



wwPDB EM Validation Summary Report ⓘ

Nov 22, 2022 – 04:31 pm GMT

PDB ID : 7QCA
EMDB ID : EMD-13892
Title : Spraguea lophii ribosome
Authors : Gil Diez, P.; McLaren, M.; Isupov, M.N.; Daum, B.; Connors, R.; Williams, B.
Deposited on : 2021-11-22
Resolution : 2.78 Å(reported)
Based on initial model : 6RM3

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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

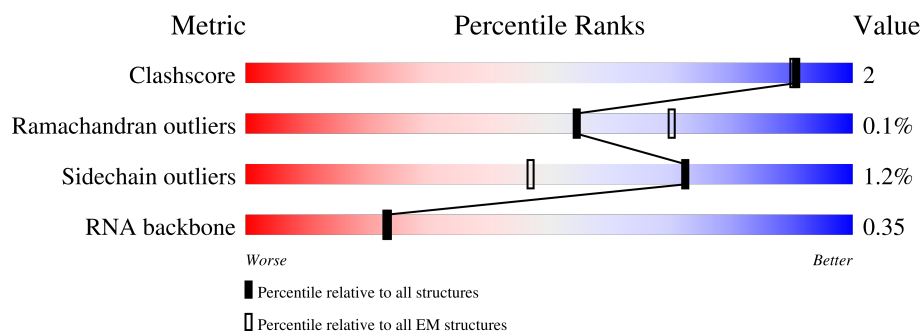
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY



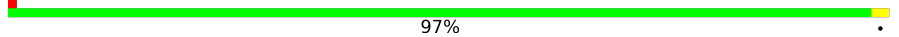

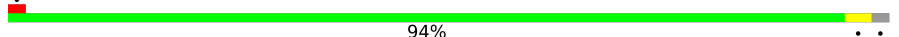
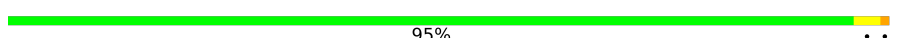

The reported resolution of this entry is 2.78 Å.

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.



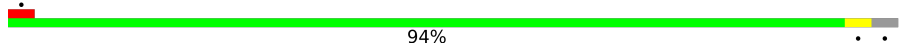


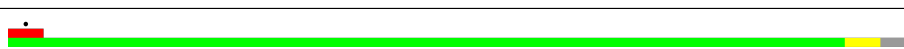
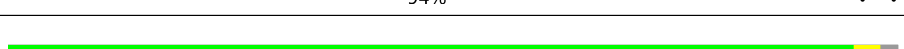
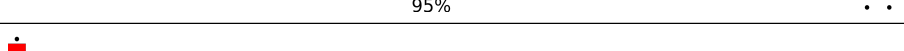
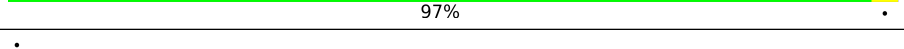
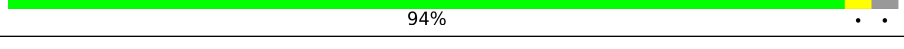
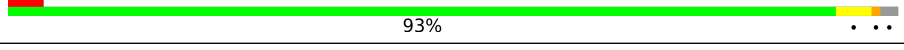
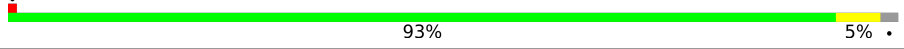
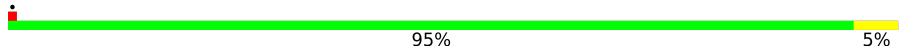
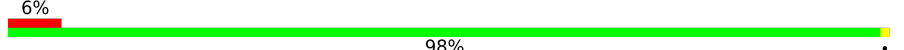
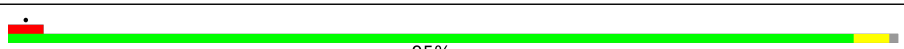

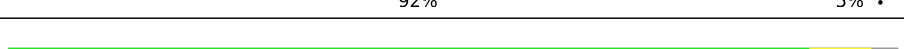
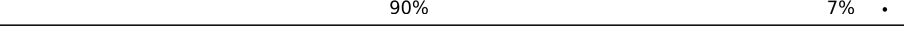
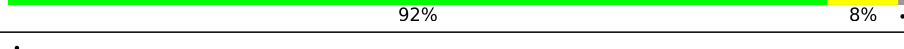
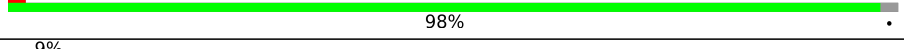
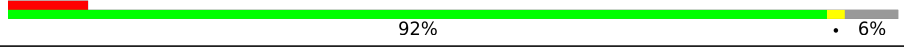

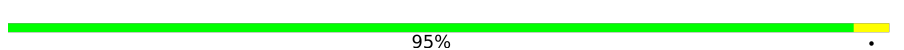
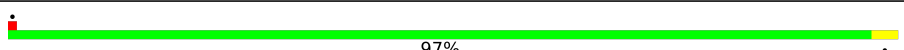
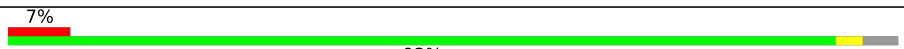
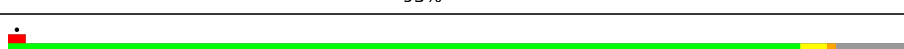
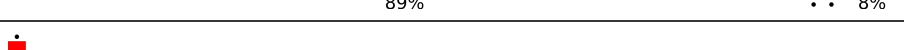
| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Clashscore | 158937 | 4297 |
| Ramachandran outliers | 154571 | 4023 |
| Sidechain outliers | 154315 | 3826 |
| RNA backbone | 4643 | 859 |

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 | L50 | 2618 |  |
| 2 | L70 | 119 |  |
| 3 | LA0 | 246 |  |
| 4 | LAA | 147 |  |
| 5 | LB0 | 392 |  |
| 6 | LC0 | 328 |  |
| 7 | LCC | 110 |  |

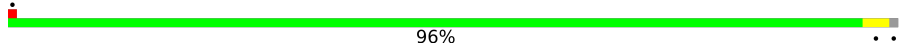
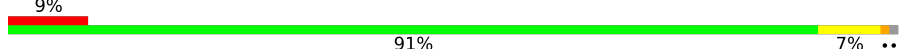
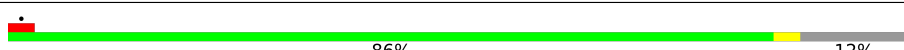
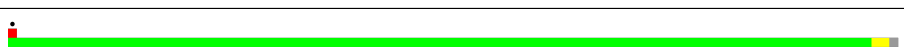
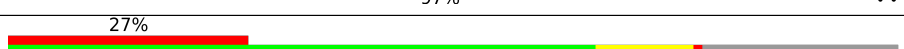
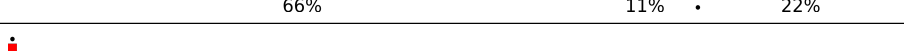
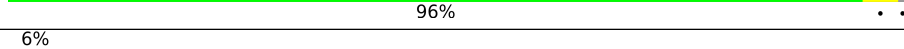
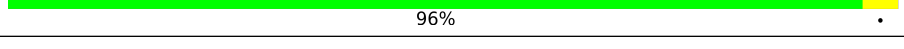




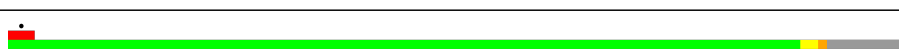

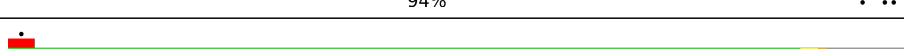
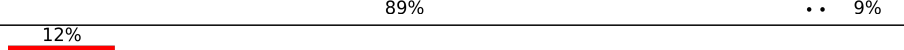


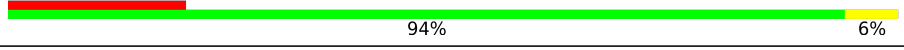





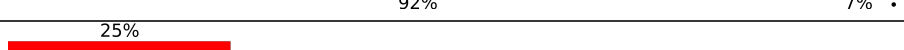
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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 8 | LD0 | 291 |  |
| 9 | LDD | 110 |  |
| 10 | LE0 | 171 |  |
| 11 | LEE | 139 |  |
| 12 | LF0 | 235 |  |
| 13 | LFF | 111 |  |
| 14 | LG0 | 206 |  |
| 15 | LGG | 106 |  |
| 16 | LH0 | 187 |  |
| 17 | LHH | 119 |  |
| 18 | LI0 | 218 |  |
| 19 | LII | 98 |  |
| 20 | LJ0 | 171 |  |
| 21 | LJJ | 92 |  |
| 22 | LL0 | 165 |  |
| 23 | LLL | 52 |  |
| 24 | LM0 | 122 |  |
| 25 | LMM | 127 |  |
| 26 | LN0 | 204 |  |
| 27 | LO0 | 198 |  |
| 28 | LOO | 104 |  |
| 29 | LP0 | 167 |  |
| 30 | LPP | 89 |  |
| 31 | LQ0 | 183 |  |
| 32 | LR0 | 168 |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 33 | LS0 | 171 |  |
| 34 | LT0 | 158 |  |
| 35 | LU0 | 113 |  |
| 36 | LV0 | 142 |  |
| 37 | LW0 | 131 |  |
| 38 | LX0 | 113 |  |
| 39 | LY0 | 131 |  |
| 40 | LZ0 | 153 |  |
| 41 | S60 | 1368 |  |
| 42 | SA0 | 233 |  |
| 43 | SAA | 102 |  |
| 44 | SB0 | 230 |  |
| 45 | SBB | 82 |  |
| 46 | SC0 | 248 |  |
| 47 | SCC | 65 |  |
| 48 | SD0 | 242 |  |
| 49 | SDD | 65 |  |
| 50 | SE0 | 280 |  |
| 51 | SEE | 60 |  |
| 52 | SF0 | 195 |  |
| 53 | SFF | 150 |  |
| 54 | SG0 | 230 |  |
| 55 | SGG | 326 |  |
| 56 | SH0 | 164 |  |
| 57 | SI0 | 173 |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 58 | SJ0 | 184 | |
| 59 | SK0 | 107 | |
| 60 | SL0 | 155 | |
| 61 | SM0 | 130 | |
| 62 | SN0 | 143 | |
| 63 | SO0 | 135 | |
| 64 | SP0 | 163 | |
| 65 | SQ0 | 143 | |
| 66 | SR0 | 120 | |
| 67 | SS0 | 160 | |
| 68 | ST0 | 143 | |
| 69 | SU0 | 119 | |
| 70 | SV0 | 67 | |
| 71 | SW0 | 128 | |
| 72 | SX0 | 141 | |
| 73 | SY0 | 146 | |
| 74 | SZ0 | 128 | |

2 Entry composition

There are 77 unique types of molecules in this entry. The entry contains 171001 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA 23S.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 1 | L50 | 2499 | Total | C | N | O | P | 0 | 0 |
| | | | 53655 | 23950 | 9876 | 17330 | 2499 | | |

- Molecule 2 is a RNA chain called RNA 5S.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 2 | L70 | 119 | Total | C | N | O | P | 0 | 0 |
| | | | 2542 | 1136 | 459 | 828 | 119 | | |

- Molecule 3 is a protein called 60S ribosomal protein L8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 3 | LA0 | 245 | Total | C | N | O | S | 0 | 0 |
| | | | 1889 | 1189 | 361 | 334 | 5 | | |

- Molecule 4 is a protein called uL15 LAA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 4 | LAA | 147 | Total | C | N | O | S | 0 | 0 |
| | | | 1167 | 738 | 229 | 194 | 6 | | |

- Molecule 5 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 5 | LB0 | 383 | Total | C | N | O | S | 0 | 0 |
| | | | 3039 | 1926 | 559 | 543 | 11 | | |

- Molecule 6 is a protein called 60S ribosomal protein L4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 6 | LC0 | 327 | Total | C | N | O | S | 0 | 0 |
| | | | 2604 | 1629 | 478 | 485 | 12 | | |

- Molecule 7 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 7 | LCC | 99 | Total | C | N | O | S | 0 | 0 |
| | | | 781 | 504 | 126 | 148 | 3 | | |

- Molecule 8 is a protein called 60S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 8 | LD0 | 281 | Total | C | N | O | S | 0 | 0 |
| | | | 2298 | 1451 | 410 | 426 | 11 | | |

- Molecule 9 is a protein called 60S ribosomal protein L31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 9 | LDD | 109 | Total | C | N | O | S | 0 | 0 |
| | | | 895 | 575 | 163 | 154 | 3 | | |

- Molecule 10 is a protein called 60S ribosomal protein L6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10 | LE0 | 165 | Total | C | N | O | S | 0 | 0 |
| | | | 1371 | 879 | 227 | 262 | 3 | | |

- Molecule 11 is a protein called 60S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 11 | LEE | 135 | Total | C | N | O | S | 0 | 0 |
| | | | 1090 | 697 | 205 | 182 | 6 | | |

- Molecule 12 is a protein called 60S ribosomal protein L7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 12 | LF0 | 231 | Total | C | N | O | S | 0 | 0 |
| | | | 1933 | 1234 | 342 | 350 | 7 | | |

- Molecule 13 is a protein called 60S ribosomal protein L35a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 13 | LFF | 111 | Total | C | N | O | S | 0 | 0 |
| | | | 893 | 567 | 159 | 162 | 5 | | |

- Molecule 14 is a protein called 60S ribosomal protein L8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 14 | LG0 | 199 | Total | C | N | O | S | 0 | 0 |
| | | | 1590 | 1015 | 275 | 290 | 10 | | |

- Molecule 15 is a protein called Ribosomal protein L34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15 | LGG | 104 | Total | C | N | O | S | 0 | 0 |
| | | | 819 | 504 | 169 | 139 | 7 | | |

- Molecule 16 is a protein called 60S ribosomal protein L9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16 | LH0 | 183 | Total | C | N | O | S | 0 | 0 |
| | | | 1477 | 951 | 252 | 266 | 8 | | |

- Molecule 17 is a protein called Ribosomal L29 protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17 | LHH | 119 | Total | C | N | O | S | 0 | 0 |
| | | | 992 | 626 | 188 | 175 | 3 | | |

- Molecule 18 is a protein called S60 ribosomal protein L10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 18 | LI0 | 217 | Total | C | N | O | S | 0 | 0 |
| | | | 1750 | 1096 | 333 | 308 | 13 | | |

- Molecule 19 is a protein called 60S ribosomal protein L36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19 | LII | 97 | Total | C | N | O | S | 0 | 0 |
| | | | 784 | 496 | 146 | 136 | 6 | | |

- Molecule 20 is a protein called 60S ribosomal protein L11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20 | LJ0 | 167 | Total | C | N | O | S | 0 | 0 |
| | | | 1332 | 847 | 242 | 236 | 7 | | |

- Molecule 21 is a protein called eL37 LJJ.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 21 | LJJ | 89 | Total | C | N | O | S | 0 | 0 |
| | | | 701 | 427 | 146 | 118 | 10 | | |

- Molecule 22 is a protein called 60S ribosomal protein L13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 22 | LL0 | 164 | Total | C | N | O | S | 0 | 0 |
| | | | 1353 | 857 | 252 | 232 | 12 | | |

- Molecule 23 is a protein called 60S ribosomal protein L39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 23 | LLL | 51 | Total | C | N | O | S | 0 | 0 |
| | | | 427 | 272 | 87 | 65 | 3 | | |

- Molecule 24 is a protein called eL14 LM0.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24 | LM0 | 115 | Total | C | N | O | S | 0 | 0 |
| | | | 927 | 588 | 151 | 183 | 5 | | |

- Molecule 25 is a protein called Ubiquitin.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 25 | LMM | 52 | Total | C | N | O | S | 0 | 0 |
| | | | 427 | 264 | 89 | 70 | 4 | | |

- Molecule 26 is a protein called Ribosomal protein L15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 26 | LN0 | 203 | Total | C | N | O | S | 0 | 0 |
| | | | 1688 | 1055 | 346 | 276 | 11 | | |

- Molecule 27 is a protein called Ribosomal protein L13A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 27 | LO0 | 198 | Total | C | N | O | S | 0 | 0 |
| | | | 1598 | 1018 | 286 | 280 | 14 | | |

- Molecule 28 is a protein called 60S ribosomal protein L44.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 28 | LOO | 100 | Total | C | N | O | S | 0 | 0 |
| | | | 801 | 504 | 163 | 130 | 4 | | |

- Molecule 29 is a protein called 60S ribosomal protein L17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29 | LP0 | 154 | Total | C | N | O | S | 0 | 0 |
| | | | 1238 | 794 | 225 | 213 | 6 | | |

- Molecule 30 is a protein called 60S ribosomal protein L37a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 30 | LPP | 87 | Total | C | N | O | S | 0 | 0 |
| | | | 684 | 427 | 131 | 116 | 10 | | |

- Molecule 31 is a protein called 60S ribosomal protein L18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 31 | LQ0 | 182 | Total | C | N | O | S | 0 | 0 |
| | | | 1491 | 950 | 270 | 266 | 5 | | |

- Molecule 32 is a protein called 60S ribosomal protein L19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32 | LR0 | 164 | Total | C | N | O | S | 0 | 0 |
| | | | 1336 | 832 | 261 | 236 | 7 | | |

- Molecule 33 is a protein called 60S ribosomal protein L20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33 | LS0 | 170 | Total | C | N | O | S | 0 | 0 |
| | | | 1400 | 898 | 241 | 256 | 5 | | |

- Molecule 34 is a protein called 60s ribosomal protein L21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 34 | LT0 | 156 | Total | C | N | O | S | 0 | 0 |
| | | | 1270 | 808 | 233 | 224 | 5 | | |

- Molecule 35 is a protein called 60S ribosomal protein L22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 35 | LU0 | 100 | Total | C | N | O | S | 0 | 0 |
| | | | 810 | 526 | 135 | 147 | 2 | | |

- Molecule 36 is a protein called Ribosomal protein L23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 36 | LV0 | 141 | Total | C | N | O | S | 0 | 0 |
| | | | 1057 | 663 | 200 | 189 | 5 | | |

- Molecule 37 is a protein called Ribosomal protein L24E.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 37 | LW0 | 102 | Total | C | N | O | S | 0 | 0 |
| | | | 832 | 539 | 143 | 147 | 3 | | |

- Molecule 38 is a protein called 60S ribosomal protein L23a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 38 | LX0 | 112 | Total | C | N | O | S | 0 | 0 |
| | | | 874 | 562 | 156 | 155 | 1 | | |

- Molecule 39 is a protein called 60S ribosomal protein L26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 39 | LY0 | 131 | Total | C | N | O | S | 0 | 0 |
| | | | 1048 | 658 | 197 | 186 | 7 | | |

- Molecule 40 is a protein called 60S ribosomal protein L27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 40 | LZ0 | 118 | Total | C | N | O | S | 0 | 0 |
| | | | 963 | 618 | 172 | 169 | 4 | | |

- Molecule 41 is a RNA chain called RNA SSU.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|------|------|---------|-------|
| 41 | S60 | 1354 | Total | C | N | O | P | 0 | 0 |
| | | | 29181 | 13024 | 5463 | 9340 | 1354 | | |

- Molecule 42 is a protein called 40S ribosomal protein S0.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 42 | SA0 | 220 | Total | C | N | O | S | 0 | 0 |
| | | | 1725 | 1091 | 292 | 328 | 14 | | |

- Molecule 43 is a protein called 40S ribosomal protein S26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 43 | SAA | 101 | Total | C | N | O | S | 0 | 0 |
| | | | 827 | 513 | 163 | 145 | 6 | | |

- Molecule 44 is a protein called eS1 SB0.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 44 | SB0 | 204 | Total | C | N | O | S | 0 | 0 |
| | | | 1609 | 1018 | 286 | 298 | 7 | | |

- Molecule 45 is a protein called eS27 SBB.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 45 | SBB | 81 | Total | C | N | O | S | 0 | 0 |
| | | | 627 | 394 | 108 | 116 | 9 | | |

- Molecule 46 is a protein called 40S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 46 | SC0 | 226 | Total | C | N | O | S | 0 | 0 |
| | | | 1727 | 1099 | 300 | 321 | 7 | | |

- Molecule 47 is a protein called eS28 SCC.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 47 | SCC | 62 | Total | C | N | O | S | 0 | 0 |
| | | | 476 | 295 | 86 | 91 | 4 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 48 | SD0 | 216 | Total | C | N | O | S | 0 | 0 |
| | | | 1700 | 1085 | 300 | 307 | 8 | | |

- Molecule 49 is a protein called 40S ribosomal protein S29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 49 | SDD | 65 | Total | C | N | O | S | 0 | 0 |
| | | | 550 | 345 | 102 | 96 | 7 | | |

- Molecule 50 is a protein called 40S ribosomal protein S4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 50 | SE0 | 260 | Total | C | N | O | S | 0 | 0 |
| | | | 2044 | 1297 | 361 | 379 | 7 | | |

- Molecule 51 is a protein called eS30 SEE.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 51 | SEE | 56 | Total | C | N | O | S | 0 | 0 |
| | | | 447 | 284 | 89 | 74 | | | |

- Molecule 52 is a protein called 40S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 52 | SF0 | 192 | Total | C | N | O | S | 0 | 0 |
| | | | 1509 | 953 | 275 | 275 | 6 | | |

- Molecule 53 is a protein called Ubiquitin/40s ribosomal protein S27a fusion.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 53 | SFF | 58 | Total | C | N | O | S | 0 | 0 |
| | | | 447 | 278 | 81 | 83 | 5 | | |

- Molecule 54 is a protein called 40S ribosomal protein S6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 54 | SG0 | 229 | Total | C | N | O | S | 0 | 0 |
| | | | 1835 | 1178 | 325 | 328 | 4 | | |

- Molecule 55 is a protein called Guanine nucleotide binding protein beta subunit.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 55 | SGG | 319 | Total | C | N | O | S | 0 | 0 |
| | | | 2478 | 1558 | 411 | 494 | 15 | | |

- Molecule 56 is a protein called 40S ribosomal protein S7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 56 | SH0 | 163 | Total | C | N | O | S | 0 | 0 |
| | | | 1335 | 855 | 219 | 255 | 6 | | |

- Molecule 57 is a protein called 40S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 57 | SI0 | 167 | Total | C | N | O | S | 0 | 0 |
| | | | 1347 | 834 | 266 | 240 | 7 | | |

- Molecule 58 is a protein called 40S ribosomal protein S9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 58 | SJ0 | 168 | Total | C | N | O | S | 0 | 0 |
| | | | 1379 | 880 | 252 | 243 | 4 | | |

- Molecule 59 is a protein called 40S ribosomal protein S10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 59 | SK0 | 91 | Total | C | N | O | S | 0 | 0 |
| | | | 764 | 490 | 130 | 140 | 4 | | |

- Molecule 60 is a protein called 40S ribosomal protein S11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 60 | SL0 | 150 | Total | C | N | O | S | 0 | 0 |
| | | | 1229 | 790 | 217 | 216 | 6 | | |

- Molecule 61 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 61 | SM0 | 113 | Total | C | N | O | S | 0 | 0 |
| | | | 876 | 553 | 156 | 162 | 5 | | |

- Molecule 62 is a protein called 40S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 62 | SN0 | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1130 | 728 | 196 | 202 | 4 | | |

- Molecule 63 is a protein called 40S ribosomal protein S14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 63 | SO0 | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 983 | 606 | 191 | 183 | 3 | | |

- Molecule 64 is a protein called Ribosomal protein S19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 64 | SP0 | 117 | Total | C | N | O | S | 0 | 0 |
| | | | 950 | 598 | 172 | 173 | 7 | | |

- Molecule 65 is a protein called 40S ribosomal protein S16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 65 | SQ0 | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1143 | 726 | 204 | 207 | 6 | | |

- Molecule 66 is a protein called eS17 SR0.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 66 | SR0 | 119 | Total | C | N | O | S | 0 | 0 |
| | | | 977 | 616 | 172 | 186 | 3 | | |

- Molecule 67 is a protein called 40S ribosomal protein S18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 67 | SS0 | 144 | Total | C | N | O | S | 0 | 0 |
| | | | 1150 | 720 | 220 | 207 | 3 | | |

- Molecule 68 is a protein called 40S Ribosomal protein S19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 68 | ST0 | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1161 | 741 | 208 | 211 | 1 | | |

- Molecule 69 is a protein called 40S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 69 | SU0 | 100 | Total | C | N | O | S | 0 | 0 |
| | | | 809 | 515 | 144 | 143 | 7 | | |

- Molecule 70 is a protein called Ribosomal protein S21E.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|---|---------|-------|
| 70 | SV0 | 65 | Total | C | N | O | S | 0 | 0 |
| | | | 521 | 319 | 96 | 101 | 5 | | |

- Molecule 71 is a protein called 40S ribosomal protein S15A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 71 | SW0 | 128 | Total | C | N | O | S | 0 | 0 |
| | | | 1022 | 639 | 195 | 180 | 8 | | |

- Molecule 72 is a protein called uS12 SX0.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 72 | SX0 | 140 | Total | C | N | O | S | 0 | 0 |
| | | | 1098 | 692 | 216 | 186 | 4 | | |

- Molecule 73 is a protein called 40s ribosomal protein s24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 73 | SY0 | 136 | Total | C | N | O | S | 0 | 0 |
| | | | 1118 | 693 | 215 | 204 | 6 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 74 | SZ0 | 76 | Total | C | N | O | S | 0 | 0 |
| | | | 633 | 403 | 116 | 113 | 1 | | |

- Molecule 75 is POTASSIUM ION (three-letter code: K) (formula: K).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|-----|---------|
| 75 | L50 | 145 | Total | K | 0 |
| | | | 145 | 145 | |
| 75 | LA0 | 2 | Total | K | 0 |
| | | | 2 | 2 | |
| 75 | LEE | 1 | Total | K | 0 |
| | | | 1 | 1 | |
| 75 | LLL | 1 | Total | K | 0 |
| | | | 1 | 1 | |
| 75 | LN0 | 1 | Total | K | 0 |
| | | | 1 | 1 | |
| 75 | S60 | 44 | Total | K | 0 |
| | | | 44 | 44 | |

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| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|--------|---------|
| 75 | SN0 | 3 | Total 3 | K 3 | 0 |
| 75 | SO0 | 2 | Total 2 | K 2 | 0 |

- Molecule 76 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|--------------|-----------|---------|
| 76 | L50 | 104 | Total 104 | Mg 104 | 0 |
| 76 | L70 | 4 | Total 4 | Mg 4 | 0 |
| 76 | LB0 | 1 | Total 1 | Mg 1 | 0 |
| 76 | LF0 | 1 | Total 1 | Mg 1 | 0 |
| 76 | LII | 1 | Total 1 | Mg 1 | 0 |
| 76 | LJJ | 1 | Total 1 | Mg 1 | 0 |
| 76 | LV0 | 1 | Total 1 | Mg 1 | 0 |
| 76 | S60 | 46 | Total 46 | Mg 46 | 0 |
| 76 | SI0 | 1 | Total 1 | Mg 1 | 0 |

- Molecule 77 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|---------|---------|
| 77 | LGG | 1 | Total 1 | Zn 1 | 0 |
| 77 | LJJ | 1 | Total 1 | Zn 1 | 0 |
| 77 | LMM | 1 | Total 1 | Zn 1 | 0 |
| 77 | LOO | 1 | Total 1 | Zn 1 | 0 |
| 77 | LPP | 1 | Total 1 | Zn 1 | 0 |
| 77 | SAA | 1 | Total 1 | Zn 1 | 0 |

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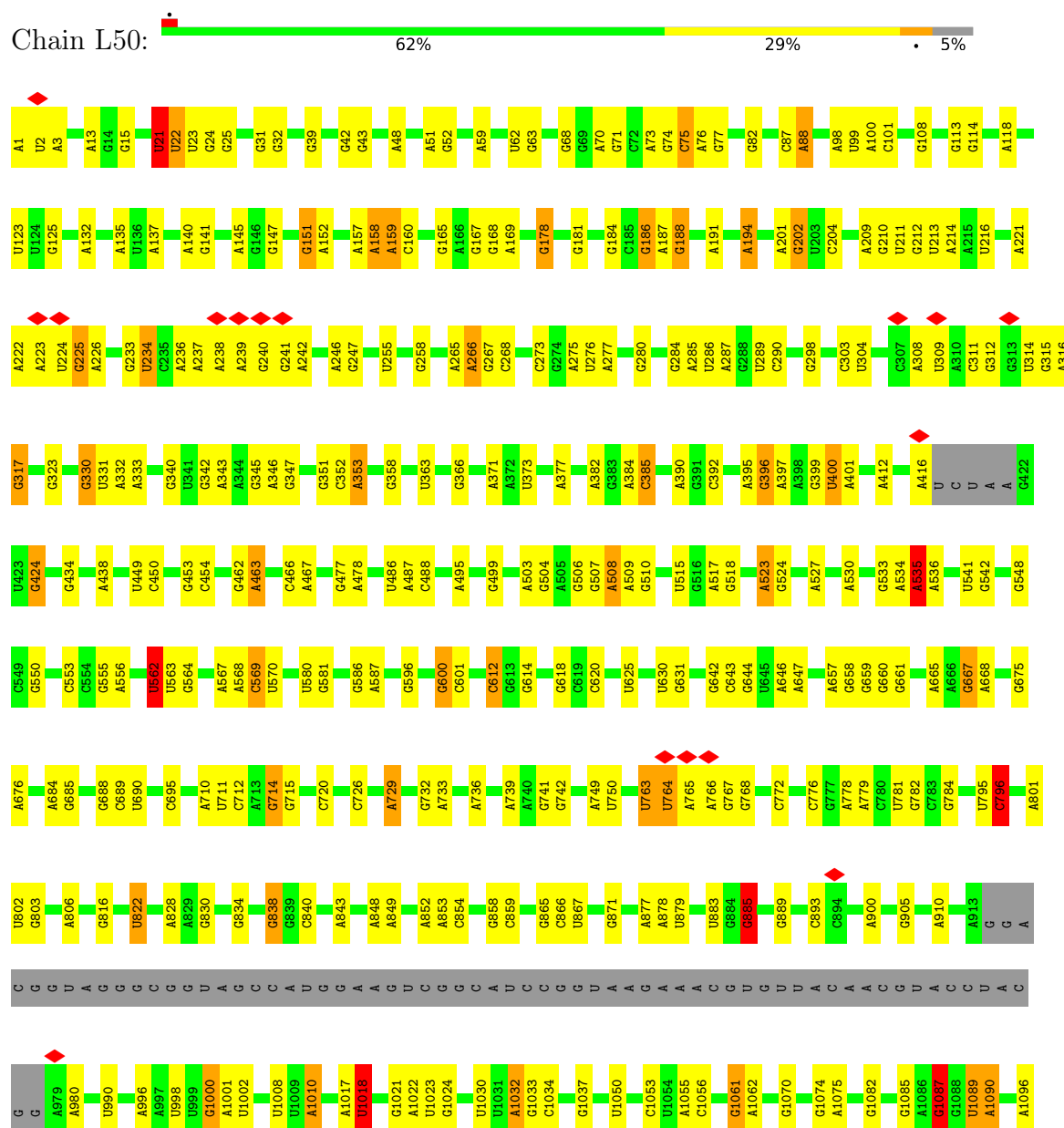
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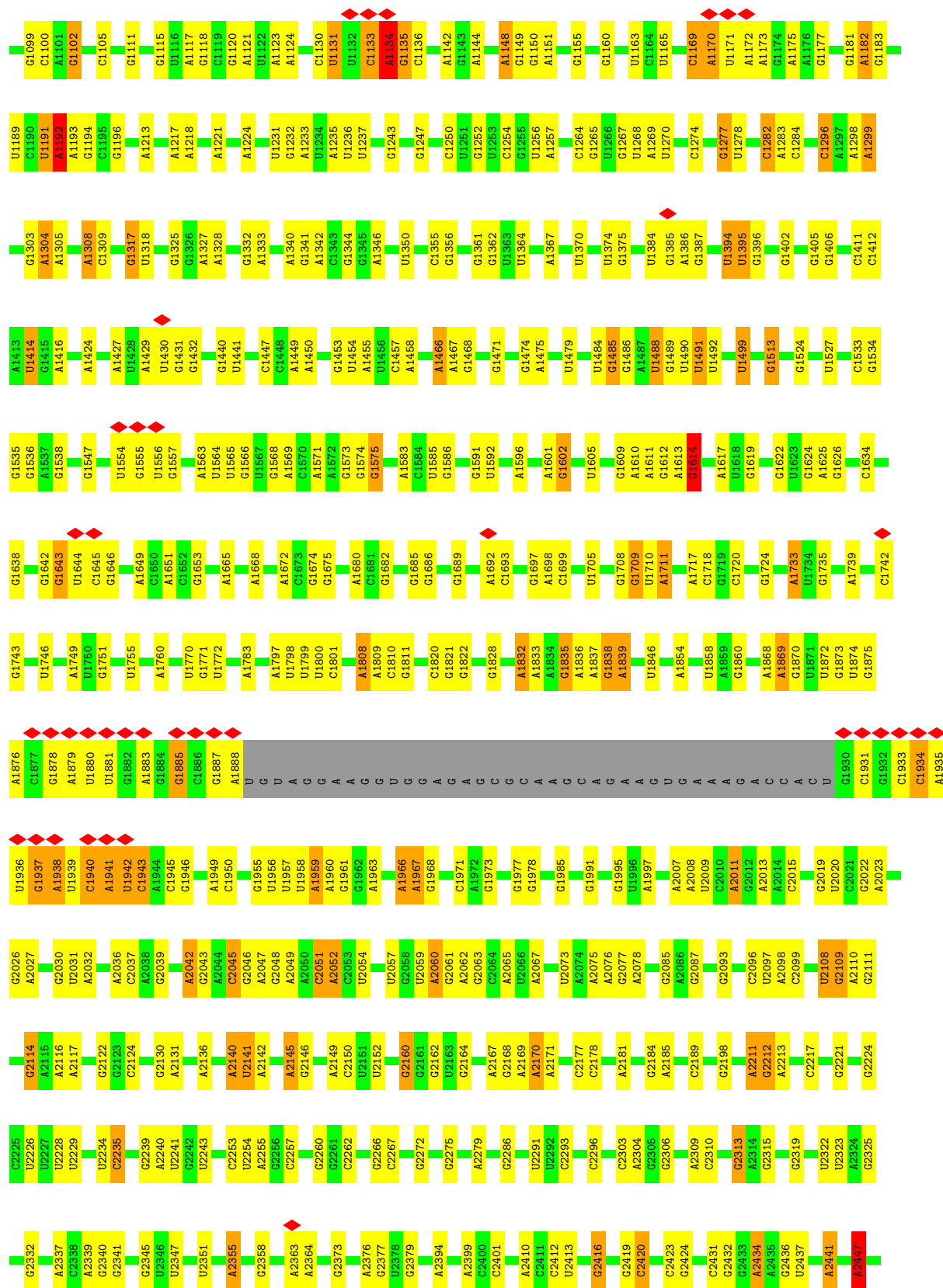
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|---------|---------|
| 77 | SBB | 1 | Total 1 | Zn 1 | 0 |
| 77 | SDD | 1 | Total 1 | Zn 1 | 0 |
| 77 | SFF | 1 | Total 1 | Zn 1 | 0 |

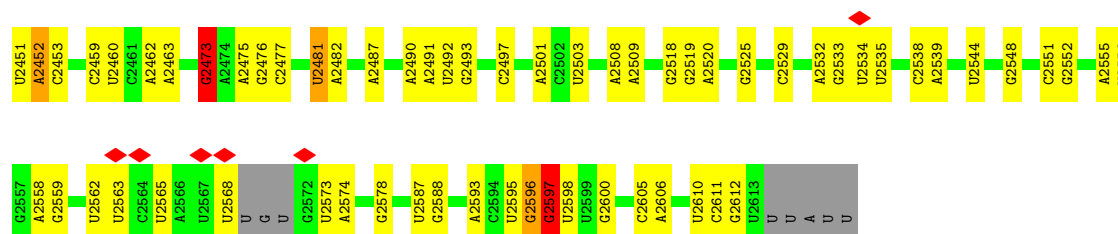
3 Residue-property plots

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

• Molecule 1: RNA 23S







- Molecule 2: RNA 5S

Chain L70: 60% 35% 5%



- Molecule 3: 60S ribosomal protein L8

Chain LA0: 97%



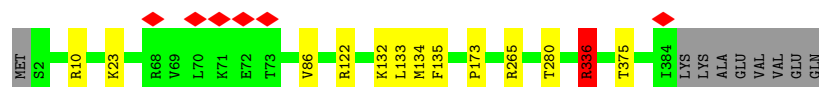
- Molecule 4: uL15 LAA

Chain LAA: 93% 7%



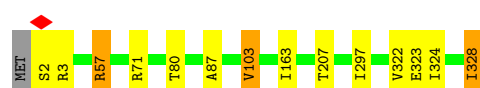
- Molecule 5: 60S ribosomal protein L3

Chain LB0: 94%

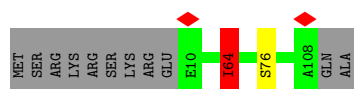
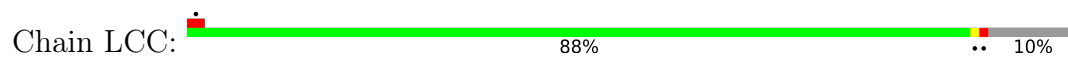


- Molecule 6: 60S ribosomal protein L4

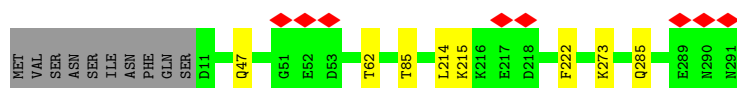
Chain LC0: 95%



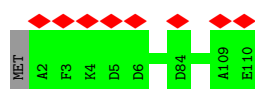
- Molecule 7: 60S ribosomal protein L3



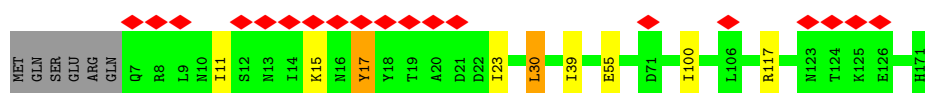
- Molecule 8: 60S ribosomal protein L5



- Molecule 9: 60S ribosomal protein L31



- Molecule 10: 60S ribosomal protein L6



- Molecule 11: 60S ribosomal protein L32



- Molecule 12: 60S ribosomal protein L7

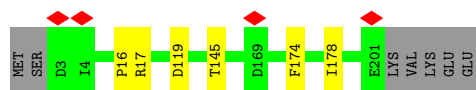


- Molecule 13: 60S ribosomal protein L35a



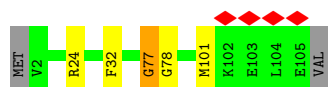
- Molecule 14: 60S ribosomal protein L8

Chain LG0:  94% . .



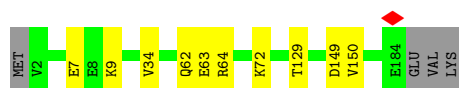
- Molecule 15: Ribosomal protein L34

Chain LGG:  93% . . .



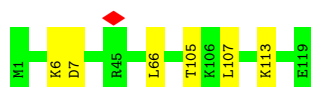
- Molecule 16: 60S ribosomal protein L9

Chain LH0:  93% 5% .



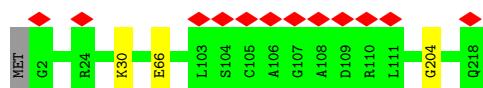
- Molecule 17: Ribosomal L29 protein

Chain LHH:  95% 5%



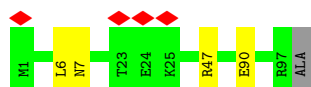
- Molecule 18: S60 ribosomal protein L10

Chain LI0:  98% .



- Molecule 19: 60S ribosomal protein L36

Chain LII:  95% . .



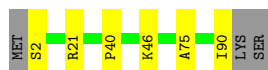
- Molecule 20: 60S ribosomal protein L11

Chain LJ0:  92% 5% .



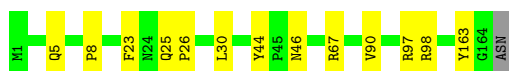
- Molecule 21: eL37 LJJ

Chain LJJ: 90% 7% .



- Molecule 22: 60S ribosomal protein L13

Chain LL0: 92% 8% .



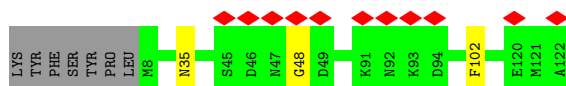
- Molecule 23: 60S ribosomal protein L39

Chain LLL: 98% .



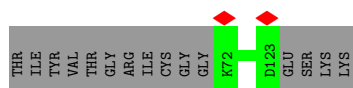
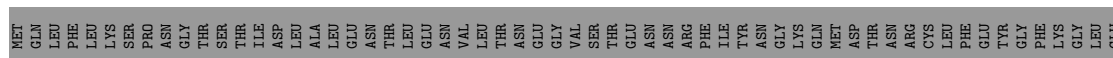
- Molecule 24: eL14 LM0

Chain LM0: 9% 92% 6% .



- Molecule 25: Ubiquitin

Chain LMM: 41% 59% .



- Molecule 26: Ribosomal protein L15

Chain LN0: 95% .



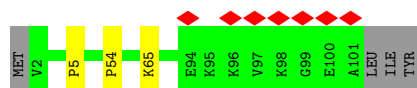
- Molecule 27: Ribosomal protein L13A

Chain LO0:  97%



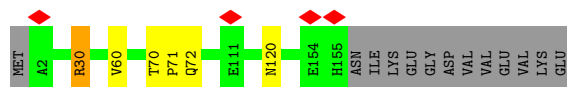
- Molecule 28: 60S ribosomal protein L44

Chain LOO:  93%



- Molecule 29: 60S ribosomal protein L17

Chain LP0:  89%



- Molecule 30: 60S ribosomal protein L37a

Chain LPP:  92%



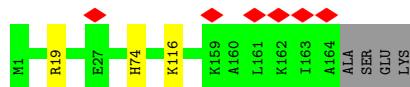
- Molecule 31: 60S ribosomal protein L18

Chain LQ0:  96%



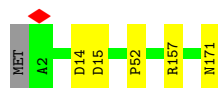
- Molecule 32: 60S ribosomal protein L19

Chain LR0:  96%

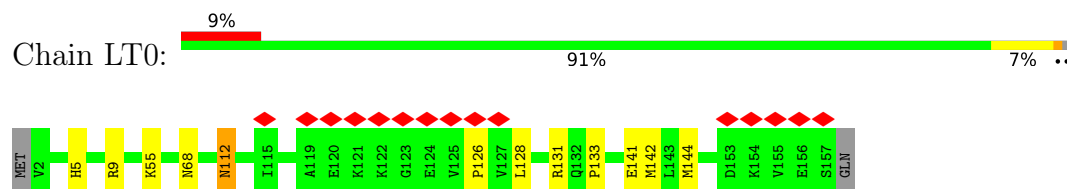


- Molecule 33: 60S ribosomal protein L20

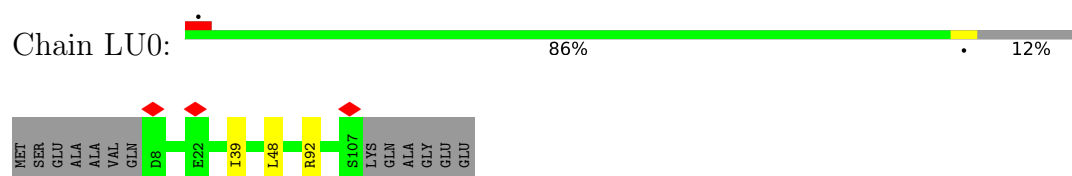
Chain LS0:  96%



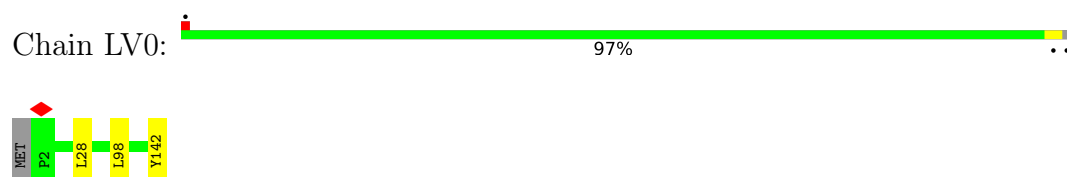
- Molecule 34: 60s ribosomal protein L21



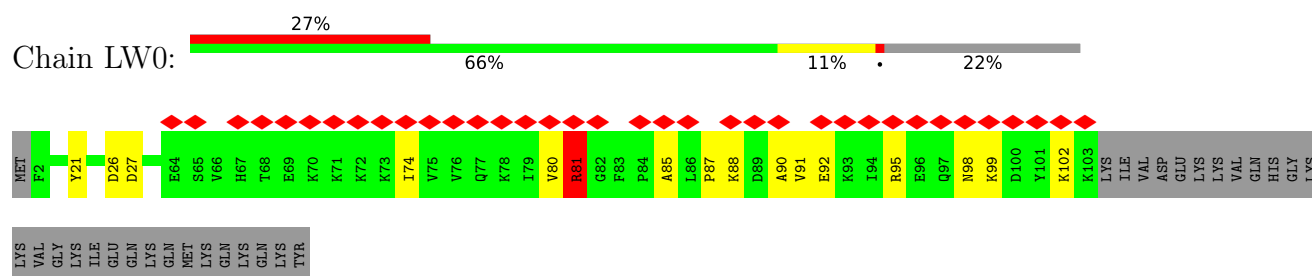
- Molecule 35: 60S ribosomal protein L22



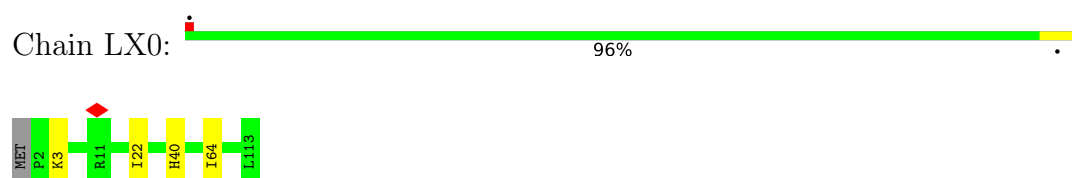
- Molecule 36: Ribosomal protein L23



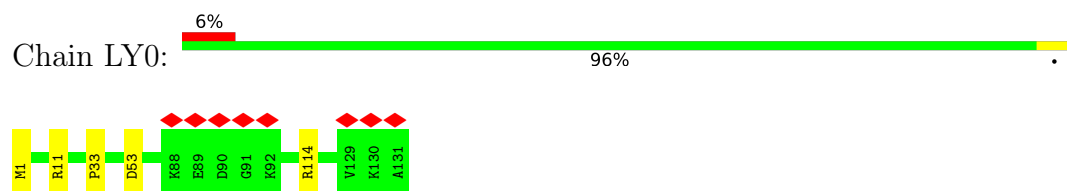
- Molecule 37: Ribosomal protein L24E



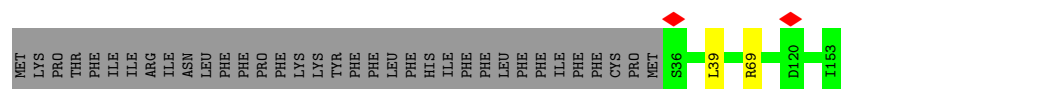
- Molecule 38: 60S ribosomal protein L23a



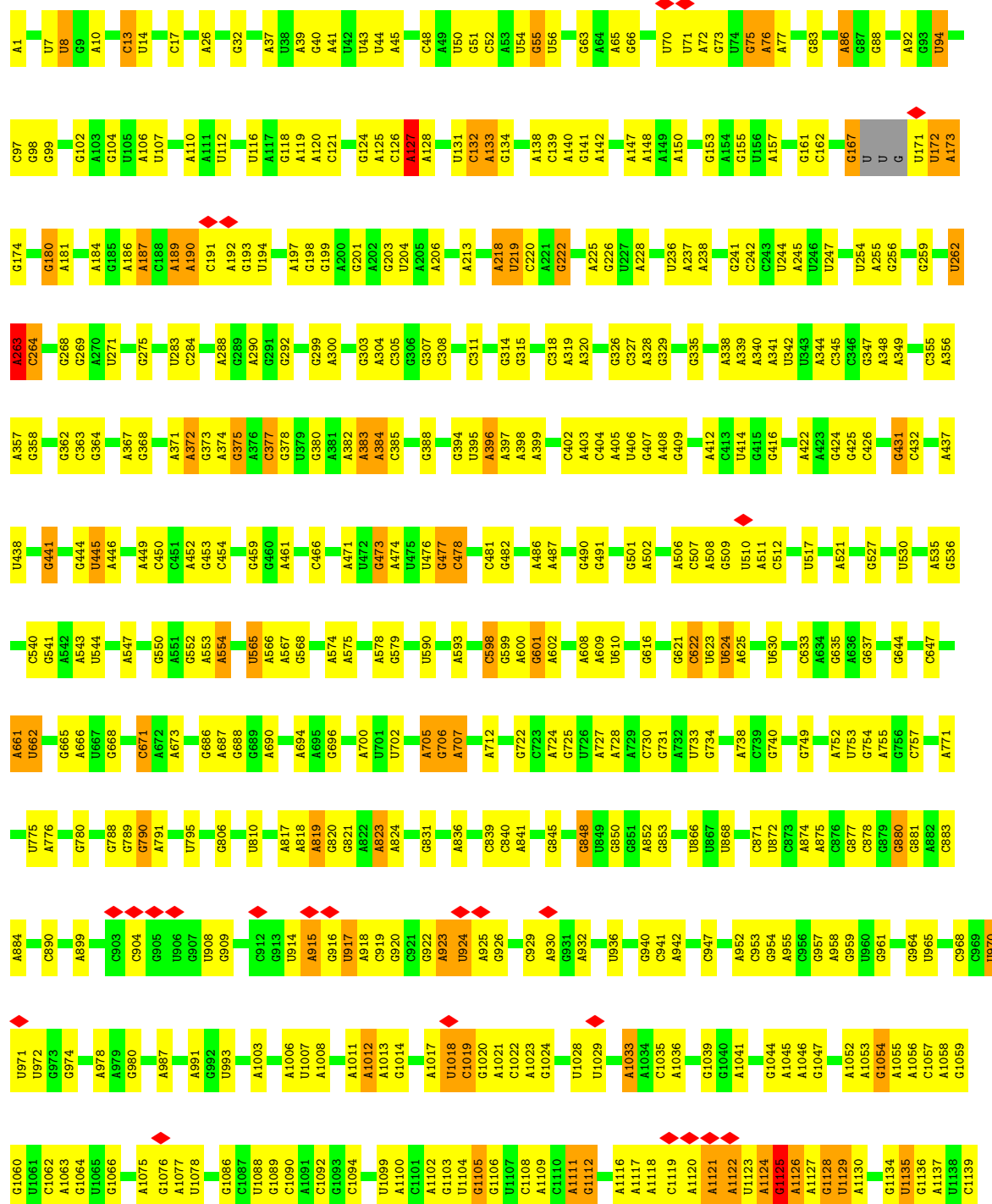
- Molecule 39: 60S ribosomal protein L26

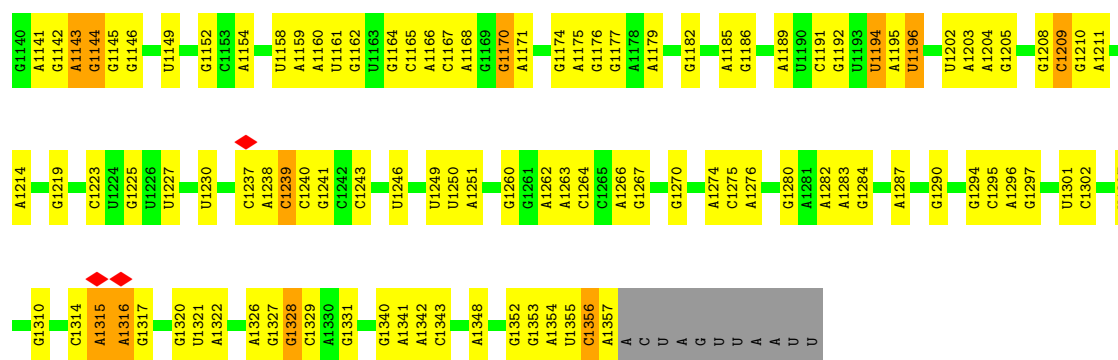


- Molecule 40: 60S ribosomal protein L27

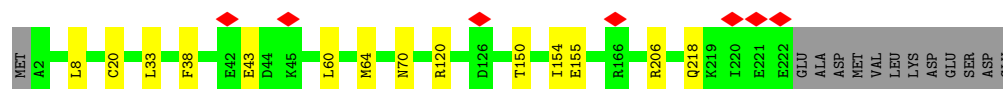


Chain S60: 56% 37% 6%





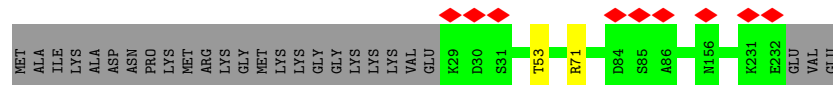
- Molecule 42: 40S ribosomal protein S0



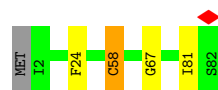
- Molecule 43: 40S ribosomal protein S26



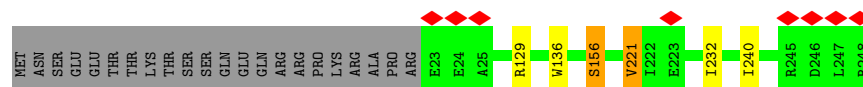
- Molecule 44: eS1 SB0




- Molecule 45: eS27 SBB

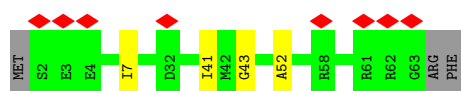


- Molecule 46: 40S ribosomal protein S2




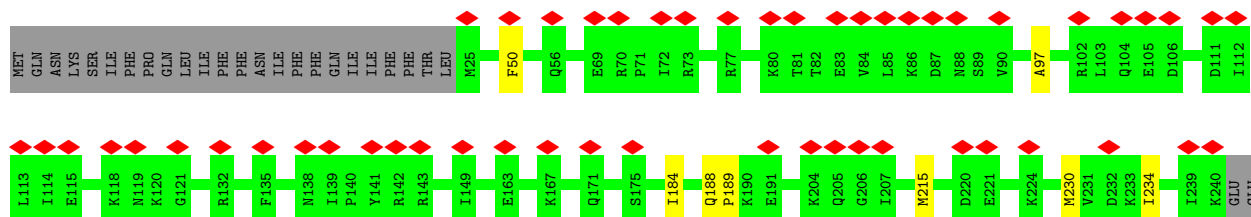
- Molecule 47: eS28 SCC

Chain SCC: 



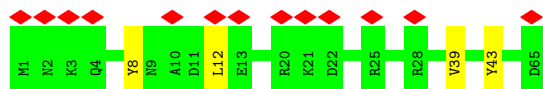
- Molecule 48: 40S ribosomal protein S3

Chain SD0: 



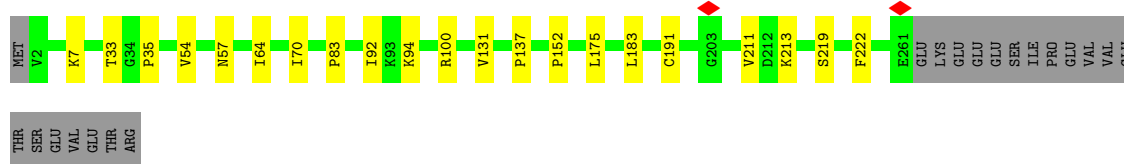
- Molecule 49: 40S ribosomal protein S29

Chain SDD: 



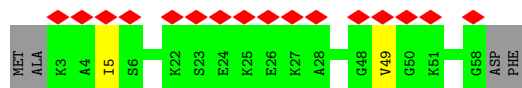
- Molecule 50: 40S ribosomal protein S4

Chain SE0: 




- Molecule 51: eS30 SEE

Chain SEE: 




- Molecule 52: 40S ribosomal protein S5

Chain SF0: 




- Molecule 53: Ubiquitin/40s ribosomal protein S27a fusion

Chain SJ0:  86% 5% 9%



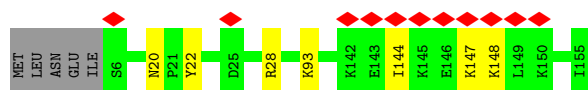
- Molecule 59: 40S ribosomal protein S10

Chain SK0:  34% 81% 15%




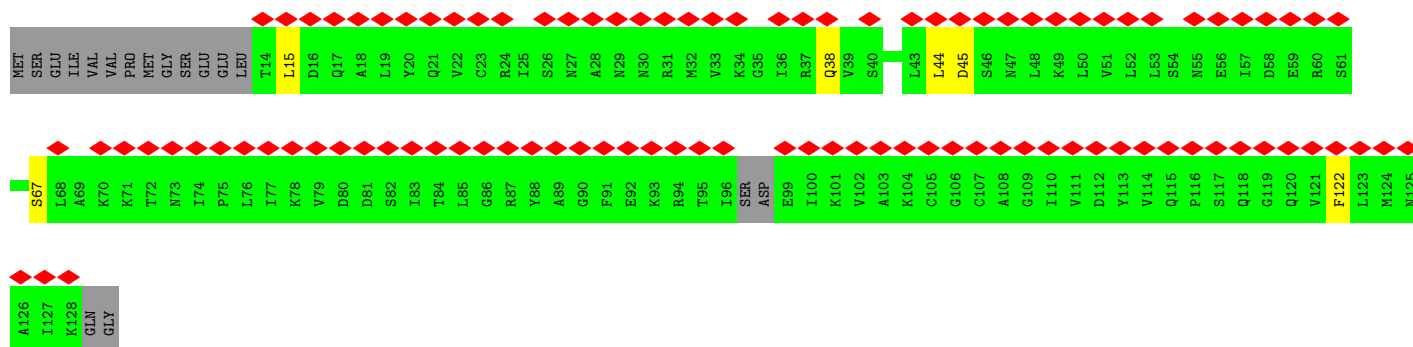
- Molecule 60: 40S ribosomal protein S11

Chain SL0:  7% 92% 5%



- Molecule 61: 40S ribosomal protein S12

Chain SM0:  77% 82% 5% 13%



- Molecule 62: 40S ribosomal protein S13

Chain SN0:  94% 5%

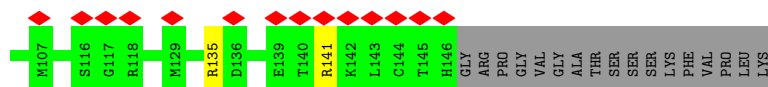
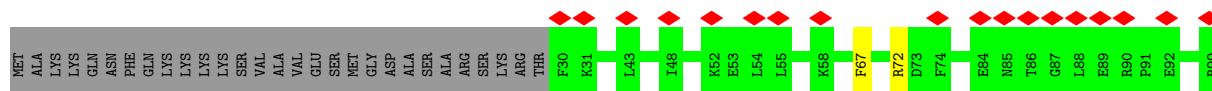
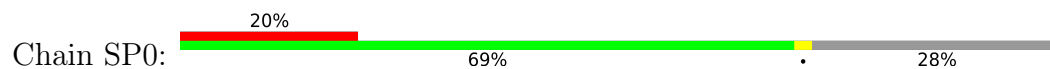


- Molecule 63: 40S ribosomal protein S14

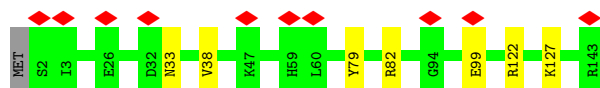
Chain SO0:  91% 5% 5%



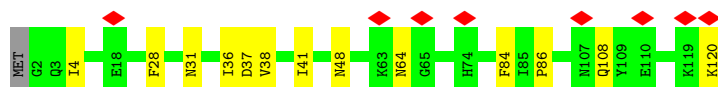
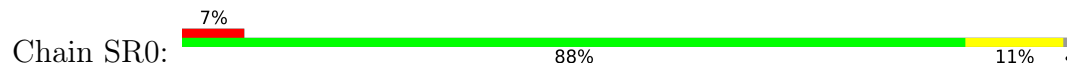
- Molecule 64: Ribosomal protein S19



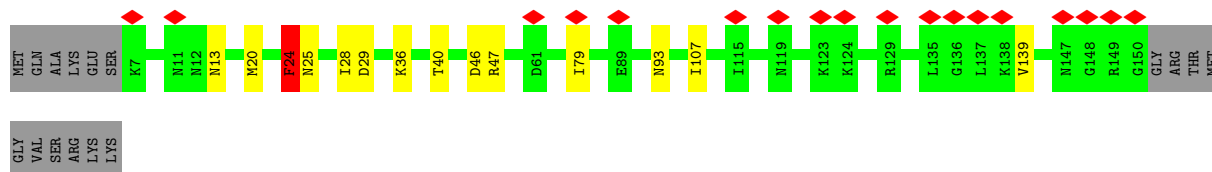
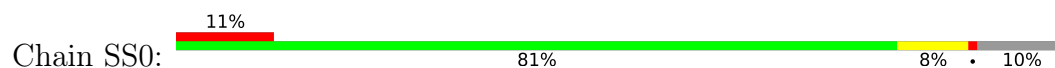
- Molecule 65: 40S ribosomal protein S16



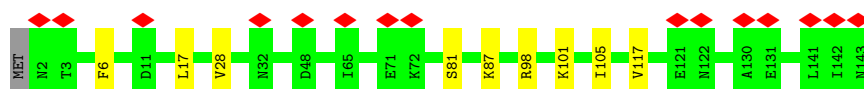
- Molecule 66: eS17 SR0



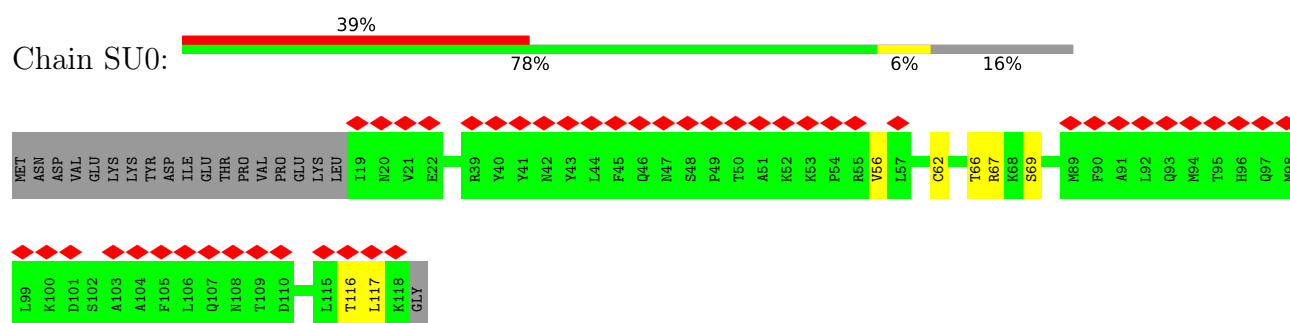
- Molecule 67: 40S ribosomal protein S18



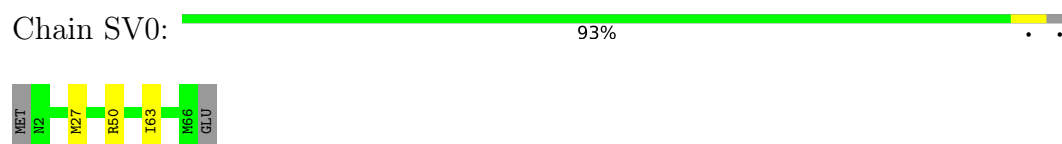
- Molecule 68: 40S Ribosomal protein S19



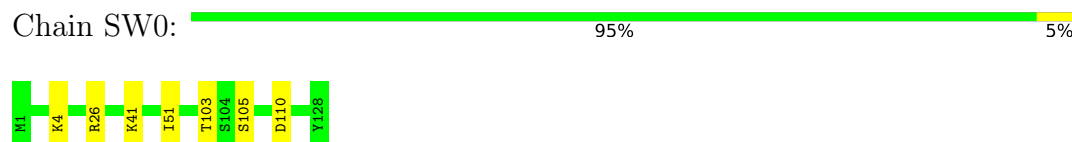
- Molecule 69: 40S ribosomal protein S20



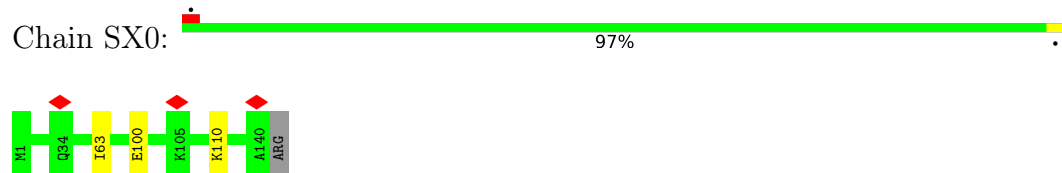
- Molecule 70: Ribosomal protein S21E



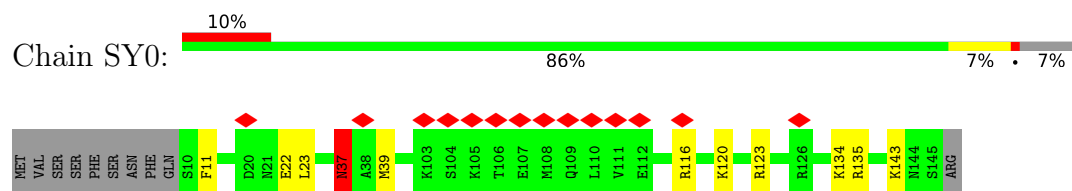
- Molecule 71: 40S ribosomal protein S15A



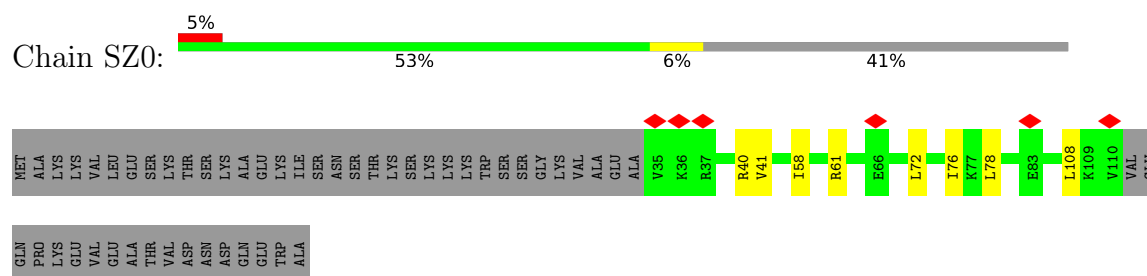
- Molecule 72: uS12 SX0



- Molecule 73: 40s ribosomal protein s24



- Molecule 74: 40S ribosomal protein S25



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 285940 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | TFS KRIOS, TFS TALOS | Depositor |
| Voltage (kV) | 300, 200 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 41.5, 41.34 | Depositor |
| Minimum defocus (nm) | 1200, 1200 | Depositor |
| Maximum defocus (nm) | 2500, 2500 | Depositor |
| Magnification | Not provided, Not provided | Depositor |
| Image detector | GATAN K3 BIOQUANTUM (6k x 4k), GATAN K2 SUMMIT (4k x 4k) | Depositor |
| Maximum map value | 2.403 | Depositor |
| Minimum map value | -0.069 | Depositor |
| Average map value | 0.008 | Depositor |
| Map value standard deviation | 0.061 | Depositor |
| Recommended contour level | 0.05356 | Depositor |
| Map size (Å) | 337.28, 337.28, 337.28 | wwPDB |
| Map dimensions | 320, 320, 320 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.054, 1.054, 1.054 | Depositor |

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, K, MG

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

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|----------------|-------------|------------------|
| | | RMSZ | $\# Z > 5$ | RMSZ | $\# Z > 5$ |
| 1 | L50 | 0.75 | 1/60107 (0.0%) | 1.19 | 158/93753 (0.2%) |
| 2 | L70 | 0.75 | 1/2844 (0.0%) | 1.10 | 6/4429 (0.1%) |
| 3 | LA0 | 0.32 | 0/1926 | 0.74 | 0/2590 |
| 4 | LAA | 0.34 | 0/1191 | 0.66 | 0/1586 |
| 5 | LB0 | 0.32 | 0/3092 | 0.70 | 1/4144 (0.0%) |
| 6 | LC0 | 0.32 | 0/2646 | 0.75 | 1/3555 (0.0%) |
| 7 | LCC | 0.32 | 0/794 | 0.62 | 0/1067 |
| 8 | LD0 | 0.28 | 0/2328 | 0.67 | 0/3098 |
| 9 | LDD | 0.29 | 0/913 | 0.66 | 0/1223 |
| 10 | LE0 | 0.27 | 0/1394 | 0.65 | 0/1875 |
| 11 | LEE | 0.32 | 0/1108 | 0.69 | 0/1477 |
| 12 | LF0 | 0.30 | 0/1963 | 0.68 | 0/2618 |
| 13 | LFF | 0.33 | 0/906 | 0.70 | 0/1207 |
| 14 | LG0 | 0.28 | 0/1612 | 0.63 | 0/2163 |
| 15 | LGG | 0.34 | 0/825 | 0.77 | 1/1090 (0.1%) |
| 16 | LH0 | 0.30 | 0/1503 | 0.65 | 0/2018 |
| 17 | LHH | 0.28 | 0/999 | 0.66 | 0/1324 |
| 18 | LI0 | 0.31 | 0/1781 | 0.69 | 0/2382 |
| 19 | LII | 0.29 | 0/790 | 0.59 | 0/1041 |
| 20 | LJ0 | 0.30 | 0/1350 | 0.66 | 0/1797 |
| 21 | LJJ | 0.40 | 0/710 | 0.82 | 2/932 (0.2%) |
| 22 | LL0 | 0.30 | 0/1374 | 0.76 | 1/1827 (0.1%) |
| 23 | LLL | 0.34 | 0/435 | 0.72 | 0/576 |
| 24 | LM0 | 0.31 | 0/935 | 0.66 | 0/1251 |
| 25 | LMM | 0.41 | 0/431 | 0.68 | 0/568 |
| 26 | LN0 | 0.35 | 0/1722 | 0.74 | 1/2297 (0.0%) |
| 27 | LO0 | 0.30 | 0/1626 | 0.65 | 0/2168 |
| 28 | LOO | 0.34 | 0/811 | 0.69 | 0/1071 |
| 29 | LP0 | 0.31 | 0/1262 | 0.77 | 0/1689 |
| 30 | LPP | 0.40 | 0/693 | 0.78 | 2/918 (0.2%) |
| 31 | LQ0 | 0.30 | 0/1512 | 0.64 | 0/2014 |
| 32 | LR0 | 0.31 | 0/1352 | 0.65 | 1/1790 (0.1%) |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-----------------|-------------|-------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 33 | LS0 | 0.30 | 0/1422 | 0.66 | 0/1898 |
| 34 | LT0 | 0.31 | 0/1294 | 0.68 | 0/1736 |
| 35 | LU0 | 0.30 | 0/826 | 0.67 | 0/1104 |
| 36 | LV0 | 0.31 | 0/1068 | 0.70 | 0/1429 |
| 37 | LW0 | 0.30 | 0/849 | 0.69 | 0/1129 |
| 38 | LX0 | 0.28 | 0/883 | 0.67 | 0/1175 |
| 39 | LY0 | 0.29 | 0/1058 | 0.68 | 1/1399 (0.1%) |
| 40 | LZ0 | 0.29 | 0/976 | 0.73 | 1/1302 (0.1%) |
| 41 | S60 | 0.71 | 1/32725 (0.0%) | 1.07 | 53/51066 (0.1%) |
| 42 | SA0 | 0.35 | 1/1751 (0.1%) | 0.64 | 0/2358 |
| 43 | SAA | 0.38 | 0/839 | 0.72 | 0/1120 |
| 44 | SB0 | 0.29 | 0/1623 | 0.67 | 0/2169 |
| 45 | SBB | 0.47 | 1/634 (0.2%) | 0.65 | 0/844 |
| 46 | SC0 | 0.31 | 0/1751 | 0.69 | 2/2359 (0.1%) |
| 47 | SCC | 0.33 | 0/480 | 0.73 | 0/644 |
| 48 | SD0 | 0.30 | 0/1721 | 0.66 | 0/2304 |
| 49 | SDD | 0.39 | 0/559 | 0.75 | 1/742 (0.1%) |
| 50 | SE0 | 0.32 | 0/2080 | 0.72 | 3/2804 (0.1%) |
| 51 | SEE | 0.35 | 0/453 | 0.74 | 1/596 (0.2%) |
| 52 | SF0 | 0.31 | 0/1527 | 0.68 | 0/2045 |
| 53 | SFF | 0.42 | 0/453 | 0.68 | 0/606 |
| 54 | SG0 | 0.29 | 0/1863 | 0.68 | 0/2483 |
| 55 | SGG | 0.34 | 0/2517 | 0.71 | 1/3397 (0.0%) |
| 56 | SH0 | 0.31 | 0/1356 | 0.66 | 0/1820 |
| 57 | SI0 | 0.33 | 0/1369 | 0.67 | 0/1825 |
| 58 | SJ0 | 0.32 | 0/1403 | 0.68 | 0/1880 |
| 59 | SK0 | 0.30 | 0/778 | 0.70 | 0/1047 |
| 60 | SL0 | 0.32 | 0/1252 | 0.72 | 2/1672 (0.1%) |
| 61 | SM0 | 0.32 | 0/881 | 0.71 | 0/1182 |
| 62 | SN0 | 0.37 | 0/1154 | 0.78 | 0/1557 |
| 63 | SO0 | 0.32 | 0/993 | 0.72 | 0/1326 |
| 64 | SP0 | 0.33 | 0/964 | 0.71 | 0/1289 |
| 65 | SQ0 | 0.32 | 0/1163 | 0.74 | 3/1556 (0.2%) |
| 66 | SR0 | 0.33 | 0/988 | 0.75 | 1/1319 (0.1%) |
| 67 | SS0 | 0.34 | 0/1165 | 0.74 | 0/1566 |
| 68 | ST0 | 0.34 | 0/1181 | 0.75 | 1/1585 (0.1%) |
| 69 | SU0 | 0.32 | 0/824 | 0.74 | 2/1110 (0.2%) |
| 70 | SV0 | 0.33 | 0/525 | 0.65 | 0/700 |
| 71 | SW0 | 0.32 | 0/1037 | 0.71 | 0/1389 |
| 72 | SX0 | 0.31 | 0/1113 | 0.70 | 0/1486 |
| 73 | SY0 | 0.30 | 0/1131 | 0.72 | 1/1503 (0.1%) |
| 74 | SZ0 | 0.33 | 0/640 | 0.75 | 0/855 |
| All | All | 0.58 | 5/182204 (0.0%) | 0.98 | 247/264914 (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 |
|-----|-------|---------------------|---------------------|
| 6 | LC0 | 0 | 1 |
| 13 | LFF | 0 | 1 |
| 15 | LGG | 0 | 1 |
| 66 | SR0 | 0 | 1 |
| All | All | 0 | 4 |

All (5) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 42 | SA0 | 20 | CYS | C-N | 8.40 | 1.53 | 1.34 |
| 1 | L50 | 1 | A | OP3-P | -8.34 | 1.51 | 1.61 |
| 41 | S60 | 1 | A | OP3-P | -7.55 | 1.52 | 1.61 |
| 2 | L70 | 1 | A | OP3-P | -7.35 | 1.52 | 1.61 |
| 45 | SBB | 58 | CYS | CB-SG | -5.21 | 1.73 | 1.81 |

The worst 5 of 247 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-------------|--------|-------------|----------|
| 41 | S60 | 1356 | C | O5'-P-OP1 | -18.04 | 89.06 | 110.70 |
| 1 | L50 | 330 | G | C2'-C3'-O3' | 10.41 | 132.39 | 109.50 |
| 1 | L50 | 1265 | G | OP1-P-OP2 | -9.86 | 104.81 | 119.60 |
| 1 | L50 | 535 | A | P-O3'-C3' | 9.42 | 131.00 | 119.70 |
| 1 | L50 | 1395 | U | C2'-C3'-O3' | 9.04 | 129.39 | 109.50 |

There are no chirality outliers.

All (4) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 6 | LC0 | 87 | ALA | Peptide |
| 13 | LFF | 101 | ILE | Peptide |
| 15 | LGG | 77 | GLY | Peptide |
| 66 | SR0 | 64 | ASN | Peptide |

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 | L50 | 53655 | 0 | 26937 | 97 | 0 |
| 2 | L70 | 2542 | 0 | 1282 | 8 | 0 |
| 3 | LA0 | 1889 | 0 | 1985 | 3 | 0 |
| 4 | LAA | 1167 | 0 | 1214 | 5 | 0 |
| 5 | LB0 | 3039 | 0 | 3183 | 5 | 0 |
| 6 | LC0 | 2604 | 0 | 2638 | 10 | 0 |
| 7 | LCC | 781 | 0 | 803 | 2 | 0 |
| 8 | LD0 | 2298 | 0 | 2384 | 7 | 0 |
| 9 | LDD | 895 | 0 | 948 | 0 | 0 |
| 10 | LE0 | 1371 | 0 | 1389 | 13 | 0 |
| 11 | LEE | 1090 | 0 | 1173 | 10 | 0 |
| 12 | LF0 | 1933 | 0 | 2011 | 10 | 0 |
| 13 | LFF | 893 | 0 | 945 | 2 | 0 |
| 14 | LG0 | 1590 | 0 | 1709 | 4 | 0 |
| 15 | LGG | 819 | 0 | 882 | 1 | 0 |
| 16 | LH0 | 1477 | 0 | 1528 | 4 | 0 |
| 17 | LHH | 992 | 0 | 1097 | 5 | 0 |
| 18 | LI0 | 1750 | 0 | 1797 | 2 | 0 |
| 19 | LII | 784 | 0 | 873 | 2 | 0 |
| 20 | LJ0 | 1332 | 0 | 1411 | 6 | 0 |
| 21 | LJJ | 701 | 0 | 753 | 4 | 0 |
| 22 | LL0 | 1353 | 0 | 1433 | 4 | 0 |
| 23 | LLL | 427 | 0 | 468 | 0 | 0 |
| 24 | LM0 | 927 | 0 | 961 | 3 | 0 |
| 25 | LMM | 427 | 0 | 461 | 0 | 0 |
| 26 | LN0 | 1688 | 0 | 1752 | 5 | 0 |
| 27 | LO0 | 1598 | 0 | 1681 | 4 | 0 |
| 28 | LOO | 801 | 0 | 886 | 3 | 0 |
| 29 | LP0 | 1238 | 0 | 1304 | 3 | 0 |
| 30 | LPP | 684 | 0 | 720 | 2 | 0 |
| 31 | LQ0 | 1491 | 0 | 1587 | 7 | 0 |
| 32 | LR0 | 1336 | 0 | 1430 | 1 | 0 |
| 33 | LS0 | 1400 | 0 | 1450 | 1 | 0 |
| 34 | LT0 | 1270 | 0 | 1321 | 16 | 0 |
| 35 | LU0 | 810 | 0 | 834 | 1 | 0 |
| 36 | LV0 | 1057 | 0 | 1139 | 2 | 0 |
| 37 | LW0 | 832 | 0 | 873 | 31 | 0 |
| 38 | LX0 | 874 | 0 | 956 | 5 | 0 |
| 39 | LY0 | 1048 | 0 | 1135 | 2 | 0 |
| 40 | LZ0 | 963 | 0 | 1022 | 2 | 0 |
| 41 | S60 | 29181 | 0 | 14618 | 125 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 42 | SA0 | 1725 | 0 | 1750 | 15 | 0 |
| 43 | SAA | 827 | 0 | 859 | 1 | 0 |
| 44 | SB0 | 1609 | 0 | 1728 | 6 | 0 |
| 45 | SBB | 627 | 0 | 651 | 3 | 0 |
| 46 | SC0 | 1727 | 0 | 1802 | 4 | 0 |
| 47 | SCC | 476 | 0 | 488 | 4 | 0 |
| 48 | SD0 | 1700 | 0 | 1815 | 7 | 0 |
| 49 | SDD | 550 | 0 | 542 | 4 | 0 |
| 50 | SE0 | 2044 | 0 | 2116 | 26 | 0 |
| 51 | SEE | 447 | 0 | 483 | 1 | 0 |
| 52 | SF0 | 1509 | 0 | 1604 | 22 | 0 |
| 53 | SFF | 447 | 0 | 456 | 14 | 0 |
| 54 | SG0 | 1835 | 0 | 1968 | 27 | 0 |
| 55 | SGG | 2478 | 0 | 2458 | 4 | 0 |
| 56 | SH0 | 1335 | 0 | 1356 | 2 | 0 |
| 57 | SI0 | 1347 | 0 | 1379 | 9 | 0 |
| 58 | SJ0 | 1379 | 0 | 1436 | 6 | 0 |
| 59 | SK0 | 764 | 0 | 771 | 2 | 0 |
| 60 | SL0 | 1229 | 0 | 1302 | 5 | 0 |
| 61 | SM0 | 876 | 0 | 937 | 10 | 0 |
| 62 | SN0 | 1130 | 0 | 1188 | 7 | 0 |
| 63 | SO0 | 983 | 0 | 1028 | 9 | 0 |
| 64 | SP0 | 950 | 0 | 984 | 4 | 0 |
| 65 | SQ0 | 1143 | 0 | 1171 | 6 | 0 |
| 66 | SR0 | 977 | 0 | 1012 | 12 | 0 |
| 67 | SS0 | 1150 | 0 | 1207 | 17 | 0 |
| 68 | ST0 | 1161 | 0 | 1219 | 10 | 0 |
| 69 | SU0 | 809 | 0 | 838 | 5 | 0 |
| 70 | SV0 | 521 | 0 | 525 | 6 | 0 |
| 71 | SW0 | 1022 | 0 | 1052 | 7 | 0 |
| 72 | SX0 | 1098 | 0 | 1183 | 3 | 0 |
| 73 | SY0 | 1118 | 0 | 1166 | 13 | 0 |
| 74 | SZ0 | 633 | 0 | 678 | 16 | 0 |
| 75 | L50 | 145 | 0 | 0 | 0 | 0 |
| 75 | LA0 | 2 | 0 | 0 | 0 | 0 |
| 75 | LEE | 1 | 0 | 0 | 0 | 0 |
| 75 | LLL | 1 | 0 | 0 | 0 | 0 |
| 75 | LN0 | 1 | 0 | 0 | 0 | 0 |
| 75 | S60 | 44 | 0 | 0 | 0 | 0 |
| 75 | SN0 | 3 | 0 | 0 | 0 | 0 |
| 75 | SO0 | 2 | 0 | 0 | 0 | 0 |
| 76 | L50 | 104 | 0 | 0 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 76 | L70 | 4 | 0 | 0 | 0 | 0 |
| 76 | LB0 | 1 | 0 | 0 | 0 | 0 |
| 76 | LF0 | 1 | 0 | 0 | 0 | 0 |
| 76 | LII | 1 | 0 | 0 | 0 | 0 |
| 76 | LJJ | 1 | 0 | 0 | 0 | 0 |
| 76 | LV0 | 1 | 0 | 0 | 0 | 0 |
| 76 | S60 | 46 | 0 | 0 | 0 | 0 |
| 76 | SI0 | 1 | 0 | 0 | 0 | 0 |
| 77 | LGG | 1 | 0 | 0 | 0 | 0 |
| 77 | LJJ | 1 | 0 | 0 | 0 | 0 |
| 77 | LMM | 1 | 0 | 0 | 0 | 0 |
| 77 | LOO | 1 | 0 | 0 | 0 | 0 |
| 77 | LPP | 1 | 0 | 0 | 0 | 0 |
| 77 | SAA | 1 | 0 | 0 | 0 | 0 |
| 77 | SBB | 1 | 0 | 0 | 0 | 0 |
| 77 | SDD | 1 | 0 | 0 | 0 | 0 |
| 77 | SFF | 1 | 0 | 0 | 0 | 0 |
| All | All | 171001 | 0 | 132125 | 475 | 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 475 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) |
|--------------------|--------------------|--------------------------|-------------------|
| 52:SF0:90:ILE:HG23 | 74:SZ0:58:ILE:CD1 | 1.58 | 1.33 |
| 37:LW0:99:LYS:HA | 37:LW0:102:LYS:HE2 | 1.32 | 1.09 |
| 73:SY0:22:GLU:O | 73:SY0:23:LEU:HG | 1.54 | 1.08 |
| 74:SZ0:61:ARG:HD3 | 74:SZ0:76:ILE:HD11 | 1.36 | 1.07 |
| 34:LT0:126:PRO:HB2 | 34:LT0:128:LEU:HG | 1.34 | 1.07 |

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 | |
|-----|-------|---------------|------------|---------|----------|-------------|-----|
| 3 | LA0 | 243/246 (99%) | 236 (97%) | 7 (3%) | 0 | 100 | 100 |
| 4 | LAA | 145/147 (99%) | 142 (98%) | 3 (2%) | 0 | 100 | 100 |
| 5 | LB0 | 381/392 (97%) | 372 (98%) | 9 (2%) | 0 | 100 | 100 |
| 6 | LC0 | 325/328 (99%) | 313 (96%) | 11 (3%) | 1 (0%) | 41 | 70 |
| 7 | LCC | 97/110 (88%) | 94 (97%) | 2 (2%) | 1 (1%) | 15 | 41 |
| 8 | LD0 | 279/291 (96%) | 274 (98%) | 5 (2%) | 0 | 100 | 100 |
| 9 | LDD | 107/110 (97%) | 104 (97%) | 3 (3%) | 0 | 100 | 100 |
| 10 | LE0 | 163/171 (95%) | 154 (94%) | 9 (6%) | 0 | 100 | 100 |
| 11 | LEE | 133/139 (96%) | 127 (96%) | 6 (4%) | 0 | 100 | 100 |
| 12 | LF0 | 229/235 (97%) | 224 (98%) | 5 (2%) | 0 | 100 | 100 |
| 13 | LFF | 109/111 (98%) | 106 (97%) | 3 (3%) | 0 | 100 | 100 |
| 14 | LG0 | 197/206 (96%) | 194 (98%) | 3 (2%) | 0 | 100 | 100 |
| 15 | LGG | 102/106 (96%) | 96 (94%) | 5 (5%) | 1 (1%) | 15 | 41 |
| 16 | LH0 | 181/187 (97%) | 177 (98%) | 4 (2%) | 0 | 100 | 100 |
| 17 | LHH | 117/119 (98%) | 109 (93%) | 8 (7%) | 0 | 100 | 100 |
| 18 | LI0 | 215/218 (99%) | 214 (100%) | 1 (0%) | 0 | 100 | 100 |
| 19 | LII | 95/98 (97%) | 91 (96%) | 4 (4%) | 0 | 100 | 100 |
| 20 | LJ0 | 165/171 (96%) | 156 (94%) | 9 (6%) | 0 | 100 | 100 |
| 21 | LJJ | 87/92 (95%) | 86 (99%) | 1 (1%) | 0 | 100 | 100 |
| 22 | LL0 | 162/165 (98%) | 155 (96%) | 6 (4%) | 1 (1%) | 25 | 54 |
| 23 | LLL | 49/52 (94%) | 48 (98%) | 1 (2%) | 0 | 100 | 100 |
| 24 | LM0 | 113/122 (93%) | 106 (94%) | 6 (5%) | 1 (1%) | 17 | 44 |
| 25 | LMM | 50/127 (39%) | 50 (100%) | 0 | 0 | 100 | 100 |
| 26 | LN0 | 201/204 (98%) | 195 (97%) | 6 (3%) | 0 | 100 | 100 |
| 27 | LO0 | 196/198 (99%) | 193 (98%) | 3 (2%) | 0 | 100 | 100 |
| 28 | LOO | 98/104 (94%) | 96 (98%) | 2 (2%) | 0 | 100 | 100 |
| 29 | LP0 | 152/167 (91%) | 145 (95%) | 7 (5%) | 0 | 100 | 100 |
| 30 | LPP | 85/89 (96%) | 80 (94%) | 4 (5%) | 1 (1%) | 13 | 36 |
| 31 | LQ0 | 180/183 (98%) | 175 (97%) | 5 (3%) | 0 | 100 | 100 |
| 32 | LR0 | 162/168 (96%) | 160 (99%) | 2 (1%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|------------|---------|----------|-------------|-----|
| 33 | LS0 | 168/171 (98%) | 159 (95%) | 9 (5%) | 0 | 100 | 100 |
| 34 | LT0 | 154/158 (98%) | 145 (94%) | 9 (6%) | 0 | 100 | 100 |
| 35 | LU0 | 98/113 (87%) | 93 (95%) | 5 (5%) | 0 | 100 | 100 |
| 36 | LV0 | 139/142 (98%) | 137 (99%) | 2 (1%) | 0 | 100 | 100 |
| 37 | LW0 | 100/131 (76%) | 94 (94%) | 5 (5%) | 1 (1%) | 15 | 41 |
| 38 | LX0 | 110/113 (97%) | 106 (96%) | 4 (4%) | 0 | 100 | 100 |
| 39 | LY0 | 129/131 (98%) | 123 (95%) | 6 (5%) | 0 | 100 | 100 |
| 40 | LZ0 | 116/153 (76%) | 116 (100%) | 0 | 0 | 100 | 100 |
| 42 | SA0 | 218/233 (94%) | 206 (94%) | 12 (6%) | 0 | 100 | 100 |
| 43 | SAA | 99/102 (97%) | 98 (99%) | 1 (1%) | 0 | 100 | 100 |
| 44 | SB0 | 202/230 (88%) | 197 (98%) | 5 (2%) | 0 | 100 | 100 |
| 45 | SBB | 79/82 (96%) | 77 (98%) | 2 (2%) | 0 | 100 | 100 |
| 46 | SC0 | 224/248 (90%) | 220 (98%) | 4 (2%) | 0 | 100 | 100 |
| 47 | SCC | 60/65 (92%) | 57 (95%) | 3 (5%) | 0 | 100 | 100 |
| 48 | SD0 | 214/242 (88%) | 212 (99%) | 2 (1%) | 0 | 100 | 100 |
| 49 | SDD | 63/65 (97%) | 58 (92%) | 5 (8%) | 0 | 100 | 100 |
| 50 | SE0 | 258/280 (92%) | 247 (96%) | 11 (4%) | 0 | 100 | 100 |
| 51 | SEE | 54/60 (90%) | 53 (98%) | 1 (2%) | 0 | 100 | 100 |
| 52 | SF0 | 190/195 (97%) | 180 (95%) | 10 (5%) | 0 | 100 | 100 |
| 53 | SFF | 56/150 (37%) | 52 (93%) | 4 (7%) | 0 | 100 | 100 |
| 54 | SG0 | 227/230 (99%) | 213 (94%) | 14 (6%) | 0 | 100 | 100 |
| 55 | SGG | 315/326 (97%) | 295 (94%) | 19 (6%) | 1 (0%) | 41 | 70 |
| 56 | SH0 | 161/164 (98%) | 156 (97%) | 4 (2%) | 1 (1%) | 25 | 54 |
| 57 | SI0 | 165/173 (95%) | 161 (98%) | 4 (2%) | 0 | 100 | 100 |
| 58 | SJ0 | 166/184 (90%) | 165 (99%) | 1 (1%) | 0 | 100 | 100 |
| 59 | SK0 | 89/107 (83%) | 84 (94%) | 4 (4%) | 1 (1%) | 14 | 38 |
| 60 | SL0 | 148/155 (96%) | 141 (95%) | 7 (5%) | 0 | 100 | 100 |
| 61 | SM0 | 109/130 (84%) | 106 (97%) | 3 (3%) | 0 | 100 | 100 |
| 62 | SN0 | 140/143 (98%) | 134 (96%) | 6 (4%) | 0 | 100 | 100 |
| 63 | SO0 | 127/135 (94%) | 120 (94%) | 7 (6%) | 0 | 100 | 100 |
| 64 | SP0 | 115/163 (71%) | 113 (98%) | 2 (2%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 65 | SQ0 | 140/143 (98%) | 134 (96%) | 6 (4%) | 0 | 100 | 100 |
| 66 | SR0 | 117/120 (98%) | 112 (96%) | 5 (4%) | 0 | 100 | 100 |
| 67 | SS0 | 142/160 (89%) | 137 (96%) | 4 (3%) | 1 (1%) | 22 | 50 |
| 68 | ST0 | 140/143 (98%) | 140 (100%) | 0 | 0 | 100 | 100 |
| 69 | SU0 | 98/119 (82%) | 94 (96%) | 4 (4%) | 0 | 100 | 100 |
| 70 | SV0 | 63/67 (94%) | 62 (98%) | 1 (2%) | 0 | 100 | 100 |
| 71 | SW0 | 126/128 (98%) | 124 (98%) | 2 (2%) | 0 | 100 | 100 |
| 72 | SX0 | 138/141 (98%) | 136 (99%) | 2 (1%) | 0 | 100 | 100 |
| 73 | SY0 | 134/146 (92%) | 122 (91%) | 10 (8%) | 2 (2%) | 10 | 30 |
| 74 | SZ0 | 74/128 (58%) | 69 (93%) | 5 (7%) | 0 | 100 | 100 |
| All | All | 10483/11325 (93%) | 10120 (96%) | 350 (3%) | 13 (0%) | 54 | 80 |

5 of 13 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 15 | LGG | 78 | GLY |
| 73 | SY0 | 134 | LYS |
| 30 | LPP | 18 | TYR |
| 37 | LW0 | 81 | ARG |
| 67 | SS0 | 24 | PHE |

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 | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 3 | LA0 | 202/203 (100%) | 199 (98%) | 3 (2%) | 65 | 87 |
| 4 | LAA | 123/123 (100%) | 119 (97%) | 4 (3%) | 38 | 69 |
| 5 | LB0 | 328/336 (98%) | 319 (97%) | 9 (3%) | 44 | 75 |
| 6 | LC0 | 277/278 (100%) | 274 (99%) | 3 (1%) | 73 | 90 |
| 7 | LCC | 87/97 (90%) | 85 (98%) | 2 (2%) | 50 | 79 |
| 8 | LD0 | 251/261 (96%) | 249 (99%) | 2 (1%) | 81 | 93 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 9 | LDD | 99/100 (99%) | 99 (100%) | 0 | 100 | 100 |
| 10 | LE0 | 153/159 (96%) | 150 (98%) | 3 (2%) | 55 | 82 |
| 11 | LEE | 118/122 (97%) | 118 (100%) | 0 | 100 | 100 |
| 12 | LF0 | 212/216 (98%) | 211 (100%) | 1 (0%) | 88 | 95 |
| 13 | LFF | 98/98 (100%) | 98 (100%) | 0 | 100 | 100 |
| 14 | LG0 | 183/190 (96%) | 183 (100%) | 0 | 100 | 100 |
| 15 | LGG | 88/90 (98%) | 86 (98%) | 2 (2%) | 50 | 79 |
| 16 | LH0 | 165/169 (98%) | 161 (98%) | 4 (2%) | 49 | 78 |
| 17 | LHH | 110/110 (100%) | 109 (99%) | 1 (1%) | 78 | 92 |
| 18 | LI0 | 188/189 (100%) | 188 (100%) | 0 | 100 | 100 |
| 19 | LII | 84/84 (100%) | 82 (98%) | 2 (2%) | 49 | 78 |
| 20 | LJ0 | 146/149 (98%) | 144 (99%) | 2 (1%) | 67 | 87 |
| 21 | LJJ | 78/81 (96%) | 77 (99%) | 1 (1%) | 69 | 89 |
| 22 | LL0 | 148/149 (99%) | 142 (96%) | 6 (4%) | 30 | 61 |
| 23 | LLL | 46/47 (98%) | 46 (100%) | 0 | 100 | 100 |
| 24 | LM0 | 110/117 (94%) | 110 (100%) | 0 | 100 | 100 |
| 25 | LMM | 46/112 (41%) | 46 (100%) | 0 | 100 | 100 |
| 26 | LN0 | 175/176 (99%) | 171 (98%) | 4 (2%) | 50 | 79 |
| 27 | LO0 | 178/178 (100%) | 177 (99%) | 1 (1%) | 86 | 95 |
| 28 | LOO | 85/89 (96%) | 85 (100%) | 0 | 100 | 100 |
| 29 | LP0 | 135/147 (92%) | 132 (98%) | 3 (2%) | 52 | 80 |
| 30 | LPP | 75/77 (97%) | 73 (97%) | 2 (3%) | 44 | 75 |
| 31 | LQ0 | 165/166 (99%) | 165 (100%) | 0 | 100 | 100 |
| 32 | LR0 | 142/145 (98%) | 141 (99%) | 1 (1%) | 84 | 94 |
| 33 | LS0 | 155/156 (99%) | 152 (98%) | 3 (2%) | 57 | 83 |
| 34 | LT0 | 140/142 (99%) | 138 (99%) | 2 (1%) | 67 | 87 |
| 35 | LU0 | 89/98 (91%) | 88 (99%) | 1 (1%) | 73 | 90 |
| 36 | LV0 | 113/114 (99%) | 112 (99%) | 1 (1%) | 78 | 92 |
| 37 | LW0 | 93/120 (78%) | 89 (96%) | 4 (4%) | 29 | 59 |
| 38 | LX0 | 92/93 (99%) | 91 (99%) | 1 (1%) | 73 | 90 |
| 39 | LY0 | 116/116 (100%) | 114 (98%) | 2 (2%) | 60 | 85 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 40 | LZ0 | 106/141 (75%) | 106 (100%) | 0 | 100 | 100 |
| 42 | SA0 | 194/206 (94%) | 192 (99%) | 2 (1%) | 76 | 91 |
| 43 | SAA | 92/93 (99%) | 92 (100%) | 0 | 100 | 100 |
| 44 | SB0 | 182/203 (90%) | 182 (100%) | 0 | 100 | 100 |
| 45 | SBB | 72/73 (99%) | 71 (99%) | 1 (1%) | 67 | 87 |
| 46 | SC0 | 187/209 (90%) | 185 (99%) | 2 (1%) | 73 | 90 |
| 47 | SCC | 51/54 (94%) | 51 (100%) | 0 | 100 | 100 |
| 48 | SD0 | 189/215 (88%) | 189 (100%) | 0 | 100 | 100 |
| 49 | SDD | 57/57 (100%) | 57 (100%) | 0 | 100 | 100 |
| 50 | SE0 | 231/251 (92%) | 229 (99%) | 2 (1%) | 78 | 92 |
| 51 | SEE | 44/47 (94%) | 44 (100%) | 0 | 100 | 100 |
| 52 | SF0 | 167/170 (98%) | 163 (98%) | 4 (2%) | 49 | 78 |
| 53 | SFF | 52/136 (38%) | 51 (98%) | 1 (2%) | 57 | 83 |
| 54 | SG0 | 199/200 (100%) | 194 (98%) | 5 (2%) | 47 | 77 |
| 55 | SGG | 282/288 (98%) | 278 (99%) | 4 (1%) | 67 | 87 |
| 56 | SH0 | 153/154 (99%) | 153 (100%) | 0 | 100 | 100 |
| 57 | SI0 | 147/153 (96%) | 147 (100%) | 0 | 100 | 100 |
| 58 | SJ0 | 152/165 (92%) | 150 (99%) | 2 (1%) | 69 | 89 |
| 59 | SK0 | 86/99 (87%) | 85 (99%) | 1 (1%) | 71 | 90 |
| 60 | SL0 | 140/145 (97%) | 139 (99%) | 1 (1%) | 84 | 94 |
| 61 | SM0 | 99/114 (87%) | 99 (100%) | 0 | 100 | 100 |
| 62 | SN0 | 126/127 (99%) | 126 (100%) | 0 | 100 | 100 |
| 63 | SO0 | 102/108 (94%) | 101 (99%) | 1 (1%) | 76 | 91 |
| 64 | SP0 | 107/144 (74%) | 106 (99%) | 1 (1%) | 78 | 92 |
| 65 | SQ0 | 120/121 (99%) | 119 (99%) | 1 (1%) | 81 | 93 |
| 66 | SR0 | 110/111 (99%) | 109 (99%) | 1 (1%) | 78 | 92 |
| 67 | SS0 | 125/138 (91%) | 124 (99%) | 1 (1%) | 81 | 93 |
| 68 | ST0 | 129/130 (99%) | 127 (98%) | 2 (2%) | 62 | 86 |
| 69 | SU0 | 92/110 (84%) | 92 (100%) | 0 | 100 | 100 |
| 70 | SV0 | 61/63 (97%) | 61 (100%) | 0 | 100 | 100 |
| 71 | SW0 | 111/111 (100%) | 110 (99%) | 1 (1%) | 78 | 92 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|------------------|------------|----------|-------------|-----|
| 72 | SX0 | 115/116 (99%) | 115 (100%) | 0 | 100 | 100 |
| 73 | SY0 | 126/136 (93%) | 121 (96%) | 5 (4%) | 31 | 62 |
| 74 | SZ0 | 73/118 (62%) | 73 (100%) | 0 | 100 | 100 |
| All | All | 9372/10003 (94%) | 9264 (99%) | 108 (1%) | 72 | 90 |

5 of 108 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 33 | LS0 | 157 | ARG |
| 42 | SA0 | 154 | ILE |
| 67 | SS0 | 24 | PHE |
| 34 | LT0 | 55 | LYS |
| 37 | LW0 | 91 | VAL |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 1 | L50 | 2494/2618 (95%) | 738 (29%) | 102 (4%) |
| 2 | L70 | 118/119 (99%) | 36 (30%) | 4 (3%) |
| 41 | S60 | 1352/1368 (98%) | 507 (37%) | 65 (4%) |
| All | All | 3964/4105 (96%) | 1281 (32%) | 171 (4%) |

5 of 1281 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | L50 | 2 | U |
| 1 | L50 | 3 | A |
| 1 | L50 | 13 | A |
| 1 | L50 | 15 | G |
| 1 | L50 | 21 | U |

5 of 171 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 41 | S60 | 225 | A |
| 41 | S60 | 877 | G |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 41 | S60 | 283 | U |
| 41 | S60 | 445 | U |
| 41 | S60 | 980 | G |

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 368 ligands modelled in this entry, 368 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

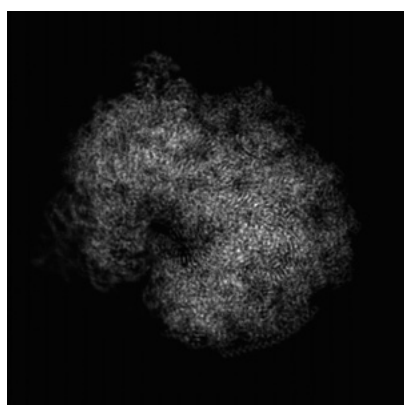
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13892. These allow visual inspection of the internal detail of the map and identification of artifacts.

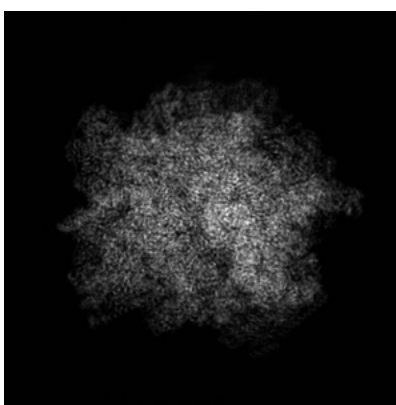
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

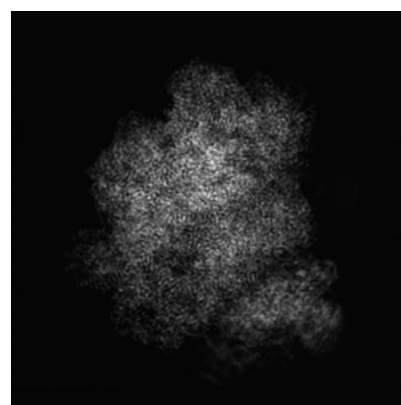
6.1.1 Primary map



X



Y



Z

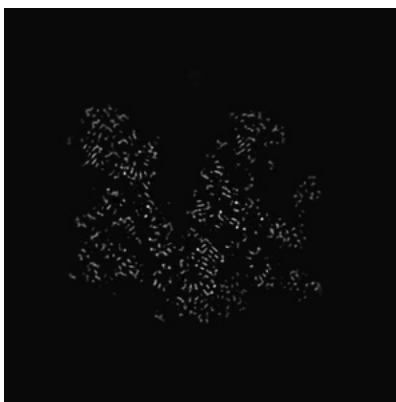
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 160



Y Index: 160



Z Index: 160

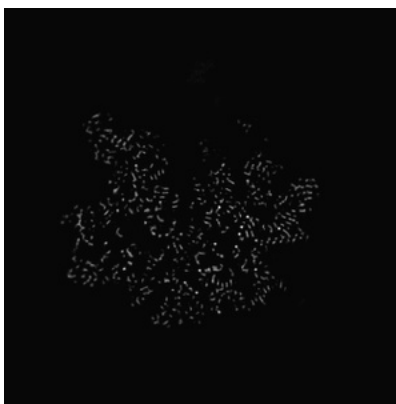
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 164



Y Index: 170

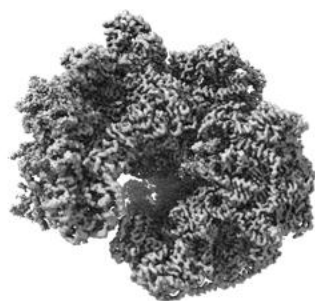


Z Index: 185

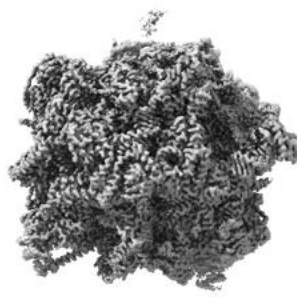
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

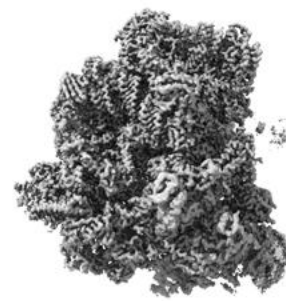
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05356. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

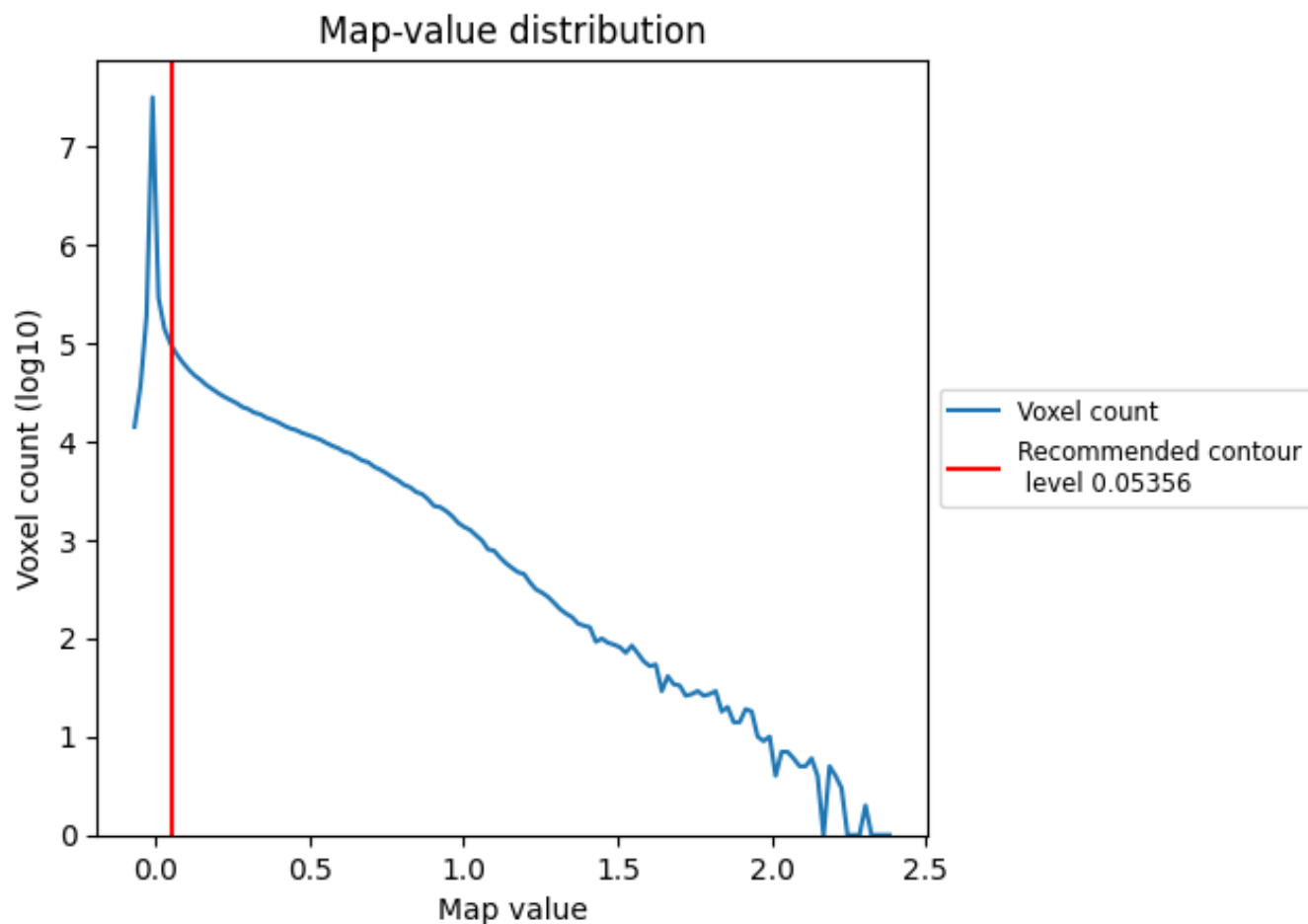
6.5 Mask visualisation

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

7 Map analysis [i](#)

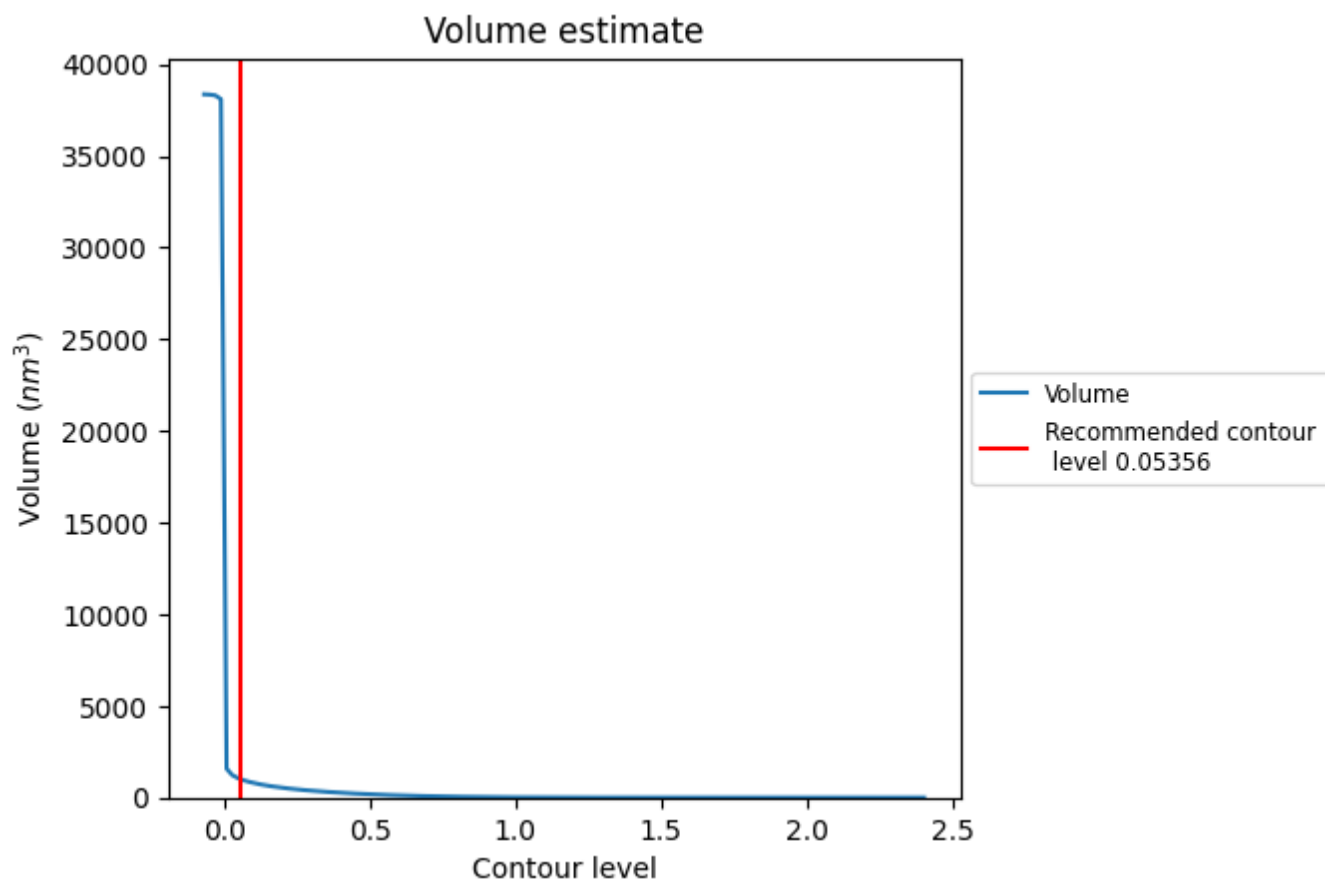
This section contains the results of statistical analysis of the map.

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.

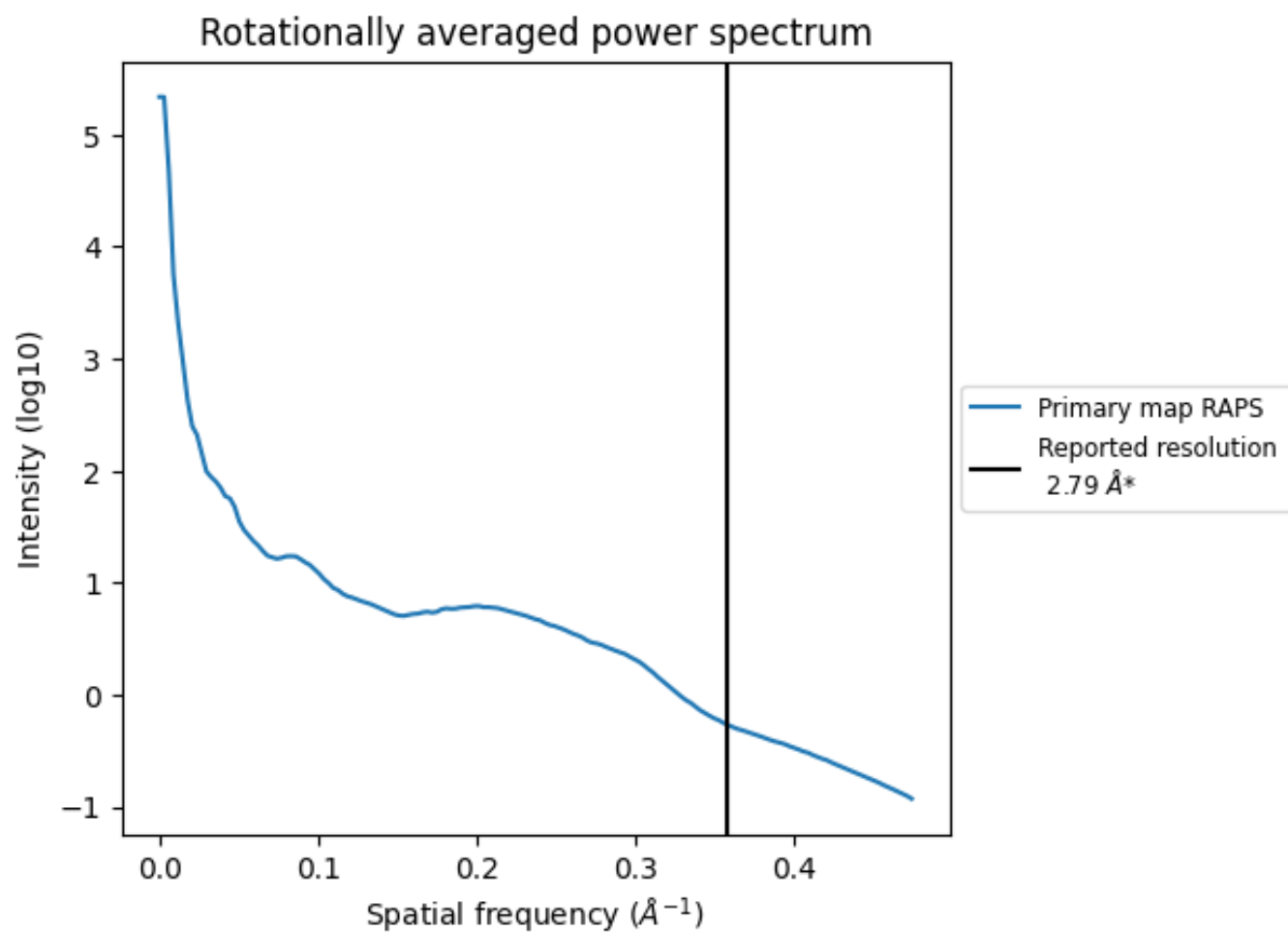
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1025 nm³; this corresponds to an approximate mass of 926 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 ⓘ

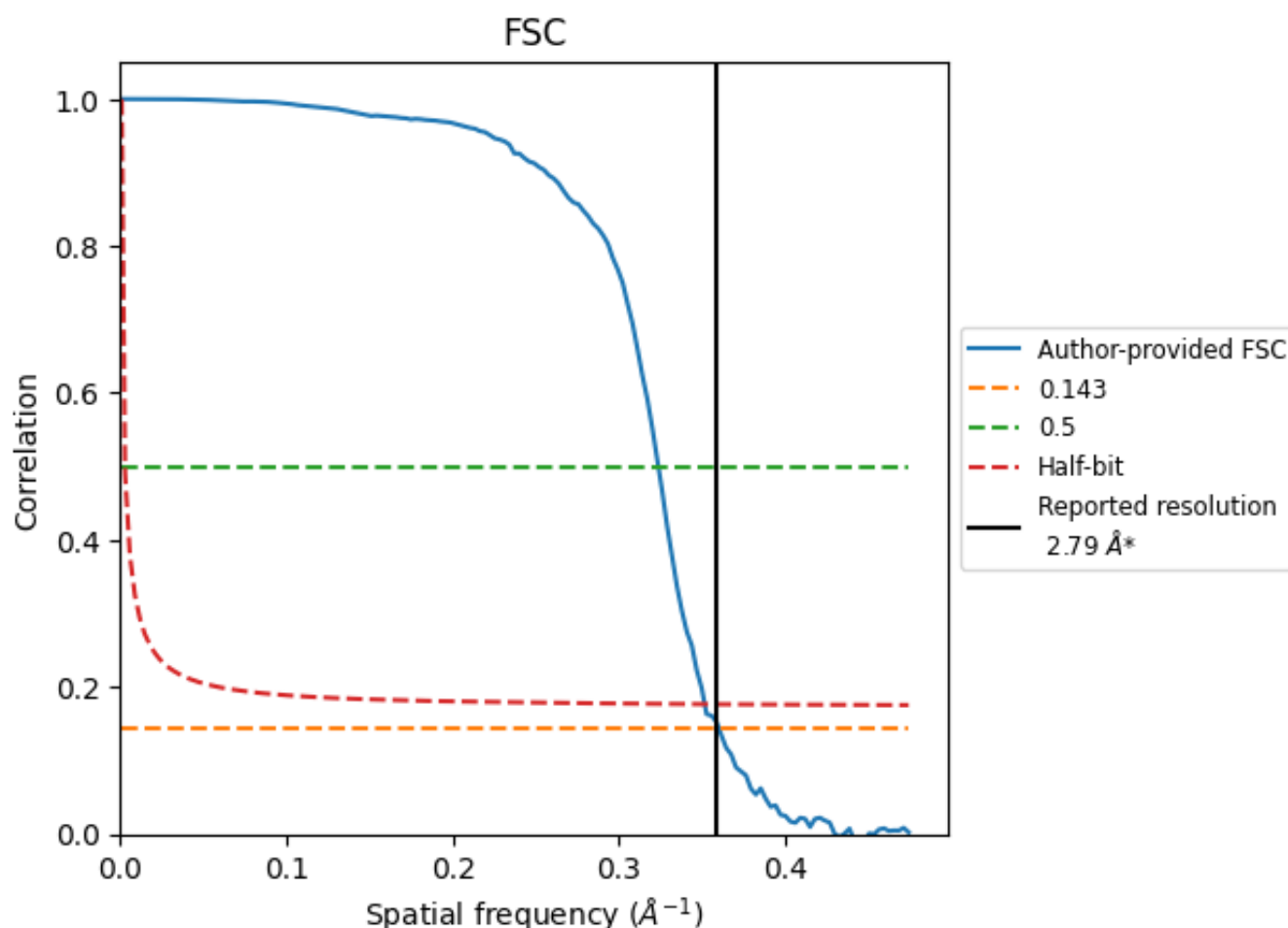


*Reported resolution corresponds to spatial frequency of 0.358 Å⁻¹

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 0.358 Å⁻¹

8.2 Resolution estimates [i](#)

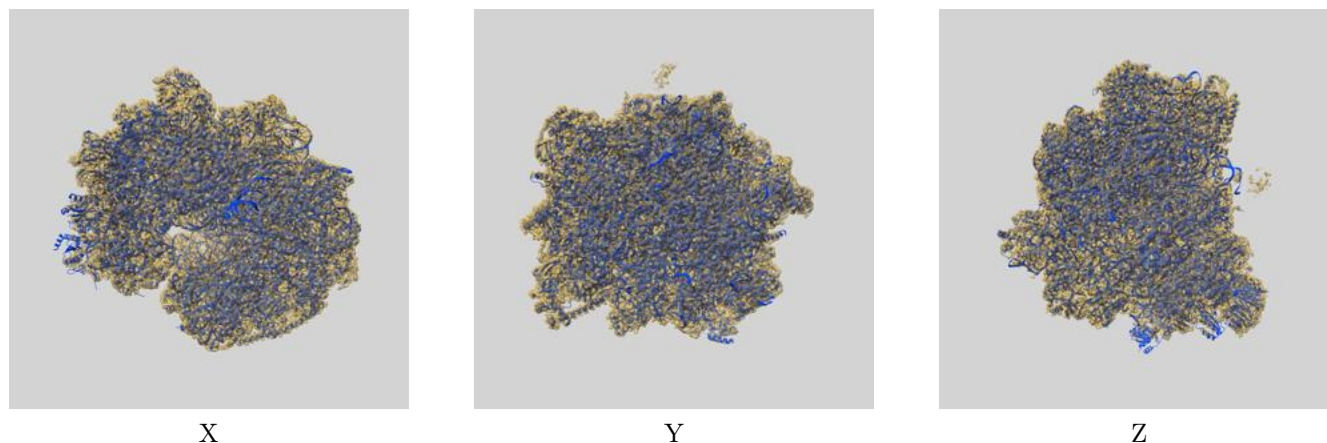
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 2.79 | - | - |
| Author-provided FSC curve | 2.78 | 3.09 | 2.84 |
| Unmasked-calculated* | - | - | - |

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

9 Map-model fit [i](#)

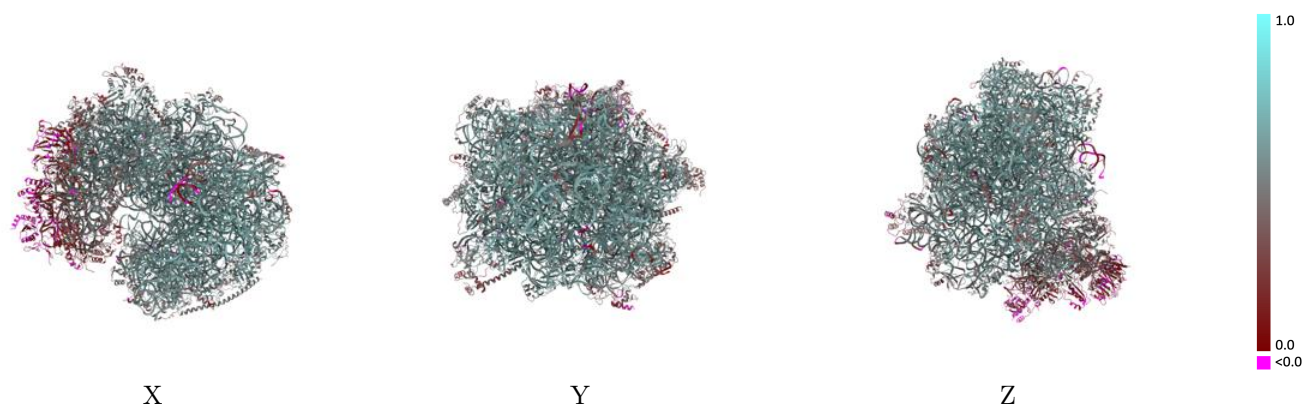
This section contains information regarding the fit between EMDB map EMD-13892 and PDB model 7QCA. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



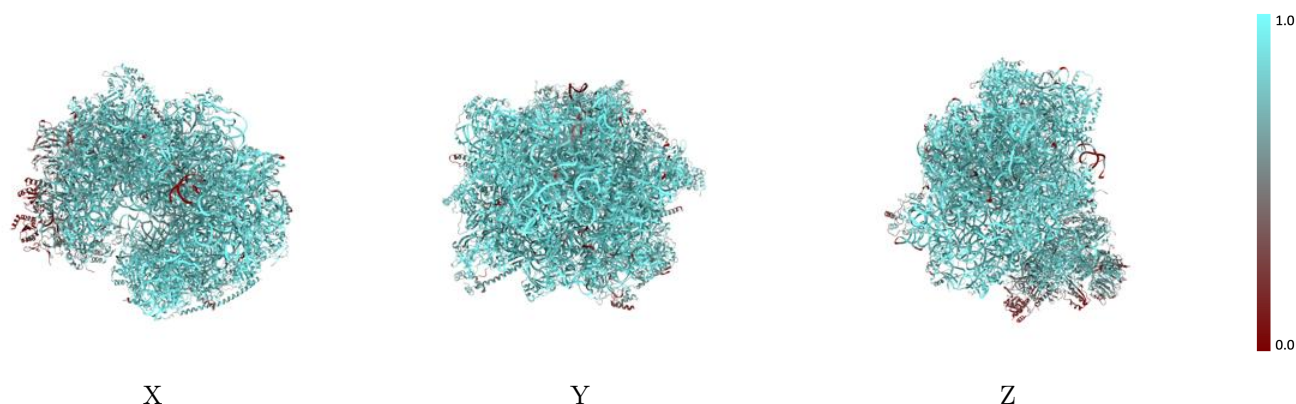
The images above show the 3D surface view of the map at the recommended contour level 0.05356 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



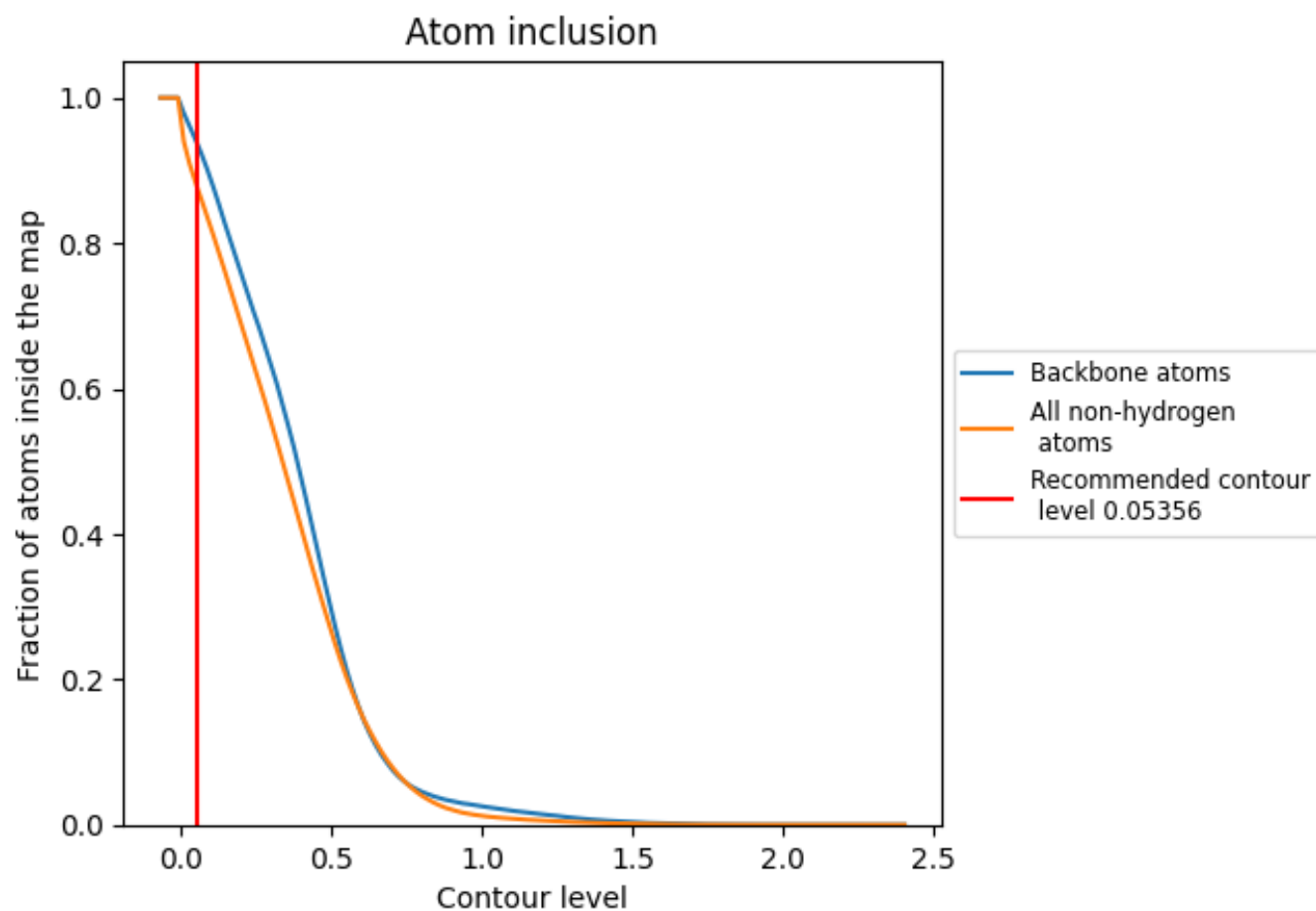
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05356).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 94% of all backbone atoms, 88% 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 (0.05356) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.8758 |  0.5380 |
| L50 |  0.9571 |  0.6180 |
| L70 |  0.9823 |  0.6100 |
| LA0 |  0.9152 |  0.6140 |
| LAA |  0.9394 |  0.6260 |
| LB0 |  0.9016 |  0.5950 |
| LC0 |  0.8954 |  0.5850 |
| LCC |  0.8846 |  0.5500 |
| LD0 |  0.8319 |  0.5000 |
| LDD |  0.8408 |  0.5610 |
| LE0 |  0.6949 |  0.4160 |
| LEE |  0.8717 |  0.5690 |
| LF0 |  0.8883 |  0.5650 |
| LFF |  0.8923 |  0.5860 |
| LG0 |  0.8534 |  0.5190 |
| LGG |  0.8766 |  0.5700 |
| LH0 |  0.8928 |  0.5730 |
| LHH |  0.8595 |  0.5520 |
| LI0 |  0.8708 |  0.5640 |
| LII |  0.8253 |  0.5130 |
| LJ0 |  0.8046 |  0.4680 |
| LJJ |  0.9197 |  0.6250 |
| LL0 |  0.8892 |  0.5740 |
| LLL |  0.9225 |  0.6080 |
| LM0 |  0.7636 |  0.4460 |
| LMM |  0.8683 |  0.5660 |
| LN0 |  0.9733 |  0.6600 |
| LO0 |  0.8702 |  0.5570 |
| LOO |  0.8524 |  0.5540 |
| LP0 |  0.8923 |  0.5830 |
| LPP |  0.9140 |  0.6080 |
| LQ0 |  0.8868 |  0.5790 |
| LR0 |  0.8421 |  0.5420 |
| LS0 |  0.8808 |  0.5620 |
| LT0 |  0.8266 |  0.5340 |



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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| LU0 |  0.8105 |  0.4960 |
| LV0 |  0.9071 |  0.6030 |
| LW0 |  0.5831 |  0.4010 |
| LX0 |  0.8621 |  0.5650 |
| LY0 |  0.8202 |  0.5360 |
| LZ0 |  0.8150 |  0.4790 |
| S60 |  0.9328 |  0.5490 |
| SA0 |  0.7814 |  0.4370 |
| SAA |  0.8697 |  0.5430 |
| SB0 |  0.8293 |  0.5060 |
| SBB |  0.8774 |  0.5250 |
| SC0 |  0.8400 |  0.5030 |
| SCC |  0.6746 |  0.4050 |
| SD0 |  0.5728 |  0.2460 |
| SDD |  0.6061 |  0.2920 |
| SE0 |  0.8342 |  0.5000 |
| SEE |  0.6124 |  0.4200 |
| SF0 |  0.7493 |  0.4160 |
| SFF |  0.1091 |  0.0310 |
| SG0 |  0.7032 |  0.4000 |
| SGG |  0.5549 |  0.1570 |
| SH0 |  0.8184 |  0.4420 |
| SI0 |  0.8881 |  0.5450 |
| SJ0 |  0.8682 |  0.5180 |
| SK0 |  0.4450 |  0.1240 |
| SL0 |  0.8354 |  0.5200 |
| SM0 |  0.1138 |  0.0140 |
| SN0 |  0.9128 |  0.5590 |
| SO0 |  0.8822 |  0.5480 |
| SP0 |  0.5179 |  0.1740 |
| SQ0 |  0.7363 |  0.3400 |
| SR0 |  0.6848 |  0.2960 |
| SS0 |  0.6414 |  0.2850 |
| ST0 |  0.6954 |  0.2540 |
| SU0 |  0.4053 |  0.1760 |
| SV0 |  0.8425 |  0.4920 |
| SW0 |  0.9333 |  0.5830 |
| SX0 |  0.8447 |  0.5300 |
| SY0 |  0.6700 |  0.3780 |
| SZ0 |  0.6591 |  0.2470 |