



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 12:40 pm GMT

PDB ID : 4V6I
EMDB ID: : EMD-1669
Title : Localization of the small subunit ribosomal proteins into a 6.1 Å cryo-EM map of *Saccharomyces cerevisiae* translating 80S ribosome
Authors : Armache, J.-P.; Jarasch, A.; Anger, A.M.; Villa, E.; Becker, T.; Bhushan, S.; Jossinet, F.; Habeck, M.; Dindar, G.; Franckenberg, S.; Marquez, V.; Mielke, T.; Thomm, M.; Berninghausen, O.; Beatrix, B.; Soeding, J.; Westhof, E.; Wilson, D.N.; Beckmann, R.
Deposited on : 2010-10-12
Resolution : 8.80 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

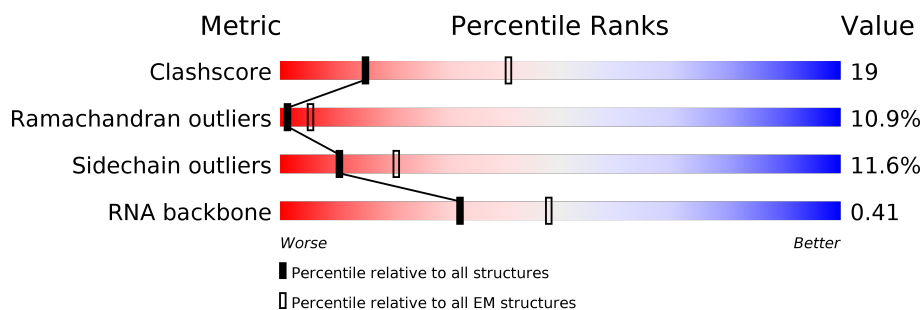
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.80 Å.

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



| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Clashscore | 125131 | 1336 |
| Ramachandran outliers | 121729 | 1120 |
| Sidechain outliers | 121581 | 1026 |
| RNA backbone | 3398 | 335 |

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--------------------|
| 1 | Aa | 319 | 72% 19% 8% . |
| 2 | AA | 252 | 57% 26% 10% 7% |
| 3 | AB | 240 | 45% 23% 13% . 15% |
| 4 | AD | 261 | 34% 23% 13% 7% 23% |
| 5 | AC | 197 | 43% 31% 17% 8% |
| 6 | AE | 254 | 51% 28% 12% 8% |
| 7 | AG | 144 | 74% 17% 8% . |
| 8 | AF | 225 | 53% 24% 9% . 12% |




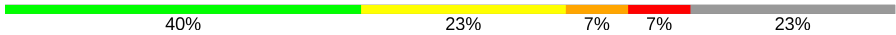

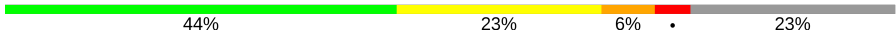

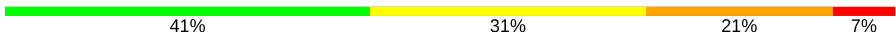

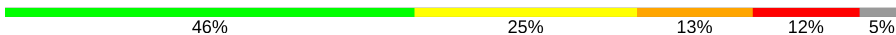

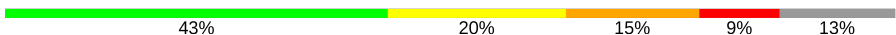













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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 9 | AH | 130 | |
| 10 | AI | 143 | |
| 11 | AJ | 121 | |
| 12 | AK | 137 | |
| 13 | AL | 145 | |
| 14 | AM | 146 | |
| 15 | AN | 56 | |
| 16 | AO | 151 | |
| 17 | AQ | 136 | |
| 18 | AP | 156 | |
| 19 | AR | 142 | |
| 20 | AS | 144 | |
| 21 | AT | 87 | |
| 22 | AV | 108 | |
| 23 | AW | 93 | |
| 24 | AX | 82 | |
| 25 | AY | 67 | |
| 26 | AZ | 63 | |
| 27 | Ab | 37 | |
| 28 | Ac | 26 | |
| 29 | AU | 135 | |
| 30 | BA | 217 | |
| 31 | BB | 254 | |
| 32 | BC | 388 | |
| 33 | BD | 362 | |



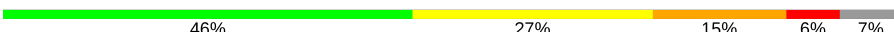











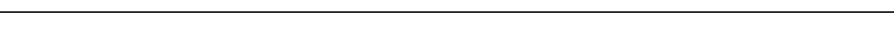
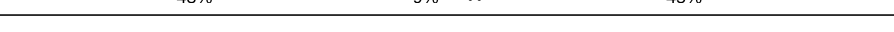
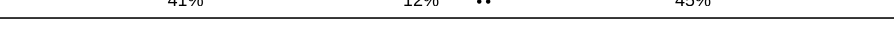
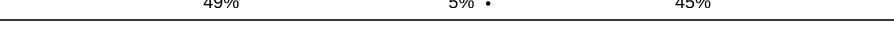
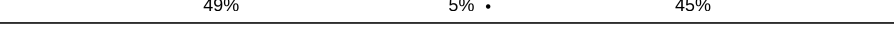


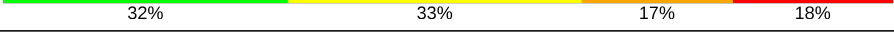



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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 34 | BE | 174 |  |
| 35 | BG | 176 |  |
| 36 | BF | 191 |  |
| 37 | BH | 256 |  |
| 38 | Bs | 312 |  |
| 39 | BJ | 165 |  |
| 40 | BK | 199 |  |
| 41 | BN | 138 |  |
| 42 | BM | 137 |  |
| 43 | BP | 204 |  |
| 44 | BO | 149 |  |
| 45 | BR | 186 |  |
| 46 | BT | 189 |  |
| 47 | BU | 160 |  |
| 48 | BW | 121 |  |
| 49 | BV | 170 |  |
| 50 | BX | 142 |  |
| 51 | BZ | 155 |  |
| 52 | BY | 123 |  |
| 53 | Ba | 136 |  |
| 54 | Bd | 59 |  |
| 55 | Bc | 120 |  |
| 56 | Bf | 105 |  |
| 57 | Be | 244 |  |
| 58 | Bg | 113 |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 59 | Bh | 130 |  |
| 60 | Bi | 118 |  |
| 61 | Bj | 107 |  |
| 62 | Bk | 100 |  |
| 63 | Bm | 92 |  |
| 64 | Bl | 88 |  |
| 65 | Bn | 78 |  |
| 66 | Bo | 51 |  |
| 67 | Bp | 52 |  |
| 68 | Bq | 25 |  |
| 69 | Br | 106 |  |
| 70 | Bx | 21 |  |
| 70 | By | 21 |  |
| 71 | Bz | 15 |  |
| 72 | Bt | 106 |  |
| 72 | Bu | 106 |  |
| 73 | Bv | 106 |  |
| 73 | Bw | 106 |  |
| 74 | BQ | 297 |  |
| 75 | BL | 170 |  |
| 76 | BS | 167 |  |
| 77 | BI | 221 |  |
| 78 | CA | 1800 |  |
| 79 | CB | 75 |  |
| 80 | CC | 11 |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 81 | DA | 3396 | <div><div></div><div>6%37%38%18%</div><div></div></div> |
| 82 | DB | 158 | <div><div></div><div>7%35%39%18%</div><div></div></div> |
| 83 | DC | 118 | <div><div></div><div>24%47%29%</div><div></div></div> |

2 Entry composition [i](#)

There are 83 unique types of molecules in this entry. The entry contains 191627 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S ribosomal protein RACK1 (RACK1).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 1 | Aa | 319 | Total | C | N | O | S | 0 | 0 |
| | | | 2442 | 1544 | 420 | 469 | 9 | | |

- Molecule 2 is a protein called 40S ribosomal protein rpS0 (S2p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 2 | AA | 252 | Total | C | N | O | S | 0 | 0 |
| | | | 1922 | 1204 | 336 | 380 | 2 | | |

- Molecule 3 is a protein called 40S ribosomal protein rpS3 (S3p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 3 | AB | 204 | Total | C | N | O | S | 0 | 0 |
| | | | 1511 | 945 | 282 | 278 | 6 | | |

- Molecule 4 is a protein called 40S ribosomal protein rpS4 (S4e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 4 | AD | 200 | Total | C | N | O | S | 0 | 0 |
| | | | 1591 | 1018 | 288 | 283 | 2 | | |

- Molecule 5 is a protein called 40S ribosomal protein rpS9 (S4p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 5 | AC | 197 | Total | C | N | O | S | 0 | 0 |
| | | | 1521 | 951 | 298 | 270 | 2 | | |

- Molecule 6 is a protein called 40S ribosomal protein rpS2 (S5p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 6 | AE | 254 | Total | C | N | O | S | 0 | 0 |
| | | | 1936 | 1224 | 360 | 349 | 3 | | |

- Molecule 7 is a protein called 40S ribosomal protein rpS7 (S7e).

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 7 | AG | 143 | Total | C | N | O | 0 | 0 |
| | | | 716 | 429 | 143 | 144 | | |

- Molecule 8 is a protein called 40S ribosomal protein rpS5 (S7p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 8 | AF | 199 | Total | C | N | O | S | 0 | 0 |
| | | | 1543 | 958 | 293 | 289 | 3 | | |

- Molecule 9 is a protein called 40S ribosomal protein rpS22 (S8p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 9 | AH | 130 | Total | C | N | O | S | 0 | 0 |
| | | | 1030 | 655 | 189 | 182 | 4 | | |

- Molecule 10 is a protein called 40S ribosomal protein rpS16 (S9p).

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 10 | AI | 126 | Total | C | N | O | 0 | 0 |
| | | | 998 | 639 | 184 | 175 | | |

- Molecule 11 is a protein called 40S ribosomal protein rpS20 (S10p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 11 | AJ | 113 | Total | C | N | O | S | 0 | 0 |
| | | | 849 | 528 | 158 | 162 | 1 | | |

- Molecule 12 is a protein called 40S ribosomal protein rpS14 (S11p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12 | AK | 119 | Total | C | N | O | S | 0 | 0 |
| | | | 833 | 508 | 157 | 165 | 3 | | |

- Molecule 13 is a protein called 40S ribosomal protein rpS23 (S12p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 13 | AL | 145 | Total | C | N | O | S | 0 | 0 |
| | | | 978 | 588 | 203 | 184 | 3 | | |

- Molecule 14 is a protein called 40S ribosomal protein rpS18 (S13p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 14 | AM | 140 | Total | C | N | O | S | 0 | 0 |
| | | | 1156 | 719 | 231 | 204 | 2 | | |

- Molecule 15 is a protein called 40S ribosomal protein rpS29 (S14p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 15 | AN | 48 | Total | C | N | O | S | 0 | 0 |
| | | | 353 | 209 | 79 | 61 | 4 | | |

- Molecule 16 is a protein called 40S ribosomal protein rpS13 (S15p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16 | AO | 121 | Total | C | N | O | S | 0 | 0 |
| | | | 978 | 624 | 183 | 170 | 1 | | |

- Molecule 17 is a protein called 40S ribosomal protein rpS17 (S17e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17 | AQ | 136 | Total | C | N | O | S | 0 | 0 |
| | | | 1098 | 682 | 213 | 201 | 2 | | |

- Molecule 18 is a protein called 40S ribosomal protein rpS11 (S17p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 18 | AP | 85 | Total | C | N | O | S | 0 | 0 |
| | | | 631 | 402 | 124 | 104 | 1 | | |

- Molecule 19 is a protein called 40S ribosomal protein rpS15 (S19p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19 | AR | 88 | Total | C | N | O | S | 0 | 0 |
| | | | 676 | 429 | 123 | 118 | 6 | | |

- Molecule 20 is a protein called 40S ribosomal protein rpS19 (S19e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20 | AS | 144 | Total | C | N | O | S | 0 | 0 |
| | | | 1120 | 699 | 209 | 209 | 3 | | |

- Molecule 21 is a protein called 40S ribosomal protein rpS21 (S21e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21 | AT | 87 | Total | C | N | O | S | 0 | 0 |
| | | | 685 | 420 | 125 | 138 | 2 | | |

- Molecule 22 is a protein called 40S ribosomal protein rpS25 (S25e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 22 | AV | 85 | Total | C | N | O | S | 0 | 0 |
| | | | 688 | 437 | 128 | 122 | 1 | | |

- Molecule 23 is a protein called 40S ribosomal protein rpS26 (S26e).

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 23 | AW | 92 | Total | C | N | O | 0 | 0 |
| | | | 461 | 276 | 92 | 93 | | |

- Molecule 24 is a protein called 40S ribosomal protein rpS27 (S27e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 24 | AX | 50 | Total | C | N | O | S | 0 | 0 |
| | | | 366 | 229 | 60 | 72 | 5 | | |

- Molecule 25 is a protein called 40S ribosomal protein rpS28 (S28e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 25 | AY | 60 | Total | C | N | O | S | 0 | 0 |
| | | | 445 | 276 | 80 | 87 | 2 | | |

- Molecule 26 is a protein called 40S ribosomal protein rpS30 (S30e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 26 | AZ | 63 | Total | C | N | O | S | 0 | 0 |
| | | | 492 | 307 | 102 | 81 | 2 | | |

- Molecule 27 is a protein called Unknown 40S ribosomal protein XS1.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 27 | Ab | 36 | Total | C | N | O | 0 | 0 |
| | | | 181 | 108 | 36 | 37 | | |

- Molecule 28 is a protein called Unknown 40S ribosomal protein XS2.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---------|-------|
| 28 | Ac | 25 | Total | C | N | O | 0 | 0 |
| | | | 126 | 75 | 25 | 26 | | |

- Molecule 29 is a protein called 40S ribosomal protein S24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29 | AU | 96 | Total | C | N | O | S | 0 | 0 |
| | | | 714 | 450 | 134 | 129 | 1 | | |

- Molecule 30 is a protein called 60S ribosomal protein rpL1 (L1p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 30 | BA | 217 | Total | C | N | O | S | 0 | 0 |
| | | | 1718 | 1097 | 299 | 312 | 10 | | |

- Molecule 31 is a protein called 60S ribosomal protein rpL2 (L2p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 31 | BB | 254 | Total | C | N | O | S | 0 | 0 |
| | | | 1904 | 1183 | 385 | 334 | 2 | | |

- Molecule 32 is a protein called 60S ribosomal protein rpL3 (L3p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 32 | BC | 388 | Total | C | N | O | S | 0 | 0 |
| | | | 3055 | 1933 | 579 | 534 | 9 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| BC | 388 | GLY | - | EXPRESSION TAG | UNP P14126 |

- Molecule 33 is a protein called 60S ribosomal protein rpL4 (L4p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 33 | BD | 329 | Total | C | N | O | S | 0 | 0 |
| | | | 2486 | 1564 | 480 | 438 | 4 | | |

- Molecule 34 is a protein called 60S ribosomal protein rpL11 (L5p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 34 | BE | 168 | Total | C | N | O | S | 0 | 0 |
| | | | 1341 | 839 | 252 | 245 | 5 | | |

- Molecule 35 is a protein called 60S ribosomal protein rpL6 (L6e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 35 | BG | 176 | Total | C | N | O | S | 0 | 0 |
| | | | 1409 | 907 | 252 | 248 | 2 | | |

- Molecule 36 is a protein called 60S ribosomal protein rpL9 (L6p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 36 | BF | 191 | Total | C | N | O | S | 0 | 0 |
| | | | 1516 | 961 | 274 | 277 | 4 | | |

- Molecule 37 is a protein called 60S ribosomal protein rpL8 (L7ae).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 37 | BH | 197 | Total | C | N | O | S | 0 | 0 |
| | | | 1505 | 959 | 269 | 274 | 3 | | |

- Molecule 38 is a protein called 60S acidic ribosomal protein rpP0 (L10P).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 38 | Bs | 257 | Total | C | N | O | S | 0 | 0 |
| | | | 1976 | 1269 | 334 | 368 | 5 | | |

- Molecule 39 is a protein called 60S ribosomal protein rpL12 (L11p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 39 | BJ | 127 | Total | C | N | O | S | 0 | 0 |
| | | | 954 | 601 | 174 | 178 | 1 | | |

- Molecule 40 is a protein called 60S ribosomal protein rpL16 (L13p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 40 | BK | 199 | Total | C | N | O | S | 0 | 0 |
| | | | 1570 | 1011 | 291 | 266 | 2 | | |

- Molecule 41 is a protein called 60S ribosomal protein rpL14 (L14e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 41 | BN | 138 | Total | C | N | O | S | 0 | 0 |
| | | | 1068 | 683 | 201 | 181 | 3 | | |

- Molecule 42 is a protein called 60S ribosomal protein rpL23 (L14p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42 | BM | 131 | Total | C | N | O | S | 0 | 0 |
| | | | 972 | 611 | 182 | 172 | 7 | | |

- Molecule 43 is a protein called 60S ribosomal protein rpL15 (L15e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 43 | BP | 193 | Total | C | N | O | S | 0 | 0 |
| | | | 1625 | 1016 | 341 | 266 | 2 | | |

- Molecule 44 is a protein called 60S ribosomal protein rpL28 (L15p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 44 | BO | 149 | Total | C | N | O | S | 0 | 0 |
| | | | 1182 | 754 | 232 | 192 | 4 | | |

- Molecule 45 is a protein called 60S ribosomal protein rpL18 (L18e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 45 | BR | 161 | Total | C | N | O | S | 0 | 0 |
| | | | 1243 | 786 | 242 | 212 | 3 | | |

- Molecule 46 is a protein called 60S ribosomal protein rpL19 (L19e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 46 | BT | 189 | Total | C | N | O | S | 0 | 0 |
| | | | 1530 | 940 | 327 | 262 | 1 | | |

- Molecule 47 is a protein called 60S ribosomal protein rpL21 (L21e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 47 | BU | 160 | Total | C | N | O | S | 0 | 0 |
| | | | 1261 | 793 | 242 | 222 | 4 | | |

- Molecule 48 is a protein called 60S ribosomal protein rpL22 (L22e).

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 48 | BW | 105 | Total | C | N | O | 0 | 0 |
| | | | 830 | 535 | 140 | 155 | | |

- Molecule 49 is a protein called 60S ribosomal protein rpL17 (L22p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 49 | BV | 170 | Total | C | N | O | S | 0 | 0 |
| | | | 1312 | 814 | 254 | 243 | 1 | | |

- Molecule 50 is a protein called 60S ribosomal protein rpL25 (L23p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 50 | BX | 122 | Total | C | N | O | S | 0 | 0 |
| | | | 978 | 629 | 172 | 175 | 2 | | |

- Molecule 51 is a protein called 60S ribosomal protein rpL24 (L24e).

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---------|-------|
| 51 | BZ | 73 | Total | C | N | O | 0 | 0 |
| | | | 579 | 366 | 115 | 98 | | |

- Molecule 52 is a protein called 60S ribosomal protein rpL26 (L24p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 52 | BY | 123 | Total | C | N | O | S | 0 | 0 |
| | | | 972 | 611 | 188 | 172 | 1 | | |

- Molecule 53 is a protein called 60S ribosomal protein rpL27 (L27e).

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 53 | Ba | 95 | Total | C | N | O | 0 | 0 |
| | | | 708 | 455 | 134 | 119 | | |

- Molecule 54 is a protein called 60S ribosomal protein rpL29 (L29e).

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 54 | Bd | 22 | Total | C | N | O | 0 | 0 |
| | | | 174 | 109 | 40 | 25 | | |

- Molecule 55 is a protein called 60S ribosomal protein rpL35 (L29p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 55 | Bc | 118 | Total | C | N | O | S | 0 | 0 |
| | | | 965 | 612 | 185 | 167 | 1 | | |

- Molecule 56 is a protein called 60S ribosomal protein rpL30 (L30e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 56 | Bf | 105 | Total | C | N | O | S | 0 | 0 |
| | | | 785 | 501 | 133 | 150 | 1 | | |

- Molecule 57 is a protein called 60S ribosomal protein rpL7 (L30p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 57 | Be | 239 | Total | C | N | O | S | 0 | 0 |
| | | | 1919 | 1235 | 348 | 335 | 1 | | |

- Molecule 58 is a protein called 60S ribosomal protein rpL31 (L31e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 58 | Bg | 110 | Total | C | N | O | S | 0 | 0 |
| | | | 873 | 552 | 169 | 150 | 2 | | |

- Molecule 59 is a protein called 60S ribosomal protein pL32 (L32e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 59 | Bh | 130 | Total | C | N | O | S | 0 | 0 |
| | | | 1043 | 660 | 208 | 173 | 2 | | |

- Molecule 60 is a protein called 60S ribosomal protein rpL34 (L34e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 60 | Bi | 118 | Total | C | N | O | S | 0 | 0 |
| | | | 926 | 572 | 188 | 161 | 5 | | |

- Molecule 61 is a protein called 60S ribosomal protein rpL33 (L35ae).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 61 | Bj | 100 | Total | C | N | O | S | 0 | 0 |
| | | | 738 | 461 | 147 | 128 | 2 | | |

- Molecule 62 is a protein called 60S ribosomal protein rpL36 (L36e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 62 | Bk | 77 | Total | C | N | O | S | 0 | 0 |
| | | | 619 | 384 | 129 | 105 | 1 | | |

- Molecule 63 is a protein called 60S ribosomal protein rpL43 (L37ae).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 63 | Bm | 92 | Total | C | N | O | S | 0 | 0 |
| | | | 703 | 434 | 139 | 123 | 7 | | |

- Molecule 64 is a protein called 60S ribosomal protein rpL37 (L37e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 64 | Bl | 88 | Total | C | N | O | S | 0 | 0 |
| | | | 678 | 410 | 148 | 114 | 6 | | |

- Molecule 65 is a protein called 60S ribosomal protein rpL38 (L38e).

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 65 | Bn | 78 | Total | C | N | O | 0 | 0 |
| | | | 604 | 385 | 113 | 106 | | |

- Molecule 66 is a protein called 60S ribosomal protein rpL39 (L39e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 66 | Bo | 51 | Total | C | N | O | S | 0 | 0 |
| | | | 445 | 277 | 98 | 67 | 3 | | |

- Molecule 67 is a protein called 60S ribosomal protein rpL40 (L40e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 67 | Bp | 40 | Total | C | N | O | S | 0 | 0 |
| | | | 330 | 201 | 72 | 52 | 5 | | |

- Molecule 68 is a protein called 60S ribosomal protein rpL41 (L41e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 68 | Bq | 25 | Total | C | N | O | S | 0 | 0 |
| | | | 234 | 142 | 63 | 28 | 1 | | |

- Molecule 69 is a protein called 60S ribosomal protein rpL42 (L44e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 69 | Br | 106 | Total | C | N | O | S | 0 | 0 |
| | | | 834 | 521 | 169 | 138 | 6 | | |

- Molecule 70 is a protein called Unknown protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|--|---------|-------|
| 70 | Bx | 20 | Total | C | N | O | | 0 | 0 |
| | | | 100 | 60 | 20 | 20 | | | |
| 70 | By | 20 | Total | C | N | O | | 0 | 0 |
| | | | 100 | 60 | 20 | 20 | | | |

- Molecule 71 is a protein called Unknown protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|--|---------|-------|
| 71 | Bz | 14 | Total | C | N | O | | 0 | 0 |
| | | | 70 | 42 | 14 | 14 | | | |

- Molecule 72 is a protein called 60S acidic ribosomal protein rpP11 (P1).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|--|---------|-------|
| 72 | Bt | 58 | Total | C | N | O | | 0 | 0 |
| | | | 440 | 281 | 68 | 91 | | | |
| 72 | Bu | 58 | Total | C | N | O | | 0 | 0 |
| | | | 440 | 281 | 68 | 91 | | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| Bt | 37 | ASP | VAL | CONFLICT | UNP P05318 |
| Bu | 37 | ASP | VAL | CONFLICT | UNP P05318 |

- Molecule 73 is a protein called 60S acidic ribosomal protein (P2).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 73 | Bv | 58 | Total | C | N | O | S | 0 | 0 |
| | | | 429 | 271 | 66 | 91 | 1 | | |
| 73 | Bw | 58 | Total | C | N | O | S | 0 | 0 |
| | | | 429 | 271 | 66 | 91 | 1 | | |

- Molecule 74 is a protein called 60S ribosomal protein rpL5 (L18p).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 74 | BQ | 297 | Total | C | N | O | S | 0 | 0 |
| | | | 2356 | 1485 | 414 | 454 | 3 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| BQ | 112 | ARG | LYS | CONFLICT | UNP P26321 |

- Molecule 75 is a protein called 60S ribosomal protein rpL13 (L13e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 75 | BL | 169 | Total | C | N | O | | 0 | 0 |
| | | | 845 | 507 | 169 | 169 | | | |

- Molecule 76 is a protein called 60S ribosomal protein rpL20 (L18ae).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 76 | BS | 167 | Total | C | N | O | S | 0 | 0 |
| | | | 1420 | 916 | 263 | 234 | 7 | | |

- Molecule 77 is a protein called 60S ribosomal protein rpL10 (L10e).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 77 | BI | 181 | Total | C | N | O | S | 0 | 0 |
| | | | 1444 | 907 | 281 | 248 | 8 | | |

- Molecule 78 is a RNA chain called 18S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 78 | CA | 1721 | Total | C | N | O | P | 0 | 10 |
| | | | 33643 | 14904 | 5670 | 11348 | 1721 | | |

- Molecule 79 is a RNA chain called P-SITE TRNA ASP.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 79 | CB | 75 | Total | C | N | O | P | 0 | 0 |
| | | | 1599 | 712 | 280 | 532 | 75 | | |

- Molecule 80 is a RNA chain called MRNA, RNA (5'-R(P*AP*AP*AP*AP*GP*AP*CP*U P*UP*CP*A)-3').

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|----|---------|-------|
| 80 | CC | 11 | Total | C | N | O | P | 0 | 0 |
| | | | 236 | 106 | 45 | 74 | 11 | | |

- Molecule 81 is a RNA chain called 25S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 81 | DA | 3354 | Total | C | N | O | P | 0 | 75 |
| | | | 68830 | 30640 | 12220 | 22616 | 3354 | | |

- Molecule 82 is a RNA chain called 5.8S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|---------|-------|
| 82 | DB | 157 | Total | C | N | O | P | 0 | 0 |
| | | | 3129 | 1391 | 523 | 1058 | 157 | | |

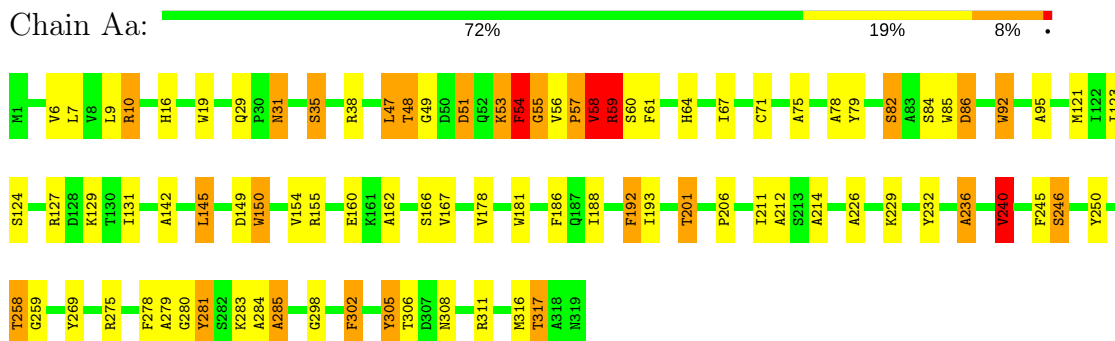
- Molecule 83 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 83 | DC | 118 | Total | C | N | O | P | 0 | 0 |
| | | | 2513 | 1122 | 446 | 827 | 118 | | |

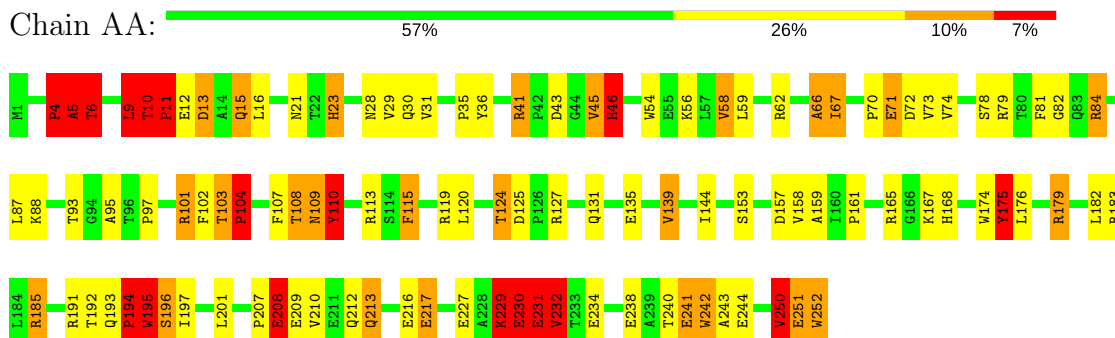
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

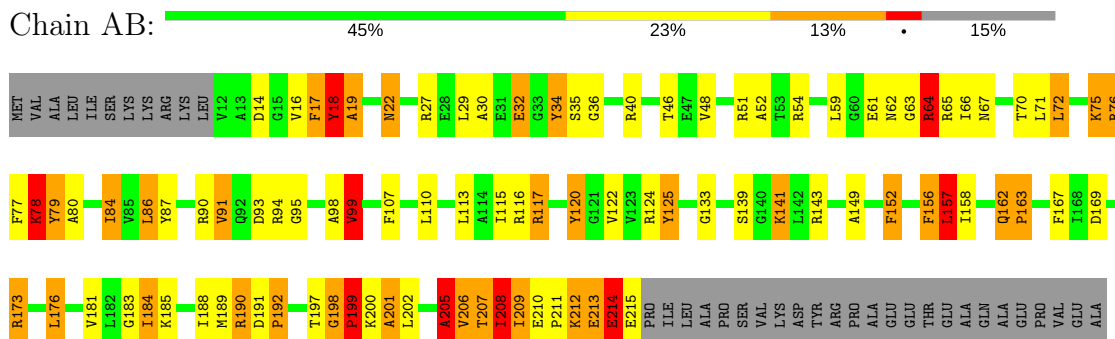
- Molecule 1: 40S ribosomal protein RACK1 (RACK1)



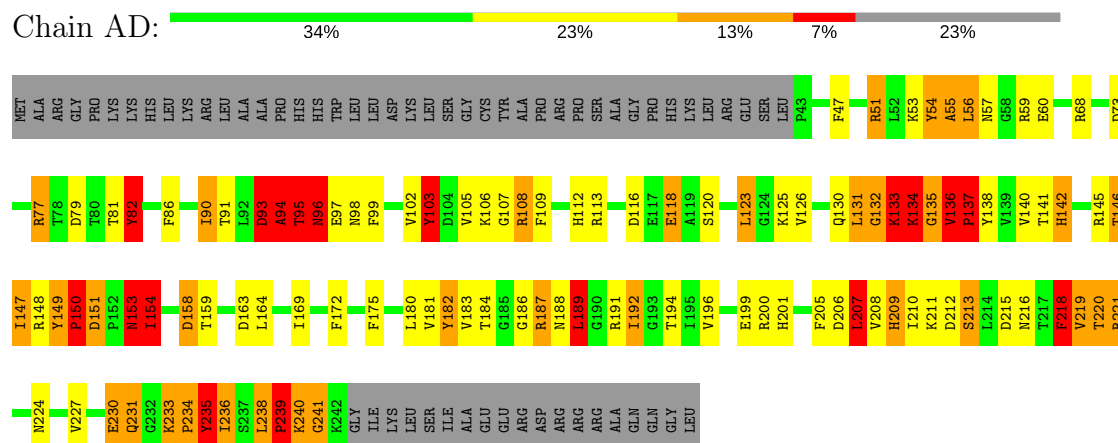
- Molecule 2: 40S ribosomal protein rpS0 (S2p)



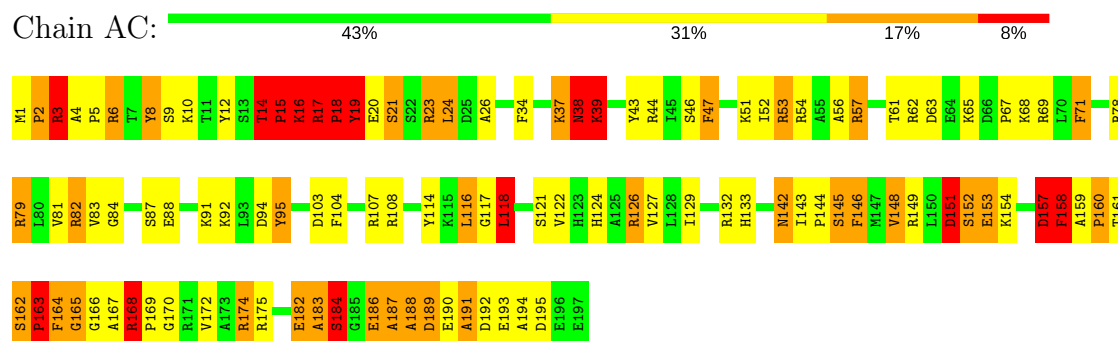
- Molecule 3: 40S ribosomal protein rpS3 (S3p)



- Molecule 4: 40S ribosomal protein rpS4 (S4e)



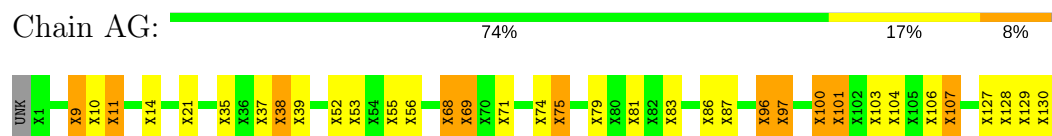
• Molecule 5: 40S ribosomal protein rpS9 (S4p)



• Molecule 6: 40S ribosomal protein rpS2 (S5p)

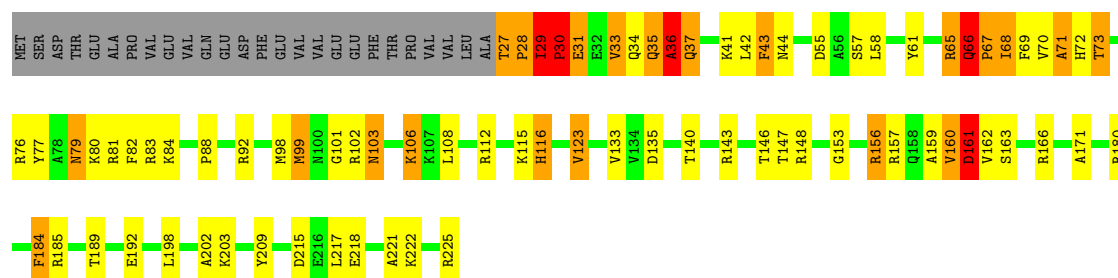


• Molecule 7: 40S ribosomal protein rpS7 (S7e)



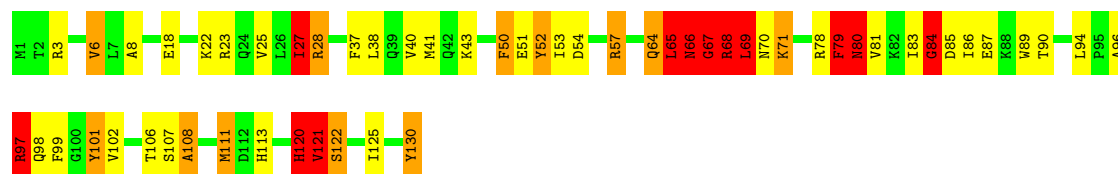
• Molecule 8: 40S ribosomal protein rpS5 (S7p)





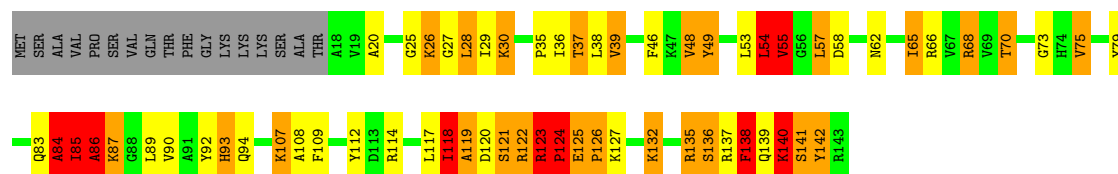
- Molecule 9: 40S ribosomal protein rpS22 (S8p)

Chain AH: 57% 25% 9% 9%



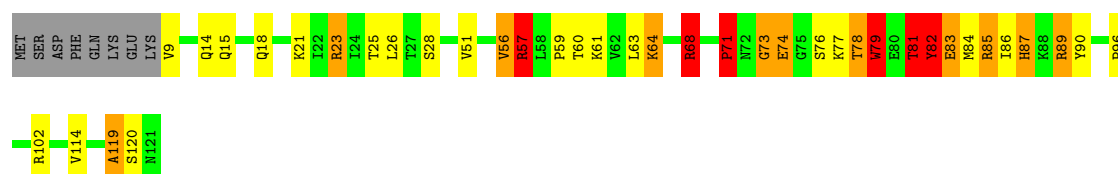
- Molecule 10: 40S ribosomal protein rpS16 (S9p)

Chain AI: 44% 20% 17% 7% 12%



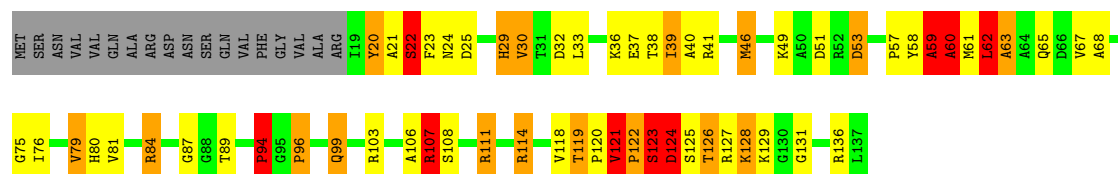
- Molecule 11: 40S ribosomal protein rpS20 (S10p)

Chain AJ: 61% 18% 9% 5% 7%

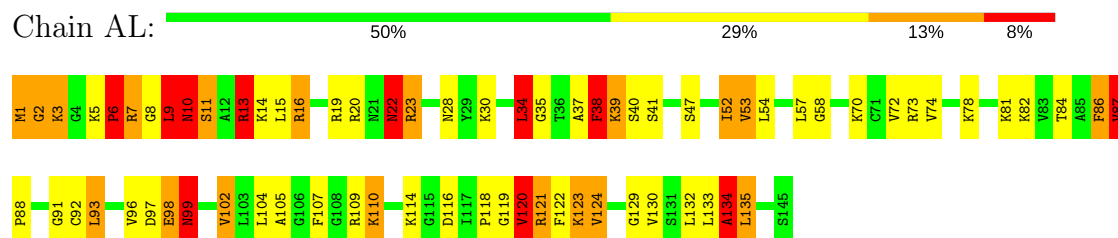


- Molecule 12: 40S ribosomal protein rpS14 (S11p)

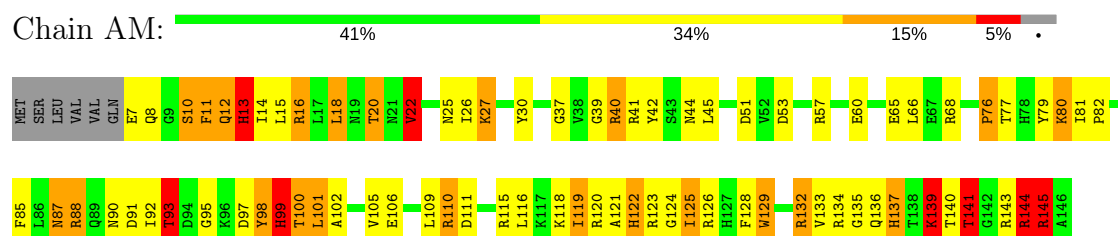
Chain AK: 42% 26% 12% 7% 13%



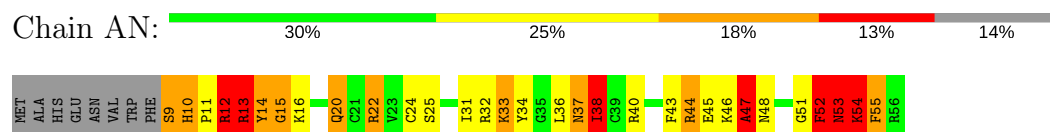
- Molecule 13: 40S ribosomal protein rpS23 (S12p)



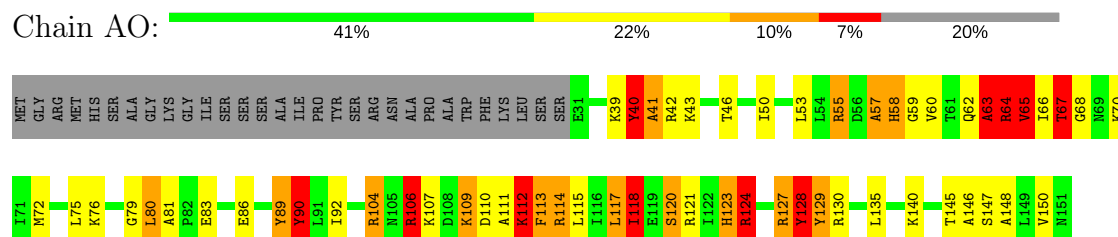
- Molecule 14: 40S ribosomal protein rpS18 (S13p)



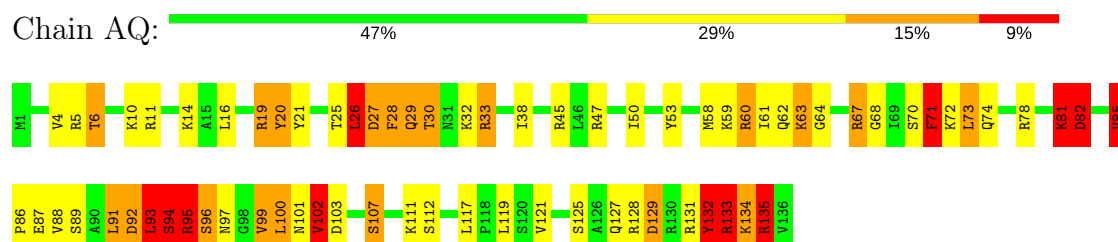
- Molecule 15: 40S ribosomal protein rpS29 (S14p)



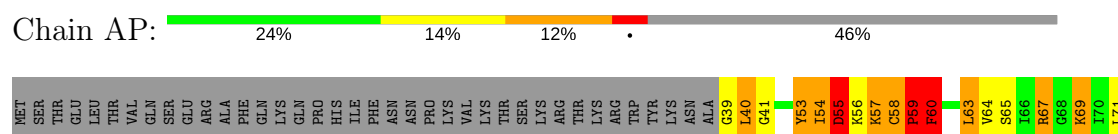
- Molecule 16: 40S ribosomal protein rpS13 (S15p)

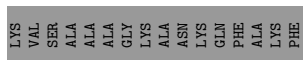



- Molecule 17: 40S ribosomal protein rpS17 (S17e)



- Molecule 18: 40S ribosomal protein rpS11 (S17p)

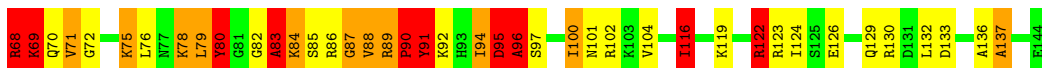




- Chain AR: 



- Chain AS:

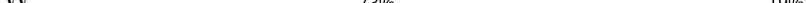


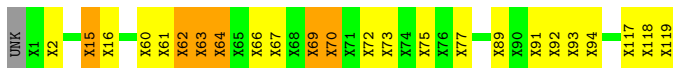
- Chain AT: 




- Chain AV: 



- Chain AW:  73% 19% 6%



- 


Chain AX: 



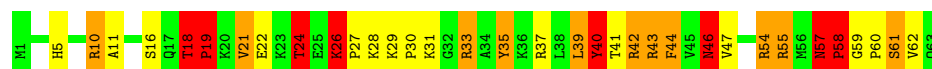
- Molecule 25: 40S ribosomal protein rpS28 (S28e)

Chain AY: 



- Molecule 26: 40S ribosomal protein rpS30 (S30e)

Chain AZ: 



- Molecule 27: Unknown 40S ribosomal protein XS1

Chain Ab: 




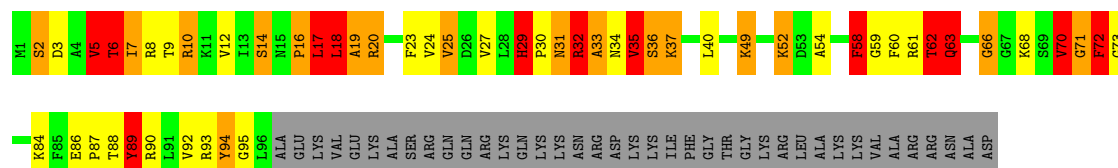
- Molecule 28: Unknown 40S ribosomal protein XS2

Chain Ac: 



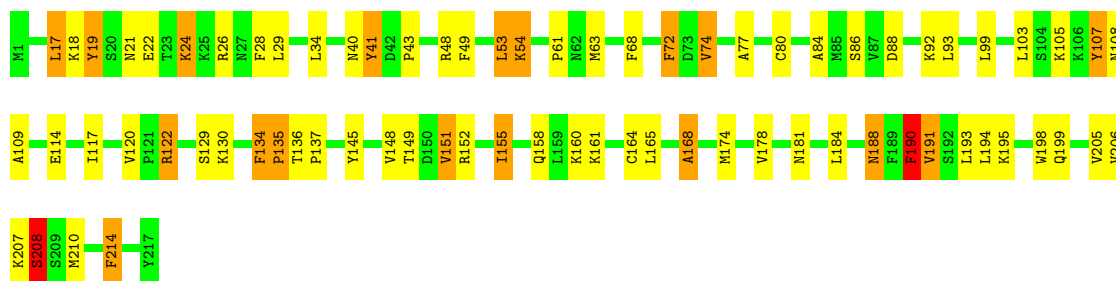
- Molecule 29: 40S ribosomal protein S24

Chain AU: 



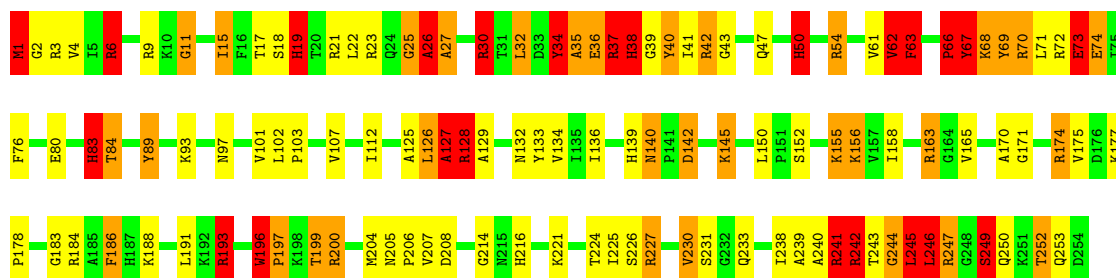
- Molecule 30: 60S ribosomal protein rpL1 (L1p)

Chain BA: 



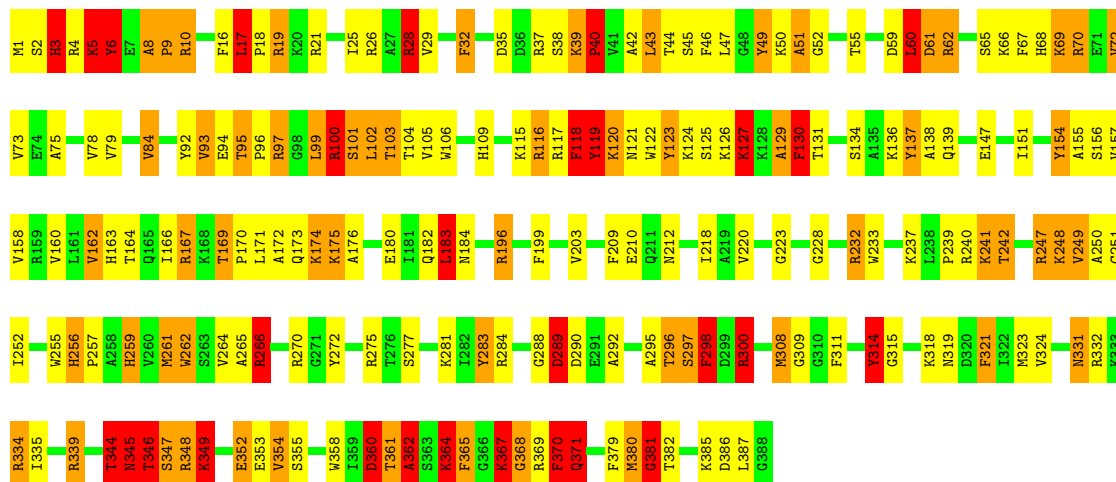
- Molecule 31: 60S ribosomal protein rpL2 (L2p)

Chain BB: 



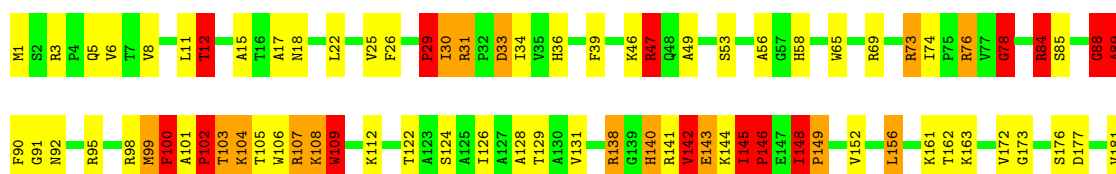
- Molecule 32: 60S ribosomal protein rpL3 (L3p)

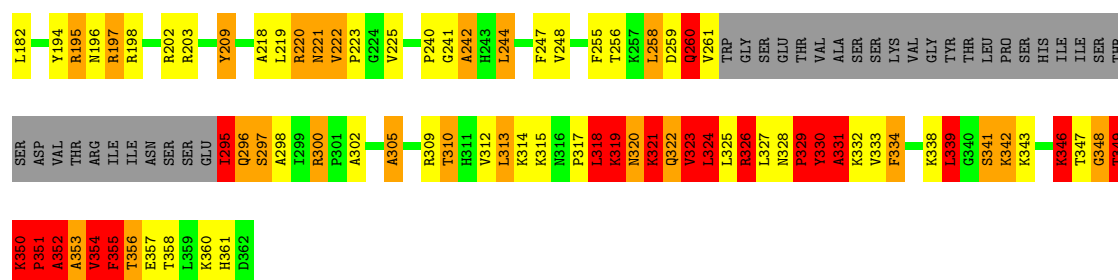
Chain BC: 



- Molecule 33: 60S ribosomal protein rpL4 (L4p)

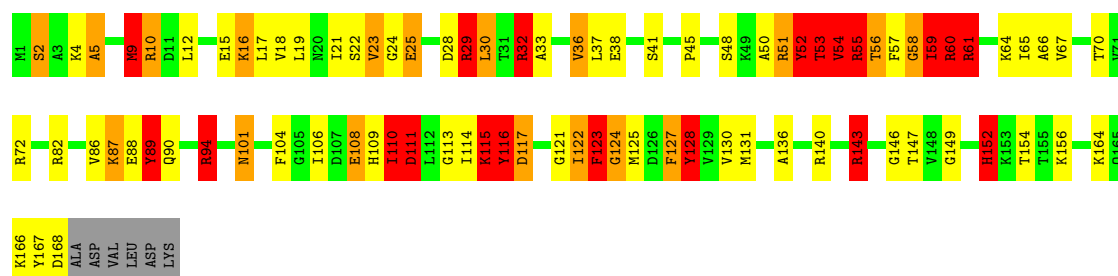
Chain BD: 





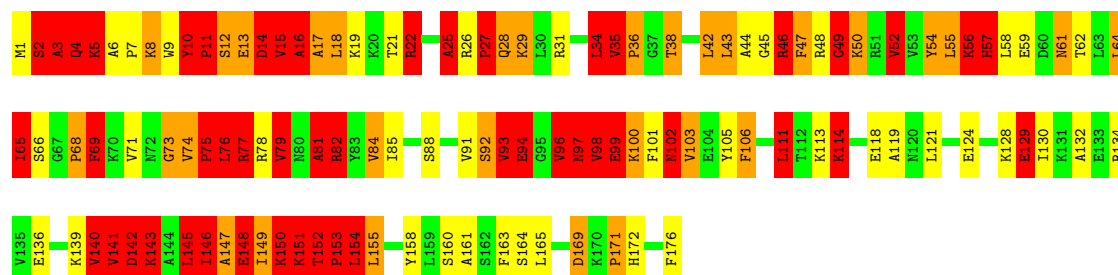
• Molecule 34: 60S ribosomal protein rpL11 (L5p)

Chain BE: 47% 28% 10% 11% .



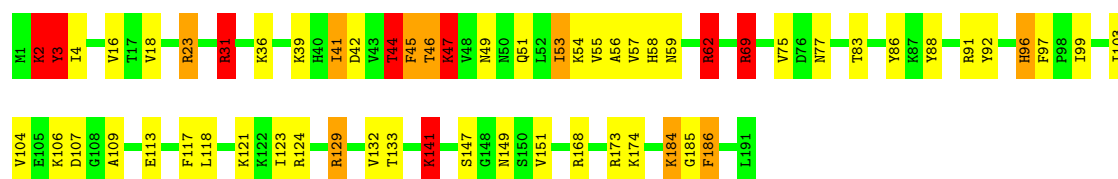
• Molecule 35: 60S ribosomal protein rpL6 (L6e)

Chain BG: 32% 23% 17% 28% .



• Molecule 36: 60S ribosomal protein rpL9 (L6p)

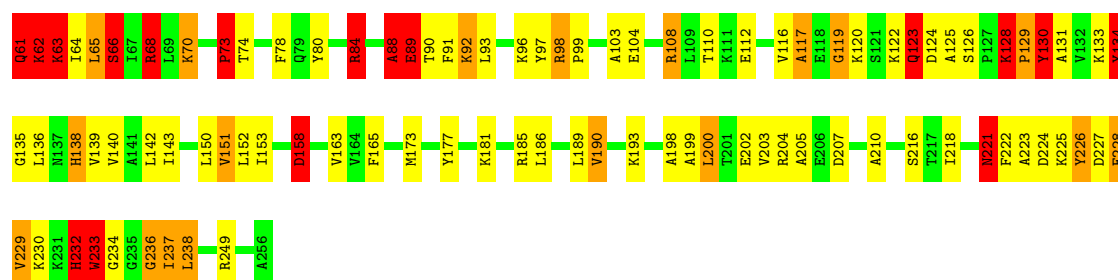
Chain BF: 69% 23% 5% .



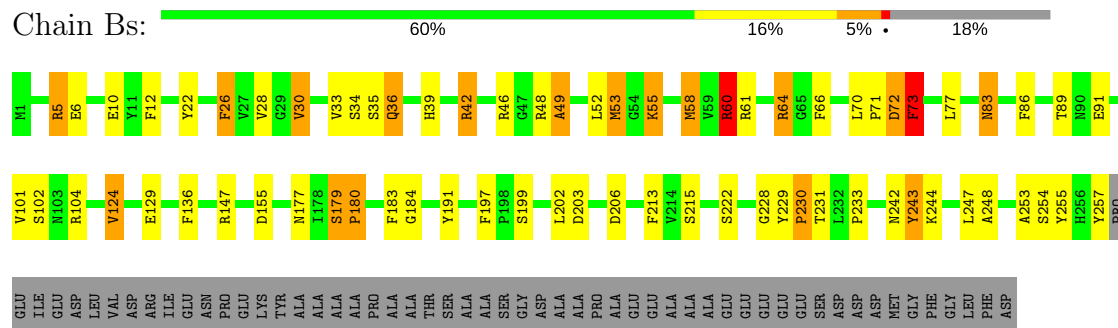
• Molecule 37: 60S ribosomal protein rpL8 (L7ae)

Chain BH: 40% 23% 7% 7% 23%

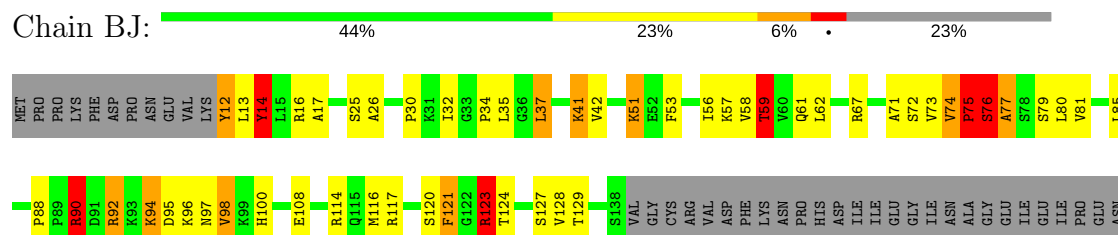




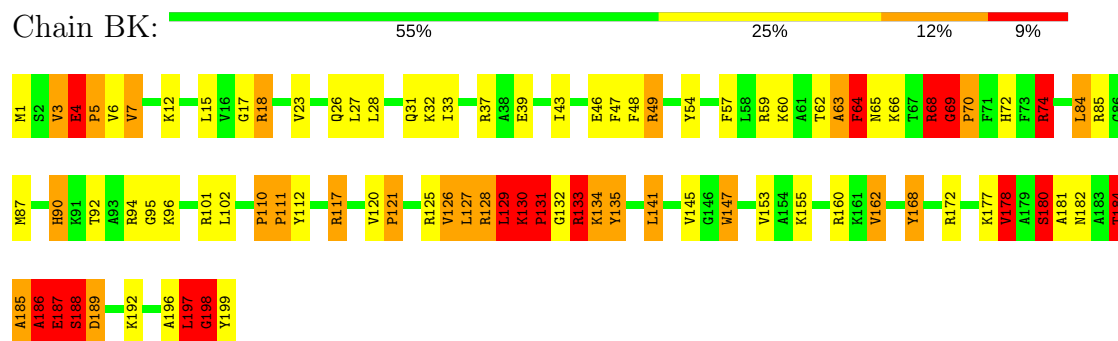
- Molecule 38: 60S acidic ribosomal protein rpP0 (L10P)



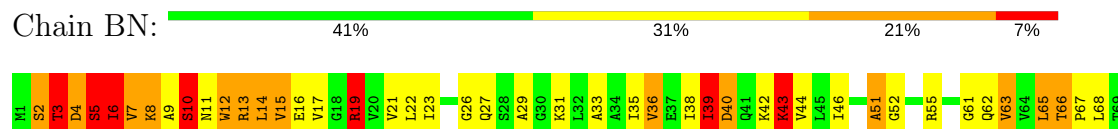
- Molecule 39: 60S ribosomal protein rpL12 (L11p)



- Molecule 40: 60S ribosomal protein rpL16 (L13p)



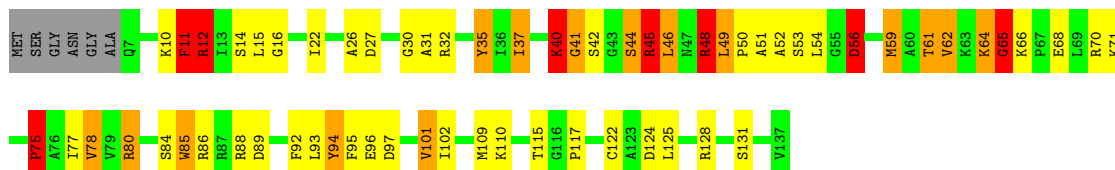
- Molecule 41: 60S ribosomal protein rpL14 (L14e)





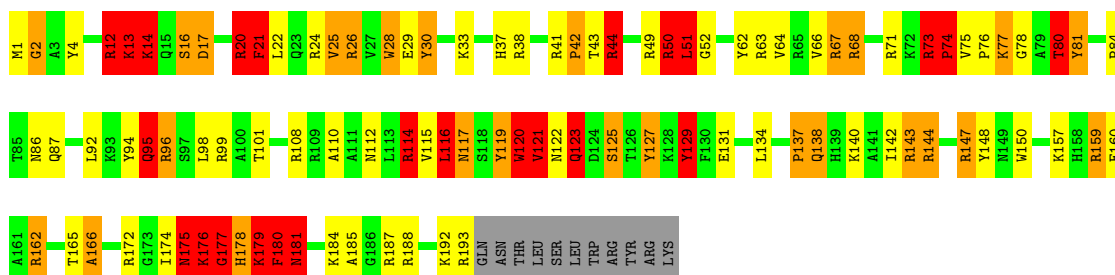
• Molecule 42: 60S ribosomal protein rpL23 (L14p)

Chain BM: 50% 29% 11% 6%



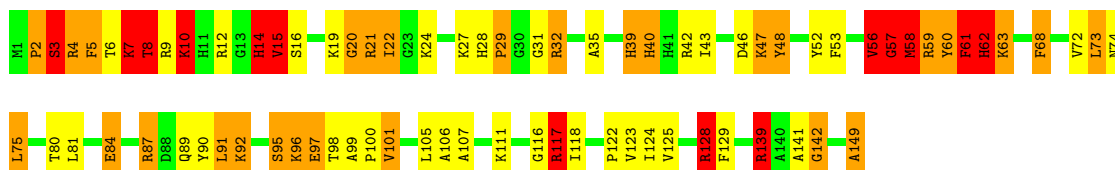
• Molecule 43: 60S ribosomal protein rpL15 (L15e)

Chain BP: 46% 25% 13% 12% 5%



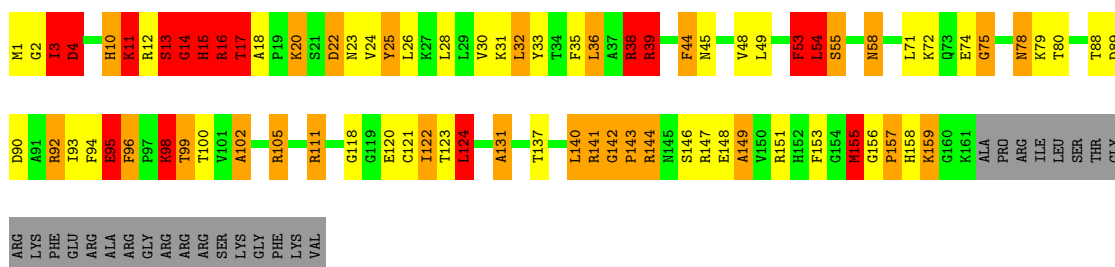
• Molecule 44: 60S ribosomal protein rpL28 (L15p)

Chain BO: 48% 24% 19% 9%

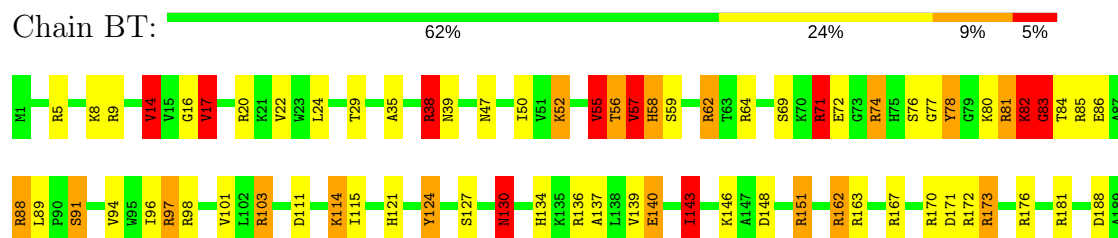


• Molecule 45: 60S ribosomal protein rpL18 (L18e)

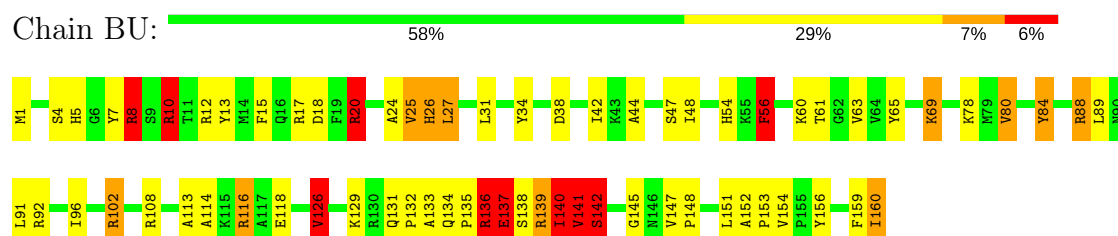
Chain BR: 43% 20% 15% 9% 13%



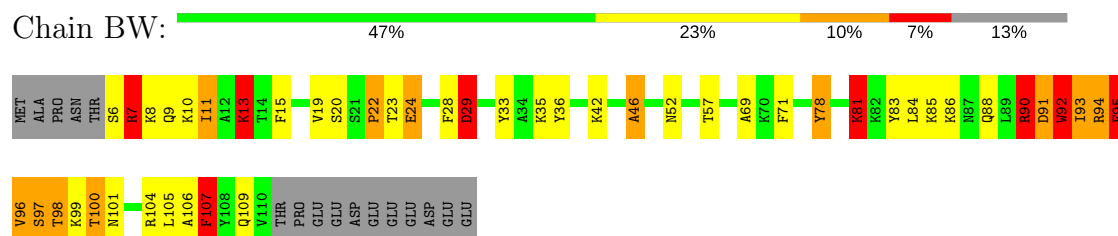
• Molecule 46: 60S ribosomal protein rpL19 (L19e)



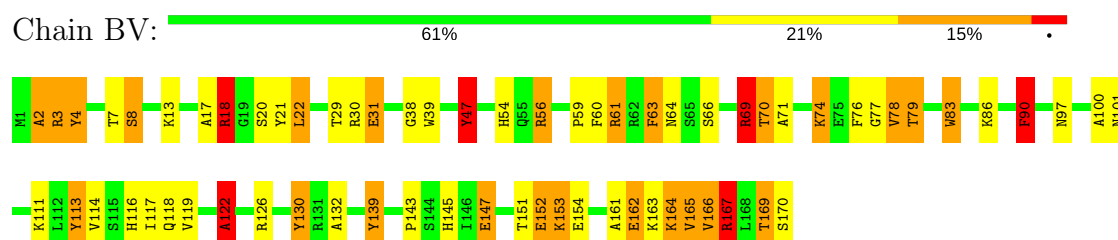
- Molecule 47: 60S ribosomal protein rpL21 (L21e)



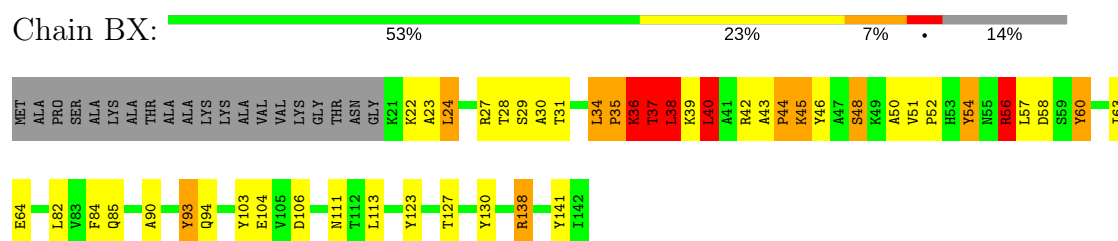
- Molecule 48: 60S ribosomal protein rpL22 (L22e)



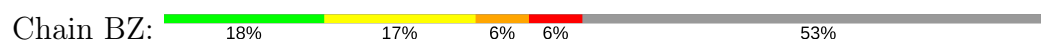
- Molecule 49: 60S ribosomal protein rpL17 (L22p)

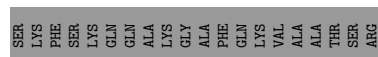
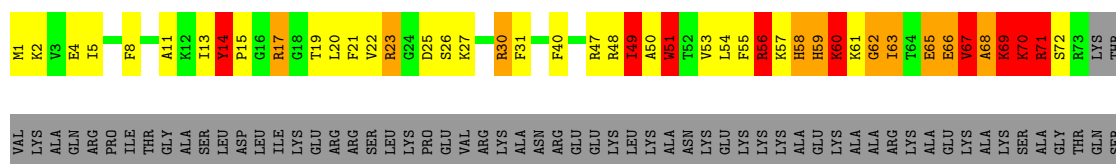


- Molecule 50: 60S ribosomal protein rpL25 (L23p)



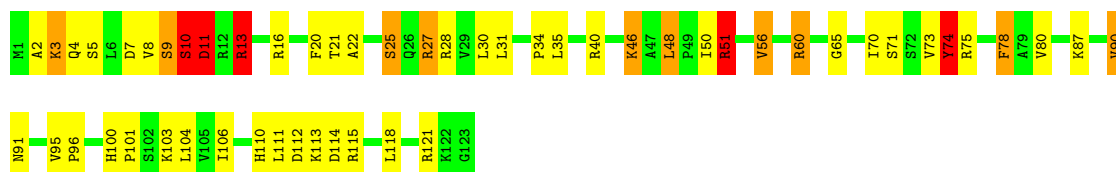
- Molecule 51: 60S ribosomal protein rpL24 (L24e)





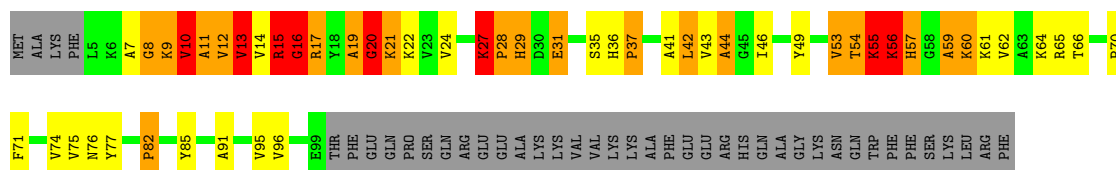
- Molecule 52: 60S ribosomal protein rpL26 (L24p)

Chain BY: 56% 32% 8%



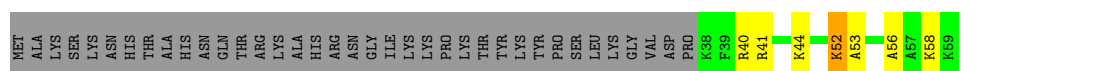
- Molecule 53: 60S ribosomal protein rpL27 (L27e)

Chain Ba: 32% 18% 14% 6% 30%



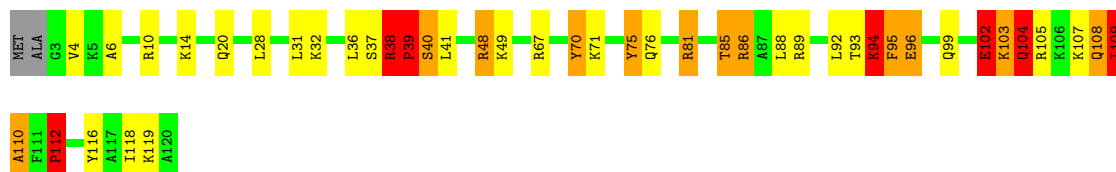
- Molecule 54: 60S ribosomal protein rpL29 (L29e)

Chain Bd: 25% 10% 63%



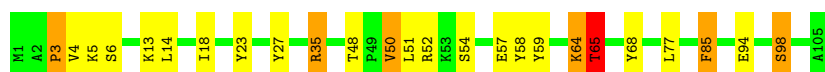
- Molecule 55: 60S ribosomal protein rpL35 (L29p)

Chain Bc: 62% 21% 10% 6%

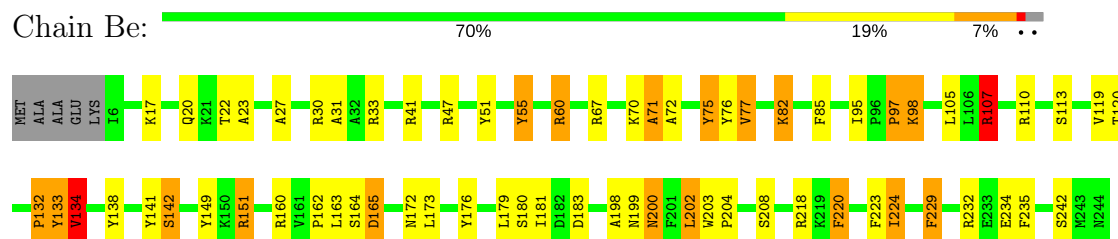


- Molecule 56: 60S ribosomal protein rpL30 (L30e)

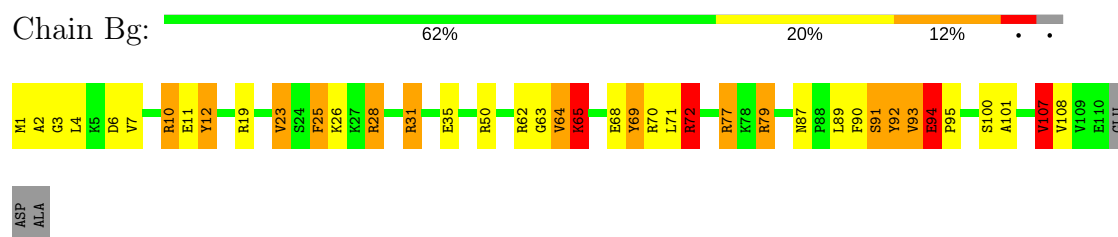
Chain Bf: 76% 17% 6%



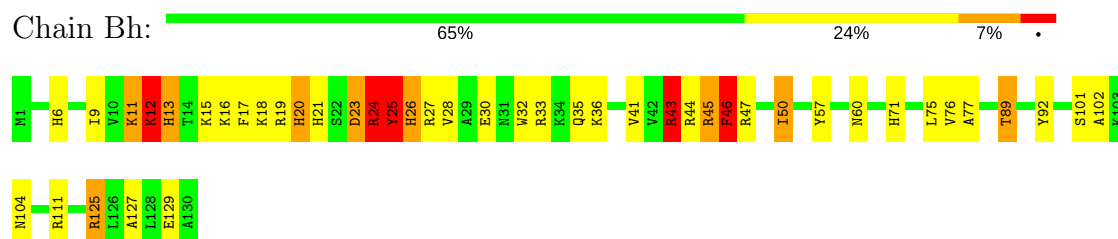
- Molecule 57: 60S ribosomal protein rpL7 (L30p)



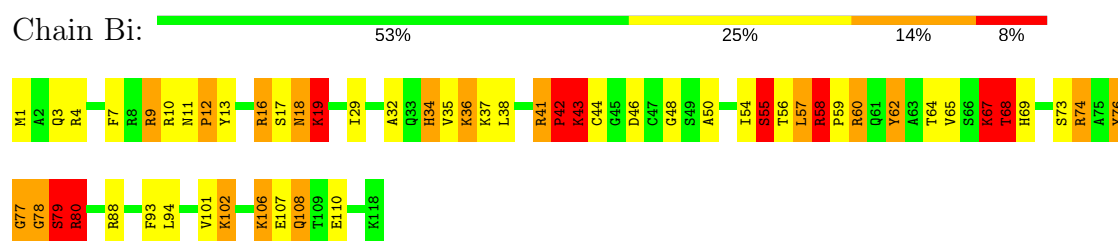
- Molecule 58: 60S ribosomal protein rpL31 (L31e)



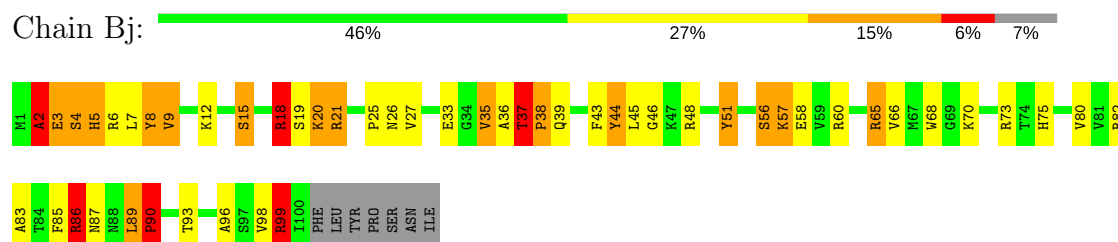
- Molecule 59: 60S ribosomal protein pL32 (L32e)



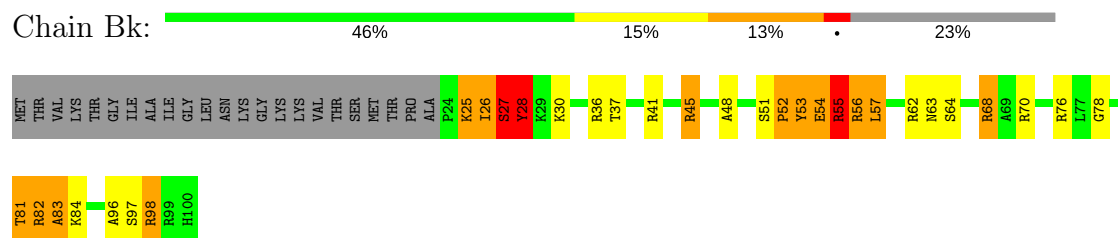
- Molecule 60: 60S ribosomal protein rpL34 (L34e)



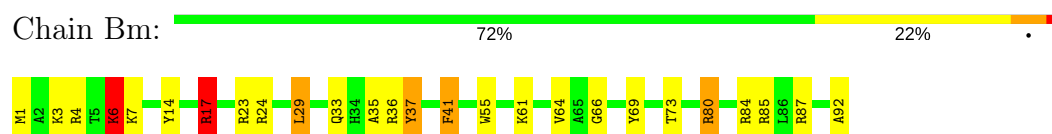
- Molecule 61: 60S ribosomal protein rpL33 (L35ae)



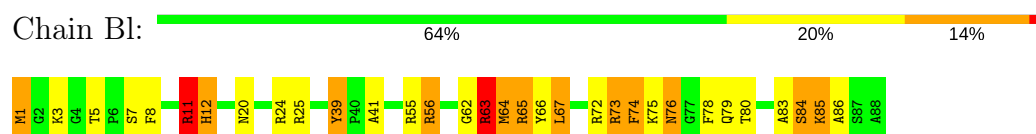
- Molecule 62: 60S ribosomal protein rpL36 (L36e)



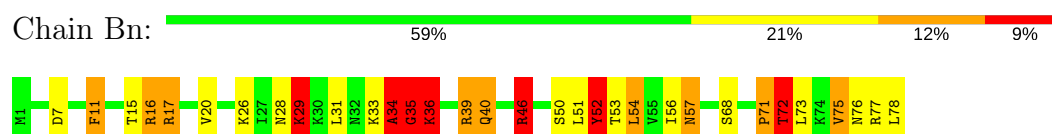
- Molecule 63: 60S ribosomal protein rpL43 (L37ae)



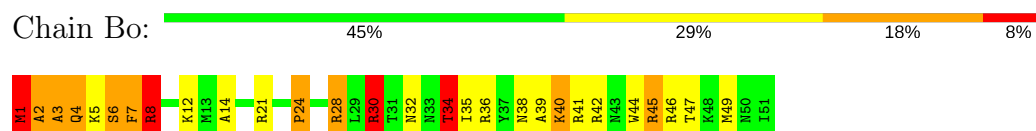
- Molecule 64: 60S ribosomal protein rpL37 (L37e)



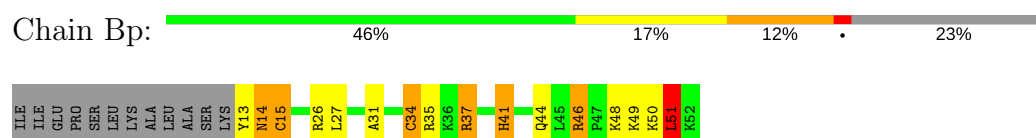
- Molecule 65: 60S ribosomal protein rpL38 (L38e)



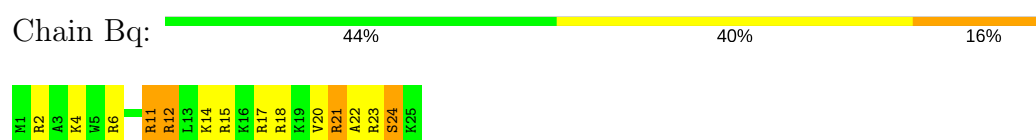
- Molecule 66: 60S ribosomal protein rpL39 (L39e)



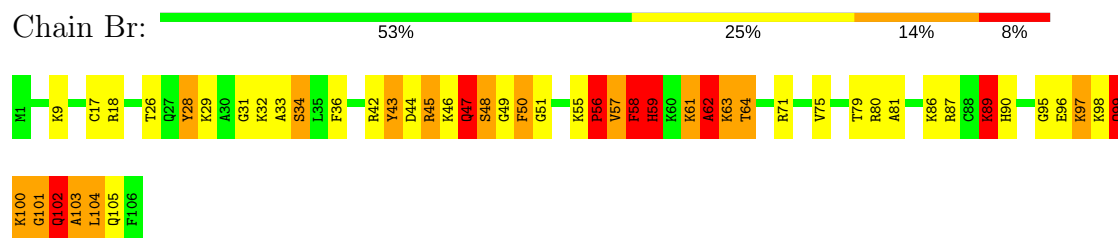
- Molecule 67: 60S ribosomal protein rpL40 (L40e)



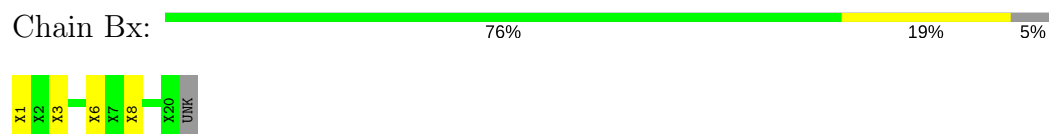
- Molecule 68: 60S ribosomal protein rpL41 (L41e)



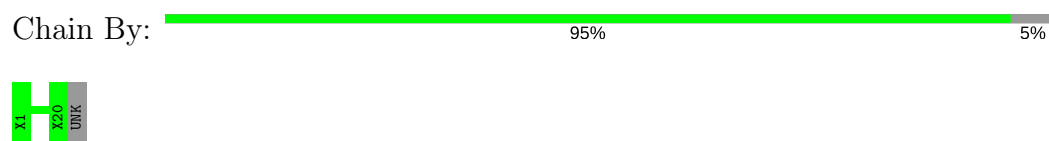
- Molecule 69: 60S ribosomal protein rpL42 (L44e)



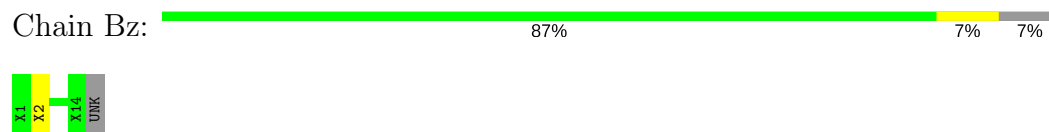
- Molecule 70: Unknown protein



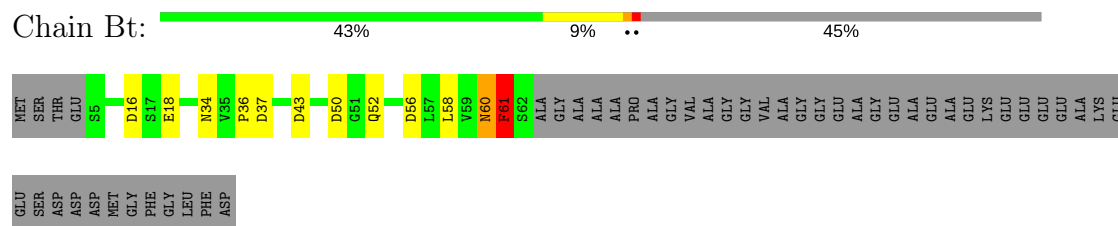
- Molecule 70: Unknown protein



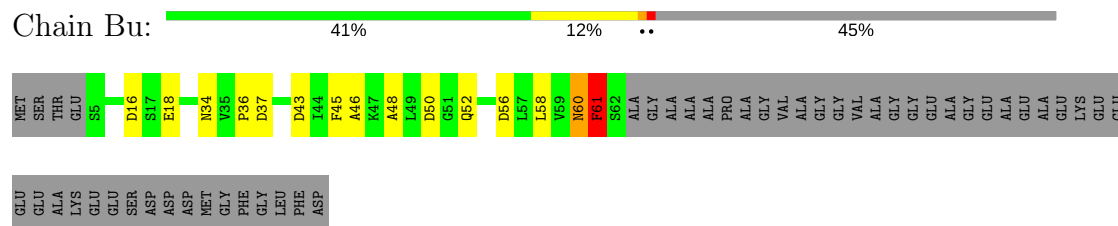
- Molecule 71: Unknown protein



- Molecule 72: 60S acidic ribosomal protein rpP11 (P1)

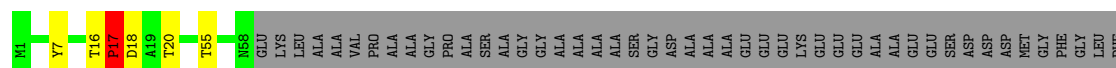


- Molecule 72: 60S acidic ribosomal protein rpP11 (P1)



- Molecule 73: 60S acidic ribosomal protein (P2)

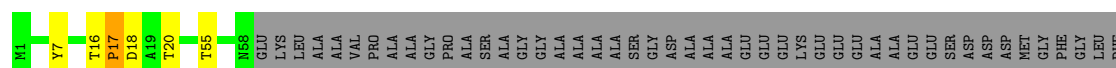
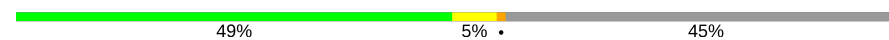
Chain Bv:



ASP

- Molecule 73: 60S acidic ribosomal protein (P2)

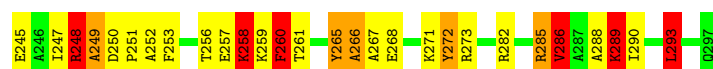
Chain Bw:



ASP

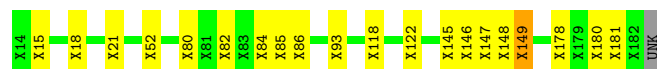
- Molecule 74: 60S ribosomal protein rpL5 (L18p)

Chain BQ:



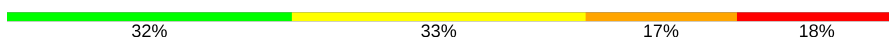
- Molecule 75: 60S ribosomal protein rpL13 (L13e)

Chain BL:



- Molecule 76: 60S ribosomal protein rpL20 (L18ae)

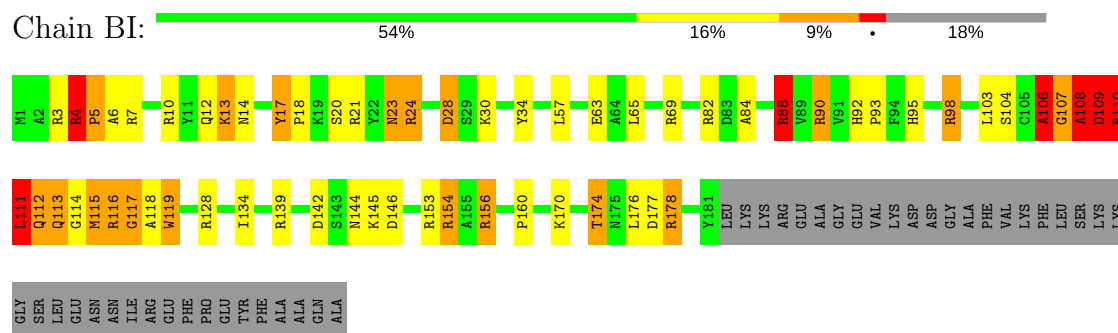
Chain BS:





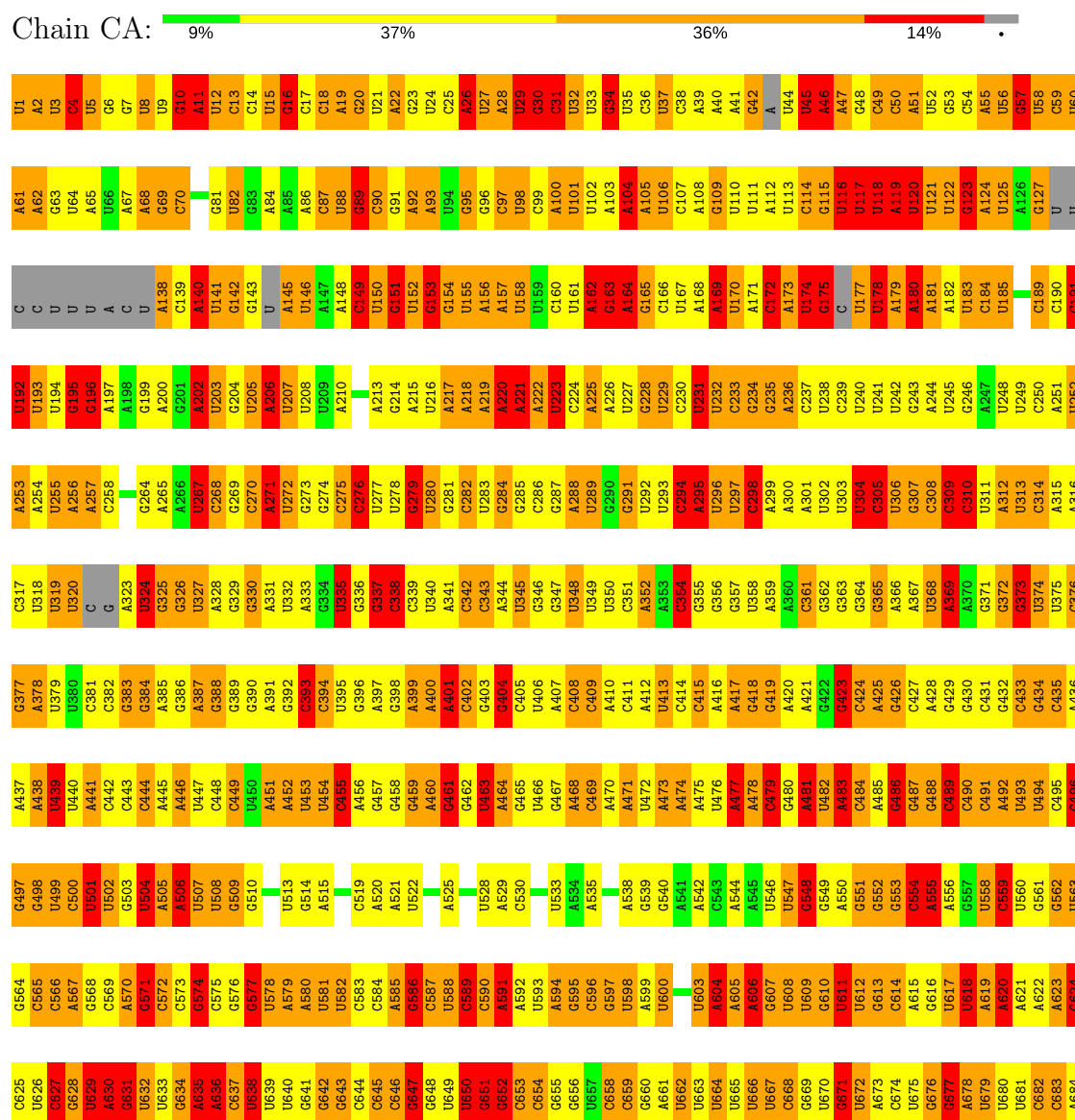
• Molecule 77: 60S ribosomal protein rpL10 (L10e)

Chain BI:

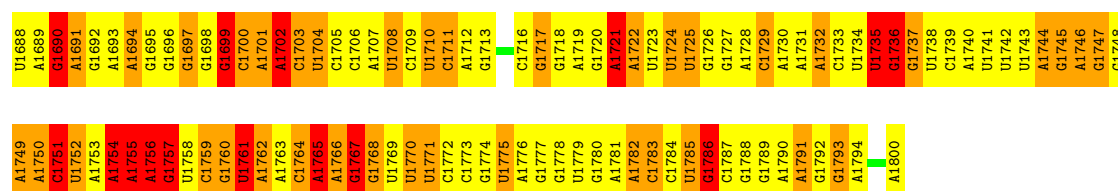


• Molecule 78: 18S rRNA

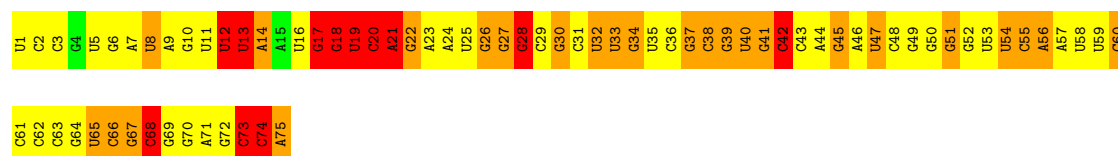
Chain CA:



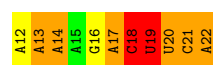
| | | | | | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|------|------|------|------|
| U1628 | G1668 | G1568 | G1502 | G1438 | U1378 | C1317 | U1257 | U1191 | A1131 | U1071 | G1011 | A951 | A891 | U831 | A | A686 |
| G1629 | A1569 | C1379 | U1258 | C1439 | C1379 | G1318 | U1258 | C1192 | A1132 | C1072 | U1012 | A952 | A892 | U832 | G | C686 |
| U1630 | A1570 | U1380 | U1259 | C1440 | U1381 | A1319 | U1260 | A1193 | A1133 | G1073 | A1013 | G953 | U893 | U833 | A | G687 |
| A1631 | C1571 | U1381 | U1260 | C1441 | U1382 | U1320 | U1261 | A1194 | C1134 | G1074 | G1014 | G954 | U894 | G688 | G | G688 |
| C1632 | G1572 | G1382 | G1261 | U1442 | A1321 | A1321 | G1262 | C1195 | U1135 | A1075 | U1015 | A955 | G895 | U835 | U764 | G689 |
| A1633 | A1573 | G1383 | G1262 | U1443 | A1322 | A1322 | G1263 | A1196 | U1136 | A1076 | C1016 | G956 | U896 | U836 | C | G690 |
| G1634 | G1574 | A1384 | G1263 | U1444 | C1323 | C1323 | G1264 | C1197 | A1137 | C1077 | U1017 | G957 | G897 | G637 | C | G690 |
| A1635 | G1575 | G1386 | G1264 | G | G1324 | G1324 | G1265 | C1198 | A1138 | C1078 | U1018 | U958 | G898 | G638 | C | G690 |
| C1636 | A1576 | A1446 | G1265 | A1446 | A1325 | A1325 | G1266 | G1199 | A1139 | U1079 | A1019 | U959 | G899 | U839 | U | C |
| C1637 | A1577 | G1387 | U1266 | C1447 | C1326 | A1326 | G1267 | G1200 | G1140 | U1080 | A1020 | U960 | A900 | U840 | U | C |
| G1638 | U1578 | A1388 | G1267 | G1448 | C1327 | C1327 | G1268 | G1201 | G1141 | A1081 | C1021 | U961 | A901 | U841 | C | U |
| C1639 | U1579 | C1389 | G1268 | U1449 | G1328 | A1328 | G1269 | A1202 | A1142 | C | C1022 | G962 | G902 | U842 | C | U |
| G1640 | U1580 | U1390 | U1269 | U1450 | A1329 | A1329 | U1270 | A1203 | A1143 | G1083 | A1023 | U963 | G903 | U843 | C | U |
| C1641 | C1581 | A1391 | G1270 | C1451 | G1330 | G1330 | G1271 | A1204 | U1144 | A1084 | U1024 | U964 | G904 | A844 | C | U |
| G1642 | U1582 | U1392 | G1271 | U1452 | C1331 | A1331 | G1272 | C1205 | U1145 | G1085 | U1025 | U965 | A905 | U845 | C | U |
| U1643 | A1583 | C1393 | U1272 | G1453 | C1332 | A1332 | U1273 | U1206 | G1146 | A1086 | A1026 | U966 | A906 | G846 | C | U |
| G1644 | G1584 | G1394 | G1273 | G1454 | C1333 | A1333 | G1274 | C1207 | A1087 | A1087 | A1027 | U967 | A907 | A847 | C | U |
| U1645 | U1585 | G1395 | C1274 | G1455 | U1334 | A1334 | U1275 | A1208 | C1148 | A1088 | C1028 | U968 | U908 | C848 | C | U |
| C1646 | A1586 | U1396 | U1276 | C | U1335 | A1335 | U1276 | C1209 | G1149 | U1089 | U1029 | G969 | U909 | C849 | C | U |
| U1647 | U1587 | U1397 | U1277 | U1456 | A1336 | A1336 | U1277 | C1210 | G1150 | U1090 | A1030 | A970 | C910 | A850 | C | U |
| G1648 | G1588 | U1398 | G1278 | G1458 | A1337 | A1337 | U1282 | A1211 | A1151 | A1091 | U1031 | A971 | U911 | A851 | C | U |
| G1649 | C1589 | C1399 | G1278 | C1459 | C1338 | A1338 | U1283 | G1212 | A1152 | A1092 | G1032 | G972 | U912 | C852 | C | U |
| U1650 | U1590 | A1400 | C1279 | A1460 | C1339 | A1339 | U1284 | G1213 | G1153 | A1093 | C1033 | A973 | G913 | C853 | C | U |
| A1651 | G1591 | A1401 | G1280 | G1461 | U1340 | A1340 | U1285 | U1214 | G1154 | A1094 | C1034 | A974 | G914 | U854 | C | U |
| C1652 | A1592 | G1402 | U1281 | G1462 | C1341 | A1341 | U1286 | C1215 | G1155 | U1095 | G1035 | C975 | A915 | A855 | C | U |
| C1653 | A1593 | C1403 | U1282 | C1463 | C1342 | A1342 | U1287 | C1096 | C1156 | C1096 | A1036 | G976 | U916 | A856 | C | U |
| G1654 | G1594 | U1404 | U1283 | G1464 | U1343 | A1343 | U1288 | C1220 | A1157 | U1097 | A1037 | A977 | U917 | U857 | C | U |
| U1655 | U1595 | G1405 | U1284 | C1465 | A1344 | A1344 | U1289 | A1221 | C1158 | U1098 | U1038 | A978 | U918 | G858 | C | U |
| C1656 | C1596 | A1406 | U1285 | G1466 | A1345 | A1345 | U1290 | C1222 | C1159 | U1099 | A1039 | A979 | A919 | A | C | U |
| U1657 | A1597 | U1407 | U1286 | C1467 | A1346 | A1346 | G1291 | A1223 | A1160 | G1100 | G1040 | A980 | U920 | A | C | U |
| G1658 | U1598 | G1408 | U1287 | U1468 | U1347 | A1347 | U1292 | A1224 | G1161 | G1101 | G1041 | U981 | U921 | U | C | U |
| C1659 | C1599 | G1409 | U1288 | A1469 | A1348 | A1348 | U1293 | U1225 | C1162 | G1102 | G1042 | U982 | G922 | U | C | U |
| U1660 | A1600 | A1410 | U1289 | C1470 | G1349 | A1349 | U1294 | A1226 | A1163 | U1103 | A1043 | A983 | A923 | A | C | U |
| G1661 | G1601 | U1411 | U1290 | A1471 | U1350 | A1350 | U1295 | A1227 | G1170 | G1110 | G1050 | G990 | A930 | G | C | U |
| C1662 | C1602 | G1412 | U1291 | C1472 | G1351 | A1351 | U1296 | G1235 | G1171 | G1111 | G1051 | G991 | C931 | A | C | U |
| G1663 | U1603 | U1413 | U1292 | U1473 | G1352 | A1352 | U1297 | A1236 | G1172 | G1112 | U1052 | A992 | U932 | A | C | U |
| C1664 | U1604 | U | U1293 | G1474 | U1353 | A1353 | U1298 | G1237 | C1173 | A1113 | G1053 | A993 | A933 | U | C | U |
| U1665 | G1605 | U1415 | U1294 | A1475 | G1354 | A1354 | U1299 | A1238 | G1174 | G1114 | U1054 | G994 | C934 | A | C | U |
| U1666 | C1606 | U1416 | U1295 | C1476 | C1355 | A1355 | U1299 | U1239 | U1175 | U1115 | U1055 | A995 | U935 | U | C | U |
| A1667 | G1607 | G1417 | U1296 | G1477 | U1356 | A1356 | U1299 | U1240 | U1176 | A1116 | U1056 | U996 | G936 | U | C | U |
| G1668 | U1608 | U1418 | U1297 | C1478 | A1357 | A1357 | U1299 | G1241 | C1177 | U1117 | U1057 | G997 | G937 | A | C | U |
| U1669 | U1609 | G1419 | U1298 | A1479 | G1358 | A1358 | U1299 | A1242 | G1178 | G1118 | U1058 | U998 | G938 | C | C | U |
| G1670 | G1610 | A1420 | U1299 | G1480 | C1359 | A1359 | U1299 | G1243 | G1179 | G1119 | U1059 | U999 | A939 | U | C | U |
| A1671 | U1611 | U1421 | U1300 | C1481 | C1359 | A1359 | U1299 | A1244 | U1180 | U1120 | U1060 | C1000 | A940 | U | C | U |
| G1672 | U1612 | A1422 | U1301 | C1482 | U1362 | A1362 | U1301 | G1245 | U1181 | C1121 | A1061 | A1001 | A941 | U | C | U |
| C1673 | U1613 | U1423 | U1302 | G1487 | U1363 | A1363 | U1302 | C1246 | U1182 | G1122 | A1062 | G942 | G942 | U | C | U |
| A1674 | A1614 | A1424 | U1303 | G1488 | G1364 | A1364 | U1303 | U1250 | A1183 | C1123 | U1063 | C943 | C943 | U | C | U |
| C1675 | C1615 | A1425 | G1304 | U1489 | C1365 | A1365 | G1304 | U1251 | A1184 | A1124 | G1064 | A944 | A884 | A | C | U |
| U1676 | G1616 | A1426 | U1305 | U1490 | U1366 | A1366 | U1305 | C1252 | U1185 | A1125 | A1065 | U945 | G885 | A | C | U |
| C1677 | U1617 | U1427 | U1306 | U1491 | G1367 | A1367 | U1306 | U1253 | U1186 | A1126 | C1066 | U946 | G886 | A | C | U |
| A1678 | C1618 | G1428 | U1307 | U1491 | G1368 | A1368 | U1307 | G1245 | U1187 | G1127 | C1067 | C1007 | U947 | A | C | U |
| G1679 | U1619 | U1429 | U1308 | A1492 | U1369 | A1369 | U1308 | C1246 | U1188 | U1128 | G1068 | G948 | G948 | A | C | U |
| C1680 | C1620 | U1430 | U1309 | G1493 | U1370 | A1370 | U1309 | U1254 | A1189 | C1129 | A1069 | C949 | U889 | U | C | U |
| A1681 | U1621 | A1431 | U1310 | C1495 | A1371 | A1371 | U1310 | U1255 | A1190 | A1129 | U1069 | C950 | C950 | U | C | U |
| G1682 | G1622 | U1432 | U1311 | U1496 | C1372 | A1372 | U1311 | C1256 | U1191 | G1129 | C1070 | C1010 | C950 | U | C | U |
| C1683 | C1623 | G1433 | U1312 | U1497 | C1373 | A1373 | U1312 | U1257 | U1192 | U1129 | C1070 | C1010 | C950 | U | C | U |
| U1684 | C1624 | U1434 | U1313 | U1498 | C1374 | A1374 | U1313 | U1258 | U1193 | U1130 | C1070 | C1010 | C950 | U | C | U |
| G1685 | U1625 | G1435 | U1314 | G1499 | A1375 | A1375 | U1314 | U1259 | U1194 | U1130 | C1070 | C1010 | C950 | U | C | U |
| C1686 | C1626 | U1436 | U1315 | C1500 | C1376 | A1376 | U1315 | U1260 | U1195 | U1130 | C1070 | C1010 | C950 | U | C | U |
| U1687 | U1627 | U1437 | U1316 | C1501 | U1377 | A1377 | U1316 | U1261 | U1196 | U1130 | C1070 | C1010 | C950 | U | C | U |



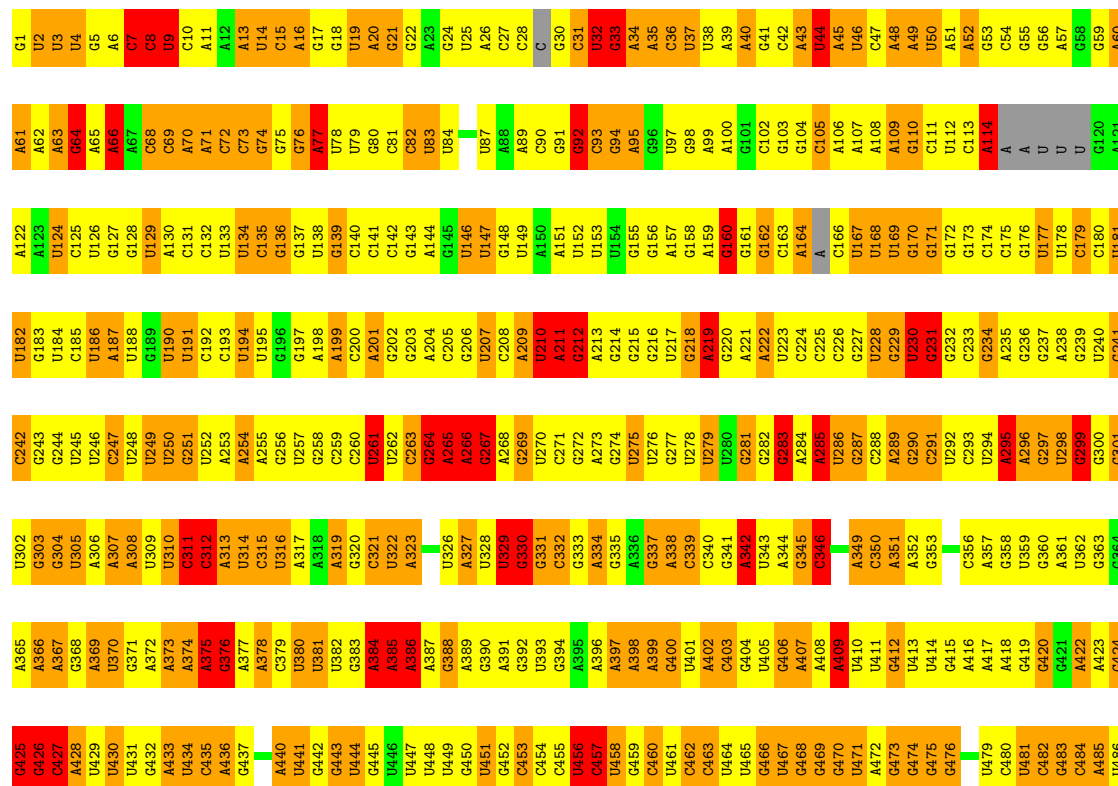
• Molecule 79: P-SITE TRNA ASP



• Molecule 80: MRNA, RNA (5'-R(P*AP*AP*AP*AP*GP*AP*CP*UP*UP*CP*A)-3')



• Molecule 81: 25S rRNA

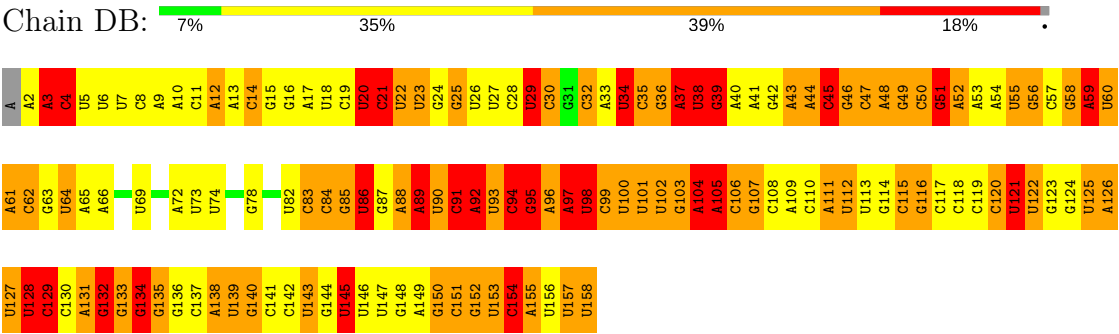




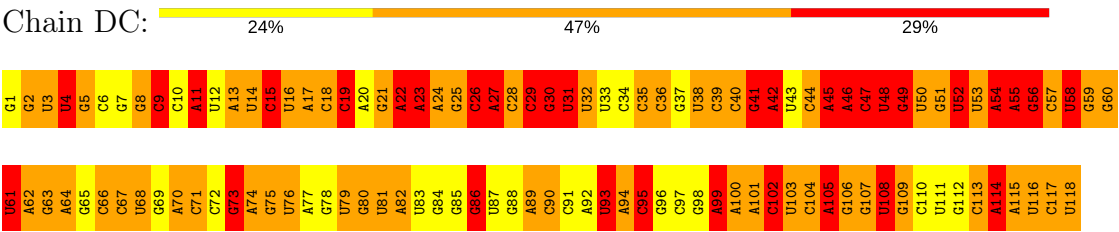

| | | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| C9378 | U2318 | U2288 | C2078 | G2017 | G1957 | G1897 | C1836 | G1775 | A1715 | G1655 | A1594 | C1532 | U1472 |
| U2379 | U2319 | A2259 | C2079 | C2018 | U1958 | G1898 | U1837 | G1776 | U1716 | A1656 | U1595 | U1533 | G1473 |
| G2381 | A2320 | G2261 | C2080 | U2019 | G1959 | G1899 | A1838 | G1778 | U1717 | G1657 | C1596 | A1534 | A1474 |
| G2382 | A2321 | A2262 | U2081 | A2020 | A1960 | U1960 | A1839 | U1778 | G1718 | G1658 | C1597 | A1535 | A1475 |
| G2383 | G2323 | G2263 | G2083 | G2021 | G1961 | A1901 | A1840 | C1779 | G1719 | U1659 | G1598 | G1536 | A1476 |
| A2384 | A2324 | U2264 | G2084 | C2023 | G1963 | U1903 | A1842 | G1781 | U1720 | C1660 | G1599 | A1537 | A1477 |
| G2385 | G2325 | C2265 | U2085 | G2024 | C1964 | C1904 | C1843 | U1782 | U1721 | G1661 | U1600 | G1538 | A1478 |
| A2386 | A2326 | U2266 | A2086 | G2025 | C1965 | G1905 | C1844 | U1783 | A1722 | G1662 | U1601 | A1539 | U1479 |
| A2387 | A2327 | A2267 | C2087 | A2026 | U1966 | G1906 | G1845 | G1784 | U1723 | C1663 | A1602 | U1540 | G1480 |
| U2388 | U2328 | U2268 | A2088 | C2027 | U1967 | C1907 | G1846 | U1785 | G1724 | G1664 | G1603 | G1541 | A1481 |
| U2389 | C2329 | U2269 | A2089 | C2028 | G1968 | A1908 | A1847 | G1786 | C1726 | G1665 | G1604 | G1542 | A1482 |
| C2390 | G2330 | G2210 | U2090 | A2029 | G1969 | A1909 | A1848 | A1787 | G1727 | G1666 | U1605 | G1543 | G1483 |
| C2391 | C2331 | A2271 | U2091 | C2030 | U1970 | U1910 | C1849 | C1788 | G1728 | G1668 | U1606 | G1544 | U1484 |
| G2392 | A2332 | G2272 | A2092 | U2031 | C1971 | A1911 | A1850 | C1789 | A1729 | C1669 | U1607 | A1545 | G1485 |
| G2393 | C2333 | G2273 | A2093 | U2032 | A1972 | U1912 | A1851 | G1790 | U1730 | C1670 | C1608 | A1546 | G1486 |
| G2394 | U2334 | A2274 | C2094 | G2033 | G1973 | A1913 | G1852 | C1791 | U1731 | C1671 | G1610 | C1548 | G1488 |
| G2395 | G2335 | G2275 | G2095 | C2034 | A1974 | G1914 | U1853 | C1792 | U1732 | U1672 | G1611 | U1549 | A1489 |
| G2396 | U2336 | G2276 | A2096 | G2035 | C1975 | A1915 | C1854 | C1793 | G1733 | G1673 | A1612 | C1550 | A1490 |
| A2397 | C2337 | C2277 | U2097 | U2036 | G1976 | U1916 | U1855 | G1794 | G1734 | G1674 | A1613 | C1551 | A1491 |
| A2398 | G2338 | G2278 | C2098 | G2037 | C1977 | C1917 | C1856 | G1795 | G1735 | G1675 | C1614 | G1552 | G1492 |
| A2399 | C2339 | A2279 | A2099 | C2038 | A1978 | U1918 | C1857 | G1796 | g | A1676 | C1615 | C1556 | G1493 |
| G2400 | U2340 | G2280 | A2100 | C2039 | G1979 | G1919 | A1858 | A1797 | U1737 | G1677 | U1616 | A1557 | U1494 |
| A2401 | A2341 | A2281 | C2101 | U2040 | C1980 | U1920 | A1859 | A1798 | U1738 | G1678 | G1617 | A1558 | U1495 |
| G2402 | U2342 | G2282 | U2102 | U2041 | G1981 | A1921 | G1860 | A1799 | U1739 | A1679 | G1618 | A1559 | C1496 |
| G2403 | C2343 | A2283 | U2103 | G2042 | G1982 | A1922 | G1861 | A1800 | U1740 | G1680 | A | G1560 | C1497 |
| A2404 | U2344 | C2284 | A2104 | U2043 | C1983 | C1923 | U1862 | U1801 | A1741 | U1681 | U1620 | G1561 | A1498 |
| A2405 | A2345 | G2285 | G2105 | U2044 | G1984 | U1924 | G1863 | C1802 | U1742 | U1682 | A1621 | G1562 | C1499 |
| G2406 | C2346 | U2286 | A2106 | G2045 | G1985 | U1925 | A1864 | C1803 | G1743 | A1683 | U1622 | C1563 | U1500 |
| C2407 | U2347 | C2287 | A2107 | U2046 | U1986 | C1926 | A1865 | A1804 | G1744 | U1684 | G1623 | C1564 | U1501 |
| U2408 | A2348 | G2288 | C2108 | A2047 | G1987 | G1927 | C1866 | C1805 | G1745 | G1685 | G1624 | U1564 | C1502 |
| G2409 | U2349 | A2289 | U2109 | G2048 | C1988 | G1928 | A1867 | A1806 | U1746 | U1686 | A1625 | G1565 | A1503 |
| U2410 | C2350 | C2290 | G2110 | A2049 | U1989 | G1929 | G1868 | G1807 | G1747 | U1687 | U1626 | A1566 | A1504 |
| G2411 | U2351 | A2291 | G2111 | C2050 | U1990 | A1930 | C1869 | A1808 | G1748 | U1688 | U1627 | U1567 | C1505 |
| A2412 | A2352 | G2292 | U2112 | G2051 | G1991 | U1931 | C1870 | A1809 | A1749 | C1628 | C1628 | U1568 | A1506 |
| G2413 | G2353 | C2293 | A2113 | G2052 | U1992 | A1932 | U1871 | A1810 | U1750 | C1690 | U1629 | G1569 | G1507 |
| G2414 | C2354 | U2294 | C2114 | C2053 | G1993 | A1933 | C1872 | G1811 | G1751 | U1691 | U1630 | U1570 | C1508 |
| C2415 | G2355 | A2295 | G2115 | C2054 | G1994 | G1934 | U1873 | G1812 | A1752 | U1692 | C1631 | A1571 | A1509 |
| U2416 | A2356 | A2296 | G2116 | U2055 | A1995 | G1935 | U1876 | A1813 | G1753 | C1693 | A1632 | U1572 | G1510 |
| U2417 | U2357 | G2297 | A2117 | U2056 | C1996 | A1936 | U1877 | A1814 | G1754 | U1694 | C1633 | G1573 | U1511 |
| G2418 | A2358 | U2298 | C2118 | G2057 | U1997 | U1937 | G1878 | A1815 | C1755 | U1695 | G1634 | C1574 | U1512 |
| A2419 | C2359 | G2299 | A2119 | G2058 | G1998 | U1938 | A1879 | A1816 | G1756 | A1696 | G1635 | A1575 | G1513 |
| C2420 | C2360 | G2300 | G2120 | U2059 | C1999 | G1939 | U1880 | U1817 | A1757 | A1697 | U | G1576 | G1514 |
| U2421 | A2361 | U2301 | G2121 | A2060 | U2000 | G1940 | A1881 | U1818 | G1758 | C1698 | A1637 | G1577 | A1515 |
| C2422 | C2362 | G2302 | A2122 | G2061 | U2001 | C1941 | A1881 | U1819 | C1759 | A1699 | A1638 | C1578 | C1516 |
| U2423 | A2363 | A2303 | G2123 | G2062 | G2002 | U1942 | G1882 | U1820 | A1760 | G1700 | C1639 | C1579 | C1517 |
| A2424 | G2364 | U2184 | G2124 | U2063 | C2003 | C1943 | A1883 | U1821 | C1761 | G1701 | G1640 | A1580 | U1518 |
| G2425 | C2365 | G2305 | A2125 | C2064 | U2004 | U1944 | A1884 | C | U1762 | U1702 | U1541 | C1581 | G1519 |
| U2426 | C2366 | G2246 | A2126 | U2065 | G2005 | A1945 | U1885 | U1823 | C1763 | U1703 | C1582 | C1582 | G1520 |
| U2427 | A2367 | G2247 | U2127 | C2066 | G2006 | A1946 | A1886 | U1824 | U1764 | A1704 | U1583 | G1521 | G1521 |
| U2428 | A2368 | C2248 | C2128 | U2067 | G2007 | G1947 | A1887 | G1825 | U1765 | U1705 | U1644 | U1584 | U1522 |
| G2429 | G2369 | G2249 | U2129 | U2068 | G2008 | G1948 | U1888 | C1826 | G1766 | G1706 | U1646 | C1585 | U1523 |
| A2430 | U2370 | G2250 | G2130 | G2069 | C2009 | G1949 | U1889 | C1827 | C1767 | A1647 | A1647 | C1586 | A1524 |
| C2431 | G2371 | G2251 | A2131 | U2070 | U1950 | U1950 | A1890 | A1828 | U1768 | C1708 | A1648 | A1587 | G1525 |
| A2432 | A2372 | C2192 | C2132 | U2071 | U2011 | G1951 | A1891 | G1929 | U1769 | C1709 | U1649 | U1588 | U1526 |
| U2433 | G2373 | G2253 | U2133 | G2072 | G2012 | G1952 | G1892 | G1830 | G1770 | C1710 | G1650 | A1589 | G1527 |
| U2434 | C2374 | U2254 | G2134 | A2073 | C2013 | G1953 | A1893 | U1831 | C1771 | C1711 | U1651 | G1590 | G1528 |
| G2435 | G2375 | A2255 | C2135 | C2074 | U2014 | G1954 | U1894 | U1832 | U1772 | G1712 | G1652 | G1591 | A1529 |
| U2436 | G2376 | A2256 | U2136 | C2075 | C2015 | U1955 | A1895 | G1833 | C1773 | G1713 | G1653 | G1592 | U1530 |
| G2437 | G2377 | C2257 | U2137 | C2076 | U2016 | A1956 | A1896 | | C1774 | A1714 | A1654 | A1593 | C1531 |



● Molecule 82: 5.8S rRNA



● Molecule 83: 5S rRNA



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---------------------|-----------|
| Reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | Depositor |
| Number of particles used | Not provided | Depositor |
| Resolution determination method | Not provided | Depositor |
| CTF correction method | Not provided | Depositor |
| Microscope | Not provided | Depositor |
| Voltage (kV) | Not provided | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | Not provided | Depositor |
| Minimum defocus (nm) | Not provided | Depositor |
| Maximum defocus (nm) | Not provided | Depositor |
| Magnification | Not provided | Depositor |
| Image detector | Not provided | Depositor |

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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 >2 | RMSZ | # Z >2 |
| 1 | Aa | 1.65 | 23/2495 (0.9%) | 2.01 | 81/3391 (2.4%) |
| 10 | AI | 1.94 | 15/1016 (1.5%) | 2.50 | 48/1362 (3.5%) |
| 11 | AJ | 1.93 | 13/857 (1.5%) | 2.90 | 38/1148 (3.3%) |
| 12 | AK | 1.98 | 14/843 (1.7%) | 2.28 | 38/1134 (3.4%) |
| 13 | AL | 2.41 | 23/990 (2.3%) | 3.21 | 80/1304 (6.1%) |
| 14 | AM | 1.85 | 23/1175 (2.0%) | 2.38 | 47/1577 (3.0%) |
| 15 | AN | 1.78 | 5/358 (1.4%) | 2.77 | 29/469 (6.2%) |
| 16 | AO | 1.85 | 10/994 (1.0%) | 2.70 | 58/1339 (4.3%) |
| 17 | AQ | 2.16 | 24/1109 (2.2%) | 3.08 | 59/1483 (4.0%) |
| 18 | AP | 2.29 | 17/646 (2.6%) | 3.39 | 49/867 (5.7%) |
| 19 | AR | 1.65 | 5/691 (0.7%) | 2.07 | 20/931 (2.1%) |
| 2 | AA | 1.99 | 33/1962 (1.7%) | 2.62 | 83/2674 (3.1%) |
| 20 | AS | 1.83 | 17/1138 (1.5%) | 2.73 | 74/1527 (4.8%) |
| 21 | AT | 2.06 | 13/694 (1.9%) | 2.67 | 32/935 (3.4%) |
| 22 | AV | 1.91 | 14/698 (2.0%) | 2.68 | 44/932 (4.7%) |
| 24 | AX | 1.77 | 5/372 (1.3%) | 2.15 | 13/504 (2.6%) |
| 25 | AY | 1.80 | 3/447 (0.7%) | 2.08 | 19/601 (3.2%) |
| 26 | AZ | 2.63 | 17/499 (3.4%) | 3.77 | 31/660 (4.7%) |
| 29 | AU | 1.93 | 8/725 (1.1%) | 2.49 | 45/969 (4.6%) |
| 3 | AB | 1.87 | 20/1530 (1.3%) | 2.48 | 72/2049 (3.5%) |
| 30 | BA | 1.42 | 4/1745 (0.2%) | 1.78 | 32/2342 (1.4%) |
| 31 | BB | 2.07 | 31/1938 (1.6%) | 2.90 | 100/2600 (3.8%) |
| 32 | BC | 2.25 | 65/3124 (2.1%) | 3.27 | 171/4196 (4.1%) |
| 33 | BD | 2.15 | 53/2531 (2.1%) | 2.93 | 146/3414 (4.3%) |
| 34 | BE | 2.08 | 25/1362 (1.8%) | 3.17 | 79/1824 (4.3%) |
| 35 | BG | 2.50 | 42/1433 (2.9%) | 3.60 | 142/1922 (7.4%) |
| 36 | BF | 1.65 | 9/1537 (0.6%) | 2.05 | 27/2068 (1.3%) |
| 37 | BH | 2.09 | 26/1527 (1.7%) | 2.60 | 82/2052 (4.0%) |
| 38 | Bs | 1.71 | 18/2013 (0.9%) | 2.32 | 75/2731 (2.7%) |
| 39 | BJ | 1.89 | 16/964 (1.7%) | 2.63 | 44/1295 (3.4%) |
| 4 | AD | 1.95 | 29/1620 (1.8%) | 2.88 | 94/2182 (4.3%) |
| 40 | BK | 1.93 | 21/1600 (1.3%) | 2.78 | 76/2146 (3.5%) |
| 41 | BN | 1.88 | 15/1083 (1.4%) | 2.30 | 56/1456 (3.8%) |
| 42 | BM | 1.73 | 12/987 (1.2%) | 2.20 | 45/1326 (3.4%) |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-------------------|-------------|--------------------|
| | | RMSZ | # Z >2 | RMSZ | # Z >2 |
| 43 | BP | 2.03 | 23/1659 (1.4%) | 2.68 | 113/2221 (5.1%) |
| 44 | BO | 2.47 | 29/1213 (2.4%) | 3.20 | 74/1623 (4.6%) |
| 45 | BR | 2.41 | 29/1264 (2.3%) | 3.18 | 68/1701 (4.0%) |
| 46 | BT | 1.82 | 26/1547 (1.7%) | 2.27 | 54/2060 (2.6%) |
| 47 | BU | 1.78 | 21/1285 (1.6%) | 2.44 | 54/1720 (3.1%) |
| 48 | BW | 2.02 | 13/846 (1.5%) | 2.75 | 47/1142 (4.1%) |
| 49 | BV | 1.71 | 14/1335 (1.0%) | 2.03 | 40/1794 (2.2%) |
| 5 | AC | 2.12 | 34/1544 (2.2%) | 3.02 | 112/2059 (5.4%) |
| 50 | BX | 1.58 | 5/993 (0.5%) | 2.19 | 41/1336 (3.1%) |
| 51 | BZ | 2.29 | 14/590 (2.4%) | 2.74 | 40/783 (5.1%) |
| 52 | BY | 1.61 | 10/983 (1.0%) | 1.95 | 25/1312 (1.9%) |
| 53 | Ba | 2.24 | 20/722 (2.8%) | 3.30 | 75/967 (7.8%) |
| 54 | Bd | 1.63 | 2/177 (1.1%) | 1.91 | 5/231 (2.2%) |
| 55 | Bc | 2.06 | 14/974 (1.4%) | 2.76 | 53/1294 (4.1%) |
| 56 | Bf | 1.59 | 7/793 (0.9%) | 1.92 | 17/1062 (1.6%) |
| 57 | Be | 1.85 | 25/1957 (1.3%) | 2.29 | 69/2631 (2.6%) |
| 58 | Bg | 1.83 | 16/887 (1.8%) | 2.38 | 32/1185 (2.7%) |
| 59 | Bh | 1.80 | 11/1064 (1.0%) | 2.30 | 47/1423 (3.3%) |
| 6 | AE | 1.82 | 21/1971 (1.1%) | 2.46 | 79/2664 (3.0%) |
| 60 | Bi | 2.51 | 24/935 (2.6%) | 3.64 | 59/1242 (4.8%) |
| 61 | Bj | 2.79 | 19/751 (2.5%) | 3.05 | 68/1004 (6.8%) |
| 62 | Bk | 2.48 | 19/625 (3.0%) | 3.48 | 45/826 (5.4%) |
| 63 | Bm | 1.73 | 9/710 (1.3%) | 2.09 | 24/944 (2.5%) |
| 64 | Bl | 2.03 | 9/693 (1.3%) | 2.42 | 34/915 (3.7%) |
| 65 | Bn | 2.32 | 13/610 (2.1%) | 3.37 | 37/813 (4.6%) |
| 66 | Bo | 1.80 | 4/452 (0.9%) | 2.23 | 17/598 (2.8%) |
| 67 | Bp | 1.57 | 2/335 (0.6%) | 2.25 | 18/442 (4.1%) |
| 68 | Bq | 1.98 | 3/235 (1.3%) | 2.32 | 14/300 (4.7%) |
| 69 | Br | 2.01 | 14/846 (1.7%) | 2.74 | 44/1113 (4.0%) |
| 72 | Bt | 0.69 | 1/445 (0.2%) | 1.49 | 16/606 (2.6%) |
| 72 | Bu | 0.92 | 1/445 (0.2%) | 1.63 | 18/606 (3.0%) |
| 73 | Bv | 0.97 | 0/431 | 1.29 | 4/582 (0.7%) |
| 73 | Bw | 0.96 | 0/431 | 1.28 | 4/582 (0.7%) |
| 74 | BQ | 2.23 | 50/2404 (2.1%) | 3.27 | 146/3236 (4.5%) |
| 76 | BS | 1.92 | 23/1458 (1.6%) | 2.70 | 109/1957 (5.6%) |
| 77 | BI | 0.95 | 1/1473 (0.1%) | 1.60 | 29/1976 (1.5%) |
| 78 | CA | 2.64 | 1783/37406 (4.8%) | 2.65 | 3176/57948 (5.5%) |
| 79 | CB | 2.75 | 77/1785 (4.3%) | 2.58 | 142/2779 (5.1%) |
| 8 | AF | 1.70 | 13/1561 (0.8%) | 1.94 | 47/2103 (2.2%) |
| 80 | CC | 3.40 | 11/264 (4.2%) | 3.22 | 29/407 (7.1%) |
| 81 | DA | 2.74 | 3996/76832 (5.2%) | 2.77 | 7042/119578 (5.9%) |
| 82 | DB | 2.68 | 166/3480 (4.8%) | 2.64 | 305/5395 (5.7%) |
| 83 | DC | 2.90 | 156/2808 (5.6%) | 3.09 | 331/4372 (7.6%) |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|--------------------|-------------|---------------------|
| | | RMSZ | # Z >2 | RMSZ | # Z >2 |
| 9 | AH | 1.85 | 10/1047 (1.0%) | 2.39 | 47/1405 (3.3%) |
| All | All | 2.44 | 7406/202969 (3.6%) | 2.70 | 14979/298347 (5.0%) |

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 |
|-----|-------|---------------------|---------------------|
| 1 | Aa | 0 | 18 |
| 10 | AI | 0 | 14 |
| 11 | AJ | 0 | 17 |
| 12 | AK | 1 | 15 |
| 13 | AL | 0 | 14 |
| 14 | AM | 0 | 12 |
| 15 | AN | 0 | 12 |
| 16 | AO | 2 | 15 |
| 17 | AQ | 0 | 29 |
| 18 | AP | 0 | 15 |
| 19 | AR | 0 | 8 |
| 2 | AA | 1 | 30 |
| 20 | AS | 0 | 19 |
| 21 | AT | 0 | 15 |
| 22 | AV | 0 | 12 |
| 23 | AW | 5 | 20 |
| 24 | AX | 0 | 2 |
| 25 | AY | 0 | 4 |
| 26 | AZ | 0 | 25 |
| 27 | Ab | 0 | 3 |
| 28 | Ac | 0 | 1 |
| 29 | AU | 2 | 12 |
| 3 | AB | 0 | 29 |
| 30 | BA | 0 | 8 |
| 31 | BB | 2 | 45 |
| 32 | BC | 2 | 56 |
| 33 | BD | 2 | 53 |
| 34 | BE | 2 | 25 |
| 35 | BG | 2 | 57 |
| 36 | BF | 0 | 10 |
| 37 | BH | 0 | 36 |
| 38 | Bs | 0 | 18 |
| 39 | BJ | 1 | 10 |

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| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 4 | AD | 0 | 36 |
| 40 | BK | 0 | 29 |
| 41 | BN | 1 | 13 |
| 42 | BM | 0 | 11 |
| 43 | BP | 4 | 44 |
| 44 | BO | 1 | 28 |
| 45 | BR | 0 | 31 |
| 46 | BT | 0 | 17 |
| 47 | BU | 1 | 16 |
| 48 | BW | 0 | 12 |
| 49 | BV | 0 | 20 |
| 5 | AC | 2 | 40 |
| 50 | BX | 0 | 13 |
| 51 | BZ | 0 | 18 |
| 52 | BY | 0 | 8 |
| 53 | Ba | 0 | 25 |
| 54 | Bd | 0 | 1 |
| 55 | Bc | 0 | 16 |
| 56 | Bf | 0 | 6 |
| 57 | Be | 1 | 14 |
| 58 | Bg | 0 | 13 |
| 59 | Bh | 0 | 14 |
| 6 | AE | 3 | 29 |
| 60 | Bi | 0 | 25 |
| 61 | Bj | 1 | 26 |
| 62 | Bk | 1 | 15 |
| 63 | Bm | 1 | 5 |
| 64 | Bl | 0 | 13 |
| 65 | Bn | 0 | 15 |
| 66 | Bo | 0 | 15 |
| 67 | Bp | 0 | 8 |
| 68 | Bq | 0 | 4 |
| 69 | Br | 0 | 23 |
| 7 | AG | 0 | 52 |
| 70 | Bx | 0 | 7 |
| 71 | Bz | 0 | 1 |
| 72 | Bt | 0 | 3 |
| 72 | Bu | 0 | 3 |
| 73 | Bv | 0 | 1 |
| 73 | Bw | 0 | 1 |
| 74 | BQ | 0 | 48 |
| 75 | BL | 6 | 5 |

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| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 76 | BS | 1 | 41 |
| 77 | BI | 2 | 24 |
| 78 | CA | 10 | 22 |
| 79 | CB | 1 | 0 |
| 8 | AF | 0 | 14 |
| 80 | CC | 1 | 0 |
| 81 | DA | 32 | 15 |
| 82 | DB | 5 | 0 |
| 9 | AH | 0 | 15 |
| All | All | 96 | 1514 |

The worst 5 of 7406 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|---------|--------|-------------|----------|
| 81 | DA | 1261 | G | C2'-C1' | 59.16 | 2.18 | 1.53 |
| 79 | CB | 55 | C | C2'-C1' | -55.11 | 0.92 | 1.53 |
| 78 | CA | 636 | A | C2'-C1' | 54.35 | 2.13 | 1.53 |
| 81 | DA | 3215 | A | C2'-C1' | -49.15 | 0.99 | 1.53 |
| 78 | CA | 1190 | C | O5'-C5' | -48.72 | 0.65 | 1.42 |

The worst 5 of 14979 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|-----------|--------|-------------|----------|
| 32 | BC | 266 | ARG | NE-CZ-NH1 | -73.84 | 83.38 | 120.30 |
| 81 | DA | 3305 | A | P-O3'-C3' | 50.10 | 179.82 | 119.70 |
| 81 | DA | 3047 | U | P-O3'-C3' | 47.61 | 176.83 | 119.70 |
| 81 | DA | 2046 | U | P-O3'-C3' | 47.25 | 176.40 | 119.70 |
| 81 | DA | 2071 | A | P-O3'-C3' | 46.20 | 175.13 | 119.70 |

5 of 96 chirality outliers are listed below:

| Mol | Chain | Res | Type | Atom |
|-----|-------|-----|------|------|
| 2 | AA | 241 | GLU | CA |
| 5 | AC | 129 | ILE | CA |
| 5 | AC | 162 | SER | CA |
| 6 | AE | 28 | ARG | CA |
| 6 | AE | 30 | THR | CA |

5 of 1514 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|-----------|
| 1 | Aa | 10 | ARG | Sidechain |

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| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|-------------------|
| 1 | Aa | 48 | THR | Peptide |
| 1 | Aa | 49 | GLY | Peptide |
| 1 | Aa | 53 | LYS | Mainchain,Peptide |
| 1 | Aa | 54 | PHE | Mainchain |

5.2 Too-close contacts

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | Aa | 2442 | 0 | 2396 | 0 | 0 |
| 2 | AA | 1922 | 0 | 1841 | 43 | 0 |
| 3 | AB | 1511 | 0 | 1503 | 22 | 0 |
| 4 | AD | 1591 | 0 | 1653 | 82 | 0 |
| 5 | AC | 1521 | 0 | 1546 | 63 | 0 |
| 6 | AE | 1936 | 0 | 2030 | 86 | 0 |
| 7 | AG | 716 | 0 | 164 | 27 | 0 |
| 8 | AF | 1543 | 0 | 1589 | 34 | 0 |
| 9 | AH | 1030 | 0 | 1072 | 29 | 0 |
| 10 | AI | 998 | 0 | 1048 | 51 | 0 |
| 11 | AJ | 849 | 0 | 864 | 17 | 0 |
| 12 | AK | 833 | 0 | 824 | 78 | 0 |
| 13 | AL | 978 | 0 | 899 | 111 | 0 |
| 14 | AM | 1156 | 0 | 1176 | 153 | 0 |
| 15 | AN | 353 | 0 | 332 | 21 | 0 |
| 16 | AO | 978 | 0 | 1039 | 70 | 0 |
| 17 | AQ | 1098 | 0 | 1163 | 24 | 0 |
| 18 | AP | 631 | 0 | 634 | 93 | 0 |
| 19 | AR | 676 | 0 | 696 | 90 | 0 |
| 20 | AS | 1120 | 0 | 1131 | 87 | 0 |
| 21 | AT | 685 | 0 | 672 | 23 | 0 |
| 22 | AV | 688 | 0 | 734 | 25 | 0 |
| 23 | AW | 461 | 0 | 106 | 16 | 0 |
| 24 | AX | 366 | 0 | 364 | 19 | 0 |
| 25 | AY | 445 | 0 | 461 | 12 | 0 |
| 26 | AZ | 492 | 0 | 535 | 7 | 0 |
| 27 | Ab | 181 | 0 | 38 | 0 | 0 |
| 28 | Ac | 126 | 0 | 28 | 0 | 0 |
| 29 | AU | 714 | 0 | 711 | 46 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 30 | BA | 1718 | 0 | 1811 | 35 | 0 |
| 31 | BB | 1904 | 0 | 1951 | 143 | 0 |
| 32 | BC | 3055 | 0 | 3108 | 127 | 0 |
| 33 | BD | 2486 | 0 | 2587 | 125 | 0 |
| 34 | BE | 1341 | 0 | 1376 | 115 | 0 |
| 35 | BG | 1409 | 0 | 1512 | 119 | 0 |
| 36 | BF | 1516 | 0 | 1581 | 47 | 0 |
| 37 | BH | 1505 | 0 | 1582 | 64 | 0 |
| 38 | Bs | 1976 | 0 | 2017 | 0 | 0 |
| 39 | BJ | 954 | 0 | 1025 | 23 | 0 |
| 40 | BK | 1570 | 0 | 1675 | 50 | 0 |
| 41 | BN | 1068 | 0 | 1166 | 105 | 0 |
| 42 | BM | 972 | 0 | 1019 | 67 | 0 |
| 43 | BP | 1625 | 0 | 1685 | 71 | 0 |
| 44 | BO | 1182 | 0 | 1220 | 66 | 0 |
| 45 | BR | 1243 | 0 | 1327 | 63 | 0 |
| 46 | BT | 1530 | 0 | 1629 | 39 | 0 |
| 47 | BU | 1261 | 0 | 1281 | 34 | 0 |
| 48 | BW | 830 | 0 | 845 | 28 | 0 |
| 49 | BV | 1312 | 0 | 1313 | 23 | 0 |
| 50 | BX | 978 | 0 | 1049 | 4 | 0 |
| 51 | BZ | 579 | 0 | 591 | 55 | 0 |
| 52 | BY | 972 | 0 | 1060 | 17 | 0 |
| 53 | Ba | 708 | 0 | 741 | 0 | 0 |
| 54 | Bd | 174 | 0 | 188 | 0 | 0 |
| 55 | Bc | 965 | 0 | 1073 | 0 | 0 |
| 56 | Bf | 785 | 0 | 819 | 0 | 0 |
| 57 | Be | 1919 | 0 | 2013 | 0 | 0 |
| 58 | Bg | 873 | 0 | 913 | 0 | 0 |
| 59 | Bh | 1043 | 0 | 1113 | 0 | 0 |
| 60 | Bi | 926 | 0 | 998 | 0 | 0 |
| 61 | Bj | 738 | 0 | 730 | 0 | 0 |
| 62 | Bk | 619 | 0 | 673 | 0 | 0 |
| 63 | Bm | 703 | 0 | 750 | 0 | 0 |
| 64 | Bl | 678 | 0 | 667 | 0 | 0 |
| 65 | Bn | 604 | 0 | 664 | 0 | 0 |
| 66 | Bo | 445 | 0 | 487 | 0 | 0 |
| 67 | Bp | 330 | 0 | 356 | 0 | 0 |
| 68 | Bq | 234 | 0 | 284 | 0 | 0 |
| 69 | Br | 834 | 0 | 894 | 0 | 0 |
| 70 | Bx | 100 | 0 | 22 | 0 | 0 |
| 70 | By | 100 | 0 | 22 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 71 | Bz | 70 | 0 | 18 | 0 | 0 |
| 72 | Bt | 440 | 0 | 439 | 0 | 0 |
| 72 | Bu | 440 | 0 | 439 | 0 | 0 |
| 73 | Bv | 429 | 0 | 445 | 0 | 0 |
| 73 | Bw | 429 | 0 | 442 | 0 | 0 |
| 74 | BQ | 2356 | 0 | 2288 | 101 | 0 |
| 75 | BL | 845 | 0 | 192 | 38 | 0 |
| 76 | BS | 1420 | 0 | 1465 | 74 | 0 |
| 77 | BI | 1444 | 0 | 1477 | 35 | 0 |
| 78 | CA | 33643 | 0 | 16491 | 1332 | 0 |
| 79 | CB | 1599 | 0 | 807 | 34 | 0 |
| 80 | CC | 236 | 0 | 121 | 10 | 0 |
| 81 | DA | 68830 | 0 | 34361 | 1790 | 0 |
| 82 | DB | 3129 | 0 | 1554 | 73 | 0 |
| 83 | DC | 2513 | 0 | 1271 | 125 | 0 |
| All | All | 191627 | 0 | 136876 | 4881 | 0 |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

The worst 5 of 4881 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|-------------------|--------------------------|-------------------|
| 37:BH:158:ASP:CB | 37:BH:158:ASP:CA | 1.74 | 1.66 |
| 14:AM:12:GLN:HG3 | 34:BE:116:TYR:CD1 | 1.28 | 1.65 |
| 78:CA:960:U:C1' | 78:CA:960:U:C2' | 1.75 | 1.63 |
| 82:DB:50:C:C1' | 82:DB:50:C:C2' | 1.74 | 1.62 |
| 22:AV:105:THR:CA | 22:AV:105:THR:CB | 1.74 | 1.62 |

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|----------|-------------|----|
| 1 | Aa | 317/319 (99%) | 274 (86%) | 23 (7%) | 20 (6%) | 1 | 22 |
| 2 | AA | 250/252 (99%) | 199 (80%) | 21 (8%) | 30 (12%) | 0 | 7 |
| 3 | AB | 202/240 (84%) | 137 (68%) | 30 (15%) | 35 (17%) | 0 | 4 |
| 4 | AD | 198/261 (76%) | 160 (81%) | 17 (9%) | 21 (11%) | 0 | 10 |
| 5 | AC | 192/197 (98%) | 136 (71%) | 28 (15%) | 28 (15%) | 0 | 5 |
| 6 | AE | 252/254 (99%) | 176 (70%) | 36 (14%) | 40 (16%) | 0 | 4 |
| 8 | AF | 197/225 (88%) | 170 (86%) | 9 (5%) | 18 (9%) | 1 | 15 |
| 9 | AH | 128/130 (98%) | 95 (74%) | 17 (13%) | 16 (12%) | 0 | 7 |
| 10 | AI | 124/143 (87%) | 84 (68%) | 16 (13%) | 24 (19%) | 0 | 3 |
| 11 | AJ | 108/121 (89%) | 92 (85%) | 8 (7%) | 8 (7%) | 1 | 18 |
| 12 | AK | 117/137 (85%) | 81 (69%) | 9 (8%) | 27 (23%) | 0 | 2 |
| 13 | AL | 143/145 (99%) | 100 (70%) | 22 (15%) | 21 (15%) | 0 | 5 |
| 14 | AM | 138/146 (94%) | 107 (78%) | 21 (15%) | 10 (7%) | 1 | 19 |
| 15 | AN | 46/56 (82%) | 31 (67%) | 2 (4%) | 13 (28%) | 0 | 0 |
| 16 | AO | 119/151 (79%) | 95 (80%) | 12 (10%) | 12 (10%) | 1 | 12 |
| 17 | AQ | 134/136 (98%) | 90 (67%) | 22 (16%) | 22 (16%) | 0 | 4 |
| 18 | AP | 83/156 (53%) | 65 (78%) | 12 (14%) | 6 (7%) | 1 | 19 |
| 19 | AR | 86/142 (61%) | 64 (74%) | 10 (12%) | 12 (14%) | 0 | 5 |
| 20 | AS | 142/144 (99%) | 118 (83%) | 8 (6%) | 16 (11%) | 0 | 8 |
| 21 | AT | 85/87 (98%) | 66 (78%) | 10 (12%) | 9 (11%) | 0 | 10 |
| 22 | AV | 83/108 (77%) | 66 (80%) | 7 (8%) | 10 (12%) | 0 | 7 |
| 24 | AX | 48/82 (58%) | 37 (77%) | 7 (15%) | 4 (8%) | 1 | 16 |
| 25 | AY | 58/67 (87%) | 46 (79%) | 7 (12%) | 5 (9%) | 1 | 15 |
| 26 | AZ | 61/63 (97%) | 41 (67%) | 6 (10%) | 14 (23%) | 0 | 2 |
| 29 | AU | 94/135 (70%) | 62 (66%) | 14 (15%) | 18 (19%) | 0 | 3 |
| 30 | BA | 215/217 (99%) | 194 (90%) | 11 (5%) | 10 (5%) | 3 | 28 |
| 31 | BB | 252/254 (99%) | 208 (82%) | 18 (7%) | 26 (10%) | 0 | 11 |
| 32 | BC | 386/388 (100%) | 316 (82%) | 33 (8%) | 37 (10%) | 1 | 13 |
| 33 | BD | 325/362 (90%) | 250 (77%) | 34 (10%) | 41 (13%) | 0 | 7 |
| 34 | BE | 166/174 (95%) | 136 (82%) | 11 (7%) | 19 (11%) | 0 | 8 |
| 35 | BG | 174/176 (99%) | 108 (62%) | 15 (9%) | 51 (29%) | 0 | 0 |
| 36 | BF | 189/191 (99%) | 173 (92%) | 13 (7%) | 3 (2%) | 11 | 51 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 37 | BH | 195/256 (76%) | 156 (80%) | 18 (9%) | 21 (11%) | 0 | 10 |
| 38 | Bs | 255/312 (82%) | 224 (88%) | 16 (6%) | 15 (6%) | 2 | 23 |
| 39 | BJ | 125/165 (76%) | 107 (86%) | 11 (9%) | 7 (6%) | 2 | 25 |
| 40 | BK | 197/199 (99%) | 161 (82%) | 15 (8%) | 21 (11%) | 0 | 10 |
| 41 | BN | 136/138 (99%) | 104 (76%) | 14 (10%) | 18 (13%) | 0 | 6 |
| 42 | BM | 129/137 (94%) | 124 (96%) | 5 (4%) | 0 | 100 | 100 |
| 43 | BP | 191/204 (94%) | 168 (88%) | 14 (7%) | 9 (5%) | 3 | 28 |
| 44 | BO | 147/149 (99%) | 100 (68%) | 24 (16%) | 23 (16%) | 0 | 4 |
| 45 | BR | 159/186 (86%) | 116 (73%) | 22 (14%) | 21 (13%) | 0 | 6 |
| 46 | BT | 187/189 (99%) | 163 (87%) | 14 (8%) | 10 (5%) | 2 | 26 |
| 47 | BU | 158/160 (99%) | 144 (91%) | 7 (4%) | 7 (4%) | 3 | 29 |
| 48 | BW | 103/121 (85%) | 79 (77%) | 15 (15%) | 9 (9%) | 1 | 15 |
| 49 | BV | 168/170 (99%) | 135 (80%) | 20 (12%) | 13 (8%) | 1 | 18 |
| 50 | BX | 120/142 (84%) | 95 (79%) | 11 (9%) | 14 (12%) | 0 | 8 |
| 51 | BZ | 71/155 (46%) | 48 (68%) | 13 (18%) | 10 (14%) | 0 | 5 |
| 52 | BY | 121/123 (98%) | 115 (95%) | 2 (2%) | 4 (3%) | 4 | 35 |
| 53 | Ba | 93/136 (68%) | 62 (67%) | 15 (16%) | 16 (17%) | 0 | 4 |
| 54 | Bd | 20/59 (34%) | 19 (95%) | 1 (5%) | 0 | 100 | 100 |
| 55 | Bc | 116/120 (97%) | 92 (79%) | 11 (10%) | 13 (11%) | 0 | 9 |
| 56 | Bf | 103/105 (98%) | 91 (88%) | 7 (7%) | 5 (5%) | 2 | 27 |
| 57 | Be | 237/244 (97%) | 213 (90%) | 14 (6%) | 10 (4%) | 3 | 30 |
| 58 | Bg | 108/113 (96%) | 95 (88%) | 4 (4%) | 9 (8%) | 1 | 16 |
| 59 | Bh | 128/130 (98%) | 115 (90%) | 7 (6%) | 6 (5%) | 3 | 28 |
| 60 | Bi | 116/118 (98%) | 76 (66%) | 13 (11%) | 27 (23%) | 0 | 2 |
| 61 | Bj | 98/107 (92%) | 66 (67%) | 15 (15%) | 17 (17%) | 0 | 4 |
| 62 | Bk | 75/100 (75%) | 61 (81%) | 6 (8%) | 8 (11%) | 0 | 10 |
| 63 | Bm | 90/92 (98%) | 78 (87%) | 10 (11%) | 2 (2%) | 8 | 44 |
| 64 | Bl | 86/88 (98%) | 65 (76%) | 14 (16%) | 7 (8%) | 1 | 16 |
| 65 | Bn | 76/78 (97%) | 56 (74%) | 10 (13%) | 10 (13%) | 0 | 6 |
| 66 | Bo | 49/51 (96%) | 38 (78%) | 3 (6%) | 8 (16%) | 0 | 4 |
| 67 | Bp | 38/52 (73%) | 28 (74%) | 7 (18%) | 3 (8%) | 1 | 17 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|------------------|------------|-----------|------------|-------------|----|
| 68 | Bq | 23/25 (92%) | 21 (91%) | 1 (4%) | 1 (4%) | 3 | 29 |
| 69 | Br | 104/106 (98%) | 71 (68%) | 14 (14%) | 19 (18%) | 0 | 3 |
| 72 | Bt | 56/106 (53%) | 53 (95%) | 0 | 3 (5%) | 2 | 25 |
| 72 | Bu | 56/106 (53%) | 53 (95%) | 0 | 3 (5%) | 2 | 25 |
| 73 | Bv | 56/106 (53%) | 53 (95%) | 1 (2%) | 2 (4%) | 4 | 33 |
| 73 | Bw | 56/106 (53%) | 53 (95%) | 1 (2%) | 2 (4%) | 4 | 33 |
| 74 | BQ | 295/297 (99%) | 232 (79%) | 27 (9%) | 36 (12%) | 0 | 7 |
| 76 | BS | 165/167 (99%) | 116 (70%) | 15 (9%) | 34 (21%) | 0 | 2 |
| 77 | BI | 179/221 (81%) | 135 (75%) | 23 (13%) | 21 (12%) | 0 | 8 |
| All | All | 9997/11298 (88%) | 7958 (80%) | 949 (10%) | 1090 (11%) | 1 | 10 |

5 of 1090 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | Aa | 29 | GLN |
| 1 | Aa | 51 | ASP |
| 1 | Aa | 55 | GLY |
| 1 | Aa | 57 | PRO |
| 1 | Aa | 84 | SER |

5.3.2 Protein sidechains [i](#)

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 1 | Aa | 259/262 (99%) | 238 (92%) | 21 (8%) | 14 | 44 |
| 2 | AA | 198/210 (94%) | 180 (91%) | 18 (9%) | 11 | 38 |
| 3 | AB | 148/195 (76%) | 136 (92%) | 12 (8%) | 14 | 44 |
| 4 | AD | 173/222 (78%) | 158 (91%) | 15 (9%) | 12 | 40 |
| 5 | AC | 153/166 (92%) | 132 (86%) | 21 (14%) | 4 | 23 |
| 6 | AE | 205/205 (100%) | 188 (92%) | 17 (8%) | 13 | 43 |
| 8 | AF | 163/191 (85%) | 144 (88%) | 19 (12%) | 6 | 27 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 9 | AH | 111/111 (100%) | 98 (88%) | 13 (12%) | 6 | 27 |
| 10 | AI | 105/119 (88%) | 93 (89%) | 12 (11%) | 7 | 28 |
| 11 | AJ | 93/114 (82%) | 88 (95%) | 5 (5%) | 26 | 58 |
| 12 | AK | 82/105 (78%) | 77 (94%) | 5 (6%) | 22 | 55 |
| 13 | AL | 87/120 (72%) | 75 (86%) | 12 (14%) | 4 | 23 |
| 14 | AM | 123/129 (95%) | 104 (85%) | 19 (15%) | 3 | 19 |
| 15 | AN | 34/49 (69%) | 30 (88%) | 4 (12%) | 6 | 27 |
| 16 | AO | 105/128 (82%) | 91 (87%) | 14 (13%) | 4 | 24 |
| 17 | AQ | 122/124 (98%) | 109 (89%) | 13 (11%) | 8 | 31 |
| 18 | AP | 63/137 (46%) | 56 (89%) | 7 (11%) | 7 | 29 |
| 19 | AR | 71/118 (60%) | 62 (87%) | 9 (13%) | 5 | 25 |
| 20 | AS | 115/116 (99%) | 100 (87%) | 15 (13%) | 5 | 25 |
| 21 | AT | 74/74 (100%) | 67 (90%) | 7 (10%) | 10 | 36 |
| 22 | AV | 74/89 (83%) | 67 (90%) | 7 (10%) | 10 | 36 |
| 24 | AX | 43/71 (61%) | 33 (77%) | 10 (23%) | 1 | 6 |
| 25 | AY | 50/60 (83%) | 47 (94%) | 3 (6%) | 22 | 55 |
| 26 | AZ | 51/54 (94%) | 47 (92%) | 4 (8%) | 15 | 46 |
| 29 | AU | 72/113 (64%) | 62 (86%) | 10 (14%) | 4 | 23 |
| 30 | BA | 198/198 (100%) | 184 (93%) | 14 (7%) | 17 | 49 |
| 31 | BB | 189/196 (96%) | 177 (94%) | 12 (6%) | 21 | 53 |
| 32 | BC | 315/323 (98%) | 265 (84%) | 50 (16%) | 3 | 18 |
| 33 | BD | 253/289 (88%) | 222 (88%) | 31 (12%) | 5 | 26 |
| 34 | BE | 145/150 (97%) | 118 (81%) | 27 (19%) | 2 | 11 |
| 35 | BG | 153/153 (100%) | 124 (81%) | 29 (19%) | 2 | 11 |
| 36 | BF | 170/171 (99%) | 152 (89%) | 18 (11%) | 8 | 31 |
| 37 | BH | 154/208 (74%) | 136 (88%) | 18 (12%) | 6 | 27 |
| 38 | Bs | 216/254 (85%) | 209 (97%) | 7 (3%) | 44 | 71 |
| 39 | BJ | 102/136 (75%) | 94 (92%) | 8 (8%) | 15 | 46 |
| 40 | BK | 162/162 (100%) | 143 (88%) | 19 (12%) | 6 | 27 |
| 41 | BN | 109/109 (100%) | 96 (88%) | 13 (12%) | 6 | 27 |
| 42 | BM | 101/105 (96%) | 85 (84%) | 16 (16%) | 3 | 18 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|-----|
| 43 | BP | 165/176 (94%) | 141 (86%) | 24 (14%) | 4 | 21 |
| 44 | BO | 119/119 (100%) | 100 (84%) | 19 (16%) | 3 | 18 |
| 45 | BR | 131/151 (87%) | 106 (81%) | 25 (19%) | 2 | 11 |
| 46 | BT | 154/154 (100%) | 144 (94%) | 10 (6%) | 20 | 52 |
| 47 | BU | 132/137 (96%) | 113 (86%) | 19 (14%) | 4 | 22 |
| 48 | BW | 90/107 (84%) | 77 (86%) | 13 (14%) | 4 | 22 |
| 49 | BV | 131/137 (96%) | 117 (89%) | 14 (11%) | 8 | 31 |
| 50 | BX | 106/118 (90%) | 99 (93%) | 7 (7%) | 19 | 52 |
| 51 | BZ | 59/129 (46%) | 51 (86%) | 8 (14%) | 4 | 23 |
| 52 | BY | 107/107 (100%) | 93 (87%) | 14 (13%) | 5 | 24 |
| 53 | Ba | 73/116 (63%) | 63 (86%) | 10 (14%) | 4 | 23 |
| 54 | Bd | 15/47 (32%) | 13 (87%) | 2 (13%) | 4 | 24 |
| 55 | Bc | 104/105 (99%) | 88 (85%) | 16 (15%) | 3 | 19 |
| 56 | Bf | 83/88 (94%) | 75 (90%) | 8 (10%) | 10 | 35 |
| 57 | Be | 202/205 (98%) | 182 (90%) | 20 (10%) | 9 | 34 |
| 58 | Bg | 90/97 (93%) | 79 (88%) | 11 (12%) | 6 | 26 |
| 59 | Bh | 111/111 (100%) | 95 (86%) | 16 (14%) | 4 | 22 |
| 60 | Bi | 99/101 (98%) | 87 (88%) | 12 (12%) | 6 | 27 |
| 61 | Bj | 71/91 (78%) | 63 (89%) | 8 (11%) | 7 | 29 |
| 62 | Bk | 64/82 (78%) | 58 (91%) | 6 (9%) | 10 | 36 |
| 63 | Bm | 72/72 (100%) | 67 (93%) | 5 (7%) | 18 | 51 |
| 64 | Bl | 68/71 (96%) | 61 (90%) | 7 (10%) | 8 | 32 |
| 65 | Bn | 66/69 (96%) | 53 (80%) | 13 (20%) | 1 | 10 |
| 66 | Bo | 46/46 (100%) | 38 (83%) | 8 (17%) | 2 | 14 |
| 67 | Bp | 37/47 (79%) | 35 (95%) | 2 (5%) | 26 | 58 |
| 68 | Bq | 23/23 (100%) | 21 (91%) | 2 (9%) | 12 | 40 |
| 69 | Br | 87/91 (96%) | 76 (87%) | 11 (13%) | 5 | 26 |
| 72 | Bt | 48/76 (63%) | 48 (100%) | 0 | 100 | 100 |
| 72 | Bu | 48/76 (63%) | 48 (100%) | 0 | 100 | 100 |
| 73 | Bv | 47/74 (64%) | 45 (96%) | 2 (4%) | 33 | 64 |
| 73 | Bw | 47/74 (64%) | 46 (98%) | 1 (2%) | 59 | 80 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|------------|-----------|-------------|----|
| 74 | BQ | 238/245 (97%) | 196 (82%) | 42 (18%) | 2 | 14 |
| 76 | BS | 153/153 (100%) | 116 (76%) | 37 (24%) | 1 | 5 |
| 77 | BI | 151/187 (81%) | 133 (88%) | 18 (12%) | 6 | 27 |
| All | All | 8278/9418 (88%) | 7314 (88%) | 964 (12%) | 10 | 28 |

5 of 964 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 35 | BG | 56 | LYS |
| 42 | BM | 22 | ILE |
| 74 | BQ | 159 | VAL |
| 35 | BG | 102 | ASN |
| 37 | BH | 225 | LYS |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 133 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 35 | BG | 125 | GLN |
| 42 | BM | 47 | ASN |
| 67 | Bp | 43 | ASN |
| 35 | BG | 138 | GLN |
| 37 | BH | 243 | GLN |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 78 | CA | 1483/1800 (82%) | 521 (35%) | 0 |
| 79 | CB | 74/75 (98%) | 26 (35%) | 0 |
| 80 | CC | 10/11 (90%) | 7 (70%) | 0 |
| 81 | DA | 3150/3396 (92%) | 1246 (39%) | 0 |
| 82 | DB | 141/158 (89%) | 65 (46%) | 0 |
| 83 | DC | 117/118 (99%) | 60 (51%) | 0 |
| All | All | 4975/5558 (89%) | 1925 (38%) | 0 |

5 of 1925 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 78 | CA | 3 | U |
| 78 | CA | 4 | C |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 78 | CA | 5 | U |
| 78 | CA | 10 | G |
| 78 | CA | 11 | A |

There are no RNA pucker outliers to report.

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 |
|-----|-------|------------------|
| 44 | BO | 3 |
| 23 | AW | 1 |
| 80 | CC | 1 |
| 74 | BQ | 1 |
| 78 | CA | 1 |

The worst 5 of 7 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | AW | 31:UNK | C | 59:UNK | N | 10.96 |
| 1 | CC | 18:C | O3' | 19:U | P | 2.07 |

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| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | CA | 1255:G | O3' | 1256:A | P | 1.94 |
| 1 | BQ | 39:GLN | C | 40:HIS | N | 1.90 |
| 1 | BO | 21:ARG | C | 22:ILE | N | 1.82 |