | 0 | 0 |
| | | | 617 | 388 | 124 | 104 | 1 | | |

- Molecule 48 is a protein called Small ribosomal subunit protein uS17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 48 | q | 79 | Total | C | N | O | S | 0 | 0 |
| | | | 630 | 400 | 116 | 111 | 3 | | |

- Molecule 49 is a protein called Small ribosomal subunit protein bS18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 49 | r | 62 | Total | C | N | O | S | 0 | 0 |
| | | | 481 | 304 | 90 | 87 | | | |

- Molecule 50 is a protein called Small ribosomal subunit protein uS19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 50 | s | 82 | Total | C | N | O | S | 0 | 0 |
| | | | 639 | 410 | 123 | 105 | 1 | | |

- Molecule 51 is a protein called Small ribosomal subunit protein bS20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 51 | t | 85 | Total | C | N | O | S | 0 | 0 |
| | | | 652 | 403 | 135 | 111 | 3 | | |

- Molecule 52 is a protein called 30S ribosomal protein S21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 52 | u | 70 | Total | C | N | O | S | 0 | 0 |
| | | | 521 | 329 | 111 | 80 | 1 | | |

- Molecule 53 is a protein called Ribosome hibernation promoting factor.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 53 | v | 95 | Total | C | N | O | S | 0 | 0 |
| | | | 722 | 458 | 129 | 134 | 1 | | |

- Molecule 54 is a protein called Ribosome modulation factor.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 54 | y | 54 | Total | C | N | O | S | 0 | 0 |
| | | | 440 | 269 | 91 | 76 | 4 | | |

- Molecule 55 is a protein called Ribonuclease I.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 55 | z | 245 | Total | C | N | O | S | 6 | 0 |
| | | | 1852 | 1169 | 326 | 345 | 12 | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------------------|------------|
| z | 55 | PHE | HIS | engineered mutation | UNP P21338 |
| z | 133 | PHE | HIS | engineered mutation | UNP P21338 |

- Molecule 56 is a protein called Small ribosomal subunit protein bS1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 56 | 8 | 90 | Total | C | N | O | S | 0 | 0 |
| | | | 696 | 437 | 121 | 135 | 3 | | |

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|-----|---------|
| 57 | 3 | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 57 | B | 6 | Total | Mg | 0 |
| | | | 6 | 6 | |
| 57 | D | 2 | Total | Mg | 0 |
| | | | 2 | 2 | |
| 57 | E | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 57 | O | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 57 | A | 337 | Total | Mg | 0 |
| | | | 337 | 337 | |
| 57 | a | 127 | Total | Mg | 0 |
| | | | 127 | 127 | |

- Molecule 58 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 58 | z | 1 | Total | Ca | 0 |
| | | | 1 | 1 | |

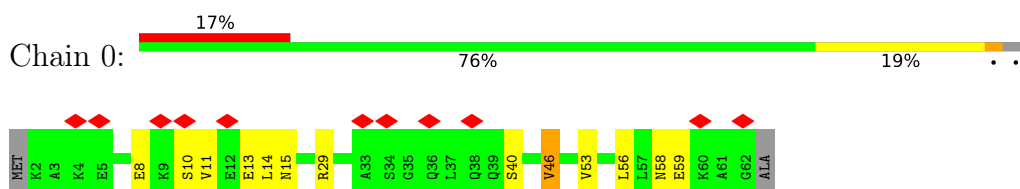
- Molecule 59 is water.

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------------|---------|---------|
| 59 | N | 1 | Total 1 | O 1 | 0 |
| 59 | Y | 1 | Total 1 | O 1 | 0 |
| 59 | A | 25 | Total 25 | O 25 | 0 |
| 59 | a | 5 | Total 5 | O 5 | 0 |

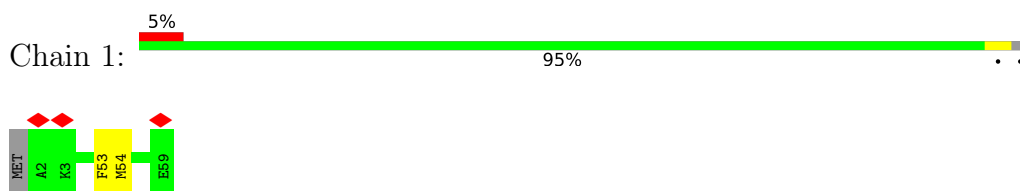
3 Residue-property plots [i](#)

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.

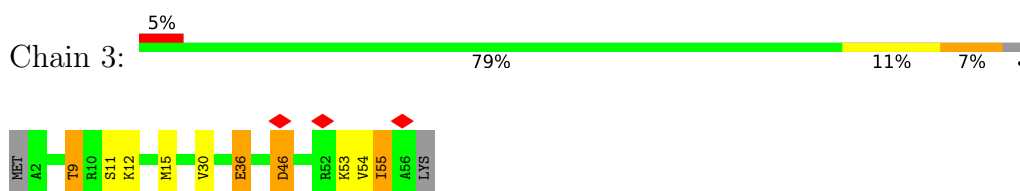
- Molecule 1: Large ribosomal subunit protein uL29



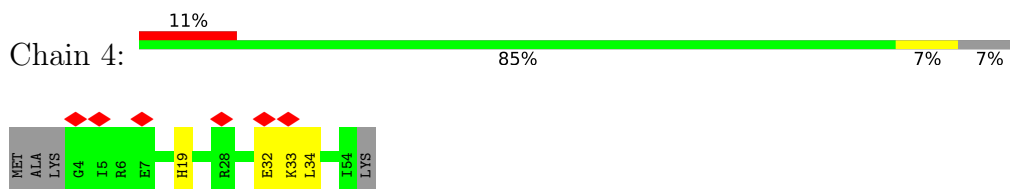
- Molecule 2: Large ribosomal subunit protein uL30



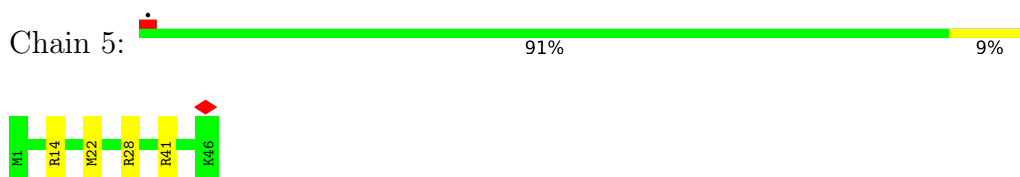
- Molecule 3: Large ribosomal subunit protein bL32




- Molecule 4: Large ribosomal subunit protein bL33



- Molecule 5: 50S ribosomal protein L34




- Molecule 6: Large ribosomal subunit protein bL35

Chain 6:  88% 11%



- Molecule 7: 50S ribosomal protein L36

Chain 7:  5% 79% 21%



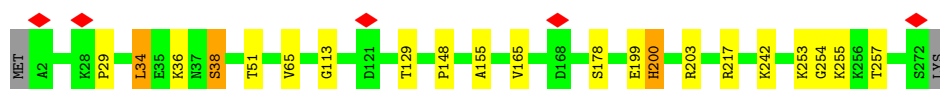
- Molecule 8: 5S rRNA

Chain B:  71% 26%

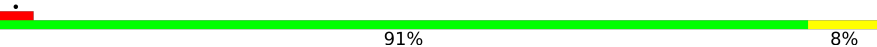


- Molecule 9: Large ribosomal subunit protein uL2

Chain D:  92% 7%

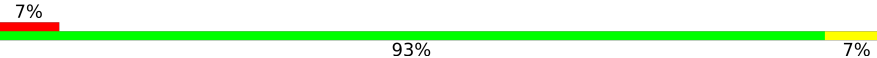


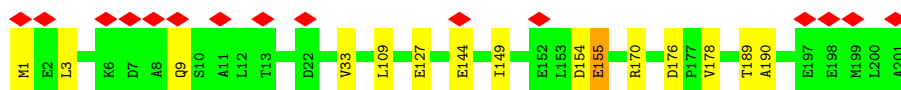
- Molecule 10: 50S ribosomal protein L3

Chain E:  91% 8%




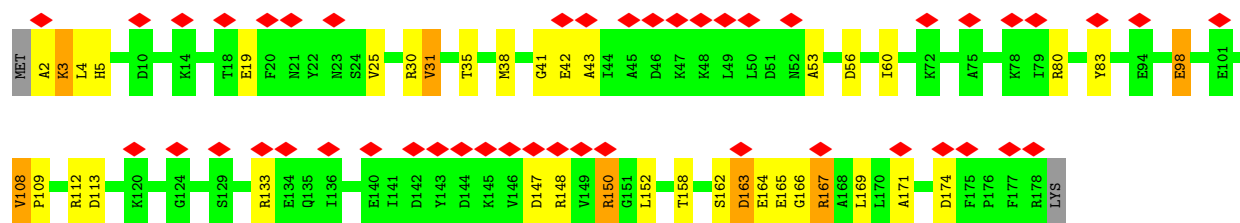
- Molecule 11: 50S ribosomal protein L4

Chain F:  7% 93% 7%

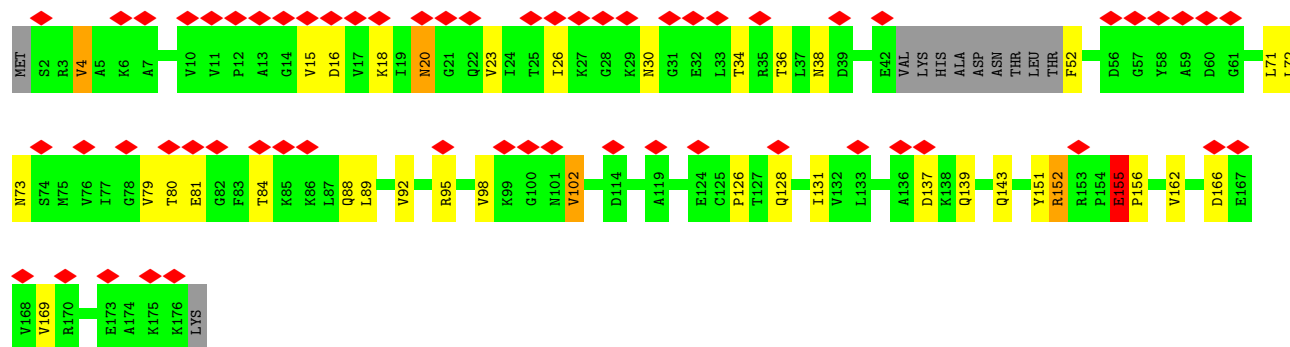
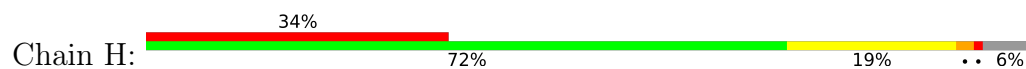


- Molecule 12: Large ribosomal subunit protein uL5

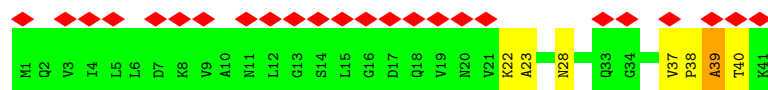
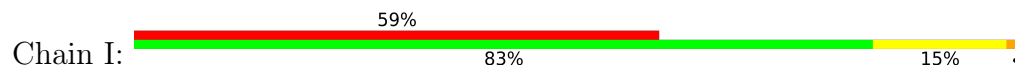
Chain G:  26% 78% 17%



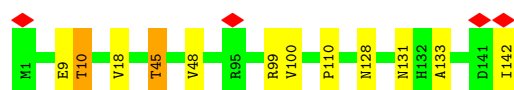
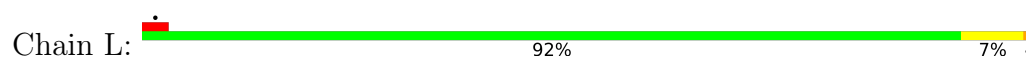
- Molecule 13: Large ribosomal subunit protein uL6



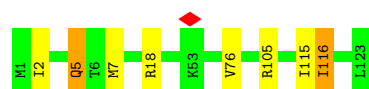
- Molecule 14: Large ribosomal subunit protein bL9



- Molecule 15: 50S ribosomal protein L13



- Molecule 16: 50S ribosomal protein L14

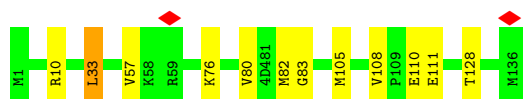


- Molecule 17: Large ribosomal subunit protein uL15

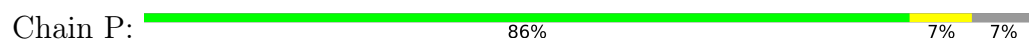




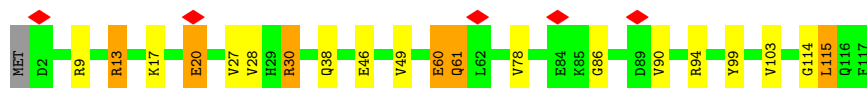
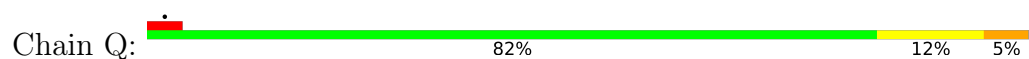
- Molecule 18: Large ribosomal subunit protein uL16



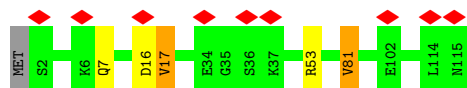
- Molecule 19: Large ribosomal subunit protein bL17



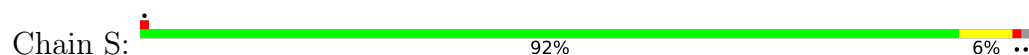
- Molecule 20: Large ribosomal subunit protein uL18



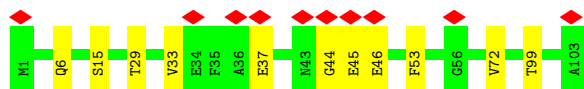
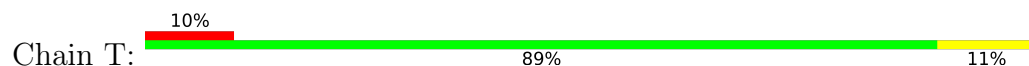
- Molecule 21: Large ribosomal subunit protein bL19



- Molecule 22: Large ribosomal subunit protein bL20

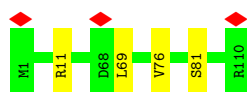


- Molecule 23: 50S ribosomal protein L21




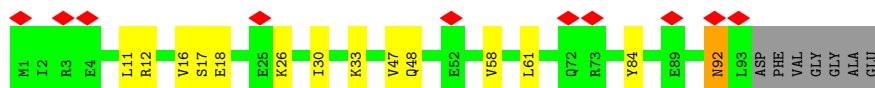
- Molecule 24: 50S ribosomal protein L22

Chain U:  96%




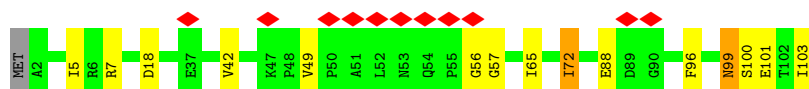
- Molecule 25: Large ribosomal subunit protein uL23

Chain V:  10% 79% 13% 7%




- Molecule 26: Large ribosomal subunit protein uL24

Chain W:  11% 84% 13% ..




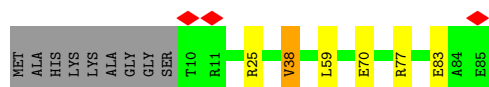
- Molecule 27: 50S ribosomal protein L25

Chain X:  12% 85% 13% .




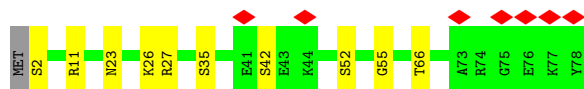
- Molecule 28: Large ribosomal subunit protein bL27

Chain Y:  82% 6% 11%




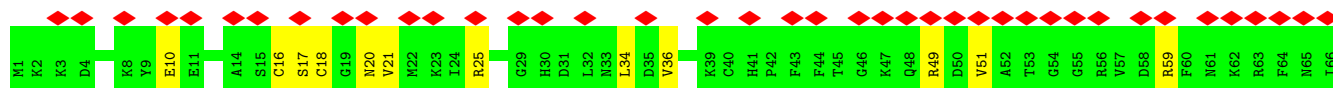
- Molecule 29: Large ribosomal subunit protein bL28

Chain Z:  9% 86% 13% .

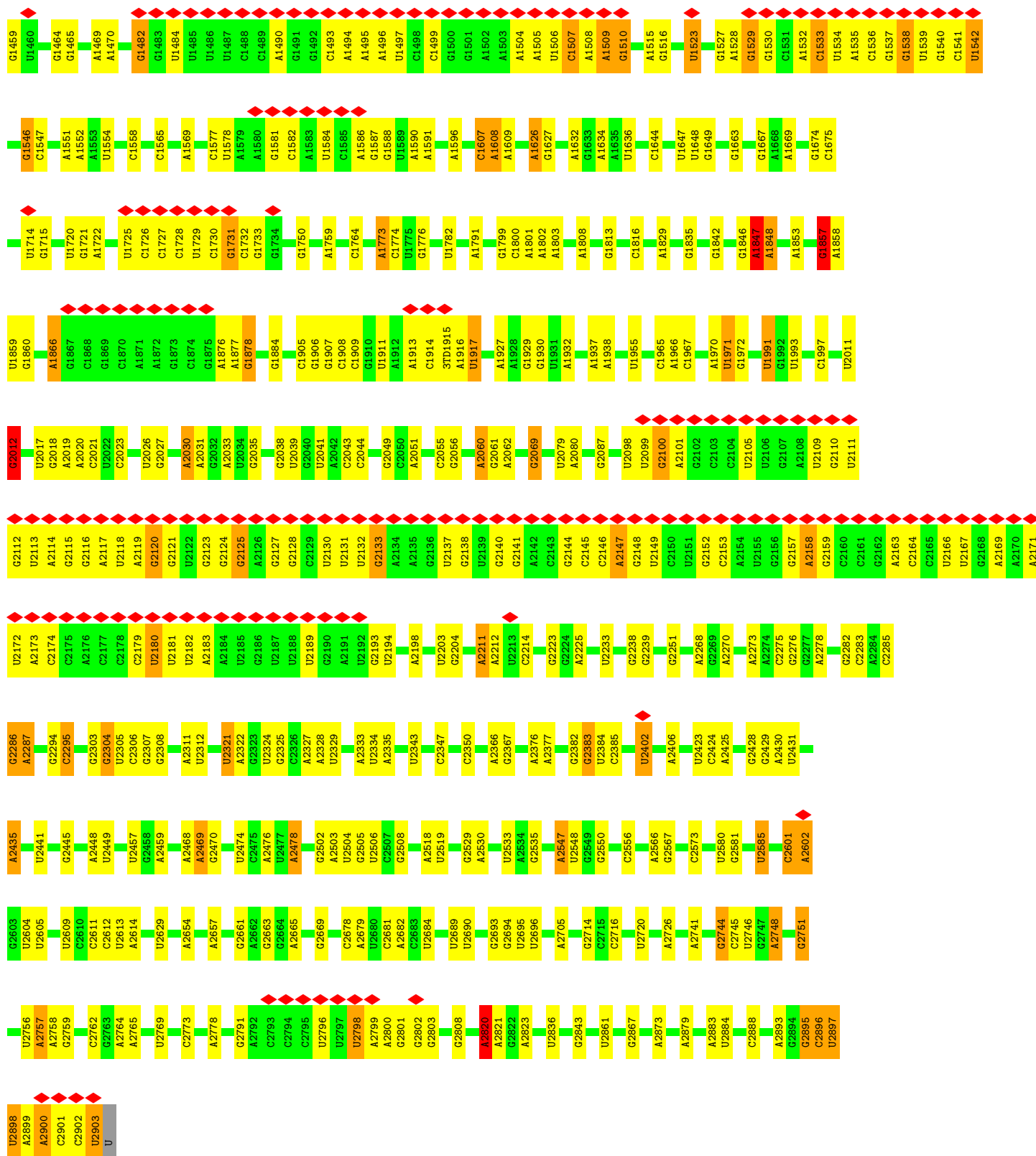


- Molecule 30: Large ribosomal subunit protein bL31

Chain 2:  61% 82% 18%

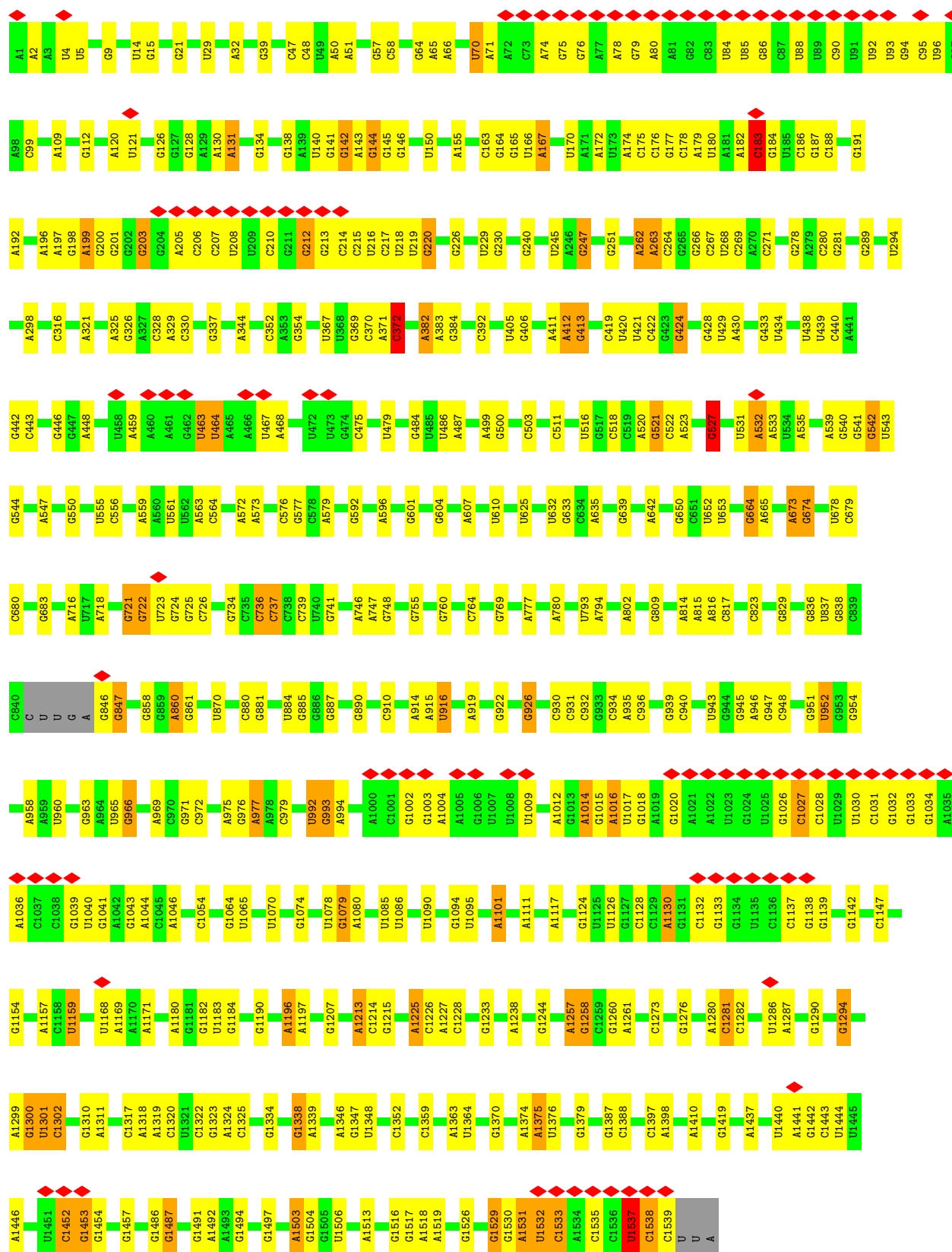


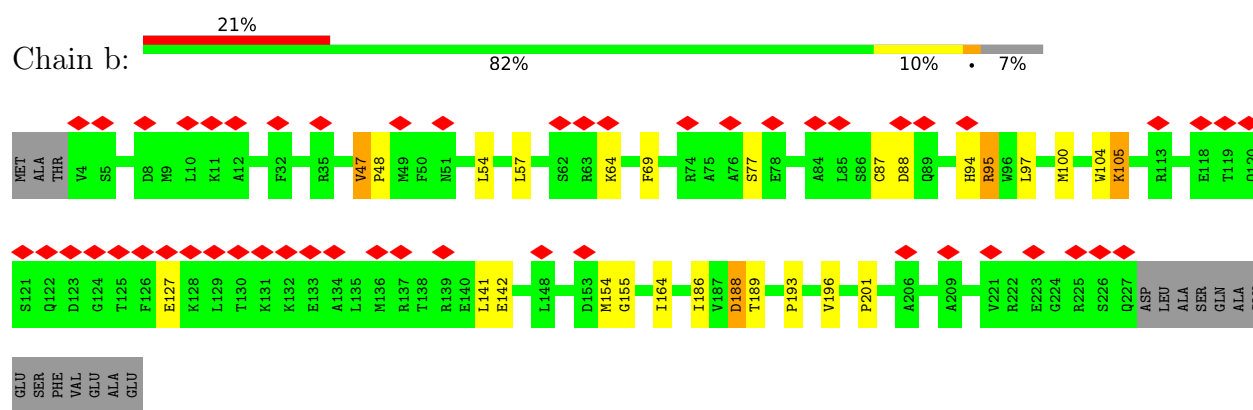




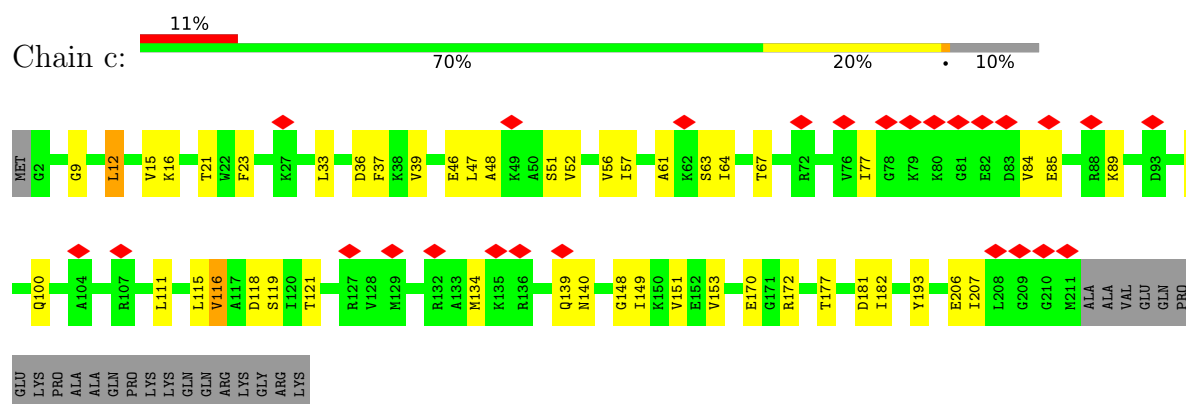
• Molecule 32: 16S rRNA



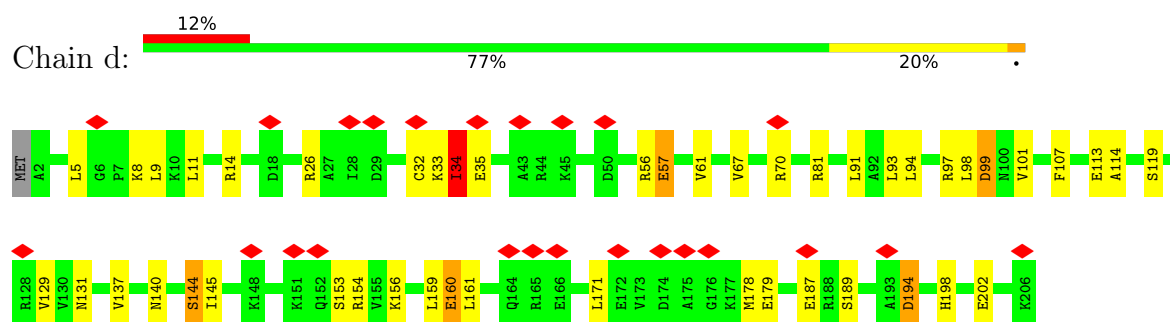




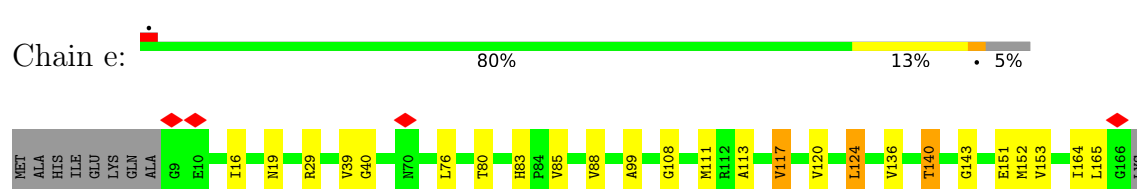
- Molecule 34: Small ribosomal subunit protein uS3



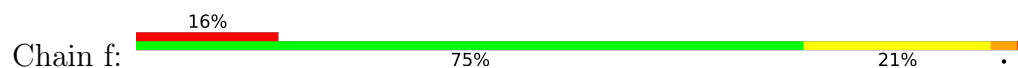
- Molecule 35: Small ribosomal subunit protein uS4

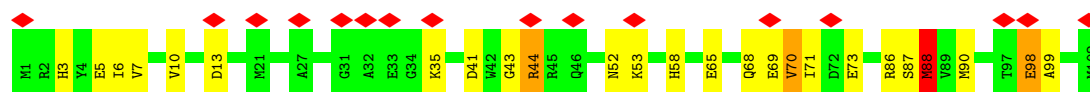


- Molecule 36: Small ribosomal subunit protein uS5

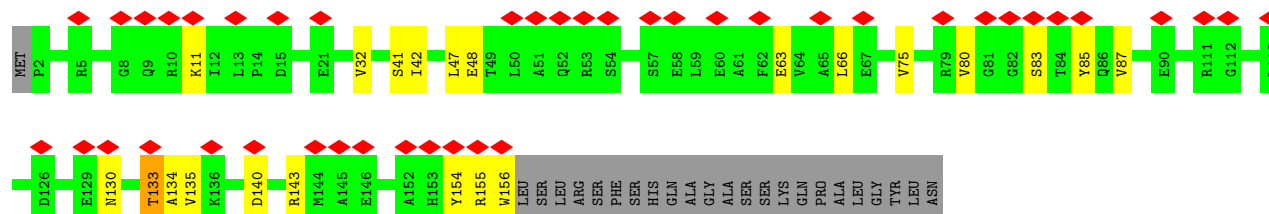
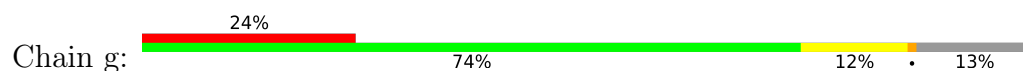


- Molecule 37: Small ribosomal subunit protein bS6, fully modified isoform

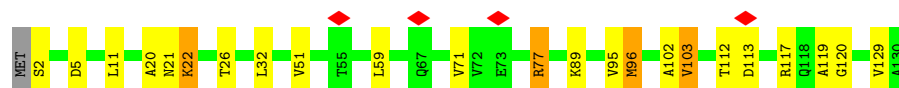
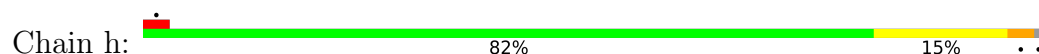




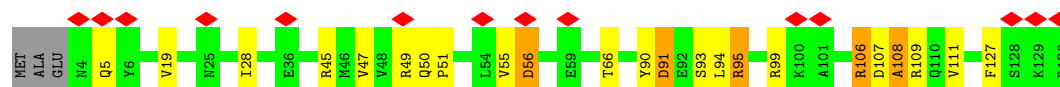
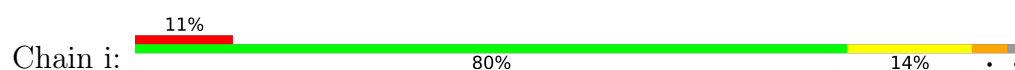
- Molecule 38: Small ribosomal subunit protein uS7



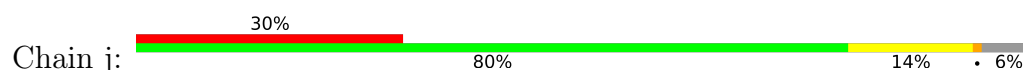
- Molecule 39: Small ribosomal subunit protein uS8



- Molecule 40: Small ribosomal subunit protein uS9



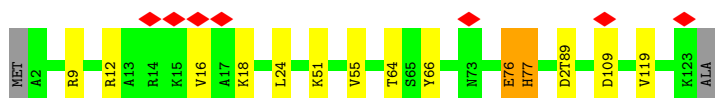
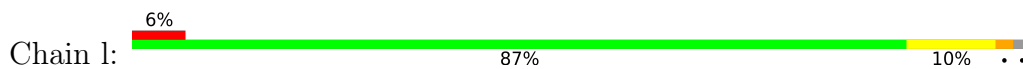
- Molecule 41: Small ribosomal subunit protein uS10



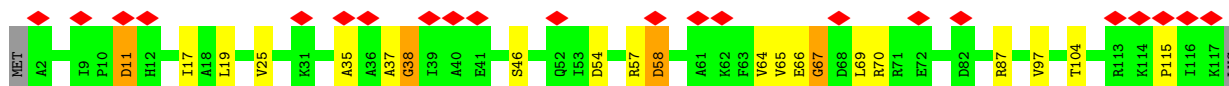
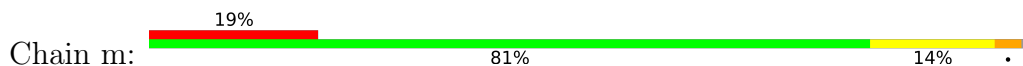
- Molecule 42: Small ribosomal subunit protein uS11



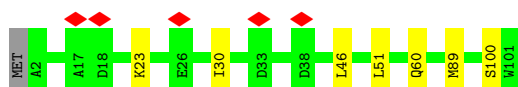
- Molecule 43: Small ribosomal subunit protein uS12



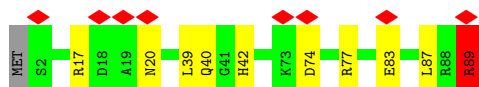
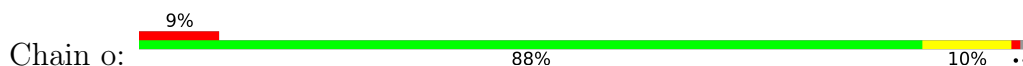
- Molecule 44: Small ribosomal subunit protein uS13



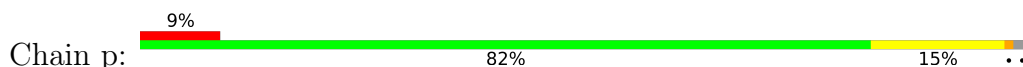
- Molecule 45: Small ribosomal subunit protein uS14



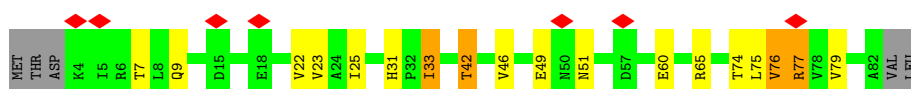
- Molecule 46: Small ribosomal subunit protein uS15



- Molecule 47: Small ribosomal subunit protein bS16



- Molecule 48: Small ribosomal subunit protein uS17

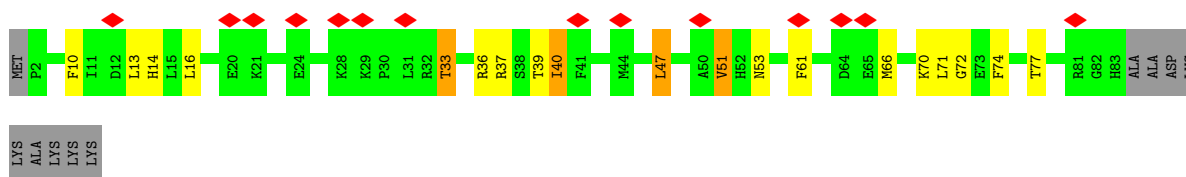


- Molecule 49: Small ribosomal subunit protein bS18

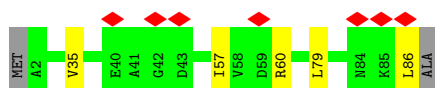




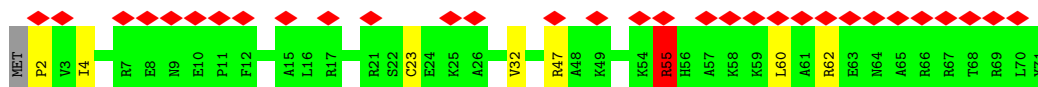
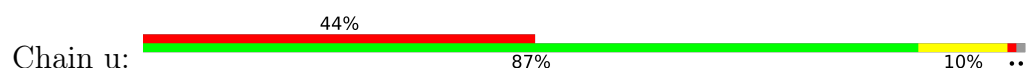
- Molecule 50: Small ribosomal subunit protein uS19



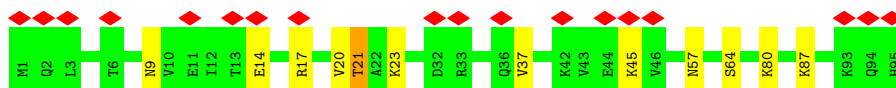
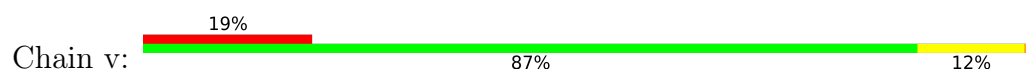
- Molecule 51: Small ribosomal subunit protein bS20



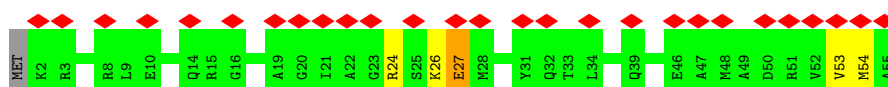
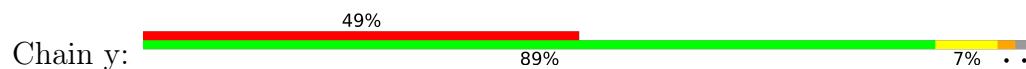
- Molecule 52: 30S ribosomal protein S21



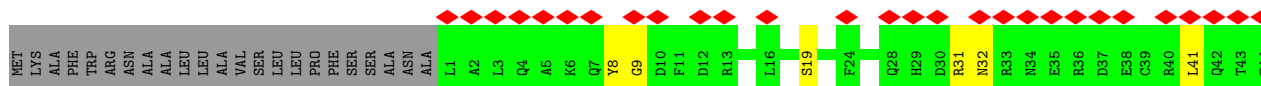
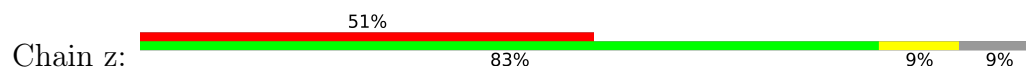
- Molecule 53: Ribosome hibernation promoting factor



- Molecule 54: Ribosome modulation factor



- Molecule 55: Ribonuclease I



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 50955 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | JEOL CRYO ARM 300 | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 50 | Depositor |
| Minimum defocus (nm) | 1000 | Depositor |
| Maximum defocus (nm) | 2000 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K3 BIOQUANTUM (6k x 4k) | Depositor |
| Maximum map value | 3.297 | Depositor |
| Minimum map value | -1.544 | Depositor |
| Average map value | 0.001 | Depositor |
| Map value standard deviation | 0.120 | Depositor |
| Recommended contour level | 0.5 | Depositor |
| Map size (Å) | 487.2, 487.2, 487.2 | wwPDB |
| Map dimensions | 400, 400, 400 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.218, 1.218, 1.218 | Depositor |

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 4D4, 5MC, 4OC, 2MA, D2T, 1MG, 5MU, 3TD, MG, H2U, 2MG, UR3, G7M, MA6, CA, OMC, OMU, OMG, IAS, PSU, MEQ, 6MZ

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 | 0 | 0.49 | 0/496 | 1.14 | 2/660 (0.3%) |
| 2 | 1 | 0.53 | 0/453 | 0.93 | 0/605 |
| 3 | 3 | 0.56 | 0/440 | 1.01 | 1/588 (0.2%) |
| 4 | 4 | 0.57 | 0/417 | 0.98 | 0/557 |
| 5 | 5 | 0.56 | 0/380 | 1.03 | 0/498 |
| 6 | 6 | 0.55 | 0/513 | 0.97 | 0/676 |
| 7 | 7 | 0.50 | 0/303 | 0.88 | 0/397 |
| 8 | B | 0.59 | 0/2876 | 0.90 | 5/4483 (0.1%) |
| 9 | D | 0.57 | 0/2114 | 0.97 | 0/2842 |
| 10 | E | 0.55 | 1/1566 (0.1%) | 0.93 | 0/2107 |
| 11 | F | 0.50 | 0/1555 | 0.95 | 0/2092 |
| 12 | G | 0.53 | 0/1409 | 1.01 | 1/1896 (0.1%) |
| 13 | H | 0.56 | 0/1244 | 1.02 | 1/1685 (0.1%) |
| 14 | I | 0.66 | 0/306 | 0.98 | 0/413 |
| 15 | L | 0.49 | 0/1142 | 0.94 | 0/1539 |
| 16 | M | 0.54 | 0/948 | 0.92 | 1/1270 (0.1%) |
| 17 | N | 0.66 | 2/1054 (0.2%) | 0.99 | 1/1403 (0.1%) |
| 18 | O | 0.53 | 0/1076 | 0.92 | 0/1436 |
| 19 | P | 0.53 | 0/952 | 0.94 | 0/1272 |
| 20 | Q | 0.56 | 0/883 | 1.01 | 0/1188 |
| 21 | R | 0.53 | 0/925 | 0.89 | 1/1238 (0.1%) |
| 22 | S | 0.59 | 1/957 (0.1%) | 1.04 | 0/1274 |
| 23 | T | 0.53 | 0/825 | 0.88 | 0/1102 |
| 24 | U | 0.56 | 0/857 | 0.91 | 0/1149 |
| 25 | V | 0.53 | 0/744 | 1.01 | 0/994 |
| 26 | W | 0.55 | 0/777 | 0.99 | 0/1038 |
| 27 | X | 0.51 | 0/759 | 0.98 | 0/1018 |
| 28 | Y | 0.55 | 0/589 | 0.96 | 0/779 |
| 29 | Z | 0.54 | 0/635 | 0.93 | 0/848 |
| 30 | 2 | 0.59 | 0/514 | 0.98 | 0/690 |
| 31 | A | 0.60 | 2/67756 (0.0%) | 0.90 | 99/105698 (0.1%) |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|------------------|-------------|-------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 32 | a | 0.59 | 2/36585 (0.0%) | 0.90 | 45/57065 (0.1%) |
| 33 | b | 0.56 | 0/1555 | 1.01 | 2/2123 (0.1%) |
| 34 | c | 0.54 | 0/1663 | 0.98 | 2/2241 (0.1%) |
| 35 | d | 0.51 | 0/1641 | 1.08 | 2/2200 (0.1%) |
| 36 | e | 0.56 | 0/1142 | 0.99 | 0/1541 |
| 37 | f | 0.56 | 0/789 | 1.05 | 2/1077 (0.2%) |
| 38 | g | 0.55 | 0/1202 | 0.99 | 0/1622 |
| 39 | h | 0.53 | 0/976 | 1.01 | 0/1309 |
| 40 | i | 0.56 | 0/967 | 1.00 | 0/1295 |
| 41 | j | 0.57 | 0/677 | 0.95 | 0/926 |
| 42 | k | 0.56 | 0/860 | 0.96 | 0/1162 |
| 43 | l | 0.53 | 0/936 | 0.91 | 0/1260 |
| 44 | m | 0.59 | 0/854 | 1.07 | 0/1149 |
| 45 | n | 0.53 | 0/806 | 1.03 | 0/1075 |
| 46 | o | 1.02 | 4/704 (0.6%) | 1.07 | 1/944 (0.1%) |
| 47 | p | 0.73 | 2/627 (0.3%) | 1.02 | 1/846 (0.1%) |
| 48 | q | 0.54 | 0/639 | 1.04 | 0/859 |
| 49 | r | 0.56 | 0/488 | 0.99 | 0/659 |
| 50 | s | 0.56 | 0/656 | 0.97 | 0/887 |
| 51 | t | 0.51 | 0/658 | 1.05 | 0/875 |
| 52 | u | 0.66 | 1/529 (0.2%) | 1.07 | 0/712 |
| 53 | v | 0.49 | 0/732 | 0.94 | 0/990 |
| 54 | y | 0.58 | 0/447 | 0.99 | 0/594 |
| 55 | z | 0.60 | 0/1928 | 0.98 | 0/2611 |
| 56 | 8 | 0.67 | 0/707 | 1.04 | 0/960 |
| All | All | 0.59 | 15/154233 (0.0%) | 0.92 | 167/230417 (0.1%) |

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 |
|-----|-------|---------------------|---------------------|
| 3 | 3 | 0 | 1 |
| 5 | 5 | 0 | 2 |
| 9 | D | 0 | 1 |
| 11 | F | 0 | 1 |
| 12 | G | 0 | 2 |
| 17 | N | 0 | 2 |
| 18 | O | 0 | 1 |
| 19 | P | 0 | 1 |
| 20 | Q | 0 | 4 |

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| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 22 | S | 0 | 1 |
| 24 | U | 0 | 1 |
| 28 | Y | 0 | 2 |
| 29 | Z | 0 | 2 |
| 33 | b | 0 | 1 |
| 35 | d | 0 | 3 |
| 36 | e | 0 | 1 |
| 37 | f | 0 | 1 |
| 41 | j | 0 | 1 |
| 42 | k | 0 | 2 |
| 43 | l | 0 | 1 |
| 45 | n | 0 | 1 |
| 52 | u | 0 | 1 |
| 53 | v | 0 | 1 |
| 54 | y | 0 | 1 |
| All | All | 0 | 35 |

The worst 5 of 15 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|--------|-------|-------------|----------|
| 46 | o | 89 | ARG | CB-CG | 15.38 | 1.98 | 1.52 |
| 46 | o | 89 | ARG | CA-C | 8.82 | 1.71 | 1.52 |
| 46 | o | 89 | ARG | CA-CB | 8.61 | 1.70 | 1.53 |
| 46 | o | 89 | ARG | CZ-NH1 | 8.52 | 1.44 | 1.32 |
| 47 | p | 80 | LYS | C-O | 8.15 | 1.39 | 1.23 |

The worst 5 of 167 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-----------|-------|-------------|----------|
| 32 | a | 652 | U | O3'-P-O5' | -8.92 | 90.63 | 104.00 |
| 32 | a | 1375 | A | O3'-P-O5' | -8.82 | 90.77 | 104.00 |
| 32 | a | 1347 | G | O3'-P-O5' | -8.81 | 90.79 | 104.00 |
| 31 | A | 1378 | A | O3'-P-O5' | -8.64 | 91.04 | 104.00 |
| 31 | A | 2367 | G | O3'-P-O5' | -8.60 | 91.10 | 104.00 |

There are no chirality outliers.

5 of 35 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|-----------|
| 3 | 3 | 46 | ASP | Peptide |
| 5 | 5 | 14 | ARG | Sidechain |

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| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|-----------|
| 5 | 5 | 41 | ARG | Sidechain |
| 9 | D | 203 | ARG | Sidechain |
| 11 | F | 170 | ARG | Sidechain |

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | 0 | 495 | 0 | 526 | 3 | 0 |
| 2 | 1 | 449 | 0 | 488 | 1 | 0 |
| 3 | 3 | 434 | 0 | 445 | 5 | 0 |
| 4 | 4 | 410 | 0 | 431 | 1 | 0 |
| 5 | 5 | 377 | 0 | 418 | 1 | 0 |
| 6 | 6 | 504 | 0 | 572 | 2 | 0 |
| 7 | 7 | 302 | 0 | 343 | 5 | 0 |
| 8 | B | 2572 | 0 | 1301 | 9 | 0 |
| 9 | D | 2075 | 0 | 2144 | 7 | 0 |
| 10 | E | 1556 | 0 | 1605 | 4 | 0 |
| 11 | F | 1536 | 0 | 1594 | 3 | 0 |
| 12 | G | 1385 | 0 | 1402 | 19 | 0 |
| 13 | H | 1226 | 0 | 1258 | 9 | 0 |
| 14 | I | 303 | 0 | 327 | 3 | 0 |
| 15 | L | 1119 | 0 | 1144 | 5 | 0 |
| 16 | M | 939 | 0 | 1014 | 2 | 0 |
| 17 | N | 1045 | 0 | 1121 | 1 | 0 |
| 18 | O | 1070 | 0 | 1150 | 4 | 0 |
| 19 | P | 939 | 0 | 989 | 3 | 0 |
| 20 | Q | 873 | 0 | 877 | 6 | 0 |
| 21 | R | 913 | 0 | 958 | 2 | 0 |
| 22 | S | 944 | 0 | 1017 | 4 | 0 |
| 23 | T | 812 | 0 | 835 | 2 | 0 |
| 24 | U | 850 | 0 | 911 | 0 | 0 |
| 25 | V | 738 | 0 | 807 | 6 | 0 |
| 26 | W | 769 | 0 | 812 | 4 | 0 |
| 27 | X | 746 | 0 | 762 | 7 | 0 |
| 28 | Y | 582 | 0 | 599 | 1 | 0 |
| 29 | Z | 625 | 0 | 652 | 4 | 0 |
| 30 | 2 | 504 | 0 | 483 | 5 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 31 | A | 61011 | 0 | 30710 | 162 | 0 |
| 32 | a | 32925 | 0 | 16593 | 143 | 0 |
| 33 | b | 1527 | 0 | 1353 | 8 | 0 |
| 34 | c | 1636 | 0 | 1709 | 16 | 0 |
| 35 | d | 1619 | 0 | 1659 | 15 | 0 |
| 36 | e | 1129 | 0 | 1149 | 9 | 0 |
| 37 | f | 770 | 0 | 717 | 8 | 0 |
| 38 | g | 1183 | 0 | 1176 | 9 | 0 |
| 39 | h | 966 | 0 | 1012 | 11 | 0 |
| 40 | i | 955 | 0 | 938 | 16 | 0 |
| 41 | j | 668 | 0 | 612 | 4 | 0 |
| 42 | k | 853 | 0 | 838 | 11 | 0 |
| 43 | l | 933 | 0 | 968 | 6 | 0 |
| 44 | m | 845 | 0 | 867 | 8 | 0 |
| 45 | n | 794 | 0 | 827 | 1 | 0 |
| 46 | o | 696 | 0 | 706 | 6 | 0 |
| 47 | p | 617 | 0 | 619 | 5 | 0 |
| 48 | q | 630 | 0 | 657 | 5 | 0 |
| 49 | r | 481 | 0 | 486 | 2 | 0 |
| 50 | s | 639 | 0 | 645 | 12 | 0 |
| 51 | t | 652 | 0 | 688 | 1 | 0 |
| 52 | u | 521 | 0 | 512 | 0 | 0 |
| 53 | v | 722 | 0 | 704 | 3 | 0 |
| 54 | y | 440 | 0 | 434 | 2 | 0 |
| 55 | z | 1852 | 0 | 1738 | 9 | 0 |
| 56 | 8 | 696 | 0 | 677 | 13 | 0 |
| 57 | 3 | 1 | 0 | 0 | 0 | 0 |
| 57 | A | 337 | 0 | 0 | 0 | 0 |
| 57 | B | 6 | 0 | 0 | 0 | 0 |
| 57 | D | 2 | 0 | 0 | 0 | 0 |
| 57 | E | 1 | 0 | 0 | 0 | 0 |
| 57 | O | 1 | 0 | 0 | 0 | 0 |
| 57 | a | 127 | 0 | 0 | 0 | 0 |
| 58 | z | 1 | 0 | 0 | 0 | 0 |
| 59 | A | 25 | 0 | 0 | 0 | 0 |
| 59 | N | 1 | 0 | 0 | 0 | 0 |
| 59 | Y | 1 | 0 | 0 | 0 | 0 |
| 59 | a | 5 | 0 | 0 | 0 | 0 |
| All | All | 143360 | 0 | 95979 | 558 | 0 |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 558 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|-----------------|------------------|--------------------------|-------------------|
| 47:p:80:LYS:CG | 47:p:80:LYS:CB | 1.76 | 1.63 |
| 46:o:89:ARG:CG | 46:o:89:ARG:CB | 1.98 | 1.38 |
| 56:8:286:ASN:O | 56:8:292:CYS:O | 1.96 | 0.83 |
| 12:G:56:ASP:OD2 | 12:G:150:ARG:NH1 | 2.16 | 0.78 |
| 31:A:1857:G:O2' | 31:A:1884:G:N2 | 2.18 | 0.76 |

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 1 | 0 | 59/63 (94%) | 58 (98%) | 1 (2%) | 0 | 100 | 100 |
| 2 | 1 | 56/59 (95%) | 55 (98%) | 1 (2%) | 0 | 100 | 100 |
| 3 | 3 | 53/57 (93%) | 51 (96%) | 2 (4%) | 0 | 100 | 100 |
| 4 | 4 | 49/55 (89%) | 45 (92%) | 3 (6%) | 1 (2%) | 6 | 16 |
| 5 | 5 | 44/46 (96%) | 42 (96%) | 2 (4%) | 0 | 100 | 100 |
| 6 | 6 | 62/65 (95%) | 59 (95%) | 3 (5%) | 0 | 100 | 100 |
| 7 | 7 | 36/38 (95%) | 35 (97%) | 0 | 1 (3%) | 4 | 10 |
| 9 | D | 269/273 (98%) | 253 (94%) | 12 (4%) | 4 (2%) | 8 | 22 |
| 10 | E | 206/209 (99%) | 191 (93%) | 14 (7%) | 1 (0%) | 25 | 49 |
| 11 | F | 199/201 (99%) | 184 (92%) | 12 (6%) | 3 (2%) | 8 | 22 |
| 12 | G | 175/179 (98%) | 149 (85%) | 20 (11%) | 6 (3%) | 3 | 7 |
| 13 | H | 162/177 (92%) | 134 (83%) | 22 (14%) | 6 (4%) | 2 | 6 |
| 14 | I | 39/41 (95%) | 35 (90%) | 3 (8%) | 1 (3%) | 4 | 11 |
| 15 | L | 140/142 (99%) | 132 (94%) | 5 (4%) | 3 (2%) | 5 | 15 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 16 | M | 121/123 (98%) | 113 (93%) | 6 (5%) | 2 (2%) | 7 | 20 |
| 17 | N | 142/144 (99%) | 135 (95%) | 6 (4%) | 1 (1%) | 19 | 42 |
| 18 | O | 133/136 (98%) | 125 (94%) | 8 (6%) | 0 | 100 | 100 |
| 19 | P | 116/127 (91%) | 109 (94%) | 7 (6%) | 0 | 100 | 100 |
| 20 | Q | 114/117 (97%) | 102 (90%) | 9 (8%) | 3 (3%) | 4 | 11 |
| 21 | R | 112/115 (97%) | 104 (93%) | 7 (6%) | 1 (1%) | 14 | 35 |
| 22 | S | 115/118 (98%) | 112 (97%) | 3 (3%) | 0 | 100 | 100 |
| 23 | T | 101/103 (98%) | 95 (94%) | 5 (5%) | 1 (1%) | 13 | 33 |
| 24 | U | 108/110 (98%) | 107 (99%) | 1 (1%) | 0 | 100 | 100 |
| 25 | V | 91/100 (91%) | 80 (88%) | 9 (10%) | 2 (2%) | 5 | 15 |
| 26 | W | 100/103 (97%) | 88 (88%) | 8 (8%) | 4 (4%) | 2 | 5 |
| 27 | X | 92/94 (98%) | 83 (90%) | 9 (10%) | 0 | 100 | 100 |
| 28 | Y | 74/85 (87%) | 71 (96%) | 3 (4%) | 0 | 100 | 100 |
| 29 | Z | 75/78 (96%) | 71 (95%) | 4 (5%) | 0 | 100 | 100 |
| 30 | 2 | 65/67 (97%) | 51 (78%) | 11 (17%) | 3 (5%) | 2 | 4 |
| 33 | b | 222/241 (92%) | 184 (83%) | 32 (14%) | 6 (3%) | 4 | 10 |
| 34 | c | 208/233 (89%) | 184 (88%) | 21 (10%) | 3 (1%) | 9 | 24 |
| 35 | d | 203/206 (98%) | 177 (87%) | 24 (12%) | 2 (1%) | 13 | 33 |
| 36 | e | 156/167 (93%) | 146 (94%) | 9 (6%) | 1 (1%) | 22 | 45 |
| 37 | f | 100/102 (98%) | 83 (83%) | 13 (13%) | 4 (4%) | 2 | 5 |
| 38 | g | 153/179 (86%) | 131 (86%) | 21 (14%) | 1 (1%) | 19 | 42 |
| 39 | h | 127/130 (98%) | 110 (87%) | 14 (11%) | 3 (2%) | 5 | 13 |
| 40 | i | 125/130 (96%) | 110 (88%) | 12 (10%) | 3 (2%) | 5 | 13 |
| 41 | j | 95/103 (92%) | 81 (85%) | 10 (10%) | 4 (4%) | 2 | 5 |
| 42 | k | 113/129 (88%) | 95 (84%) | 16 (14%) | 2 (2%) | 7 | 18 |
| 43 | l | 119/124 (96%) | 113 (95%) | 4 (3%) | 2 (2%) | 7 | 20 |
| 44 | m | 114/118 (97%) | 102 (90%) | 8 (7%) | 4 (4%) | 3 | 7 |
| 45 | n | 98/101 (97%) | 95 (97%) | 3 (3%) | 0 | 100 | 100 |
| 46 | o | 86/89 (97%) | 74 (86%) | 11 (13%) | 1 (1%) | 11 | 28 |
| 47 | p | 78/82 (95%) | 69 (88%) | 6 (8%) | 3 (4%) | 2 | 6 |
| 48 | q | 77/84 (92%) | 64 (83%) | 13 (17%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 49 | r | 60/75 (80%) | 51 (85%) | 9 (15%) | 0 | 100 | 100 |
| 50 | s | 80/92 (87%) | 64 (80%) | 16 (20%) | 0 | 100 | 100 |
| 51 | t | 83/87 (95%) | 79 (95%) | 4 (5%) | 0 | 100 | 100 |
| 52 | u | 68/71 (96%) | 61 (90%) | 7 (10%) | 0 | 100 | 100 |
| 53 | v | 93/95 (98%) | 82 (88%) | 9 (10%) | 2 (2%) | 5 | 15 |
| 54 | y | 52/55 (94%) | 48 (92%) | 2 (4%) | 2 (4%) | 2 | 6 |
| 55 | z | 249/268 (93%) | 216 (87%) | 30 (12%) | 3 (1%) | 11 | 28 |
| 56 | 8 | 88/557 (16%) | 65 (74%) | 17 (19%) | 6 (7%) | 1 | 1 |
| All | All | 5955/6743 (88%) | 5353 (90%) | 507 (8%) | 95 (2%) | 10 | 21 |

5 of 95 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 12 | G | 3 | LYS |
| 12 | G | 42 | GLU |
| 12 | G | 163 | ASP |
| 14 | I | 39 | ALA |
| 15 | L | 133 | ALA |

5.3.2 Protein sidechains ⓘ

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|-------------|-----|
| 1 | 0 | 54/55 (98%) | 46 (85%) | 8 (15%) | 2 | 6 |
| 2 | 1 | 48/49 (98%) | 48 (100%) | 0 | 100 | 100 |
| 3 | 3 | 46/48 (96%) | 42 (91%) | 4 (9%) | 8 | 20 |
| 4 | 4 | 44/49 (90%) | 43 (98%) | 1 (2%) | 45 | 74 |
| 5 | 5 | 38/38 (100%) | 38 (100%) | 0 | 100 | 100 |
| 6 | 6 | 51/52 (98%) | 48 (94%) | 3 (6%) | 16 | 38 |
| 7 | 7 | 34/34 (100%) | 33 (97%) | 1 (3%) | 37 | 67 |
| 9 | D | 212/218 (97%) | 204 (96%) | 8 (4%) | 28 | 56 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|-------------|----|
| 10 | E | 160/163 (98%) | 149 (93%) | 11 (7%) | 13 | 31 |
| 11 | F | 161/165 (98%) | 154 (96%) | 7 (4%) | 25 | 52 |
| 12 | G | 142/150 (95%) | 132 (93%) | 10 (7%) | 12 | 31 |
| 13 | H | 124/138 (90%) | 102 (82%) | 22 (18%) | 1 | 4 |
| 14 | I | 32/32 (100%) | 30 (94%) | 2 (6%) | 15 | 35 |
| 15 | L | 113/116 (97%) | 108 (96%) | 5 (4%) | 24 | 51 |
| 16 | M | 102/104 (98%) | 98 (96%) | 4 (4%) | 27 | 56 |
| 17 | N | 101/103 (98%) | 97 (96%) | 4 (4%) | 27 | 55 |
| 18 | O | 107/108 (99%) | 102 (95%) | 5 (5%) | 22 | 49 |
| 19 | P | 95/103 (92%) | 91 (96%) | 4 (4%) | 25 | 53 |
| 20 | Q | 81/87 (93%) | 70 (86%) | 11 (14%) | 3 | 7 |
| 21 | R | 98/100 (98%) | 96 (98%) | 2 (2%) | 50 | 78 |
| 22 | S | 88/90 (98%) | 85 (97%) | 3 (3%) | 32 | 61 |
| 23 | T | 83/84 (99%) | 77 (93%) | 6 (7%) | 12 | 30 |
| 24 | U | 92/93 (99%) | 89 (97%) | 3 (3%) | 33 | 62 |
| 25 | V | 80/84 (95%) | 76 (95%) | 4 (5%) | 20 | 46 |
| 26 | W | 80/84 (95%) | 73 (91%) | 7 (9%) | 8 | 20 |
| 27 | X | 76/78 (97%) | 69 (91%) | 7 (9%) | 7 | 18 |
| 28 | Y | 58/63 (92%) | 55 (95%) | 3 (5%) | 19 | 44 |
| 29 | Z | 67/68 (98%) | 64 (96%) | 3 (4%) | 23 | 50 |
| 30 | 2 | 53/60 (88%) | 51 (96%) | 2 (4%) | 28 | 56 |
| 33 | b | 118/199 (59%) | 111 (94%) | 7 (6%) | 16 | 38 |
| 34 | c | 168/190 (88%) | 148 (88%) | 20 (12%) | 4 | 10 |
| 35 | d | 167/173 (96%) | 145 (87%) | 22 (13%) | 3 | 8 |
| 36 | e | 111/126 (88%) | 99 (89%) | 12 (11%) | 5 | 13 |
| 37 | f | 73/89 (82%) | 63 (86%) | 10 (14%) | 3 | 7 |
| 38 | g | 112/147 (76%) | 105 (94%) | 7 (6%) | 15 | 35 |
| 39 | h | 100/105 (95%) | 90 (90%) | 10 (10%) | 6 | 16 |
| 40 | i | 87/107 (81%) | 79 (91%) | 8 (9%) | 7 | 18 |
| 41 | j | 53/90 (59%) | 48 (91%) | 5 (9%) | 7 | 18 |
| 42 | k | 82/98 (84%) | 73 (89%) | 9 (11%) | 5 | 12 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|-------------|----|
| 43 | l | 98/103 (95%) | 92 (94%) | 6 (6%) | 15 | 36 |
| 44 | m | 79/96 (82%) | 70 (89%) | 9 (11%) | 4 | 11 |
| 45 | n | 80/84 (95%) | 75 (94%) | 5 (6%) | 15 | 35 |
| 46 | o | 72/77 (94%) | 69 (96%) | 3 (4%) | 25 | 53 |
| 47 | p | 59/65 (91%) | 52 (88%) | 7 (12%) | 4 | 10 |
| 48 | q | 70/78 (90%) | 57 (81%) | 13 (19%) | 1 | 3 |
| 49 | r | 47/65 (72%) | 44 (94%) | 3 (6%) | 14 | 34 |
| 50 | s | 66/79 (84%) | 61 (92%) | 5 (8%) | 11 | 27 |
| 51 | t | 62/66 (94%) | 58 (94%) | 4 (6%) | 14 | 34 |
| 52 | u | 43/61 (70%) | 35 (81%) | 8 (19%) | 1 | 3 |
| 53 | v | 71/81 (88%) | 66 (93%) | 5 (7%) | 12 | 31 |
| 54 | y | 42/44 (96%) | 41 (98%) | 1 (2%) | 44 | 73 |
| 55 | z | 181/215 (84%) | 176 (97%) | 5 (3%) | 38 | 68 |
| 56 | 8 | 75/461 (16%) | 67 (89%) | 8 (11%) | 5 | 13 |
| All | All | 4636/5515 (84%) | 4294 (93%) | 342 (7%) | 14 | 28 |

5 of 342 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 39 | h | 59 | LEU |
| 47 | p | 60 | TRP |
| 40 | i | 19 | VAL |
| 43 | l | 16 | VAL |
| 48 | q | 76 | VAL |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 81 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 40 | i | 5 | GLN |
| 47 | p | 9 | HIS |
| 41 | j | 99 | GLN |
| 44 | m | 8 | ASN |
| 50 | s | 83 | HIS |

5.3.3 RNA [i](#)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 31 | A | 2839/2904 (97%) | 546 (19%) | 71 (2%) |
| 32 | a | 1532/1542 (99%) | 305 (19%) | 0 |
| 8 | B | 119/120 (99%) | 21 (17%) | 3 (2%) |
| All | All | 4490/4566 (98%) | 872 (19%) | 74 (1%) |

5 of 872 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 8 | B | 4 | C |
| 8 | B | 9 | G |
| 8 | B | 14 | U |
| 8 | B | 15 | A |
| 8 | B | 25 | U |

5 of 74 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 31 | A | 2163 | A |
| 31 | A | 2820 | A |
| 31 | A | 2275 | C |
| 31 | A | 2518 | A |
| 31 | A | 895 | U |

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

39 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 | $\# Z > 2$ |
| 31 | 6MZ | A | 1618 | 31 | 18,25,26 | 0.70 | 0 | 16,36,39 | 0.70 | 0 |
| 31 | 5MU | A | 1939 | 31 | 19,22,23 | 0.30 | 0 | 28,32,35 | 0.40 | 0 |
| 42 | IAS | k | 119 | 42 | 6,7,8 | 0.86 | 0 | 6,8,10 | 0.96 | 0 |
| 31 | PSU | A | 1917 | 31 | 18,21,22 | 0.93 | 1 (5%) | 22,30,33 | 0.63 | 0 |
| 32 | 5MC | a | 1407 | 32 | 18,22,23 | 0.31 | 0 | 26,32,35 | 0.61 | 0 |
| 31 | H2U | A | 2449 | 31 | 18,21,22 | 0.74 | 1 (5%) | 21,30,33 | 0.81 | 1 (4%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|------|-------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 31 | PSU | A | 2604 | 31 | 18,21,22 | 0.98 | 1 (5%) | 22,30,33 | 0.92 | 1 (4%) |
| 31 | PSU | A | 2457 | 31 | 18,21,22 | 0.89 | 1 (5%) | 22,30,33 | 0.69 | 0 |
| 31 | 2MG | A | 2445 | 31 | 18,26,27 | 1.05 | 3 (16%) | 16,38,41 | 0.71 | 0 |
| 31 | 5MU | A | 747 | 31 | 19,22,23 | 0.31 | 0 | 28,32,35 | 0.33 | 0 |
| 32 | G7M | a | 527 | 32 | 20,26,27 | 1.22 | 3 (15%) | 17,39,42 | 0.57 | 0 |
| 32 | 2MG | a | 966 | 32 | 18,26,27 | 1.02 | 2 (11%) | 16,38,41 | 0.69 | 0 |
| 31 | 5MC | A | 1962 | 31 | 18,22,23 | 0.36 | 0 | 26,32,35 | 0.48 | 0 |
| 10 | MEQ | E | 150 | 10 | 8,9,10 | 0.45 | 0 | 5,10,12 | 1.48 | 1 (20%) |
| 31 | PSU | A | 2504 | 31 | 18,21,22 | 0.89 | 1 (5%) | 22,30,33 | 0.85 | 1 (4%) |
| 31 | PSU | A | 2605 | 31 | 18,21,22 | 0.87 | 1 (5%) | 22,30,33 | 0.79 | 0 |
| 43 | D2T | l | 89 | 43 | 7,9,10 | 1.02 | 0 | 6,11,13 | 1.76 | 3 (50%) |
| 31 | 6MZ | A | 2030 | 31 | 18,25,26 | 0.71 | 0 | 16,36,39 | 0.94 | 1 (6%) |
| 31 | 1MG | A | 745 | 31 | 18,26,27 | 1.02 | 2 (11%) | 19,39,42 | 0.63 | 0 |
| 31 | 2MG | A | 1835 | 31 | 18,26,27 | 1.03 | 3 (16%) | 16,38,41 | 0.78 | 0 |
| 32 | UR3 | a | 1498 | 32 | 19,22,23 | 0.32 | 0 | 26,32,35 | 0.73 | 0 |
| 32 | MA6 | a | 1518 | 32 | 18,26,27 | 0.73 | 0 | 19,38,41 | 0.49 | 0 |
| 31 | 3TD | A | 1915 | 31 | 18,22,23 | 1.05 | 1 (5%) | 22,32,35 | 0.77 | 0 |
| 32 | 5MC | a | 967 | 32 | 18,22,23 | 0.33 | 0 | 26,32,35 | 0.56 | 0 |
| 31 | OMC | A | 2498 | 57,31 | 19,22,23 | 0.32 | 0 | 26,31,34 | 0.54 | 0 |
| 31 | PSU | A | 1911 | 31 | 18,21,22 | 0.90 | 1 (5%) | 22,30,33 | 0.74 | 1 (4%) |
| 31 | 2MA | A | 2503 | 57,31 | 19,25,26 | 0.97 | 1 (5%) | 21,37,40 | 1.76 | 3 (14%) |
| 31 | PSU | A | 2580 | 31 | 18,21,22 | 0.91 | 1 (5%) | 22,30,33 | 0.84 | 1 (4%) |
| 31 | OMU | A | 2552 | 31 | 19,22,23 | 0.32 | 0 | 26,31,34 | 0.46 | 0 |
| 32 | 4OC | a | 1402 | 32 | 20,23,24 | 0.41 | 0 | 26,32,35 | 0.56 | 0 |
| 31 | PSU | A | 955 | 31 | 18,21,22 | 0.94 | 1 (5%) | 22,30,33 | 0.61 | 0 |
| 31 | OMG | A | 2251 | 31 | 18,26,27 | 1.04 | 3 (16%) | 19,38,41 | 0.70 | 0 |
| 31 | G7M | A | 2069 | 31 | 20,26,27 | 1.11 | 2 (10%) | 17,39,42 | 0.55 | 0 |
| 32 | 2MG | a | 1516 | 32 | 18,26,27 | 1.05 | 3 (16%) | 16,38,41 | 0.89 | 0 |
| 32 | PSU | a | 516 | 32 | 18,21,22 | 0.89 | 1 (5%) | 22,30,33 | 0.64 | 0 |
| 18 | 4D4 | O | 81 | 18 | 9,11,12 | 0.53 | 0 | 8,13,15 | 0.81 | 0 |
| 31 | PSU | A | 746 | 57,31 | 18,21,22 | 0.93 | 1 (5%) | 22,30,33 | 0.63 | 0 |
| 32 | 2MG | a | 1207 | 32 | 18,26,27 | 1.02 | 2 (11%) | 16,38,41 | 0.83 | 1 (6%) |
| 32 | MA6 | a | 1519 | 32 | 18,26,27 | 0.74 | 0 | 19,38,41 | 0.62 | 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 |
|-----|------|-------|------|-------|---------|------------|---------|
| 31 | 6MZ | A | 1618 | 31 | - | 0/5/27/28 | 0/3/3/3 |
| 31 | 5MU | A | 1939 | 31 | - | 0/7/25/26 | 0/2/2/2 |
| 42 | IAS | k | 119 | 42 | - | 0/7/7/8 | - |
| 31 | PSU | A | 1917 | 31 | - | 0/7/25/26 | 0/2/2/2 |
| 32 | 5MC | a | 1407 | 32 | - | 1/7/25/26 | 0/2/2/2 |
| 31 | H2U | A | 2449 | 31 | - | 0/7/38/39 | 0/2/2/2 |
| 31 | PSU | A | 2604 | 31 | - | 0/7/25/26 | 0/2/2/2 |
| 31 | PSU | A | 2457 | 31 | - | 0/7/25/26 | 0/2/2/2 |
| 31 | 2MG | A | 2445 | 31 | - | 2/5/27/28 | 0/3/3/3 |
| 31 | 5MU | A | 747 | 31 | - | 0/7/25/26 | 0/2/2/2 |
| 32 | G7M | a | 527 | 32 | - | 2/3/25/26 | 0/3/3/3 |
| 32 | 2MG | a | 966 | 32 | - | 2/5/27/28 | 0/3/3/3 |
| 31 | 5MC | A | 1962 | 31 | - | 0/7/25/26 | 0/2/2/2 |
| 10 | MEQ | E | 150 | 10 | - | 2/8/9/11 | - |
| 31 | PSU | A | 2504 | 31 | - | 0/7/25/26 | 0/2/2/2 |
| 31 | PSU | A | 2605 | 31 | - | 0/7/25/26 | 0/2/2/2 |
| 43 | D2T | l | 89 | 43 | - | 1/7/12/14 | - |
| 31 | 6MZ | A | 2030 | 31 | - | 1/5/27/28 | 0/3/3/3 |
| 31 | 1MG | A | 745 | 31 | - | 0/3/25/26 | 0/3/3/3 |
| 31 | 2MG | A | 1835 | 31 | - | 0/5/27/28 | 0/3/3/3 |
| 32 | UR3 | a | 1498 | 32 | - | 0/7/25/26 | 0/2/2/2 |
| 32 | MA6 | a | 1518 | 32 | - | 0/7/29/30 | 0/3/3/3 |
| 31 | 3TD | A | 1915 | 31 | - | 1/7/25/26 | 0/2/2/2 |
| 32 | 5MC | a | 967 | 32 | - | 0/7/25/26 | 0/2/2/2 |
| 31 | OMC | A | 2498 | 57,31 | - | 0/9/27/28 | 0/2/2/2 |
| 31 | PSU | A | 1911 | 31 | - | 0/7/25/26 | 0/2/2/2 |
| 31 | 2MA | A | 2503 | 57,31 | - | 1/3/25/26 | 0/3/3/3 |
| 31 | PSU | A | 2580 | 31 | - | 0/7/25/26 | 0/2/2/2 |
| 31 | OMU | A | 2552 | 31 | - | 1/9/27/28 | 0/2/2/2 |
| 32 | 4OC | a | 1402 | 32 | - | 1/9/29/30 | 0/2/2/2 |
| 31 | PSU | A | 955 | 31 | - | 0/7/25/26 | 0/2/2/2 |
| 31 | OMG | A | 2251 | 31 | - | 0/5/27/28 | 0/3/3/3 |
| 31 | G7M | A | 2069 | 31 | - | 2/3/25/26 | 0/3/3/3 |
| 32 | 2MG | a | 1516 | 32 | - | 0/5/27/28 | 0/3/3/3 |
| 32 | PSU | a | 516 | 32 | - | 0/7/25/26 | 0/2/2/2 |
| 18 | 4D4 | O | 81 | 18 | - | 1/11/12/14 | - |
| 31 | PSU | A | 746 | 57,31 | - | 1/7/25/26 | 0/2/2/2 |
| 32 | 2MG | a | 1207 | 32 | - | 0/5/27/28 | 0/3/3/3 |
| 32 | MA6 | a | 1519 | 32 | - | 1/7/29/30 | 0/3/3/3 |

The worst 5 of 36 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|------|-------------|----------|
| 31 | A | 1915 | 3TD | C6-C5 | 3.76 | 1.39 | 1.35 |
| 31 | A | 2604 | PSU | C6-C5 | 3.69 | 1.39 | 1.35 |
| 31 | A | 746 | PSU | C6-C5 | 3.62 | 1.39 | 1.35 |
| 31 | A | 1917 | PSU | C6-C5 | 3.59 | 1.39 | 1.35 |
| 31 | A | 955 | PSU | C6-C5 | 3.58 | 1.39 | 1.35 |

The worst 5 of 14 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-------------|-------|-------------|----------|
| 31 | A | 2503 | 2MA | C5-C6-N1 | -4.81 | 117.85 | 121.01 |
| 31 | A | 2503 | 2MA | C5-C6-N6 | 4.13 | 126.63 | 120.35 |
| 31 | A | 2503 | 2MA | CM2-C2-N1 | 3.10 | 121.99 | 117.15 |
| 31 | A | 2580 | PSU | C3'-C2'-C1' | 2.77 | 104.86 | 101.64 |
| 10 | E | 150 | MEQ | CB-CG-CD | 2.46 | 118.53 | 113.04 |

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|-----|------|-----------------|
| 32 | a | 527 | G7M | O4'-C4'-C5'-O5' |
| 32 | a | 527 | G7M | C3'-C4'-C5'-O5' |
| 32 | a | 966 | 2MG | O4'-C4'-C5'-O5' |
| 32 | a | 966 | 2MG | C3'-C4'-C5'-O5' |
| 10 | E | 150 | MEQ | OE1-CD-CG-CB |

There are no ring outliers.

5 monomers are involved in 4 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|------|------|---------|--------------|
| 31 | A | 1917 | PSU | 1 | 0 |
| 32 | a | 527 | G7M | 1 | 0 |
| 31 | A | 2030 | 6MZ | 1 | 0 |
| 32 | a | 1518 | MA6 | 1 | 0 |
| 32 | a | 1519 | MA6 | 1 | 0 |

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 476 ligands modelled in this entry, 476 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

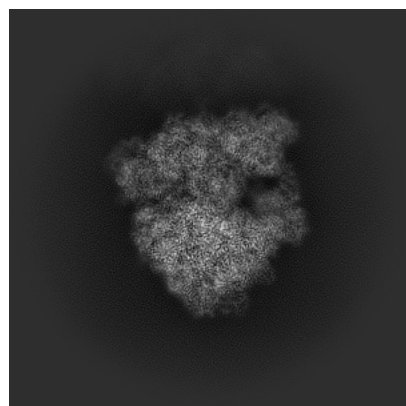
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60747. These allow visual inspection of the internal detail of the map and identification of artifacts.

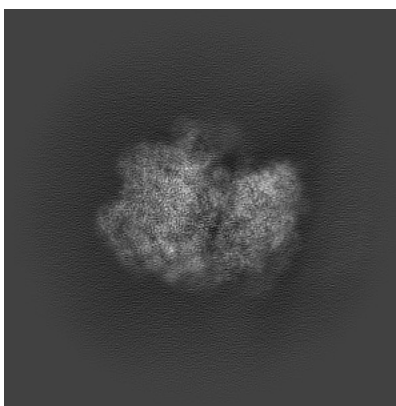
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

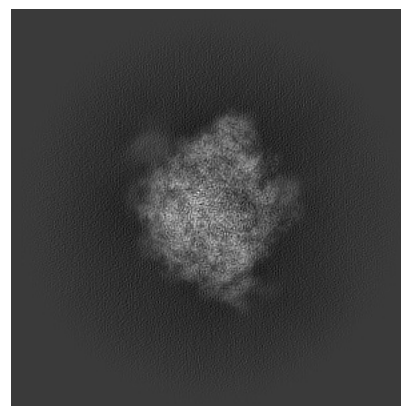
6.1.1 Primary map



X

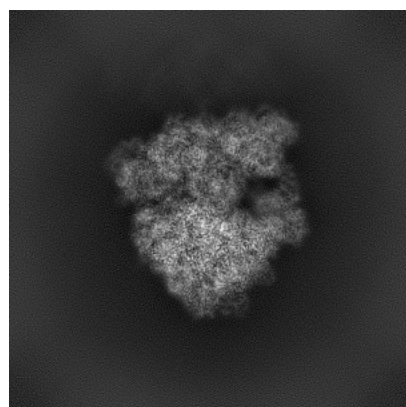


Y

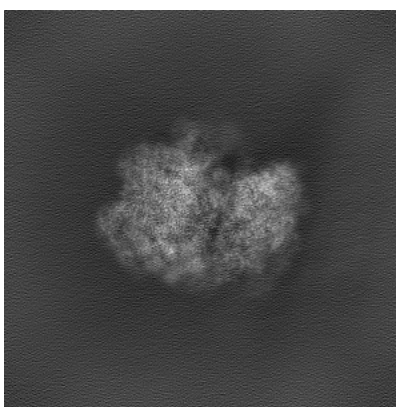


Z

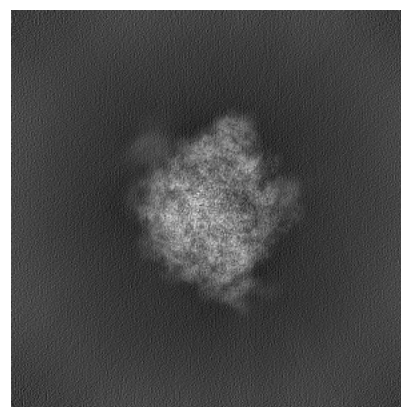
6.1.2 Raw map



X



Y

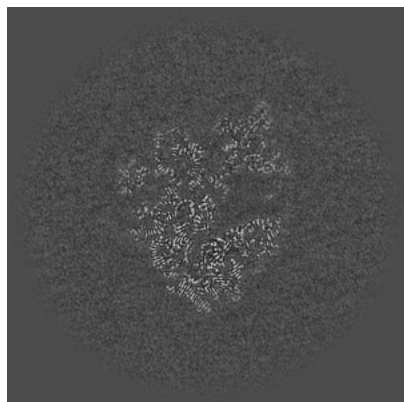


Z

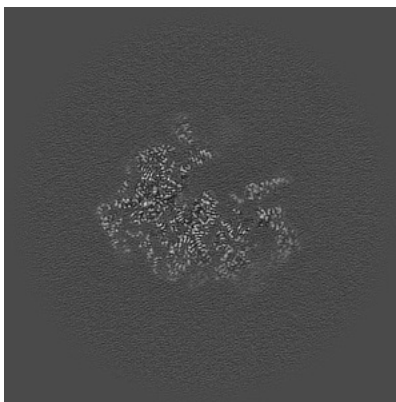
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

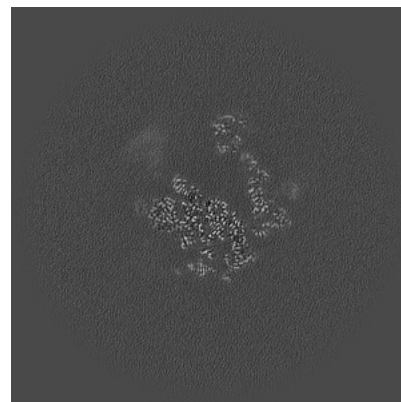
6.2.1 Primary map



X Index: 200

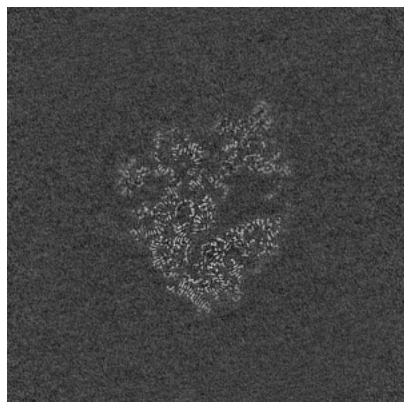


Y Index: 200

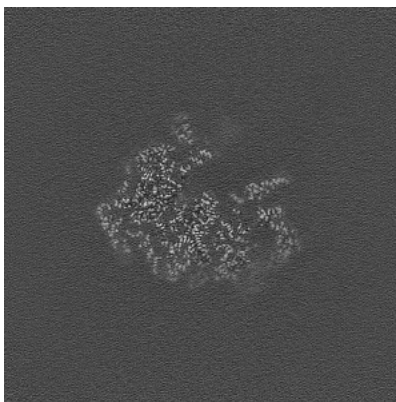


Z Index: 200

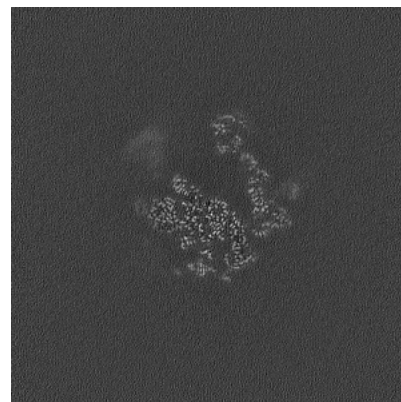
6.2.2 Raw map



X Index: 200



Y Index: 200

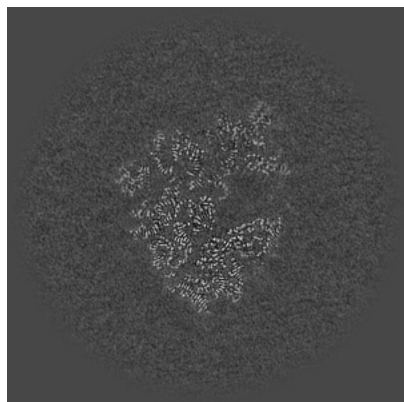


Z Index: 200

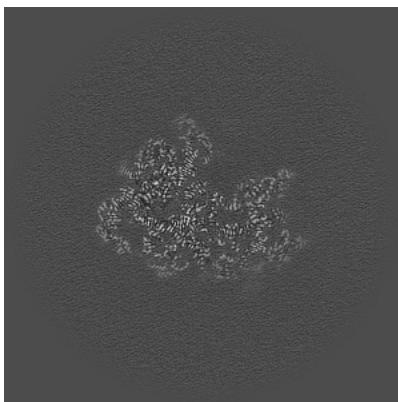
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

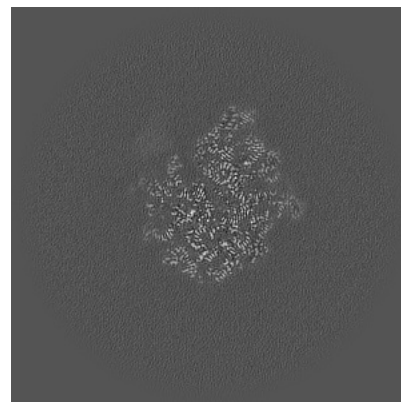
6.3.1 Primary map



X Index: 199

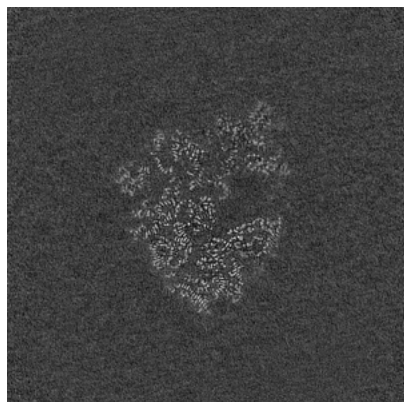


Y Index: 193

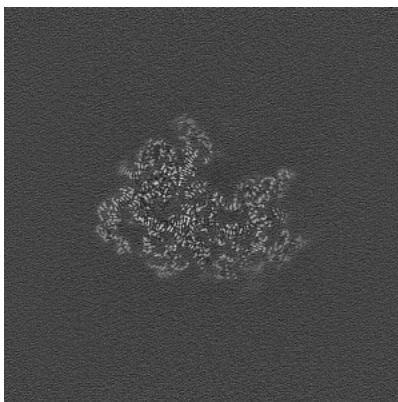


Z Index: 179

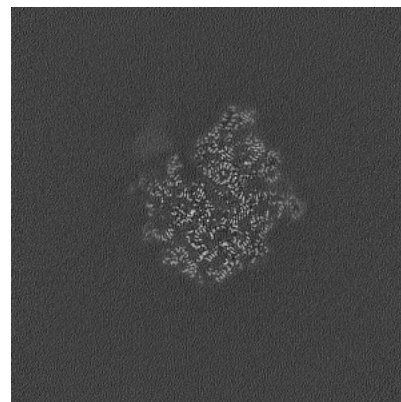
6.3.2 Raw map



X Index: 199



Y Index: 193

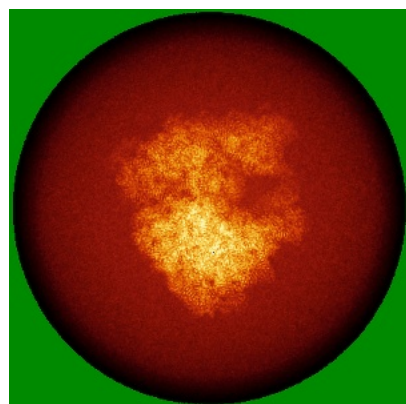


Z Index: 179

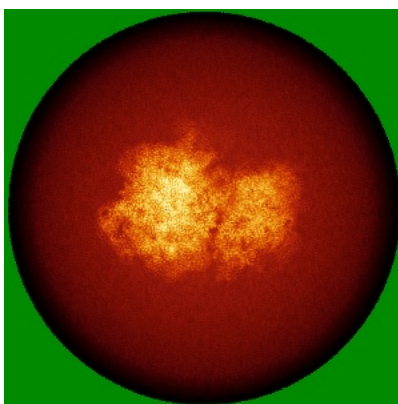
The images above show the largest variance slices of the map in three orthogonal directions.

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

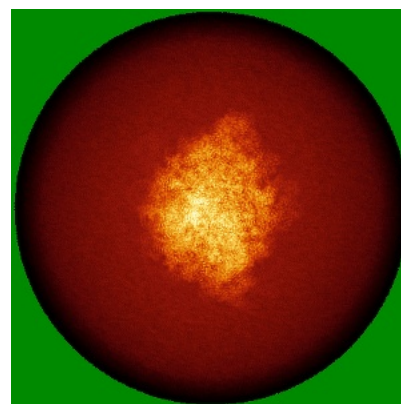
6.4.1 Primary map



X

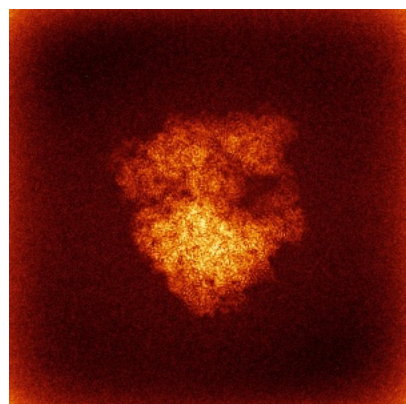


Y

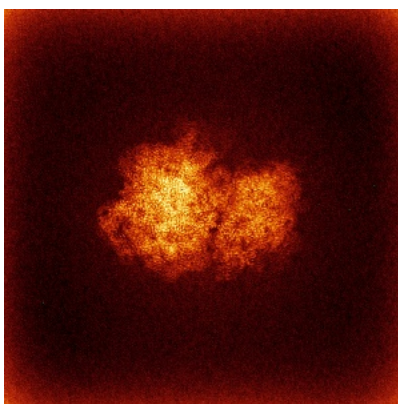


Z

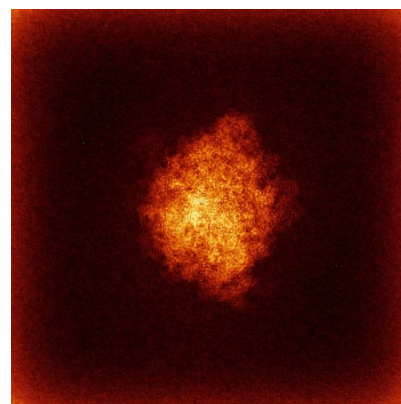
6.4.2 Raw map



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



X



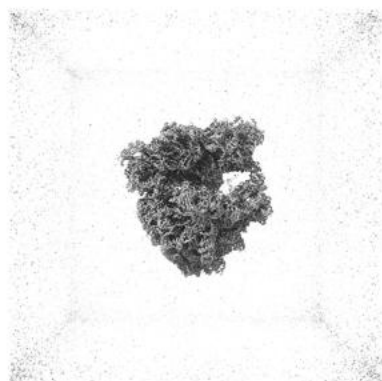
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

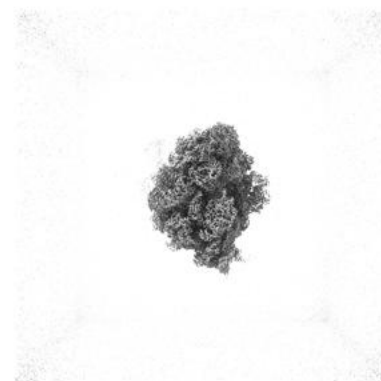
6.5.2 Raw map



X



Y



Z

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.

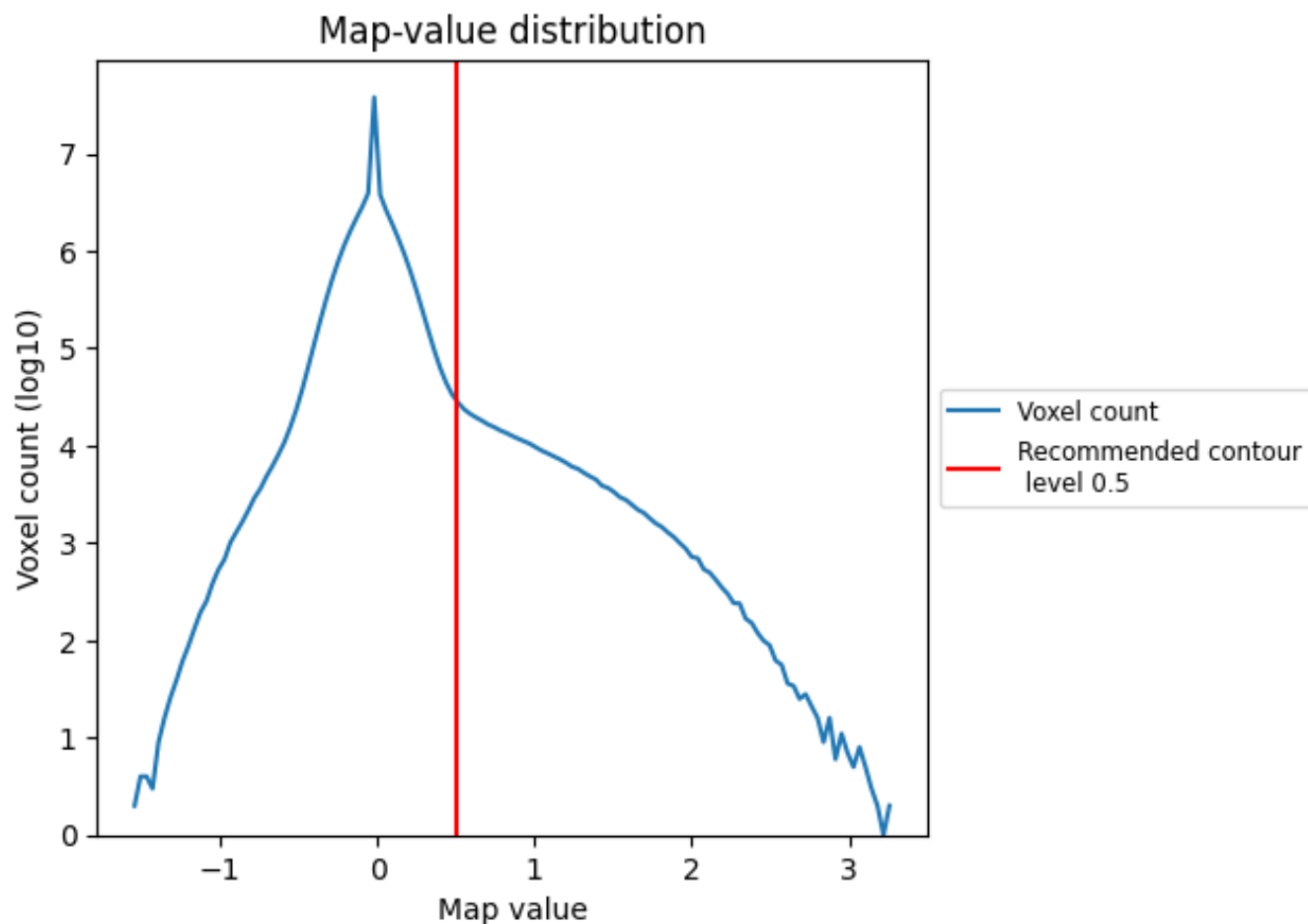
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

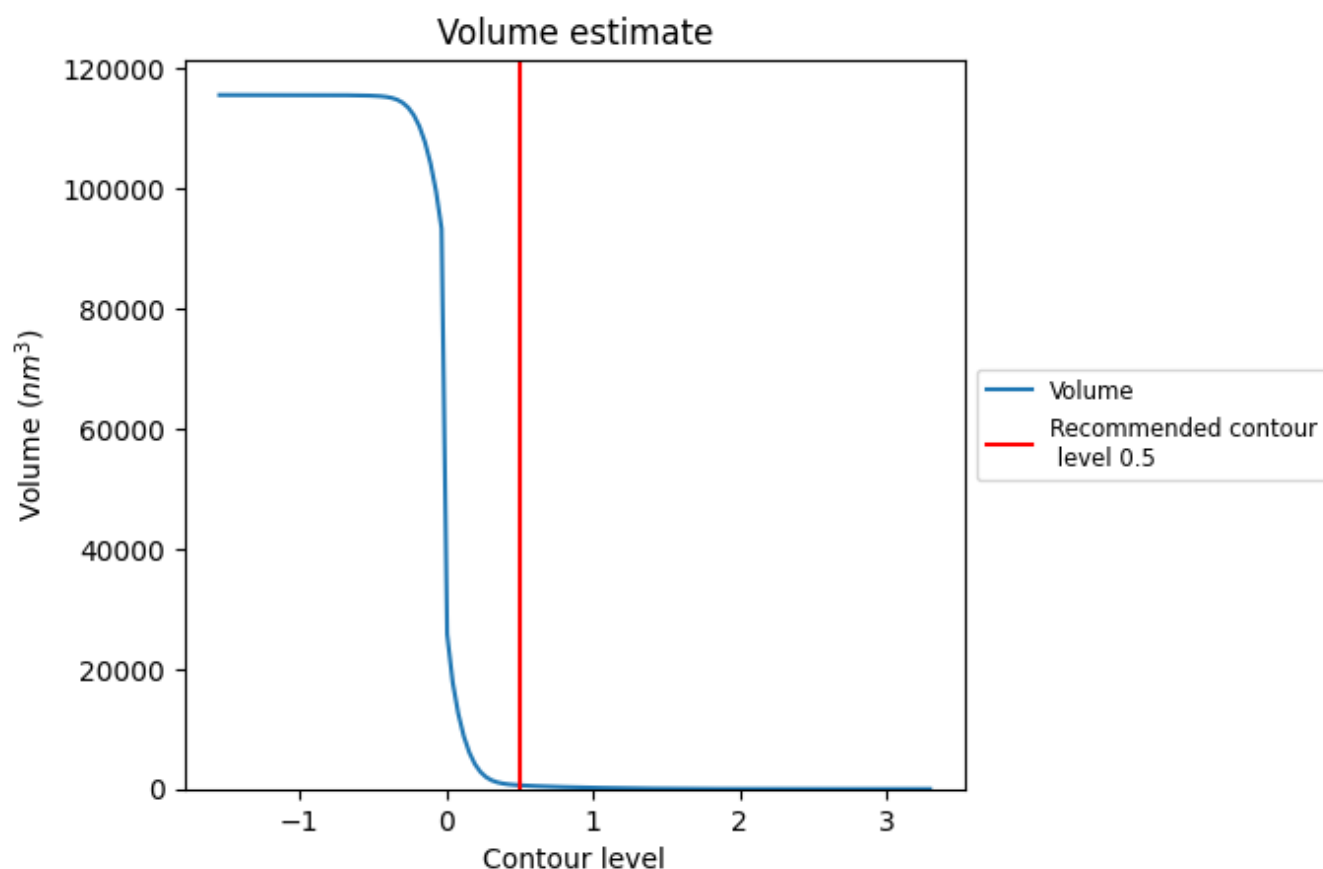
This section contains the results of statistical analysis of the map.

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.

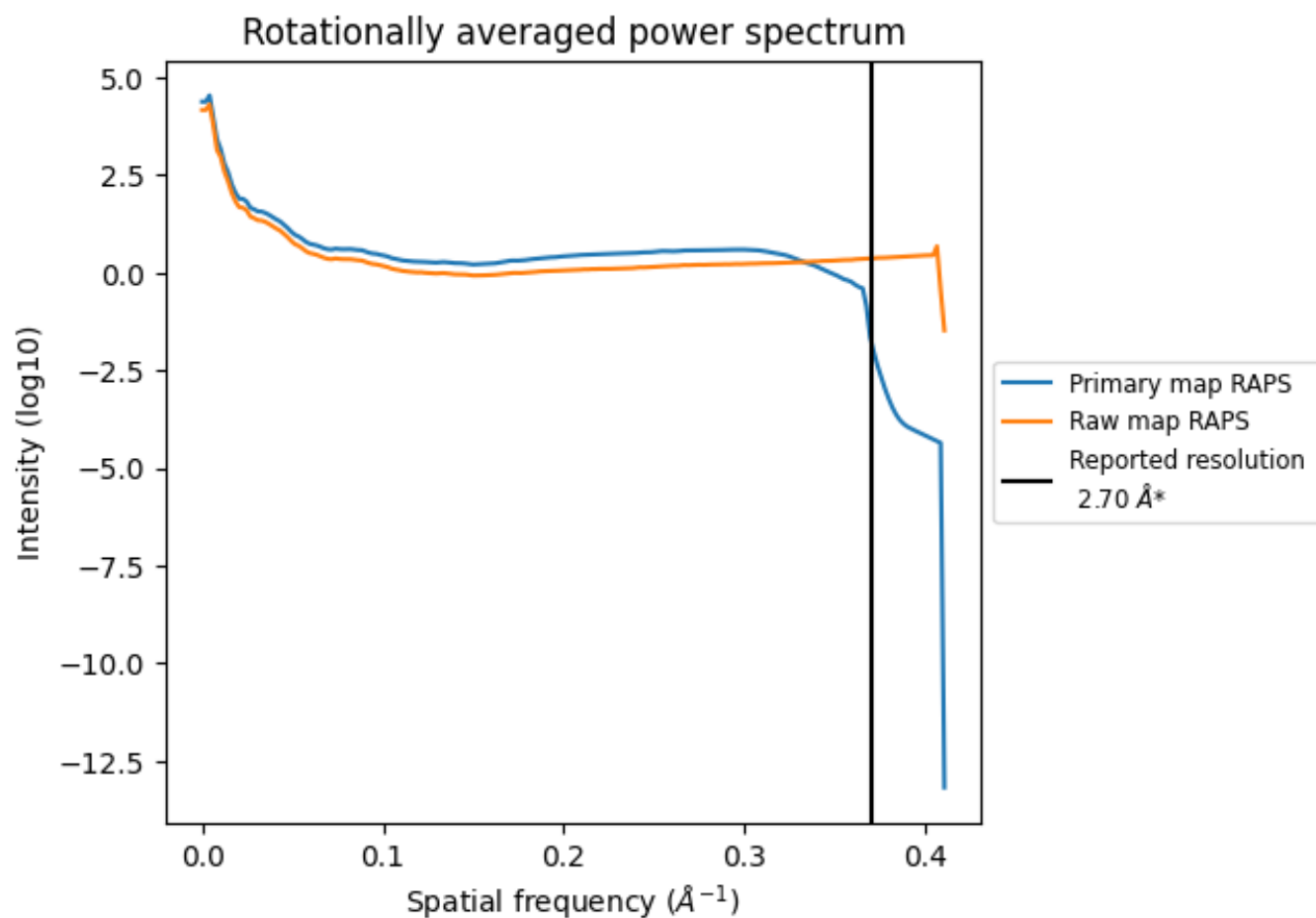
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 613 nm³; this corresponds to an approximate mass of 554 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

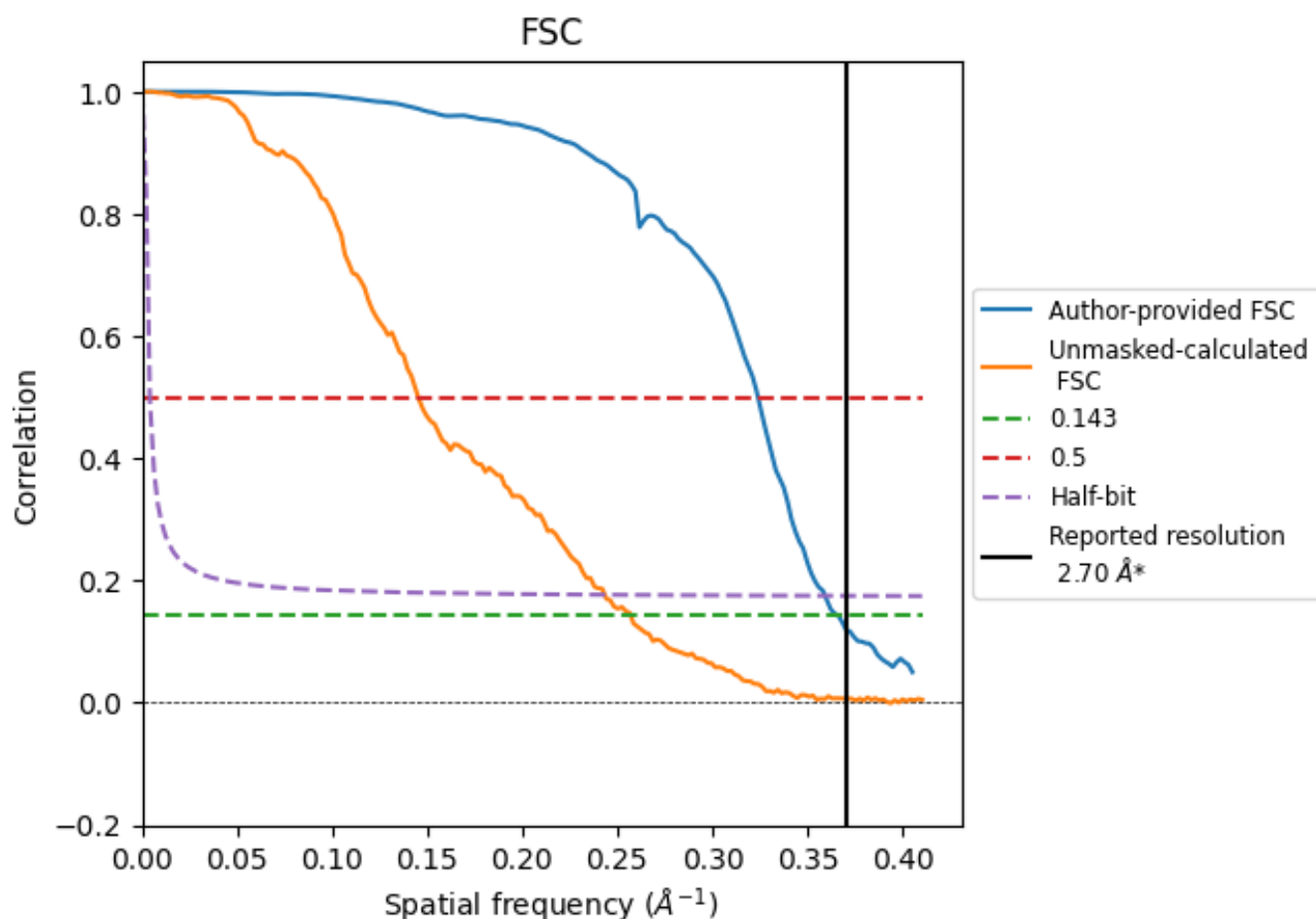


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

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 0.370 \AA^{-1}

8.2 Resolution estimates [i](#)

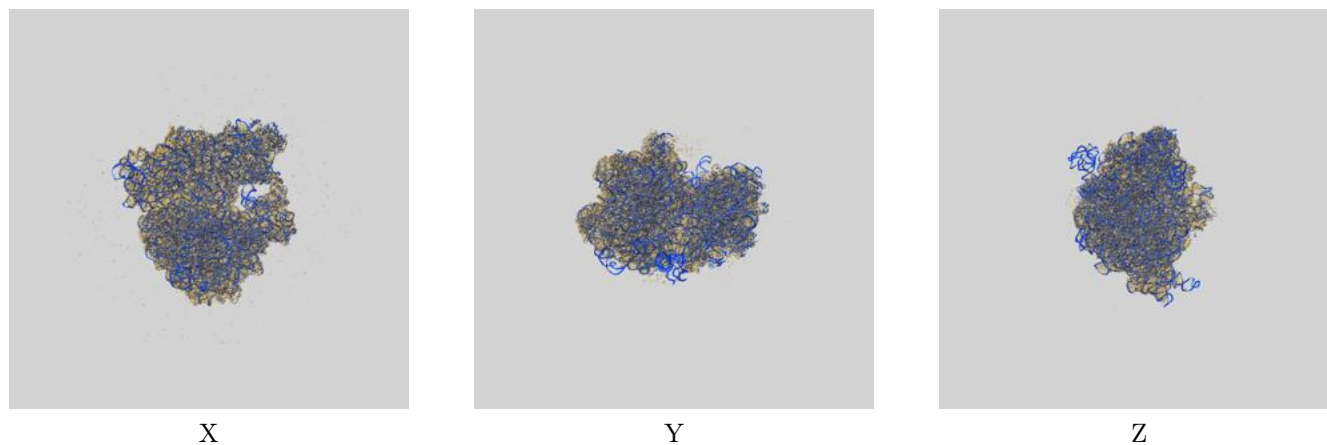
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 2.70 | - | - |
| Author-provided FSC curve | 2.73 | 3.09 | 2.78 |
| Unmasked-calculated* | 3.89 | 6.88 | 4.11 |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.89 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

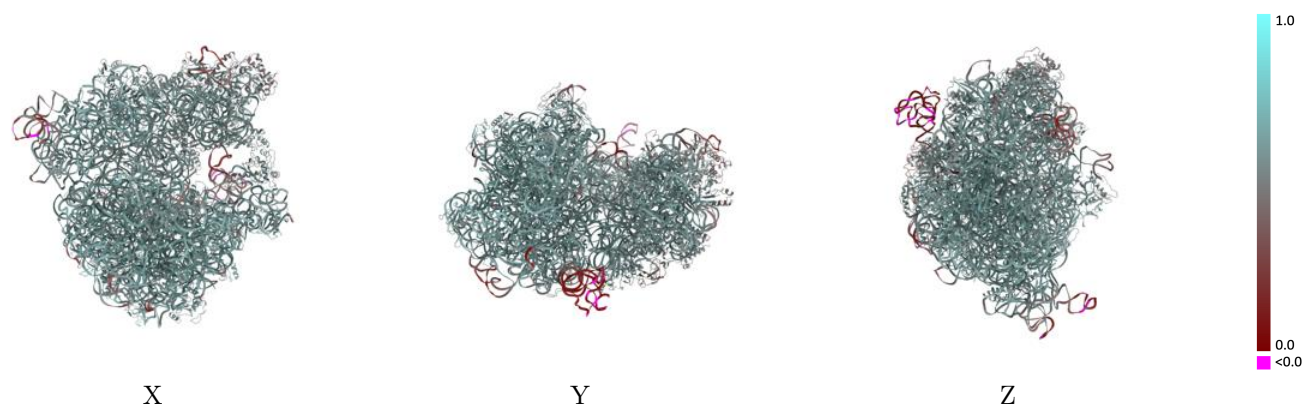
This section contains information regarding the fit between EMDB map EMD-60747 and PDB model 9IOT. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



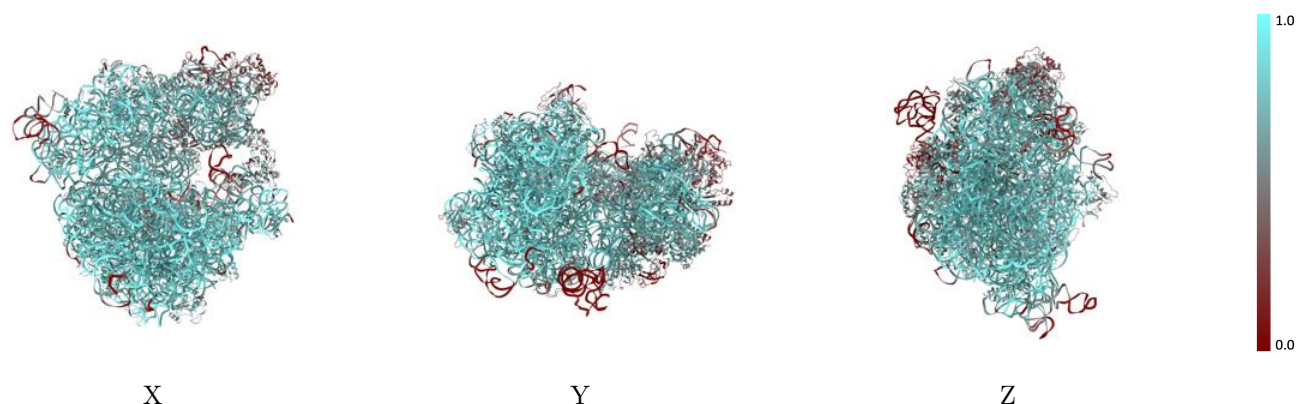
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



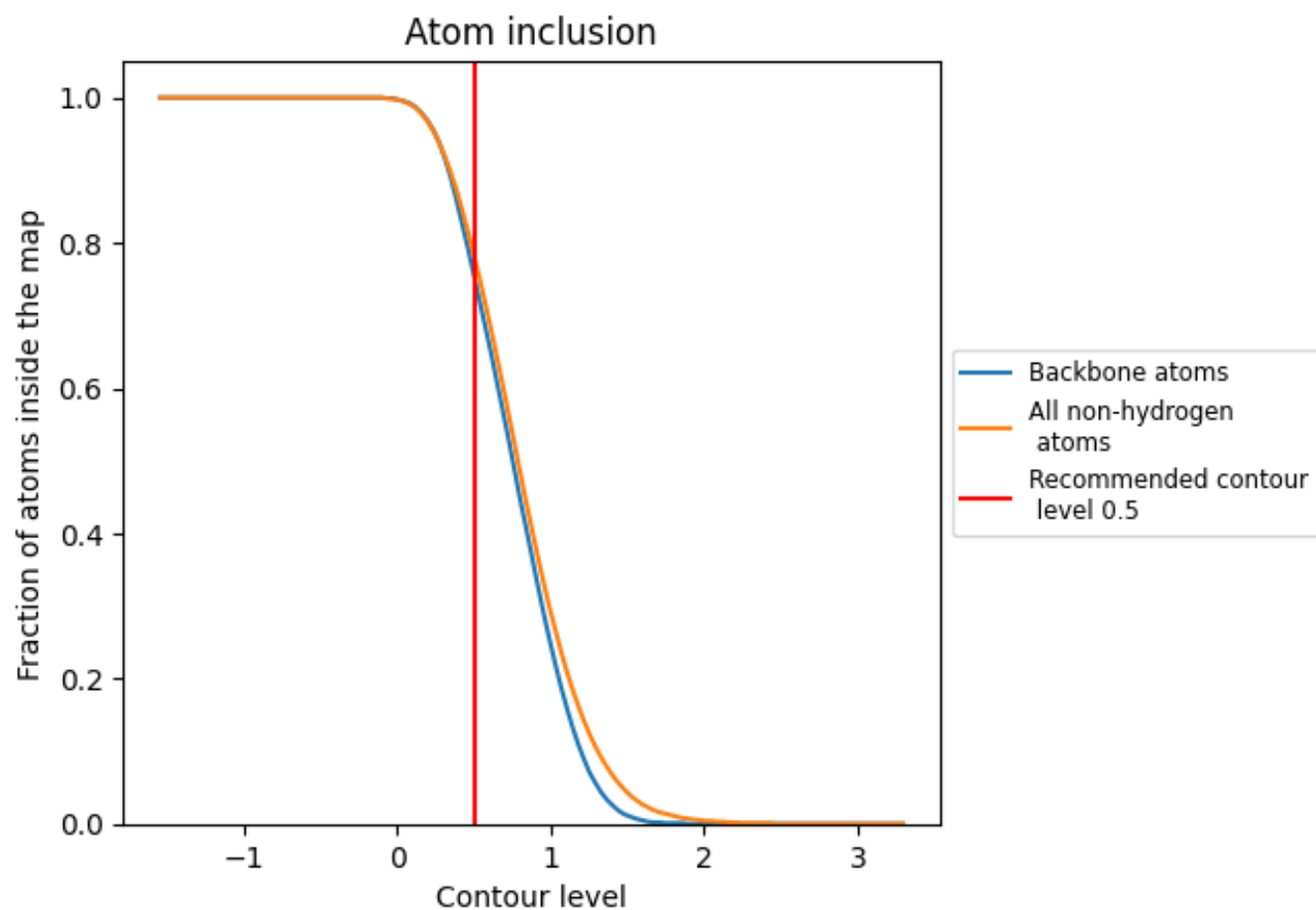
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 78% 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 (0.5) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.7830 |  0.5850 |
| 0 |  0.6460 |  0.5730 |
| 1 |  0.7530 |  0.6060 |
| 2 |  0.3780 |  0.5070 |
| 3 |  0.8110 |  0.6240 |
| 4 |  0.7110 |  0.5940 |
| 5 |  0.8620 |  0.6370 |
| 6 |  0.8700 |  0.6340 |
| 7 |  0.7500 |  0.5980 |
| 8 |  0.0950 |  0.4070 |
| A |  0.8430 |  0.5870 |
| B |  0.8320 |  0.5870 |
| D |  0.8170 |  0.6260 |
| E |  0.7880 |  0.6180 |
| F |  0.7500 |  0.6050 |
| G |  0.5290 |  0.5350 |
| H |  0.5200 |  0.5310 |
| I |  0.3670 |  0.5370 |
| L |  0.7980 |  0.6130 |
| M |  0.7830 |  0.6170 |
| N |  0.8120 |  0.6220 |
| O |  0.7800 |  0.6190 |
| P |  0.8580 |  0.6270 |
| Q |  0.7250 |  0.5890 |
| R |  0.7650 |  0.6160 |
| S |  0.8520 |  0.6250 |
| T |  0.7680 |  0.6110 |
| U |  0.8100 |  0.6210 |
| V |  0.6760 |  0.5790 |
| W |  0.7000 |  0.5830 |
| X |  0.6800 |  0.5850 |
| Y |  0.7900 |  0.6170 |
| Z |  0.7550 |  0.6140 |
| a |  0.8250 |  0.5830 |
| b |  0.6040 |  0.5550 |



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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| c |  0.6580 |  0.5730 |
| d |  0.6680 |  0.5810 |
| e |  0.7610 |  0.6020 |
| f |  0.6030 |  0.5560 |
| g |  0.5340 |  0.5550 |
| h |  0.7440 |  0.6020 |
| i |  0.6440 |  0.5660 |
| j |  0.6060 |  0.5500 |
| k |  0.6680 |  0.5730 |
| l |  0.7230 |  0.6060 |
| m |  0.5840 |  0.5670 |
| n |  0.6970 |  0.5900 |
| o |  0.6970 |  0.5880 |
| p |  0.7530 |  0.5950 |
| q |  0.6440 |  0.5720 |
| r |  0.6640 |  0.5670 |
| s |  0.5890 |  0.5530 |
| t |  0.6860 |  0.5750 |
| u |  0.4650 |  0.5310 |
| v |  0.5760 |  0.5860 |
| y |  0.4600 |  0.5740 |
| z |  0.3780 |  0.5000 |