



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 1, 2020 – 11:59 AM BST

PDB ID : 5DC3
Title : Complex of yeast 80S ribosome with non-modified eIF5A
Authors : Melnikov, S.; Mailliot, J.; Shin, B.-S.; Rigger, L.; Yusupova, G.; Micura, R.;
Dever, T.E.; Yusupov, M.
Deposited on : 2015-08-23
Resolution : 3.25 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.14.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.14.1

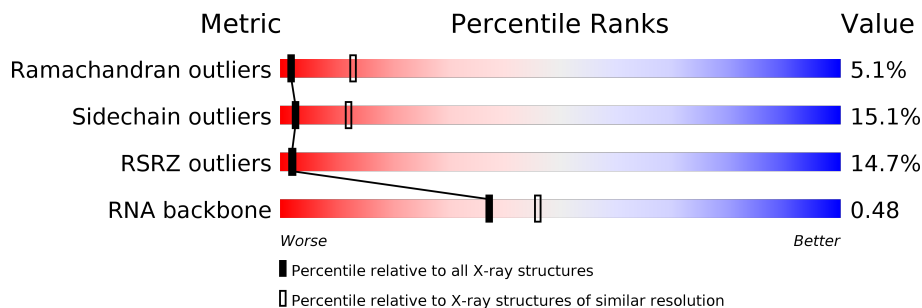
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 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) | Similar resolution (#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|---|
| Ramachandran outliers | 138981 | 1229 (3.30-3.22) |
| Sidechain outliers | 138945 | 1228 (3.30-3.22) |
| RSRZ outliers | 127900 | 1154 (3.30-3.22) |
| RNA backbone | 3102 | 1072 (3.62-2.90) |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower 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 electron density. The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | 2 | 1800 | |
| 1 | 6 | 1800 | |
| 2 | S0 | 251 | |
| 2 | s0 | 251 | |
| 3 | S1 | 254 | |
| 3 | s1 | 254 | |
| 4 | S2 | 253 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|-------------------------------|
| 4 | s2 | 253 | 23% 68% 16% 14% |
| 5 | S3 | 239 | 37% 77% 16% 7% |
| 5 | s3 | 239 | 47% 77% 15% 7% |
| 6 | S4 | 260 | 28% 82% 17% . |
| 6 | s4 | 260 | 9% 84% 15% . |
| 7 | S5 | 224 | 18% 79% 12% 8% |
| 7 | s5 | 224 | 23% 74% 17% 8% |
| 8 | S6 | 236 | 25% 81% 15% . |
| 8 | s6 | 236 | 11% 78% 14% 8% |
| 9 | S7 | 189 | 20% 75% 20% .. |
| 9 | s7 | 189 | 14% 81% 16% .. |
| 10 | S8 | 200 | 28% 82% 12% 6% |
| 10 | s8 | 200 | 18% 82% 13% 6% |
| 11 | S9 | 196 | 25% 79% 14% 6% |
| 11 | s9 | 196 | 8% 76% 17% 6% |
| 12 | C0 | 105 | 26% 74% 16% 9% |
| 13 | C1 | 155 | 46% 91% 8% . |
| 13 | c1 | 155 | 21% 83% 10% 6% |
| 14 | C2 | 142 | 21% 68% 18% 13% |
| 14 | c2 | 142 | 36% 68% 20% 13% |
| 15 | C3 | 150 | 27% 83% 15% . |
| 15 | c3 | 150 | 30% 83% 15% . |
| 16 | C4 | 136 | 18% 74% 17% 7% |
| 16 | c4 | 136 | 26% 79% 13% 6% |
| 17 | C5 | 141 | 6% 68% 16% .. 12% |

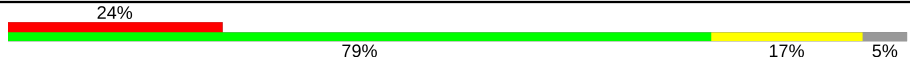
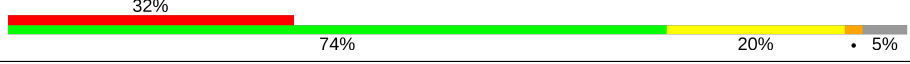



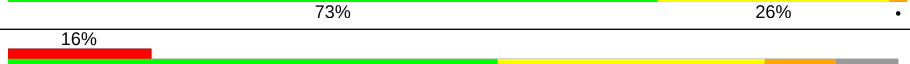
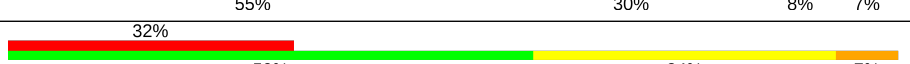
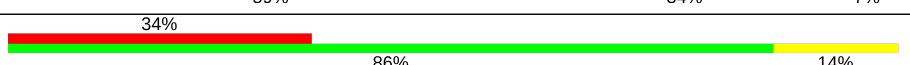
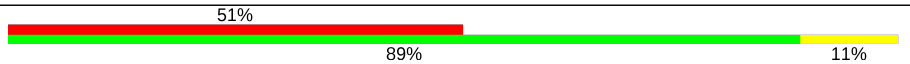
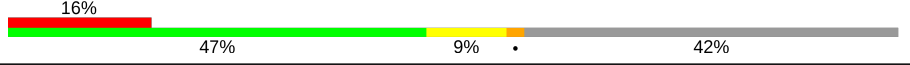
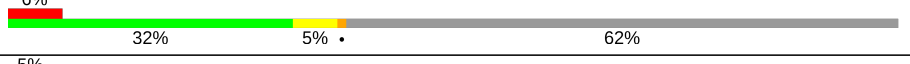
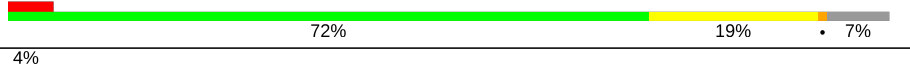

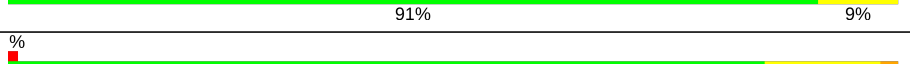
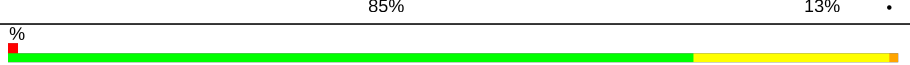










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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--------------------------|
| 17 | c5 | 141 | 19% 75% 17% |
| 18 | C6 | 142 | 65% 82% 17% |
| 18 | c6 | 142 | 52% 79% 21% |
| 19 | C7 | 136 | 60% 72% 13% 12% |
| 19 | c7 | 136 | 31% 73% 12% 14% |
| 20 | C8 | 145 | 6% 81% 18% |
| 20 | c8 | 145 | 4% 80% 19% |
| 21 | C9 | 143 | 57% 84% 16% |
| 21 | c9 | 143 | 19% 92% 6% |
| 22 | D0 | 120 | 35% 74% 15% 11% |
| 22 | d0 | 120 | 44% 76% 16% 8% |
| 23 | D1 | 87 | 49% 77% 23% |
| 23 | d1 | 87 | 21% 82% 17% |
| 24 | D2 | 129 | 82% 82% 16% |
| 24 | d2 | 129 | 29% 84% 15% |
| 25 | D3 | 144 | 28% 82% 16% |
| 25 | d3 | 144 | 15% 90% 10% |
| 26 | D4 | 134 | 9% 87% 13% |
| 26 | d4 | 134 | 3% 83% 16% |
| 27 | D5 | 107 | 5% 48% 18% 35% |
| 27 | d5 | 107 | 6% 55% 9% 36% |
| 28 | D6 | 97 | 59% 78% 16% 5% |
| 28 | d6 | 97 | 54% 86% 14% |
| 29 | D7 | 81 | 43% 89% 11% |
| 29 | d7 | 81 | 41% 84% 16% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 30 | D8 | 66 |  |
| 30 | d8 | 66 |  |
| 31 | D9 | 55 |  |
| 31 | d9 | 55 |  |
| 32 | E0 | 62 |  |
| 32 | e0 | 62 |  |
| 33 | E1 | 76 |  |
| 33 | e1 | 76 |  |
| 34 | SR | 318 |  |
| 34 | sR | 318 |  |
| 35 | SM | 273 |  |
| 35 | sM | 273 |  |
| 36 | 1 | 3396 |  |
| 36 | 5 | 3396 |  |
| 37 | 3 | 121 |  |
| 37 | 7 | 121 |  |
| 38 | 4 | 158 |  |
| 38 | 8 | 158 |  |
| 39 | L2 | 253 |  |
| 39 | l2 | 253 |  |
| 40 | L3 | 386 |  |
| 40 | l3 | 386 |  |
| 41 | L4 | 361 |  |
| 41 | l4 | 361 |  |
| 42 | L5 | 296 |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 42 | l5 | 296 | |
| 43 | L6 | 175 | |
| 43 | l6 | 175 | |
| 44 | L7 | 243 | |
| 44 | l7 | 243 | |
| 45 | L8 | 255 | |
| 45 | l8 | 255 | |
| 46 | L9 | 191 | |
| 46 | l9 | 191 | |
| 47 | M0 | 220 | |
| 47 | m0 | 220 | |
| 48 | M1 | 173 | |
| 48 | m1 | 173 | |
| 49 | M3 | 198 | |
| 49 | m3 | 198 | |
| 50 | M4 | 137 | |
| 50 | m4 | 137 | |
| 51 | M5 | 203 | |
| 51 | m5 | 203 | |
| 52 | M6 | 198 | |
| 52 | m6 | 198 | |
| 53 | M7 | 183 | |
| 53 | m7 | 183 | |
| 54 | M8 | 185 | |
| 54 | m8 | 185 | |

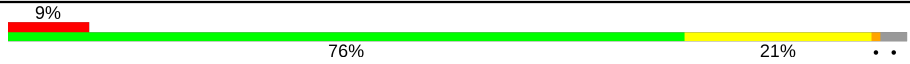
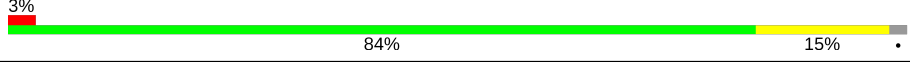

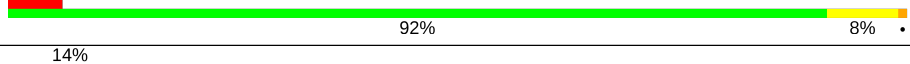

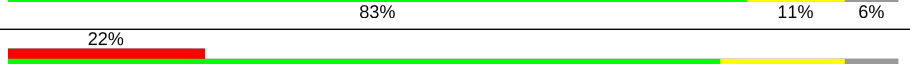
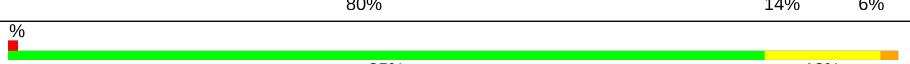
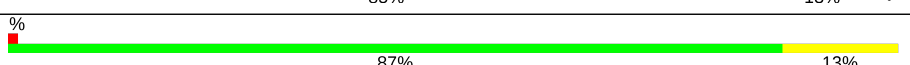
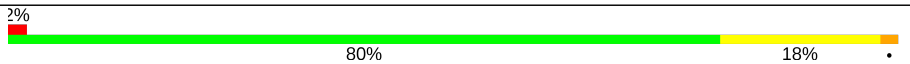


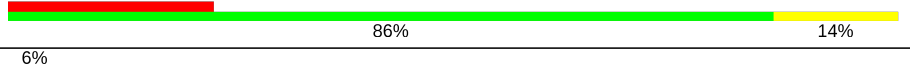

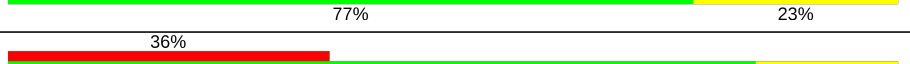
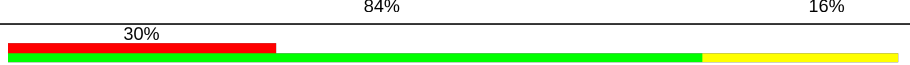










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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--------------------------|
| 55 | M9 | 188 | 11% 87% 13% |
| 55 | m9 | 188 | 7% 87% 13% |
| 56 | N0 | 172 | 3% 84% 16% |
| 56 | n0 | 172 | % 87% 13% |
| 57 | N1 | 159 | 3% 80% 18% |
| 57 | n1 | 159 | 3% 83% 16% |
| 58 | N2 | 120 | 21% 73% 10% 17% |
| 58 | n2 | 120 | 18% 68% 14% 18% |
| 59 | N3 | 136 | 22% 85% 15% |
| 59 | n3 | 136 | 7% 85% 14% |
| 60 | N4 | 155 | 25% 55% 8% 37% |
| 60 | n4 | 155 | 12% 75% 12% 13% |
| 61 | N5 | 141 | 8% 72% 13% 14% |
| 61 | n5 | 141 | 6% 74% 11% 15% |
| 62 | N6 | 126 | 2% 84% 13% |
| 62 | n6 | 126 | 5% 82% 17% |
| 63 | N7 | 135 | 10% 86% 12% |
| 63 | n7 | 135 | 11% 81% 19% |
| 64 | N8 | 148 | 14% 85% 14% |
| 64 | n8 | 148 | 17% 84% 15% |
| 65 | N9 | 58 | 10% 84% 16% |
| 65 | n9 | 58 | 5% 81% 17% |
| 66 | O0 | 104 | 2% 83% 11% 7% |
| 66 | o0 | 104 | 5% 81% 14% |
| 67 | O1 | 112 | 24% 81% 14% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 67 | o1 | 112 |  |
| 68 | O2 | 129 |  |
| 68 | o2 | 129 |  |
| 69 | O3 | 106 |  |
| 69 | o3 | 106 |  |
| 70 | O4 | 119 |  |
| 70 | o4 | 119 |  |
| 71 | O5 | 119 |  |
| 71 | o5 | 119 |  |
| 72 | O6 | 99 |  |
| 72 | o6 | 99 |  |
| 73 | O7 | 87 |  |
| 73 | o7 | 87 |  |
| 74 | O8 | 77 |  |
| 74 | o8 | 77 |  |
| 75 | O9 | 50 |  |
| 75 | o9 | 50 |  |
| 76 | Q0 | 52 |  |
| 76 | q0 | 52 |  |
| 77 | Q1 | 25 |  |
| 77 | q1 | 25 |  |
| 78 | Q2 | 105 |  |
| 78 | q2 | 105 |  |
| 79 | Q3 | 91 |  |
| 79 | q3 | 91 |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---------------------------|
| 80 | c0 | 105 | <p>59% 71% 17% 9%</p> |
| 81 | m2 | 150 | <p>100%</p> |
| 82 | p0 | 311 | <p>6% 40% 5% 54%</p> |
| 83 | p1 | 47 | <p>100%</p> |
| 84 | p2 | 46 | <p>100%</p> |
| 85 | f | 157 | <p>61% 74% 18% 6%</p> |

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 404042 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|---------|-------|
| | | | Total | C | N | O | P | | | |
| 1 | 2 | 1781 | Total | C | N | O | P | 0 | 1 | 0 |
| | | | 37970 | 16975 | 6720 | 12493 | 1782 | | | |
| 1 | 6 | 1795 | Total | C | N | O | P | 0 | 1 | 0 |
| | | | 38260 | 17105 | 6763 | 12596 | 1796 | | | |

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 2 | S0 | 206 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1577 | 1014 | 278 | 283 | 2 | | | |
| 2 | s0 | 206 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1583 | 1017 | 281 | 283 | 2 | | | |

- Molecule 3 is a protein called 40S ribosomal protein S1-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 3 | S1 | 214 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1709 | 1084 | 310 | 311 | 4 | | | |
| 3 | s1 | 216 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1722 | 1091 | 312 | 315 | 4 | | | |

- Molecule 4 is a protein called 40S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 4 | S2 | 217 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1635 | 1047 | 289 | 297 | 2 | | | |
| 4 | s2 | 217 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1635 | 1047 | 289 | 297 | 2 | | | |

- Molecule 5 is a protein called 40S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 5 | S3 | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1734 | 1101 | 313 | 314 | 6 | | | |
| 5 | s3 | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1734 | 1101 | 313 | 314 | 6 | | | |

- Molecule 6 is a protein called 40S ribosomal protein S4-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 6 | S4 | 260 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2068 | 1316 | 389 | 360 | 3 | | | |
| 6 | s4 | 260 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2068 | 1316 | 389 | 360 | 3 | | | |

- Molecule 7 is a protein called 40S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 7 | S5 | 206 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1609 | 1007 | 300 | 299 | 3 | | | |
| 7 | s5 | 206 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1609 | 1007 | 300 | 299 | 3 | | | |

- Molecule 8 is a protein called 40S ribosomal protein S6-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 8 | S6 | 226 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1799 | 1129 | 346 | 321 | 3 | | | |
| 8 | s6 | 218 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1755 | 1102 | 337 | 313 | 3 | | | |

- Molecule 9 is a protein called 40S ribosomal protein S7-A.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| 9 | S7 | 184 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1481 | 951 | 265 | 265 | | | |
| 9 | s7 | 186 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1491 | 957 | 267 | 267 | | | |

- Molecule 10 is a protein called 40S ribosomal protein S8-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 10 | S8 | 188 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1489 | 925 | 298 | 264 | 2 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 10 | s8 | 188 | 1489 | 925 | 298 | 264 | 2 | 0 | 0 | 0 |

- Molecule 11 is a protein called 40S ribosomal protein S9-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 11 | S9 | 185 | 1494 | 943 | 289 | 261 | 1 | 0 | 0 | 0 |
| 11 | s9 | 185 | 1494 | 943 | 289 | 261 | 1 | 0 | 0 | 0 |

- Molecule 12 is a protein called 40S ribosomal protein S10-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 12 | C0 | 96 | 772 | 499 | 126 | 145 | 2 | 0 | 0 | 0 |

- Molecule 13 is a protein called 40S ribosomal protein S11-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 13 | C1 | 155 | 1213 | 774 | 230 | 206 | 3 | 0 | 0 | 0 |
| 13 | c1 | 146 | 1168 | 747 | 221 | 197 | 3 | 0 | 0 | 0 |

- Molecule 14 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 14 | C2 | 124 | 890 | 560 | 156 | 172 | 2 | 0 | 0 | 0 |
| 14 | c2 | 124 | 890 | 560 | 156 | 172 | 2 | 0 | 0 | 0 |

- Molecule 15 is a protein called 40S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 15 | C3 | 150 | 1192 | 759 | 224 | 207 | 2 | 0 | 0 | 0 |
| 15 | c3 | 150 | 1192 | 759 | 224 | 207 | 2 | 0 | 0 | 0 |

- Molecule 16 is a protein called 40S ribosomal protein S14-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 16 | C4 | 127 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 891 | 545 | 182 | 163 | 1 | | | |
| 16 | c4 | 128 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 949 | 582 | 188 | 176 | 3 | | | |

- Molecule 17 is a protein called 40S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 17 | C5 | 124 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 977 | 622 | 182 | 166 | 7 | | | |
| 17 | c5 | 135 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1039 | 658 | 196 | 178 | 7 | | | |

- Molecule 18 is a protein called 40S ribosomal protein S16-A.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| 18 | C6 | 141 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1105 | 708 | 203 | 194 | | | |
| 18 | c6 | 142 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1111 | 711 | 204 | 196 | | | |

- Molecule 19 is a protein called 40S ribosomal protein S17-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 19 | C7 | 120 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 926 | 577 | 177 | 170 | 2 | | | |
| 19 | c7 | 117 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 906 | 563 | 174 | 167 | 2 | | | |

- Molecule 20 is a protein called 40S ribosomal protein S18-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 20 | C8 | 145 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1192 | 743 | 237 | 210 | 2 | | | |
| 20 | c8 | 145 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1192 | 743 | 237 | 210 | 2 | | | |

- Molecule 21 is a protein called 40S ribosomal protein S19-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 21 | C9 | 143 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1112 | 694 | 208 | 208 | 2 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 21 | c9 | 143 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1112 | 694 | 208 | 208 | 2 | | | |

- Molecule 22 is a protein called 40S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 22 | D0 | 107 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 855 | 539 | 156 | 159 | 1 | | | |
| 22 | d0 | 110 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 882 | 554 | 161 | 166 | 1 | | | |

- Molecule 23 is a protein called 40S ribosomal protein S21-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 23 | D1 | 87 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 684 | 420 | 125 | 137 | 2 | | | |
| 23 | d1 | 87 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 684 | 420 | 125 | 137 | 2 | | | |

- Molecule 24 is a protein called 40S ribosomal protein S22-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 24 | D2 | 129 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1021 | 650 | 188 | 180 | 3 | | | |
| 24 | d2 | 129 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1021 | 650 | 188 | 180 | 3 | | | |

- Molecule 25 is a protein called 40S ribosomal protein S23-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 25 | D3 | 144 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1121 | 708 | 220 | 191 | 2 | | | |
| 25 | d3 | 144 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1121 | 708 | 220 | 191 | 2 | | | |

- Molecule 26 is a protein called 40S ribosomal protein S24-A.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| 26 | D4 | 134 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1073 | 676 | 208 | 189 | | | |
| 26 | d4 | 134 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1073 | 676 | 208 | 189 | | | |

- Molecule 27 is a protein called 40S ribosomal protein S25-A.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---------|---------|-------|
| 27 | D5 | 70 | Total | C | N | O | 0 | 0 | 0 |
| | | | 563 | 360 | 104 | 99 | | | |
| 27 | d5 | 69 | Total | C | N | O | 0 | 0 | 0 |
| | | | 558 | 357 | 103 | 98 | | | |

- Molecule 28 is a protein called 40S ribosomal protein S26-B.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 28 | D6 | 97 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 769 | 475 | 160 | 129 | 5 | | | |
| 28 | d6 | 97 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 769 | 475 | 160 | 129 | 5 | | | |

- Molecule 29 is a protein called 40S ribosomal protein S27-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 29 | D7 | 81 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 610 | 382 | 110 | 113 | 5 | | | |
| 29 | d7 | 81 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 610 | 382 | 110 | 113 | 5 | | | |

- Molecule 30 is a protein called 40S ribosomal protein S28-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 30 | D8 | 63 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 497 | 306 | 99 | 91 | 1 | | | |
| 30 | d8 | 63 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 497 | 306 | 99 | 91 | 1 | | | |

- Molecule 31 is a protein called 40S ribosomal protein S29-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 31 | D9 | 53 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 442 | 274 | 92 | 72 | 4 | | | |
| 31 | d9 | 53 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 442 | 274 | 92 | 72 | 4 | | | |

- Molecule 32 is a protein called 40S ribosomal protein S30-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|---------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 32 | E0 | 60 | Total 475 | C 299 | N 98 | O 77 | S 1 | 0 | 0 | 0 |
| 32 | e0 | 62 | Total 491 | C 309 | N 101 | O 80 | S 1 | 0 | 0 | 0 |

- Molecule 33 is a protein called Ubiquitin-40S ribosomal protein S31.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|---------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 33 | E1 | 71 | Total 566 | C 362 | N 106 | O 94 | S 4 | 0 | 0 | 0 |
| 33 | e1 | 76 | Total 608 | C 388 | N 117 | O 99 | S 4 | 0 | 0 | 0 |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| E1 | 77 | ALA | GLY | conflict | UNP P05759 |
| e1 | 77 | ALA | GLY | conflict | UNP P05759 |

- Molecule 34 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|---------------|-----------|----------|----------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 34 | SR | 318 | Total 2437 | C 1541 | N 418 | O 470 | S 8 | 0 | 0 | 0 |
| 34 | sR | 318 | Total 2442 | C 1544 | N 418 | O 472 | S 8 | 0 | 0 | 0 |

- Molecule 35 is a protein called Suppressor protein STM1.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|---------|---------|-------|
| | | | Total | C | N | O | | | |
| 35 | SM | 159 | Total 1104 | C 652 | N 221 | O 231 | 0 | 0 | 0 |
| 35 | sM | 104 | Total 679 | C 402 | N 140 | O 137 | 0 | 0 | 0 |

- Molecule 36 is a RNA chain called 25S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|----------------|------------|------------|------------|-----------|---------|---------|-------|
| | | | Total | C | N | O | P | | | |
| 36 | 1 | 3149 | Total 67355 | C 30086 | N 12142 | O 21978 | P 3149 | 0 | 0 | 0 |
| 36 | 5 | 3169 | Total 67780 | C 30276 | N 12216 | O 22120 | P 3168 | 0 | 0 | 0 |

- Molecule 37 is a RNA chain called 5S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|---------|-------|
| 37 | 3 | 121 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 2579 | 1152 | 461 | 845 | 121 | | | |
| 37 | 7 | 121 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 2579 | 1152 | 461 | 845 | 121 | | | |

- Molecule 38 is a RNA chain called 5.8S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|---------|---------|-------|
| 38 | 4 | 158 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 3353 | 1500 | 586 | 1109 | 158 | | | |
| 38 | 8 | 158 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 3353 | 1500 | 586 | 1109 | 158 | | | |

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 39 | L2 | 252 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1914 | 1191 | 388 | 334 | 1 | | | |
| 39 | 12 | 252 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1912 | 1190 | 388 | 333 | 1 | | | |

- Molecule 40 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 40 | L3 | 386 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3075 | 1950 | 584 | 533 | 8 | | | |
| 40 | 13 | 386 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3075 | 1950 | 584 | 533 | 8 | | | |

- Molecule 41 is a protein called 60S ribosomal protein L4-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 41 | L4 | 361 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2748 | 1729 | 522 | 494 | 3 | | | |
| 41 | 14 | 361 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2748 | 1729 | 522 | 494 | 3 | | | |

- Molecule 42 is a protein called 60S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 42 | L5 | 296 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2375 | 1501 | 414 | 458 | 2 | | | |
| 42 | 15 | 294 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2359 | 1489 | 412 | 456 | 2 | | | |

- Molecule 43 is a protein called 60S ribosomal protein L6-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 43 | L6 | 156 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1239 | 800 | 222 | 216 | 1 | | | |
| 43 | 16 | 157 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1248 | 806 | 224 | 217 | 1 | | | |

- Molecule 44 is a protein called 60S ribosomal protein L7-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 44 | L7 | 222 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1784 | 1151 | 324 | 308 | 1 | | | |
| 44 | 17 | 223 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1791 | 1155 | 325 | 310 | 1 | | | |

- Molecule 45 is a protein called 60S ribosomal protein L8-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 45 | L8 | 233 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1804 | 1151 | 323 | 327 | 3 | | | |
| 45 | 18 | 231 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1763 | 1130 | 316 | 314 | 3 | | | |

- Molecule 46 is a protein called 60S ribosomal protein L9-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 46 | L9 | 191 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1518 | 963 | 274 | 277 | 4 | | | |
| 46 | 19 | 191 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1518 | 963 | 274 | 277 | 4 | | | |

- Molecule 47 is a protein called 60S ribosomal protein L10.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 47 | M0 | 211 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1705 | 1083 | 322 | 294 | 6 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 47 | m0 | 213 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1722 | 1094 | 325 | 297 | 6 | | | |

- Molecule 48 is a protein called 60S ribosomal protein L11-B.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 48 | M1 | 169 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1353 | 847 | 253 | 249 | 4 | | | |
| 48 | m1 | 169 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1353 | 847 | 253 | 249 | 4 | | | |

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 49 | M3 | 193 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1543 | 962 | 315 | 266 | | | | |
| 49 | m3 | 194 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1548 | 965 | 316 | 267 | | | | |

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 50 | M4 | 136 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1053 | 675 | 199 | 177 | 2 | | | |
| 50 | m4 | 137 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1059 | 678 | 200 | 179 | 2 | | | |

- Molecule 51 is a protein called 60S ribosomal protein L15-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 51 | M5 | 203 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1720 | 1077 | 361 | 281 | 1 | | | |
| 51 | m5 | 203 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1720 | 1077 | 361 | 281 | 1 | | | |

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 52 | M6 | 197 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1555 | 1003 | 289 | 262 | 1 | | | |
| 52 | m6 | 197 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1555 | 1003 | 289 | 262 | 1 | | | |

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| | | | Total | C | N | O | | | |
| 53 | M7 | 183 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1420 | 882 | 281 | 257 | | | |
| 53 | m7 | 155 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1227 | 764 | 238 | 225 | | | |

- Molecule 54 is a protein called 60S ribosomal protein L18-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 54 | M8 | 185 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1441 | 908 | 290 | 241 | 2 | | | |
| 54 | m8 | 185 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1441 | 908 | 290 | 241 | 2 | | | |

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| | | | Total | C | N | O | | | |
| 55 | M9 | 188 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1521 | 935 | 326 | 260 | | | |
| 55 | m9 | 188 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1521 | 935 | 326 | 260 | | | |

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 56 | N0 | 172 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1445 | 930 | 267 | 244 | 4 | | | |
| 56 | n0 | 172 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1445 | 930 | 267 | 244 | 4 | | | |

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 57 | N1 | 159 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1276 | 805 | 246 | 221 | 4 | | | |
| 57 | n1 | 159 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1276 | 805 | 246 | 221 | 4 | | | |

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| 58 | N2 | 100 | Total | C | N | O | 0 | 0 | 0 |
| | | | 796 | 516 | 131 | 149 | | | |
| 58 | n2 | 98 | Total | C | N | O | 0 | 0 | 0 |
| | | | 778 | 505 | 127 | 146 | | | |

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 59 | N3 | 136 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1003 | 628 | 189 | 179 | 7 | | | |
| 59 | n3 | 136 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1003 | 628 | 189 | 179 | 7 | | | |

- Molecule 60 is a protein called 60S ribosomal protein L24-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 60 | N4 | 98 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 699 | 443 | 137 | 118 | 1 | | | |
| 60 | n4 | 135 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1038 | 651 | 206 | 180 | 1 | | | |

- Molecule 61 is a protein called 60S ribosomal protein L25.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 61 | N5 | 121 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 964 | 620 | 169 | 173 | 2 | | | |
| 61 | n5 | 120 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 959 | 617 | 168 | 172 | 2 | | | |

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| 62 | N6 | 126 | Total | C | N | O | 0 | 0 | 0 |
| | | | 993 | 625 | 192 | 176 | | | |
| 62 | n6 | 126 | Total | C | N | O | 0 | 0 | 0 |
| | | | 993 | 625 | 192 | 176 | | | |

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| 63 | N7 | 135 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1092 | 710 | 202 | 180 | | | |

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| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| | | | Total | C | N | O | | | |
| 63 | n7 | 135 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1092 | 710 | 202 | 180 | | | |

- Molecule 64 is a protein called 60S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 64 | N8 | 148 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1173 | 749 | 231 | 190 | 3 | | | |
| 64 | n8 | 148 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1173 | 749 | 231 | 190 | 3 | | | |

- Molecule 65 is a protein called 60S ribosomal protein L29.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---------|---------|-------|
| | | | Total | C | N | O | | | |
| 65 | N9 | 58 | Total | C | N | O | 0 | 0 | 0 |
| | | | 462 | 289 | 100 | 73 | | | |
| 65 | n9 | 58 | Total | C | N | O | 0 | 0 | 0 |
| | | | 462 | 289 | 100 | 73 | | | |

- Molecule 66 is a protein called 60S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 66 | O0 | 97 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 743 | 479 | 124 | 139 | 1 | | | |
| 66 | o0 | 100 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 767 | 492 | 128 | 146 | 1 | | | |

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 67 | O1 | 109 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 876 | 556 | 167 | 152 | 1 | | | |
| 67 | o1 | 109 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 883 | 559 | 167 | 156 | 1 | | | |

- Molecule 68 is a protein called 60S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 68 | O2 | 127 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1020 | 647 | 205 | 167 | 1 | | | |
| 68 | o2 | 127 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1020 | 647 | 205 | 167 | 1 | | | |

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 69 | O3 | 106 | Total 850 | C 540 | N 165 | O 144 | S 1 | 0 | 0 | 0 |
| 69 | o3 | 106 | Total 850 | C 540 | N 165 | O 144 | S 1 | 0 | 0 | 0 |

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 70 | O4 | 112 | Total 880 | C 545 | N 179 | O 152 | S 4 | 0 | 0 | 0 |
| 70 | o4 | 112 | Total 880 | C 545 | N 179 | O 152 | S 4 | 0 | 0 | 0 |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| O4 | ? | - | LYS | deletion | UNP P87262 |
| o4 | ? | - | LYS | deletion | UNP P87262 |

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 71 | O5 | 119 | Total 969 | C 615 | N 186 | O 167 | S 1 | 0 | 0 | 0 |
| 71 | o5 | 119 | Total 965 | C 612 | N 185 | O 167 | S 1 | 0 | 0 | 0 |

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 72 | O6 | 99 | Total 771 | C 481 | N 156 | O 132 | S 2 | 0 | 0 | 0 |
| 72 | o6 | 99 | Total 770 | C 481 | N 156 | O 131 | S 2 | 0 | 0 | 0 |

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 73 | O7 | 87 | Total 681 | C 414 | N 148 | O 114 | S 5 | 0 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 73 | o7 | 87 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 681 | 414 | 148 | 114 | 5 | | | |

- Molecule 74 is a protein called 60S ribosomal protein L38.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|---------|-------|
| 74 | O8 | 77 | Total | C | N | O | | 0 | 0 | 0 |
| | | | 612 | 391 | 115 | 106 | | | | |
| 74 | o8 | 77 | Total | C | N | O | | 0 | 0 | 0 |
| | | | 608 | 388 | 114 | 106 | | | | |

- Molecule 75 is a protein called 60S ribosomal protein L39.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 75 | O9 | 50 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 436 | 272 | 97 | 65 | 2 | | | |
| 75 | o9 | 50 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 436 | 272 | 97 | 65 | 2 | | | |

- Molecule 76 is a protein called Ubiquitin-60S ribosomal protein L40.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 76 | Q0 | 52 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 417 | 259 | 86 | 67 | 5 | | | |
| 76 | q0 | 52 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 417 | 259 | 86 | 67 | 5 | | | |

- Molecule 77 is a protein called 60S ribosomal protein L41-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 77 | Q1 | 25 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 233 | 142 | 63 | 27 | 1 | | | |
| 77 | q1 | 25 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 233 | 142 | 63 | 27 | 1 | | | |

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 78 | Q2 | 105 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 847 | 534 | 170 | 138 | 5 | | | |
| 78 | q2 | 105 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 847 | 534 | 170 | 138 | 5 | | | |

- Molecule 79 is a protein called 60S ribosomal protein L43-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 79 | Q3 | 91 | Total 694 | C 429 | N 138 | O 121 | S 6 | 0 | 0 | 0 |
| 79 | q3 | 91 | Total 694 | C 429 | N 138 | O 121 | S 6 | 0 | 0 | 0 |

- Molecule 80 is a protein called 40S ribosomal protein S10-A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 80 | c0 | 96 | Total 762 | C 491 | N 125 | O 144 | S 2 | 0 | 0 | 0 |

- Molecule 81 is a protein called 60S ribosomal protein L12-A (uL11).

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|---------|---------|-------|
| | | | Total | C | N | O | | | |
| 81 | m2 | 150 | Total 750 | C 450 | N 150 | O 150 | 0 | 0 | 0 |

- Molecule 82 is a protein called 60S acidic ribosomal protein P0.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 82 | p0 | 143 | Total 1076 | C 686 | N 192 | O 195 | S 3 | 0 | 0 | 0 |

- Molecule 83 is a protein called 60S ribosomal protein P1 alpha.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|---------|---------|---------|---------|-------|
| | | | Total | C | N | O | | | |
| 83 | p1 | 47 | Total 235 | C 141 | N 47 | O 47 | 0 | 0 | 0 |

- Molecule 84 is a protein called 60S ribosomal P2 beta.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|---------|---------|---------|---------|-------|
| | | | Total | C | N | O | | | |
| 84 | p2 | 46 | Total 230 | C 138 | N 46 | O 46 | 0 | 0 | 0 |

- Molecule 85 is a protein called Eukaryotic translation initiation factor 5A-1.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|---------------|----------|----------|----------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 85 | f | 148 | Total 1116 | C 692 | N 188 | O 227 | S 9 | 0 | 0 | 0 |

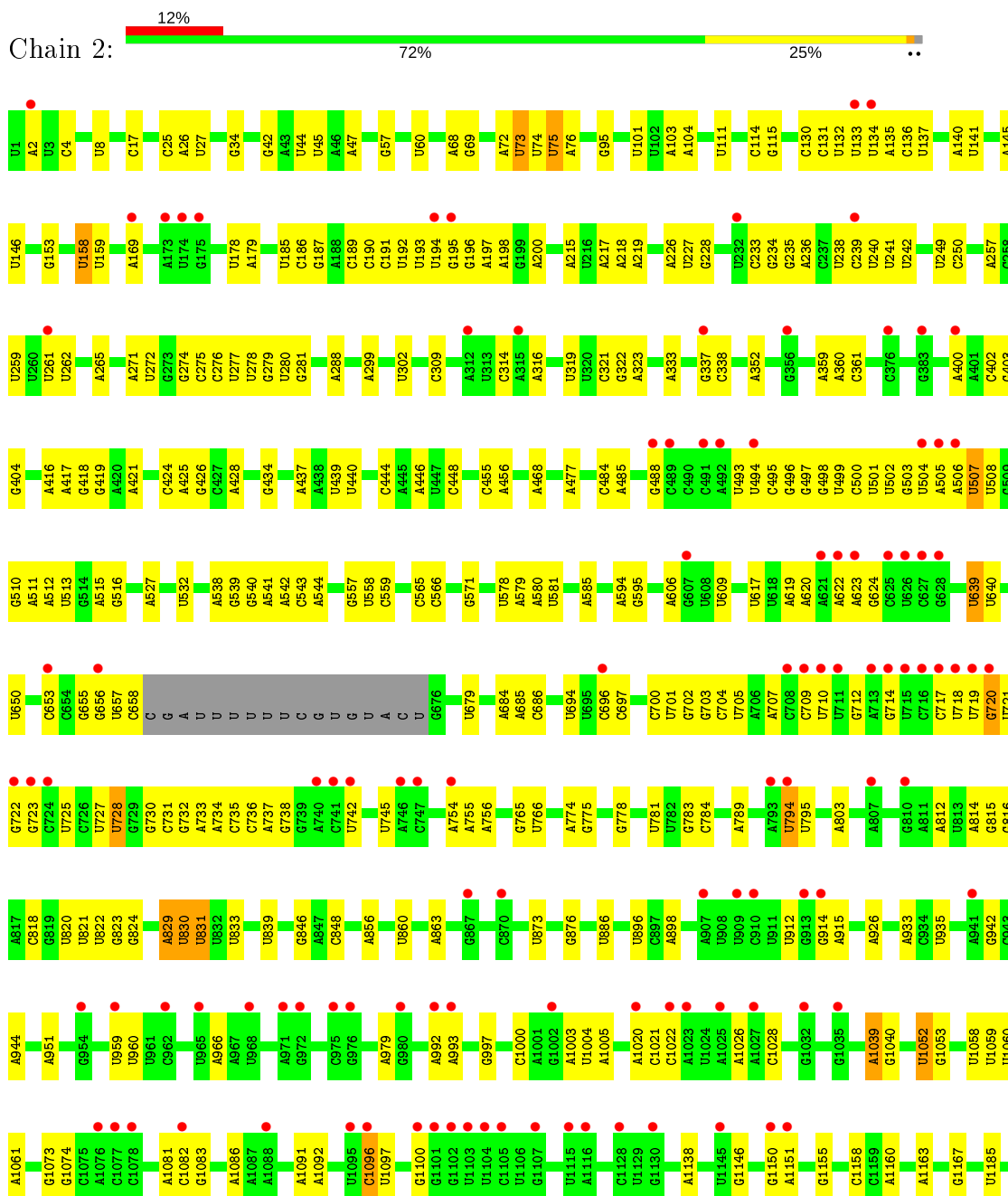
- Molecule 86 is ZINC ION (three-letter code: ZN) (formula: Zn).

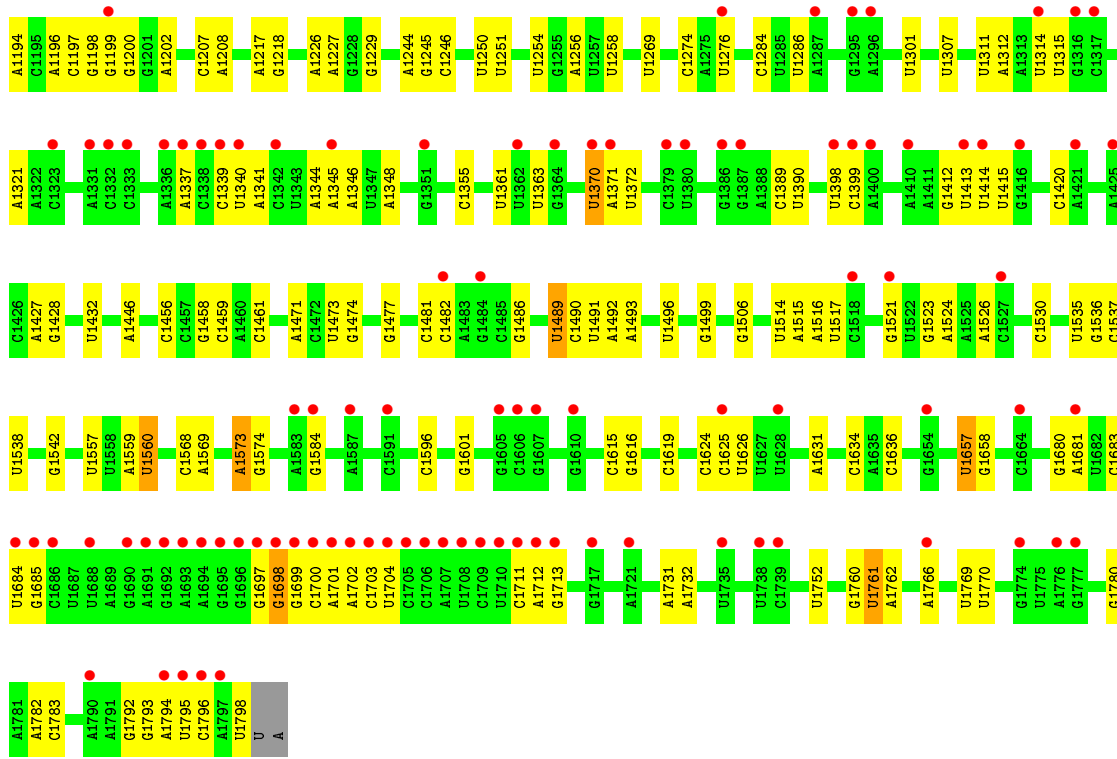
| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 86 | q0 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | D6 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | Q2 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | e1 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | Q3 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | D9 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | E1 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | Q0 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | d7 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | q3 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | d9 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | D7 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | d6 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | o7 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | O7 | 1 | Total Zn 1 1 | 0 | 0 |
| 86 | q2 | 1 | Total Zn 1 1 | 0 | 0 |

3 Residue-property plots [i](#)

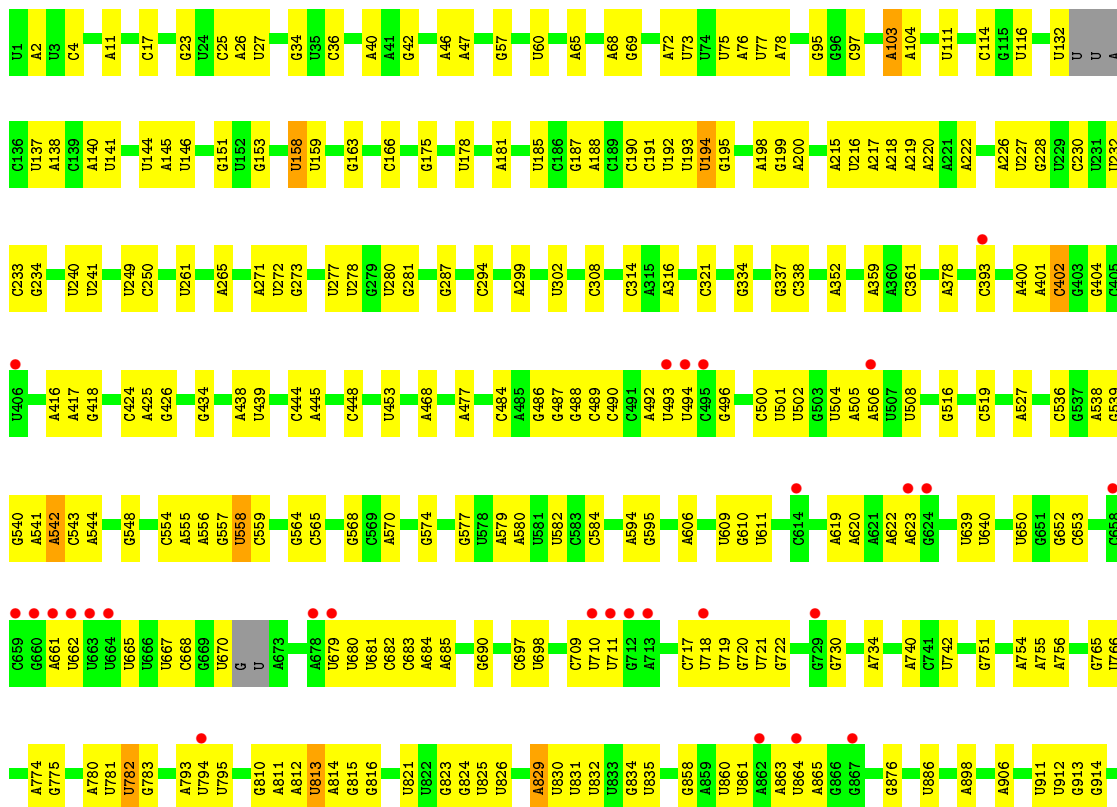
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

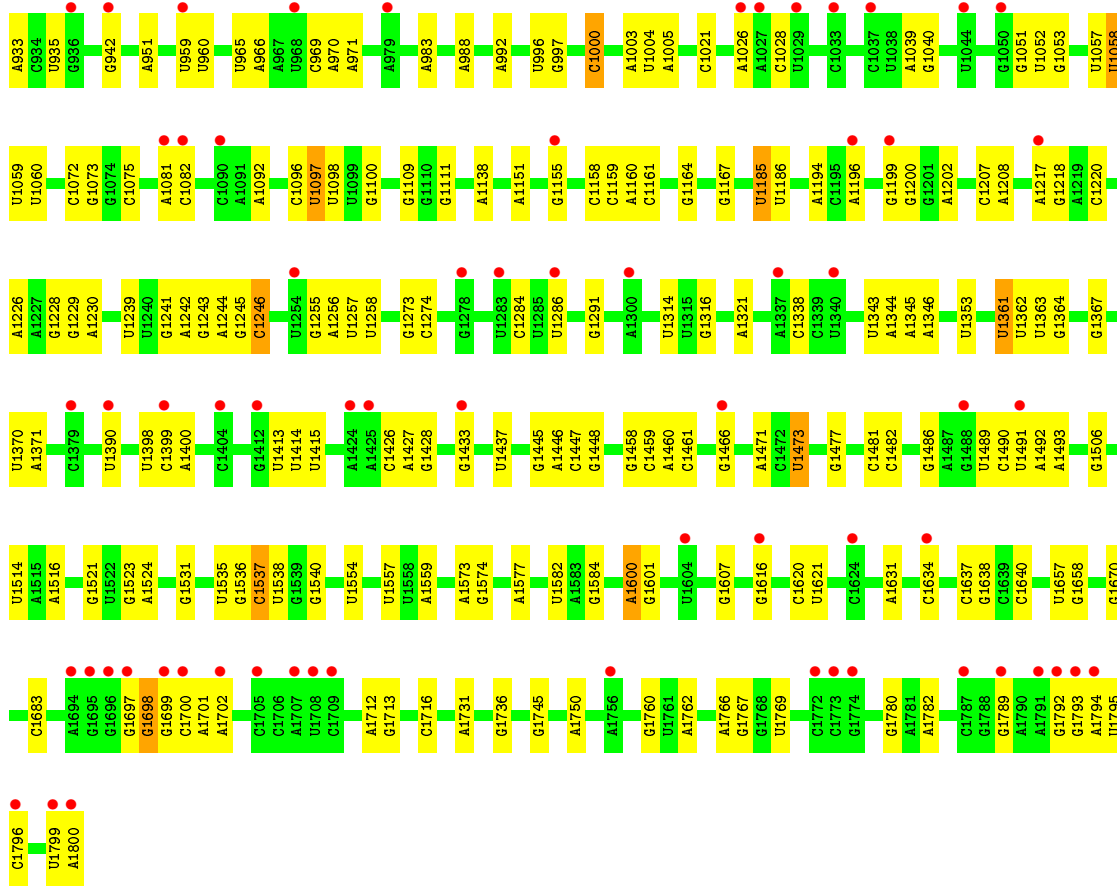
- Molecule 1: 18S ribosomal RNA



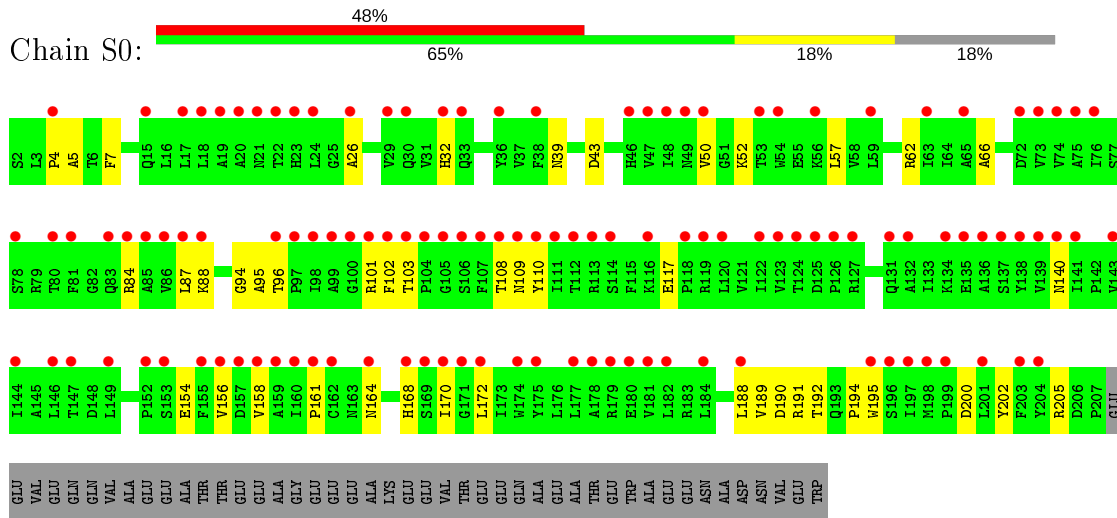


• Molecule 1: 18S ribosomal RNA

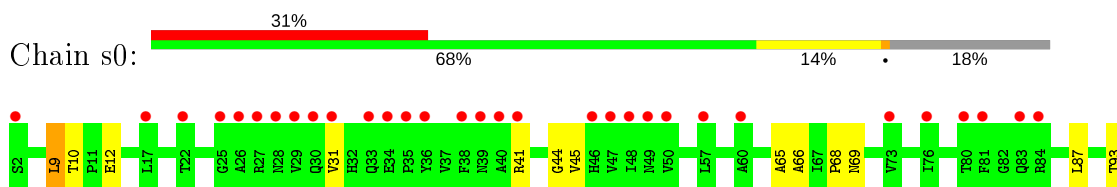


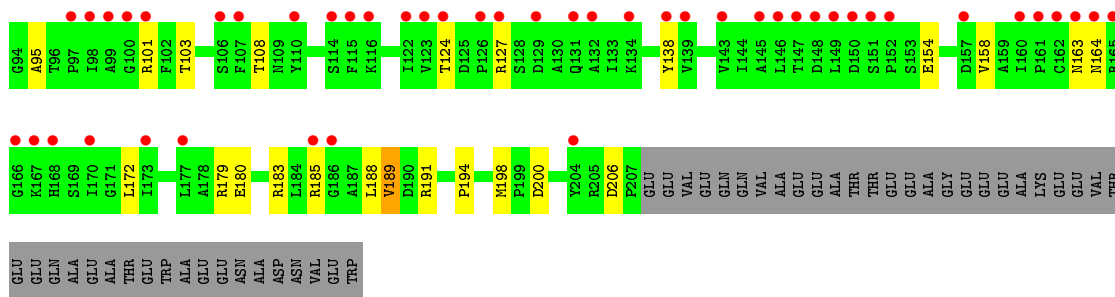


• Molecule 2: 40S ribosomal protein S0-A

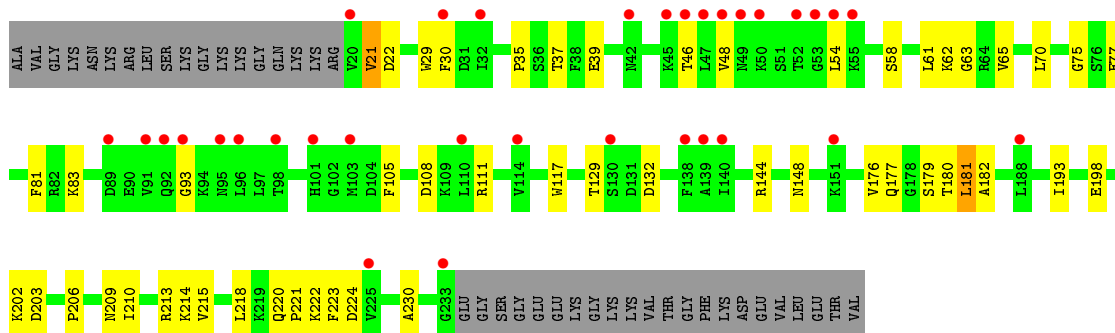


• Molecule 2: 40S ribosomal protein S0-A

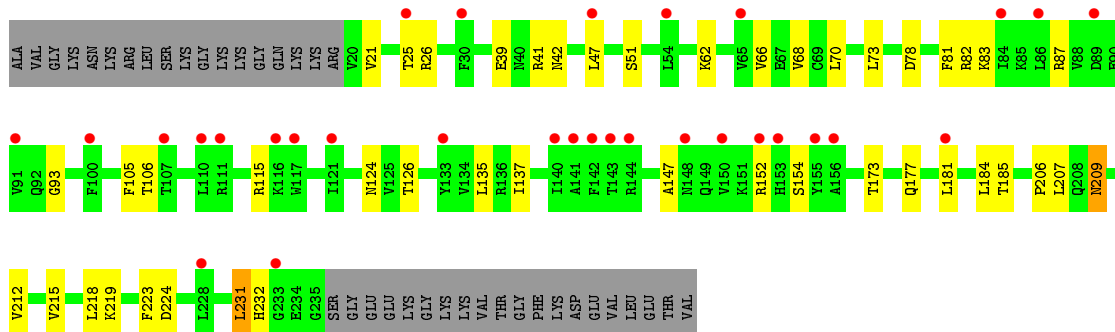




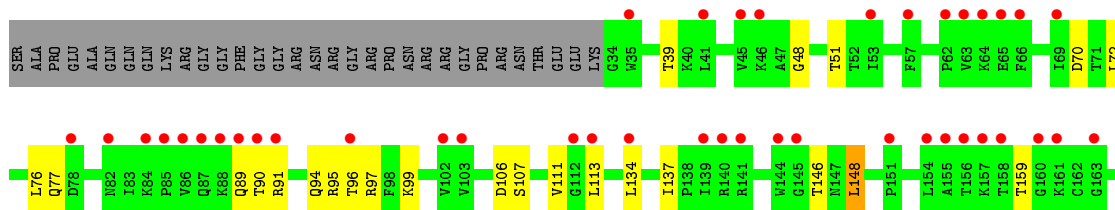
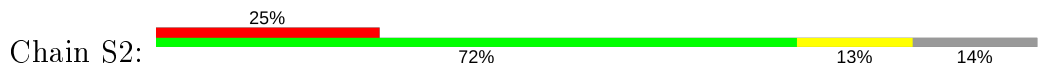
• Molecule 3: 40S ribosomal protein S1-A

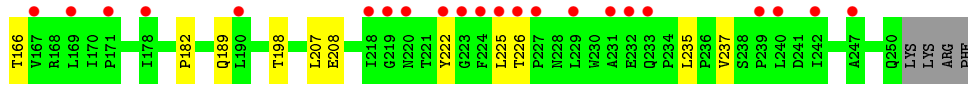


• Molecule 3: 40S ribosomal protein S1-A

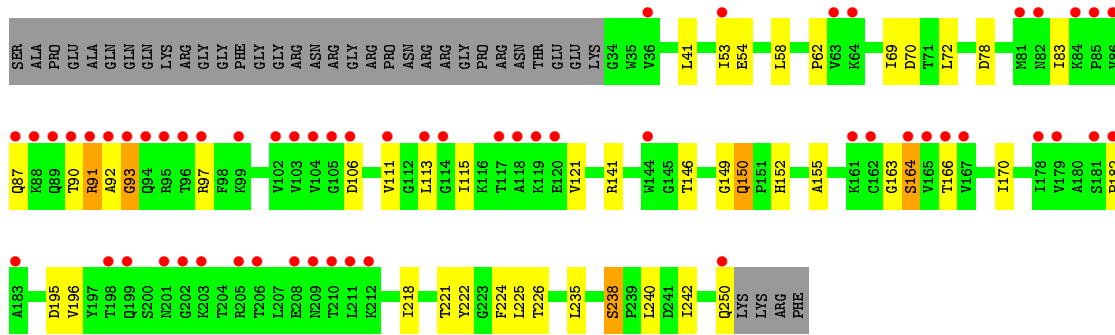


• Molecule 4: 40S ribosomal protein S2

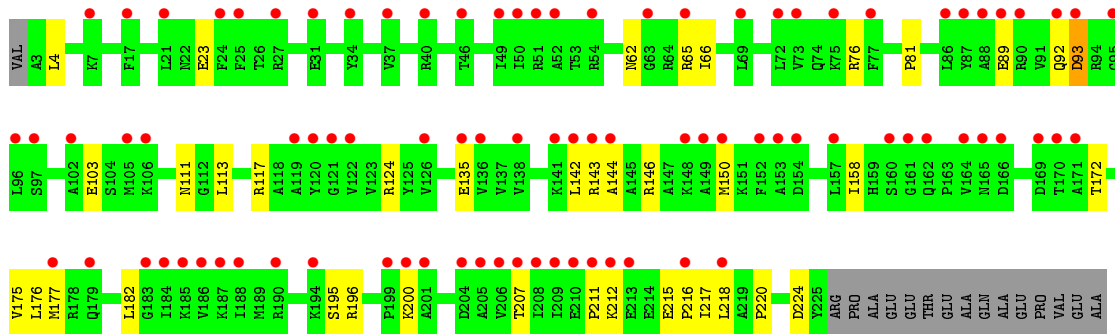
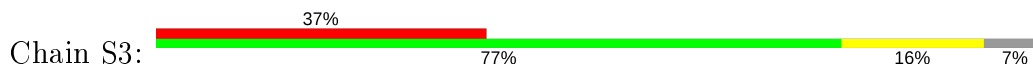




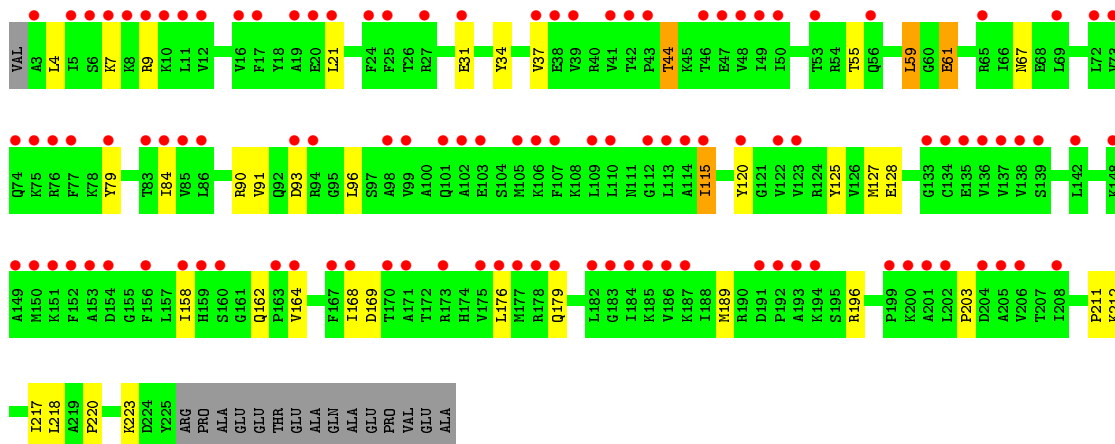
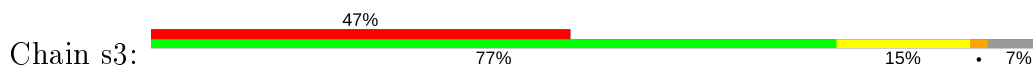
• Molecule 4: 40S ribosomal protein S2



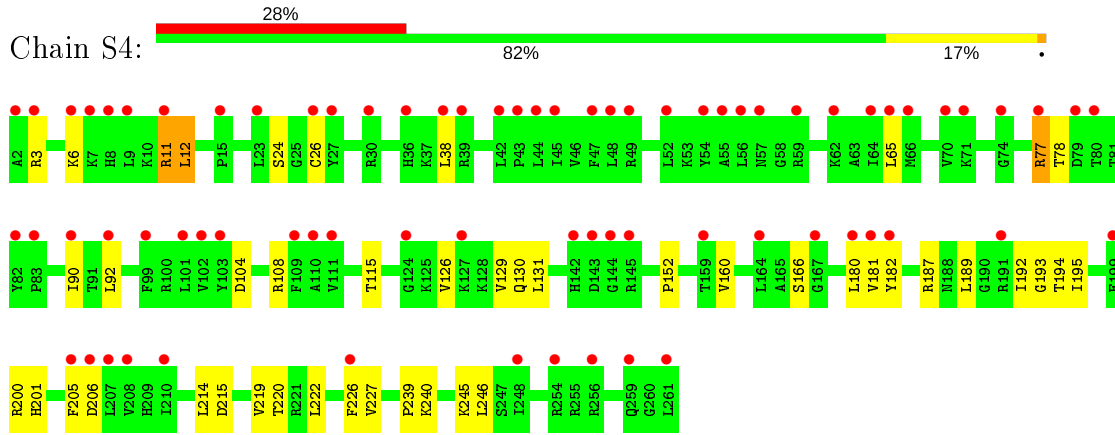
• Molecule 5: 40S ribosomal protein S3



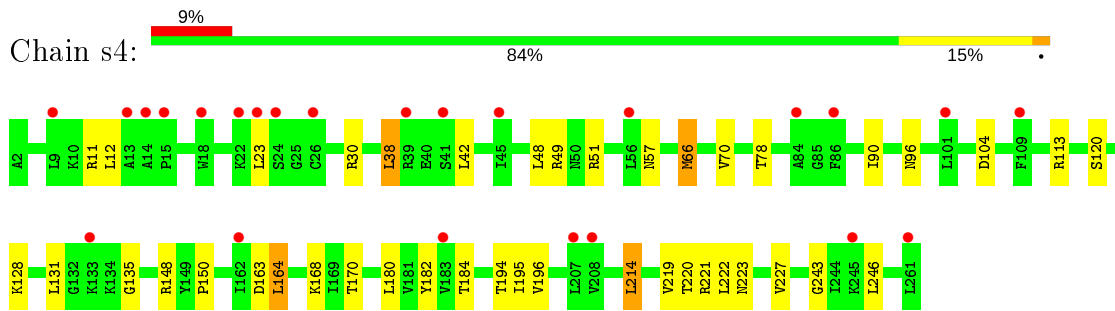
• Molecule 5: 40S ribosomal protein S3



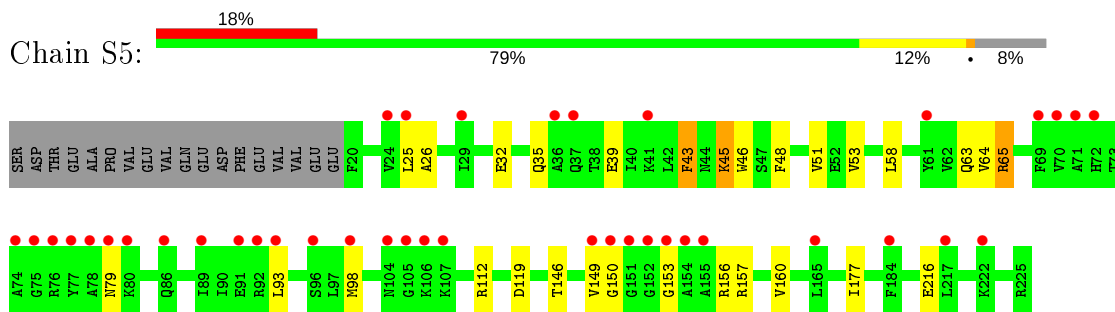
• Molecule 6: 40S ribosomal protein S4-A



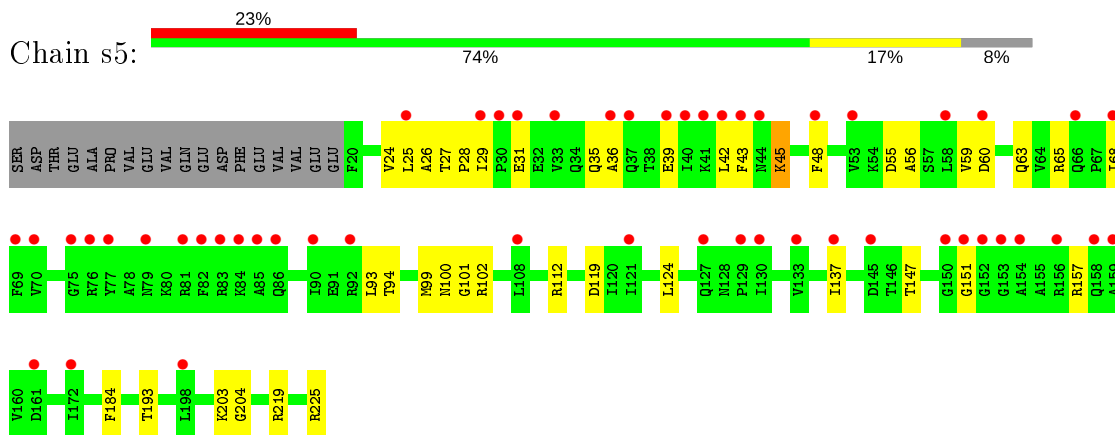
• Molecule 6: 40S ribosomal protein S4-A



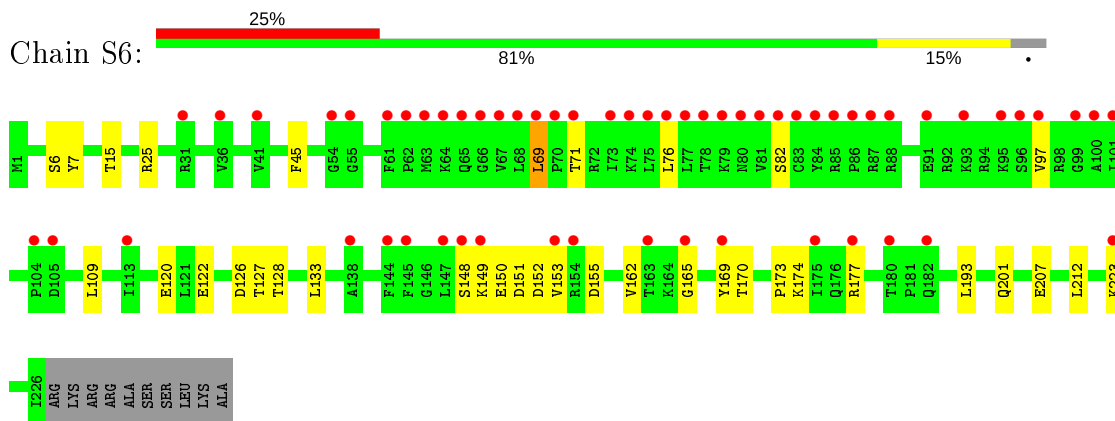
• Molecule 7: 40S ribosomal protein S5



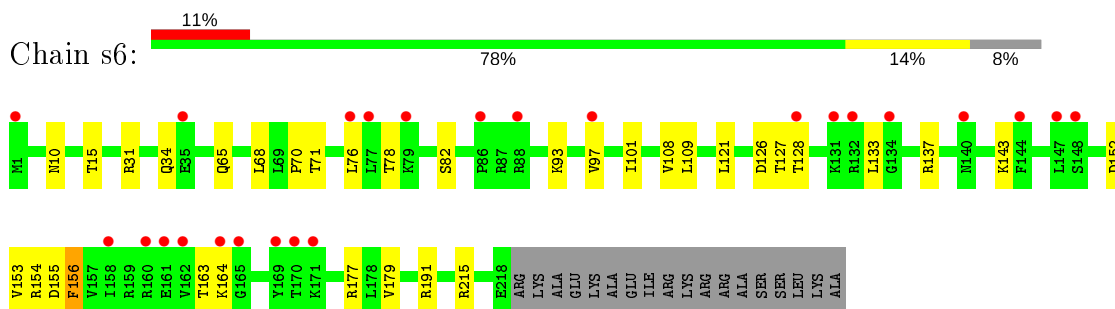
• Molecule 7: 40S ribosomal protein S5



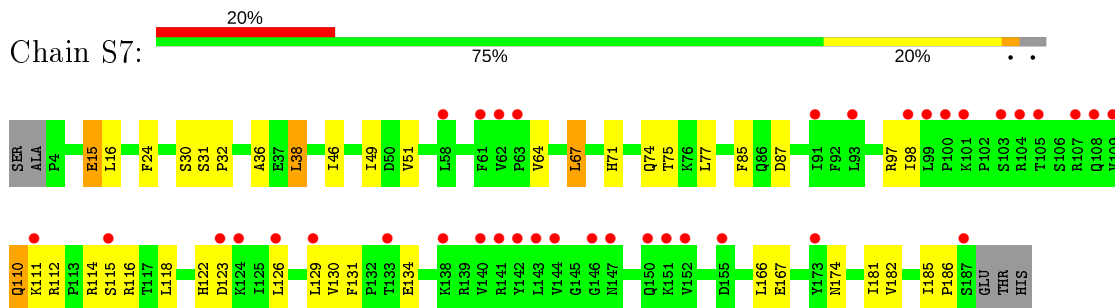
- Molecule 8: 40S ribosomal protein S6-A



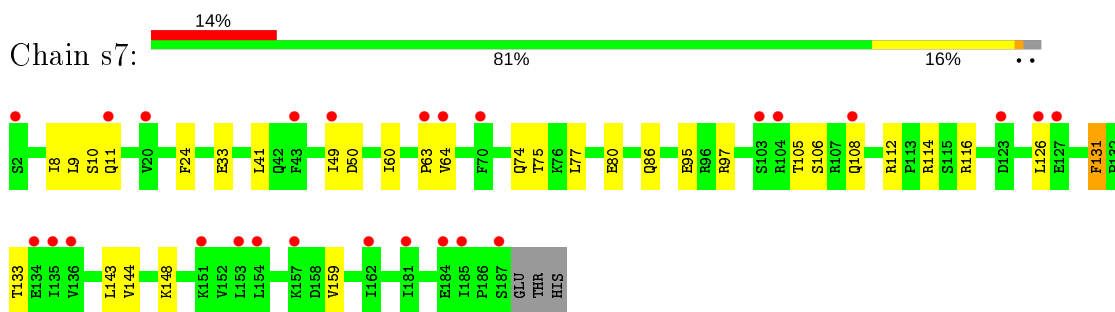
- Molecule 8: 40S ribosomal protein S6-A



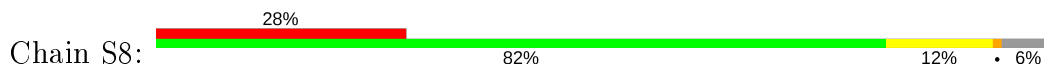
- Molecule 9: 40S ribosomal protein S7-A

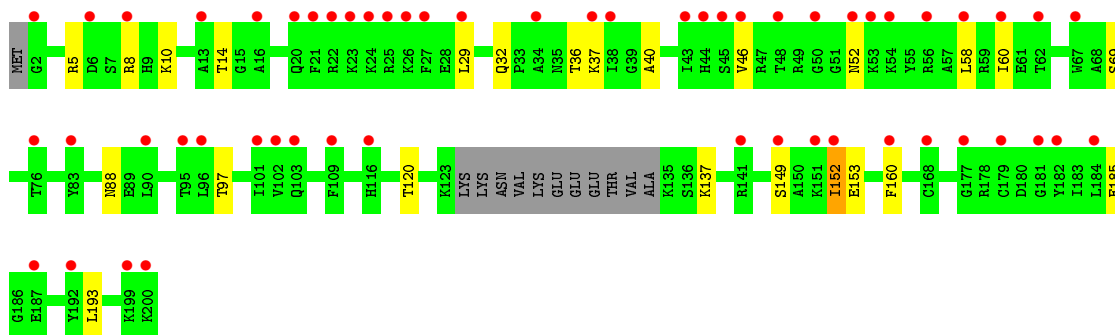


- Molecule 9: 40S ribosomal protein S7-A

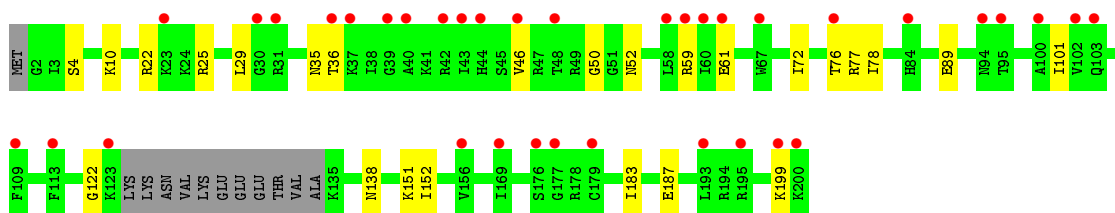
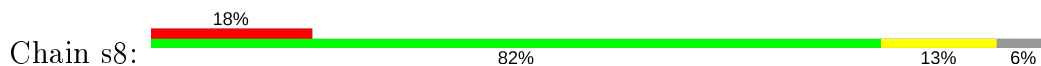


- Molecule 10: 40S ribosomal protein S8-A

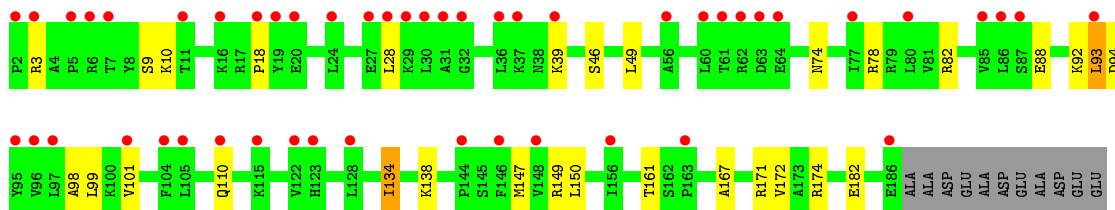
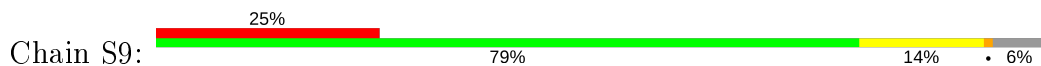




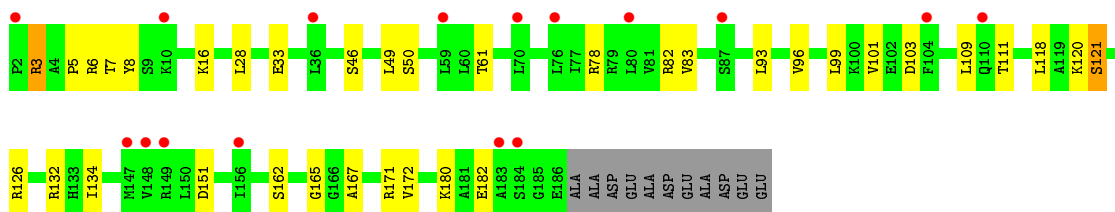
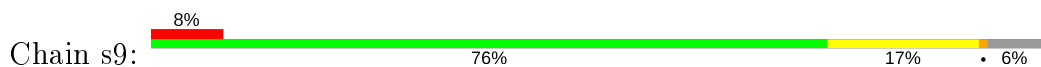
- Molecule 10: 40S ribosomal protein S8-A



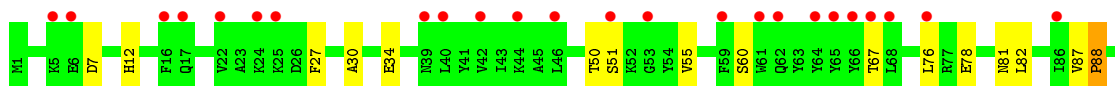
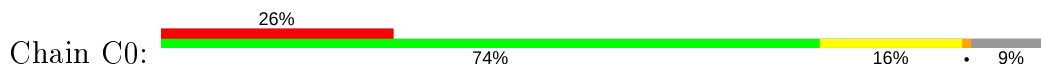
- Molecule 11: 40S ribosomal protein S9-A

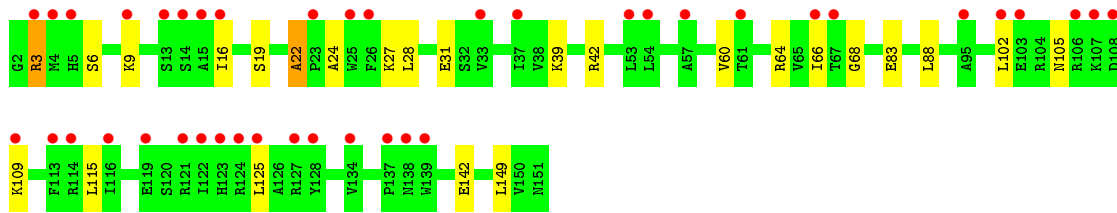


- Molecule 11: 40S ribosomal protein S9-A

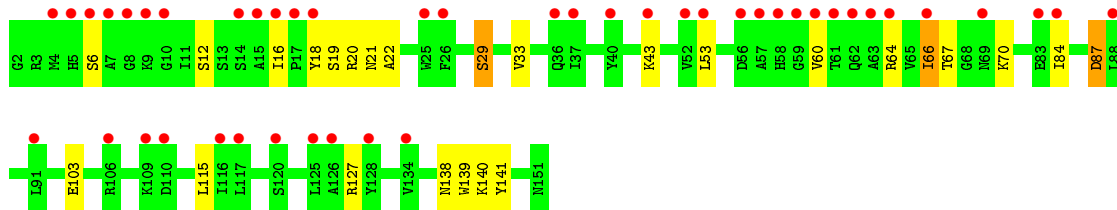
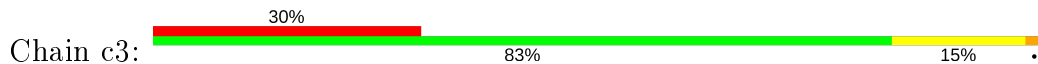


- Molecule 12: 40S ribosomal protein S10-A

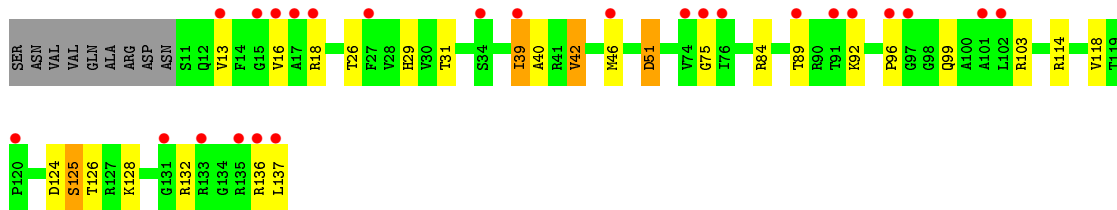
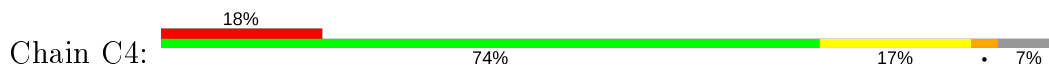




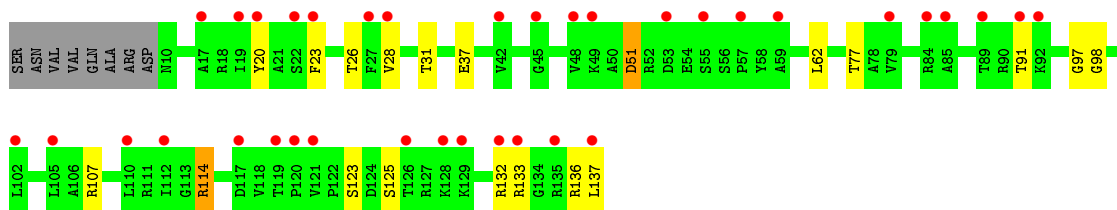
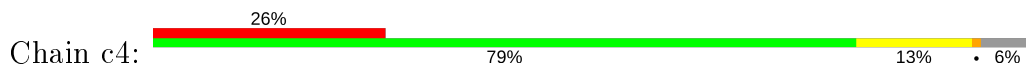
• Molecule 15: 40S ribosomal protein S13



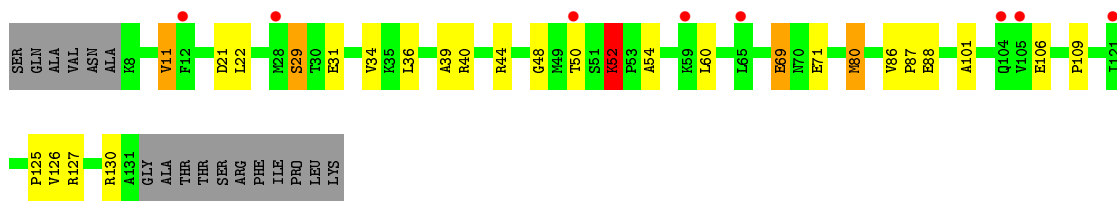
• Molecule 16: 40S ribosomal protein S14-A



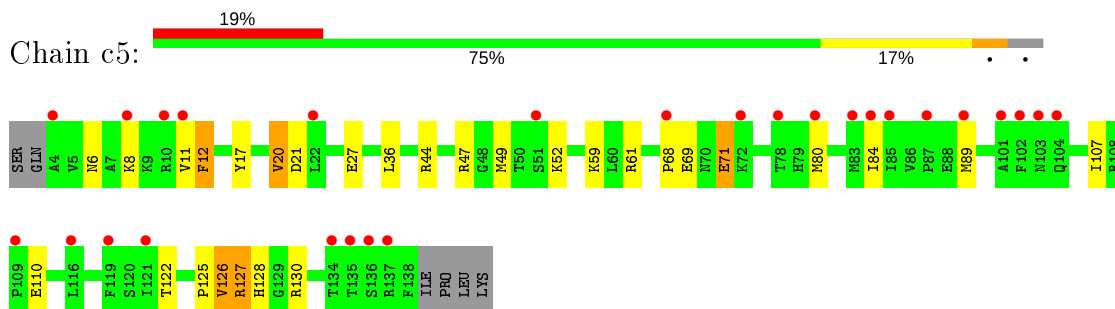
• Molecule 16: 40S ribosomal protein S14-A



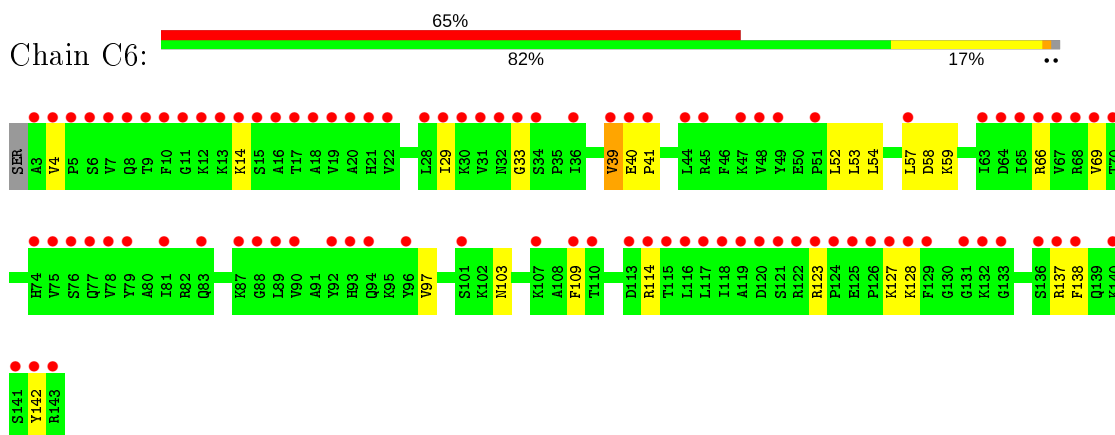
• Molecule 17: 40S ribosomal protein S15



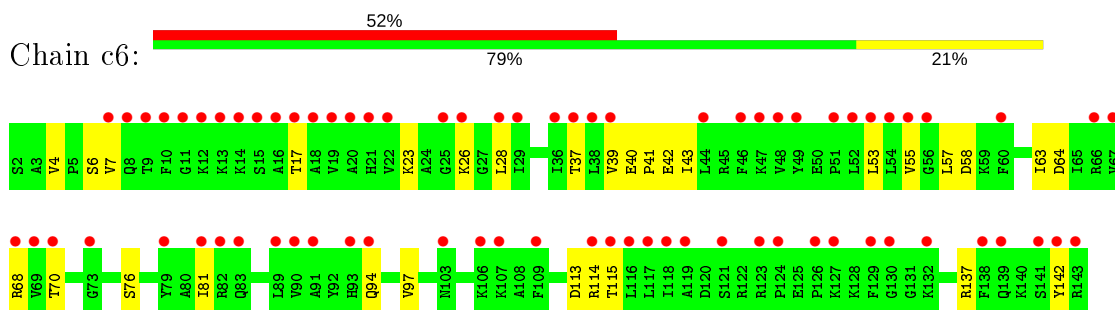
• Molecule 17: 40S ribosomal protein S15



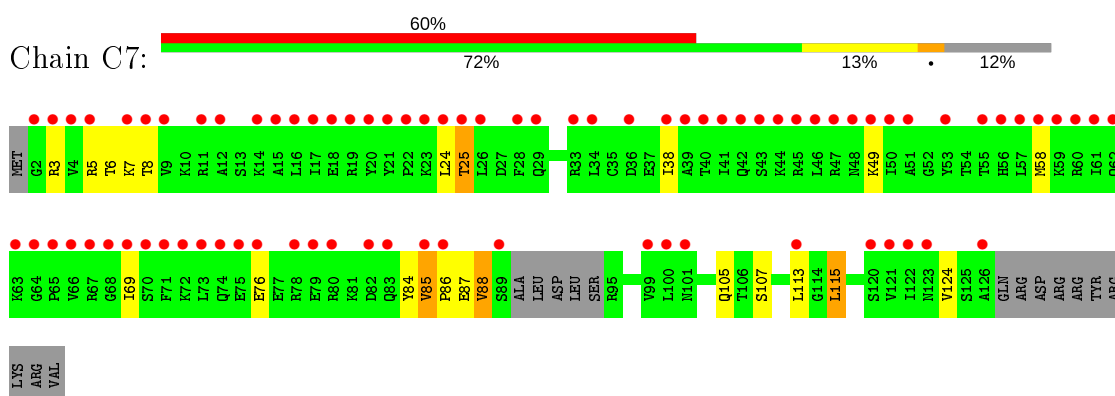
• Molecule 18: 40S ribosomal protein S16-A



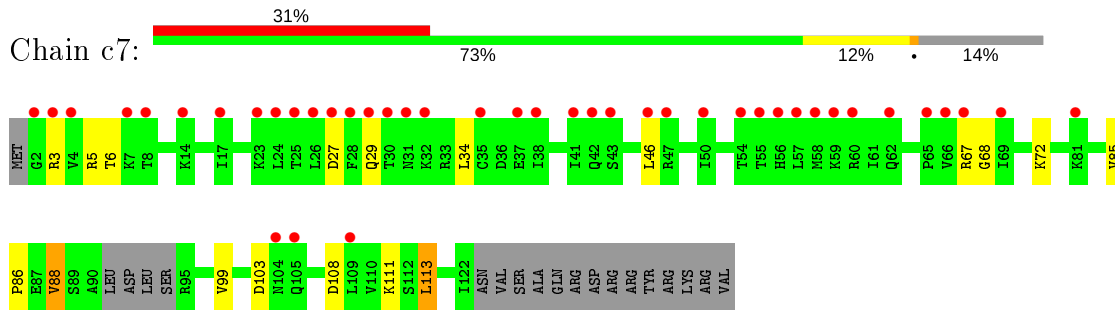
• Molecule 18: 40S ribosomal protein S16-A



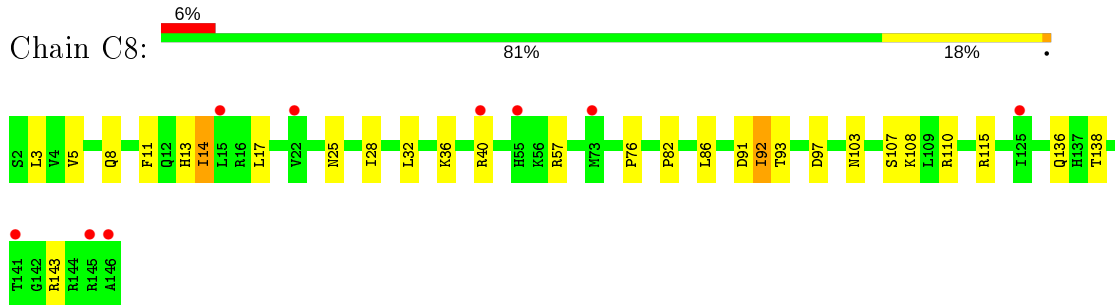
• Molecule 19: 40S ribosomal protein S17-A



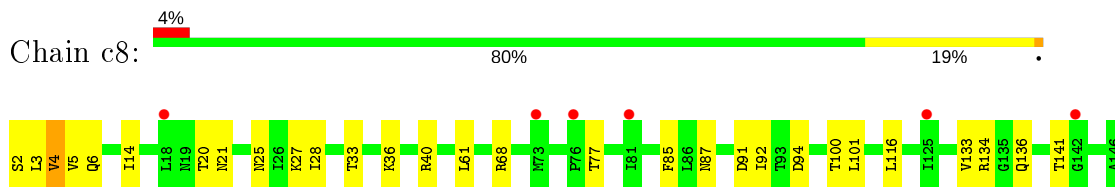
• Molecule 19: 40S ribosomal protein S17-A



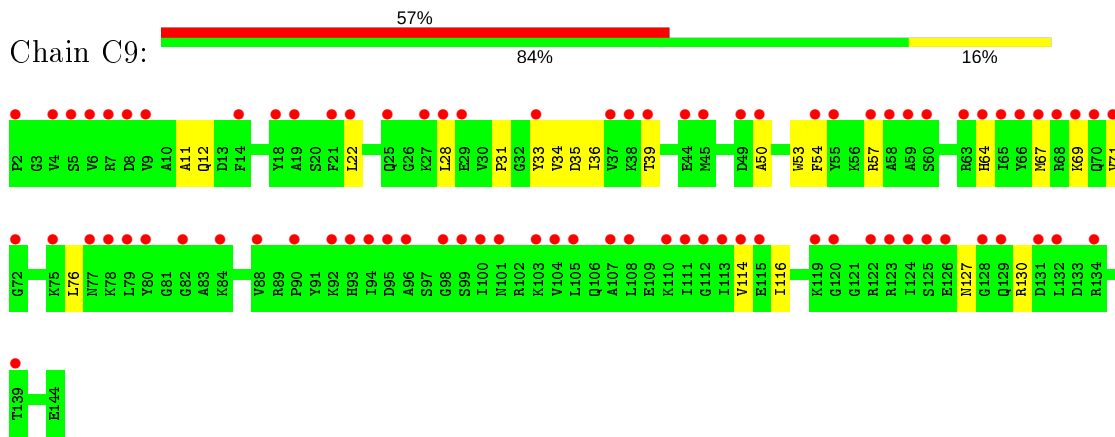
• Molecule 20: 40S ribosomal protein S18-A



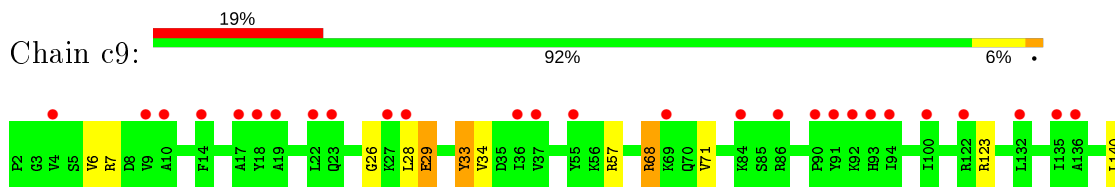
• Molecule 20: 40S ribosomal protein S18-A



• Molecule 21: 40S ribosomal protein S19-A

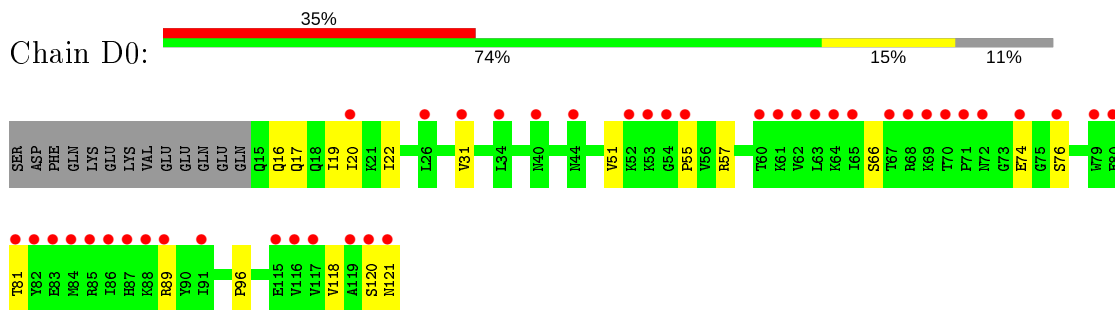


• Molecule 21: 40S ribosomal protein S19-A

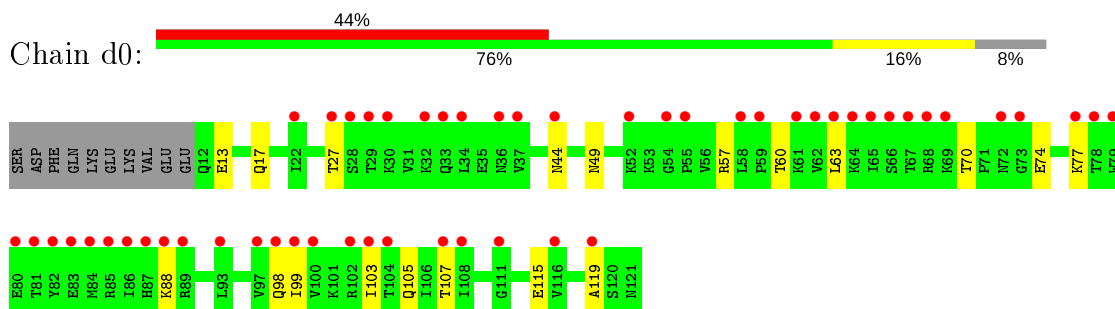


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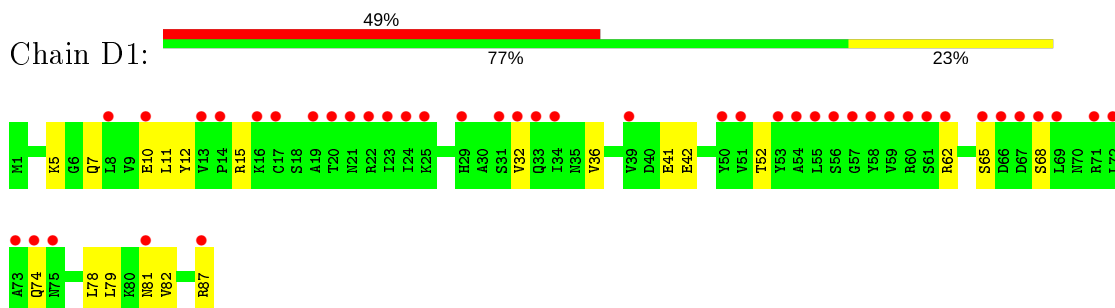
- Molecule 22: 40S ribosomal protein S20



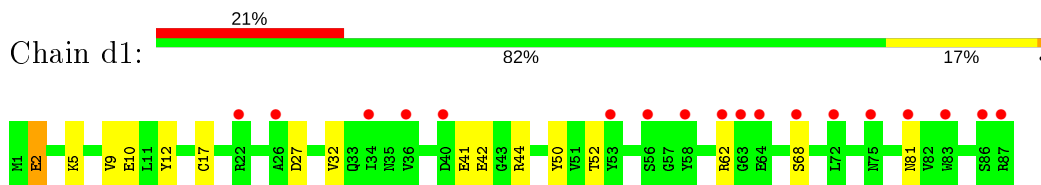
- Molecule 22: 40S ribosomal protein S20



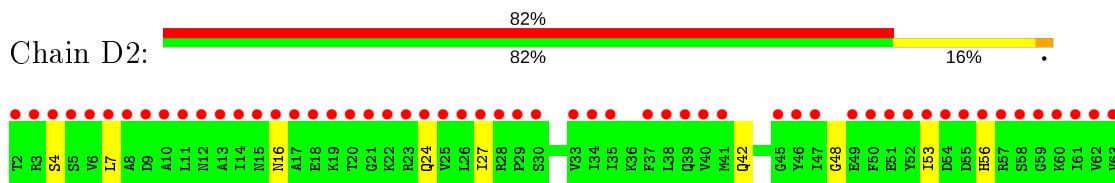
- Molecule 23: 40S ribosomal protein S21-A

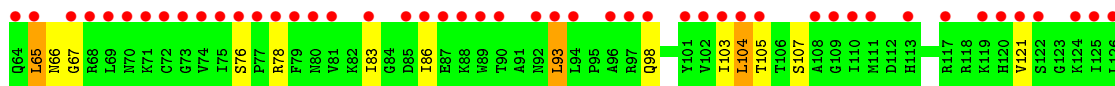


- Molecule 23: 40S ribosomal protein S21-A

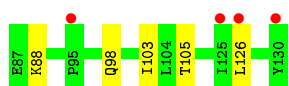
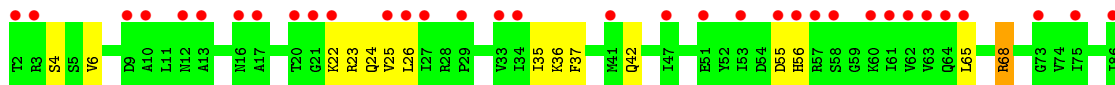
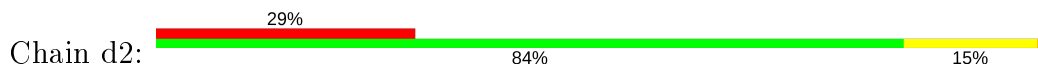


- Molecule 24: 40S ribosomal protein S22-A

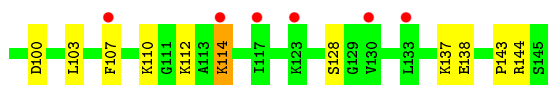
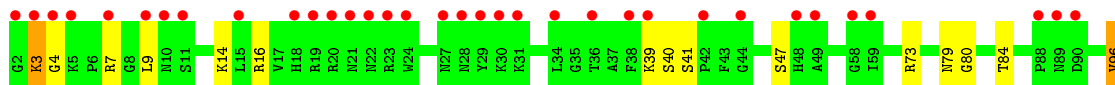
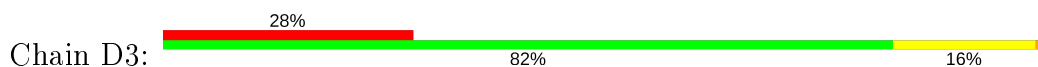




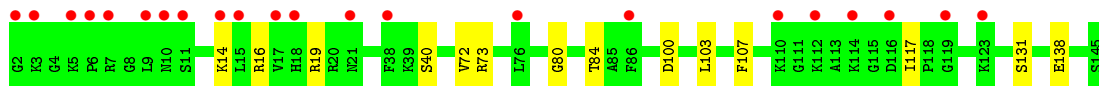
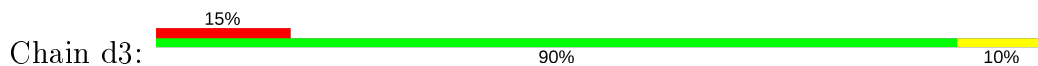
• Molecule 24: 40S ribosomal protein S22-A



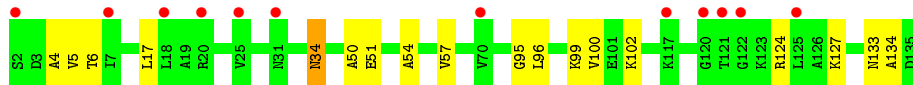
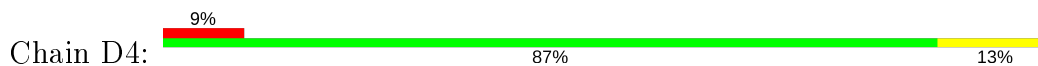
• Molecule 25: 40S ribosomal protein S23-A



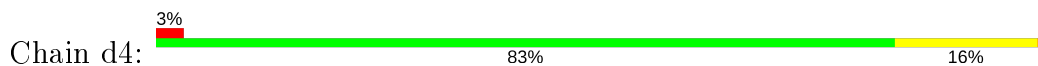
• Molecule 25: 40S ribosomal protein S23-A



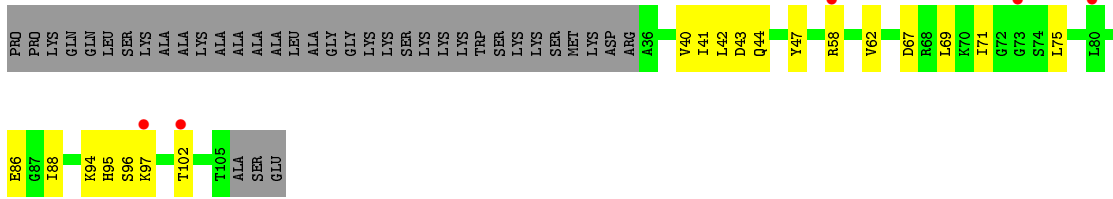
• Molecule 26: 40S ribosomal protein S24-A



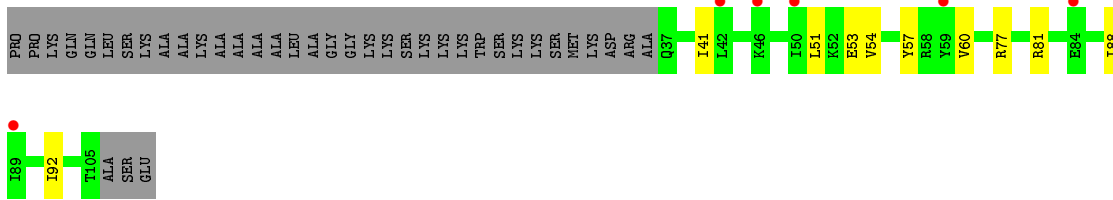
• Molecule 26: 40S ribosomal protein S24-A



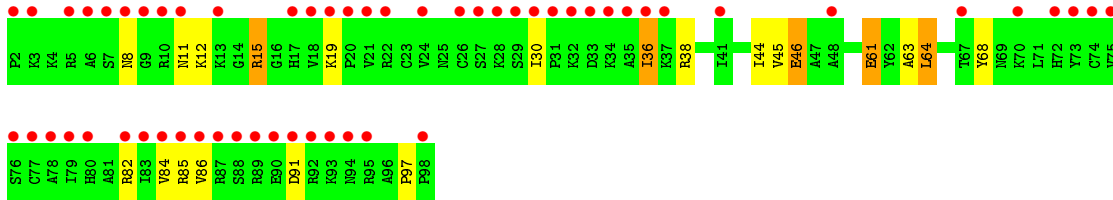
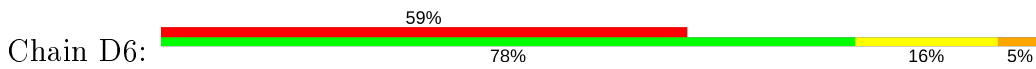
• Molecule 27: 40S ribosomal protein S25-A



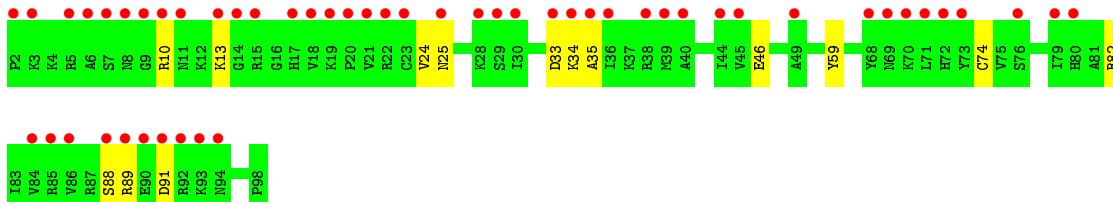
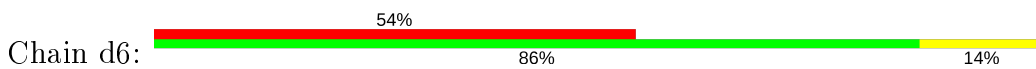
• Molecule 27: 40S ribosomal protein S25-A



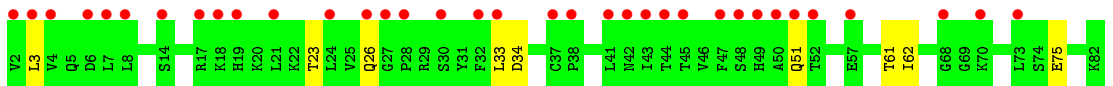
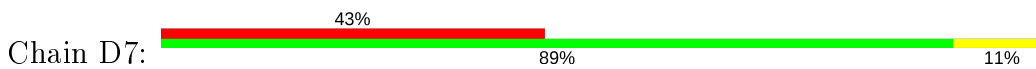
• Molecule 28: 40S ribosomal protein S26-B



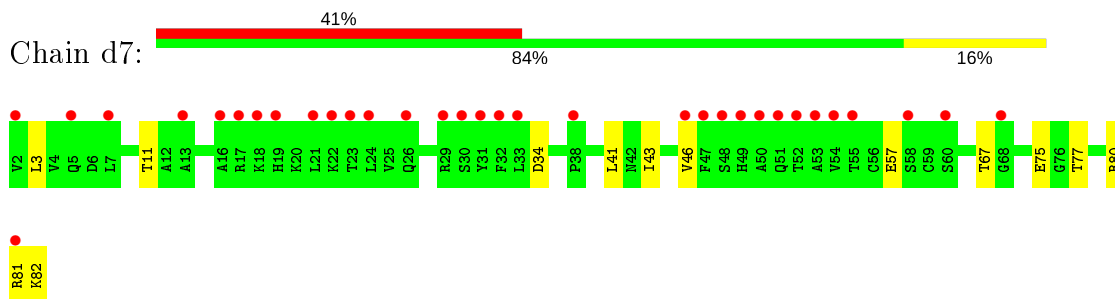
• Molecule 28: 40S ribosomal protein S26-B



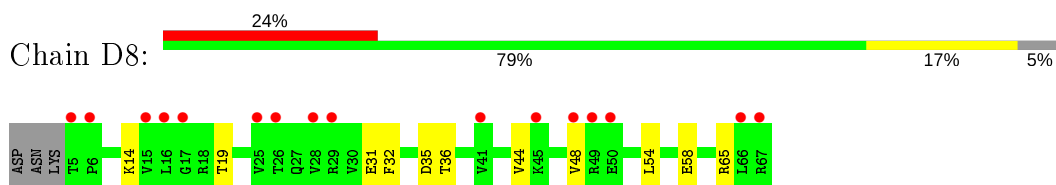
• Molecule 29: 40S ribosomal protein S27-A



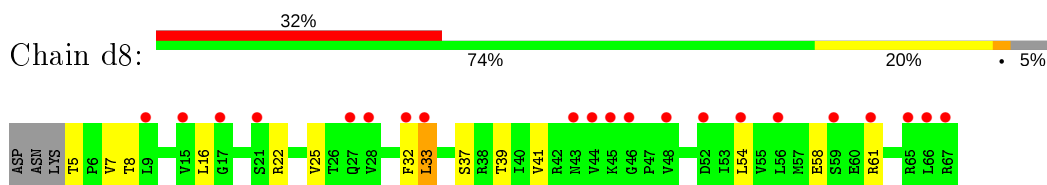
- Molecule 29: 40S ribosomal protein S27-A



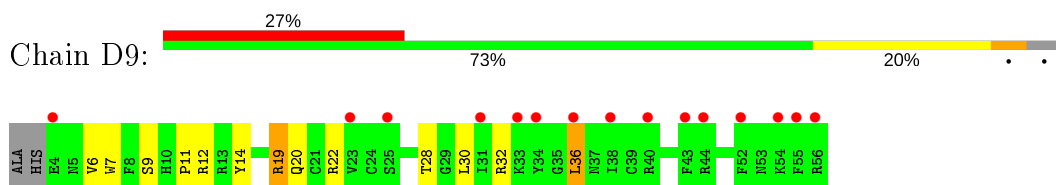
- Molecule 30: 40S ribosomal protein S28-A



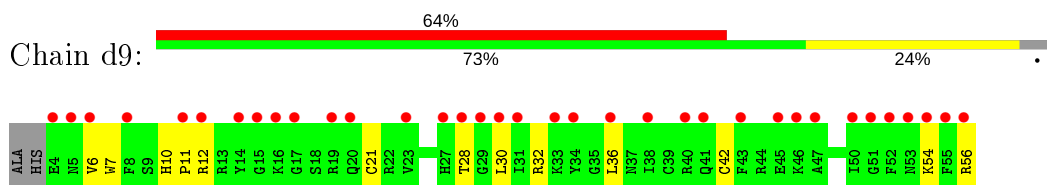
- Molecule 30: 40S ribosomal protein S28-A



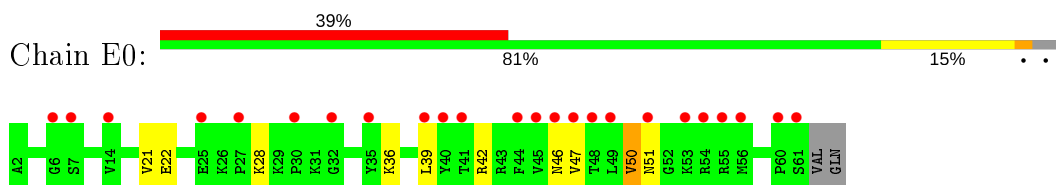
- Molecule 31: 40S ribosomal protein S29-A



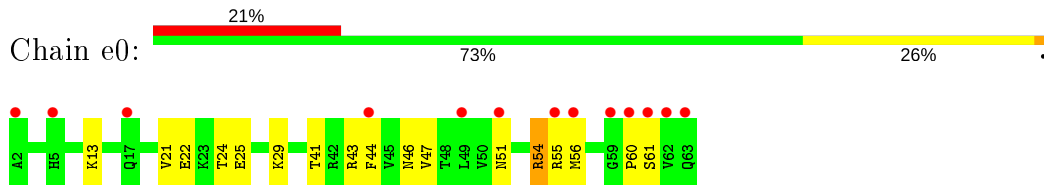
- Molecule 31: 40S ribosomal protein S29-A



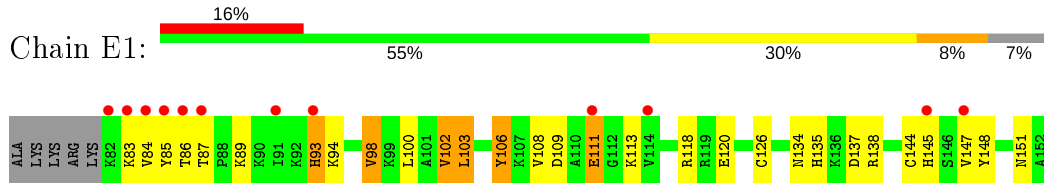
- Molecule 32: 40S ribosomal protein S30-A



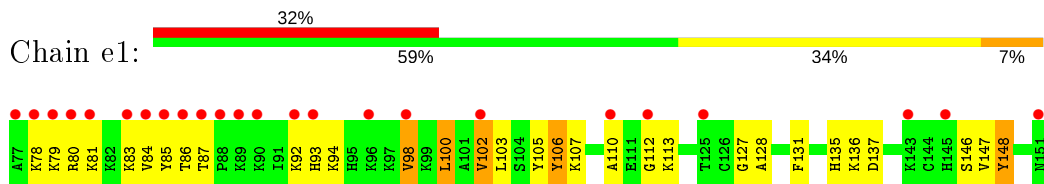
- Molecule 32: 40S ribosomal protein S30-A



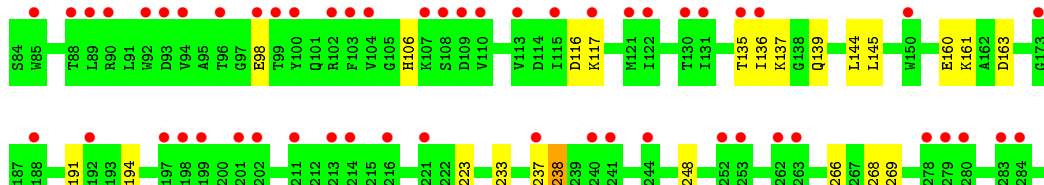
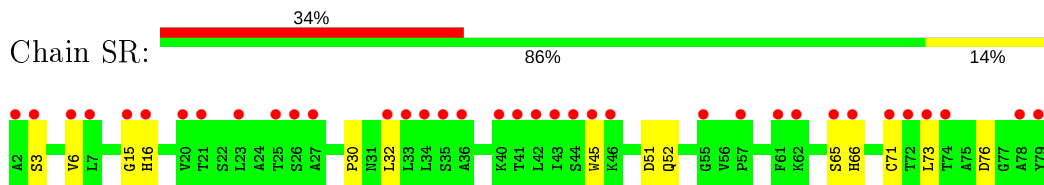
• Molecule 33: Ubiquitin-40S ribosomal protein S31



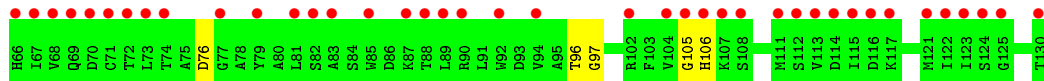
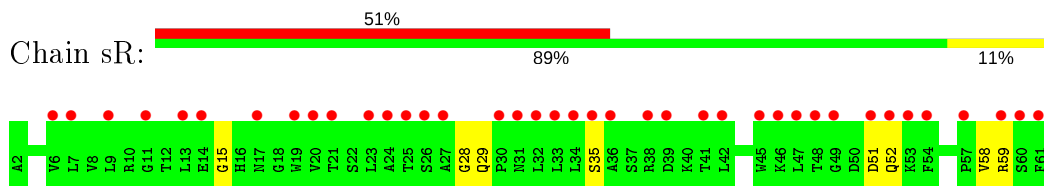
• Molecule 33: Ubiquitin-40S ribosomal protein S31

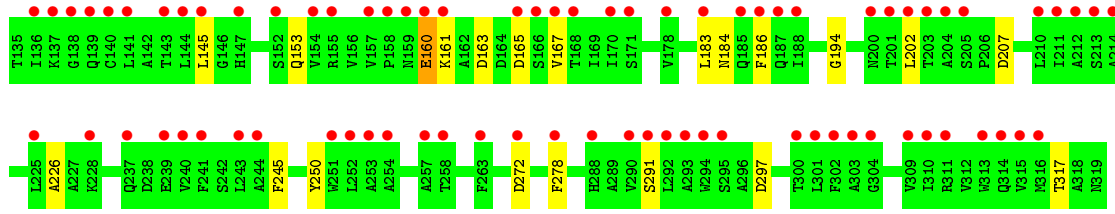


• Molecule 34: Guanine nucleotide-binding protein subunit beta-like protein

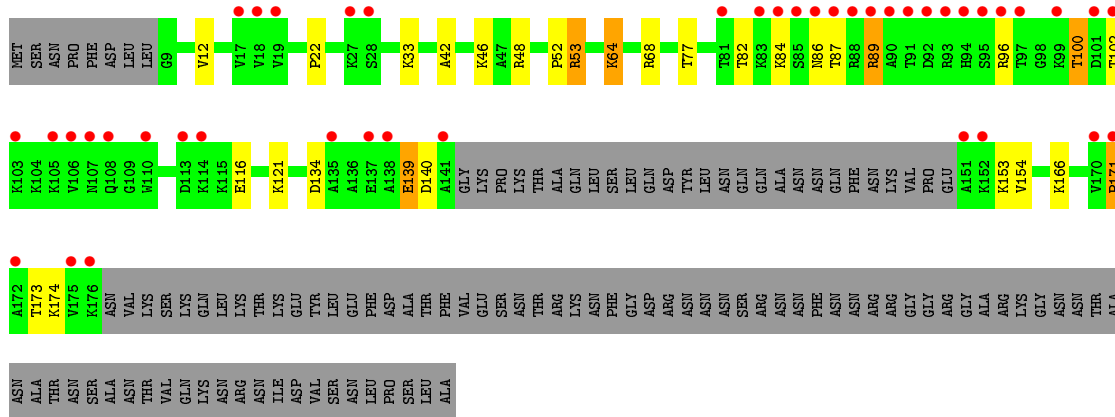


• Molecule 34: Guanine nucleotide-binding protein subunit beta-like protein

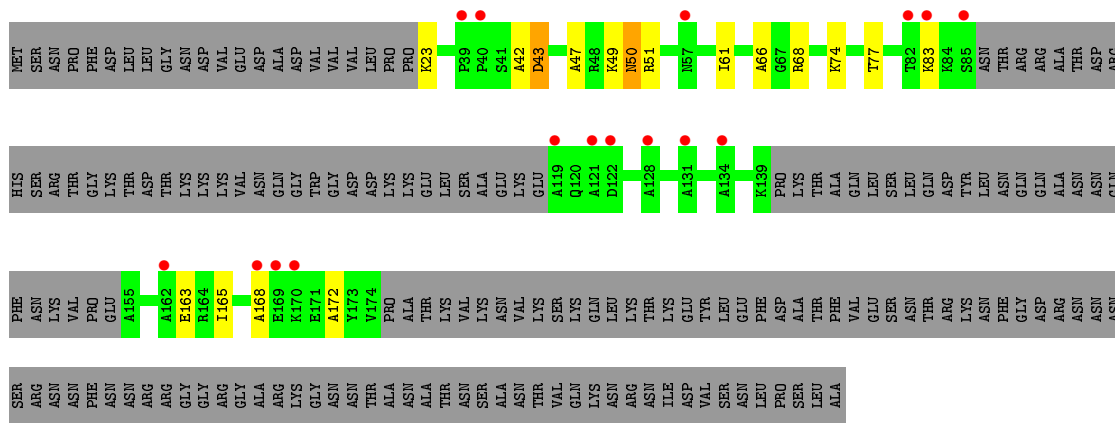




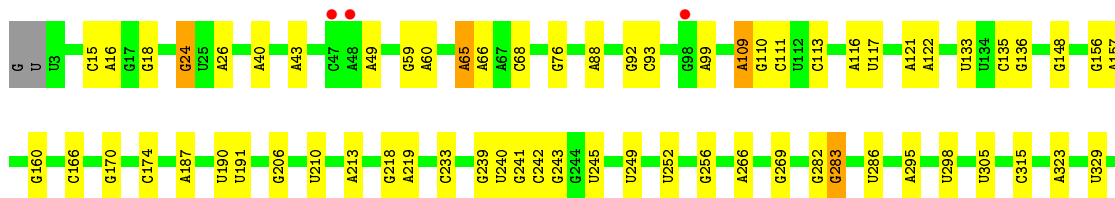
● Molecule 35: Suppressor protein STM1

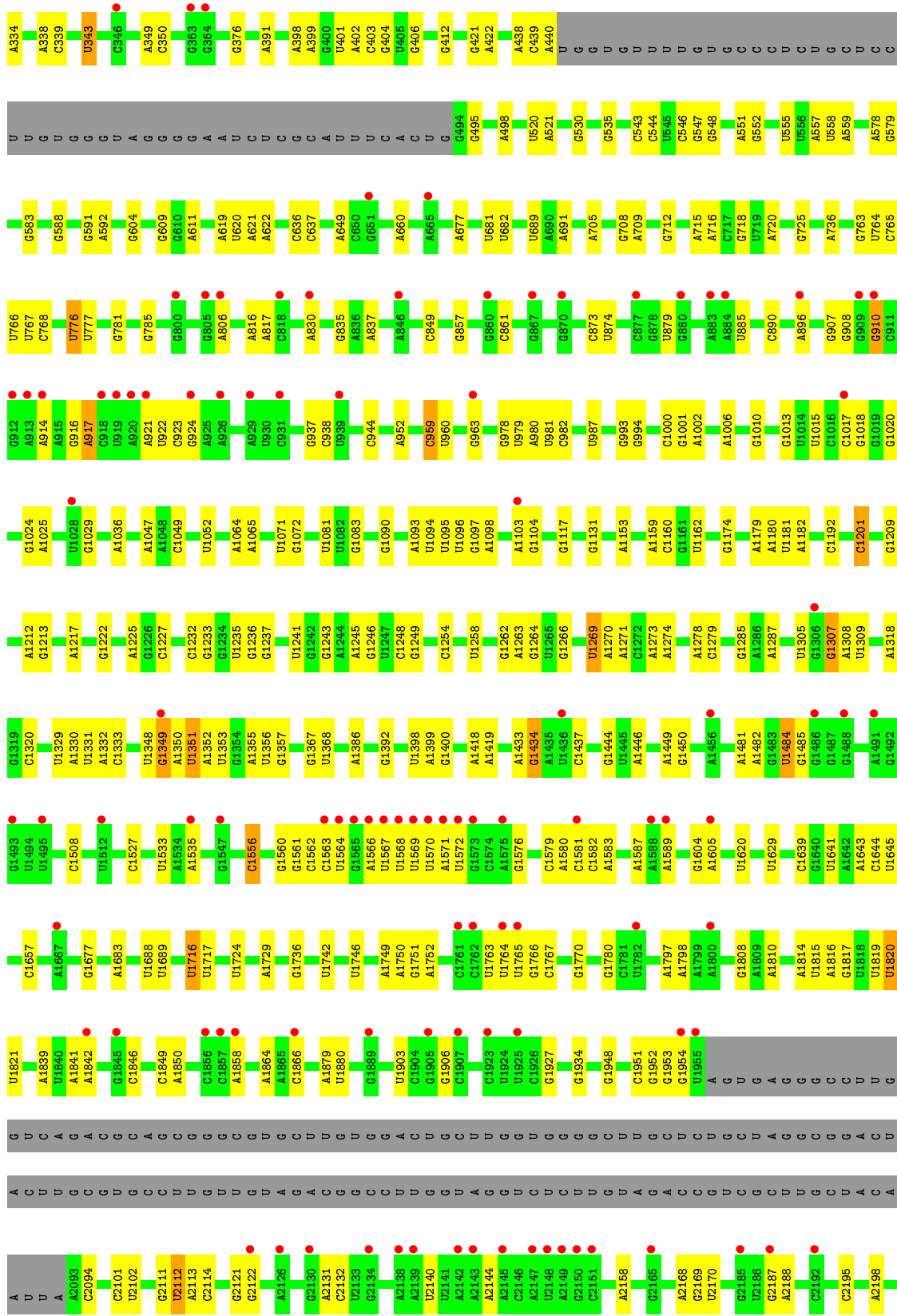


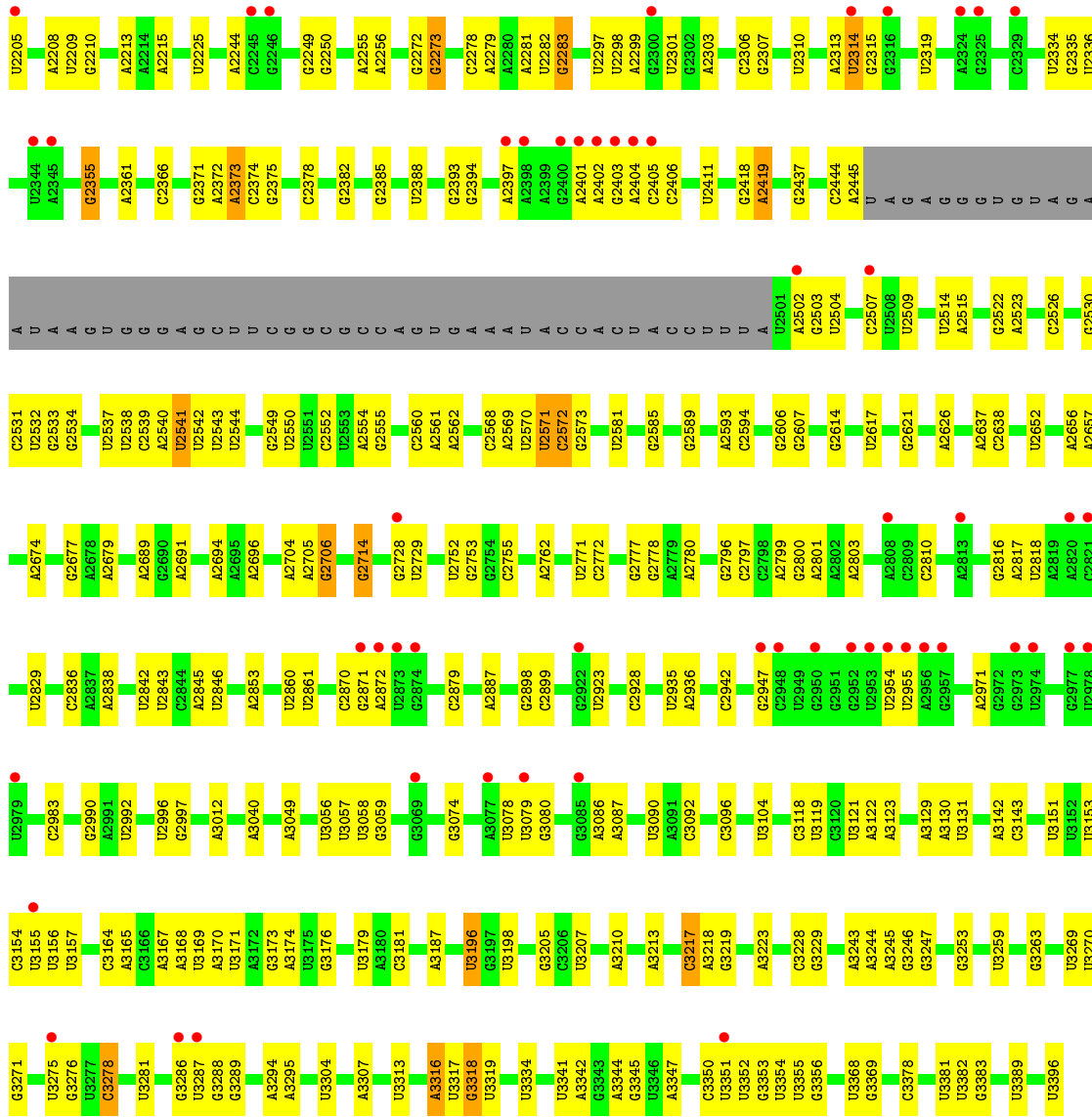
● Molecule 35: Suppressor protein STM1



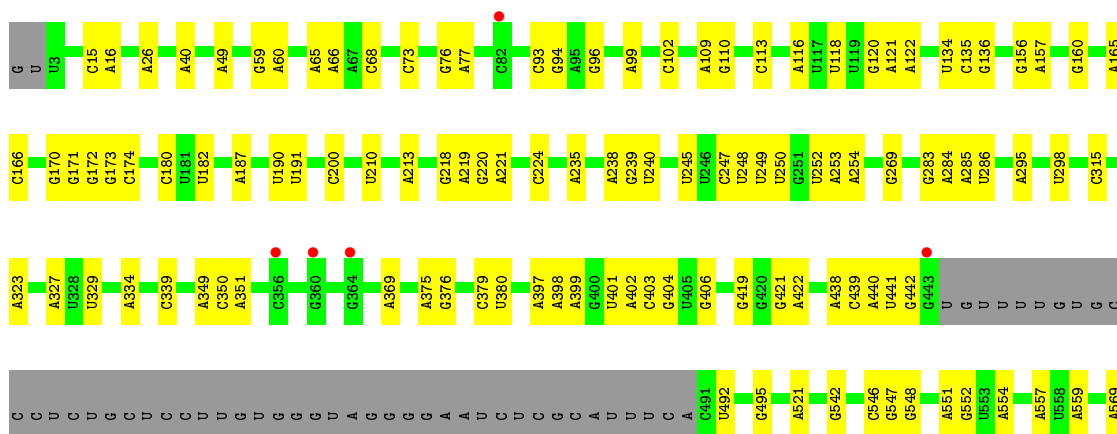
● Molecule 36: 25S ribosomal RNA

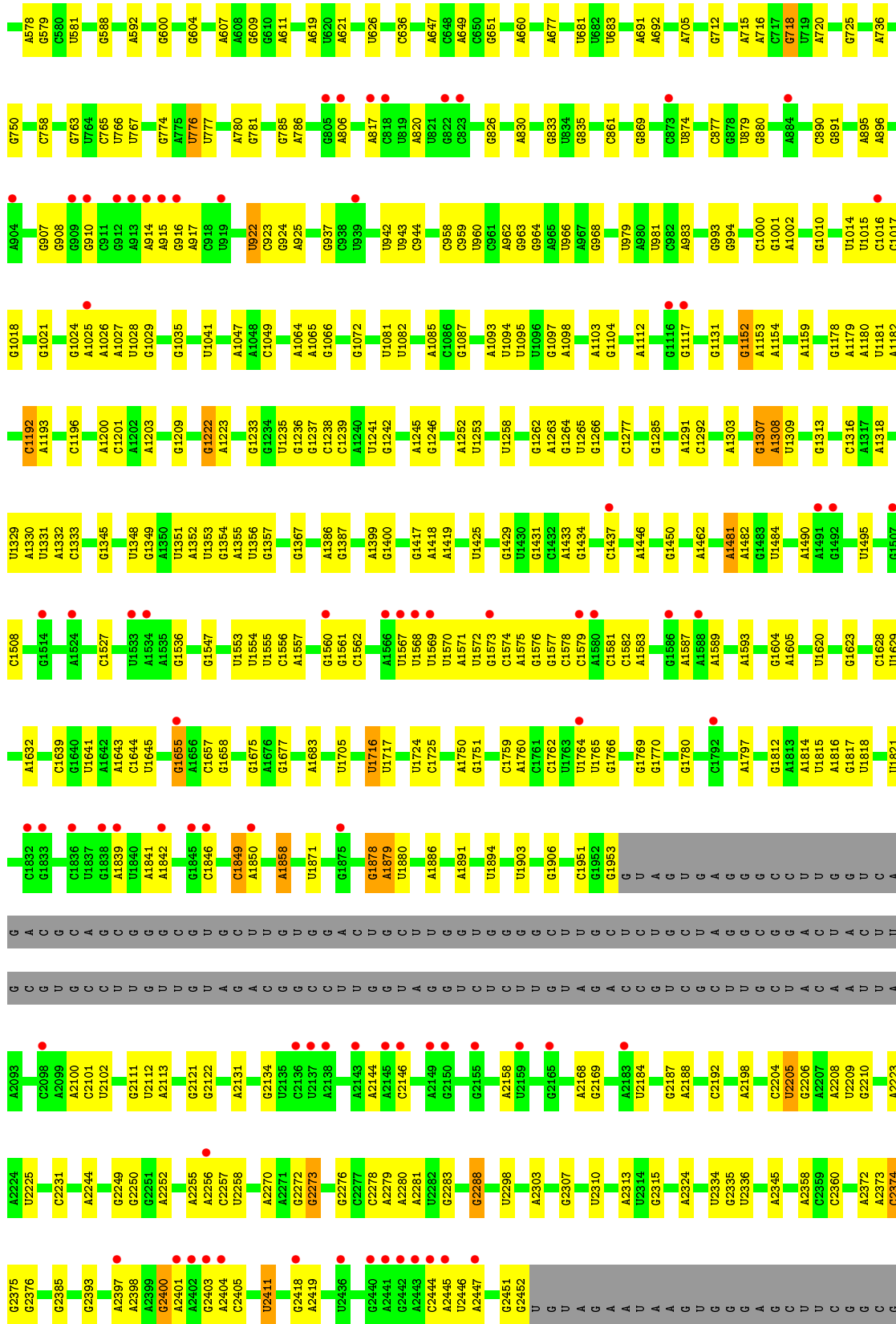


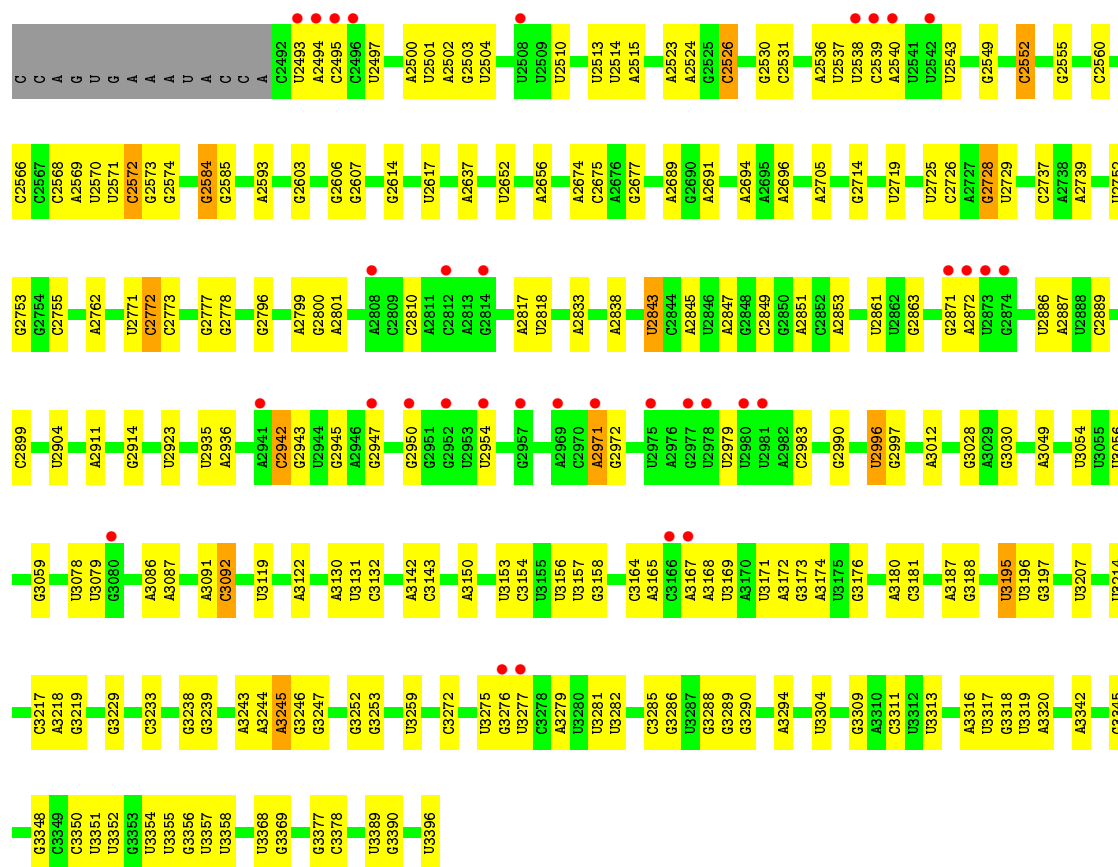




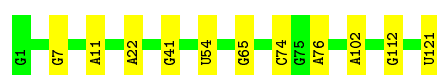
• Molecule 36: 25S ribosomal RNA



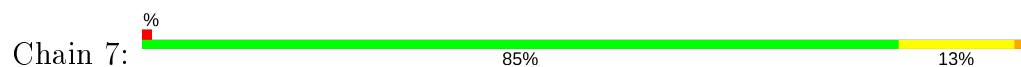




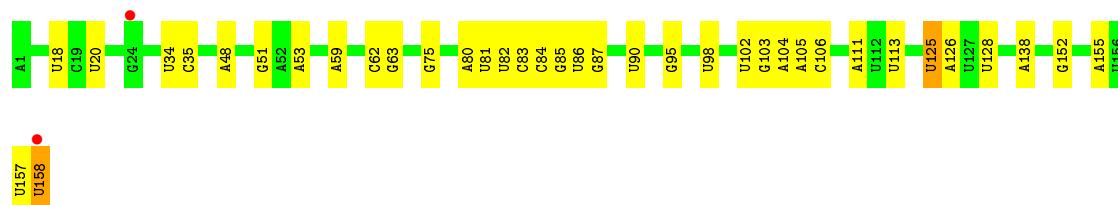
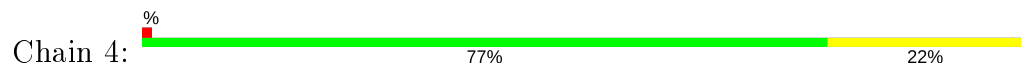
● Molecule 37: 5S ribosomal RNA



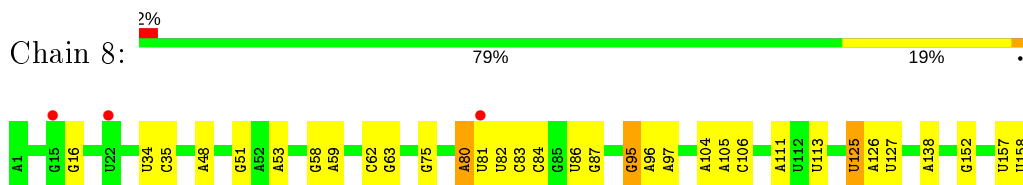
● Molecule 37: 5S ribosomal RNA



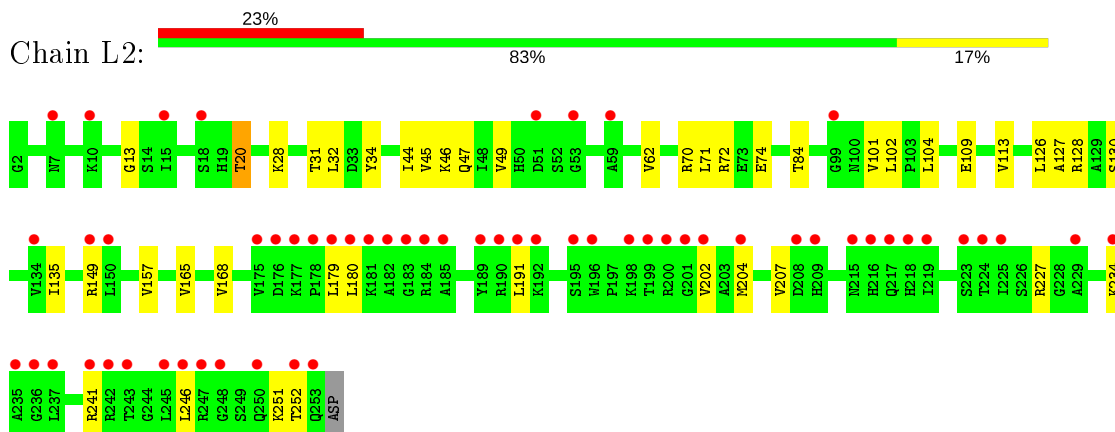
● Molecule 38: 5.8S ribosomal RNA



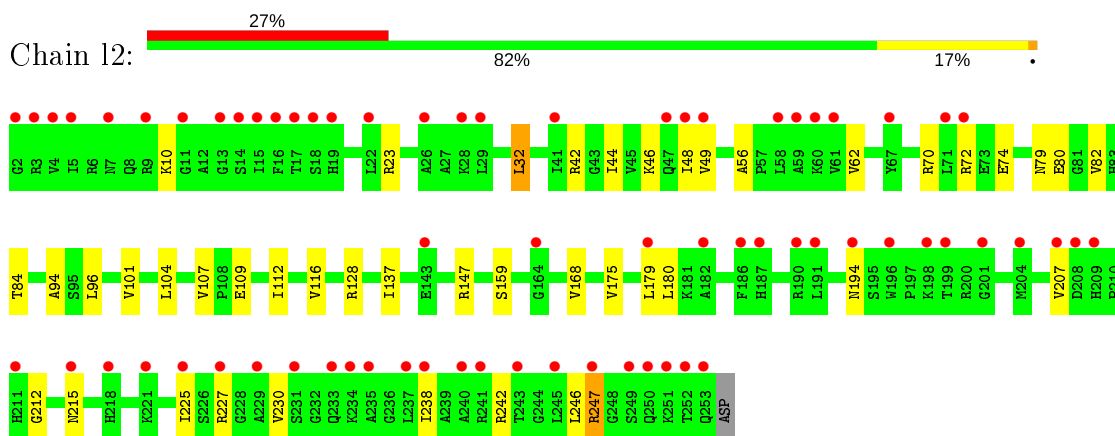
- Molecule 38: 5.8S ribosomal RNA



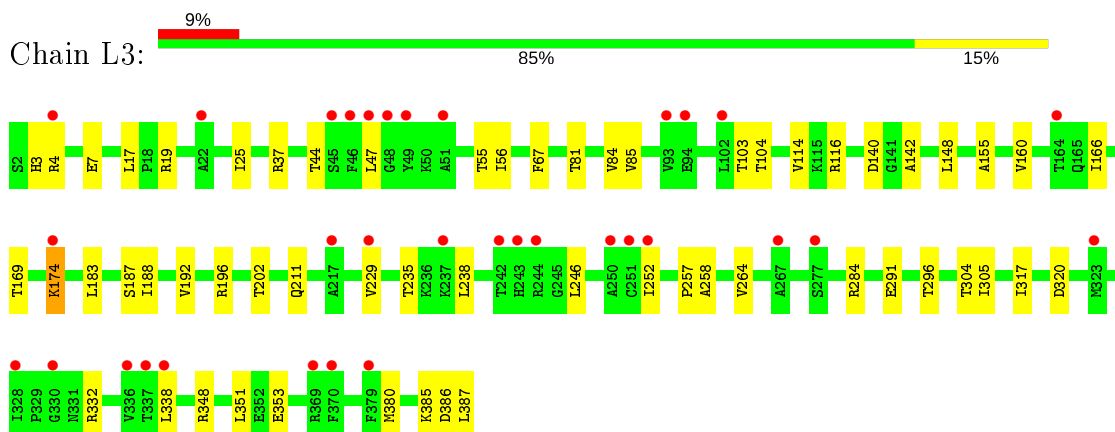
- Molecule 39: 60S ribosomal protein L2-A



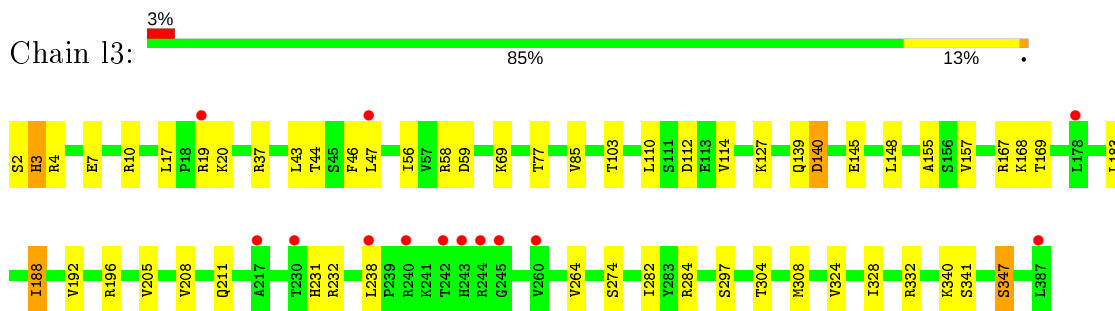
- Molecule 39: 60S ribosomal protein L2-A



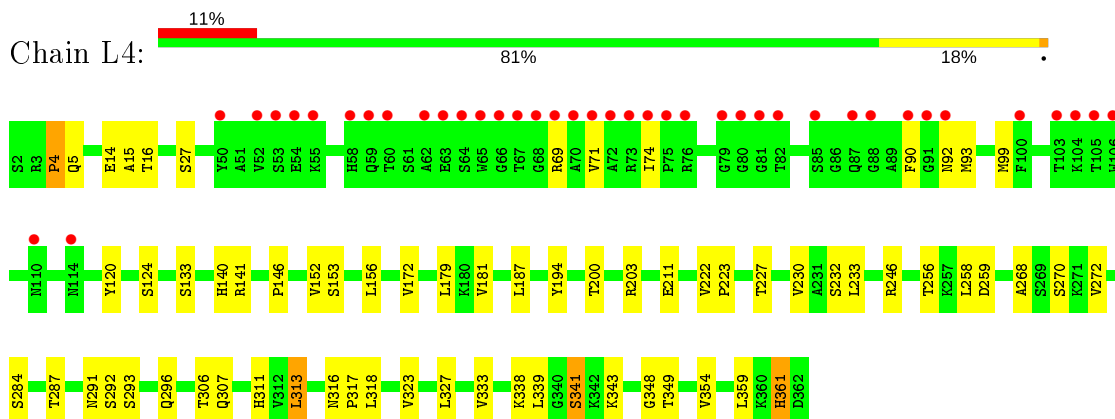
- Molecule 40: 60S ribosomal protein L3



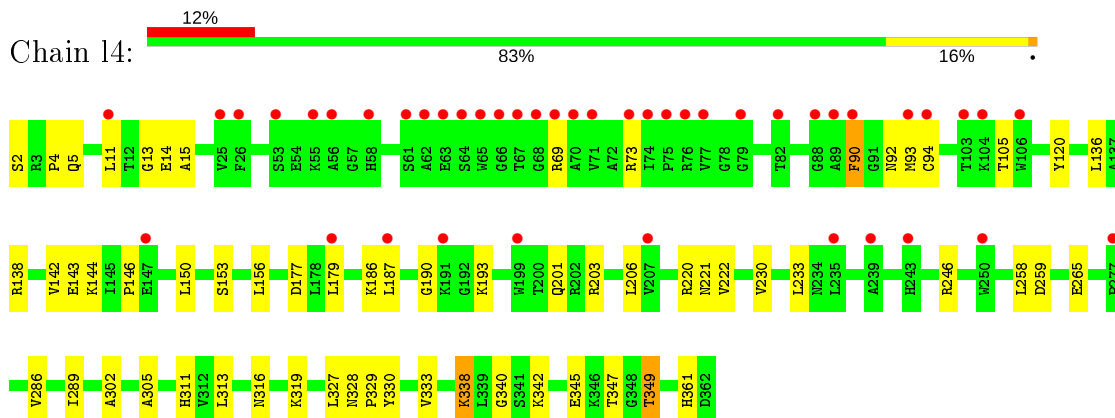
- Molecule 40: 60S ribosomal protein L3



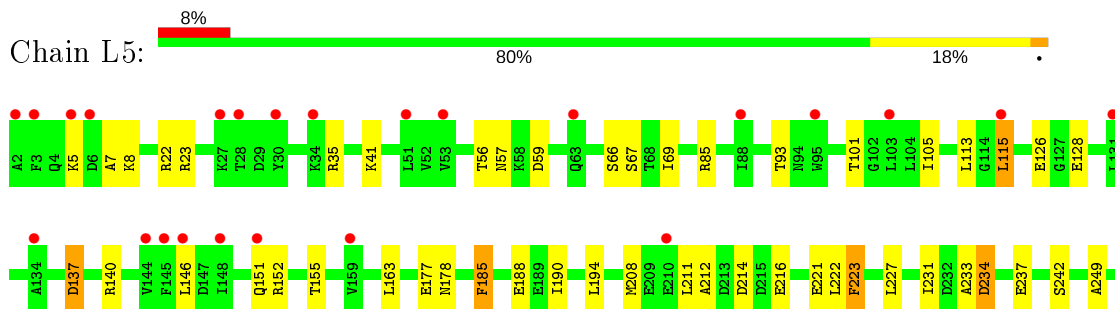
- Molecule 41: 60S ribosomal protein L4-A



- Molecule 41: 60S ribosomal protein L4-A

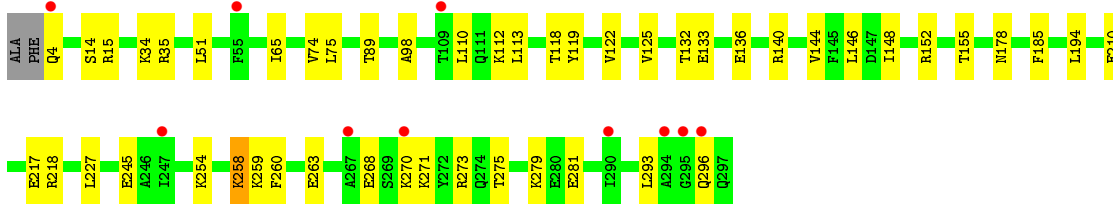
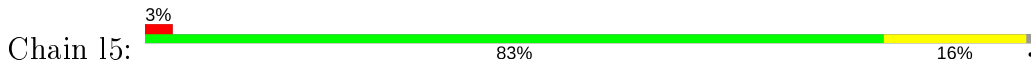


- Molecule 42: 60S ribosomal protein L5

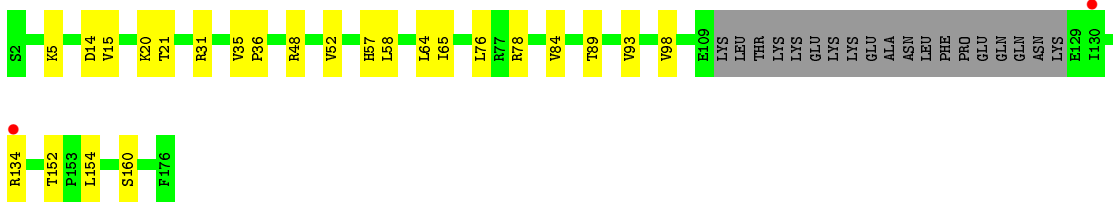
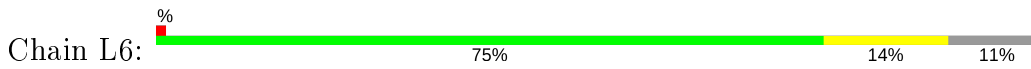




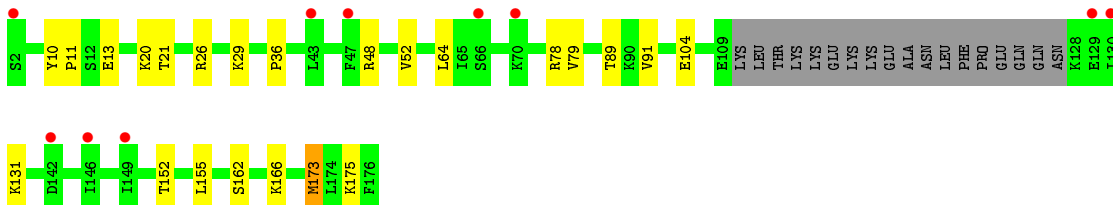
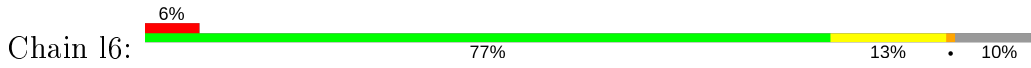
• Molecule 42: 60S ribosomal protein L5



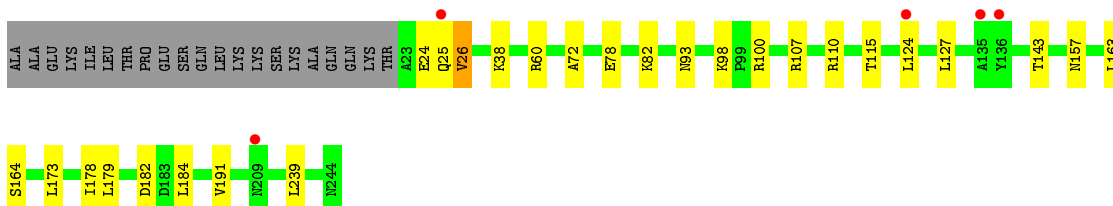
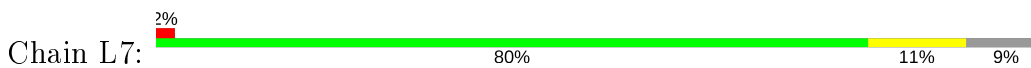
• Molecule 43: 60S ribosomal protein L6-A



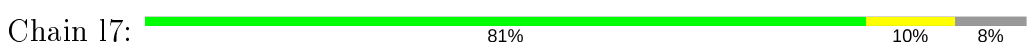
• Molecule 43: 60S ribosomal protein L6-A



• Molecule 44: 60S ribosomal protein L7-A

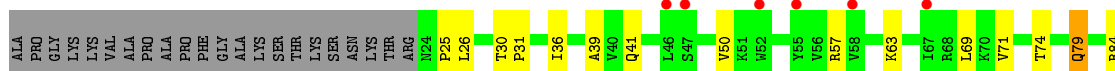
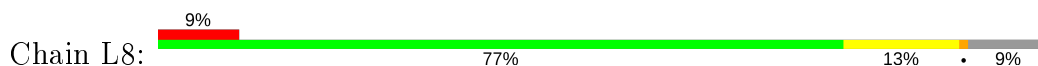


• Molecule 44: 60S ribosomal protein L7-A

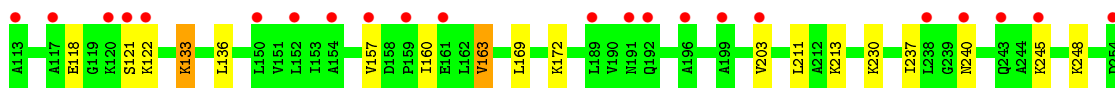
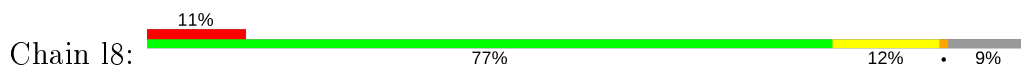




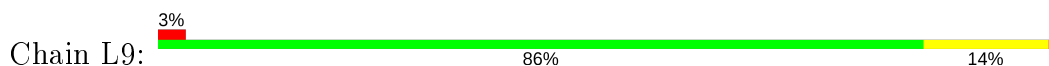
• Molecule 45: 60S ribosomal protein L8-A



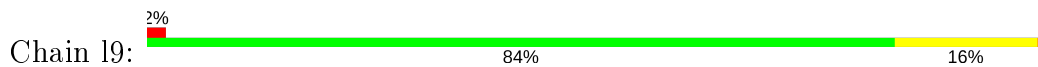
• Molecule 45: 60S ribosomal protein L8-A



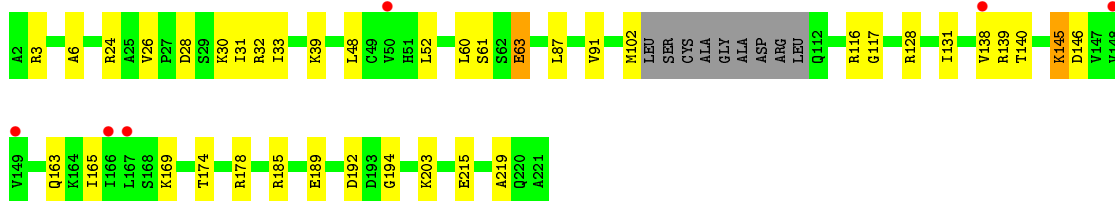
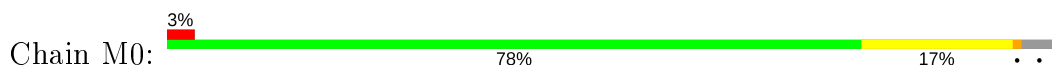
• Molecule 46: 60S ribosomal protein L9-A



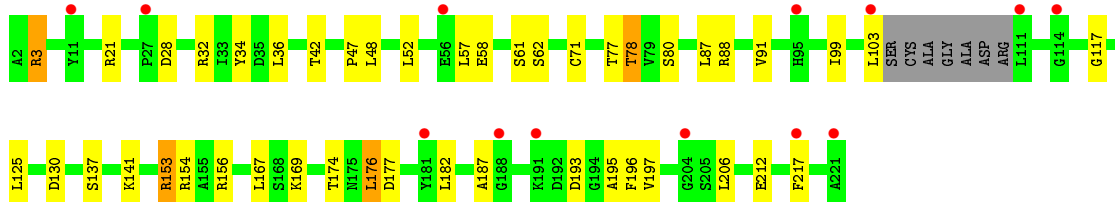
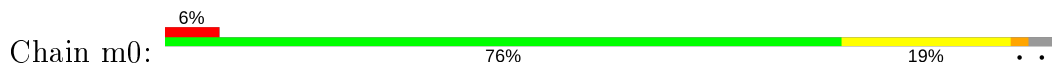
• Molecule 46: 60S ribosomal protein L9-A



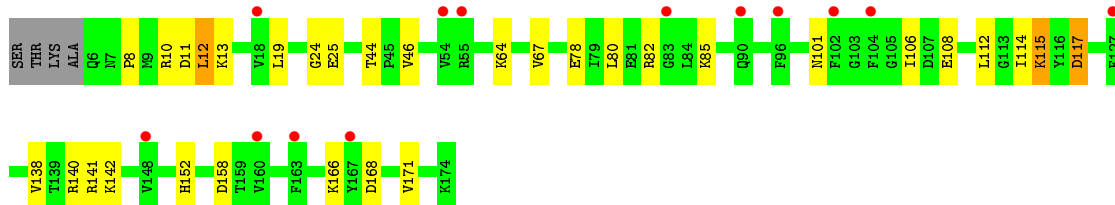
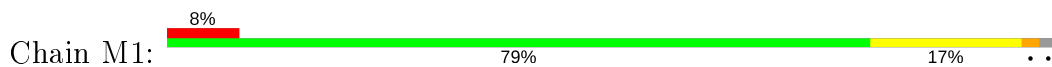
• Molecule 47: 60S ribosomal protein L10



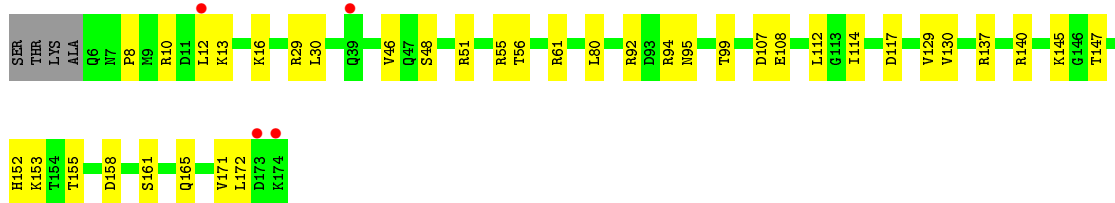
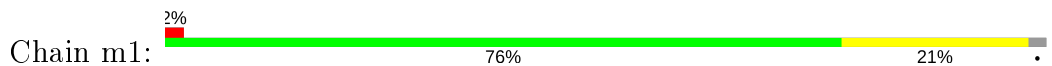
- Molecule 47: 60S ribosomal protein L10



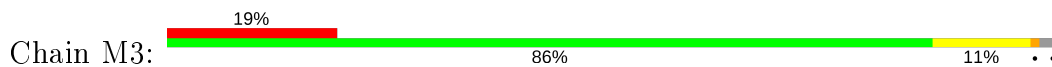
- Molecule 48: 60S ribosomal protein L11-B

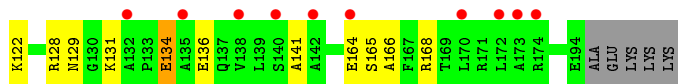


- Molecule 48: 60S ribosomal protein L11-B

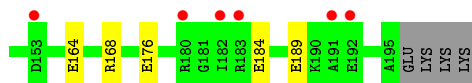
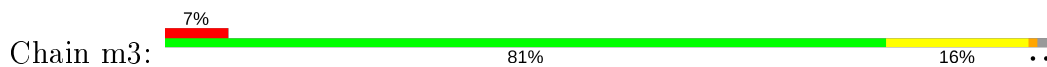


- Molecule 49: 60S ribosomal protein L13-A

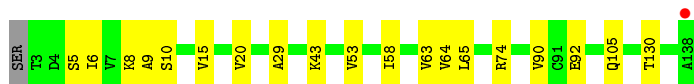
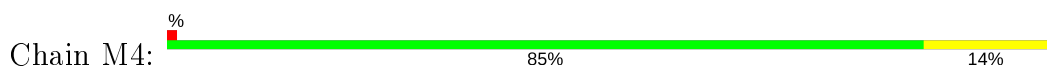




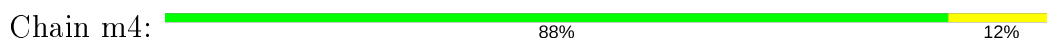
- Molecule 49: 60S ribosomal protein L13-A



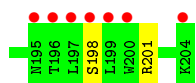
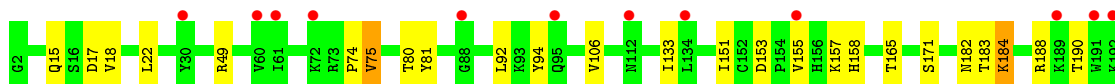
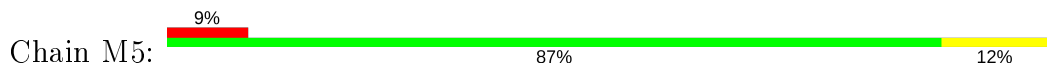
- Molecule 50: 60S ribosomal protein L14-A



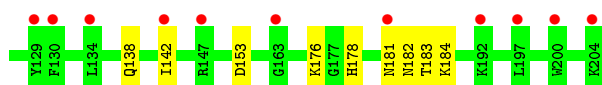
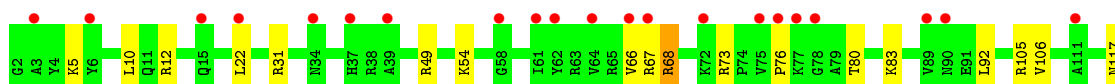
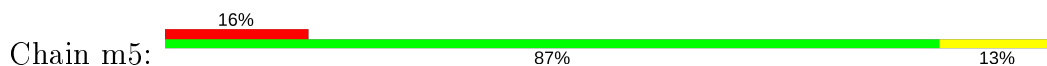
- Molecule 50: 60S ribosomal protein L14-A



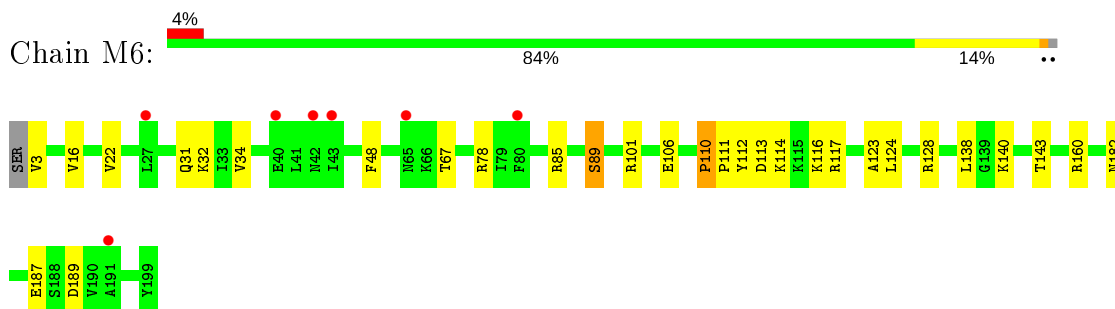
- Molecule 51: 60S ribosomal protein L15-A



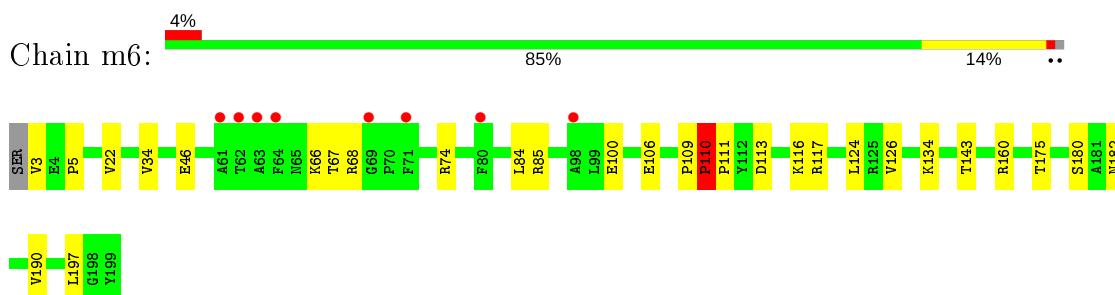
- Molecule 51: 60S ribosomal protein L15-A



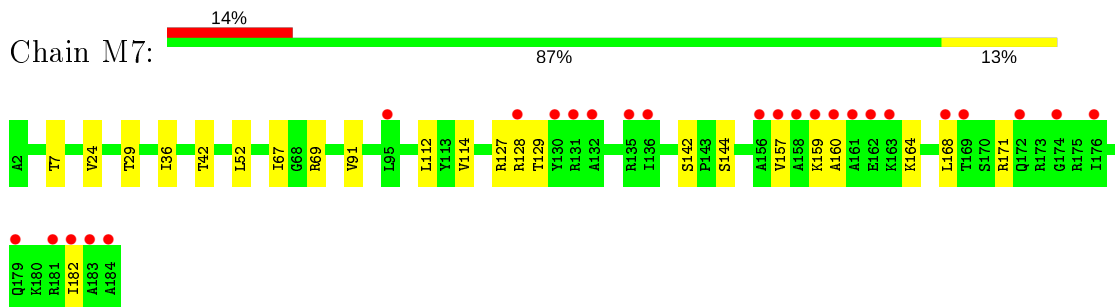
- Molecule 52: 60S ribosomal protein L16-A



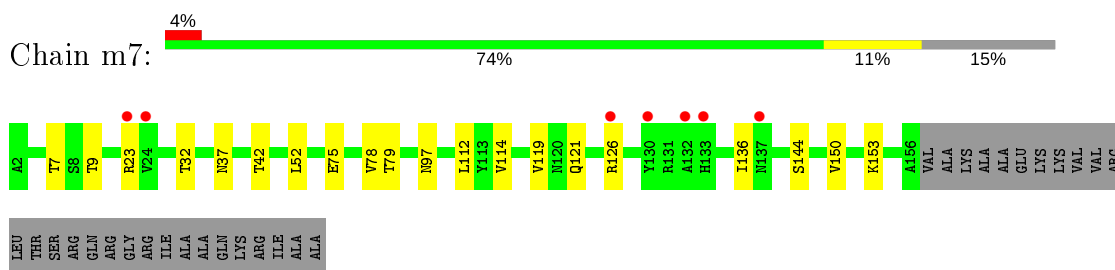
- Molecule 52: 60S ribosomal protein L16-A



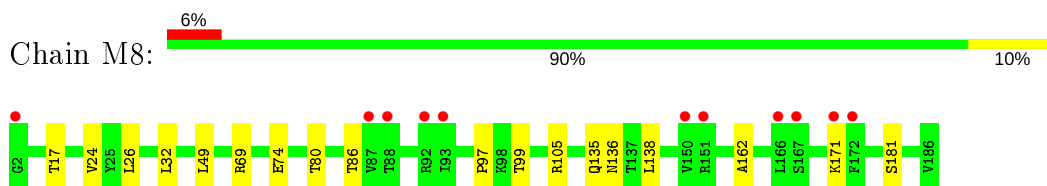
- Molecule 53: 60S ribosomal protein L17-A



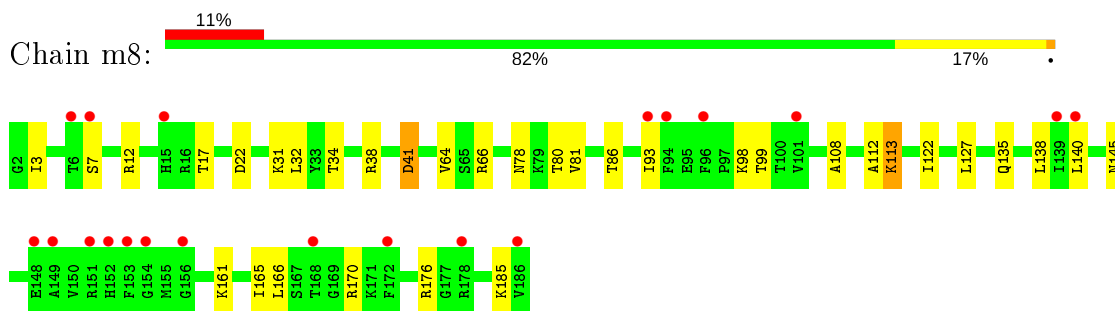
- Molecule 53: 60S ribosomal protein L17-A



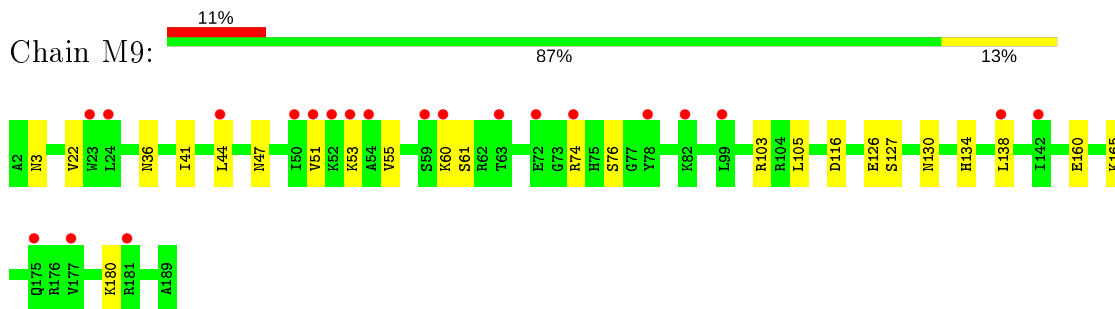
- Molecule 54: 60S ribosomal protein L18-A



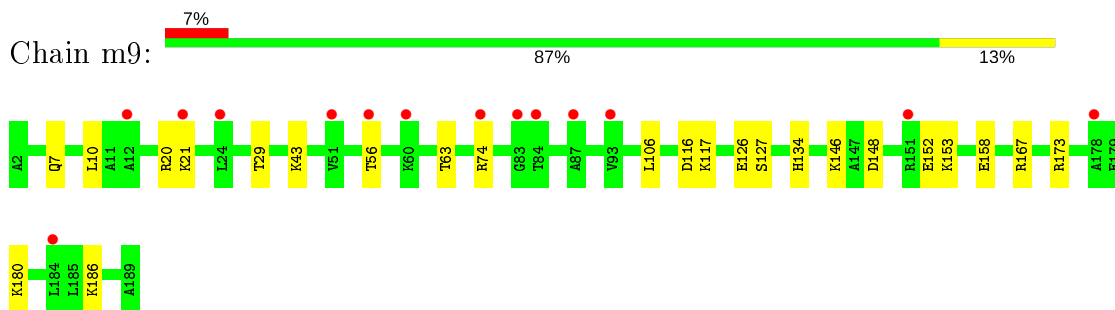
- Molecule 54: 60S ribosomal protein L18-A



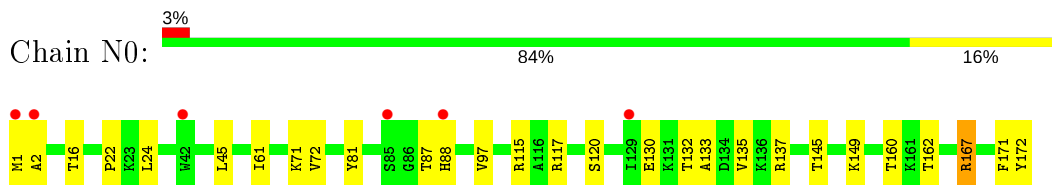
- Molecule 55: 60S ribosomal protein L19-A



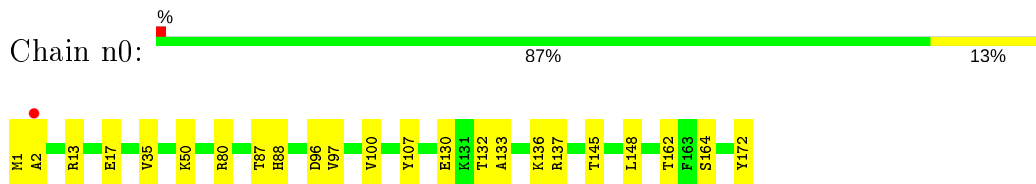
- Molecule 55: 60S ribosomal protein L19-A



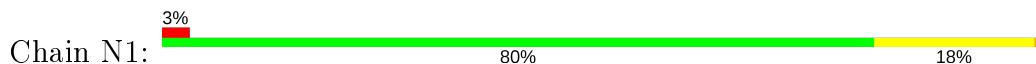
- Molecule 56: 60S ribosomal protein L20-A

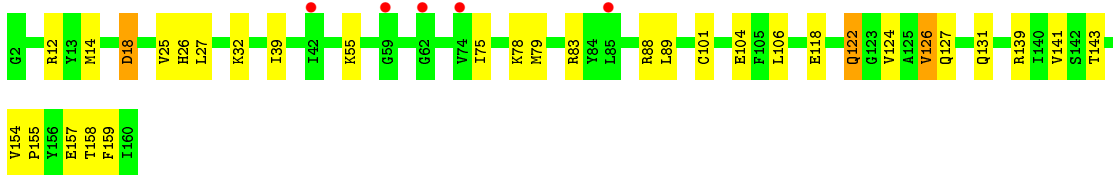


- Molecule 56: 60S ribosomal protein L20-A

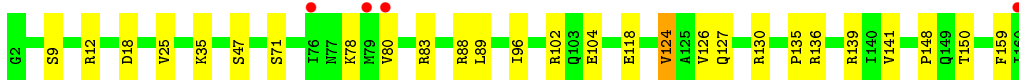
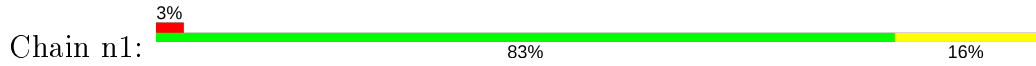


- Molecule 57: 60S ribosomal protein L21-A

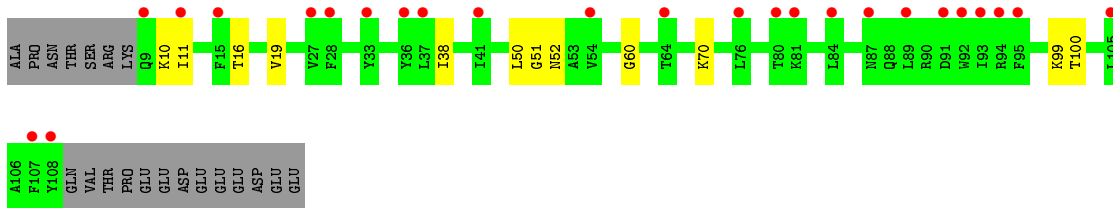
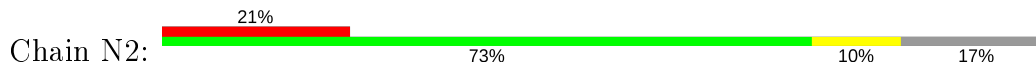




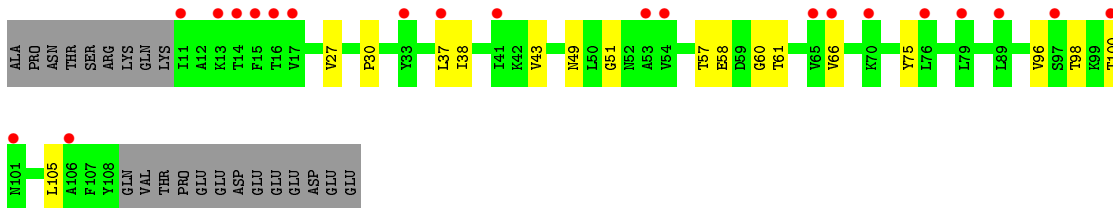
- Molecule 57: 60S ribosomal protein L21-A



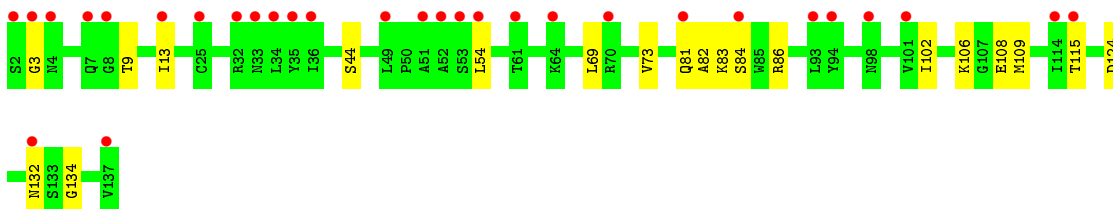
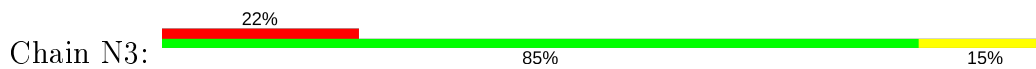
- Molecule 58: 60S ribosomal protein L22-A



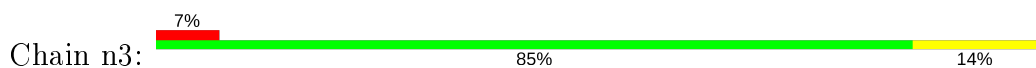
- Molecule 58: 60S ribosomal protein L22-A

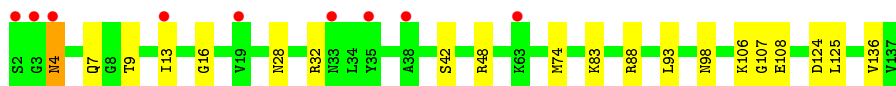


- Molecule 59: 60S ribosomal protein L23-A

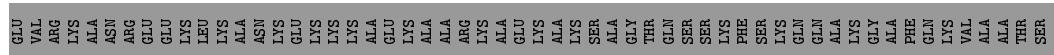
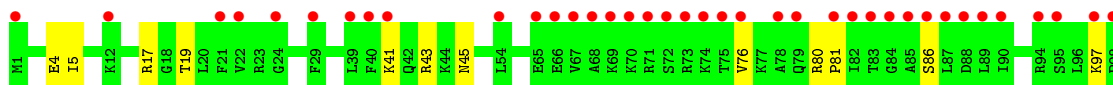


- Molecule 59: 60S ribosomal protein L23-A

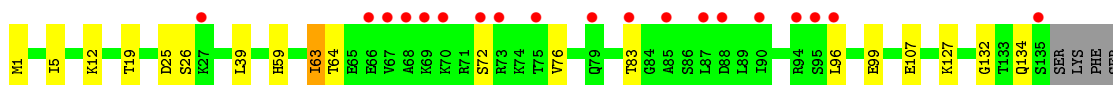
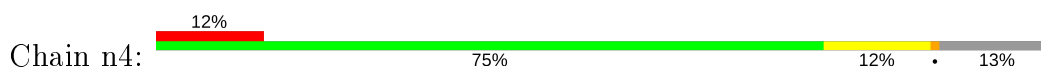




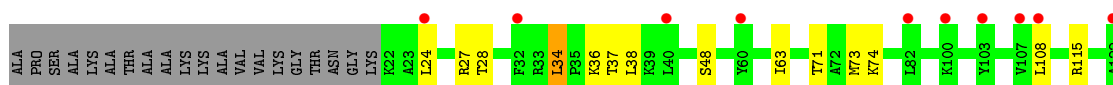
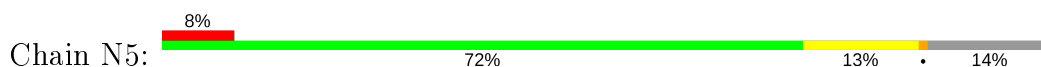
- Molecule 60: 60S ribosomal protein L24-A



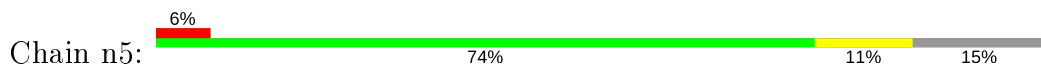
- Molecule 60: 60S ribosomal protein L24-A



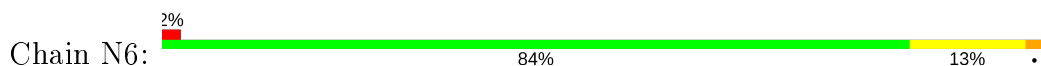
- Molecule 61: 60S ribosomal protein L25

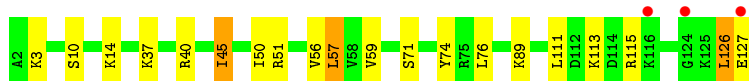


- Molecule 61: 60S ribosomal protein L25

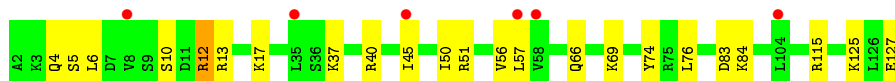
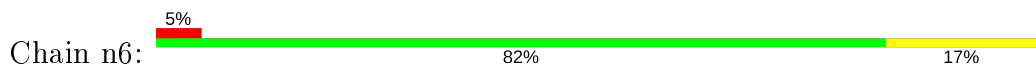


- Molecule 62: 60S ribosomal protein L26-A

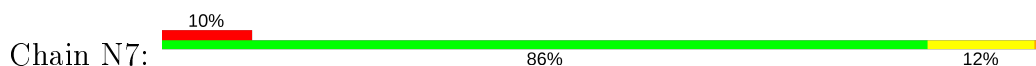




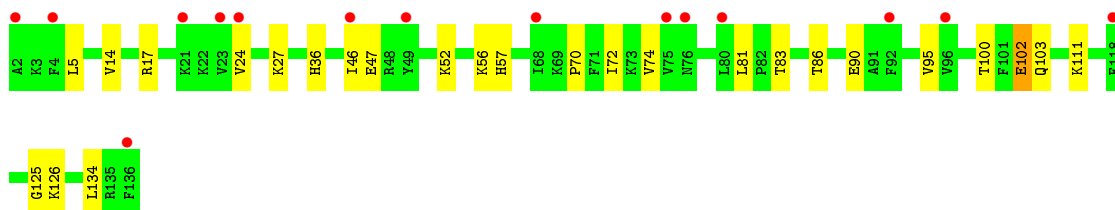
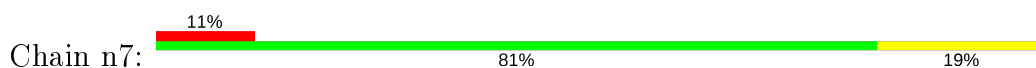
- Molecule 62: 60S ribosomal protein L26-A



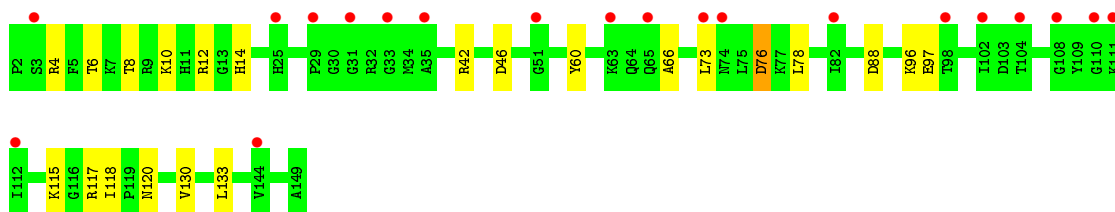
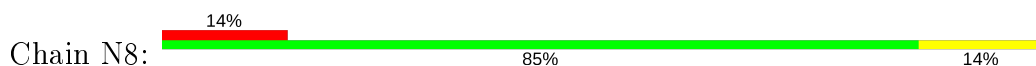
- Molecule 63: 60S ribosomal protein L27-A



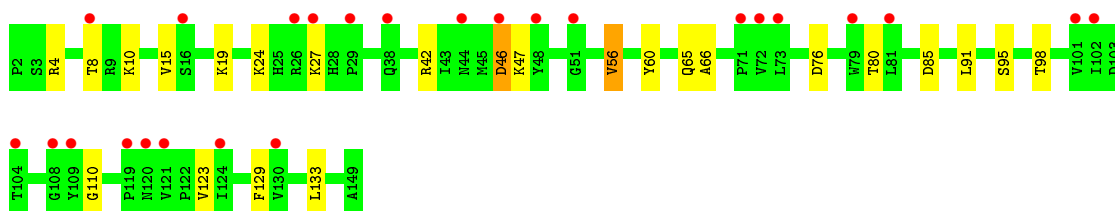
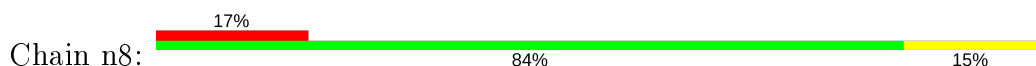
- Molecule 63: 60S ribosomal protein L27-A



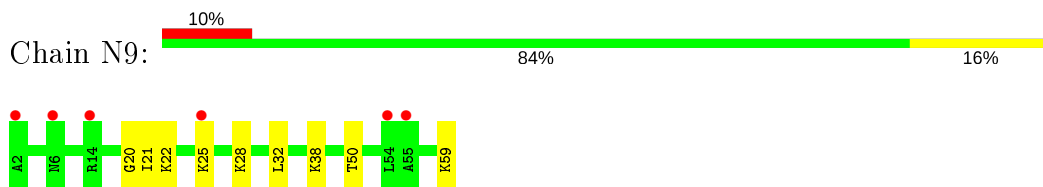
- Molecule 64: 60S ribosomal protein L28



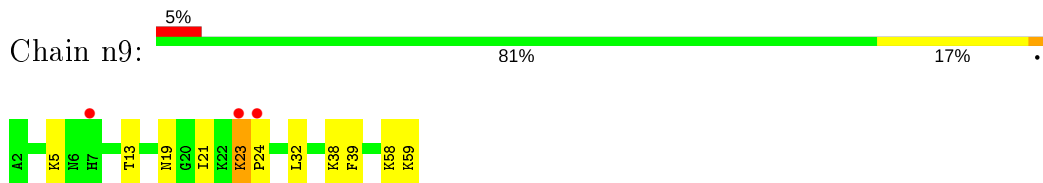
- Molecule 64: 60S ribosomal protein L28



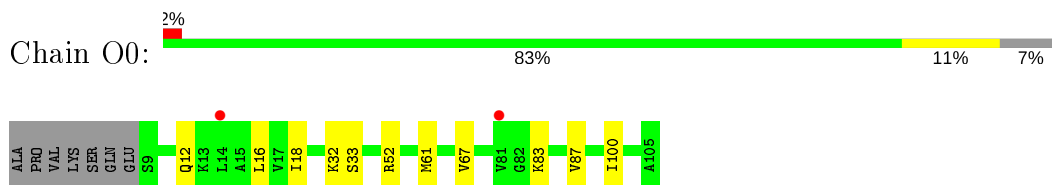
- Molecule 65: 60S ribosomal protein L29



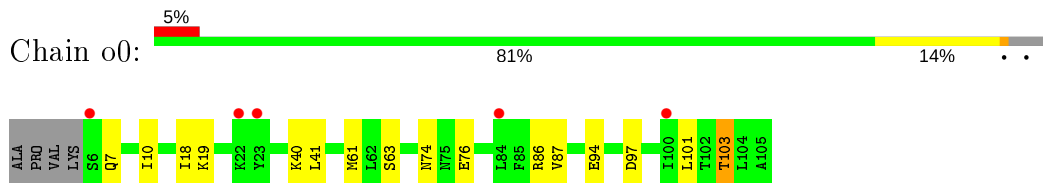
- Molecule 65: 60S ribosomal protein L29



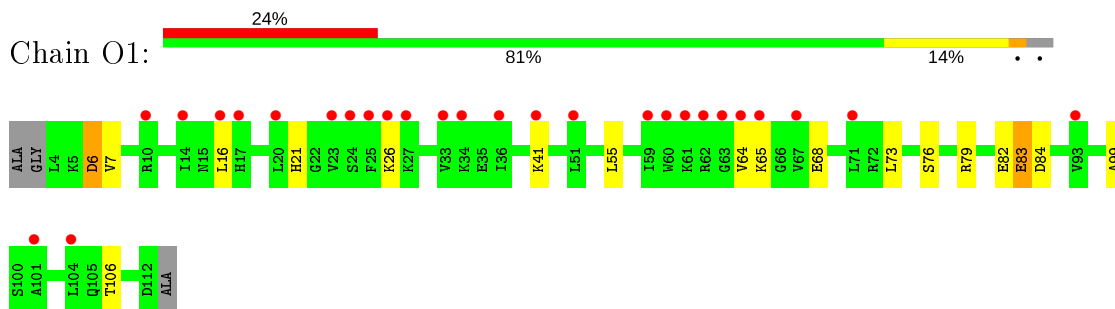
- Molecule 66: 60S ribosomal protein L30



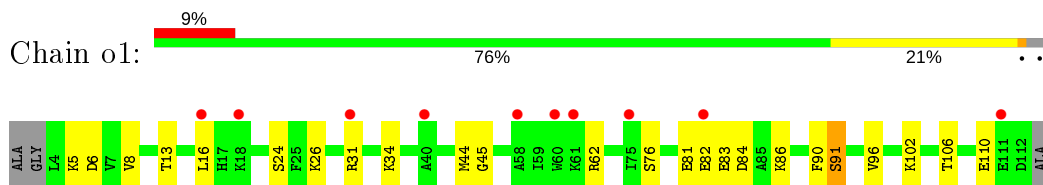
- Molecule 66: 60S ribosomal protein L30



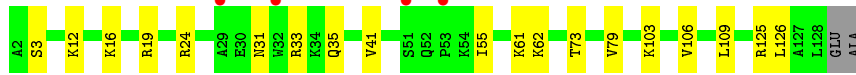
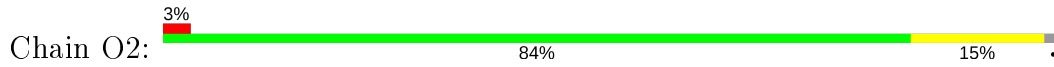
- Molecule 67: 60S ribosomal protein L31-A



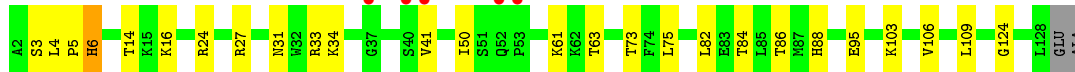
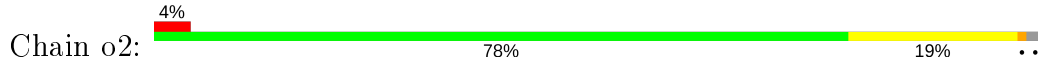
- Molecule 67: 60S ribosomal protein L31-A



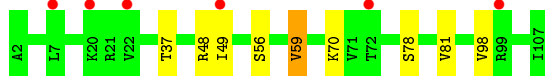
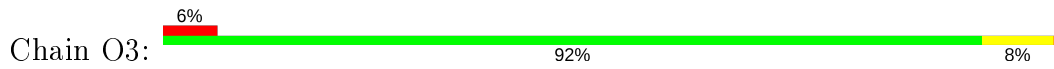
- Molecule 68: 60S ribosomal protein L32



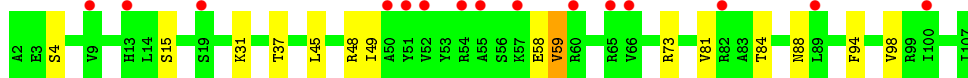
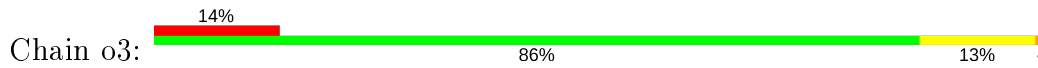
- Molecule 68: 60S ribosomal protein L32



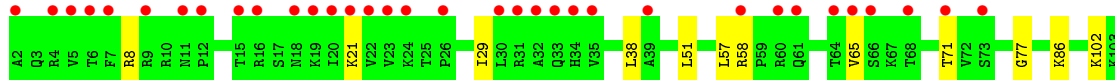
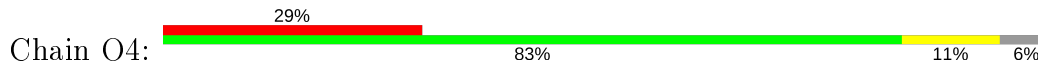
- Molecule 69: 60S ribosomal protein L33-A



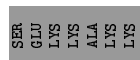
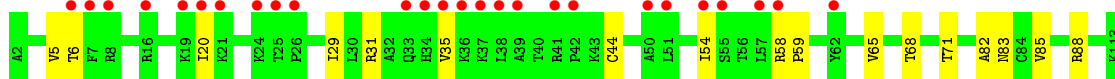
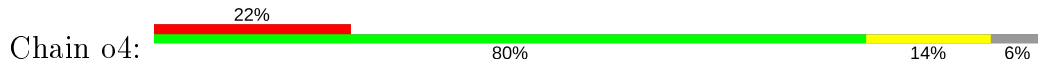
- Molecule 69: 60S ribosomal protein L33-A



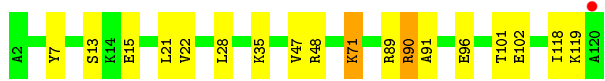
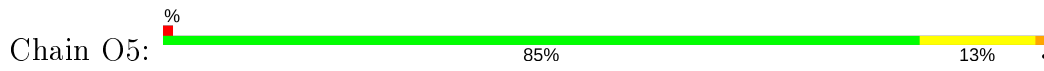
- Molecule 70: 60S ribosomal protein L34-A



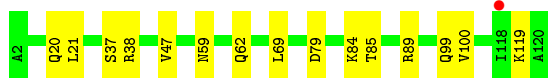
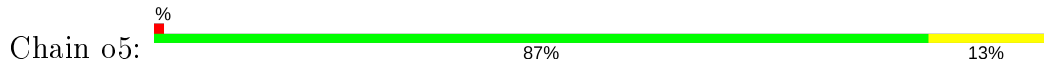
- Molecule 70: 60S ribosomal protein L34-A



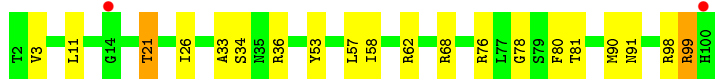
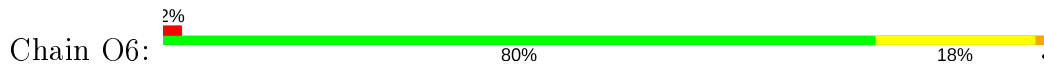
- Molecule 71: 60S ribosomal protein L35-A



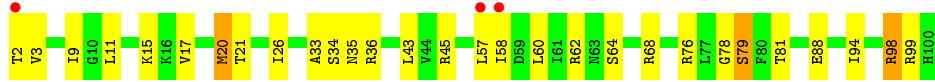
- Molecule 71: 60S ribosomal protein L35-A



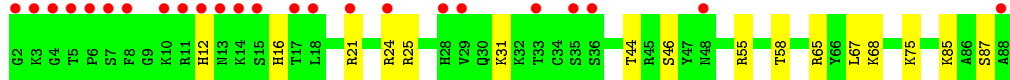
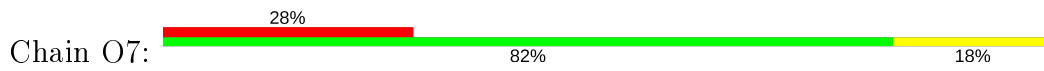
- Molecule 72: 60S ribosomal protein L36-A



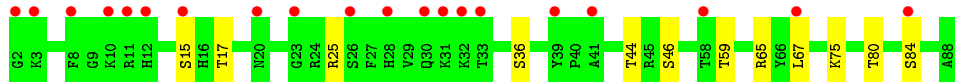
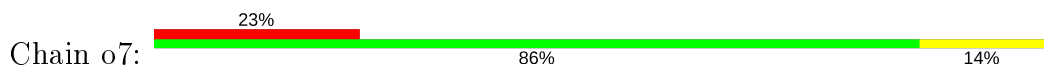
- Molecule 72: 60S ribosomal protein L36-A



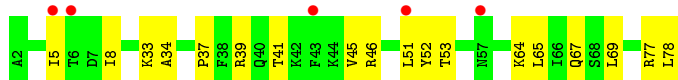
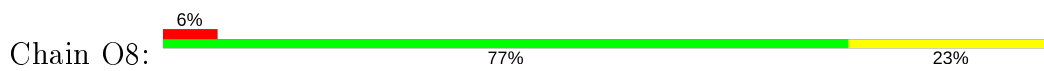
- Molecule 73: 60S ribosomal protein L37-A



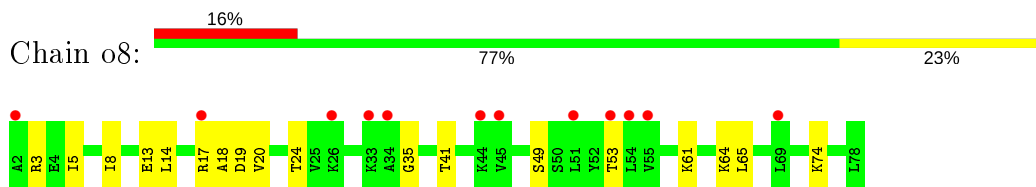
- Molecule 73: 60S ribosomal protein L37-A



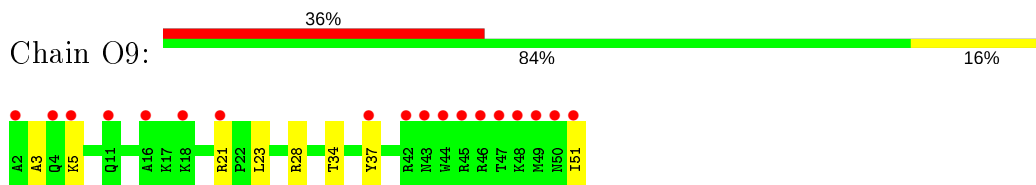
- Molecule 74: 60S ribosomal protein L38



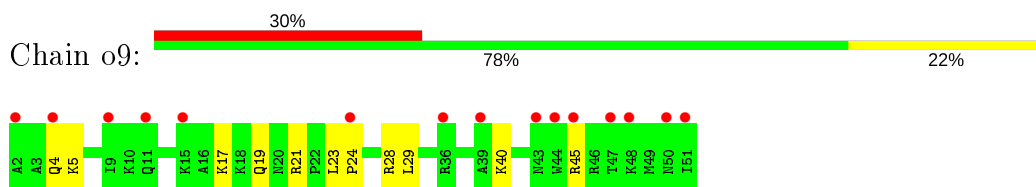
- Molecule 74: 60S ribosomal protein L38



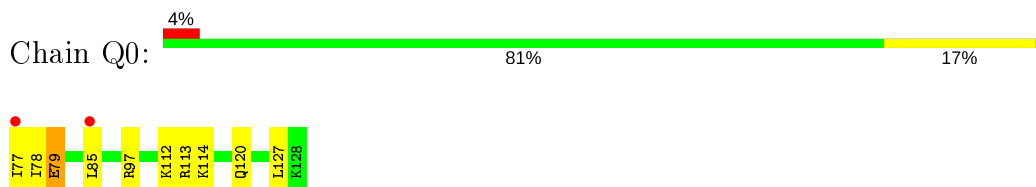
- Molecule 75: 60S ribosomal protein L39



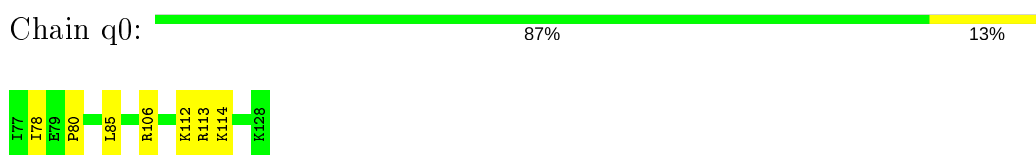
- Molecule 75: 60S ribosomal protein L39



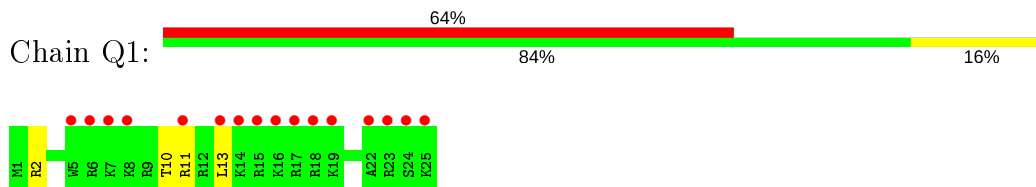
- Molecule 76: Ubiquitin-60S ribosomal protein L40



- Molecule 76: Ubiquitin-60S ribosomal protein L40



- Molecule 77: 60S ribosomal protein L41-A

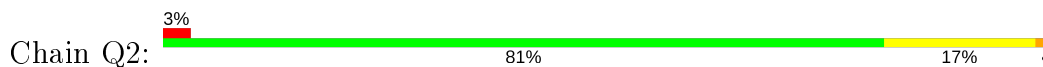


- Molecule 77: 60S ribosomal protein L41-A

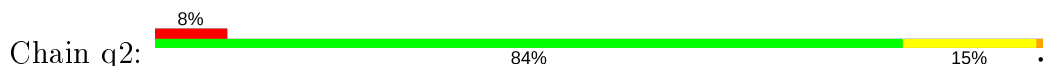




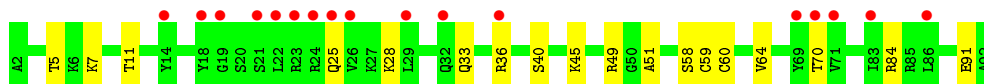
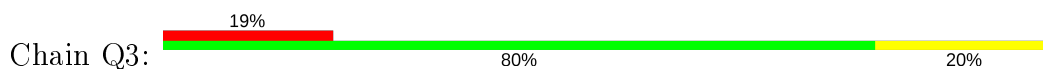
- Molecule 78: 60S ribosomal protein L42-A



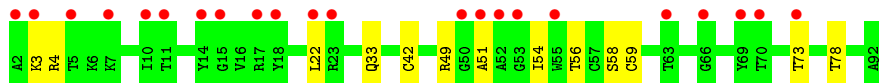
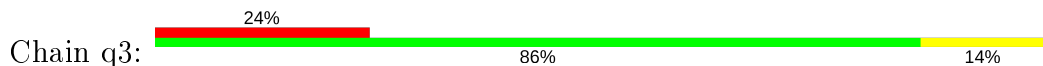
- Molecule 78: 60S ribosomal protein L42-A



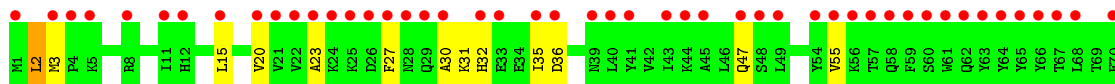
- Molecule 79: 60S ribosomal protein L43-A



- Molecule 79: 60S ribosomal protein L43-A



- Molecule 80: 40S ribosomal protein S10-A

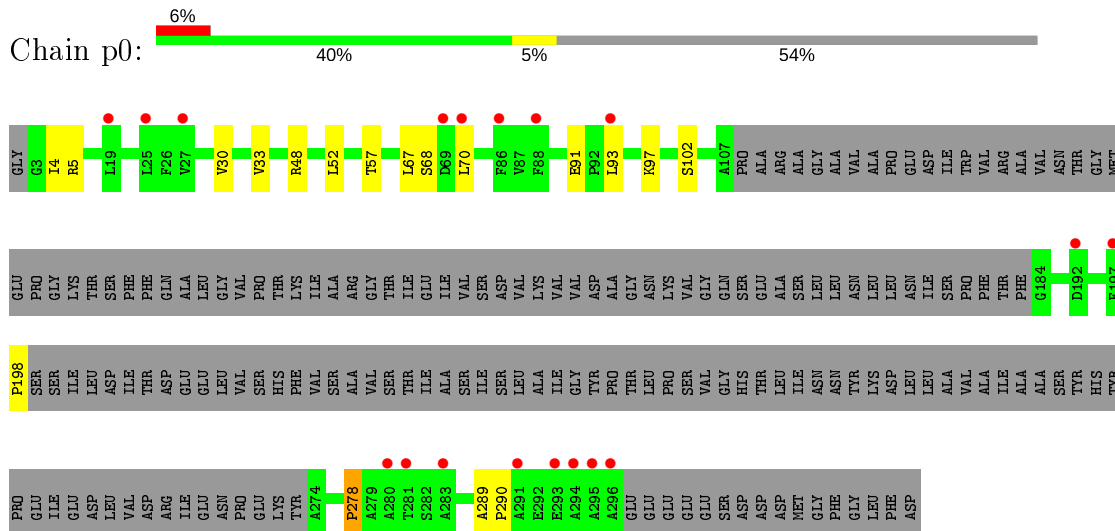


- Molecule 81: 60S ribosomal protein L12-A (uL11)



There are no outlier residues recorded for this chain.

- Molecule 82: 60S acidic ribosomal protein P0



- Molecule 83: 60S ribosomal protein P1 alpha



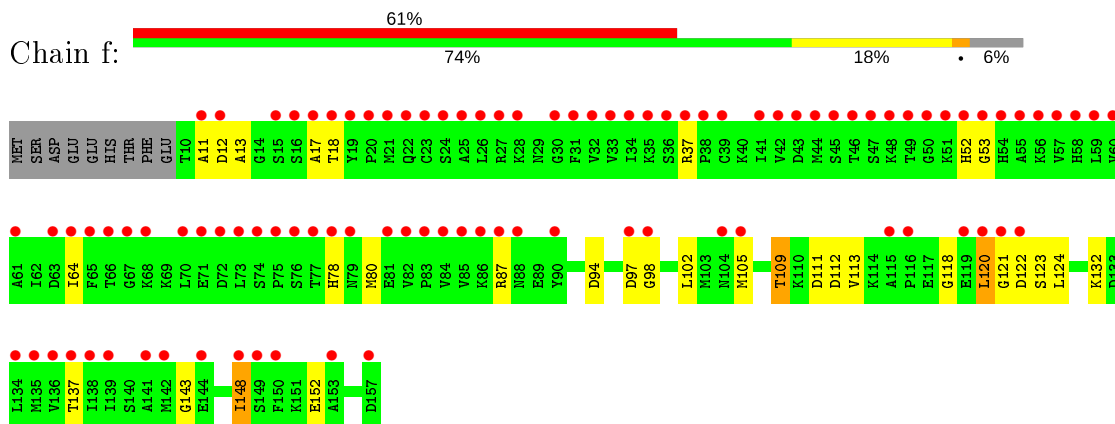
There are no outlier residues recorded for this chain.

- Molecule 84: 60S ribosomal P2 beta



There are no outlier residues recorded for this chain.

- Molecule 85: Eukaryotic translation initiation factor 5A-1



4 Data and refinement statistics

| Property | Value | Source |
|---|---|------------------|
| Space group | P 1 21 1 | Depositor |
| Cell constants a, b, c, α , β , γ | 438.23Å 289.33Å 305.47Å 90.00° 98.95° 90.00° | Depositor |
| Resolution (Å) | 190.48 – 3.25 196.56 – 3.25 | Depositor EDS |
| % Data completeness (in resolution range) | 100.0 (190.48-3.25) 99.9 (196.56-3.25) | Depositor EDS |
| R_{merge} | 0.41 | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 1.37 (at 3.26Å) | Xtrriage |
| Refinement program | PHENIX | Depositor |
| R, R_{free} | 0.252 , 0.301 0.257 , (Not available) | Depositor DCC |
| R_{free} test set | No test flags present. | wwPDB-VP |
| Wilson B-factor (Å ²) | 86.7 | Xtrriage |
| Anisotropy | 0.117 | Xtrriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.33 , 78.2 | EDS |
| L-test for twinning ² | $\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$ | Xtrriage |
| Estimated twinning fraction | No twinning to report. | Xtrriage |
| F_o, F_c correlation | 0.84 | EDS |
| Total number of atoms | 404042 | wwPDB-VP |
| Average B, all atoms (Å ²) | 80.0 | wwPDB-VP |

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

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

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

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|-----------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 1 | 2 | 0.37 | 0/42467 | 0.89 | 53/66169 (0.1%) |
| 1 | 6 | 0.43 | 0/42790 | 0.93 | 47/66673 (0.1%) |
| 2 | S0 | 0.28 | 0/1617 | 0.51 | 0/2215 |
| 2 | s0 | 0.30 | 0/1623 | 0.52 | 0/2222 |
| 3 | S1 | 0.27 | 0/1735 | 0.53 | 0/2335 |
| 3 | s1 | 0.29 | 0/1748 | 0.52 | 0/2352 |
| 4 | S2 | 0.30 | 0/1665 | 0.52 | 0/2263 |
| 4 | s2 | 0.33 | 0/1665 | 0.57 | 1/2263 (0.0%) |
| 5 | S3 | 0.31 | 0/1759 | 0.49 | 0/2368 |
| 5 | s3 | 0.29 | 0/1759 | 0.47 | 0/2368 |
| 6 | S4 | 0.29 | 0/2109 | 0.53 | 0/2839 |
| 6 | s4 | 0.34 | 0/2109 | 0.57 | 1/2839 (0.0%) |
| 7 | S5 | 0.27 | 0/1629 | 0.49 | 0/2202 |
| 7 | s5 | 0.28 | 0/1629 | 0.50 | 0/2202 |
| 8 | S6 | 0.29 | 0/1823 | 0.48 | 0/2439 |
| 8 | s6 | 0.33 | 0/1779 | 0.52 | 0/2379 |
| 9 | S7 | 0.29 | 0/1506 | 0.54 | 0/2028 |
| 9 | s7 | 0.29 | 0/1516 | 0.53 | 1/2043 (0.0%) |
| 10 | S8 | 0.32 | 0/1514 | 0.51 | 0/2021 |
| 10 | s8 | 0.35 | 0/1514 | 0.51 | 0/2021 |
| 11 | S9 | 0.29 | 0/1519 | 0.49 | 0/2035 |
| 11 | s9 | 0.31 | 0/1519 | 0.51 | 0/2035 |
| 12 | C0 | 0.29 | 0/789 | 0.48 | 1/1067 (0.1%) |
| 13 | C1 | 0.32 | 0/1239 | 0.51 | 0/1673 |
| 13 | c1 | 0.36 | 0/1194 | 0.52 | 0/1610 |
| 14 | C2 | 0.28 | 0/898 | 0.52 | 1/1220 (0.1%) |
| 14 | c2 | 0.24 | 0/898 | 0.49 | 0/1220 |
| 15 | C3 | 0.31 | 0/1215 | 0.51 | 1/1638 (0.1%) |
| 15 | c3 | 0.33 | 0/1215 | 0.53 | 0/1638 |
| 16 | C4 | 0.28 | 0/901 | 0.54 | 0/1217 |
| 16 | c4 | 0.30 | 0/960 | 0.55 | 0/1290 |
| 17 | C5 | 0.31 | 0/998 | 0.55 | 1/1341 (0.1%) |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|----------------|-------------|-------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 17 | c5 | 0.31 | 0/1060 | 0.50 | 0/1426 |
| 18 | C6 | 0.29 | 0/1125 | 0.56 | 2/1510 (0.1%) |
| 18 | c6 | 0.29 | 0/1131 | 0.51 | 0/1518 |
| 19 | C7 | 0.31 | 0/935 | 0.54 | 0/1254 |
| 19 | c7 | 0.29 | 0/914 | 0.52 | 0/1224 |
| 20 | C8 | 0.30 | 0/1211 | 0.52 | 0/1628 |
| 20 | c8 | 0.29 | 0/1211 | 0.51 | 0/1628 |
| 21 | C9 | 0.28 | 0/1130 | 0.48 | 0/1517 |
| 21 | c9 | 0.29 | 0/1130 | 0.47 | 0/1517 |
| 22 | D0 | 0.30 | 0/865 | 0.55 | 0/1169 |
| 22 | d0 | 0.28 | 0/892 | 0.52 | 0/1205 |
| 23 | D1 | 0.28 | 0/693 | 0.51 | 0/935 |
| 23 | d1 | 0.30 | 0/693 | 0.49 | 0/935 |
| 24 | D2 | 0.31 | 0/1038 | 0.58 | 3/1395 (0.2%) |
| 24 | d2 | 0.34 | 0/1038 | 0.56 | 0/1395 |
| 25 | D3 | 0.34 | 0/1139 | 0.54 | 0/1518 |
| 25 | d3 | 0.38 | 0/1139 | 0.59 | 0/1518 |
| 26 | D4 | 0.29 | 0/1087 | 0.46 | 0/1449 |
| 26 | d4 | 0.31 | 0/1087 | 0.52 | 0/1449 |
| 27 | D5 | 0.28 | 0/571 | 0.57 | 0/768 |
| 27 | d5 | 0.27 | 0/566 | 0.47 | 0/761 |
| 28 | D6 | 0.30 | 0/782 | 0.53 | 0/1047 |
| 28 | d6 | 0.35 | 0/782 | 0.52 | 0/1047 |
| 29 | D7 | 0.28 | 0/620 | 0.51 | 0/838 |
| 29 | d7 | 0.28 | 0/620 | 0.50 | 0/838 |
| 30 | D8 | 0.28 | 0/499 | 0.48 | 0/670 |
| 30 | d8 | 0.28 | 0/499 | 0.54 | 0/670 |
| 31 | D9 | 0.30 | 0/452 | 0.53 | 1/600 (0.2%) |
| 31 | d9 | 0.32 | 0/452 | 0.51 | 0/600 |
| 32 | E0 | 0.28 | 0/483 | 0.47 | 0/643 |
| 32 | e0 | 0.32 | 0/499 | 0.54 | 0/665 |
| 33 | E1 | 0.30 | 0/577 | 0.60 | 0/770 |
| 33 | e1 | 0.30 | 0/619 | 0.64 | 0/822 |
| 34 | SR | 0.26 | 0/2490 | 0.49 | 0/3389 |
| 34 | sR | 0.26 | 0/2495 | 0.45 | 0/3395 |
| 35 | SM | 0.32 | 0/1113 | 0.55 | 2/1502 (0.1%) |
| 35 | sM | 0.32 | 0/682 | 0.50 | 0/921 |
| 36 | 1 | 0.55 | 0/75394 | 1.02 | 101/117545 (0.1%) |
| 36 | 5 | 0.58 | 2/75865 (0.0%) | 1.04 | 122/118275 (0.1%) |
| 37 | 3 | 0.47 | 0/2883 | 0.88 | 0/4491 |
| 37 | 7 | 0.55 | 0/2883 | 1.03 | 4/4491 (0.1%) |
| 38 | 4 | 0.51 | 0/3746 | 0.99 | 5/5832 (0.1%) |
| 38 | 8 | 0.50 | 0/3746 | 0.95 | 4/5832 (0.1%) |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------------|-------------|---------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 39 | L2 | 0.37 | 0/1948 | 0.58 | 0/2617 |
| 39 | l2 | 0.39 | 0/1946 | 0.60 | 0/2614 |
| 40 | L3 | 0.39 | 0/3146 | 0.57 | 0/4228 |
| 40 | l3 | 0.43 | 0/3146 | 0.58 | 0/4228 |
| 41 | L4 | 0.41 | 0/2800 | 0.60 | 0/3790 |
| 41 | l4 | 0.40 | 1/2800 (0.0%) | 0.62 | 1/3790 (0.0%) |
| 42 | L5 | 0.34 | 0/2425 | 0.53 | 0/3271 |
| 42 | l5 | 0.40 | 0/2408 | 0.56 | 0/3248 |
| 43 | L6 | 0.38 | 0/1260 | 0.56 | 0/1694 |
| 43 | l6 | 0.41 | 0/1269 | 0.58 | 0/1705 |
| 44 | L7 | 0.42 | 0/1821 | 0.59 | 0/2451 |
| 44 | l7 | 0.44 | 0/1828 | 0.63 | 2/2461 (0.1%) |
| 45 | L8 | 0.31 | 0/1836 | 0.52 | 1/2481 (0.0%) |
| 45 | l8 | 0.33 | 0/1795 | 0.52 | 0/2429 |
| 46 | L9 | 0.37 | 0/1539 | 0.55 | 0/2073 |
| 46 | l9 | 0.40 | 0/1539 | 0.56 | 0/2073 |
| 47 | M0 | 0.41 | 0/1741 | 0.55 | 0/2335 |
| 47 | m0 | 0.43 | 0/1758 | 0.61 | 0/2358 |
| 48 | M1 | 0.31 | 0/1374 | 0.50 | 0/1842 |
| 48 | m1 | 0.34 | 0/1374 | 0.56 | 0/1842 |
| 49 | M3 | 0.40 | 0/1568 | 0.59 | 0/2106 |
| 49 | m3 | 0.40 | 0/1573 | 0.57 | 0/2113 |
| 50 | M4 | 0.40 | 0/1068 | 0.54 | 0/1438 |
| 50 | m4 | 0.41 | 0/1074 | 0.57 | 0/1446 |
| 51 | M5 | 0.38 | 0/1757 | 0.57 | 0/2354 |
| 51 | m5 | 0.37 | 0/1757 | 0.56 | 0/2354 |
| 52 | M6 | 0.43 | 0/1585 | 0.58 | 0/2128 |
| 52 | m6 | 0.50 | 0/1585 | 0.61 | 0/2128 |
| 53 | M7 | 0.42 | 0/1443 | 0.55 | 0/1944 |
| 53 | m7 | 0.44 | 0/1250 | 0.61 | 0/1683 |
| 54 | M8 | 0.39 | 0/1465 | 0.60 | 0/1965 |
| 54 | m8 | 0.40 | 0/1465 | 0.62 | 0/1965 |
| 55 | M9 | 0.30 | 0/1538 | 0.48 | 0/2050 |
| 55 | m9 | 0.34 | 0/1538 | 0.51 | 0/2050 |
| 56 | N0 | 0.39 | 0/1481 | 0.59 | 0/1990 |
| 56 | n0 | 0.43 | 0/1481 | 0.57 | 0/1990 |
| 57 | N1 | 0.41 | 0/1300 | 0.56 | 0/1743 |
| 57 | n1 | 0.44 | 0/1300 | 0.55 | 0/1743 |
| 58 | N2 | 0.29 | 0/812 | 0.48 | 0/1099 |
| 58 | n2 | 0.32 | 0/794 | 0.54 | 0/1076 |
| 59 | N3 | 0.38 | 0/1018 | 0.56 | 0/1369 |
| 59 | n3 | 0.45 | 0/1018 | 0.64 | 0/1369 |
| 60 | N4 | 0.31 | 0/712 | 0.47 | 0/958 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-----------------|-------------|-------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 60 | n4 | 0.36 | 0/1052 | 0.53 | 0/1398 |
| 61 | N5 | 0.34 | 0/979 | 0.57 | 1/1321 (0.1%) |
| 61 | n5 | 0.34 | 0/974 | 0.56 | 0/1314 |
| 62 | N6 | 0.37 | 0/1004 | 0.63 | 2/1341 (0.1%) |
| 62 | n6 | 0.34 | 0/1004 | 0.56 | 0/1341 |
| 63 | N7 | 0.31 | 0/1118 | 0.51 | 0/1497 |
| 63 | n7 | 0.31 | 0/1118 | 0.51 | 0/1497 |
| 64 | N8 | 0.41 | 0/1204 | 0.64 | 0/1612 |
| 64 | n8 | 0.42 | 0/1204 | 0.63 | 0/1612 |
| 65 | N9 | 0.38 | 0/473 | 0.57 | 0/629 |
| 65 | n9 | 0.45 | 0/473 | 0.71 | 1/629 (0.2%) |
| 66 | O0 | 0.30 | 0/751 | 0.46 | 0/1008 |
| 66 | o0 | 0.32 | 0/775 | 0.51 | 0/1040 |
| 67 | O1 | 0.36 | 0/890 | 0.53 | 0/1196 |
| 67 | o1 | 0.43 | 0/897 | 0.59 | 0/1205 |
| 68 | O2 | 0.42 | 0/1041 | 0.61 | 0/1394 |
| 68 | o2 | 0.42 | 0/1041 | 0.59 | 0/1394 |
| 69 | O3 | 0.44 | 0/868 | 0.52 | 0/1168 |
| 69 | o3 | 0.47 | 0/868 | 0.58 | 0/1168 |
| 70 | O4 | 0.33 | 0/890 | 0.53 | 1/1189 (0.1%) |
| 70 | o4 | 0.35 | 0/890 | 0.56 | 0/1189 |
| 71 | O5 | 0.38 | 0/978 | 0.56 | 0/1301 |
| 71 | o5 | 0.33 | 0/974 | 0.53 | 0/1297 |
| 72 | O6 | 0.35 | 0/778 | 0.57 | 0/1034 |
| 72 | o6 | 0.34 | 0/777 | 0.53 | 0/1033 |
| 73 | O7 | 0.41 | 0/696 | 0.62 | 0/923 |
| 73 | o7 | 0.39 | 0/696 | 0.61 | 0/923 |
| 74 | O8 | 0.31 | 0/618 | 0.51 | 0/826 |
| 74 | o8 | 0.32 | 0/614 | 0.51 | 0/822 |
| 75 | O9 | 0.38 | 0/443 | 0.60 | 0/588 |
| 75 | o9 | 0.37 | 0/443 | 0.56 | 0/588 |
| 76 | Q0 | 0.44 | 0/423 | 0.60 | 0/562 |
| 76 | q0 | 0.46 | 0/423 | 0.62 | 0/562 |
| 77 | Q1 | 0.35 | 0/234 | 0.61 | 0/300 |
| 77 | q1 | 0.43 | 0/234 | 0.58 | 0/300 |
| 78 | Q2 | 0.51 | 1/860 (0.1%) | 0.64 | 0/1136 |
| 78 | q2 | 0.52 | 1/860 (0.1%) | 0.64 | 1/1136 (0.1%) |
| 79 | Q3 | 0.38 | 0/701 | 0.58 | 0/934 |
| 79 | q3 | 0.42 | 0/701 | 0.60 | 0/934 |
| 80 | c0 | 0.28 | 0/777 | 0.53 | 2/1049 (0.2%) |
| 82 | p0 | 0.27 | 0/1091 | 0.53 | 2/1472 (0.1%) |
| 85 | f | 0.31 | 0/1131 | 0.59 | 1/1522 (0.1%) |
| All | All | 0.45 | 5/432438 (0.0%) | 0.84 | 366/634802 (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 |
|-----|-------|---------------------|---------------------|
| 7 | s5 | 0 | 1 |
| 18 | c6 | 0 | 2 |
| 19 | C7 | 0 | 1 |
| 27 | D5 | 0 | 1 |
| 52 | M6 | 0 | 1 |
| 52 | m6 | 0 | 1 |
| 56 | n0 | 0 | 1 |
| 64 | n8 | 0 | 2 |
| 65 | N9 | 0 | 1 |
| All | All | 0 | 11 |

All (5) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|-------|-------------|----------|
| 78 | q2 | 17 | CYS | CB-SG | 8.72 | 1.97 | 1.82 |
| 78 | Q2 | 17 | CYS | CB-SG | 8.11 | 1.96 | 1.82 |
| 36 | 5 | 1152 | G | N9-C4 | -7.24 | 1.32 | 1.38 |
| 36 | 5 | 2971 | A | N9-C4 | 6.37 | 1.41 | 1.37 |
| 41 | 14 | 94 | CYS | CB-SG | -5.72 | 1.72 | 1.81 |

The worst 5 of 366 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|----------|--------|-------------|----------|
| 36 | 5 | 1152 | G | N3-C4-C5 | 13.24 | 135.22 | 128.60 |
| 36 | 5 | 1152 | G | N3-C4-N9 | -12.64 | 118.41 | 126.00 |
| 36 | 5 | 1152 | G | C2-N3-C4 | -10.83 | 106.48 | 111.90 |
| 36 | 5 | 2726 | C | C6-N1-C2 | -9.83 | 116.37 | 120.30 |
| 36 | 1 | 3217 | C | N1-C2-O2 | 8.77 | 124.16 | 118.90 |

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 19 | C7 | 85 | VAL | Peptide |
| 27 | D5 | 94 | LYS | Peptide |
| 52 | M6 | 110 | PRO | Peptide |
| 65 | N9 | 20 | GLY | Peptide |
| 7 | s5 | 99 | MET | Peptide |

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|----|
| 2 | S0 | 204/251 (81%) | 156 (76%) | 30 (15%) | 18 (9%) | 1 | 5 |
| 2 | s0 | 204/251 (81%) | 158 (78%) | 31 (15%) | 15 (7%) | 1 | 7 |
| 3 | S1 | 212/254 (84%) | 154 (73%) | 36 (17%) | 22 (10%) | 0 | 3 |
| 3 | s1 | 214/254 (84%) | 165 (77%) | 37 (17%) | 12 (6%) | 2 | 11 |
| 4 | S2 | 215/253 (85%) | 174 (81%) | 33 (15%) | 8 (4%) | 3 | 19 |
| 4 | s2 | 215/253 (85%) | 175 (81%) | 26 (12%) | 14 (6%) | 1 | 9 |
| 5 | S3 | 221/239 (92%) | 189 (86%) | 21 (10%) | 11 (5%) | 2 | 13 |
| 5 | s3 | 221/239 (92%) | 183 (83%) | 27 (12%) | 11 (5%) | 2 | 13 |
| 6 | S4 | 258/260 (99%) | 205 (80%) | 37 (14%) | 16 (6%) | 1 | 10 |
| 6 | s4 | 258/260 (99%) | 198 (77%) | 44 (17%) | 16 (6%) | 1 | 10 |
| 7 | S5 | 204/224 (91%) | 163 (80%) | 28 (14%) | 13 (6%) | 1 | 9 |
| 7 | s5 | 204/224 (91%) | 157 (77%) | 30 (15%) | 17 (8%) | 1 | 5 |
| 8 | S6 | 224/236 (95%) | 198 (88%) | 17 (8%) | 9 (4%) | 3 | 17 |
| 8 | s6 | 216/236 (92%) | 186 (86%) | 24 (11%) | 6 (3%) | 5 | 25 |
| 9 | S7 | 182/189 (96%) | 137 (75%) | 27 (15%) | 18 (10%) | 0 | 3 |
| 9 | s7 | 184/189 (97%) | 146 (79%) | 25 (14%) | 13 (7%) | 1 | 7 |
| 10 | S8 | 184/200 (92%) | 159 (86%) | 18 (10%) | 7 (4%) | 3 | 19 |
| 10 | s8 | 184/200 (92%) | 156 (85%) | 21 (11%) | 7 (4%) | 3 | 19 |
| 11 | S9 | 183/196 (93%) | 148 (81%) | 28 (15%) | 7 (4%) | 3 | 19 |
| 11 | s9 | 183/196 (93%) | 151 (82%) | 24 (13%) | 8 (4%) | 2 | 15 |
| 12 | C0 | 94/105 (90%) | 74 (79%) | 13 (14%) | 7 (7%) | 1 | 7 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|----|
| 13 | C1 | 153/155 (99%) | 123 (80%) | 23 (15%) | 7 (5%) | 2 | 15 |
| 13 | c1 | 144/155 (93%) | 122 (85%) | 20 (14%) | 2 (1%) | 11 | 40 |
| 14 | C2 | 122/142 (86%) | 73 (60%) | 32 (26%) | 17 (14%) | 0 | 1 |
| 14 | c2 | 122/142 (86%) | 76 (62%) | 30 (25%) | 16 (13%) | 0 | 1 |
| 15 | C3 | 148/150 (99%) | 122 (82%) | 20 (14%) | 6 (4%) | 3 | 17 |
| 15 | c3 | 148/150 (99%) | 117 (79%) | 21 (14%) | 10 (7%) | 1 | 8 |
| 16 | C4 | 125/136 (92%) | 92 (74%) | 21 (17%) | 12 (10%) | 0 | 4 |
| 16 | c4 | 126/136 (93%) | 98 (78%) | 19 (15%) | 9 (7%) | 1 | 7 |
| 17 | C5 | 122/141 (86%) | 90 (74%) | 17 (14%) | 15 (12%) | 0 | 2 |
| 17 | c5 | 133/141 (94%) | 98 (74%) | 19 (14%) | 16 (12%) | 0 | 2 |
| 18 | C6 | 139/142 (98%) | 111 (80%) | 19 (14%) | 9 (6%) | 1 | 9 |
| 18 | c6 | 140/142 (99%) | 123 (88%) | 11 (8%) | 6 (4%) | 2 | 16 |
| 19 | C7 | 116/136 (85%) | 89 (77%) | 20 (17%) | 7 (6%) | 1 | 10 |
| 19 | c7 | 113/136 (83%) | 89 (79%) | 16 (14%) | 8 (7%) | 1 | 7 |
| 20 | C8 | 143/145 (99%) | 109 (76%) | 27 (19%) | 7 (5%) | 2 | 14 |
| 20 | c8 | 143/145 (99%) | 116 (81%) | 21 (15%) | 6 (4%) | 3 | 16 |
| 21 | C9 | 141/143 (99%) | 115 (82%) | 19 (14%) | 7 (5%) | 2 | 13 |
| 21 | c9 | 141/143 (99%) | 119 (84%) | 17 (12%) | 5 (4%) | 3 | 21 |
| 22 | D0 | 105/120 (88%) | 90 (86%) | 9 (9%) | 6 (6%) | 1 | 11 |
| 22 | d0 | 108/120 (90%) | 87 (81%) | 18 (17%) | 3 (3%) | 5 | 25 |
| 23 | D1 | 85/87 (98%) | 61 (72%) | 17 (20%) | 7 (8%) | 1 | 6 |
| 23 | d1 | 85/87 (98%) | 71 (84%) | 8 (9%) | 6 (7%) | 1 | 7 |
| 24 | D2 | 127/129 (98%) | 111 (87%) | 12 (9%) | 4 (3%) | 4 | 24 |
| 24 | d2 | 127/129 (98%) | 117 (92%) | 7 (6%) | 3 (2%) | 6 | 28 |
| 25 | D3 | 142/144 (99%) | 109 (77%) | 20 (14%) | 13 (9%) | 1 | 4 |
| 25 | d3 | 142/144 (99%) | 125 (88%) | 14 (10%) | 3 (2%) | 7 | 32 |
| 26 | D4 | 132/134 (98%) | 114 (86%) | 8 (6%) | 10 (8%) | 1 | 6 |
| 26 | d4 | 132/134 (98%) | 110 (83%) | 14 (11%) | 8 (6%) | 1 | 10 |
| 27 | D5 | 68/107 (64%) | 47 (69%) | 15 (22%) | 6 (9%) | 1 | 5 |
| 27 | d5 | 67/107 (63%) | 52 (78%) | 14 (21%) | 1 (2%) | 10 | 39 |
| 28 | D6 | 95/97 (98%) | 62 (65%) | 19 (20%) | 14 (15%) | 0 | 1 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|----------|-------------|----|
| 28 | d6 | 95/97 (98%) | 70 (74%) | 20 (21%) | 5 (5%) | 2 | 12 |
| 29 | D7 | 79/81 (98%) | 58 (73%) | 18 (23%) | 3 (4%) | 3 | 19 |
| 29 | d7 | 79/81 (98%) | 62 (78%) | 15 (19%) | 2 (2%) | 5 | 28 |
| 30 | D8 | 61/66 (92%) | 53 (87%) | 6 (10%) | 2 (3%) | 4 | 22 |
| 30 | d8 | 61/66 (92%) | 47 (77%) | 10 (16%) | 4 (7%) | 1 | 9 |
| 31 | D9 | 51/55 (93%) | 42 (82%) | 6 (12%) | 3 (6%) | 1 | 10 |
| 31 | d9 | 51/55 (93%) | 41 (80%) | 7 (14%) | 3 (6%) | 1 | 10 |
| 32 | E0 | 58/62 (94%) | 48 (83%) | 7 (12%) | 3 (5%) | 2 | 12 |
| 32 | e0 | 60/62 (97%) | 46 (77%) | 8 (13%) | 6 (10%) | 0 | 3 |
| 33 | E1 | 69/76 (91%) | 39 (56%) | 12 (17%) | 18 (26%) | 0 | 0 |
| 33 | e1 | 74/76 (97%) | 38 (51%) | 12 (16%) | 24 (32%) | 0 | 0 |
| 34 | SR | 316/318 (99%) | 266 (84%) | 34 (11%) | 16 (5%) | 2 | 13 |
| 34 | sR | 316/318 (99%) | 264 (84%) | 39 (12%) | 13 (4%) | 3 | 17 |
| 35 | SM | 155/273 (57%) | 114 (74%) | 22 (14%) | 19 (12%) | 0 | 2 |
| 35 | sM | 98/273 (36%) | 59 (60%) | 28 (29%) | 11 (11%) | 0 | 2 |
| 39 | L2 | 250/253 (99%) | 216 (86%) | 25 (10%) | 9 (4%) | 3 | 20 |
| 39 | l2 | 250/253 (99%) | 208 (83%) | 32 (13%) | 10 (4%) | 3 | 17 |
| 40 | L3 | 384/386 (100%) | 332 (86%) | 39 (10%) | 13 (3%) | 3 | 22 |
| 40 | l3 | 384/386 (100%) | 341 (89%) | 38 (10%) | 5 (1%) | 12 | 41 |
| 41 | L4 | 359/361 (99%) | 296 (82%) | 38 (11%) | 25 (7%) | 1 | 7 |
| 41 | l4 | 359/361 (99%) | 295 (82%) | 42 (12%) | 22 (6%) | 1 | 10 |
| 42 | L5 | 294/296 (99%) | 231 (79%) | 38 (13%) | 25 (8%) | 1 | 5 |
| 42 | l5 | 292/296 (99%) | 253 (87%) | 31 (11%) | 8 (3%) | 5 | 26 |
| 43 | L6 | 152/175 (87%) | 135 (89%) | 13 (9%) | 4 (3%) | 5 | 27 |
| 43 | l6 | 153/175 (87%) | 125 (82%) | 24 (16%) | 4 (3%) | 5 | 27 |
| 44 | L7 | 220/243 (90%) | 190 (86%) | 24 (11%) | 6 (3%) | 5 | 26 |
| 44 | l7 | 221/243 (91%) | 199 (90%) | 17 (8%) | 5 (2%) | 6 | 29 |
| 45 | L8 | 231/255 (91%) | 190 (82%) | 30 (13%) | 11 (5%) | 2 | 14 |
| 45 | l8 | 229/255 (90%) | 178 (78%) | 37 (16%) | 14 (6%) | 1 | 10 |
| 46 | L9 | 189/191 (99%) | 161 (85%) | 20 (11%) | 8 (4%) | 3 | 16 |
| 46 | l9 | 189/191 (99%) | 170 (90%) | 16 (8%) | 3 (2%) | 9 | 37 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 47 | M0 | 207/220 (94%) | 169 (82%) | 32 (16%) | 6 (3%) | 4 | 25 |
| 47 | m0 | 209/220 (95%) | 161 (77%) | 35 (17%) | 13 (6%) | 1 | 10 |
| 48 | M1 | 167/173 (96%) | 130 (78%) | 25 (15%) | 12 (7%) | 1 | 7 |
| 48 | m1 | 167/173 (96%) | 139 (83%) | 18 (11%) | 10 (6%) | 1 | 10 |
| 49 | M3 | 191/198 (96%) | 149 (78%) | 34 (18%) | 8 (4%) | 3 | 16 |
| 49 | m3 | 192/198 (97%) | 148 (77%) | 30 (16%) | 14 (7%) | 1 | 7 |
| 50 | M4 | 134/137 (98%) | 116 (87%) | 14 (10%) | 4 (3%) | 4 | 24 |
| 50 | m4 | 135/137 (98%) | 120 (89%) | 13 (10%) | 2 (2%) | 10 | 39 |
| 51 | M5 | 201/203 (99%) | 178 (89%) | 16 (8%) | 7 (4%) | 3 | 21 |
| 51 | m5 | 201/203 (99%) | 178 (89%) | 18 (9%) | 5 (2%) | 5 | 28 |
| 52 | M6 | 195/198 (98%) | 171 (88%) | 17 (9%) | 7 (4%) | 3 | 20 |
| 52 | m6 | 195/198 (98%) | 173 (89%) | 18 (9%) | 4 (2%) | 7 | 32 |
| 53 | M7 | 181/183 (99%) | 149 (82%) | 26 (14%) | 6 (3%) | 4 | 22 |
| 53 | m7 | 153/183 (84%) | 140 (92%) | 11 (7%) | 2 (1%) | 12 | 41 |
| 54 | M8 | 183/185 (99%) | 157 (86%) | 22 (12%) | 4 (2%) | 6 | 31 |
| 54 | m8 | 183/185 (99%) | 152 (83%) | 25 (14%) | 6 (3%) | 4 | 22 |
| 55 | M9 | 186/188 (99%) | 164 (88%) | 19 (10%) | 3 (2%) | 9 | 37 |
| 55 | m9 | 186/188 (99%) | 166 (89%) | 20 (11%) | 0 | 100 | 100 |
| 56 | N0 | 170/172 (99%) | 150 (88%) | 13 (8%) | 7 (4%) | 3 | 17 |
| 56 | n0 | 170/172 (99%) | 156 (92%) | 13 (8%) | 1 (1%) | 25 | 59 |
| 57 | N1 | 157/159 (99%) | 135 (86%) | 16 (10%) | 6 (4%) | 3 | 19 |
| 57 | n1 | 157/159 (99%) | 138 (88%) | 14 (9%) | 5 (3%) | 4 | 23 |
| 58 | N2 | 98/120 (82%) | 73 (74%) | 21 (21%) | 4 (4%) | 3 | 17 |
| 58 | n2 | 96/120 (80%) | 84 (88%) | 8 (8%) | 4 (4%) | 3 | 16 |
| 59 | N3 | 134/136 (98%) | 117 (87%) | 11 (8%) | 6 (4%) | 2 | 15 |
| 59 | n3 | 134/136 (98%) | 121 (90%) | 7 (5%) | 6 (4%) | 2 | 15 |
| 60 | N4 | 96/155 (62%) | 76 (79%) | 15 (16%) | 5 (5%) | 2 | 12 |
| 60 | n4 | 133/155 (86%) | 109 (82%) | 16 (12%) | 8 (6%) | 1 | 10 |
| 61 | N5 | 119/141 (84%) | 101 (85%) | 16 (13%) | 2 (2%) | 9 | 36 |
| 61 | n5 | 118/141 (84%) | 101 (86%) | 13 (11%) | 4 (3%) | 3 | 22 |
| 62 | N6 | 124/126 (98%) | 109 (88%) | 13 (10%) | 2 (2%) | 9 | 37 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 62 | n6 | 124/126 (98%) | 104 (84%) | 16 (13%) | 4 (3%) | 4 | 23 |
| 63 | N7 | 133/135 (98%) | 106 (80%) | 16 (12%) | 11 (8%) | 1 | 5 |
| 63 | n7 | 133/135 (98%) | 111 (84%) | 15 (11%) | 7 (5%) | 2 | 12 |
| 64 | N8 | 146/148 (99%) | 121 (83%) | 20 (14%) | 5 (3%) | 3 | 22 |
| 64 | n8 | 146/148 (99%) | 122 (84%) | 18 (12%) | 6 (4%) | 3 | 17 |
| 65 | N9 | 56/58 (97%) | 47 (84%) | 7 (12%) | 2 (4%) | 3 | 20 |
| 65 | n9 | 56/58 (97%) | 40 (71%) | 10 (18%) | 6 (11%) | 0 | 3 |
| 66 | O0 | 95/104 (91%) | 84 (88%) | 11 (12%) | 0 | 100 | 100 |
| 66 | o0 | 98/104 (94%) | 85 (87%) | 9 (9%) | 4 (4%) | 3 | 17 |
| 67 | O1 | 107/112 (96%) | 92 (86%) | 9 (8%) | 6 (6%) | 2 | 11 |
| 67 | o1 | 107/112 (96%) | 91 (85%) | 9 (8%) | 7 (6%) | 1 | 9 |
| 68 | O2 | 125/129 (97%) | 111 (89%) | 13 (10%) | 1 (1%) | 19 | 52 |
| 68 | o2 | 125/129 (97%) | 112 (90%) | 10 (8%) | 3 (2%) | 6 | 28 |
| 69 | O3 | 104/106 (98%) | 98 (94%) | 5 (5%) | 1 (1%) | 15 | 47 |
| 69 | o3 | 104/106 (98%) | 90 (86%) | 11 (11%) | 3 (3%) | 4 | 25 |
| 70 | O4 | 110/119 (92%) | 94 (86%) | 15 (14%) | 1 (1%) | 17 | 50 |
| 70 | o4 | 110/119 (92%) | 93 (84%) | 15 (14%) | 2 (2%) | 8 | 35 |
| 71 | O5 | 117/119 (98%) | 97 (83%) | 14 (12%) | 6 (5%) | 2 | 13 |
| 71 | o5 | 117/119 (98%) | 103 (88%) | 12 (10%) | 2 (2%) | 9 | 36 |
| 72 | O6 | 97/99 (98%) | 78 (80%) | 12 (12%) | 7 (7%) | 1 | 7 |
| 72 | o6 | 97/99 (98%) | 76 (78%) | 13 (13%) | 8 (8%) | 1 | 6 |
| 73 | O7 | 85/87 (98%) | 73 (86%) | 11 (13%) | 1 (1%) | 13 | 43 |
| 73 | o7 | 85/87 (98%) | 75 (88%) | 10 (12%) | 0 | 100 | 100 |
| 74 | O8 | 75/77 (97%) | 63 (84%) | 9 (12%) | 3 (4%) | 3 | 17 |
| 74 | o8 | 75/77 (97%) | 59 (79%) | 10 (13%) | 6 (8%) | 1 | 6 |
| 75 | O9 | 48/50 (96%) | 40 (83%) | 7 (15%) | 1 (2%) | 7 | 32 |
| 75 | o9 | 48/50 (96%) | 39 (81%) | 7 (15%) | 2 (4%) | 3 | 16 |
| 76 | Q0 | 50/52 (96%) | 42 (84%) | 5 (10%) | 3 (6%) | 1 | 10 |
| 76 | q0 | 50/52 (96%) | 47 (94%) | 1 (2%) | 2 (4%) | 3 | 17 |
| 77 | Q1 | 23/25 (92%) | 19 (83%) | 4 (17%) | 0 | 100 | 100 |
| 77 | q1 | 23/25 (92%) | 22 (96%) | 1 (4%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|------------|-----------|-------------|----|
| 78 | Q2 | 103/105 (98%) | 84 (82%) | 12 (12%) | 7 (7%) | 1 | 8 |
| 78 | q2 | 103/105 (98%) | 88 (85%) | 11 (11%) | 4 (4%) | 3 | 18 |
| 79 | Q3 | 89/91 (98%) | 77 (86%) | 6 (7%) | 6 (7%) | 1 | 8 |
| 79 | q3 | 89/91 (98%) | 80 (90%) | 7 (8%) | 2 (2%) | 6 | 31 |
| 80 | c0 | 92/105 (88%) | 63 (68%) | 16 (17%) | 13 (14%) | 0 | 1 |
| 82 | p0 | 139/311 (45%) | 113 (81%) | 20 (14%) | 6 (4%) | 2 | 16 |
| 85 | f | 146/157 (93%) | 98 (67%) | 30 (20%) | 18 (12%) | 0 | 2 |
| All | All | 22479/24300 (92%) | 18504 (82%) | 2828 (13%) | 1147 (5%) | 2 | 13 |

5 of 1147 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | S0 | 4 | PRO |
| 2 | S0 | 158 | VAL |
| 2 | S0 | 190 | ASP |
| 2 | S0 | 191 | ARG |
| 2 | S0 | 192 | THR |

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 2 | S0 | 164/209 (78%) | 138 (84%) | 26 (16%) | 2 | 11 |
| 2 | s0 | 165/209 (79%) | 142 (86%) | 23 (14%) | 3 | 15 |
| 3 | S1 | 191/223 (86%) | 159 (83%) | 32 (17%) | 2 | 9 |
| 3 | s1 | 192/223 (86%) | 157 (82%) | 35 (18%) | 1 | 7 |
| 4 | S2 | 176/204 (86%) | 148 (84%) | 28 (16%) | 2 | 11 |
| 4 | s2 | 176/204 (86%) | 141 (80%) | 35 (20%) | 1 | 5 |
| 5 | S3 | 182/194 (94%) | 153 (84%) | 29 (16%) | 2 | 11 |
| 5 | s3 | 182/194 (94%) | 150 (82%) | 32 (18%) | 2 | 8 |
| 6 | S4 | 221/221 (100%) | 188 (85%) | 33 (15%) | 3 | 12 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 6 | s4 | 221/221 (100%) | 192 (87%) | 29 (13%) | 4 | 17 |
| 7 | S5 | 173/190 (91%) | 154 (89%) | 19 (11%) | 6 | 24 |
| 7 | s5 | 173/190 (91%) | 150 (87%) | 23 (13%) | 4 | 16 |
| 8 | S6 | 188/201 (94%) | 160 (85%) | 28 (15%) | 3 | 12 |
| 8 | s6 | 187/201 (93%) | 158 (84%) | 29 (16%) | 2 | 11 |
| 9 | S7 | 165/169 (98%) | 137 (83%) | 28 (17%) | 2 | 9 |
| 9 | s7 | 165/169 (98%) | 146 (88%) | 19 (12%) | 5 | 22 |
| 10 | S8 | 150/161 (93%) | 132 (88%) | 18 (12%) | 5 | 20 |
| 10 | s8 | 150/161 (93%) | 132 (88%) | 18 (12%) | 5 | 20 |
| 11 | S9 | 158/165 (96%) | 133 (84%) | 25 (16%) | 2 | 11 |
| 11 | s9 | 158/165 (96%) | 128 (81%) | 30 (19%) | 1 | 6 |
| 12 | C0 | 77/98 (79%) | 66 (86%) | 11 (14%) | 3 | 14 |
| 13 | C1 | 129/136 (95%) | 120 (93%) | 9 (7%) | 15 | 43 |
| 13 | c1 | 129/136 (95%) | 113 (88%) | 16 (12%) | 4 | 19 |
| 14 | C2 | 88/118 (75%) | 76 (86%) | 12 (14%) | 3 | 16 |
| 14 | c2 | 88/118 (75%) | 76 (86%) | 12 (14%) | 3 | 16 |
| 15 | C3 | 127/127 (100%) | 107 (84%) | 20 (16%) | 2 | 11 |
| 15 | c3 | 127/127 (100%) | 108 (85%) | 19 (15%) | 3 | 12 |
| 16 | C4 | 81/104 (78%) | 62 (76%) | 19 (24%) | 1 | 3 |
| 16 | c4 | 97/104 (93%) | 84 (87%) | 13 (13%) | 4 | 16 |
| 17 | C5 | 101/117 (86%) | 83 (82%) | 18 (18%) | 2 | 7 |
| 17 | c5 | 103/117 (88%) | 85 (82%) | 18 (18%) | 2 | 8 |
| 18 | C6 | 117/118 (99%) | 101 (86%) | 16 (14%) | 3 | 16 |
| 18 | c6 | 118/118 (100%) | 96 (81%) | 22 (19%) | 1 | 6 |
| 19 | C7 | 94/124 (76%) | 76 (81%) | 18 (19%) | 1 | 6 |
| 19 | c7 | 92/124 (74%) | 80 (87%) | 12 (13%) | 4 | 17 |
| 20 | C8 | 128/128 (100%) | 105 (82%) | 23 (18%) | 1 | 7 |
| 20 | c8 | 128/128 (100%) | 104 (81%) | 24 (19%) | 1 | 6 |
| 21 | C9 | 115/115 (100%) | 99 (86%) | 16 (14%) | 3 | 15 |
| 21 | c9 | 115/115 (100%) | 105 (91%) | 10 (9%) | 10 | 34 |
| 22 | D0 | 100/113 (88%) | 88 (88%) | 12 (12%) | 5 | 20 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 22 | d0 | 103/113 (91%) | 87 (84%) | 16 (16%) | 2 | 11 |
| 23 | D1 | 74/74 (100%) | 61 (82%) | 13 (18%) | 2 | 8 |
| 23 | d1 | 74/74 (100%) | 63 (85%) | 11 (15%) | 3 | 12 |
| 24 | D2 | 110/110 (100%) | 91 (83%) | 19 (17%) | 2 | 8 |
| 24 | d2 | 110/110 (100%) | 92 (84%) | 18 (16%) | 2 | 10 |
| 25 | D3 | 119/119 (100%) | 103 (87%) | 16 (13%) | 4 | 16 |
| 25 | d3 | 119/119 (100%) | 108 (91%) | 11 (9%) | 9 | 31 |
| 26 | D4 | 112/112 (100%) | 103 (92%) | 9 (8%) | 12 | 37 |
| 26 | d4 | 112/112 (100%) | 96 (86%) | 16 (14%) | 3 | 14 |
| 27 | D5 | 61/88 (69%) | 49 (80%) | 12 (20%) | 1 | 5 |
| 27 | d5 | 61/88 (69%) | 52 (85%) | 9 (15%) | 3 | 13 |
| 28 | D6 | 83/83 (100%) | 71 (86%) | 12 (14%) | 3 | 14 |
| 28 | d6 | 83/83 (100%) | 74 (89%) | 9 (11%) | 6 | 24 |
| 29 | D7 | 70/70 (100%) | 64 (91%) | 6 (9%) | 10 | 34 |
| 29 | d7 | 70/70 (100%) | 59 (84%) | 11 (16%) | 2 | 11 |
| 30 | D8 | 56/59 (95%) | 47 (84%) | 9 (16%) | 2 | 10 |
| 30 | d8 | 56/59 (95%) | 45 (80%) | 11 (20%) | 1 | 5 |
| 31 | D9 | 47/48 (98%) | 36 (77%) | 11 (23%) | 1 | 3 |
| 31 | d9 | 47/48 (98%) | 37 (79%) | 10 (21%) | 1 | 4 |
| 32 | E0 | 51/53 (96%) | 43 (84%) | 8 (16%) | 2 | 11 |
| 32 | e0 | 53/53 (100%) | 41 (77%) | 12 (23%) | 1 | 3 |
| 33 | E1 | 62/66 (94%) | 45 (73%) | 17 (27%) | 0 | 1 |
| 33 | e1 | 66/66 (100%) | 54 (82%) | 12 (18%) | 1 | 7 |
| 34 | SR | 259/261 (99%) | 230 (89%) | 29 (11%) | 6 | 23 |
| 34 | sR | 260/261 (100%) | 236 (91%) | 24 (9%) | 9 | 31 |
| 35 | SM | 97/228 (42%) | 82 (84%) | 15 (16%) | 2 | 11 |
| 35 | sM | 54/228 (24%) | 46 (85%) | 8 (15%) | 3 | 13 |
| 39 | L2 | 193/195 (99%) | 158 (82%) | 35 (18%) | 1 | 7 |
| 39 | l2 | 192/195 (98%) | 156 (81%) | 36 (19%) | 1 | 6 |
| 40 | L3 | 320/322 (99%) | 274 (86%) | 46 (14%) | 3 | 14 |
| 40 | l3 | 319/322 (99%) | 264 (83%) | 55 (17%) | 2 | 9 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 41 | L4 | 288/288 (100%) | 241 (84%) | 47 (16%) | 2 | 10 |
| 41 | l4 | 288/288 (100%) | 247 (86%) | 41 (14%) | 3 | 15 |
| 42 | L5 | 244/244 (100%) | 203 (83%) | 41 (17%) | 2 | 9 |
| 42 | l5 | 243/244 (100%) | 201 (83%) | 42 (17%) | 2 | 8 |
| 43 | L6 | 134/152 (88%) | 114 (85%) | 20 (15%) | 3 | 12 |
| 43 | l6 | 135/152 (89%) | 115 (85%) | 20 (15%) | 3 | 13 |
| 44 | L7 | 186/204 (91%) | 164 (88%) | 22 (12%) | 5 | 21 |
| 44 | l7 | 187/204 (92%) | 164 (88%) | 23 (12%) | 4 | 20 |
| 45 | L8 | 187/207 (90%) | 160 (86%) | 27 (14%) | 3 | 14 |
| 45 | l8 | 177/207 (86%) | 154 (87%) | 23 (13%) | 4 | 17 |
| 46 | L9 | 171/171 (100%) | 151 (88%) | 20 (12%) | 5 | 21 |
| 46 | l9 | 171/171 (100%) | 142 (83%) | 29 (17%) | 2 | 9 |
| 47 | M0 | 177/186 (95%) | 142 (80%) | 35 (20%) | 1 | 5 |
| 47 | m0 | 179/186 (96%) | 143 (80%) | 36 (20%) | 1 | 5 |
| 48 | M1 | 147/150 (98%) | 124 (84%) | 23 (16%) | 2 | 11 |
| 48 | m1 | 147/150 (98%) | 120 (82%) | 27 (18%) | 1 | 7 |
| 49 | M3 | 154/158 (98%) | 138 (90%) | 16 (10%) | 7 | 25 |
| 49 | m3 | 154/158 (98%) | 132 (86%) | 22 (14%) | 3 | 14 |
| 50 | M4 | 107/108 (99%) | 92 (86%) | 15 (14%) | 3 | 15 |
| 50 | m4 | 108/108 (100%) | 94 (87%) | 14 (13%) | 4 | 17 |
| 51 | M5 | 175/175 (100%) | 153 (87%) | 22 (13%) | 4 | 18 |
| 51 | m5 | 175/175 (100%) | 152 (87%) | 23 (13%) | 4 | 17 |
| 52 | M6 | 160/161 (99%) | 136 (85%) | 24 (15%) | 3 | 12 |
| 52 | m6 | 160/161 (99%) | 134 (84%) | 26 (16%) | 2 | 10 |
| 53 | M7 | 140/145 (97%) | 123 (88%) | 17 (12%) | 5 | 20 |
| 53 | m7 | 125/145 (86%) | 107 (86%) | 18 (14%) | 3 | 14 |
| 54 | M8 | 150/150 (100%) | 136 (91%) | 14 (9%) | 9 | 30 |
| 54 | m8 | 150/150 (100%) | 120 (80%) | 30 (20%) | 1 | 5 |
| 55 | M9 | 153/153 (100%) | 132 (86%) | 21 (14%) | 3 | 16 |
| 55 | m9 | 153/153 (100%) | 129 (84%) | 24 (16%) | 2 | 11 |
| 56 | N0 | 156/156 (100%) | 134 (86%) | 22 (14%) | 3 | 15 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 56 | n0 | 156/156 (100%) | 135 (86%) | 21 (14%) | 4 | 16 |
| 57 | N1 | 136/136 (100%) | 107 (79%) | 29 (21%) | 1 | 4 |
| 57 | n1 | 136/136 (100%) | 113 (83%) | 23 (17%) | 2 | 9 |
| 58 | N2 | 87/106 (82%) | 79 (91%) | 8 (9%) | 9 | 31 |
| 58 | n2 | 85/106 (80%) | 72 (85%) | 13 (15%) | 2 | 12 |
| 59 | N3 | 104/104 (100%) | 90 (86%) | 14 (14%) | 4 | 16 |
| 59 | n3 | 104/104 (100%) | 89 (86%) | 15 (14%) | 3 | 14 |
| 60 | N4 | 57/129 (44%) | 50 (88%) | 7 (12%) | 4 | 20 |
| 60 | n4 | 100/129 (78%) | 88 (88%) | 12 (12%) | 5 | 20 |
| 61 | N5 | 104/117 (89%) | 86 (83%) | 18 (17%) | 2 | 8 |
| 61 | n5 | 104/117 (89%) | 92 (88%) | 12 (12%) | 5 | 22 |
| 62 | N6 | 109/109 (100%) | 90 (83%) | 19 (17%) | 2 | 8 |
| 62 | n6 | 109/109 (100%) | 89 (82%) | 20 (18%) | 1 | 7 |
| 63 | N7 | 115/115 (100%) | 104 (90%) | 11 (10%) | 8 | 29 |
| 63 | n7 | 115/115 (100%) | 95 (83%) | 20 (17%) | 2 | 8 |
| 64 | N8 | 118/118 (100%) | 100 (85%) | 18 (15%) | 2 | 12 |
| 64 | n8 | 118/118 (100%) | 100 (85%) | 18 (15%) | 2 | 12 |
| 65 | N9 | 46/46 (100%) | 40 (87%) | 6 (13%) | 4 | 17 |
| 65 | n9 | 46/46 (100%) | 41 (89%) | 5 (11%) | 6 | 24 |
| 66 | O0 | 81/87 (93%) | 70 (86%) | 11 (14%) | 3 | 16 |
| 66 | o0 | 84/87 (97%) | 71 (84%) | 13 (16%) | 2 | 11 |
| 67 | O1 | 92/96 (96%) | 78 (85%) | 14 (15%) | 3 | 12 |
| 67 | o1 | 94/96 (98%) | 76 (81%) | 18 (19%) | 1 | 6 |
| 68 | O2 | 109/110 (99%) | 91 (84%) | 18 (16%) | 2 | 10 |
| 68 | o2 | 109/110 (99%) | 85 (78%) | 24 (22%) | 1 | 3 |
| 69 | O3 | 90/90 (100%) | 81 (90%) | 9 (10%) | 7 | 27 |
| 69 | o3 | 90/90 (100%) | 77 (86%) | 13 (14%) | 3 | 14 |
| 70 | O4 | 95/101 (94%) | 84 (88%) | 11 (12%) | 5 | 22 |
| 70 | o4 | 95/101 (94%) | 80 (84%) | 15 (16%) | 2 | 11 |
| 71 | O5 | 104/104 (100%) | 90 (86%) | 14 (14%) | 4 | 16 |
| 71 | o5 | 103/104 (99%) | 90 (87%) | 13 (13%) | 4 | 18 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|------------|-------------|----|
| 72 | O6 | 81/81 (100%) | 66 (82%) | 15 (18%) | 1 | 6 |
| 72 | o6 | 80/81 (99%) | 56 (70%) | 24 (30%) | 0 | 1 |
| 73 | O7 | 70/70 (100%) | 55 (79%) | 15 (21%) | 1 | 4 |
| 73 | o7 | 70/70 (100%) | 58 (83%) | 12 (17%) | 2 | 9 |
| 74 | O8 | 68/68 (100%) | 53 (78%) | 15 (22%) | 1 | 3 |
| 74 | o8 | 67/68 (98%) | 55 (82%) | 12 (18%) | 2 | 7 |
| 75 | O9 | 45/45 (100%) | 38 (84%) | 7 (16%) | 2 | 11 |
| 75 | o9 | 45/45 (100%) | 36 (80%) | 9 (20%) | 1 | 5 |
| 76 | Q0 | 47/47 (100%) | 39 (83%) | 8 (17%) | 2 | 9 |
| 76 | q0 | 47/47 (100%) | 42 (89%) | 5 (11%) | 6 | 25 |
| 77 | Q1 | 23/23 (100%) | 19 (83%) | 4 (17%) | 2 | 8 |
| 77 | q1 | 23/23 (100%) | 15 (65%) | 8 (35%) | 0 | 0 |
| 78 | Q2 | 90/90 (100%) | 76 (84%) | 14 (16%) | 2 | 11 |
| 78 | q2 | 90/90 (100%) | 77 (86%) | 13 (14%) | 3 | 14 |
| 79 | Q3 | 71/71 (100%) | 59 (83%) | 12 (17%) | 2 | 9 |
| 79 | q3 | 71/71 (100%) | 60 (84%) | 11 (16%) | 2 | 11 |
| 80 | c0 | 73/98 (74%) | 64 (88%) | 9 (12%) | 4 | 20 |
| 82 | p0 | 105/253 (42%) | 94 (90%) | 11 (10%) | 7 | 25 |
| 85 | f | 124/133 (93%) | 108 (87%) | 16 (13%) | 4 | 18 |
| All | All | 18850/20374 (92%) | 15999 (85%) | 2851 (15%) | 3 | 12 |

5 of 2851 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 71 | O5 | 102 | GLU |
| 9 | s7 | 95 | GLU |
| 66 | o0 | 18 | ILE |
| 74 | O8 | 52 | TYR |
| 4 | s2 | 87 | GLN |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 47 | M0 | 144 | ASN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 3 | s1 | 149 | GLN |
| 56 | n0 | 8 | GLN |
| 51 | M5 | 15 | GLN |
| 54 | M8 | 135 | GLN |

5.3.3 RNA [i](#)

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-------------------|-------------------|-----------------|
| 1 | 2 | 1776/1800 (98%) | 454 (25%) | 49 (2%) |
| 1 | 6 | 1791/1800 (99%) | 436 (24%) | 35 (1%) |
| 36 | 1 | 3145/3396 (92%) | 652 (20%) | 49 (1%) |
| 36 | 5 | 3163/3396 (93%) | 650 (20%) | 49 (1%) |
| 37 | 3 | 120/121 (99%) | 11 (9%) | 0 |
| 37 | 7 | 120/121 (99%) | 16 (13%) | 1 (0%) |
| 38 | 4 | 157/158 (99%) | 36 (22%) | 1 (0%) |
| 38 | 8 | 157/158 (99%) | 33 (21%) | 1 (0%) |
| All | All | 10429/10950 (95%) | 2288 (21%) | 185 (1%) |

5 of 2288 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | 2 | 2 | A |
| 1 | 2 | 4 | C |
| 1 | 2 | 8 | U |
| 1 | 2 | 17 | C |
| 1 | 2 | 25 | C |

5 of 185 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 36 | 1 | 2541 | U |
| 1 | 6 | 158 | U |
| 36 | 5 | 2446 | U |
| 36 | 1 | 2593 | A |
| 36 | 1 | 3275 | U |

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 16 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](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 1 | 2 | 2 |
| 81 | m2 | 2 |
| 80 | c0 | 1 |
| 36 | 5 | 1 |

The worst 5 of 6 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | c0 | 84:GLU | C | 87:HIS | N | 7.38 |
| 1 | 2 | 1716:C | O3' | 1717:G | P | 5.29 |
| 1 | 5 | 2437:G | O3' | 2438:A | P | 3.76 |
| 1 | m2 | 52:UNK | C | 54:UNK | N | 3.58 |
| 1 | m2 | 23:UNK | C | 28:UNK | N | 3.14 |

6 Fit of model and data i

6.1 Protein, DNA and RNA chains i

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 |
|-----|-------|-----------------|--------|---------------|-----------------------|-------|
| 1 | 2 | 1781/1800 (98%) | 0.92 | 209 (11%) 4 4 | 60, 99, 172, 210 | 0 |
| 1 | 6 | 1795/1800 (99%) | 0.61 | 93 (5%) 27 25 | 46, 86, 159, 201 | 0 |
| 2 | S0 | 206/251 (82%) | 2.50 | 120 (58%) 0 0 | 101, 114, 125, 133 | 0 |
| 2 | s0 | 206/251 (82%) | 1.66 | 78 (37%) 0 0 | 83, 99, 113, 119 | 0 |
| 3 | S1 | 214/254 (84%) | 0.78 | 33 (15%) 2 2 | 107, 142, 167, 173 | 0 |
| 3 | s1 | 216/254 (85%) | 0.84 | 31 (14%) 2 2 | 84, 98, 115, 123 | 0 |
| 4 | S2 | 217/253 (85%) | 1.54 | 64 (29%) 0 0 | 84, 97, 111, 115 | 0 |
| 4 | s2 | 217/253 (85%) | 1.43 | 58 (26%) 0 0 | 68, 81, 96, 103 | 0 |
| 5 | S3 | 223/239 (93%) | 1.74 | 89 (39%) 0 0 | 89, 100, 122, 129 | 0 |
| 5 | s3 | 223/239 (93%) | 2.19 | 112 (50%) 0 0 | 84, 111, 133, 137 | 0 |
| 6 | S4 | 260/260 (100%) | 1.35 | 74 (28%) 0 0 | 77, 102, 110, 125 | 0 |
| 6 | s4 | 260/260 (100%) | 0.69 | 24 (9%) 9 10 | 61, 83, 97, 119 | 0 |
| 7 | S5 | 206/224 (91%) | 1.02 | 40 (19%) 1 1 | 102, 123, 131, 134 | 0 |
| 7 | s5 | 206/224 (91%) | 1.26 | 52 (25%) 0 0 | 87, 108, 122, 128 | 0 |
| 8 | S6 | 226/236 (95%) | 1.16 | 59 (26%) 0 0 | 78, 110, 127, 139 | 0 |
| 8 | s6 | 218/236 (92%) | 0.77 | 25 (11%) 4 4 | 60, 89, 107, 116 | 0 |
| 9 | S7 | 184/189 (97%) | 0.93 | 37 (20%) 1 1 | 101, 123, 139, 142 | 0 |
| 9 | s7 | 186/189 (98%) | 0.79 | 26 (13%) 2 2 | 77, 105, 132, 137 | 0 |
| 10 | S8 | 188/200 (94%) | 1.50 | 56 (29%) 0 0 | 71, 89, 123, 135 | 0 |
| 10 | s8 | 188/200 (94%) | 1.08 | 36 (19%) 1 1 | 56, 75, 116, 133 | 0 |
| 11 | S9 | 185/196 (94%) | 1.33 | 49 (26%) 0 0 | 90, 107, 133, 150 | 0 |
| 11 | s9 | 185/196 (94%) | 0.82 | 16 (8%) 10 10 | 72, 90, 116, 130 | 0 |
| 12 | C0 | 96/105 (91%) | 1.39 | 27 (28%) 0 0 | 92, 113, 133, 141 | 0 |
| 13 | C1 | 155/155 (100%) | 2.03 | 71 (45%) 0 0 | 73, 85, 112, 127 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 |
|-----|-------|----------------|--------|---------------|-----------------------|-------|
| 13 | c1 | 146/155 (94%) | 1.48 | 32 (21%) 0 1 | 59, 72, 97, 121 | 0 |
| 14 | C2 | 124/142 (87%) | 1.09 | 30 (24%) 0 0 | 138, 146, 152, 159 | 0 |
| 14 | c2 | 124/142 (87%) | 2.36 | 51 (41%) 0 0 | 169, 184, 194, 196 | 0 |
| 15 | C3 | 150/150 (100%) | 1.39 | 41 (27%) 0 0 | 81, 94, 113, 116 | 0 |
| 15 | c3 | 150/150 (100%) | 1.37 | 45 (30%) 0 0 | 67, 80, 97, 102 | 0 |
| 16 | C4 | 127/136 (93%) | 1.03 | 25 (19%) 1 1 | 84, 139, 155, 159 | 0 |
| 16 | c4 | 128/136 (94%) | 1.36 | 36 (28%) 0 0 | 66, 102, 112, 119 | 0 |
| 17 | C5 | 124/141 (87%) | 0.54 | 8 (6%) 18 18 | 88, 100, 112, 119 | 0 |
| 17 | c5 | 135/141 (95%) | 1.00 | 27 (20%) 1 1 | 78, 105, 114, 118 | 0 |
| 18 | C6 | 141/142 (99%) | 3.40 | 93 (65%) 0 0 | 92, 112, 117, 120 | 0 |
| 18 | c6 | 142/142 (100%) | 2.38 | 74 (52%) 0 0 | 80, 101, 116, 125 | 0 |
| 19 | C7 | 120/136 (88%) | 2.78 | 81 (67%) 0 0 | 99, 108, 126, 129 | 0 |
| 19 | c7 | 117/136 (86%) | 1.45 | 42 (35%) 0 0 | 87, 102, 115, 118 | 0 |
| 20 | C8 | 145/145 (100%) | 0.41 | 9 (6%) 20 19 | 86, 110, 131, 137 | 0 |
| 20 | c8 | 145/145 (100%) | 0.50 | 6 (4%) 37 34 | 88, 100, 118, 127 | 0 |
| 21 | C9 | 143/143 (100%) | 2.22 | 82 (57%) 0 0 | 95, 110, 121, 126 | 0 |
| 21 | c9 | 143/143 (100%) | 1.21 | 27 (18%) 1 1 | 84, 96, 112, 121 | 0 |
| 22 | D0 | 107/120 (89%) | 1.91 | 42 (39%) 0 0 | 85, 112, 128, 130 | 0 |
| 22 | d0 | 110/120 (91%) | 2.21 | 53 (48%) 0 0 | 84, 114, 139, 156 | 0 |
| 23 | D1 | 87/87 (100%) | 2.09 | 43 (49%) 0 0 | 100, 106, 118, 127 | 0 |
| 23 | d1 | 87/87 (100%) | 0.99 | 18 (20%) 1 1 | 80, 88, 108, 116 | 0 |
| 24 | D2 | 129/129 (100%) | 3.56 | 106 (82%) 0 0 | 83, 94, 103, 112 | 0 |
| 24 | d2 | 129/129 (100%) | 1.40 | 38 (29%) 0 0 | 65, 75, 82, 89 | 0 |
| 25 | D3 | 144/144 (100%) | 1.43 | 40 (27%) 0 0 | 71, 77, 86, 97 | 0 |
| 25 | d3 | 144/144 (100%) | 1.04 | 22 (15%) 2 2 | 58, 63, 74, 82 | 0 |
| 26 | D4 | 134/134 (100%) | 0.52 | 12 (8%) 9 10 | 88, 111, 122, 128 | 0 |
| 26 | d4 | 134/134 (100%) | 0.37 | 4 (2%) 50 48 | 68, 92, 105, 108 | 0 |
| 27 | D5 | 70/107 (65%) | 0.28 | 5 (7%) 16 15 | 119, 131, 137, 138 | 0 |
| 27 | d5 | 69/107 (64%) | 0.60 | 6 (8%) 10 10 | 97, 115, 125, 126 | 0 |
| 28 | D6 | 97/97 (100%) | 2.66 | 57 (58%) 0 0 | 88, 104, 150, 154 | 0 |
| 28 | d6 | 97/97 (100%) | 2.43 | 52 (53%) 0 0 | 71, 86, 115, 119 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | | | OWAB(Å ²) | Q<0.9 |
|-----|-------|-----------------|--------|-----------|-----|-----|-----------------------|-------|
| 29 | D7 | 81/81 (100%) | 1.64 | 35 (43%) | 0 | 0 | 98, 110, 134, 137 | 0 |
| 29 | d7 | 81/81 (100%) | 1.88 | 33 (40%) | 0 | 0 | 80, 94, 124, 130 | 0 |
| 30 | D8 | 63/66 (95%) | 1.23 | 16 (25%) | 0 | 0 | 110, 125, 137, 139 | 0 |
| 30 | d8 | 63/66 (95%) | 1.62 | 21 (33%) | 0 | 0 | 103, 116, 125, 130 | 0 |
| 31 | D9 | 53/55 (96%) | 1.53 | 15 (28%) | 0 | 0 | 86, 90, 106, 111 | 0 |
| 31 | d9 | 53/55 (96%) | 2.70 | 35 (66%) | 0 | 0 | 81, 92, 128, 141 | 0 |
| 32 | E0 | 60/62 (96%) | 2.14 | 24 (40%) | 0 | 0 | 77, 108, 128, 130 | 0 |
| 32 | e0 | 62/62 (100%) | 1.01 | 13 (20%) | 1 | 1 | 66, 91, 110, 113 | 0 |
| 33 | E1 | 71/76 (93%) | 0.87 | 12 (16%) | 1 | 1 | 105, 134, 149, 153 | 0 |
| 33 | e1 | 76/76 (100%) | 1.56 | 24 (31%) | 0 | 0 | 112, 161, 175, 179 | 0 |
| 34 | SR | 318/318 (100%) | 1.65 | 109 (34%) | 0 | 0 | 108, 119, 131, 147 | 0 |
| 34 | sR | 318/318 (100%) | 2.41 | 162 (50%) | 0 | 0 | 110, 127, 139, 150 | 0 |
| 35 | SM | 159/273 (58%) | 1.25 | 43 (27%) | 0 | 0 | 62, 98, 144, 148 | 0 |
| 35 | sM | 104/273 (38%) | 0.74 | 16 (15%) | 2 | 2 | 56, 109, 181, 186 | 0 |
| 36 | 1 | 3149/3396 (92%) | 0.62 | 160 (5%) | 28 | 26 | 38, 61, 124, 213 | 0 |
| 36 | 5 | 3169/3396 (93%) | 0.65 | 120 (3%) | 40 | 37 | 37, 56, 124, 192 | 0 |
| 37 | 3 | 121/121 (100%) | 0.22 | 0 | 100 | 100 | 44, 76, 91, 98 | 0 |
| 37 | 7 | 121/121 (100%) | 0.31 | 1 (0%) | 86 | 86 | 41, 62, 74, 80 | 0 |
| 38 | 4 | 158/158 (100%) | 0.42 | 2 (1%) | 77 | 75 | 47, 64, 94, 125 | 0 |
| 38 | 8 | 158/158 (100%) | 0.45 | 3 (1%) | 66 | 64 | 46, 66, 95, 118 | 0 |
| 39 | L2 | 252/253 (99%) | 1.22 | 59 (23%) | 0 | 1 | 46, 64, 80, 86 | 0 |
| 39 | l2 | 252/253 (99%) | 1.40 | 69 (27%) | 0 | 0 | 45, 61, 75, 85 | 0 |
| 40 | L3 | 386/386 (100%) | 0.64 | 33 (8%) | 10 | 10 | 44, 64, 77, 87 | 0 |
| 40 | l3 | 386/386 (100%) | 0.43 | 13 (3%) | 45 | 42 | 37, 51, 64, 79 | 0 |
| 41 | L4 | 361/361 (100%) | 0.57 | 40 (11%) | 5 | 5 | 42, 57, 70, 74 | 0 |
| 41 | l4 | 361/361 (100%) | 0.77 | 44 (12%) | 4 | 4 | 45, 60, 74, 82 | 0 |
| 42 | L5 | 296/296 (100%) | 0.47 | 24 (8%) | 12 | 11 | 60, 83, 99, 107 | 0 |
| 42 | l5 | 294/296 (99%) | 0.36 | 10 (3%) | 45 | 42 | 50, 64, 89, 105 | 0 |
| 43 | L6 | 156/175 (89%) | 0.48 | 2 (1%) | 77 | 75 | 52, 59, 72, 82 | 0 |
| 43 | l6 | 157/175 (89%) | 0.50 | 10 (6%) | 19 | 18 | 53, 60, 78, 87 | 0 |
| 44 | L7 | 222/243 (91%) | 0.55 | 5 (2%) | 60 | 58 | 42, 52, 78, 100 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 |
|-----|-------|----------------|--------|---------------|-----------------------|-------|
| 44 | l7 | 223/243 (91%) | 0.30 | 0 100 100 | 42, 51, 80, 105 | 0 |
| 45 | L8 | 233/255 (91%) | 0.65 | 22 (9%) 8 9 | 70, 86, 109, 117 | 0 |
| 45 | l8 | 231/255 (90%) | 0.79 | 27 (11%) 4 4 | 73, 86, 106, 114 | 0 |
| 46 | L9 | 191/191 (100%) | 0.30 | 5 (2%) 56 52 | 62, 72, 83, 92 | 0 |
| 46 | l9 | 191/191 (100%) | 0.37 | 4 (2%) 63 61 | 47, 57, 72, 82 | 0 |
| 47 | M0 | 211/220 (95%) | 0.55 | 6 (2%) 53 50 | 47, 61, 88, 110 | 0 |
| 47 | m0 | 213/220 (96%) | 0.72 | 13 (6%) 21 20 | 45, 64, 88, 97 | 0 |
| 48 | M1 | 169/173 (97%) | 0.66 | 13 (7%) 13 12 | 70, 88, 99, 102 | 0 |
| 48 | m1 | 169/173 (97%) | 0.31 | 4 (2%) 59 55 | 54, 71, 79, 83 | 0 |
| 49 | M3 | 193/198 (97%) | 1.06 | 37 (19%) 1 1 | 43, 68, 93, 114 | 0 |
| 49 | m3 | 194/198 (97%) | 0.56 | 13 (6%) 17 17 | 44, 71, 100, 112 | 0 |
| 50 | M4 | 136/137 (99%) | 0.23 | 1 (0%) 87 88 | 56, 62, 74, 86 | 0 |
| 50 | m4 | 137/137 (100%) | 0.12 | 0 100 100 | 51, 57, 70, 81 | 0 |
| 51 | M5 | 203/203 (100%) | 0.87 | 19 (9%) 8 9 | 45, 59, 70, 72 | 0 |
| 51 | m5 | 203/203 (100%) | 1.08 | 32 (15%) 2 2 | 46, 63, 73, 78 | 0 |
| 52 | M6 | 197/198 (99%) | 0.57 | 7 (3%) 42 39 | 44, 51, 67, 69 | 0 |
| 52 | m6 | 197/198 (99%) | 0.50 | 8 (4%) 37 34 | 37, 45, 64, 67 | 0 |
| 53 | M7 | 183/183 (100%) | 1.25 | 25 (13%) 3 3 | 49, 56, 93, 112 | 0 |
| 53 | m7 | 155/183 (84%) | 0.45 | 7 (4%) 33 31 | 42, 50, 63, 82 | 0 |
| 54 | M8 | 185/185 (100%) | 0.67 | 11 (5%) 22 21 | 45, 58, 71, 86 | 0 |
| 54 | m8 | 185/185 (100%) | 0.80 | 20 (10%) 5 6 | 44, 60, 70, 74 | 0 |
| 55 | M9 | 188/188 (100%) | 0.86 | 21 (11%) 5 5 | 67, 80, 140, 146 | 0 |
| 55 | m9 | 188/188 (100%) | 0.68 | 14 (7%) 14 14 | 53, 67, 127, 138 | 0 |
| 56 | N0 | 172/172 (100%) | 0.65 | 6 (3%) 44 40 | 51, 59, 70, 76 | 0 |
| 56 | n0 | 172/172 (100%) | 0.30 | 1 (0%) 89 89 | 45, 52, 62, 68 | 0 |
| 57 | N1 | 159/159 (100%) | 0.57 | 5 (3%) 49 47 | 46, 58, 95, 103 | 0 |
| 57 | n1 | 159/159 (100%) | 0.43 | 4 (2%) 57 53 | 43, 52, 86, 91 | 0 |
| 58 | N2 | 100/120 (83%) | 1.18 | 25 (25%) 0 0 | 95, 107, 121, 123 | 0 |
| 58 | n2 | 98/120 (81%) | 0.99 | 21 (21%) 0 1 | 78, 90, 97, 100 | 0 |
| 59 | N3 | 136/136 (100%) | 1.36 | 30 (22%) 0 1 | 54, 62, 72, 79 | 0 |
| 59 | n3 | 136/136 (100%) | 0.79 | 9 (6%) 18 17 | 38, 47, 57, 59 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 |
|-----|-------|----------------|--------|--------------|-----------------------|-------|
| 60 | N4 | 98/155 (63%) | 2.95 | 38 (38%) 0 0 | 63, 75, 134, 138 | 0 |
| 60 | n4 | 135/155 (87%) | 1.08 | 19 (14%) 2 2 | 47, 94, 119, 124 | 0 |
| 61 | N5 | 121/141 (85%) | 0.87 | 11 (9%) 9 10 | 62, 73, 86, 99 | 0 |
| 61 | n5 | 120/141 (85%) | 0.66 | 9 (7%) 14 13 | 58, 72, 86, 98 | 0 |
| 62 | N6 | 126/126 (100%) | 0.39 | 3 (2%) 59 55 | 53, 66, 76, 81 | 0 |
| 62 | n6 | 126/126 (100%) | 0.66 | 6 (4%) 30 28 | 55, 68, 79, 85 | 0 |
| 63 | N7 | 135/135 (100%) | 0.60 | 13 (9%) 8 8 | 87, 98, 107, 111 | 0 |
| 63 | n7 | 135/135 (100%) | 0.61 | 15 (11%) 5 5 | 80, 92, 102, 106 | 0 |
| 64 | N8 | 148/148 (100%) | 1.15 | 20 (13%) 3 3 | 38, 60, 79, 86 | 0 |
| 64 | n8 | 148/148 (100%) | 1.13 | 25 (16%) 1 1 | 38, 61, 75, 78 | 0 |
| 65 | N9 | 58/58 (100%) | 0.80 | 6 (10%) 6 6 | 41, 63, 89, 95 | 0 |
| 65 | n9 | 58/58 (100%) | 0.49 | 3 (5%) 27 25 | 41, 60, 82, 89 | 0 |
| 66 | O0 | 97/104 (93%) | 0.23 | 2 (2%) 63 61 | 85, 93, 107, 109 | 0 |
| 66 | o0 | 100/104 (96%) | 0.41 | 5 (5%) 28 26 | 74, 83, 101, 111 | 0 |
| 67 | O1 | 109/112 (97%) | 1.07 | 27 (24%) 0 0 | 62, 73, 92, 98 | 0 |
| 67 | o1 | 109/112 (97%) | 0.86 | 10 (9%) 9 10 | 49, 60, 84, 98 | 0 |
| 68 | O2 | 127/129 (98%) | 0.53 | 4 (3%) 49 47 | 39, 53, 65, 71 | 0 |
| 68 | o2 | 127/129 (98%) | 0.48 | 5 (3%) 39 36 | 38, 56, 69, 72 | 0 |
| 69 | O3 | 106/106 (100%) | 0.86 | 6 (5%) 23 22 | 44, 49, 70, 78 | 0 |
| 69 | o3 | 106/106 (100%) | 1.12 | 15 (14%) 2 2 | 42, 49, 70, 78 | 0 |
| 70 | O4 | 112/119 (94%) | 1.27 | 34 (30%) 0 0 | 61, 78, 107, 113 | 0 |
| 70 | o4 | 112/119 (94%) | 1.04 | 26 (23%) 0 1 | 54, 72, 102, 107 | 0 |
| 71 | O5 | 119/119 (100%) | 0.35 | 1 (0%) 86 86 | 58, 74, 82, 87 | 0 |
| 71 | o5 | 119/119 (100%) | 0.20 | 1 (0%) 86 86 | 62, 75, 89, 98 | 0 |
| 72 | O6 | 99/99 (100%) | 0.19 | 2 (2%) 65 63 | 64, 72, 94, 105 | 0 |
| 72 | o6 | 99/99 (100%) | 0.31 | 3 (3%) 50 48 | 66, 75, 87, 101 | 0 |
| 73 | O7 | 87/87 (100%) | 1.55 | 24 (27%) 0 0 | 46, 53, 71, 76 | 0 |
| 73 | o7 | 87/87 (100%) | 1.43 | 20 (22%) 0 1 | 43, 52, 76, 93 | 0 |
| 74 | O8 | 77/77 (100%) | 0.38 | 5 (6%) 18 18 | 86, 97, 109, 114 | 0 |
| 74 | o8 | 77/77 (100%) | 0.81 | 12 (15%) 2 2 | 80, 91, 101, 103 | 0 |
| 75 | O9 | 50/50 (100%) | 1.81 | 18 (36%) 0 0 | 55, 60, 64, 65 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 |
|-----|-------|-------------------|--------|----------------|-----------------------|------------|
| 75 | o9 | 50/50 (100%) | 1.45 | 15 (30%) 0 0 | 52, 58, 66, 67 | 0 |
| 76 | Q0 | 52/52 (100%) | 0.38 | 2 (3%) 40 37 | 52, 60, 76, 79 | 0 |
| 76 | q0 | 52/52 (100%) | 0.22 | 0 100 100 | 43, 47, 56, 59 | 0 |
| 77 | Q1 | 25/25 (100%) | 2.55 | 16 (64%) 0 0 | 62, 66, 73, 73 | 0 |
| 77 | q1 | 25/25 (100%) | 1.58 | 7 (28%) 0 0 | 53, 58, 59, 59 | 0 |
| 78 | Q2 | 105/105 (100%) | 0.34 | 3 (2%) 51 50 | 46, 58, 78, 103 | 0 |
| 78 | q2 | 105/105 (100%) | 0.65 | 8 (7%) 13 12 | 45, 56, 71, 94 | 0 |
| 79 | Q3 | 91/91 (100%) | 1.02 | 17 (18%) 1 1 | 56, 68, 82, 90 | 0 |
| 79 | q3 | 91/91 (100%) | 1.08 | 22 (24%) 0 0 | 47, 60, 76, 85 | 0 |
| 80 | c0 | 96/105 (91%) | 2.71 | 62 (64%) 0 0 | 104, 135, 149, 151 | 0 |
| 81 | m2 | 0/150 | - | - | - | - |
| 82 | p0 | 143/311 (45%) | 0.82 | 18 (12%) 3 3 | 102, 125, 192, 199 | 0 |
| 83 | p1 | 0/47 | - | - | - | - |
| 84 | p2 | 0/46 | - | - | - | - |
| 85 | f | 148/157 (94%) | 3.43 | 96 (64%) 0 0 | 49, 95, 145, 147 | 148 (100%) |
| All | All | 33261/35493 (93%) | 0.94 | 4903 (14%) 2 2 | 37, 76, 134, 213 | 148 (0%) |

The worst 5 of 4903 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|------|------|------|
| 53 | M7 | 161 | ALA | 23.1 |
| 1 | 2 | 1699 | G | 20.2 |
| 60 | N4 | 86 | SER | 16.1 |
| 53 | M7 | 160 | ALA | 14.7 |
| 60 | N4 | 88 | ASP | 13.6 |

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å ²) | Q<0.9 |
|-----|------|-------|-----|-------|------|------|----------------------------|-------|
| 86 | ZN | e1 | 501 | 1/1 | 0.72 | 0.15 | 165,165,165,165 | 0 |
| 86 | ZN | D7 | 101 | 1/1 | 0.76 | 0.17 | 140,140,140,140 | 0 |
| 86 | ZN | d7 | 101 | 1/1 | 0.78 | 0.31 | 134,134,134,134 | 0 |
| 86 | ZN | E1 | 501 | 1/1 | 0.91 | 0.15 | 133,133,133,133 | 0 |
| 86 | ZN | D6 | 500 | 1/1 | 0.94 | 0.06 | 99,99,99,99 | 0 |
| 86 | ZN | d6 | 500 | 1/1 | 0.94 | 0.07 | 82,82,82,82 | 0 |
| 86 | ZN | q2 | 501 | 1/1 | 0.95 | 0.07 | 74,74,74,74 | 0 |
| 86 | ZN | d9 | 101 | 1/1 | 0.95 | 0.13 | 93,93,93,93 | 0 |
| 86 | ZN | D9 | 101 | 1/1 | 0.97 | 0.11 | 89,89,89,89 | 0 |
| 86 | ZN | Q2 | 501 | 1/1 | 0.97 | 0.08 | 78,78,78,78 | 0 |
| 86 | ZN | Q0 | 500 | 1/1 | 0.98 | 0.20 | 57,57,57,57 | 0 |
| 86 | ZN | q0 | 500 | 1/1 | 0.99 | 0.16 | 48,48,48,48 | 0 |
| 86 | ZN | q3 | 501 | 1/1 | 0.99 | 0.18 | 64,64,64,64 | 0 |
| 86 | ZN | Q3 | 501 | 1/1 | 0.99 | 0.14 | 74,74,74,74 | 0 |
| 86 | ZN | o7 | 501 | 1/1 | 0.99 | 0.14 | 53,53,53,53 | 0 |
| 86 | ZN | O7 | 100 | 1/1 | 1.00 | 0.13 | 53,53,53,53 | 0 |

6.5 Other polymers [i](#)

There are no such residues in this entry.