



wwPDB EM Validation Summary Report ⓘ

Jan 18, 2024 – 05:35 pm GMT

PDB ID : 8RJD
EMDB ID : EMD-19198
Title : Structure of the rabbit 80S ribosome stalled on a 2-TMD rhodopsin intermediate in complex with Sec61-TRAP, open conformation 2
Authors : Lewis, A.J.O.; Hegde, R.S.
Deposited on : 2023-12-20
Resolution : 2.79 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:

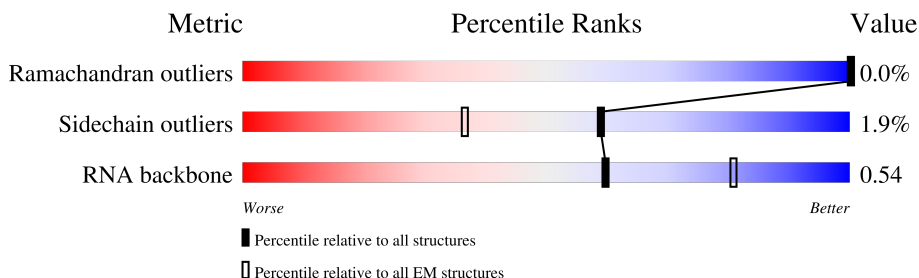
EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.79 Å.

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



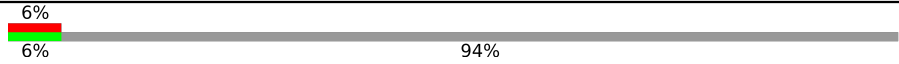
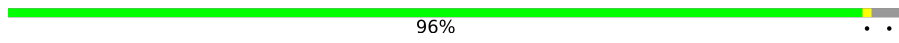


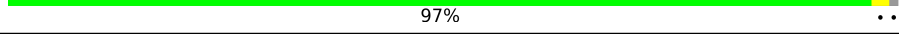
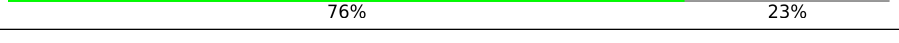
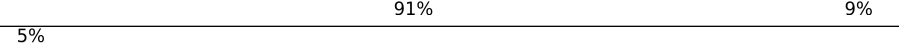
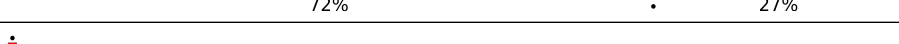
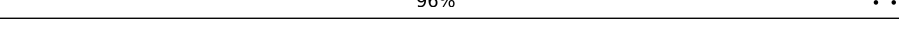
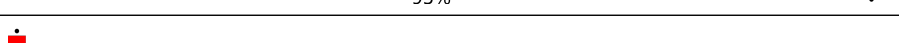


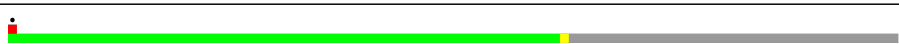

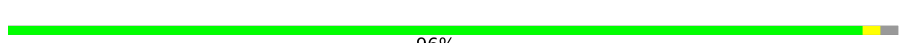
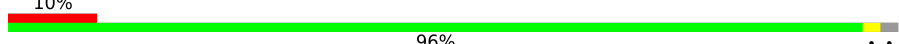
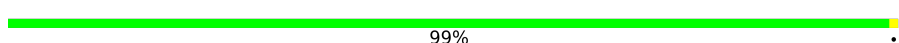

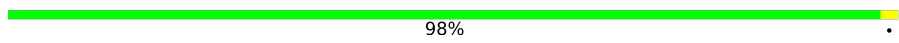
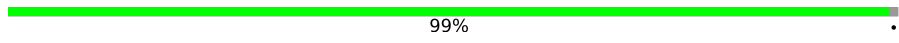

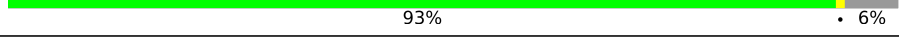



| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|--------------------------|--------------------------|
| Ramachandran outliers | 154571 | 4023 |
| Sidechain outliers | 154315 | 3826 |
| RNA backbone | 4643 | 859 |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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 | 1 | 476 | 20% (red) 95% (green) 5% (grey) |
| 2 | 2 | 96 | 9% (red) 32% (green) 67% (grey) |
| 3 | 3 | 68 | 7% (red) 91% (green) 6% (grey) |
| 4 | 4 | 66 | 9% (red) 44% (green) 53% (grey) |
| 5 | 5 | 286 | 55% (red) 60% (green) 38% (grey) |
| 6 | 6 | 183 | 88% (red) 87% (green) 11% (grey) |
| 7 | 7 | 185 | 89% (red) 94% (green) 5% (grey) |
| 8 | 8 | 173 | 84% (red) 85% (green) 13% (grey) |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|-------------------------------------------------------------------------------------------------|
| 9 | 9 | 593 |  6% 94% |
| 10 | A | 257 |  96% |
| 11 | B | 229 |  10% 25% 74% |
| 12 | C | 425 |  84% 15% |
| 13 | D | 297 |  97% |
| 14 | E | 291 |  76% 23% |
| 15 | F | 247 |  91% 9% |
| 16 | G | 319 |  5% 72% 27% |
| 17 | H | 192 |  96% |
| 18 | I | 214 |  95% |
| 19 | J | 178 |  94% |
| 20 | K | 3543 |  82% 17% |
| 21 | L | 211 |  98% |
| 22 | M | 218 |  62% 37% |
| 23 | N | 204 |  99% |
| 24 | O | 203 |  96% |
| 25 | P | 184 |  10% 96% |
| 26 | Q | 187 |  99% |
| 27 | R | 196 |  76% 21% |
| 28 | S | 176 |  98% |
| 29 | T | 160 |  99% |
| 30 | U | 128 |  74% 5% 20% |
| 31 | V | 140 |  93% 6% |
| 32 | W | 157 |  39% 60% |
| 33 | X | 156 |  75% 24% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 34 | Y | 145 | 91% 8% |
| 35 | Z | 136 | 96% |
| 36 | a | 148 | 99% |
| 37 | b | 226 | 46% 54% |
| 38 | c | 115 | 84% 15% |
| 39 | d | 125 | 85% 14% |
| 40 | e | 135 | 93% 5% |
| 41 | f | 110 | 98% |
| 42 | g | 116 | 97% |
| 43 | h | 123 | 98% |
| 44 | i | 105 | 93% |
| 45 | j | 97 | 89% 11% |
| 46 | k | 70 | 96% |
| 47 | l | 51 | 96% |
| 48 | m | 102 | 50% 49% |
| 49 | n | 25 | 96% |
| 50 | o | 106 | 97% |
| 51 | p | 92 | 97% |
| 52 | q | 76 | 11% 89% 11% |
| 53 | r | 137 | 88% 9% |
| 54 | u | 120 | 93% 7% |
| 55 | v | 156 | 83% 16% |
| 56 | w | 403 | 96% |

2 Entry composition [i](#)

There are 58 unique types of molecules in this entry. The entry contains 255550 atoms, of which 108756 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 Protein transport protein Sec61 subunit alpha isoform 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 1 | 1 | 461 | 7275 | 2347 | 3700 | 576 | 629 | 23 | 0 | 0 |

- Molecule 2 is a protein called Protein transport protein Sec61 subunit beta.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 2 | 2 | 32 | 524 | 171 | 273 | 40 | 38 | 2 | 0 | 0 |

- Molecule 3 is a protein called Protein transport protein Sec61 subunit gamma.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 3 | 3 | 66 | 1105 | 351 | 571 | 92 | 86 | 5 | 0 | 0 |

- Molecule 4 is a protein called Stress-associated endoplasmic reticulum protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 4 | 4 | 31 | 504 | 145 | 260 | 55 | 43 | 1 | 0 | 0 |

- Molecule 5 is a protein called Translocon-associated protein subunit alpha.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 5 | 5 | 178 | 2813 | 919 | 1390 | 231 | 269 | 4 | 0 | 0 |

- Molecule 6 is a protein called Translocon-associated protein subunit beta.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 6 | 6 | 162 | 2507 | 813 | 1244 | 212 | 236 | 2 | 0 | 0 |

- Molecule 7 is a protein called Translocon-associated protein subunit gamma.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 7 | 7 | 179 | 2942 | 947 | 1490 | 239 | 263 | 3 | 0 | 0 |

- Molecule 8 is a protein called Translocon-associated protein subunit delta.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 8 | 8 | 150 | 2335 | 755 | 1149 | 199 | 229 | 3 | 0 | 0 |

- Molecule 9 is a protein called Calnexin.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 9 | 9 | 38 | 610 | 206 | 309 | 43 | 50 | 2 | 0 | 0 |

- Molecule 10 is a protein called Ribosomal protein L8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 10 | A | 248 | 3892 | 1189 | 1994 | 389 | 314 | 6 | 0 | 0 |

- Molecule 11 is a protein called Nascent chain.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 11 | B | 59 | 856 | 283 | 424 | 67 | 80 | 2 | 0 | 0 |

- Molecule 12 is a protein called Large ribosomal subunit protein uL4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 12 | C | 362 | 5937 | 1812 | 3054 | 577 | 480 | 14 | 0 | 0 |

- Molecule 13 is a protein called Ribosomal_L18_c domain-containing protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 13 | D | 293 | 4816 | 1512 | 2425 | 438 | 427 | 14 | 0 | 0 |

- Molecule 14 is a protein called 60S ribosomal protein L6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 14 | E | 223 | 3754 | 1154 | 1963 | 341 | 293 | 3 | 0 | 0 |

- Molecule 15 is a protein called Ribosomal Protein uL30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 15 | F | 225 | 3872 | 1205 | 1997 | 358 | 303 | 9 | 0 | 0 |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| F | 61 | ARG | GLY | conflict | UNP G1TUB1 |
| F | 93 | ARG | GLY | conflict | UNP G1TUB1 |
| F | 131 | MET | VAL | conflict | UNP G1TUB1 |
| F | 153 | ILE | VAL | conflict | UNP G1TUB1 |

- Molecule 16 is a protein called 60S ribosomal protein L7a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 16 | G | 233 | 3908 | 1199 | 2029 | 361 | 315 | 4 | 0 | 0 |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| G | 244 | GLY | CYS | conflict | UNP G1STW0 |

- Molecule 17 is a protein called 60S ribosomal protein L9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 17 | H | 190 | 3114 | 954 | 1598 | 284 | 272 | 6 | 0 | 0 |

- Molecule 18 is a protein called 60S ribosomal protein L10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 18 | I | 205 | 3380 | 1056 | 1716 | 321 | 274 | 13 | 0 | 0 |

- Molecule 19 is a protein called 60S ribosomal protein L11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 19 | J | 170 | 2763 | 861 | 1401 | 254 | 241 | 6 | 0 | 0 |

- Molecule 20 is a RNA chain called 28S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|--------|-------|-------|-------|-------|---------|-------|---|
| | | | Total | C | H | N | O | | | P |
| 20 | K | 3543 | 114335 | 33833 | 38363 | 13910 | 24686 | 3543 | 0 | 0 |

- Molecule 21 is a protein called 60S ribosomal protein L13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 21 | L | 210 | 3525 | 1065 | 1823 | 354 | 279 | 4 | 0 | 0 |

There are 170 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------|------------|
| L | 1 | MET | ARG | conflict | UNP G1TPV0 |
| L | 3 | PRO | LEU | conflict | UNP G1TPV0 |
| L | 4 | SER | ALA | conflict | UNP G1TPV0 |
| L | 6 | ASN | - | insertion | UNP G1TPV0 |
| L | 7 | GLY | ALA | conflict | UNP G1TPV0 |
| L | 9 | ILE | ARG | conflict | UNP G1TPV0 |
| L | 10 | LEU | ARG | conflict | UNP G1TPV0 |
| L | 11 | LYS | LEU | conflict | UNP G1TPV0 |
| L | 12 | PRO | ALA | conflict | UNP G1TPV0 |
| L | 13 | HIS | LYS | conflict | UNP G1TPV0 |
| L | 14 | PHE | ALA | conflict | UNP G1TPV0 |
| L | 15 | HIS | LEU | conflict | UNP G1TPV0 |
| L | 17 | ASP | PHE | conflict | UNP G1TPV0 |
| L | 18 | TRP | PHE | conflict | UNP G1TPV0 |
| L | 19 | GLN | SER | conflict | UNP G1TPV0 |
| L | 20 | ARG | SER | conflict | UNP G1TPV0 |
| L | 21 | ARG | SER | conflict | UNP G1TPV0 |
| L | 23 | ALA | ILE | conflict | UNP G1TPV0 |
| L | 25 | TRP | - | insertion | UNP G1TPV0 |
| L | 26 | PHE | LEU | conflict | UNP G1TPV0 |
| L | 27 | ASN | ALA | conflict | UNP G1TPV0 |
| L | 28 | GLN | PHE | conflict | UNP G1TPV0 |
| L | 29 | PRO | SER | conflict | UNP G1TPV0 |
| L | 30 | ALA | PHE | conflict | UNP G1TPV0 |
| L | 31 | ARG | LEU | conflict | UNP G1TPV0 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------|------------|
| L | 33 | ILE | - | insertion | UNP G1TPV0 |
| L | 34 | ARG | THR | conflict | UNP G1TPV0 |
| L | 35 | ARG | PHE | conflict | UNP G1TPV0 |
| L | 37 | LYS | MET | conflict | UNP G1TPV0 |
| L | 38 | ALA | GLY | conflict | UNP G1TPV0 |
| L | 39 | ARG | MET | conflict | UNP G1TPV0 |
| L | 40 | GLN | THR | conflict | UNP G1TPV0 |
| L | 41 | ALA | GLY | conflict | UNP G1TPV0 |
| L | 42 | ARG | PRO | conflict | UNP G1TPV0 |
| L | 43 | ALA | VAL | conflict | UNP G1TPV0 |
| L | 44 | ARG | SER | conflict | UNP G1TPV0 |
| L | 45 | ARG | TRP | conflict | UNP G1TPV0 |
| L | 46 | ILE | VAL | conflict | UNP G1TPV0 |
| L | 48 | PRO | ASN | conflict | UNP G1TPV0 |
| L | 49 | ARG | PHE | conflict | UNP G1TPV0 |
| L | 50 | PRO | SER | conflict | UNP G1TPV0 |
| L | 51 | ALA | SER | conflict | UNP G1TPV0 |
| L | 52 | ALA | SER | conflict | UNP G1TPV0 |
| L | 53 | GLY | ALA | conflict | UNP G1TPV0 |
| L | 54 | PRO | GLU | conflict | UNP G1TPV0 |
| L | 55 | ILE | LEU | conflict | UNP G1TPV0 |
| L | 56 | ARG | SER | conflict | UNP G1TPV0 |
| L | 58 | ILE | PHE | conflict | UNP G1TPV0 |
| L | 59 | VAL | LEU | conflict | UNP G1TPV0 |
| L | 60 | ARG | GLY | conflict | UNP G1TPV0 |
| L | 61 | CYS | ALA | conflict | UNP G1TPV0 |
| L | 62 | PRO | GLU | conflict | UNP G1TPV0 |
| L | 63 | THR | GLY | conflict | UNP G1TPV0 |
| L | 64 | VAL | PHE | conflict | UNP G1TPV0 |
| L | 66 | TYR | - | insertion | UNP G1TPV0 |
| L | 67 | HIS | - | insertion | UNP G1TPV0 |
| L | 68 | THR | GLY | conflict | UNP G1TPV0 |
| L | 70 | VAL | - | insertion | UNP G1TPV0 |
| L | 71 | ARG | - | insertion | UNP G1TPV0 |
| L | 72 | ALA | - | insertion | UNP G1TPV0 |
| L | 73 | GLY | - | insertion | UNP G1TPV0 |
| L | 75 | GLY | - | insertion | UNP G1TPV0 |
| L | 76 | PHE | THR | conflict | UNP G1TPV0 |
| L | 80 | GLU | - | insertion | UNP G1TPV0 |
| L | 81 | LEU | - | insertion | UNP G1TPV0 |
| L | 83 | VAL | TYR | conflict | UNP G1TPV0 |
| L | 84 | ALA | SER | conflict | UNP G1TPV0 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------|------------|
| L | 85 | GLY | PHE | conflict | UNP G1TPV0 |
| L | 86 | ILE | SER | conflict | UNP G1TPV0 |
| L | 87 | HIS | ARG | conflict | UNP G1TPV0 |
| L | 88 | LYS | CYS | conflict | UNP G1TPV0 |
| L | 89 | LYS | THR | conflict | UNP G1TPV0 |
| L | 90 | VAL | LEU | conflict | UNP G1TPV0 |
| L | 92 | ARG | - | insertion | UNP G1TPV0 |
| L | 93 | THR | - | insertion | UNP G1TPV0 |
| L | 94 | ILE | CYS | conflict | UNP G1TPV0 |
| L | 95 | GLY | ARG | conflict | UNP G1TPV0 |
| L | 96 | ILE | ASP | conflict | UNP G1TPV0 |
| L | 100 | PRO | LEU | conflict | UNP G1TPV0 |
| L | 101 | ARG | PHE | conflict | UNP G1TPV0 |
| L | 104 | ASN | ARG | conflict | UNP G1TPV0 |
| L | 105 | LYS | GLY | conflict | UNP G1TPV0 |
| L | 109 | SER | MET | conflict | UNP G1TPV0 |
| L | 110 | LEU | PRO | conflict | UNP G1TPV0 |
| L | 111 | GLN | ILE | conflict | UNP G1TPV0 |
| L | 112 | ALA | VAL | conflict | UNP G1TPV0 |
| L | 113 | ASN | ARG | conflict | UNP G1TPV0 |
| L | 114 | VAL | ALA | conflict | UNP G1TPV0 |
| L | 115 | GLN | THR | conflict | UNP G1TPV0 |
| L | 116 | ARG | PHE | conflict | UNP G1TPV0 |
| L | ? | - | TRP | deletion | UNP G1TPV0 |
| L | ? | - | MET | deletion | UNP G1TPV0 |
| L | 118 | LYS | PRO | conflict | UNP G1TPV0 |
| L | 119 | GLU | ALA | conflict | UNP G1TPV0 |
| L | 120 | TYR | THR | conflict | UNP G1TPV0 |
| L | 123 | LYS | SER | conflict | UNP G1TPV0 |
| L | 124 | LEU | SER | conflict | UNP G1TPV0 |
| L | 125 | VAL | ARG | conflict | UNP G1TPV0 |
| L | 127 | PHE | LYS | conflict | UNP G1TPV0 |
| L | 130 | LYS | PRO | conflict | UNP G1TPV0 |
| L | 131 | PRO | ALA | conflict | UNP G1TPV0 |
| L | 132 | SER | ARG | conflict | UNP G1TPV0 |
| L | 133 | ALA | THR | conflict | UNP G1TPV0 |
| L | 134 | PRO | PHE | conflict | UNP G1TPV0 |
| L | 135 | LYS | VAL | conflict | UNP G1TPV0 |
| L | 136 | LYS | TRP | conflict | UNP G1TPV0 |
| L | 137 | GLY | TYR | conflict | UNP G1TPV0 |
| L | 138 | ASP | ARG | conflict | UNP G1TPV0 |
| L | 139 | SER | THR | conflict | UNP G1TPV0 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| L | 140 | SER | VAL | conflict | UNP G1TPV0 |
| L | 141 | ALA | GLY | conflict | UNP G1TPV0 |
| L | 142 | GLU | GLN | conflict | UNP G1TPV0 |
| L | 143 | GLU | ARG | conflict | UNP G1TPV0 |
| L | 144 | LEU | THR | conflict | UNP G1TPV0 |
| L | 145 | LYS | MET | conflict | UNP G1TPV0 |
| L | 146 | LEU | GLY | conflict | UNP G1TPV0 |
| L | 147 | ALA | ARG | conflict | UNP G1TPV0 |
| L | 148 | THR | MET | conflict | UNP G1TPV0 |
| L | 149 | GLN | GLY | conflict | UNP G1TPV0 |
| L | 151 | THR | ALA | conflict | UNP G1TPV0 |
| L | 152 | GLY | PRO | conflict | UNP G1TPV0 |
| L | 153 | PRO | ALA | conflict | UNP G1TPV0 |
| L | 154 | VAL | ASP | conflict | UNP G1TPV0 |
| L | 155 | MET | LEU | conflict | UNP G1TPV0 |
| L | 156 | PRO | ALA | conflict | UNP G1TPV0 |
| L | 157 | ILE | ARG | conflict | UNP G1TPV0 |
| L | 159 | ASN | LEU | conflict | UNP G1TPV0 |
| L | 161 | PHE | GLU | conflict | UNP G1TPV0 |
| L | 162 | LYS | PRO | conflict | UNP G1TPV0 |
| L | 163 | LYS | GLY | conflict | UNP G1TPV0 |
| L | 164 | GLU | GLY | conflict | UNP G1TPV0 |
| L | 165 | LYS | HIS | conflict | UNP G1TPV0 |
| L | 167 | ARG | PRO | conflict | UNP G1TPV0 |
| L | 168 | VAL | LEU | conflict | UNP G1TPV0 |
| L | 169 | ILE | PRO | conflict | UNP G1TPV0 |
| L | 170 | THR | VAL | conflict | UNP G1TPV0 |
| L | 171 | GLU | LEU | conflict | UNP G1TPV0 |
| L | 172 | GLU | VAL | conflict | UNP G1TPV0 |
| L | 174 | LYS | VAL | conflict | UNP G1TPV0 |
| L | 175 | ASN | ARG | conflict | UNP G1TPV0 |
| L | 176 | PHE | LEU | conflict | UNP G1TPV0 |
| L | 177 | LYS | GLN | conflict | UNP G1TPV0 |
| L | 178 | ALA | ASP | conflict | UNP G1TPV0 |
| L | 179 | PHE | HIS | conflict | UNP G1TPV0 |
| L | 181 | SER | ILE | conflict | UNP G1TPV0 |
| L | 182 | LEU | PRO | conflict | UNP G1TPV0 |
| L | 183 | ARG | ALA | conflict | UNP G1TPV0 |
| L | 184 | MET | GLY | conflict | UNP G1TPV0 |
| L | 185 | ALA | ARG | conflict | UNP G1TPV0 |
| L | 186 | ARG | HIS | conflict | UNP G1TPV0 |
| L | 187 | ALA | GLY | conflict | UNP G1TPV0 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| L | 188 | ASN | CYS | conflict | UNP G1TPV0 |
| L | 189 | ALA | VAL | conflict | UNP G1TPV0 |
| L | 190 | ARG | LEU | conflict | UNP G1TPV0 |
| L | 192 | PHE | ARG | conflict | UNP G1TPV0 |
| L | 193 | GLY | ALA | conflict | UNP G1TPV0 |
| L | 194 | ILE | ARG | conflict | UNP G1TPV0 |
| L | 195 | ARG | THR | conflict | UNP G1TPV0 |
| L | 196 | ALA | GLU | conflict | UNP G1TPV0 |
| L | 199 | ALA | LYS | conflict | UNP G1TPV0 |
| L | 200 | LYS | SER | conflict | UNP G1TPV0 |
| L | 202 | ALA | PRO | conflict | UNP G1TPV0 |
| L | 203 | ALA | GLN | conflict | UNP G1TPV0 |
| L | 204 | GLU | HIS | conflict | UNP G1TPV0 |
| L | 205 | GLN | PHE | conflict | UNP G1TPV0 |
| L | 207 | VAL | THR | conflict | UNP G1TPV0 |
| L | 208 | GLU | GLY | conflict | UNP G1TPV0 |
| L | 209 | LYS | CYS | conflict | UNP G1TPV0 |
| L | 210 | LYS | ARG | conflict | UNP G1TPV0 |
| L | 211 | LYS | HIS | conflict | UNP G1TPV0 |

- Molecule 22 is a protein called 60S ribosomal protein L14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 22 | M | 138 | 2349 | 727 | 1212 | 221 | 182 | 7 | 0 | 0 |

- Molecule 23 is a protein called Ribosomal protein L15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 23 | N | 203 | 3454 | 1072 | 1753 | 359 | 266 | 4 | 0 | 0 |

- Molecule 24 is a protein called 60S ribosomal protein L13a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 24 | O | 199 | 3410 | 1051 | 1780 | 319 | 255 | 5 | 0 | 0 |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|----------------|
| O | 174 | LEU | ILE | conflict | UNP A0A0N8ETI8 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|----------------|
| O | 194 | ASP | GLU | conflict | UNP A0A0N8ETI8 |

- Molecule 25 is a protein called uL22.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|----|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 25 | P | 181 | 3012 | 924 | 1542 | 282 | 254 | 10 | 0 | 0 |

- Molecule 26 is a protein called Ribosomal protein L18.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 26 | Q | 187 | 3153 | 946 | 1638 | 315 | 250 | 4 | 0 | 0 |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| Q | 134 | ARG | CYS | conflict | UNP F6QKI9 |

- Molecule 27 is a protein called Ribosomal protein L19.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|---|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 27 | R | 155 | 2730 | 808 | 1436 | 278 | 199 | 9 | 0 | 0 |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| R | 38 | ARG | HIS | conflict | UNP G1TYL6 |
| R | 151 | ARG | HIS | conflict | UNP G1TYL6 |

- Molecule 28 is a protein called 60S ribosomal protein L18a.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|------|-----|-----|----|---------|-------|
| | | | Total | C | H | N | O | S | | |
| 28 | S | 176 | 2972 | 930 | 1510 | 285 | 236 | 11 | 0 | 0 |

- Molecule 29 is a protein called 60S ribosomal protein L21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 29 | T | 159 | 2667 | 823 | 1369 | 252 | 217 | 6 | 0 | 0 |

- Molecule 30 is a protein called Large ribosomal subunit protein eL22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 30 | U | 102 | 1693 | 534 | 859 | 146 | 152 | 2 | 0 | 0 |

There are 5 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| U | 18 | LEU | VAL | conflict | UNP Q4R5I3 |
| U | 62 | SER | THR | conflict | UNP Q4R5I3 |
| U | 63 | LEU | ILE | conflict | UNP Q4R5I3 |
| U | 106 | THR | SER | conflict | UNP Q4R5I3 |
| U | 126 | GLU | ASP | conflict | UNP Q4R5I3 |

- Molecule 31 is a protein called Ribosomal protein L23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 31 | V | 131 | 2019 | 618 | 1040 | 184 | 172 | 5 | 0 | 0 |

- Molecule 32 is a protein called Ribosomal protein L24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 32 | W | 63 | 1070 | 337 | 542 | 103 | 85 | 3 | 0 | 0 |

- Molecule 33 is a protein called Large ribosomal subunit protein uL23 N-terminal domain-containing protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 33 | X | 118 | 2008 | 618 | 1041 | 181 | 167 | 1 | 0 | 0 |

- Molecule 34 is a protein called Ribosomal protein L26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 34 | Y | 134 | 2320 | 700 | 1205 | 226 | 186 | 3 | 0 | 0 |

- Molecule 35 is a protein called 60S ribosomal protein L27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 35 | Z | 135 | 2292 | 714 | 1185 | 208 | 182 | 3 | 0 | 0 |

- Molecule 36 is a protein called 60S ribosomal protein L27a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 36 | a | 147 | 2372 | 734 | 1210 | 239 | 185 | 4 | 0 | 0 |

- Molecule 37 is a protein called 60S ribosomal protein L29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 37 | b | 104 | 1771 | 527 | 923 | 189 | 129 | 3 | 0 | 0 |

- Molecule 38 is a protein called Large ribosomal subunit protein eL30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 38 | c | 98 | 1557 | 481 | 796 | 134 | 140 | 6 | 0 | 0 |

- Molecule 39 is a protein called 60S ribosomal protein L31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 39 | d | 107 | 1820 | 560 | 932 | 171 | 155 | 2 | 0 | 0 |

- Molecule 40 is a protein called Ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 40 | e | 128 | 2203 | 667 | 1150 | 216 | 165 | 5 | 0 | 0 |

- Molecule 41 is a protein called 60S ribosomal protein L35a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 41 | f | 109 | 1789 | 555 | 913 | 174 | 143 | 4 | 0 | 0 |

- Molecule 42 is a protein called 60S ribosomal protein L34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 42 | g | 114 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1910 | 566 | 1004 | 187 | 147 | 6 | | |

- Molecule 43 is a protein called 60S ribosomal protein L35.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| 43 | h | 122 | Total | C | H | N | O | S | 0 | 0 |
| | | | 2161 | 640 | 1148 | 204 | 168 | 1 | | |

- Molecule 44 is a protein called 60S ribosomal protein L36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 44 | i | 102 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1747 | 520 | 917 | 176 | 129 | 5 | | |

- Molecule 45 is a protein called Ribosomal protein L37.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| 45 | j | 86 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1448 | 434 | 743 | 155 | 111 | 5 | | |

- Molecule 46 is a protein called Large ribosomal subunit protein eL38.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|---|
| 46 | k | 69 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1206 | 366 | 637 | 103 | 99 | 1 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| k | 24 | LYS | ASN | conflict | UNP G1U001 |

- Molecule 47 is a protein called 60S ribosomal protein L39-like.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|---|
| 47 | l | 50 | Total | C | H | N | O | S | 0 | 0 |
| | | | 928 | 286 | 481 | 96 | 64 | 1 | | |

- Molecule 48 is a protein called eL40.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 48 | m | 52 | 899 | 266 | 470 | 90 | 67 | 6 | 0 | 0 |

- Molecule 49 is a protein called 60S ribosomal protein L41.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|----|----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 49 | n | 25 | 529 | 145 | 289 | 64 | 28 | 3 | 0 | 0 |

- Molecule 50 is a protein called 60S ribosomal protein L36a-like.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 50 | o | 104 | 1778 | 533 | 927 | 174 | 138 | 6 | 0 | 0 |

- Molecule 51 is a protein called 60S ribosomal protein L37a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 51 | p | 91 | 1470 | 445 | 762 | 136 | 120 | 7 | 0 | 0 |

- Molecule 52 is a RNA chain called P-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|-----|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | P |
| 52 | q | 76 | 2439 | 723 | 823 | 291 | 527 | 75 | 0 | 0 |

- Molecule 53 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|-----|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 53 | r | 124 | 2046 | 616 | 1052 | 205 | 167 | 6 | 0 | 0 |

- Molecule 54 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | P |
| 54 | u | 120 | 3854 | 1141 | 1296 | 456 | 842 | 119 | 0 | 0 |

- Molecule 55 is a RNA chain called 5.8S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|------|---------|-------|---|
| | | | Total | C | H | N | O | | | P |
| 55 | v | 156 | 4997 | 1480 | 1683 | 585 | 1094 | 155 | 0 | 0 |

- Molecule 56 is a protein called Ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace | |
|-----|-------|----------|-------|------|------|-----|-----|---------|-------|---|
| | | | Total | C | H | N | O | | | S |
| 56 | w | 394 | 6487 | 2020 | 3315 | 597 | 542 | 13 | 0 | 0 |

- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|--------------|-----------|---------|
| 57 | I | 1 | Total 1 | Mg 1 | 0 |
| 57 | K | 201 | Total 201 | Mg 201 | 0 |
| 57 | V | 1 | Total 1 | Mg 1 | 0 |
| 57 | a | 1 | Total 1 | Mg 1 | 0 |
| 57 | g | 1 | Total 1 | Mg 1 | 0 |
| 57 | j | 1 | Total 1 | Mg 1 | 0 |
| 57 | u | 7 | Total 7 | Mg 7 | 0 |
| 57 | v | 5 | Total 5 | Mg 5 | 0 |

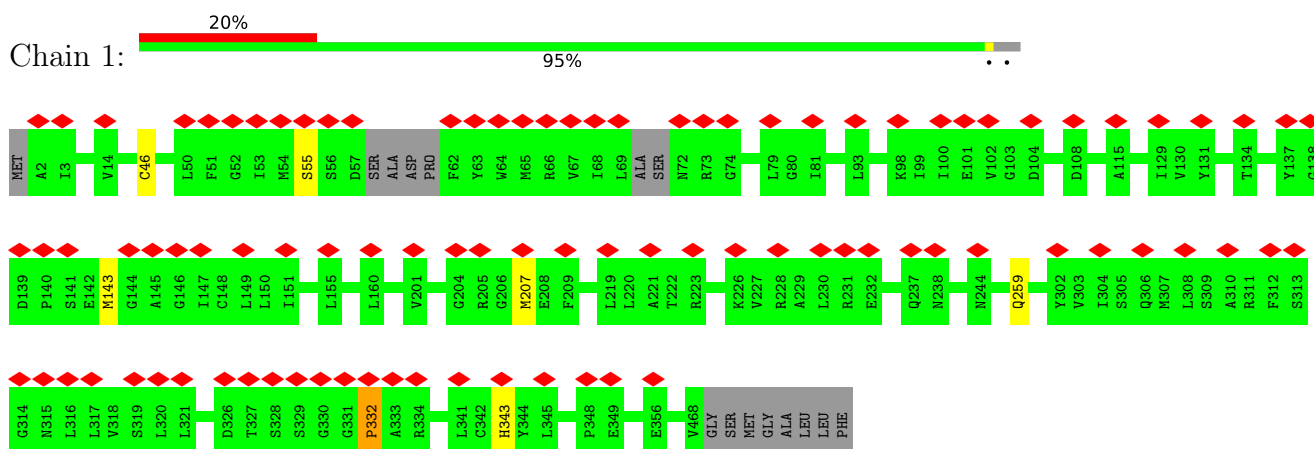
- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|---------|---------|
| 58 | g | 1 | Total 1 | Zn 1 | 0 |
| 58 | j | 1 | Total 1 | Zn 1 | 0 |
| 58 | m | 1 | Total 1 | Zn 1 | 0 |
| 58 | o | 1 | Total 1 | Zn 1 | 0 |
| 58 | p | 1 | Total 1 | Zn 1 | 0 |

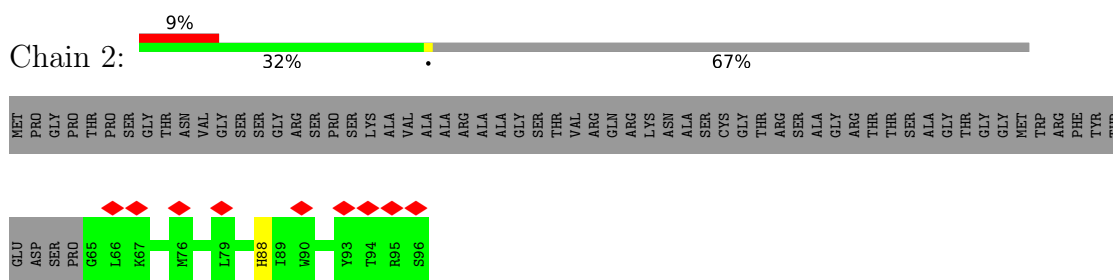
3 Residue-property plots [i](#)

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

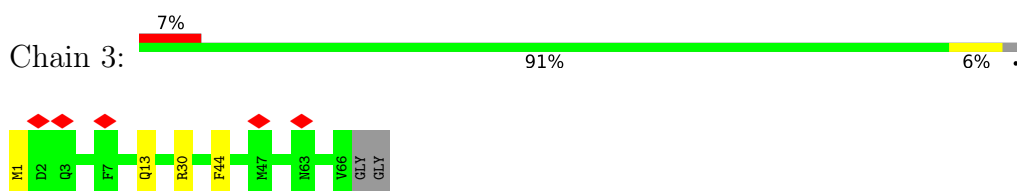
- Molecule 1: Protein transport protein Sec61 subunit alpha isoform 1



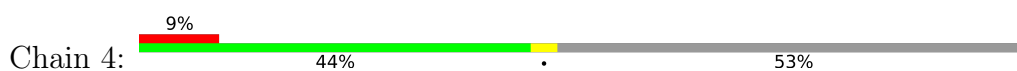
- Molecule 2: Protein transport protein Sec61 subunit beta

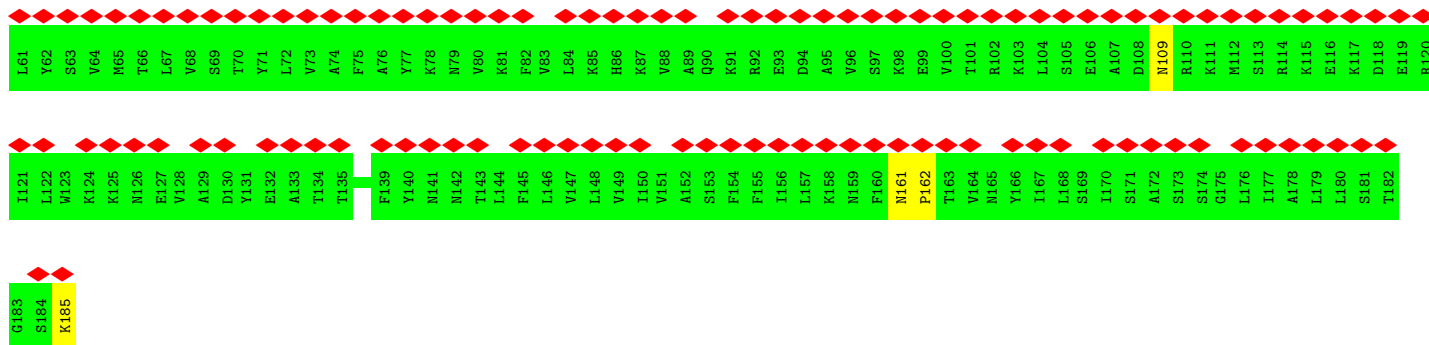


- Molecule 3: Protein transport protein Sec61 subunit gamma

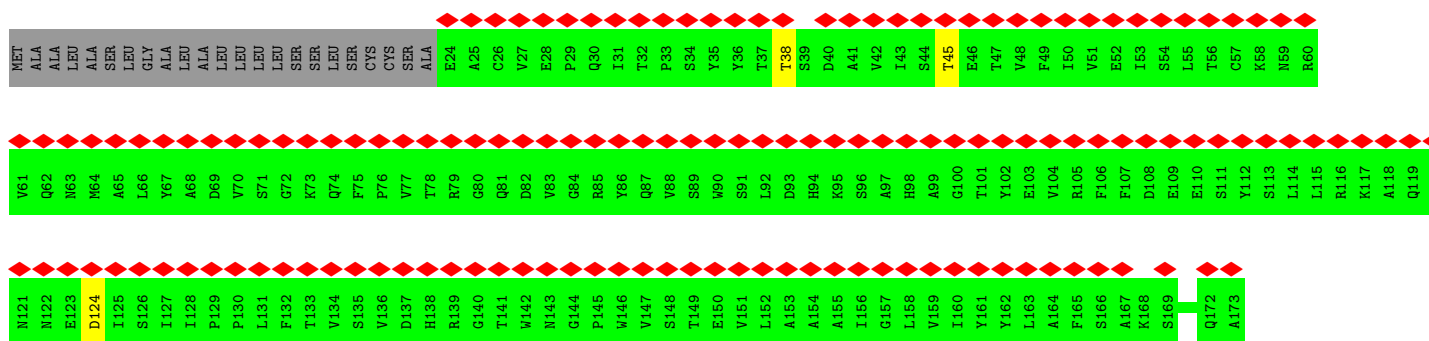
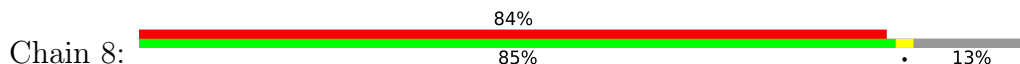


- Molecule 4: Stress-associated endoplasmic reticulum protein

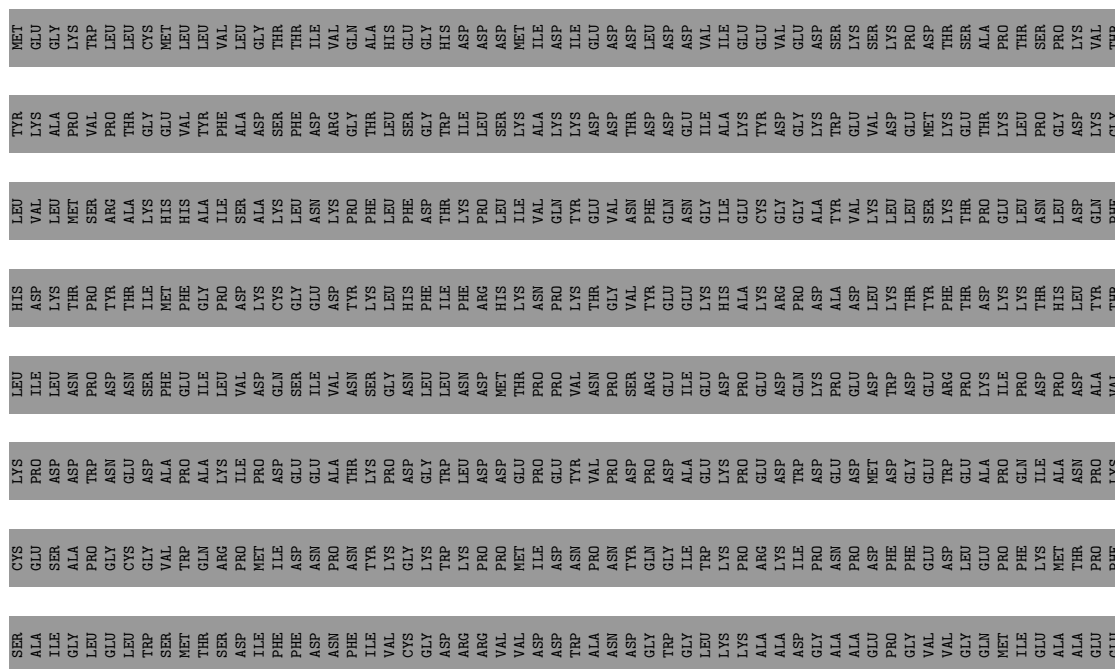


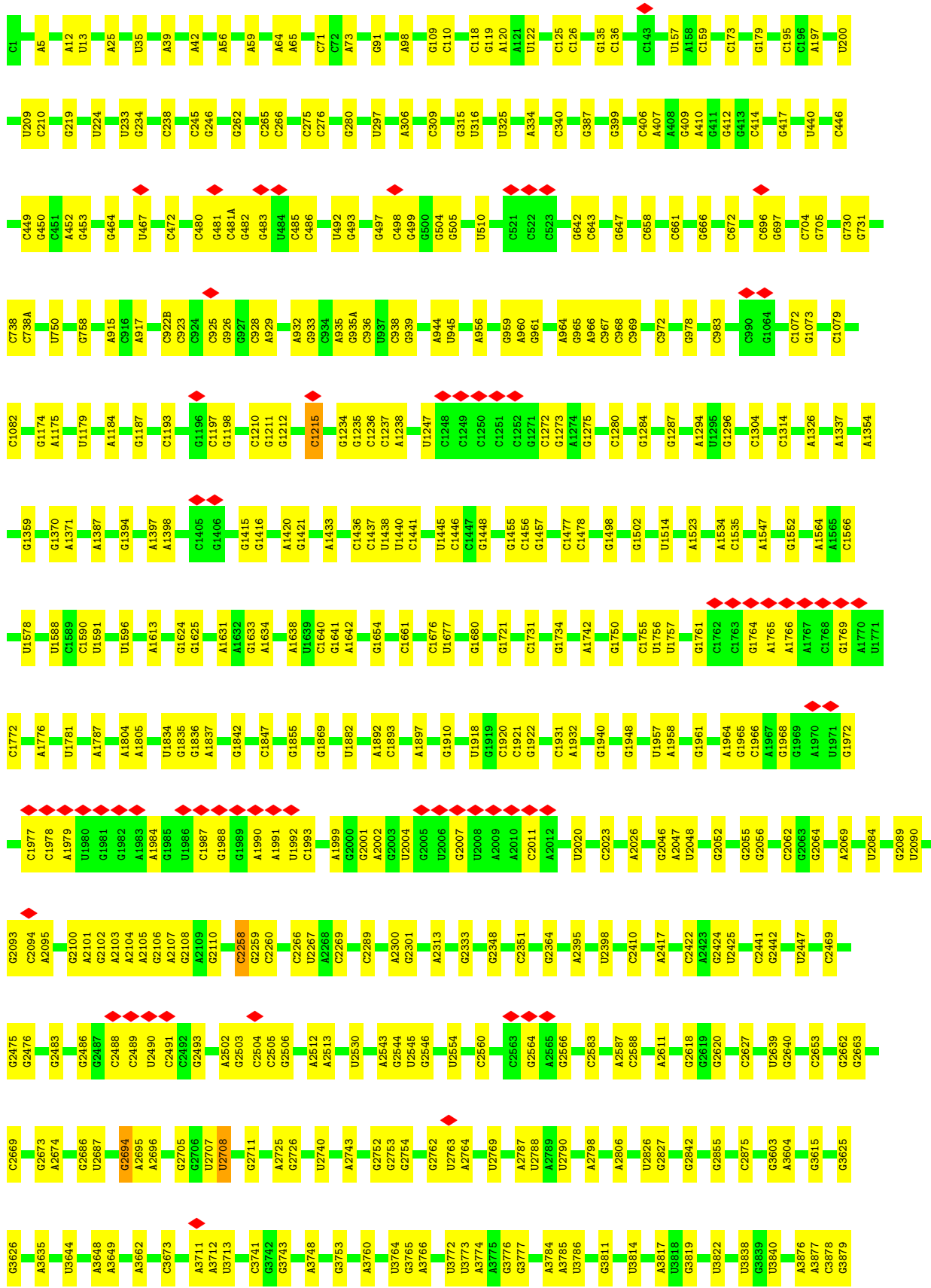


• Molecule 8: Translocon-associated protein subunit delta

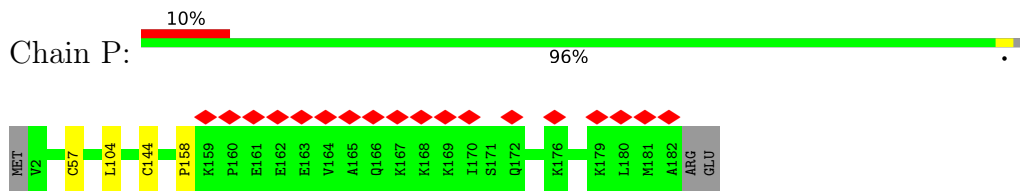


• Molecule 9: Calnexin

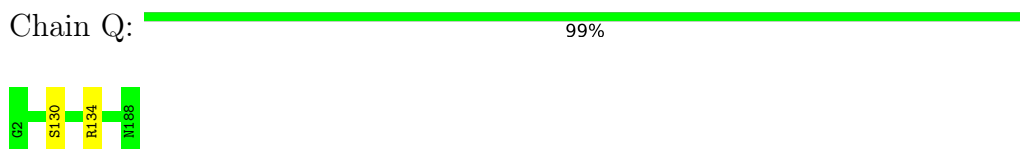




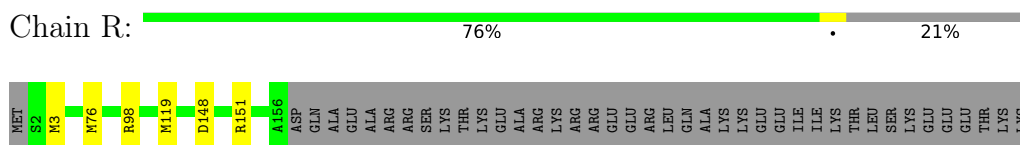
- Molecule 25: uL22



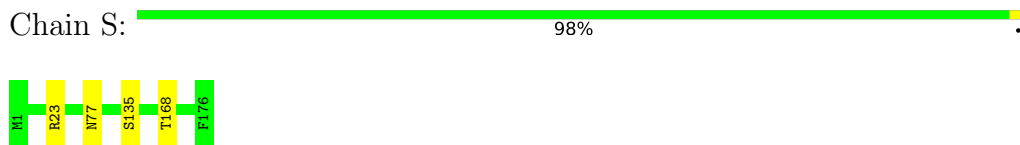
- Molecule 26: Ribosomal protein L18



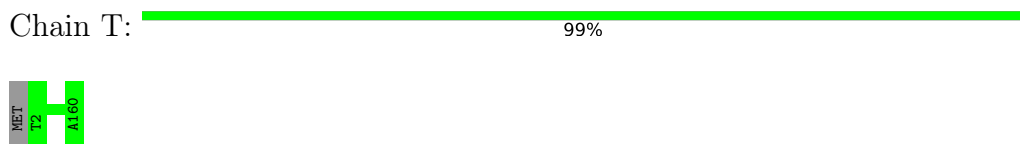
- Molecule 27: Ribosomal protein L19



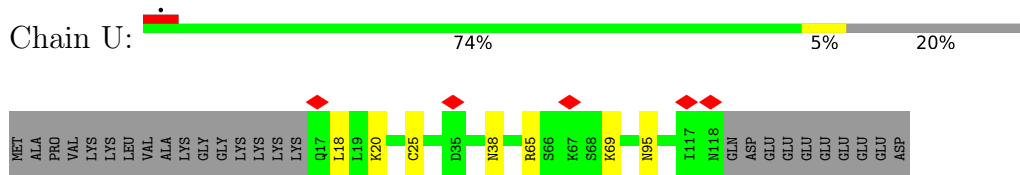
- Molecule 28: 60S ribosomal protein L18a



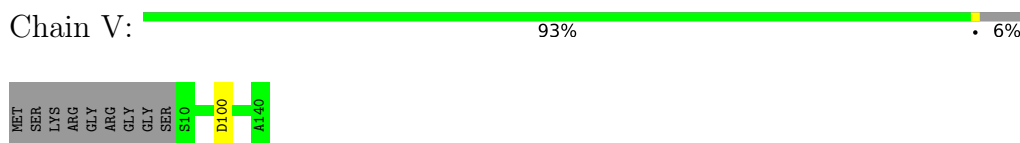
- Molecule 29: 60S ribosomal protein L21




- Molecule 30: Large ribosomal subunit protein eL22

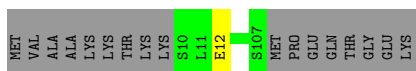


- Molecule 31: Ribosomal protein L23




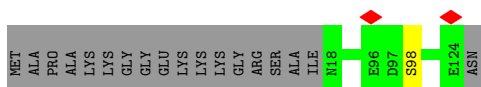
- Molecule 38: Large ribosomal subunit protein eL30

Chain c:  84% 15%



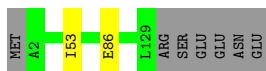
- Molecule 39: 60S ribosomal protein L31

Chain d:  85% 14%



- Molecule 40: Ribosomal protein L32

Chain e:  93% 5%



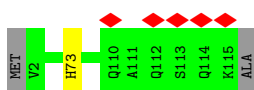
- Molecule 41: 60S ribosomal protein L35a

Chain f:  98% ..



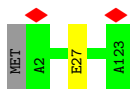
- Molecule 42: 60S ribosomal protein L34

Chain g:  97% ..



- Molecule 43: 60S ribosomal protein L35

Chain h:  98% ..




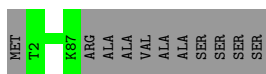
- Molecule 44: 60S ribosomal protein L36

Chain i:  93% ..



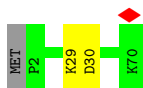
- Molecule 45: Ribosomal protein L37

Chain j:  89% 11%



- Molecule 46: Large ribosomal subunit protein eL38

Chain k:  96% ..



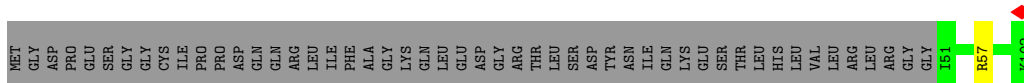
- Molecule 47: 60S ribosomal protein L39-like

Chain l:  96% ..



- Molecule 48: eL40

Chain m:  50% . 49%



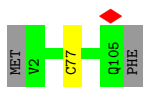
- Molecule 49: 60S ribosomal protein L41

Chain n:  96% .



- Molecule 50: 60S ribosomal protein L36a-like

Chain o:  97% ..

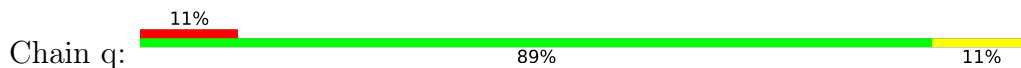


- Molecule 51: 60S ribosomal protein L37a

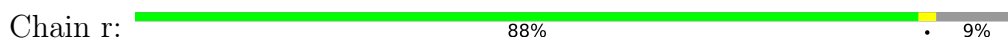
Chain p:  97% ..



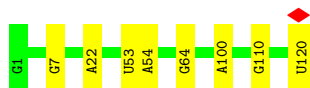
• Molecule 52: P-site tRNA



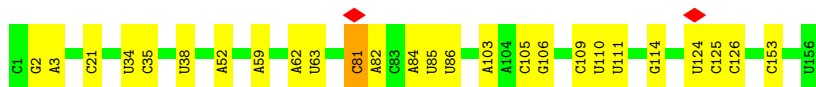
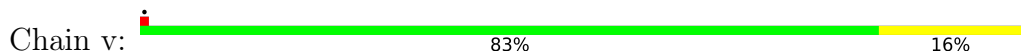
• Molecule 53: 60S ribosomal protein L28



• Molecule 54: 5S rRNA



• Molecule 55: 5.8S rRNA



• Molecule 56: Ribosomal protein L3



4 Experimental information

| Property | Value | Source |
|--------------------------------------|-------------------------------|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 282068 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | NONE | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 54 | Depositor |
| Minimum defocus (nm) | 1900 | Depositor |
| Maximum defocus (nm) | 2700 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K3 BIOQUANTUM (6k x 4k) | Depositor |
| Maximum map value | 0.218 | Depositor |
| Minimum map value | -0.064 | Depositor |
| Average map value | 0.000 | Depositor |
| Map value standard deviation | 0.007 | Depositor |
| Recommended contour level | 0.0231 | Depositor |
| Map size (\AA) | 562.7185, 562.7185, 562.7185 | wwPDB |
| Map dimensions | 420, 420, 420 | wwPDB |
| Map angles ($^\circ$) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (\AA) | 1.339806, 1.339806, 1.339806 | 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: MG, ZN

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

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------------|-------------|------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 1 | 1 | 0.31 | 1/3651 (0.0%) | 0.51 | 3/4947 (0.1%) |
| 2 | 2 | 0.29 | 0/258 | 0.42 | 0/348 |
| 3 | 3 | 0.26 | 0/544 | 0.48 | 0/728 |
| 4 | 4 | 0.26 | 0/245 | 0.54 | 0/325 |
| 5 | 5 | 0.26 | 0/1457 | 0.47 | 0/1980 |
| 6 | 6 | 0.26 | 0/1296 | 0.48 | 0/1764 |
| 7 | 7 | 0.90 | 3/1482 (0.2%) | 0.90 | 6/2001 (0.3%) |
| 8 | 8 | 0.24 | 0/1215 | 0.46 | 0/1656 |
| 9 | 9 | 0.24 | 0/311 | 0.39 | 0/427 |
| 10 | A | 0.35 | 0/1936 | 0.61 | 0/2596 |
| 11 | B | 0.27 | 0/446 | 0.48 | 0/610 |
| 12 | C | 0.32 | 0/2937 | 0.55 | 0/3946 |
| 13 | D | 0.33 | 0/2437 | 0.51 | 0/3264 |
| 14 | E | 0.30 | 0/1825 | 0.53 | 0/2445 |
| 15 | F | 0.34 | 0/1911 | 0.55 | 0/2549 |
| 16 | G | 0.30 | 0/1910 | 0.51 | 0/2569 |
| 17 | H | 0.31 | 0/1535 | 0.54 | 0/2063 |
| 18 | I | 0.33 | 0/1702 | 0.55 | 0/2272 |
| 19 | J | 0.30 | 0/1385 | 0.55 | 0/1852 |
| 20 | K | 0.67 | 0/84980 | 0.81 | 14/132536 (0.0%) |
| 21 | L | 0.31 | 0/1733 | 0.59 | 0/2316 |
| 22 | M | 0.32 | 0/1158 | 0.56 | 1/1547 (0.1%) |
| 23 | N | 0.37 | 0/1746 | 0.61 | 0/2338 |
| 24 | O | 0.34 | 0/1662 | 0.54 | 0/2222 |
| 25 | P | 0.39 | 1/1498 (0.1%) | 0.69 | 3/2003 (0.1%) |
| 26 | Q | 0.34 | 0/1539 | 0.60 | 0/2054 |
| 27 | R | 0.30 | 0/1310 | 0.58 | 0/1734 |
| 28 | S | 0.36 | 0/1501 | 0.55 | 0/2012 |
| 29 | T | 0.34 | 0/1326 | 0.56 | 0/1770 |
| 30 | U | 0.30 | 0/848 | 0.50 | 0/1138 |
| 31 | V | 0.33 | 0/993 | 0.52 | 0/1332 |
| 32 | W | 0.36 | 0/541 | 0.53 | 0/720 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-----------------|-------------|------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 33 | X | 0.32 | 0/984 | 0.50 | 0/1323 |
| 34 | Y | 0.32 | 0/1132 | 0.55 | 0/1504 |
| 35 | Z | 0.34 | 0/1130 | 0.53 | 0/1507 |
| 36 | a | 0.34 | 0/1191 | 0.55 | 0/1590 |
| 37 | b | 0.28 | 0/861 | 0.54 | 0/1138 |
| 38 | c | 0.33 | 0/771 | 0.48 | 0/1034 |
| 39 | d | 0.34 | 0/903 | 0.56 | 0/1216 |
| 40 | e | 0.34 | 0/1071 | 0.57 | 0/1429 |
| 41 | f | 0.37 | 0/895 | 0.58 | 0/1198 |
| 42 | g | 0.34 | 0/916 | 0.59 | 0/1220 |
| 43 | h | 0.30 | 0/1021 | 0.54 | 0/1348 |
| 44 | i | 0.30 | 0/841 | 0.58 | 0/1112 |
| 45 | j | 0.37 | 0/720 | 0.63 | 0/952 |
| 46 | k | 0.31 | 0/575 | 0.50 | 0/761 |
| 47 | l | 0.31 | 0/459 | 0.57 | 0/608 |
| 48 | m | 0.32 | 0/435 | 0.55 | 0/575 |
| 49 | n | 0.26 | 0/241 | 0.75 | 0/305 |
| 50 | o | 0.33 | 0/864 | 0.56 | 0/1140 |
| 51 | p | 0.34 | 0/718 | 0.60 | 0/953 |
| 52 | q | 0.27 | 0/1805 | 0.75 | 0/2809 |
| 53 | r | 0.33 | 0/1010 | 0.58 | 0/1354 |
| 54 | u | 0.67 | 0/2858 | 0.77 | 0/4455 |
| 55 | v | 0.67 | 0/3701 | 0.80 | 1/5766 (0.0%) |
| 56 | w | 0.34 | 0/3240 | 0.53 | 0/4339 |
| All | All | 0.56 | 5/157660 (0.0%) | 0.72 | 28/231700 (0.0%) |

All (5) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|--------|-------------|----------|
| 7 | 7 | 162 | PRO | CG-CD | -27.68 | 0.59 | 1.50 |
| 7 | 7 | 162 | PRO | CB-CG | 16.64 | 2.33 | 1.50 |
| 1 | 1 | 332 | PRO | CG-CD | -8.29 | 1.23 | 1.50 |
| 7 | 7 | 162 | PRO | N-CD | 5.66 | 1.55 | 1.47 |
| 25 | P | 158 | PRO | CG-CD | -5.51 | 1.32 | 1.50 |

The worst 5 of 28 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|--------|-------------|----------|
| 7 | 7 | 162 | PRO | CB-CG-CD | -27.28 | 0.11 | 106.50 |
| 25 | P | 158 | PRO | N-CD-CG | -15.91 | 79.33 | 103.20 |
| 7 | 7 | 161 | ASN | C-N-CD | 13.51 | 156.78 | 128.40 |
| 7 | 7 | 162 | PRO | CA-N-CD | -12.49 | 94.01 | 111.50 |

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| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|--------|-------------|----------|
| 1 | 1 | 332 | PRO | CA-CB-CG | -11.07 | 82.97 | 104.00 |

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 | |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 1 | 1 | 455/476 (96%) | 440 (97%) | 15 (3%) | 0 | 100 | 100 |
| 2 | 2 | 30/96 (31%) | 29 (97%) | 1 (3%) | 0 | 100 | 100 |
| 3 | 3 | 64/68 (94%) | 61 (95%) | 3 (5%) | 0 | 100 | 100 |
| 4 | 4 | 29/66 (44%) | 29 (100%) | 0 | 0 | 100 | 100 |
| 5 | 5 | 174/286 (61%) | 171 (98%) | 3 (2%) | 0 | 100 | 100 |
| 6 | 6 | 160/183 (87%) | 158 (99%) | 2 (1%) | 0 | 100 | 100 |
| 7 | 7 | 177/185 (96%) | 174 (98%) | 3 (2%) | 0 | 100 | 100 |
| 8 | 8 | 148/173 (86%) | 146 (99%) | 2 (1%) | 0 | 100 | 100 |
| 9 | 9 | 34/593 (6%) | 34 (100%) | 0 | 0 | 100 | 100 |
| 10 | A | 246/257 (96%) | 239 (97%) | 7 (3%) | 0 | 100 | 100 |
| 11 | B | 57/229 (25%) | 50 (88%) | 7 (12%) | 0 | 100 | 100 |
| 12 | C | 360/425 (85%) | 352 (98%) | 8 (2%) | 0 | 100 | 100 |
| 13 | D | 291/297 (98%) | 286 (98%) | 5 (2%) | 0 | 100 | 100 |
| 14 | E | 215/291 (74%) | 209 (97%) | 6 (3%) | 0 | 100 | 100 |
| 15 | F | 223/247 (90%) | 215 (96%) | 8 (4%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|------------|---------|----------|-------------|-----|
| 16 | G | 229/319 (72%) | 228 (100%) | 1 (0%) | 0 | 100 | 100 |
| 17 | H | 188/192 (98%) | 186 (99%) | 2 (1%) | 0 | 100 | 100 |
| 18 | I | 201/214 (94%) | 199 (99%) | 2 (1%) | 0 | 100 | 100 |
| 19 | J | 168/178 (94%) | 166 (99%) | 2 (1%) | 0 | 100 | 100 |
| 21 | L | 208/211 (99%) | 203 (98%) | 5 (2%) | 0 | 100 | 100 |
| 22 | M | 136/218 (62%) | 132 (97%) | 4 (3%) | 0 | 100 | 100 |
| 23 | N | 201/204 (98%) | 198 (98%) | 3 (2%) | 0 | 100 | 100 |
| 24 | O | 197/203 (97%) | 194 (98%) | 3 (2%) | 0 | 100 | 100 |
| 25 | P | 179/184 (97%) | 175 (98%) | 4 (2%) | 0 | 100 | 100 |
| 26 | Q | 185/187 (99%) | 181 (98%) | 4 (2%) | 0 | 100 | 100 |
| 27 | R | 153/196 (78%) | 152 (99%) | 1 (1%) | 0 | 100 | 100 |
| 28 | S | 174/176 (99%) | 170 (98%) | 4 (2%) | 0 | 100 | 100 |
| 29 | T | 157/160 (98%) | 154 (98%) | 3 (2%) | 0 | 100 | 100 |
| 30 | U | 100/128 (78%) | 97 (97%) | 3 (3%) | 0 | 100 | 100 |
| 31 | V | 129/140 (92%) | 128 (99%) | 1 (1%) | 0 | 100 | 100 |
| 32 | W | 61/157 (39%) | 61 (100%) | 0 | 0 | 100 | 100 |
| 33 | X | 116/156 (74%) | 113 (97%) | 3 (3%) | 0 | 100 | 100 |
| 34 | Y | 132/145 (91%) | 128 (97%) | 4 (3%) | 0 | 100 | 100 |
| 35 | Z | 133/136 (98%) | 131 (98%) | 2 (2%) | 0 | 100 | 100 |
| 36 | a | 145/148 (98%) | 138 (95%) | 6 (4%) | 1 (1%) | 22 | 50 |
| 37 | b | 100/226 (44%) | 98 (98%) | 2 (2%) | 0 | 100 | 100 |
| 38 | c | 96/115 (84%) | 96 (100%) | 0 | 0 | 100 | 100 |
| 39 | d | 105/125 (84%) | 105 (100%) | 0 | 0 | 100 | 100 |
| 40 | e | 126/135 (93%) | 121 (96%) | 5 (4%) | 0 | 100 | 100 |
| 41 | f | 107/110 (97%) | 105 (98%) | 2 (2%) | 0 | 100 | 100 |
| 42 | g | 112/116 (97%) | 110 (98%) | 2 (2%) | 0 | 100 | 100 |
| 43 | h | 120/123 (98%) | 118 (98%) | 2 (2%) | 0 | 100 | 100 |
| 44 | i | 100/105 (95%) | 97 (97%) | 3 (3%) | 0 | 100 | 100 |
| 45 | j | 84/97 (87%) | 83 (99%) | 1 (1%) | 0 | 100 | 100 |
| 46 | k | 67/70 (96%) | 67 (100%) | 0 | 0 | 100 | 100 |
| 47 | l | 48/51 (94%) | 48 (100%) | 0 | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 48 | m | 50/102 (49%) | 50 (100%) | 0 | 0 | 100 | 100 |
| 49 | n | 23/25 (92%) | 23 (100%) | 0 | 0 | 100 | 100 |
| 50 | o | 102/106 (96%) | 99 (97%) | 3 (3%) | 0 | 100 | 100 |
| 51 | p | 89/92 (97%) | 84 (94%) | 5 (6%) | 0 | 100 | 100 |
| 53 | r | 122/137 (89%) | 119 (98%) | 3 (2%) | 0 | 100 | 100 |
| 56 | w | 392/403 (97%) | 384 (98%) | 8 (2%) | 0 | 100 | 100 |
| All | All | 7698/9662 (80%) | 7534 (98%) | 163 (2%) | 1 (0%) | 100 | 100 |

All (1) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 36 | a | 40 | HIS |

5.3.2 Protein sidechains [i](#)

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|-------------|-----|
| 1 | 1 | 388/398 (98%) | 381 (98%) | 7 (2%) | 59 | 84 |
| 2 | 2 | 28/74 (38%) | 27 (96%) | 1 (4%) | 35 | 66 |
| 3 | 3 | 59/59 (100%) | 55 (93%) | 4 (7%) | 16 | 39 |
| 4 | 4 | 26/55 (47%) | 24 (92%) | 2 (8%) | 13 | 32 |
| 5 | 5 | 157/249 (63%) | 151 (96%) | 6 (4%) | 33 | 64 |
| 6 | 6 | 135/152 (89%) | 133 (98%) | 2 (2%) | 65 | 87 |
| 7 | 7 | 161/164 (98%) | 157 (98%) | 4 (2%) | 47 | 77 |
| 8 | 8 | 130/146 (89%) | 127 (98%) | 3 (2%) | 50 | 79 |
| 9 | 9 | 35/526 (7%) | 35 (100%) | 0 | 100 | 100 |
| 10 | A | 190/199 (96%) | 188 (99%) | 2 (1%) | 73 | 90 |
| 11 | B | 48/172 (28%) | 46 (96%) | 2 (4%) | 30 | 60 |
| 12 | C | 302/347 (87%) | 297 (98%) | 5 (2%) | 60 | 85 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 13 | D | 247/250 (99%) | 242 (98%) | 5 (2%) | 55 | 82 |
| 14 | E | 197/251 (78%) | 196 (100%) | 1 (0%) | 88 | 95 |
| 15 | F | 196/215 (91%) | 195 (100%) | 1 (0%) | 88 | 95 |
| 16 | G | 200/272 (74%) | 196 (98%) | 4 (2%) | 55 | 82 |
| 17 | H | 169/171 (99%) | 164 (97%) | 5 (3%) | 41 | 72 |
| 18 | I | 175/181 (97%) | 174 (99%) | 1 (1%) | 86 | 95 |
| 19 | J | 143/149 (96%) | 140 (98%) | 3 (2%) | 53 | 81 |
| 21 | L | 175/176 (99%) | 172 (98%) | 3 (2%) | 60 | 85 |
| 22 | M | 117/161 (73%) | 115 (98%) | 2 (2%) | 60 | 85 |
| 23 | N | 171/172 (99%) | 169 (99%) | 2 (1%) | 71 | 90 |
| 24 | O | 171/173 (99%) | 166 (97%) | 5 (3%) | 42 | 73 |
| 25 | P | 160/163 (98%) | 157 (98%) | 3 (2%) | 57 | 83 |
| 26 | Q | 164/164 (100%) | 162 (99%) | 2 (1%) | 71 | 90 |
| 27 | R | 138/175 (79%) | 132 (96%) | 6 (4%) | 29 | 59 |
| 28 | S | 157/157 (100%) | 153 (98%) | 4 (2%) | 47 | 77 |
| 29 | T | 139/140 (99%) | 139 (100%) | 0 | 100 | 100 |
| 30 | U | 92/114 (81%) | 85 (92%) | 7 (8%) | 13 | 33 |
| 31 | V | 101/107 (94%) | 100 (99%) | 1 (1%) | 76 | 91 |
| 32 | W | 55/126 (44%) | 54 (98%) | 1 (2%) | 59 | 84 |
| 33 | X | 106/134 (79%) | 105 (99%) | 1 (1%) | 78 | 92 |
| 34 | Y | 124/135 (92%) | 122 (98%) | 2 (2%) | 62 | 86 |
| 35 | Z | 117/118 (99%) | 113 (97%) | 4 (3%) | 37 | 68 |
| 36 | a | 119/120 (99%) | 119 (100%) | 0 | 100 | 100 |
| 37 | b | 84/172 (49%) | 83 (99%) | 1 (1%) | 71 | 90 |
| 38 | c | 84/98 (86%) | 83 (99%) | 1 (1%) | 71 | 90 |
| 39 | d | 98/110 (89%) | 97 (99%) | 1 (1%) | 76 | 91 |
| 40 | e | 114/121 (94%) | 112 (98%) | 2 (2%) | 59 | 84 |
| 41 | f | 88/89 (99%) | 87 (99%) | 1 (1%) | 73 | 90 |
| 42 | g | 98/99 (99%) | 97 (99%) | 1 (1%) | 76 | 91 |
| 43 | h | 109/110 (99%) | 108 (99%) | 1 (1%) | 78 | 92 |
| 44 | i | 86/89 (97%) | 82 (95%) | 4 (5%) | 26 | 56 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|-------------|-----|
| 45 | j | 73/80 (91%) | 73 (100%) | 0 | 100 | 100 |
| 46 | k | 64/65 (98%) | 62 (97%) | 2 (3%) | 40 | 71 |
| 47 | l | 47/48 (98%) | 46 (98%) | 1 (2%) | 53 | 81 |
| 48 | m | 48/90 (53%) | 47 (98%) | 1 (2%) | 53 | 81 |
| 49 | n | 24/24 (100%) | 23 (96%) | 1 (4%) | 30 | 60 |
| 50 | o | 92/94 (98%) | 91 (99%) | 1 (1%) | 73 | 90 |
| 51 | p | 74/75 (99%) | 72 (97%) | 2 (3%) | 44 | 75 |
| 53 | r | 108/121 (89%) | 105 (97%) | 3 (3%) | 43 | 74 |
| 56 | w | 342/348 (98%) | 336 (98%) | 6 (2%) | 59 | 84 |
| All | All | 6725/8198 (82%) | 6595 (98%) | 130 (2%) | 59 | 83 |

5 of 130 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 47 | l | 5 | LYS |
| 51 | p | 26 | VAL |
| 16 | G | 284 | ASP |
| 16 | G | 173 | LYS |
| 53 | r | 26 | SER |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 27 | R | 75 | HIS |
| 36 | a | 28 | HIS |
| 44 | i | 20 | ASN |

5.3.3 RNA [i](#)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 20 | K | 3521/3543 (99%) | 589 (16%) | 55 (1%) |
| 52 | q | 74/76 (97%) | 8 (10%) | 0 |
| 54 | u | 119/120 (99%) | 8 (6%) | 0 |
| 55 | v | 155/156 (99%) | 26 (16%) | 0 |
| All | All | 3869/3895 (99%) | 631 (16%) | 55 (1%) |

5 of 631 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 20 | K | 5 | A |
| 20 | K | 12 | A |
| 20 | K | 13 | U |
| 20 | K | 25 | A |
| 20 | K | 35 | U |

5 of 55 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 20 | K | 1990 | A |
| 20 | K | 2266 | C |
| 20 | K | 4947 | U |
| 20 | K | 4232 | U |
| 20 | K | 1992 | U |

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 223 ligands modelled in this entry, 223 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 20 | K | 23 |
| 52 | q | 1 |

The worst 5 of 24 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | K | 2113:G | O3' | 2258:C | P | 41.92 |
| 1 | K | 1252:C | O3' | 1271:G | P | 35.44 |
| 1 | K | 1219:G | O3' | 1233:G | P | 24.79 |
| 1 | K | 4138:C | O3' | 4146:G | P | 17.60 |
| 1 | K | 990:C | O3' | 1064:G | P | 17.52 |

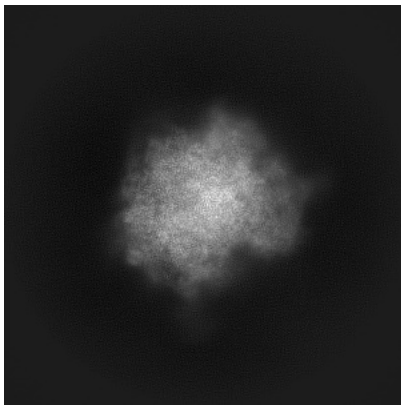
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19198. These allow visual inspection of the internal detail of the map and identification of artifacts.

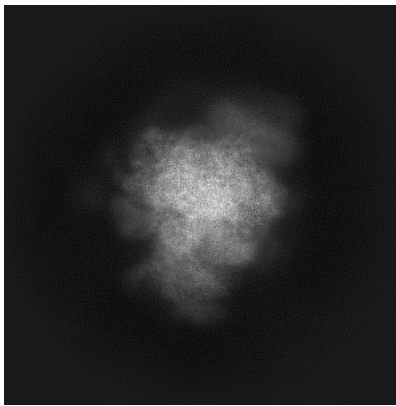
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

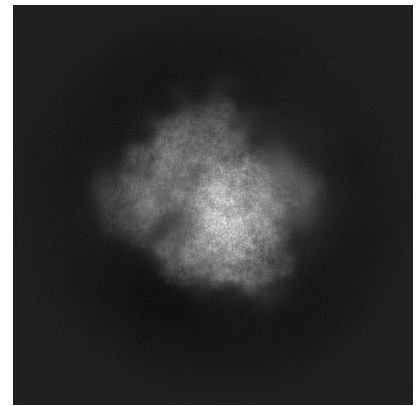
6.1.1 Primary map



X

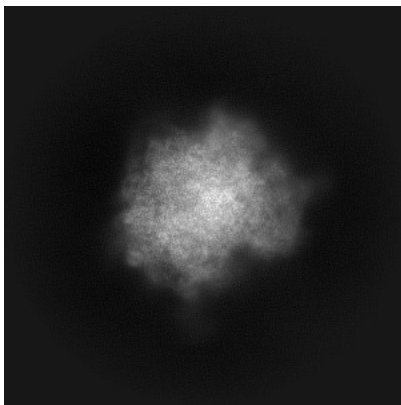


Y

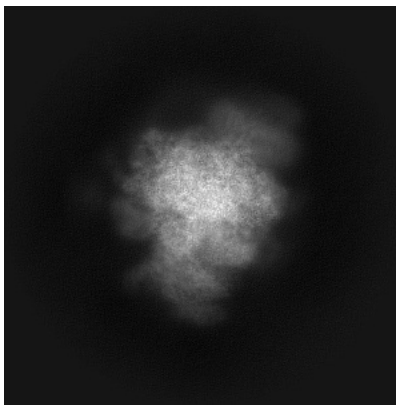


Z

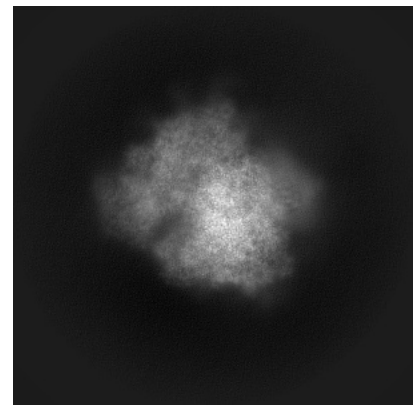
6.1.2 Raw map



X



Y

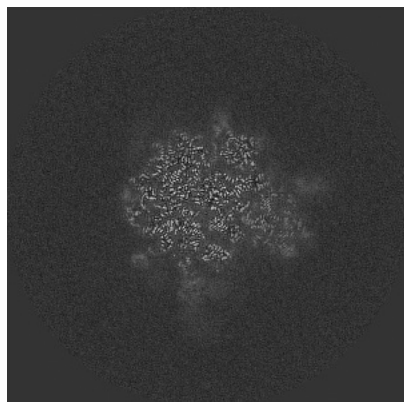


Z

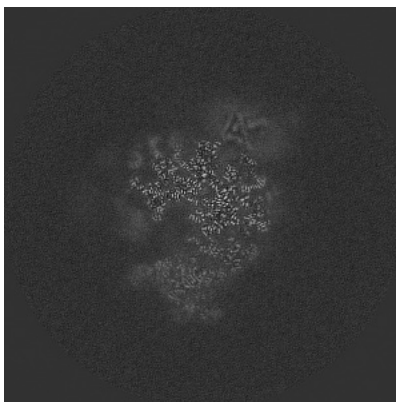
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

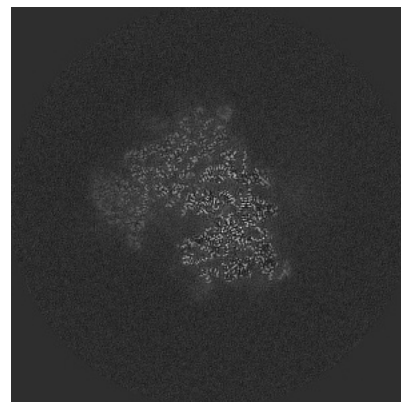
6.2.1 Primary map



X Index: 210

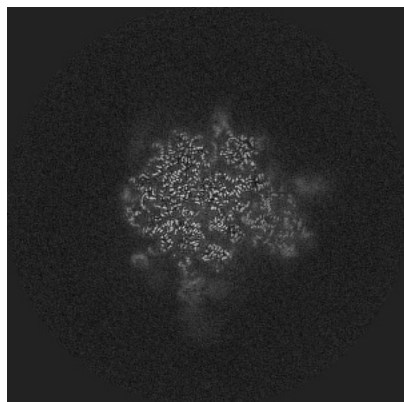


Y Index: 210

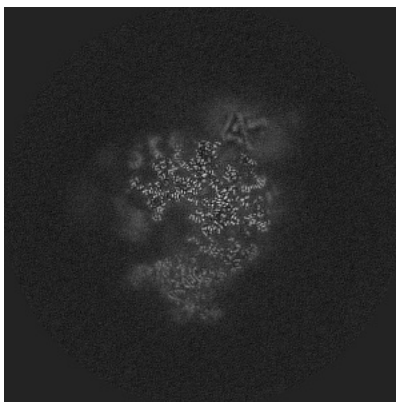


Z Index: 210

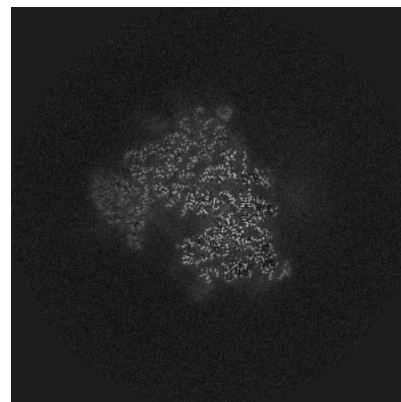
6.2.2 Raw map



X Index: 210



Y Index: 210

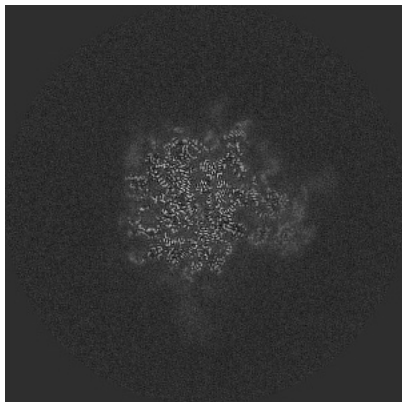


Z Index: 210

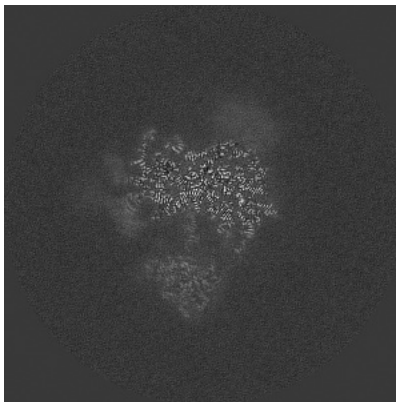
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

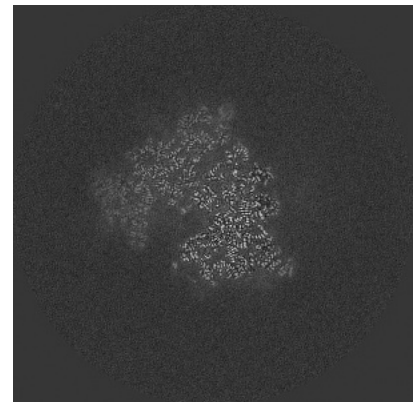
6.3.1 Primary map



X Index: 220

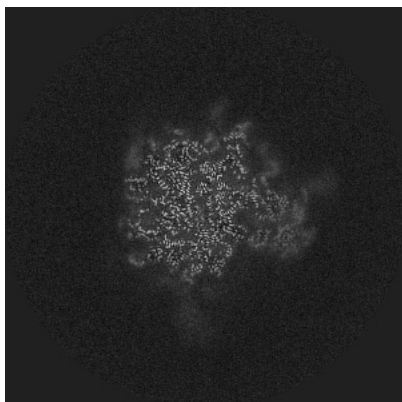


Y Index: 195

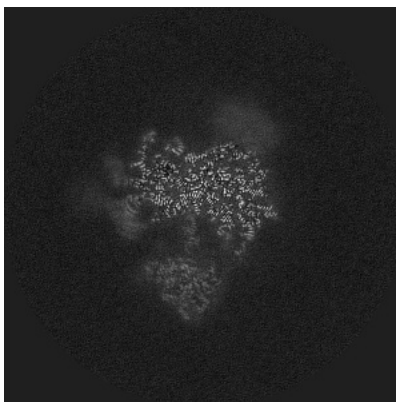


Z Index: 207

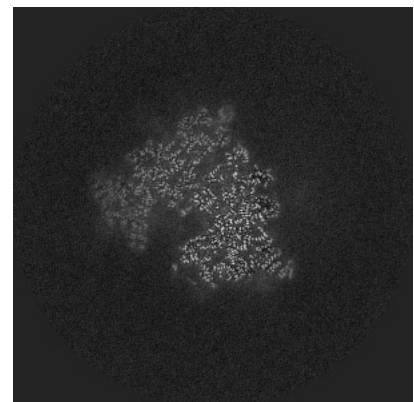
6.3.2 Raw map



X Index: 220



Y Index: 195

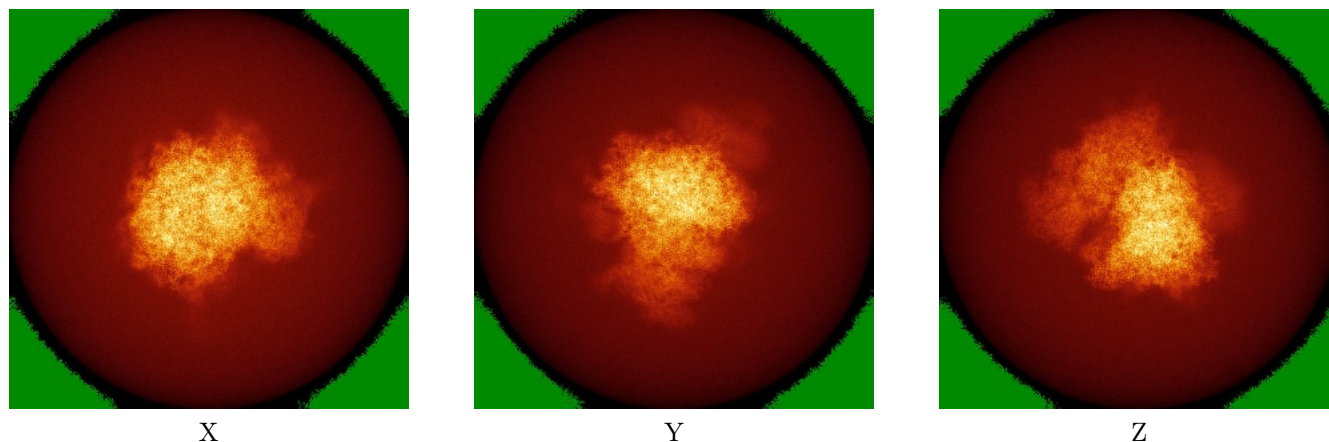


Z Index: 207

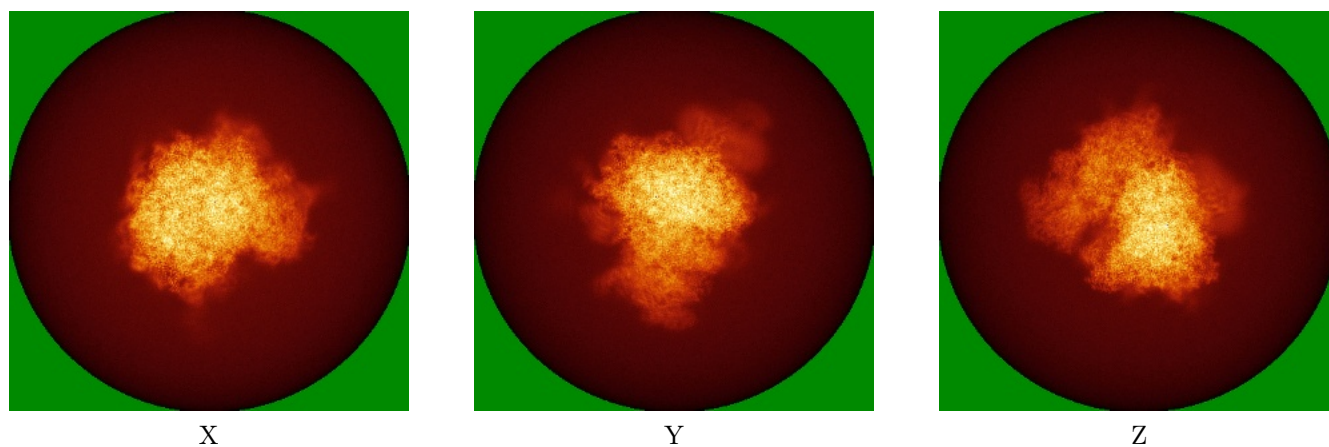
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



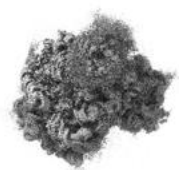
6.4.2 Raw map



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



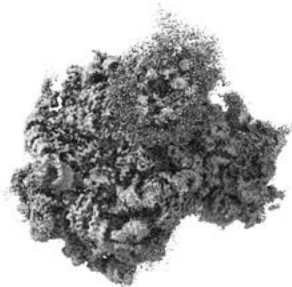
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0231. 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.

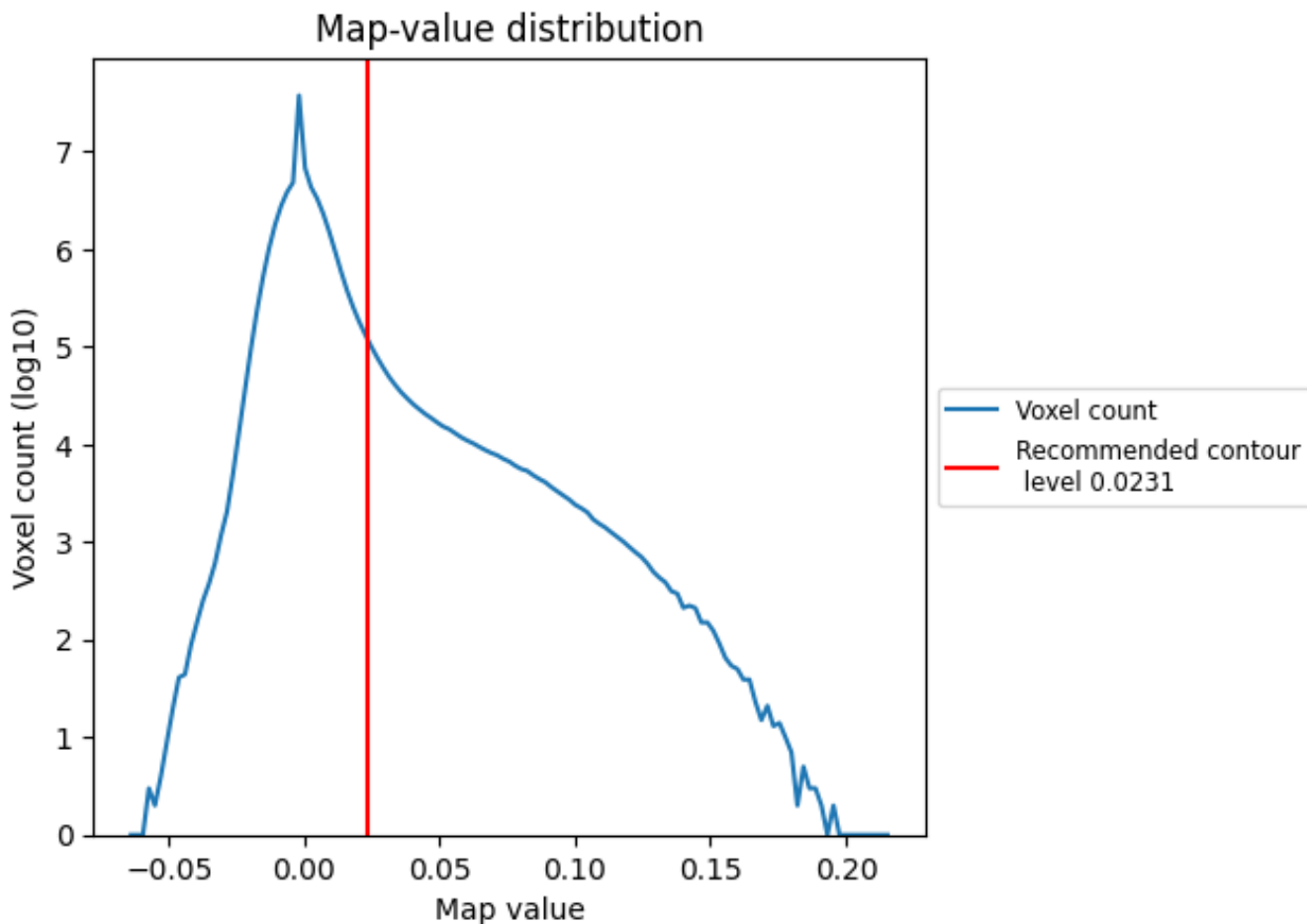
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

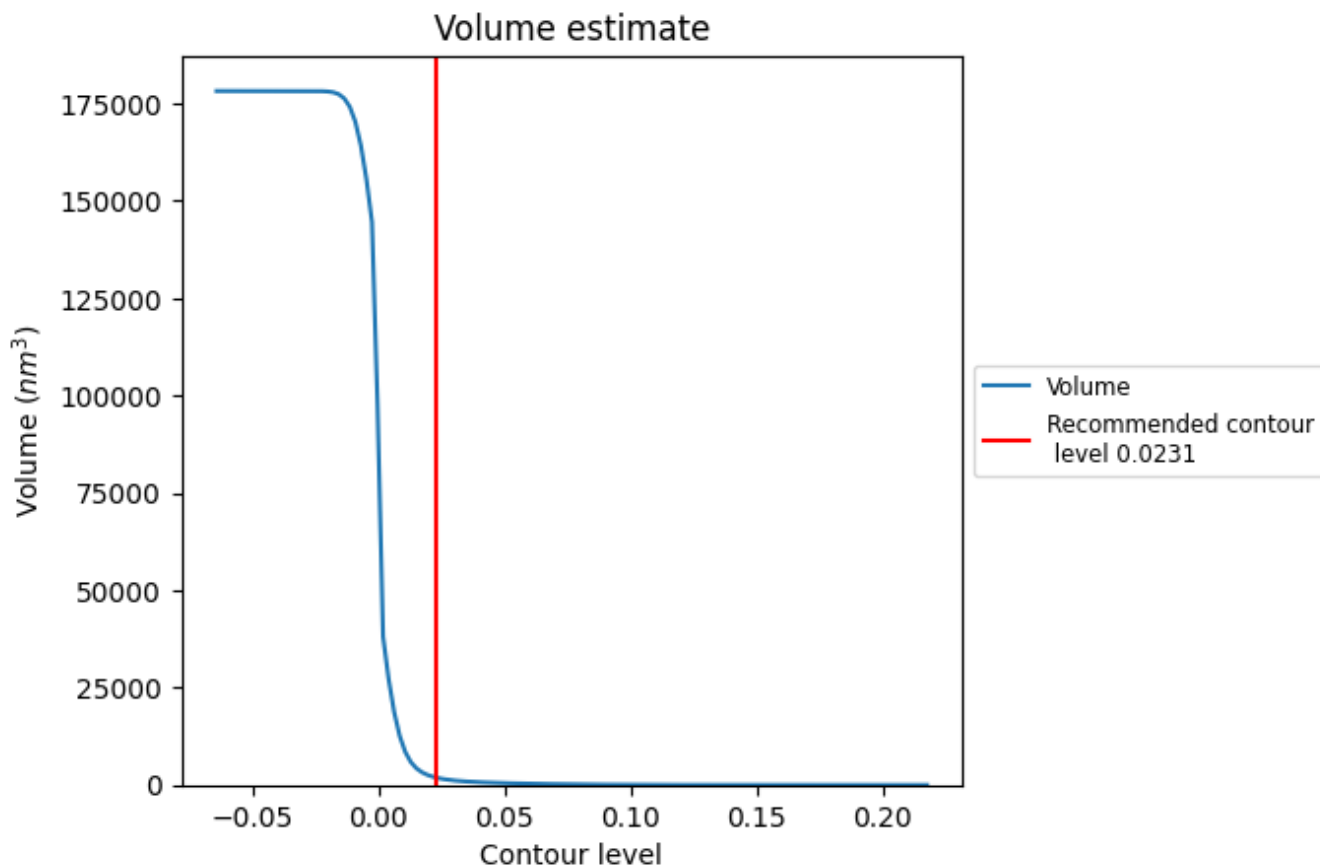
This section contains the results of statistical analysis of the map.

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.

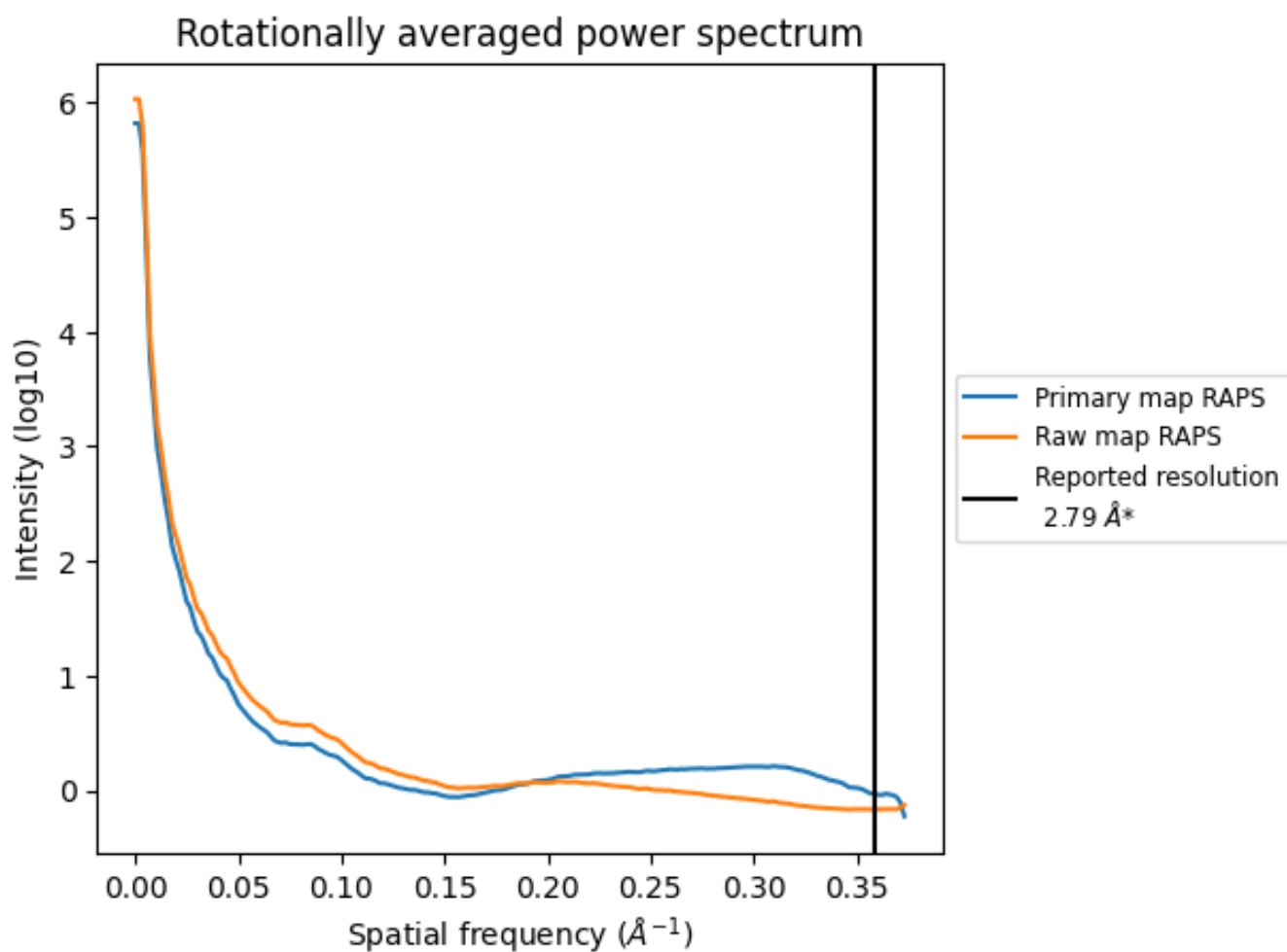
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1884 nm^3 ; this corresponds to an approximate mass of 1702 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

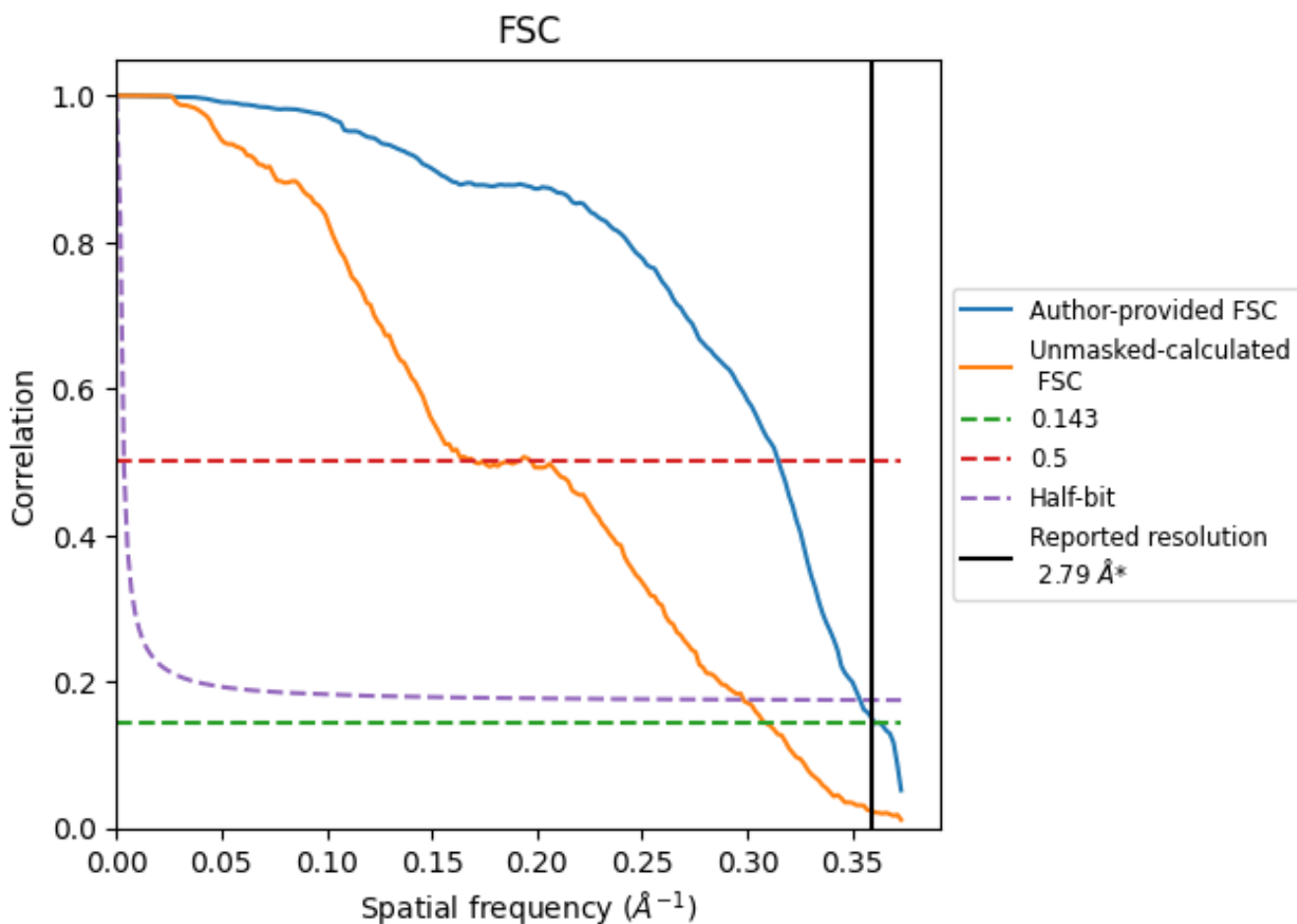


*Reported resolution corresponds to spatial frequency of 0.359 Å⁻¹

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 0.359 Å⁻¹

8.2 Resolution estimates [i](#)

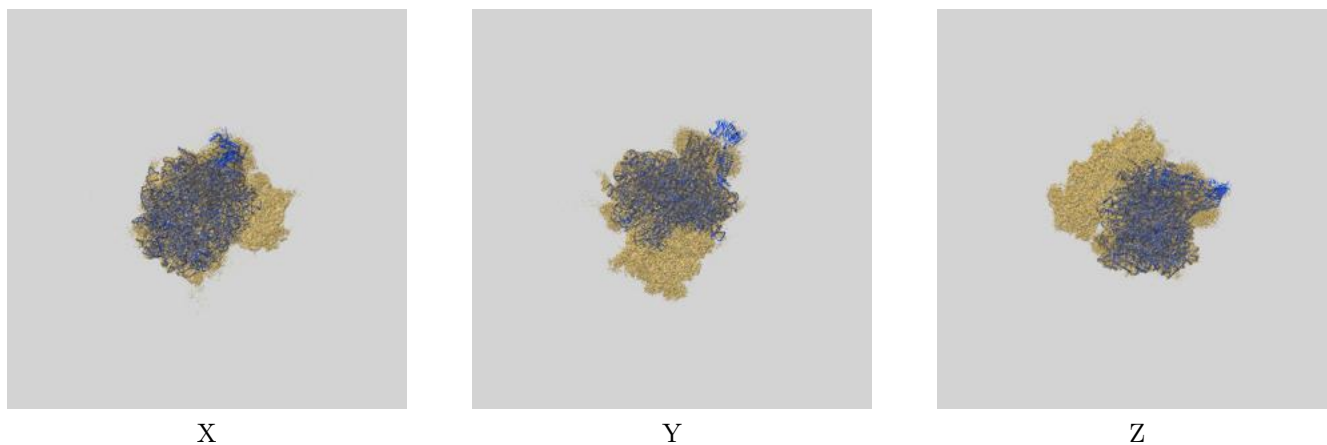
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 2.79 | - | - |
| Author-provided FSC curve | 2.77 | 3.18 | 2.83 |
| Unmasked-calculated* | 3.24 | 5.87 | 3.35 |

*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 3.24 differs from the reported value 2.78574 by more than 10 %

9 Map-model fit [i](#)

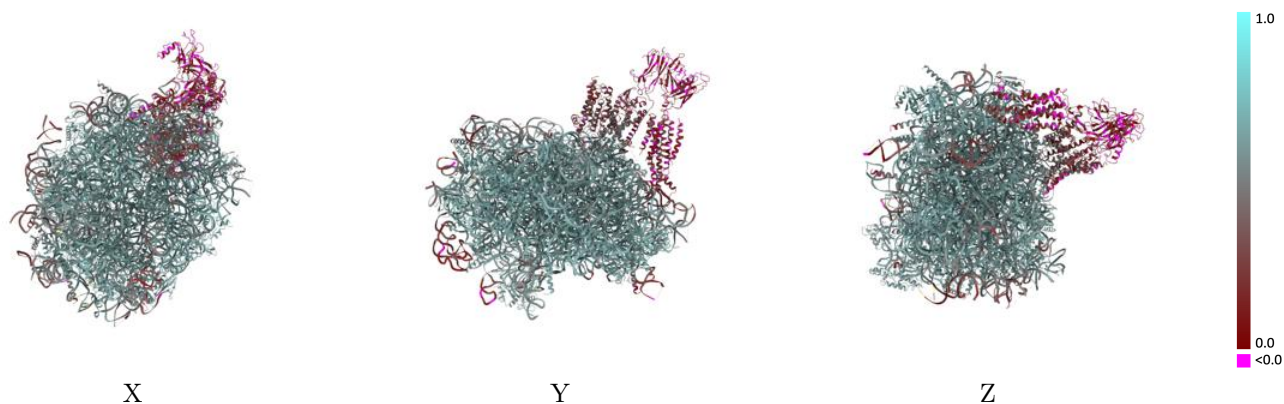
This section contains information regarding the fit between EMDB map EMD-19198 and PDB model 8RJD. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



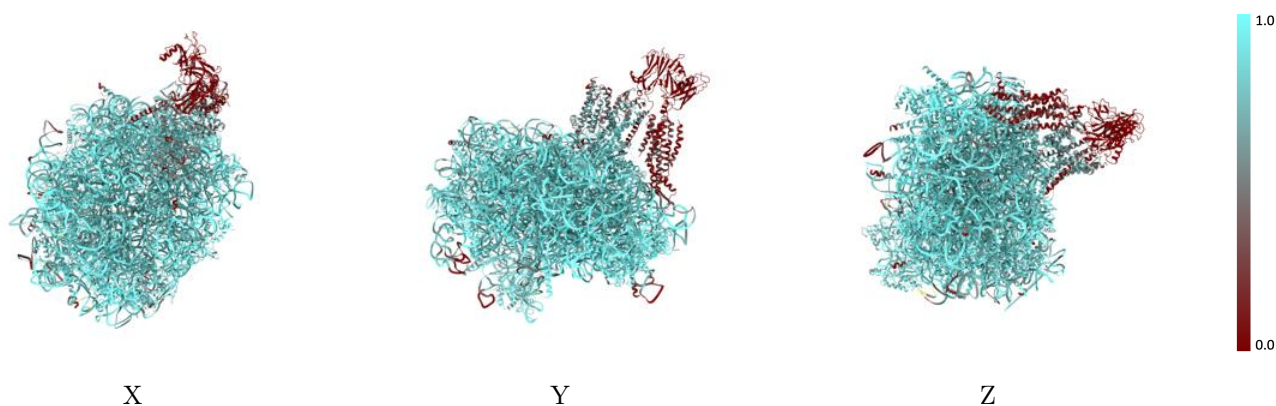
The images above show the 3D surface view of the map at the recommended contour level 0.0231 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



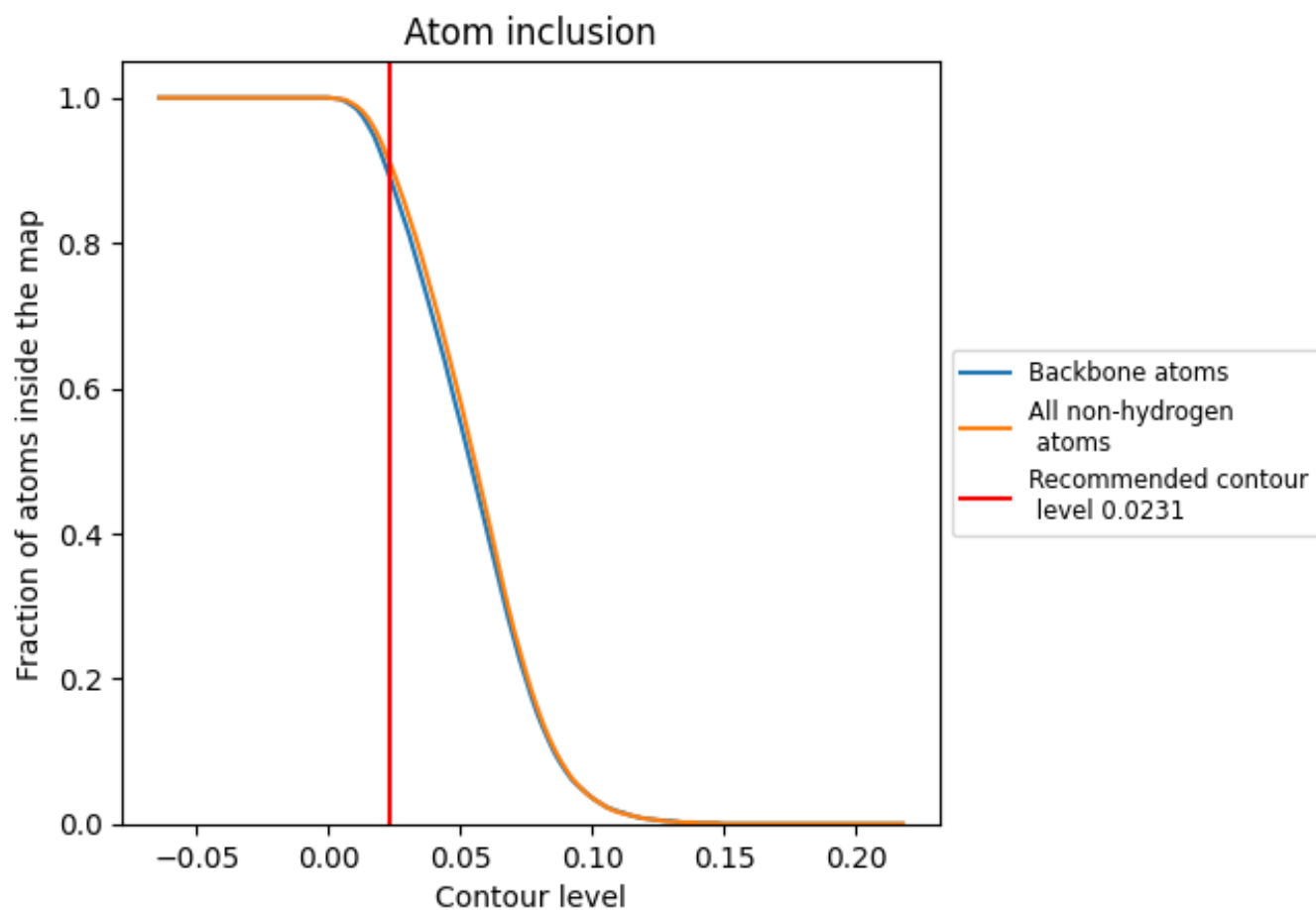
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0231).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 91% 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 (0.0231) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| All |  0.9120 |  0.5730 |
| 1 |  0.6250 |  0.3460 |
| 2 |  0.5220 |  0.2910 |
| 3 |  0.7260 |  0.4160 |
| 4 |  0.6270 |  0.5100 |
| 5 |  0.1290 |  0.1720 |
| 6 |  0.0440 |  0.1240 |
| 7 |  0.1740 |  0.1810 |
| 8 |  0.0440 |  0.1120 |
| 9 |  0.0640 |  0.1450 |
| A |  0.9890 |  0.6510 |
| B |  0.5430 |  0.3100 |
| C |  0.9670 |  0.6340 |
| D |  0.9260 |  0.6170 |
| E |  0.9140 |  0.5980 |
| F |  0.9710 |  0.6390 |
| G |  0.8820 |  0.5850 |
| H |  0.9410 |  0.6250 |
| I |  0.9650 |  0.6350 |
| J |  0.8850 |  0.5880 |
| K |  0.9500 |  0.5810 |
| L |  0.9200 |  0.6140 |
| M |  0.9420 |  0.6180 |
| N |  0.9960 |  0.6560 |
| O |  0.9750 |  0.6460 |
| P |  0.8660 |  0.6010 |
| Q |  0.9830 |  0.6470 |
| R |  0.9670 |  0.6320 |
| S |  0.9840 |  0.6420 |
| T |  0.9520 |  0.6240 |
| U |  0.8160 |  0.5280 |
| V |  0.9740 |  0.6390 |
| W |  0.9760 |  0.6410 |
| X |  0.9660 |  0.6290 |
| Y |  0.9410 |  0.6270 |



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| Chain | Atom inclusion | Q-score |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| Z |  0.9400 |  0.6140 |
| a |  0.9770 |  0.6490 |
| b |  0.8540 |  0.5680 |
| c |  0.9490 |  0.6230 |
| d |  0.9350 |  0.6200 |
| e |  0.9870 |  0.6480 |
| f |  0.9860 |  0.6520 |
| g |  0.9320 |  0.6140 |
| h |  0.9400 |  0.6220 |
| i |  0.9380 |  0.6060 |
| j |  0.9910 |  0.6500 |
| k |  0.8420 |  0.5820 |
| l |  0.9770 |  0.6300 |
| m |  0.9570 |  0.6270 |
| n |  0.9730 |  0.6180 |
| o |  0.9520 |  0.6360 |
| p |  0.9750 |  0.6340 |
| q |  0.6680 |  0.4800 |
| r |  0.9740 |  0.6360 |
| u |  0.9930 |  0.6250 |
| v |  0.9720 |  0.6040 |
| w |  0.9680 |  0.6400 |