



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Nov 22, 2016 – 04:48 PM EST

PDB ID : 5LZZ
EMDB ID: : EMD-4137
Title : Structure of the mammalian rescue complex with Pelota and Hbs1l (combined)
Authors : Shao, S.; Murray, J.; Brown, A.; Taunton, J.; Ramakrishnan, V.; Hegde, R.S.
Deposited on : 2016-10-02
Resolution : 3.47 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
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
EM map analysis : **NOT EXECUTED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028320

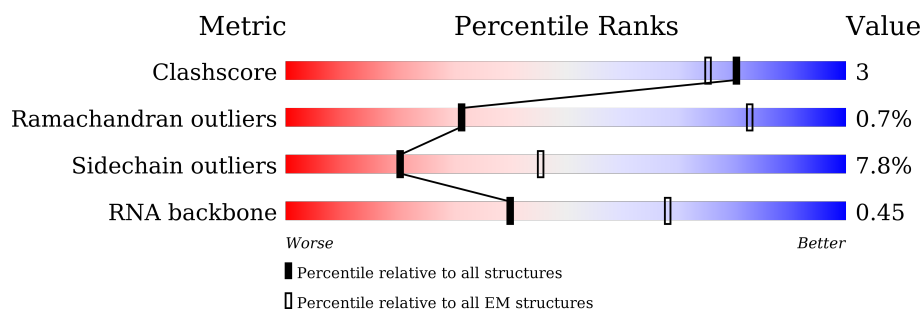
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.47 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.














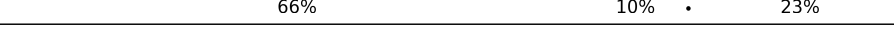





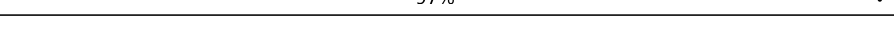

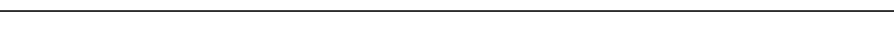

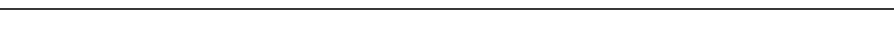
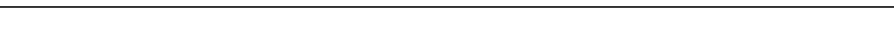


| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Clashscore | 114402 | 924 |
| Ramachandran outliers | 111179 | 726 |
| Sidechain outliers | 111093 | 686 |
| RNA backbone | 3027 | 244 |

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 | A | 257 | |
| 2 | B | 403 | |
| 3 | C | 425 | |
| 4 | D | 297 | |
| 5 | E | 291 | |
| 6 | F | 247 | |
| 7 | G | 319 | |
| 8 | H | 192 | |




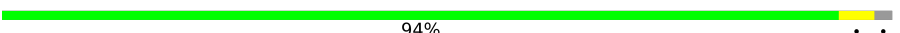





















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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 9 | I | 214 |  84% 11% . . |
| 10 | J | 178 |  82% 12% . . |
| 11 | L | 211 |  91% 8% |
| 12 | M | 218 |  54% 8% . 37% |
| 13 | N | 204 |  85% 13% . |
| 14 | O | 203 |  79% 16% . . |
| 15 | P | 184 |  72% 9% . 17% |
| 16 | Q | 188 |  84% 15% . |
| 17 | R | 196 |  77% 15% . 8% |
| 18 | S | 176 |  81% 18% . |
| 19 | T | 160 |  83% 16% .. |
| 20 | U | 128 |  66% 10% . 23% |
| 21 | V | 140 |  78% 15% . 6% |
| 22 | W | 157 |  61% 7% 32% |
| 23 | X | 156 |  71% 5% 24% |
| 24 | Y | 145 |  81% 11% . 8% |
| 25 | Z | 136 |  86% 13% . |
| 26 | a | 148 |  97% . . |
| 27 | b | 245 |  40% . 58% |
| 28 | c | 115 |  79% 6% 15% |
| 29 | d | 125 |  74% 11% 14% |
| 30 | e | 135 |  89% 6% 5% |
| 31 | f | 110 |  90% 9% . |
| 32 | g | 117 |  91% 6% . |
| 33 | h | 123 |  95% . . |


























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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 34 | i | 105 |  93% . . |
| 35 | j | 97 |  82% 6% 11% |
| 36 | k | 70 |  93% 6% . |
| 37 | l | 51 |  94% . . |
| 38 | m | 102 |  47% . 49% |
| 39 | n | 25 |  92% 8% |
| 40 | o | 106 |  94% . . |
| 41 | p | 92 |  92% 7% . |
| 42 | r | 137 |  80% 11% 9% |
| 43 | s | 318 |  59% . 38% |
| 44 | t | 165 |  89% . 7% |
| 45 | 1 | 7 |  100% |
| 46 | 2 | 76 |  79% 20% . |
| 47 | 3 | 75 |  68% 29% . |
| 48 | 5 | 3543 |  67% 28% 5% |
| 49 | 7 | 120 |  81% 19% |
| 50 | 8 | 156 |  63% 30% . . |
| 51 | 9 | 1869 |  58% 28% . 9% |
| 52 | AA | 295 |  58% 15% . 26% |
| 53 | BB | 264 |  67% 13% . 19% |
| 54 | CC | 293 |  63% 12% 25% |
| 55 | DD | 243 |  82% 11% . 6% |
| 56 | EE | 263 |  84% 16% |
| 57 | FF | 204 |  80% 9% . 9% |
| 58 | GG | 249 |  81% 14% 5% |





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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 59 | HH | 194 |  79%16%5% |
| 60 | II | 208 |  83%15%2% |
| 61 | JJ | 194 |  78%16%6% |
| 62 | KK | 165 |  50%7%42% |
| 63 | LL | 158 |  73%15%12% |
| 64 | MM | 132 |  75%13%12% |
| 65 | NN | 151 |  78%19%3% |
| 66 | OO | 168 |  69%10%21% |
| 67 | PP | 145 |  68%14%18% |
| 68 | QQ | 146 |  86%10%4% |
| 69 | RR | 135 |  83%13%4% |
| 70 | SS | 152 |  75%18%7% |
| 71 | TT | 145 |  88%8%4% |
| 72 | UU | 119 |  71%13%16% |
| 73 | VV | 83 |  86%13%1% |
| 74 | WW | 130 |  76%22%2% |
| 75 | XX | 143 |  79%17%4% |
| 76 | YY | 130 |  81%15%4% |
| 77 | ZZ | 125 |  50%10%40% |
| 78 | aa | 115 |  75%12%13% |
| 79 | bb | 84 |  87%12%1% |
| 80 | cc | 69 |  77%10%13% |
| 81 | dd | 56 |  91%7%2% |
| 82 | ee | 133 |  36%5%59% |
| 83 | ff | 156 |  41%5%54% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 84 | gg | 317 |  93%6% • |
| 85 | hh | 8 |  50%50% |
| 86 | ii | 403 |  88%•8% |
| 87 | jj | 710 |  56%•40% |

2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 222005 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 uL2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 1 | A | 248 | Total | C | N | O | S | 0 | 0 |
| | | | 1898 | 1189 | 389 | 314 | 6 | | |

- Molecule 2 is a protein called uL3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 2 | B | 394 | Total | C | N | O | S | 0 | 0 |
| | | | 3172 | 2020 | 597 | 542 | 13 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------------------|------------|
| B | 1 | MET | - | initiating methionine | UNP G1TL06 |

- Molecule 3 is a protein called uL4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 3 | C | 362 | Total | C | N | O | S | 0 | 0 |
| | | | 2883 | 1812 | 577 | 480 | 14 | | |

- Molecule 4 is a protein called 60S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 4 | D | 293 | Total | C | N | O | S | 0 | 0 |
| | | | 2391 | 1512 | 438 | 427 | 14 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------------------|------------|
| D | 1 | MET | - | initiating methionine | UNP G1SYJ6 |

- Molecule 5 is a protein called 60S ribosomal protein L6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 5 | E | 216 | Total | C | N | O | S | 0 | 0 |
| | | | 1729 | 1115 | 329 | 282 | 3 | | |

- Molecule 6 is a protein called Uncharacterized protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 6 | F | 225 | Total | C | N | O | S | 0 | 0 |
| | | | 1875 | 1205 | 358 | 303 | 9 | | |

There are 4 discrepancies between the modelled and reference sequences:

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

- Molecule 7 is a protein called 60S ribosomal protein L7a,eL8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 7 | G | 233 | Total | C | N | O | S | 0 | 0 |
| | | | 1879 | 1199 | 361 | 315 | 4 | | |

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 8 is a protein called uL6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 8 | H | 190 | Total | C | N | O | S | 0 | 0 |
| | | | 1516 | 954 | 284 | 272 | 6 | | |

- Molecule 9 is a protein called Ribosomal protein L10 (Predicted).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 9 | I | 205 | Total | C | N | O | S | 0 | 0 |
| | | | 1664 | 1056 | 321 | 274 | 13 | | |

- Molecule 10 is a protein called uL5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10 | J | 170 | Total | C | N | O | S | 0 | 0 |
| | | | 1362 | 861 | 254 | 241 | 6 | | |

- Molecule 11 is a protein called eL13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 11 | L | 210 | Total | C | N | O | S | 0 | 0 |
| | | | 1702 | 1065 | 354 | 279 | 4 | | |

- Molecule 12 is a protein called eL14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12 | M | 138 | Total | C | N | O | S | 0 | 0 |
| | | | 1137 | 727 | 221 | 182 | 7 | | |

- Molecule 13 is a protein called Ribosomal protein L15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 13 | N | 203 | Total | C | N | O | S | 0 | 0 |
| | | | 1701 | 1072 | 359 | 266 | 4 | | |

- Molecule 14 is a protein called uL13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 14 | O | 199 | Total | C | N | O | S | 0 | 0 |
| | | | 1630 | 1051 | 319 | 255 | 5 | | |

- Molecule 15 is a protein called uL22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15 | P | 153 | Total | C | N | O | S | 0 | 0 |
| | | | 1242 | 777 | 241 | 215 | 9 | | |

- Molecule 16 is a protein called eL18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16 | Q | 187 | Total | C | N | O | S | 0 | 0 |
| | | | 1515 | 946 | 315 | 250 | 4 | | |

- Molecule 17 is a protein called eL19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17 | R | 180 | Total | C | N | O | S | 0 | 0 |
| | | | 1508 | 933 | 328 | 238 | 9 | | |

- Molecule 18 is a protein called eL20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 18 | S | 176 | Total | C | N | O | S | 0 | 0 |
| | | | 1462 | 930 | 285 | 236 | 11 | | |

- Molecule 19 is a protein called eL21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19 | T | 159 | Total | C | N | O | S | 0 | 0 |
| | | | 1298 | 823 | 252 | 217 | 6 | | |

- Molecule 20 is a protein called eL22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20 | U | 99 | Total | C | N | O | S | 0 | 0 |
| | | | 809 | 519 | 141 | 147 | 2 | | |

- Molecule 21 is a protein called uL14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21 | V | 131 | Total | C | N | O | S | 0 | 0 |
| | | | 979 | 618 | 184 | 172 | 5 | | |

- Molecule 22 is a protein called eL24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 22 | W | 106 | Total | C | N | O | S | 0 | 0 |
| | | | 860 | 538 | 174 | 144 | 4 | | |

- Molecule 23 is a protein called uL23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23 | X | 118 | Total | C | N | O | S | 0 | 0 |
| | | | 967 | 618 | 181 | 167 | 1 | | |

- Molecule 24 is a protein called uL24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24 | Y | 134 | Total | C | N | O | S | 0 | 0 |
| | | | 1115 | 700 | 226 | 186 | 3 | | |

- Molecule 25 is a protein called 60S ribosomal protein L27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25 | Z | 135 | Total | C | N | O | S | 0 | 0 |
| | | | 1107 | 714 | 208 | 182 | 3 | | |

- Molecule 26 is a protein called uL15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 26 | a | 147 | Total | C | N | O | S | 0 | 0 |
| | | | 1162 | 734 | 239 | 185 | 4 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| a | 1 | MET | GLN | conflict | UNP G1SNY0 |

- Molecule 27 is a protein called eL29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27 | b | 104 | Total | C | N | O | S | 0 | 0 |
| | | | 848 | 527 | 189 | 129 | 3 | | |

- Molecule 28 is a protein called eL30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 28 | c | 98 | Total | C | N | O | S | 0 | 0 |
| | | | 761 | 481 | 134 | 140 | 6 | | |

- Molecule 29 is a protein called eL31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29 | d | 107 | Total | C | N | O | S | 0 | 0 |
| | | | 888 | 560 | 171 | 155 | 2 | | |

- Molecule 30 is a protein called eL32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 30 | e | 128 | Total | C | N | O | S | 0 | 0 |
| | | | 1053 | 667 | 216 | 165 | 5 | | |

- Molecule 31 is a protein called eL33.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 31 | f | 109 | Total | C | N | O | S | 0 | 0 |
| | | | 876 | 555 | 174 | 143 | 4 | | |

- Molecule 32 is a protein called eL34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32 | g | 114 | Total | C | N | O | S | 0 | 0 |
| | | | 906 | 566 | 187 | 147 | 6 | | |

- Molecule 33 is a protein called uL29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33 | h | 122 | Total | C | N | O | S | 0 | 0 |
| | | | 1013 | 640 | 204 | 168 | 1 | | |

- Molecule 34 is a protein called 60S ribosomal protein L36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 34 | i | 102 | Total | C | N | O | S | 0 | 0 |
| | | | 830 | 520 | 176 | 129 | 5 | | |

- Molecule 35 is a protein called Ribosomal protein L37.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 35 | j | 86 | Total | C | N | O | S | 0 | 0 |
| | | | 705 | 434 | 155 | 111 | 5 | | |

- Molecule 36 is a protein called eL38.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 36 | k | 69 | Total | C | N | O | S | 0 | 0 |
| | | | 569 | 366 | 103 | 99 | 1 | | |

- Molecule 37 is a protein called eL39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 37 | l | 50 | Total | C | N | O | S | 0 | 0 |
| | | | 447 | 286 | 96 | 64 | 1 | | |

- Molecule 38 is a protein called eL40.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 38 | m | 52 | Total | C | N | O | S | 0 | 0 |
| | | | 429 | 266 | 90 | 67 | 6 | | |

- Molecule 39 is a protein called eL41.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 39 | n | 25 | Total | C | N | O | S | 0 | 0 |
| | | | 239 | 145 | 64 | 27 | 3 | | |

- Molecule 40 is a protein called eL42.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 40 | o | 104 | Total | C | N | O | S | 0 | 0 |
| | | | 851 | 533 | 174 | 138 | 6 | | |

- Molecule 41 is a protein called eL43.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 41 | p | 91 | Total | C | N | O | S | 0 | 0 |
| | | | 708 | 445 | 136 | 120 | 7 | | |

- Molecule 42 is a protein called eL28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42 | r | 124 | Total | C | N | O | S | 0 | 0 |
| | | | 994 | 616 | 205 | 167 | 6 | | |

- Molecule 43 is a protein called uL10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 43 | s | 196 | Total | C | N | O | S | 0 | 0 |
| | | | 1507 | 959 | 263 | 276 | 9 | | |

- Molecule 44 is a protein called uL11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 44 | t | 153 | Total | C | N | O | S | 0 | 0 |
| | | | 1160 | 722 | 218 | 217 | 3 | | |

- Molecule 45 is a protein called Nascent chain.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|----|---|----|---------|-------|
| 45 | 1 | 7 | Total | C | N | O | 0 | 0 |
| | | | 49 | 31 | 8 | 10 | | |

- Molecule 46 is a RNA chain called P-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 46 | 2 | 76 | Total | C | N | O | P | 0 | 0 |
| | | | 1616 | 723 | 291 | 527 | 75 | | |

- Molecule 47 is a RNA chain called E-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 47 | 3 | 75 | Total | C | N | O | P | 0 | 0 |
| | | | 1593 | 712 | 281 | 526 | 74 | | |

- Molecule 48 is a RNA chain called 28S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 48 | 5 | 3543 | Total | C | N | O | P | 0 | 0 |
| | | | 75972 | 33833 | 13910 | 24686 | 3543 | | |

- Molecule 49 is a RNA chain called 5S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 49 | 7 | 120 | Total | C | N | O | P | 0 | 0 |
| | | | 2558 | 1141 | 456 | 842 | 119 | | |

- Molecule 50 is a RNA chain called 5.8S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|---------|-------|
| 50 | 8 | 151 | Total | C | N | O | P | 0 | 0 |
| | | | 3208 | 1432 | 564 | 1062 | 150 | | |

- Molecule 51 is a RNA chain called 18S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 51 | 9 | 1698 | Total | C | N | O | P | 0 | 0 |
| | | | 36249 | 16180 | 6508 | 11864 | 1697 | | |

- Molecule 52 is a protein called uS2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 52 | AA | 217 | Total | C | N | O | S | 0 | 0 |
| | | | 1710 | 1086 | 300 | 316 | 8 | | |

- Molecule 53 is a protein called 40S ribosomal protein S3a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 53 | BB | 213 | Total | C | N | O | S | 0 | 0 |
| | | | 1729 | 1098 | 309 | 308 | 14 | | |

- Molecule 54 is a protein called uS5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 54 | CC | 221 | Total | C | N | O | S | 0 | 0 |
| | | | 1716 | 1111 | 295 | 301 | 9 | | |

- Molecule 55 is a protein called Uncharacterized protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 55 | DD | 228 | Total | C | N | O | S | 0 | 0 |
| | | | 1768 | 1126 | 318 | 316 | 8 | | |

- Molecule 56 is a protein called eS4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 56 | EE | 262 | Total | C | N | O | S | 0 | 0 |
| | | | 2076 | 1324 | 386 | 358 | 8 | | |

- Molecule 57 is a protein called uS7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 57 | FF | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1471 | 921 | 277 | 266 | 7 | | |

- Molecule 58 is a protein called 40S ribosomal protein S6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 58 | GG | 237 | Total | C | N | O | S | 0 | 0 |
| | | | 1923 | 1200 | 387 | 329 | 7 | | |

- Molecule 59 is a protein called eS7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 59 | HH | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1488 | 952 | 271 | 264 | 1 | | |

- Molecule 60 is a protein called 40S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 60 | II | 206 | Total | C | N | O | S | 0 | 0 |
| | | | 1686 | 1058 | 332 | 291 | 5 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| II | 47 | ARG | GLY | conflict | UNP G1TJW1 |

- Molecule 61 is a protein called Ribosomal protein S9 (Predicted).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 61 | JJ | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1525 | 969 | 306 | 248 | 2 | | |

- Molecule 62 is a protein called Uncharacterized protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 62 | KK | 96 | Total | C | N | O | S | 0 | 0 |
| | | | 810 | 530 | 143 | 131 | 6 | | |

- Molecule 63 is a protein called Uncharacterized protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 63 | LL | 143 | Total | C | N | O | S | 0 | 0 |
| | | | 1175 | 749 | 222 | 198 | 6 | | |

- Molecule 64 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 64 | MM | 117 | Total | C | N | O | S | 0 | 0 |
| | | | 908 | 570 | 161 | 169 | 8 | | |

- Molecule 65 is a protein called uS15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 65 | NN | 149 | Total | C | N | O | S | 0 | 0 |
| | | | 1202 | 770 | 228 | 203 | 1 | | |

- Molecule 66 is a protein called uS11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 66 | OO | 136 | Total | C | N | O | S | 0 | 0 |
| | | | 1016 | 621 | 199 | 190 | 6 | | |

- Molecule 67 is a protein called uS19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 67 | PP | 120 | Total | C | N | O | S | 0 | 0 |
| | | | 997 | 635 | 187 | 168 | 7 | | |

- Molecule 68 is a protein called uS9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 68 | QQ | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1128 | 717 | 213 | 195 | 3 | | |

- Molecule 69 is a protein called eS17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 69 | RR | 132 | Total | C | N | O | S | 0 | 0 |
| | | | 1068 | 670 | 199 | 195 | 4 | | |

- Molecule 70 is a protein called uS13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 70 | SS | 144 | Total | C | N | O | S | 0 | 0 |
| | | | 1190 | 746 | 241 | 202 | 1 | | |

- Molecule 71 is a protein called eS19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 71 | TT | 141 | Total | C | N | O | S | 0 | 0 |
| | | | 1097 | 688 | 211 | 195 | 3 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| TT | 119 | GLY | TRP | conflict | UNP G1TN62 |

- Molecule 72 is a protein called uS10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 72 | UU | 100 | Total | C | N | O | S | 0 | 0 |
| | | | 795 | 498 | 152 | 141 | 4 | | |

- Molecule 73 is a protein called eS21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 73 | VV | 83 | Total | C | N | O | S | 0 | 0 |
| | | | 636 | 393 | 117 | 121 | 5 | | |

- Molecule 74 is a protein called uS8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 74 | WW | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1034 | 659 | 193 | 176 | 6 | | |

- Molecule 75 is a protein called uS12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 75 | XX | 141 | Total | C | N | O | S | 0 | 0 |
| | | | 1098 | 693 | 219 | 183 | 3 | | |

- Molecule 76 is a protein called 40S ribosomal protein S24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 76 | YY | 124 | Total | C | N | O | S | 0 | 0 |
| | | | 1011 | 640 | 198 | 168 | 5 | | |

- Molecule 77 is a protein called eS25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 77 | ZZ | 75 | Total | C | N | O | S | 0 | 0 |
| | | | 598 | 382 | 111 | 104 | 1 | | |

- Molecule 78 is a protein called eS26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 78 | aa | 101 | Total | C | N | O | S | 0 | 0 |
| | | | 814 | 507 | 170 | 132 | 5 | | |

- Molecule 79 is a protein called 40S ribosomal protein S27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 79 | bb | 83 | Total | C | N | O | S | 0 | 0 |
| | | | 651 | 408 | 121 | 115 | 7 | | |

- Molecule 80 is a protein called eS28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 80 | cc | 62 | Total | C | N | O | S | 0 | 0 |
| | | | 488 | 297 | 97 | 92 | 2 | | |

- Molecule 81 is a protein called uS14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 81 | dd | 55 | Total | C | N | O | S | 0 | 0 |
| | | | 459 | 286 | 94 | 74 | 5 | | |

- Molecule 82 is a protein called eS30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 82 | ee | 55 | Total | C | N | O | S | 0 | 0 |
| | | | 443 | 274 | 97 | 71 | 1 | | |

- Molecule 83 is a protein called eS31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 83 | ff | 68 | Total | C | N | O | S | 0 | 0 |
| | | | 555 | 351 | 103 | 94 | 7 | | |

- Molecule 84 is a protein called RACK1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 84 | gg | 313 | Total | C | N | O | S | 0 | 0 |
| | | | 2436 | 1535 | 424 | 465 | 12 | | |

- Molecule 85 is a RNA chain called mRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---|---------|-------|
| 85 | hh | 8 | Total | C | N | O | P | 0 | 0 |
| | | | 169 | 76 | 29 | 56 | 8 | | |

- Molecule 86 is a protein called Protein pelota homolog.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 86 | ii | 372 | Total | C | N | O | S | 0 | 0 |
| | | | 2947 | 1844 | 528 | 559 | 16 | | |

There are 19 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| ii | 221 | MET | LEU | variant | UNP Q9BRX2 |
| ii | 386 | GLY | - | expression tag | UNP Q9BRX2 |
| ii | 387 | SER | - | expression tag | UNP Q9BRX2 |
| ii | 388 | GLU | - | expression tag | UNP Q9BRX2 |
| ii | 389 | ASN | - | expression tag | UNP Q9BRX2 |
| ii | 390 | LEU | - | expression tag | UNP Q9BRX2 |
| ii | 391 | TYR | - | expression tag | UNP Q9BRX2 |
| ii | 392 | PHE | - | expression tag | UNP Q9BRX2 |
| ii | 393 | GLN | - | expression tag | UNP Q9BRX2 |
| ii | 394 | GLY | - | expression tag | UNP Q9BRX2 |
| ii | 395 | ALA | - | expression tag | UNP Q9BRX2 |
| ii | 396 | HIS | - | expression tag | UNP Q9BRX2 |
| ii | 397 | HIS | - | expression tag | UNP Q9BRX2 |
| ii | 398 | HIS | - | expression tag | UNP Q9BRX2 |
| ii | 399 | HIS | - | expression tag | UNP Q9BRX2 |
| ii | 400 | HIS | - | expression tag | UNP Q9BRX2 |
| ii | 401 | HIS | - | expression tag | UNP Q9BRX2 |
| ii | 402 | SER | - | expression tag | UNP Q9BRX2 |
| ii | 403 | THR | - | expression tag | UNP Q9BRX2 |

- Molecule 87 is a protein called HBS1-like protein.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 87 | jj | 425 | Total | C | N | O | S | 0 | 0 |
| | | | 3292 | 2100 | 565 | 609 | 18 | | |

There are 26 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------------------|------------|
| jj | -25 | MET | - | initiating methionine | UNP Q9Y450 |
| jj | -24 | ASP | - | expression tag | UNP Q9Y450 |
| jj | -23 | TYR | - | expression tag | UNP Q9Y450 |
| jj | -22 | LYS | - | expression tag | UNP Q9Y450 |
| jj | -21 | ASP | - | expression tag | UNP Q9Y450 |
| jj | -20 | HIS | - | expression tag | UNP Q9Y450 |
| jj | -19 | ASP | - | expression tag | UNP Q9Y450 |
| jj | -18 | GLY | - | expression tag | UNP Q9Y450 |
| jj | -17 | ASP | - | expression tag | UNP Q9Y450 |
| jj | -16 | TYR | - | expression tag | UNP Q9Y450 |
| jj | -15 | LYS | - | expression tag | UNP Q9Y450 |
| jj | -14 | ASP | - | expression tag | UNP Q9Y450 |
| jj | -13 | HIS | - | expression tag | UNP Q9Y450 |
| jj | -12 | ASP | - | expression tag | UNP Q9Y450 |
| jj | -11 | ILE | - | expression tag | UNP Q9Y450 |
| jj | -10 | ASP | - | expression tag | UNP Q9Y450 |
| jj | -9 | TYR | - | expression tag | UNP Q9Y450 |
| jj | -8 | LYS | - | expression tag | UNP Q9Y450 |
| jj | -7 | ASP | - | expression tag | UNP Q9Y450 |
| jj | -6 | ASP | - | expression tag | UNP Q9Y450 |
| jj | -5 | ASP | - | expression tag | UNP Q9Y450 |
| jj | -4 | ASP | - | expression tag | UNP Q9Y450 |
| jj | -3 | LYS | - | expression tag | UNP Q9Y450 |
| jj | -2 | ALA | - | expression tag | UNP Q9Y450 |
| jj | -1 | GLY | - | expression tag | UNP Q9Y450 |
| jj | 0 | SER | - | expression tag | UNP Q9Y450 |

- Molecule 88 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | AltConf |
|-----|-------|----------|-----------------|---------|
| 88 | P | 1 | Total Mg 1 1 | 0 |
| 88 | g | 1 | Total Mg 1 1 | 0 |
| 88 | j | 1 | Total Mg 1 1 | 0 |
| 88 | e | 1 | Total Mg 1 1 | 0 |
| 88 | B | 1 | Total Mg 1 1 | 0 |
| 88 | I | 1 | Total Mg 1 1 | 0 |

Continued on next page...

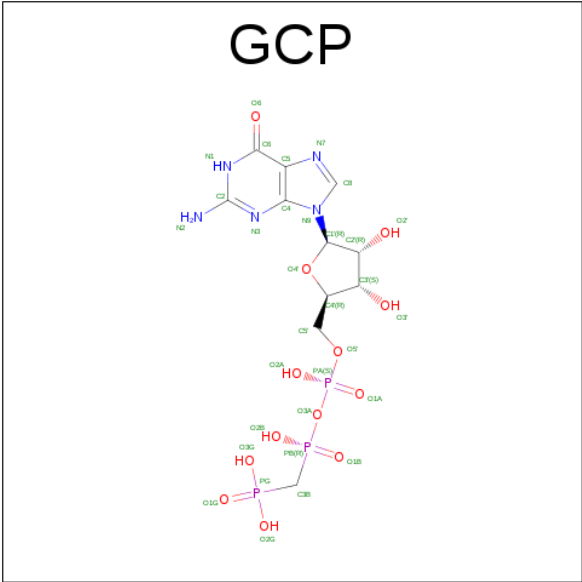
Continued from previous page...

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|--------------|-----------|---------|
| 88 | jj | 1 | Total 1 | Mg 1 | 0 |
| 88 | V | 1 | Total 1 | Mg 1 | 0 |
| 88 | 7 | 5 | Total 5 | Mg 5 | 0 |
| 88 | a | 1 | Total 1 | Mg 1 | 0 |
| 88 | 5 | 178 | Total 178 | Mg 178 | 0 |
| 88 | 8 | 5 | Total 5 | Mg 5 | 0 |
| 88 | 9 | 66 | Total 66 | Mg 66 | 0 |
| 88 | L | 1 | Total 1 | Mg 1 | 0 |

- Molecule 89 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|------------|---------|---------|
| 89 | p | 1 | Total 1 | Zn 1 | 0 |
| 89 | g | 1 | Total 1 | Zn 1 | 0 |
| 89 | j | 1 | Total 1 | Zn 1 | 0 |
| 89 | dd | 1 | Total 1 | Zn 1 | 0 |
| 89 | ff | 1 | Total 1 | Zn 1 | 0 |
| 89 | aa | 1 | Total 1 | Zn 1 | 0 |
| 89 | o | 1 | Total 1 | Zn 1 | 0 |
| 89 | m | 1 | Total 1 | Zn 1 | 0 |

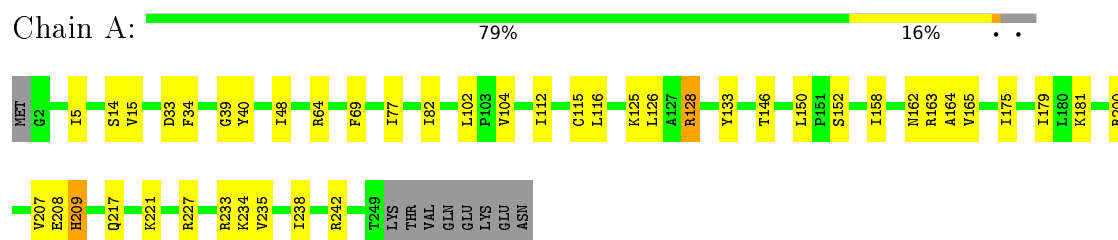
- Molecule 90 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).



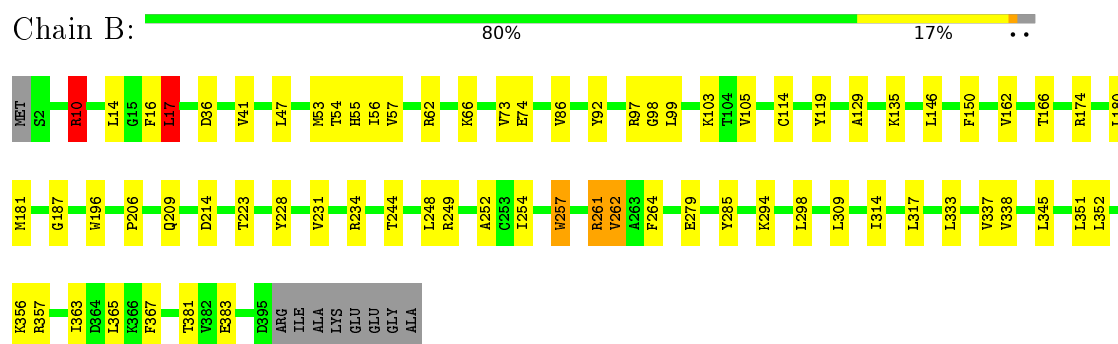
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

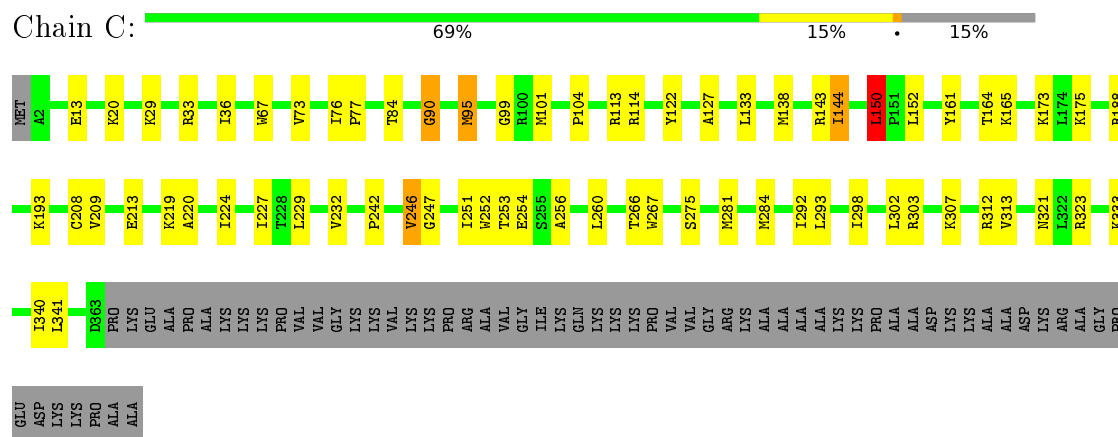
- Molecule 1: uL2




- Molecule 2: uL3

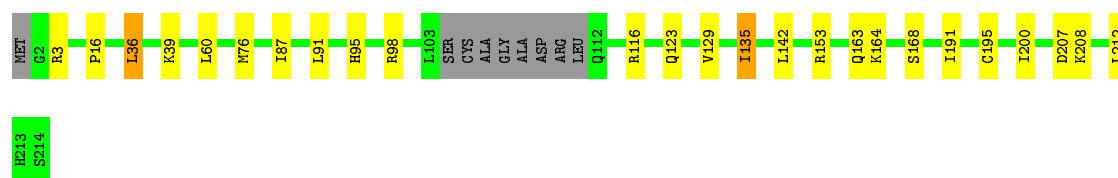


- Molecule 3: uL4



- Molecule 4: 60S ribosomal protein L5

Chain I:  84% 11% . .



- Molecule 10: uL5

Chain J: 82% 12% . .



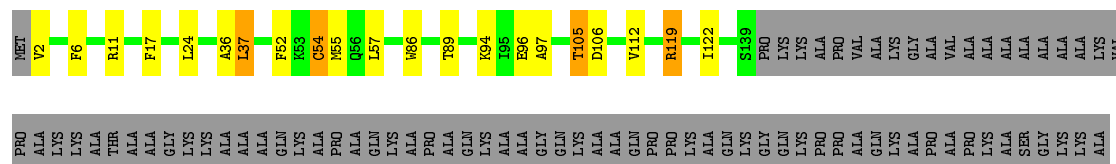
- Molecule 11: eL13

Chain L:  91% 8%



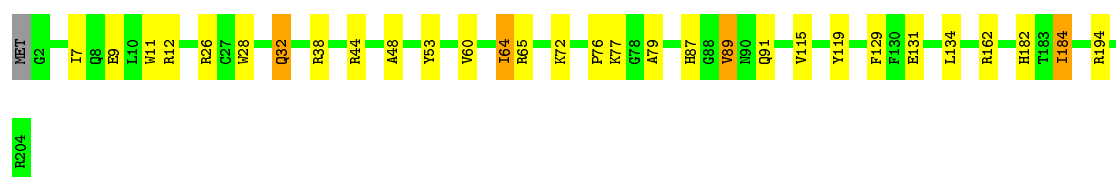
- Molecule 12: eL14

Chain M:  54% 8% • 37%



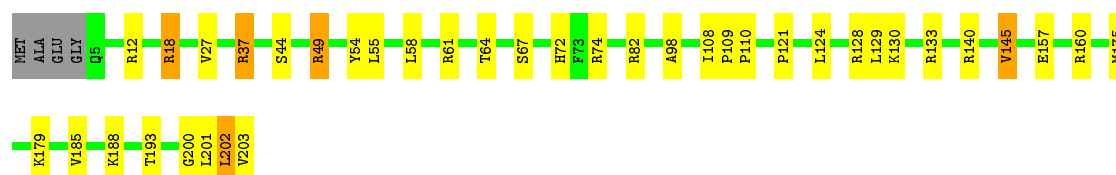
- Molecule 13: Ribosomal protein L15

Chain N: 85% 13%



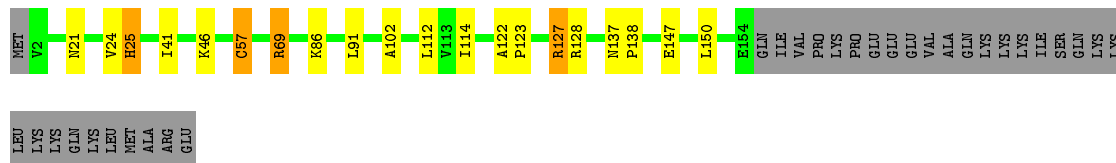
- Molecule 14: uL13

Chain 0: 79% 16% •




- Molecule 15: uL22

Chain P:  72% 9% 17%




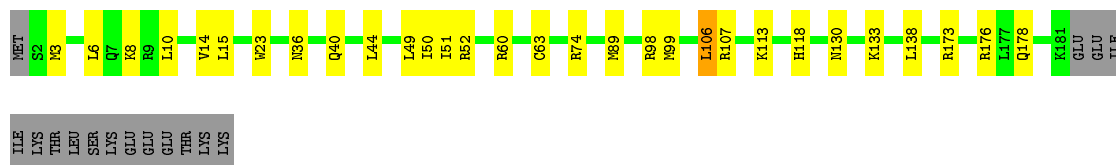
- Molecule 16: eL18

Chain Q:  84% 15%




- Molecule 17: eL19

Chain R:  77% 15% 8%




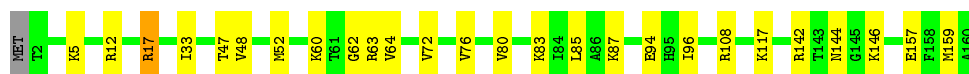
- Molecule 18: eL20

Chain S:  81% 18%



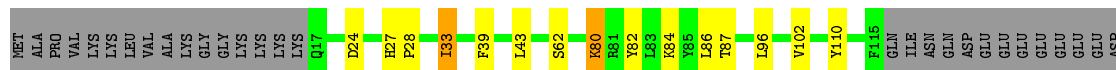
- Molecule 19: eL21

Chain T:  83% 16%



- Molecule 20: eL22

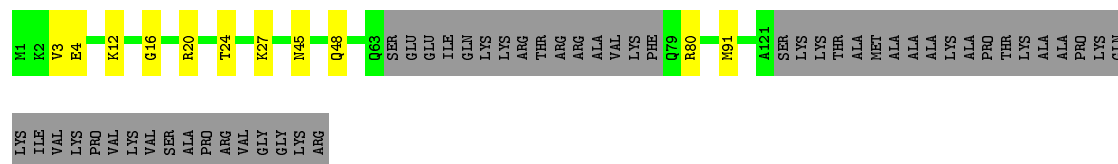
Chain U:  66% 10% 23%



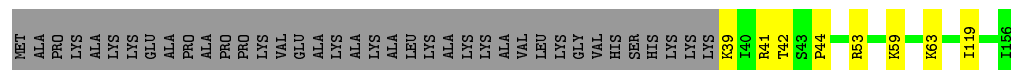
- Molecule 21: uL14



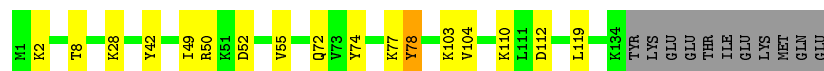
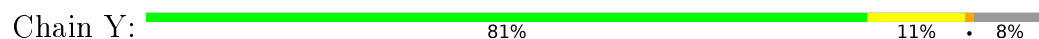
- Molecule 22: eL24



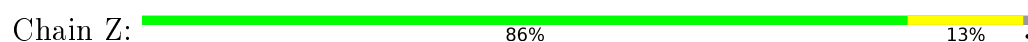
- Molecule 23: uL23



- Molecule 24: uL24



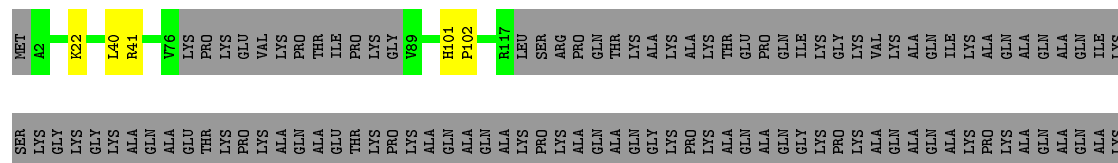
- Molecule 25: 60S ribosomal protein L27



- Molecule 26: uL15




- Molecule 27: eL29



PRO LYS ALA GLN ALA GLN THR PRO LYS LYS ALA GLN ALA THR PRO ALA ALA VAL PRO ALA GLN ALA GLN PRO LYS LYS GLY ALA GLN PRO GLN THR ALA LYS ALA PRO

• Molecule 28: eL30

Chain c:  79% 6% 15%

MET VAL ALA ALA LYS LYS THR LYS LYS S10 M37 N50 N78 L81 G82 T83 R90 V91 C92 S107 MET PRO GLN GLN THR GLY LYS

• Molecule 29: eL31

Chain d:  74% 11% 14%


MET ALA PRO ALA LYS LYS GLY GLY LYS LYS LYS GLY ARG SER SER ALA ALA ILE N18 R23 T26 K31 R44 E48 E56 M57 G58 R78 N79 R83 T84 R85 R90 S98 L117 E124 ASN

• Molecule 30: eL32

Chain e:  89% 6% 5%

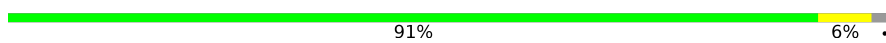
MET A2 I21 R22 R48 R64 L78 E86 K106 R128 L129 ARG SER GLU ASN GLU

• Molecule 31: eL33

Chain f:  90% 9% .

MET S2 R16 R23 L28 V33 K52 S90 I101 L105 Y106 P107 I110

• Molecule 32: eL34

Chain g:  91% 6% .

MET V2 L22 V48 R54 R60 R66 R90 Q114 K115 ALA LYS

• Molecule 33: uL29

Chain h:  95% . .


MET A2 E16 L28 E87 K77 R89 A123

• Molecule 34: 60S ribosomal protein L36

Chain i:  93% . .

MET A2 T34 C48 K36 E89 K103 LYS ASP

- Molecule 35: Ribosomal protein L37

Chain j:  82% 6% 11%



- Molecule 36: eL38

Chain k:  93% 6% .



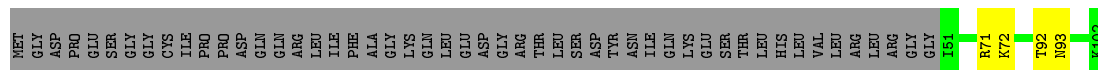
- Molecule 37: eL39

Chain l:  94% . .



- Molecule 38: eL40

Chain m:  47% . 49%



- Molecule 39: eL41

Chain n:  92% 8%



- Molecule 40: eL42

Chain o:  94% . .




- Molecule 41: eL43

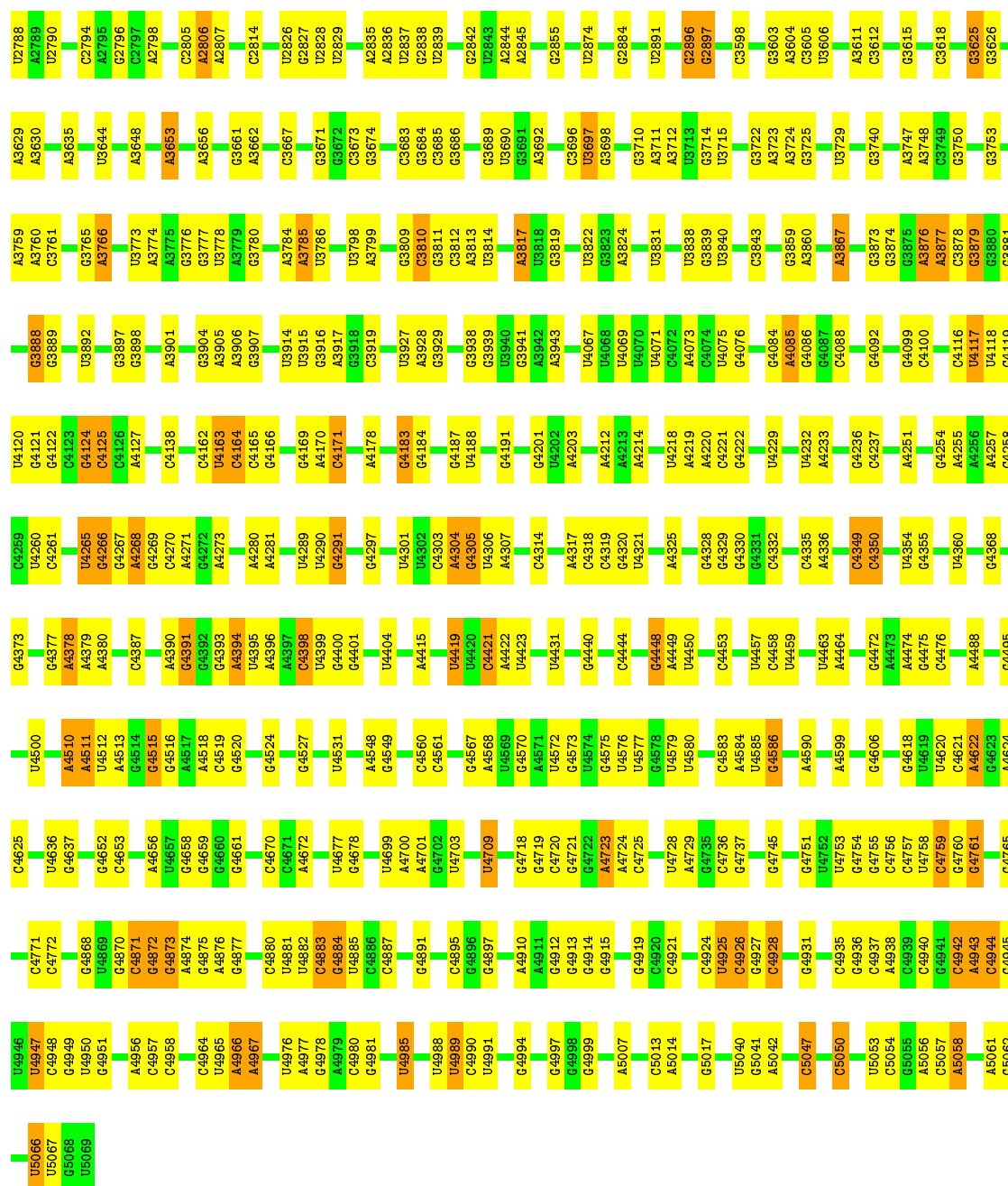
Chain p:  92% 7% .



- Molecule 42: eL28

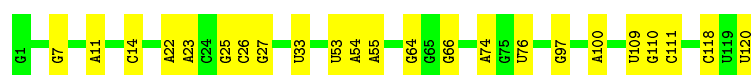
Chain r:  80% 11% 9%

| | | | | | | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|-------|-------|------|-------|------|
| G2686 | G2687 | A2513 | G2514 | G2399 | G2262 | C2031 | A1923 | G1799 | C1676 | C1546 | G1432 | A1326 | G1075 | A917 | G497 | G387 | G234 |
| G2693 | G2694 | U2519 | G2520 | U2409 | G2266 | A2032 | C1928 | G1803 | A1677 | A1547 | A1433 | C1327 | G1076 | G918 | C498 | G399 | A235 |
| G2695 | A2695 | G2521 | G2522 | G2416 | U2267 | G2034 | C1931 | A1804 | A1679 | A1554 | G1435 | G1328 | A1077 | C922 | G499 | A400 | G236 |
| A2696 | A2696 | G2523 | G2524 | A2417 | G2269 | G2044 | A1932 | A1805 | G1685 | A1563 | C1436 | A1330 | C1079 | C922A | G504 | G401 | C245 |
| C2704 | C2704 | U2524 | U2524 | G2421 | G2270 | G2045 | C1935 | G1813 | C1686 | A1564 | U1438 | A1337 | C1082 | C922B | G505 | U404 | G246 |
| U2707 | U2708 | A2529 | U2530 | G2422 | G2274 | G2046 | C1938 | G1819 | G1691 | A1565 | U1440 | G1338 | G1174 | C924 | G647 | U405 | G253 |
| C2709 | C2710 | U2537 | U2538 | G2424 | G2275 | A2047 | C1939 | U1820 | G1694 | U1566 | U1442 | G1339 | G1177 | C925 | G648 | A406 | G262 |
| G2711 | G2712 | C2540 | C2540 | U2428 | G2278 | U2048 | A1939 | U1821 | C1694 | U1567 | C1442 | C1340 | U1177 | G926 | A649 | A408 | G266 |
| G2713 | G2714 | G2433 | G2433 | G2433 | G2279 | G2052 | U1947 | U1822 | G1724 | U1568 | U1445 | G1353 | G1178 | C923 | C654 | A410 | G267 |
| G2715 | G2716 | G2439 | G2440 | U2441 | A2279 | G2055 | G1948 | C1828 | A1729 | U1577 | C1446 | A1354 | U1179 | C930 | C658 | G411 | C265 |
| G2717 | G2718 | U2442 | U2443 | U2444 | G2280 | G2056 | G1951 | G1833 | G1733 | U1578 | G1453 | G1358 | G1195 | C931 | G666 | G412 | C266 |
| C2719 | C2720 | C2441 | C2441 | U2447 | U2281 | A2057 | G1952 | U1834 | G1734 | G1586 | G1454 | G1359 | U1209 | G932 | A667 | G413 | C275 |
| G2721 | G2722 | G2450 | G2450 | G2450 | G2289 | C2062 | G1961 | G1835 | C1740 | U1591 | G1455 | U1364 | C1210 | C934 | C668 | G417 | C276 |
| G2724 | G2725 | C2455 | C2455 | C2455 | C2292 | G2063 | A1962 | G1836 | G1741 | U1596 | G1457 | G1370 | G1212 | C935A | C672 | G423 | G277 |
| G2726 | G2727 | G2466 | G2466 | U2467 | U2293 | G2064 | A1963 | U1837 | G1742 | A1600 | G1458 | A1371 | G1213 | C936 | C683 | U424 | G278 |
| C2729 | C2730 | U2468 | U2468 | U2468 | G2294 | C2068 | C1966 | G1846 | U1744 | A1601 | C1477 | G1377 | C1214 | C938 | G684 | G431 | A279 |
| U2730 | U2730 | G2469 | G2470 | G2470 | G2297 | A2069 | A1967 | C1847 | G1745 | U1602 | C1478 | G1378 | C1215 | G939 | G685 | U432 | U281 |
| G2735 | G2736 | C2471 | C2471 | C2471 | G2300 | C2072 | G1976 | C1848 | A1746 | U1612 | C1479 | G1380 | G1234 | C940 | A686 | A433 | U297 |
| C2739 | C2740 | U2472 | U2472 | U2472 | G2301 | C2081 | C1977 | U1849 | U1747 | A1613 | C1481 | U1381 | G1235 | C941 | U687 | A441 | A306 |
| U2743 | U2744 | G2473 | G2473 | G2473 | A2307 | G2082 | C1978 | G1854 | G1748 | A1624 | G1482 | G1385 | C1236 | C942 | C696 | G444 | A307 |
| G2750 | G2751 | A2587 | A2587 | A2587 | G2313 | C2083 | U1980 | G1855 | G1750 | G1625 | G1483 | G1386 | C1237 | C943 | G697 | U445 | C309 |
| G2754 | G2755 | G2601 | G2601 | G2601 | G2314 | U2084 | G1981 | G1864 | G1753 | A1633 | G1485 | A1387 | C1239 | C944 | C704 | U454 | G310 |
| G2758 | G2759 | A2611 | A2611 | A2611 | G2325 | G2085 | A1982 | U1882 | U1754 | A1634 | G1486 | A1397 | G1280 | C963 | G705 | A466 | C322 |
| G2760 | G2761 | G2620 | G2620 | G2620 | G2326 | A2088 | A1990 | G1869 | G1755 | A1635 | G1488 | A1398 | G1281 | C964 | G729 | U467 | C340 |
| G2762 | G2763 | C2627 | C2627 | C2627 | G2332 | G2089 | A1991 | U1888 | U1756 | A1638 | G1489 | G1401 | G1282 | C965 | G730 | U468 | A347 |
| A2764 | A2765 | G2638 | G2638 | G2638 | G2333 | U2090 | U1992 | G1890 | G1757 | A1639 | G1497 | C1401 | G1284 | C966 | G731 | A452 | A334 |
| U2769 | U2769 | A2647 | A2647 | A2647 | G2343 | C2091 | C1993 | G1891 | G1761 | G1640 | G1498 | A1397 | G1287 | C967 | G741 | G453 | A335 |
| A2783 | A2784 | G2649 | G2649 | G2649 | G2344 | G2092 | U1997 | A1892 | G1762 | G1641 | G1502 | A1406B | G1288 | C968 | G742 | U454 | A336 |
| A2787 | A2787 | U2490 | U2490 | U2490 | G2345 | G2093 | U1999 | G1893 | C1763 | A1641 | G1503 | G1406C | G1291 | C969 | G743 | A466 | C340 |
| | | G2658 | G2658 | G2658 | G2346 | C2094 | A2001 | C1894 | G1764 | U1649 | G1514 | G1406C | G1292 | C971A | G747 | U467 | C347 |
| | | A2647 | A2647 | A2647 | G2347 | A2101 | A2002 | G1895 | U1771 | A1650 | G1515 | G1411A | C1293 | C972 | G749 | U468 | A347 |
| | | G2660 | G2660 | G2660 | G2348 | G2102 | G2003 | A1896 | C1772 | G1651 | G1516 | G1411B | G1294 | C976 | G750 | G481A | C350 |
| | | U2661 | U2661 | U2661 | G2349 | A2103 | U2004 | A1897 | U1773 | A1652 | A1523 | G1412 | U1295 | G977 | G751 | G482 | G356 |
| | | G2662 | G2662 | G2662 | G2350 | G2104 | G2005 | U1905 | A1776 | A1653 | A1524 | G1416 | G1296 | C978 | G756 | G483 | U357 |
| | | G2663 | G2663 | G2663 | G2351 | A2105 | U2008 | U1906 | U1781 | A1654 | A1525 | G1419 | G1301 | C979 | G757 | U484 | G366 |
| | | C2669 | C2669 | C2669 | G2352 | G2106 | U2009 | G1910 | U1782 | U1656 | U1528 | A1420 | U1302 | C983 | G758 | C485 | C361 |
| | | G2670 | G2670 | G2670 | G2353 | A2107 | C2011 | G1918 | C1783 | C1661 | G1529 | G1421 | A1303 | C990 | U911 | G486 | A362 |
| | | A2676 | A2676 | A2676 | G2354 | U2109 | A2017 | G1919 | U1784 | C1665 | G1533 | G1422 | C1304 | C991 | U912 | U492 | A363 |
| | | G2681 | G2681 | G2681 | G2355 | G2110 | G2024 | G1920 | C1785 | A1666 | A1534 | G1428 | C1304 | C1072 | U913 | G483 | U365 |
| | | | | | G2356 | G2259 | A2025 | C1921 | A1786 | A1667 | C1535 | U1428 | C1313 | G1073 | U914 | C494 | A385 |
| | | | | | G2357 | G2261 | A2026 | G1922 | A1787 | | | C1429 | C1325 | G1074 | C495 | G496 | A386 |



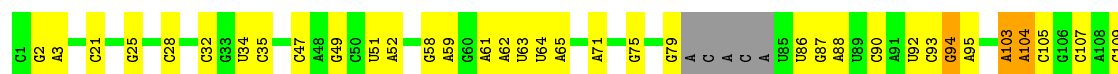
- Molecule 49: 5S ribosomal RNA

Chain 7: 81% 19%



- Molecule 50: 5.8S ribosomal RNA

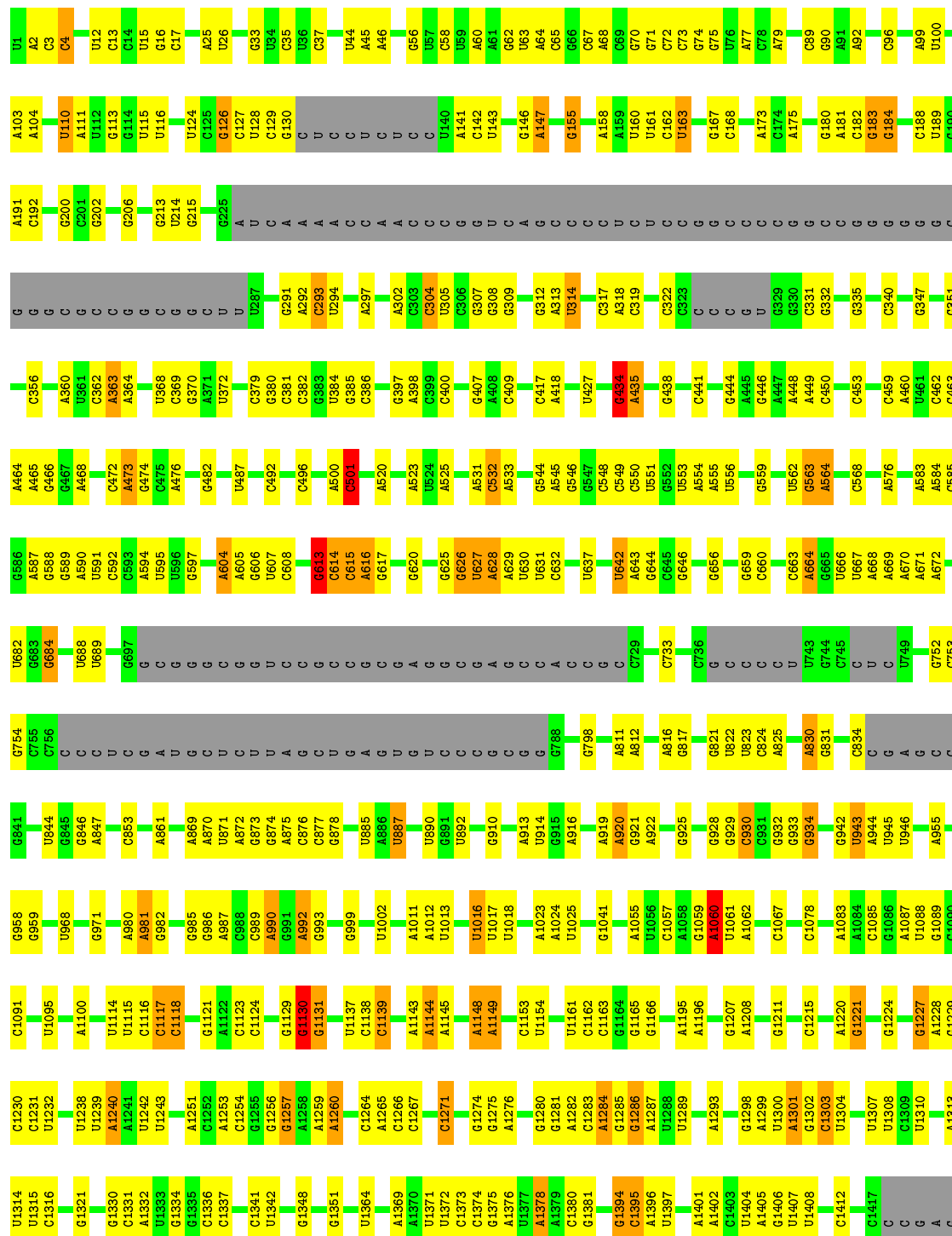
Chain 8: 63% 30%

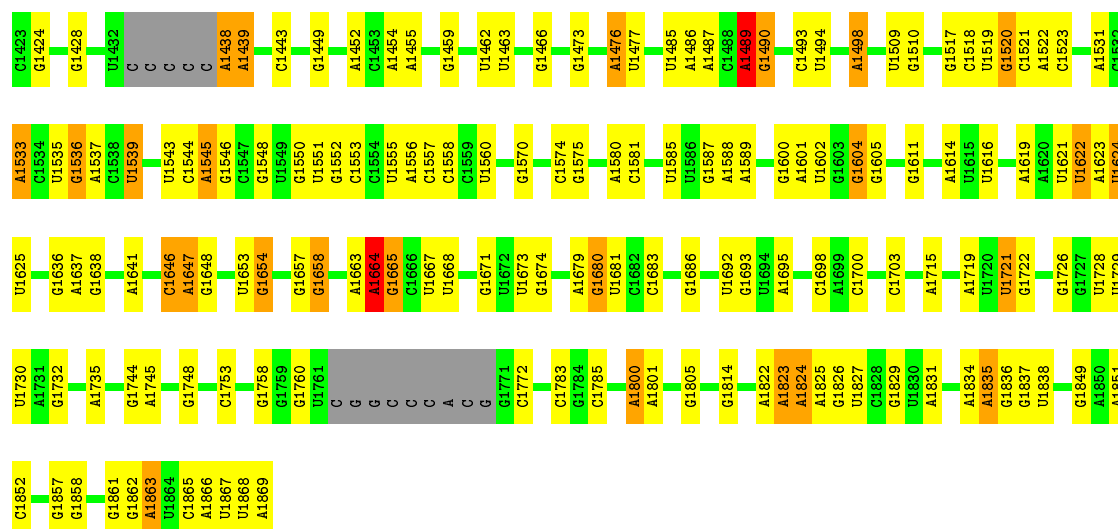




● Molecule 51: 18S ribosomal RNA

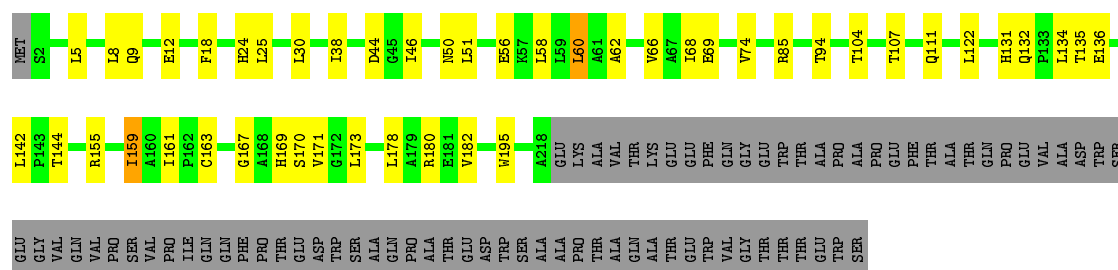
Chain 9: 58% 28% 9%





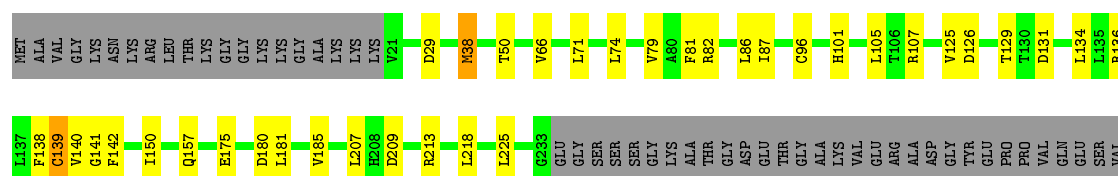
- Molecule 52: uS2

Chain AA: 58% 15% 26%



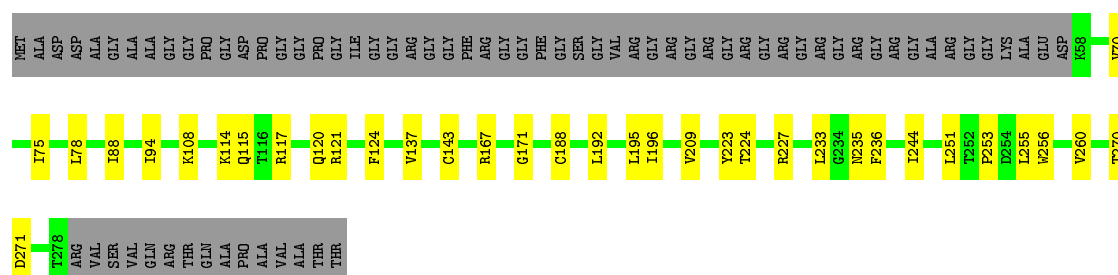
- Molecule 53: 40S ribosomal protein S3a

Chain BB: 67% 13% 19%

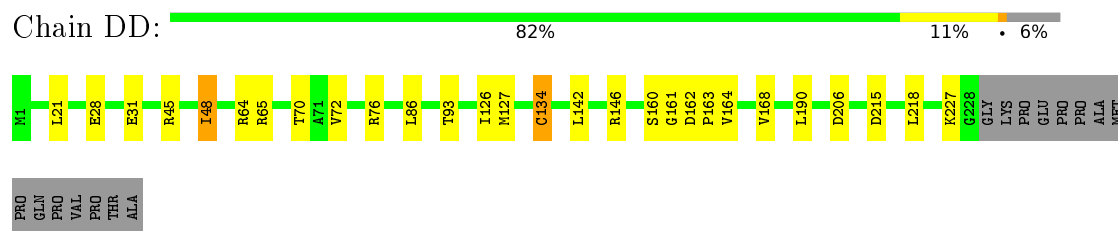


- Molecule 54: uS5

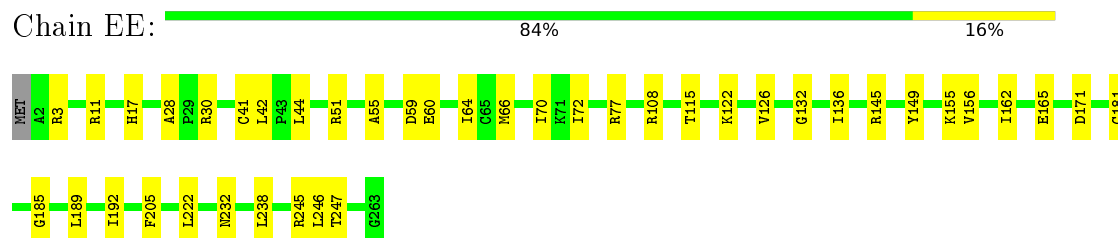
Chain CC: 63% 12% 25%



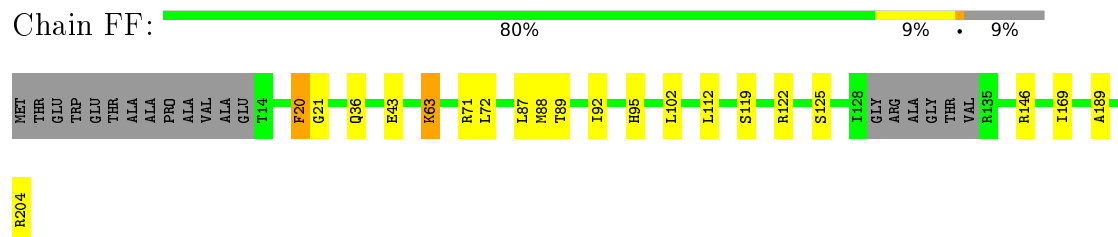
- Molecule 55: Uncharacterized protein



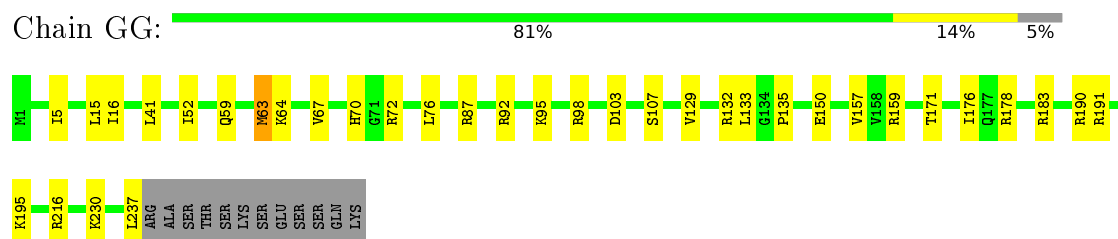
- Molecule 56: eS4



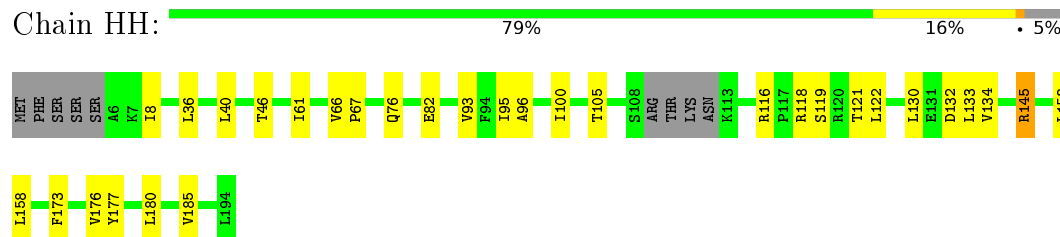
- Molecule 57: uS7



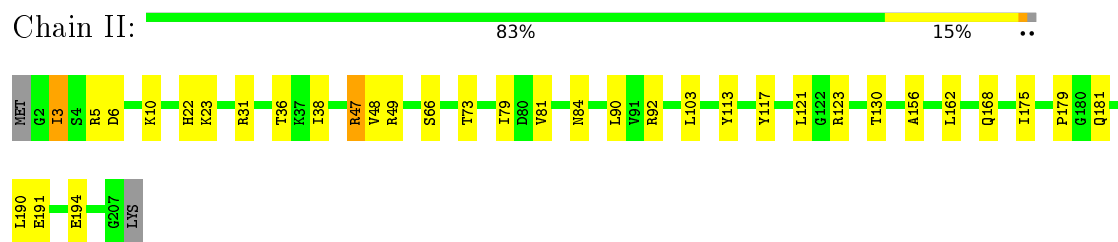
- Molecule 58: 40S ribosomal protein S6



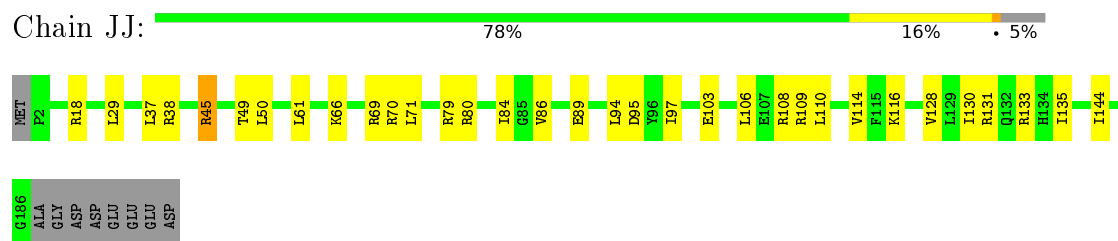
- Molecule 59: eS7



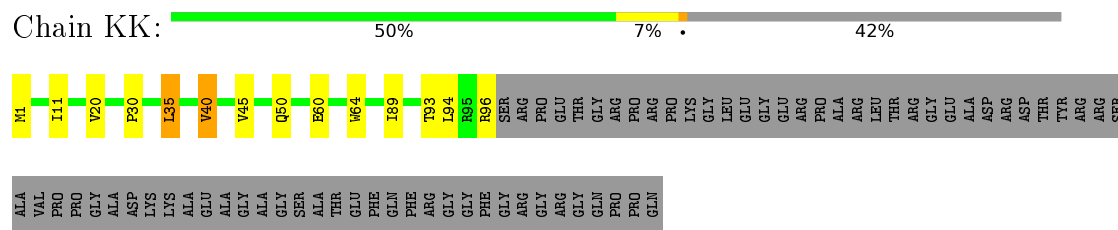
- Molecule 60: 40S ribosomal protein S8



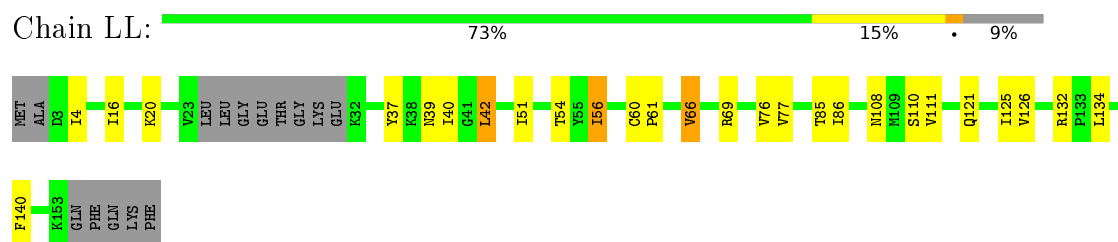
- Molecule 61: Ribosomal protein S9 (Predicted)



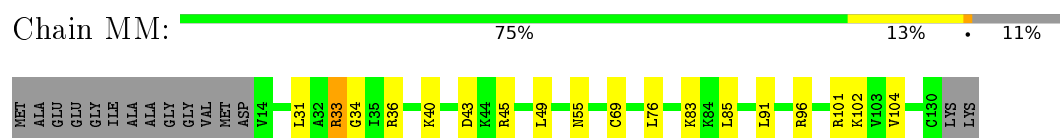
- Molecule 62: Uncharacterized protein



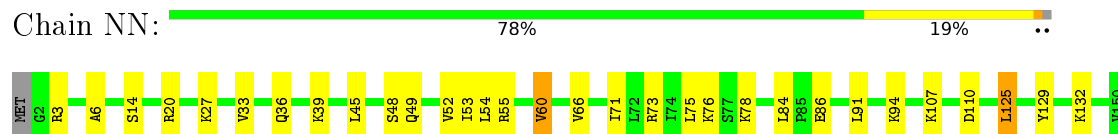
- Molecule 63: Uncharacterized protein



- Molecule 64: 40S ribosomal protein S12



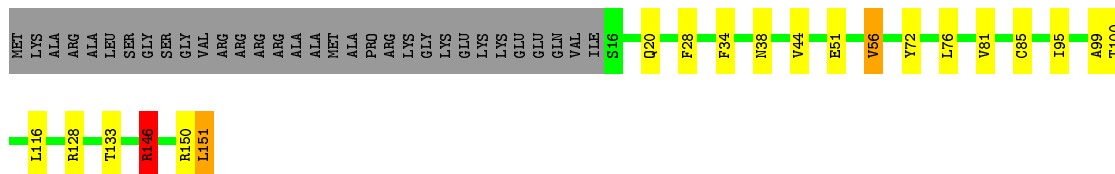
- Molecule 65: uS15



ALA

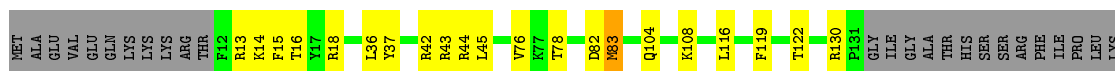
- Molecule 66: uS11

Chain OO:  69% 10% .. 19%




- Molecule 67: uS19

Chain PP:  68% 14% . 17%




- Molecule 68: uS9

Chain QQ:  86% 10% ..




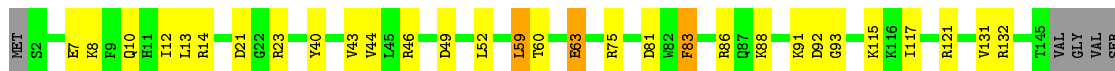
- Molecule 69: eS17

Chain RR:  83% 13% ..




- Molecule 70: uS13

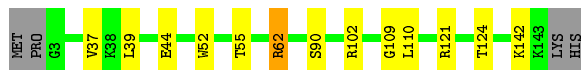
Chain SS:  75% 18% . 5%



LYS
LYS
LYS

- Molecule 71: eS19

Chain TT:  88% 8% ..




- Molecule 72: uS10

Chain UU:  71% 13% 16%




- Molecule 73: eS21

Chain VV:  86% 13%




- Molecule 74: uS8

Chain WW:  76% 22%




- Molecule 75: uS12

Chain XX:  79% 17%



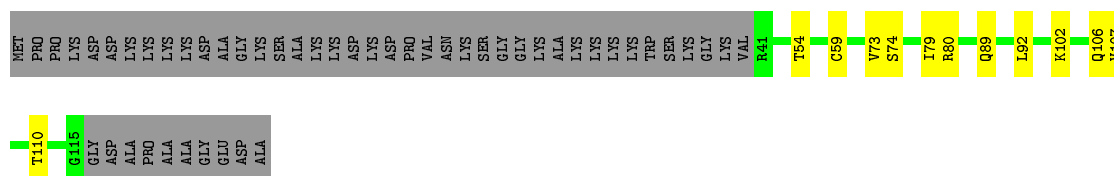
- Molecule 76: 40S ribosomal protein S24

Chain YY:  81% 15% 5%




- Molecule 77: eS25

Chain ZZ:  50% 10% 40%



- Molecule 78: eS26

Chain aa:  75% 12% 12%



- Molecule 79: 40S ribosomal protein S27

- Molecule 80: eS28

| Amino Acid | Percentage |
|------------|------------|
| MET | ~10% |
| ASP | ~10% |
| THR | ~10% |
| SER | ~10% |
| ARG | ~10% |
| VAL | ~10% |
| Q7 | ~10% |
| L18 | ~10% |
| G19 | ~10% |
| R20 | ~10% |
| T21 | ~10% |
| G22 | ~10% |
| R31 | ~10% |
| D36 | ~10% |
| R40 | ~10% |
| R44 | ~10% |
| R51 | ~10% |
| L68 | ~10% |
| ARG | ~10% |

- Molecule 81: uS14

- Molecule 82: eS30

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | GLN | LEU | PHE | VAL | ARG | ALA | GLN | GLU | LEU | HIS | THR | LEU | GLU | VAL | THR | GLY | ARG | GLU | THR | VAL | ALA | ALA | ILE | LYS | ALA | HIS | ALA | VAL | VAL | SER | LEU | GLU | ILE | GLY | ALA | PRO | ASP | GLN | VAL | VAL | VAL | LEU | LEU | ALA | GLY | PRO | LEU | ASP | GLU | THR | LEU | GLY | CYS | VAL | VAL | ILE |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------------|------------|------------|-------------|-------------|-------------|-------------|-------------|-------------|
| ALA | LEU | SER | THR | LEU | GLU | VAL | ALA | GLY | ARG | MET | LEU | GLY | GLY | LVS | VAL | HIS | GLY | \$78 | V85 | K99 | R107 | R108 | M109 | R113 | T121 | S132 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------------|------------|------------|-------------|-------------|-------------|-------------|-------------|-------------|

- Molecule 83: eS31

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| NET | GLN | ILE | PHE | VAL | LYS | THR | THR | THR | GLY | LYS | THR | ILE | THR | THR | LEU | GLU | VAL | VAL | GLU | PRO | SER | ASP | THR | THR | ILE | ILE | GLU | ASN | VAL | LYS | ALA | LYS | ILE | ILE | GLN | ASP | LYS | GLU | GLY | ILE | GLY | PRO | PRO | ASP | ASP | GLN | GLN | GLN | ARG | LEU | ILE | PHE | ALA | ALA | LYS | GLY | GLN | LEU | GLU | GLU | ASP | GLY | ARG | THR | LEU | SER | ASP | TYR | GLN |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|-----|-----|-----|-----|-----|-----|
| ILE | GLN | LYS | GLU | SER | THR | LEU | HIS | LEU | VAL | LEU | ARG | LEU | ARG | GLY | GLY | ALA | LYS | LYS | ARG | LYS | LYS | K83 | K99 | A128 | R138 | H139 | Y140 | F150 | ASN | LYS | PRO | GLU | ASP | LYS |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|-----|-----|-----|-----|-----|-----|

- Molecule 84: RACK1

| | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|
| MET | T2 | G13 | W17 | Q20 | R36 | D37 | K38 | R47 | F113 | E149 | H191 | V198 | C207 | G224 | P243 | E273 | T287 | S288 | L289 | L298 | L306 | I314 | GLY | THR | ARG |
|-----|----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|

- Molecule 85: mRNA

| | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|
| U41 | C42 | A43 | A44 | A45 | G46 | U47 | U48 |
|-----|-----|-----|-----|-----|-----|-----|-----|

4 Experimental information

| Property | Value | Source |
|--------------------------------------|---------------------|-----------|
| Reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | Depositor |
| Number of particles used | 58773 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | Not provided | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | Not provided | Depositor |
| Minimum defocus (nm) | Not provided | Depositor |
| Maximum defocus (nm) | Not provided | Depositor |
| Magnification | 104478 | Depositor |
| Image detector | Not provided | Depositor |

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-------------|-------------|---------------|
| | | RMSZ | $\# Z > 2$ | RMSZ | $\# Z > 2$ |
| 1 | A | 0.44 | 0/1936 | 0.79 | 0/2596 |
| 10 | J | 0.40 | 0/1385 | 0.70 | 0/1852 |
| 11 | L | 0.41 | 0/1733 | 0.74 | 0/2316 |
| 12 | M | 0.44 | 0/1158 | 0.72 | 0/1547 |
| 13 | N | 0.43 | 0/1746 | 0.78 | 0/2338 |
| 14 | O | 0.44 | 0/1662 | 0.73 | 0/2222 |
| 15 | P | 0.49 | 0/1268 | 0.73 | 0/1700 |
| 16 | Q | 0.44 | 0/1539 | 0.82 | 0/2054 |
| 17 | R | 0.41 | 0/1524 | 0.74 | 1/2013 (0.0%) |
| 18 | S | 0.54 | 0/1501 | 0.79 | 1/2012 (0.0%) |
| 19 | T | 0.42 | 0/1326 | 0.70 | 0/1770 |
| 2 | B | 0.48 | 0/3240 | 0.75 | 1/4339 (0.0%) |
| 20 | U | 0.39 | 0/823 | 0.64 | 0/1104 |
| 21 | V | 0.45 | 0/993 | 0.72 | 0/1332 |
| 22 | W | 0.45 | 0/873 | 0.62 | 0/1158 |
| 23 | X | 0.37 | 0/984 | 0.66 | 0/1323 |
| 24 | Y | 0.42 | 0/1132 | 0.72 | 0/1504 |
| 25 | Z | 0.44 | 0/1130 | 0.70 | 0/1507 |
| 26 | a | 0.44 | 0/1191 | 0.72 | 0/1590 |
| 27 | b | 0.37 | 0/861 | 0.63 | 0/1138 |
| 28 | c | 0.40 | 0/771 | 0.60 | 0/1034 |
| 29 | d | 0.44 | 0/903 | 0.75 | 0/1216 |
| 3 | C | 0.46 | 0/2937 | 0.77 | 2/3946 (0.1%) |
| 30 | e | 0.45 | 0/1071 | 0.74 | 0/1429 |
| 31 | f | 0.48 | 0/895 | 0.78 | 0/1198 |
| 32 | g | 0.42 | 0/916 | 0.74 | 0/1220 |
| 33 | h | 0.36 | 0/1021 | 0.66 | 0/1348 |
| 34 | i | 0.43 | 0/841 | 0.69 | 0/1112 |
| 35 | j | 0.45 | 0/720 | 0.77 | 0/952 |
| 36 | k | 0.35 | 0/575 | 0.60 | 0/761 |
| 37 | l | 0.43 | 0/459 | 0.70 | 0/608 |
| 38 | m | 0.47 | 0/435 | 0.72 | 0/575 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-----------------|-------------|------------------|
| | | RMSZ | # Z >2 | RMSZ | # Z >2 |
| 39 | n | 0.39 | 0/240 | 0.77 | 0/305 |
| 4 | D | 0.39 | 0/2437 | 0.69 | 2/3264 (0.1%) |
| 40 | o | 0.44 | 0/864 | 0.70 | 0/1140 |
| 41 | p | 0.47 | 0/718 | 0.70 | 0/953 |
| 42 | r | 0.47 | 0/1010 | 0.76 | 0/1354 |
| 43 | s | 0.37 | 0/1530 | 0.49 | 0/2064 |
| 44 | t | 0.36 | 0/1174 | 0.52 | 0/1582 |
| 45 | 1 | 0.48 | 0/49 | 0.59 | 0/65 |
| 46 | 2 | 0.26 | 0/1805 | 0.66 | 0/2809 |
| 47 | 3 | 0.23 | 0/1777 | 0.66 | 0/2763 |
| 48 | 5 | 0.41 | 15/84961 (0.0%) | 0.78 | 53/132460 (0.0%) |
| 49 | 7 | 0.37 | 0/2858 | 0.67 | 0/4455 |
| 5 | E | 0.38 | 0/1762 | 0.69 | 0/2362 |
| 50 | 8 | 0.38 | 0/3581 | 0.70 | 0/5577 |
| 51 | 9 | 0.37 | 3/40523 (0.0%) | 0.73 | 14/63130 (0.0%) |
| 52 | AA | 0.40 | 0/1747 | 0.67 | 0/2374 |
| 53 | BB | 0.38 | 0/1756 | 0.64 | 0/2350 |
| 54 | CC | 0.40 | 0/1753 | 0.70 | 0/2369 |
| 55 | DD | 0.37 | 0/1796 | 0.65 | 0/2417 |
| 56 | EE | 0.37 | 0/2118 | 0.69 | 0/2849 |
| 57 | FF | 0.35 | 0/1492 | 0.66 | 0/2005 |
| 58 | GG | 0.37 | 0/1946 | 0.69 | 0/2590 |
| 59 | HH | 0.36 | 0/1510 | 0.61 | 0/2022 |
| 6 | F | 0.54 | 0/1911 | 0.79 | 0/2549 |
| 60 | II | 0.40 | 0/1715 | 0.72 | 0/2287 |
| 61 | JJ | 0.40 | 0/1550 | 0.76 | 0/2069 |
| 62 | KK | 0.39 | 0/834 | 0.61 | 0/1125 |
| 63 | LL | 0.41 | 0/1195 | 0.73 | 0/1597 |
| 64 | MM | 0.37 | 0/918 | 0.62 | 0/1233 |
| 65 | NN | 0.40 | 0/1226 | 0.74 | 0/1649 |
| 66 | OO | 0.42 | 0/1029 | 0.83 | 1/1380 (0.1%) |
| 67 | PP | 0.40 | 0/1017 | 0.71 | 0/1358 |
| 68 | QQ | 0.36 | 0/1146 | 0.66 | 0/1534 |
| 69 | RR | 0.37 | 0/1082 | 0.65 | 0/1452 |
| 7 | G | 0.40 | 0/1910 | 0.68 | 0/2569 |
| 70 | SS | 0.37 | 0/1208 | 0.70 | 0/1618 |
| 71 | TT | 0.37 | 0/1115 | 0.66 | 0/1493 |
| 72 | UU | 0.37 | 0/805 | 0.68 | 0/1081 |
| 73 | VV | 0.41 | 0/643 | 0.73 | 0/860 |
| 74 | WW | 0.45 | 0/1051 | 0.79 | 2/1406 (0.1%) |
| 75 | XX | 0.43 | 0/1116 | 0.75 | 1/1490 (0.1%) |
| 76 | YY | 0.37 | 0/1028 | 0.67 | 0/1366 |
| 77 | ZZ | 0.36 | 0/604 | 0.66 | 0/810 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|------------------|-------------|------------------|
| | | RMSZ | # Z >2 | RMSZ | # Z >2 |
| 78 | aa | 0.42 | 0/828 | 0.80 | 0/1109 |
| 79 | bb | 0.37 | 0/665 | 0.65 | 0/891 |
| 8 | H | 0.42 | 0/1535 | 0.69 | 0/2063 |
| 80 | cc | 0.37 | 0/490 | 0.73 | 0/656 |
| 81 | dd | 0.43 | 0/470 | 0.72 | 0/623 |
| 82 | ee | 0.38 | 0/447 | 0.70 | 0/587 |
| 83 | ff | 0.37 | 0/567 | 0.53 | 0/753 |
| 84 | gg | 0.34 | 0/2493 | 0.59 | 0/3394 |
| 85 | hh | 0.28 | 0/188 | 0.79 | 0/290 |
| 86 | ii | 0.34 | 0/2996 | 0.58 | 0/4050 |
| 87 | jj | 0.34 | 0/3352 | 0.57 | 0/4523 |
| 9 | I | 0.43 | 0/1702 | 0.69 | 0/2272 |
| All | All | 0.40 | 18/237792 (0.0%) | 0.73 | 78/348210 (0.0%) |

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 |
|-----|-------|---------------------|---------------------|
| 11 | L | 0 | 1 |
| 13 | N | 0 | 1 |
| 2 | B | 0 | 2 |
| 3 | C | 0 | 1 |
| 31 | f | 0 | 1 |
| 48 | 5 | 0 | 2 |
| 56 | EE | 0 | 1 |
| 74 | WW | 0 | 1 |
| 75 | XX | 0 | 1 |
| 78 | aa | 0 | 1 |
| 80 | cc | 0 | 1 |
| All | All | 0 | 13 |

The worst 5 of 18 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|--------|------|-------|--------|-------------|----------|
| 48 | 5 | 935 | A | C5-C6 | -15.99 | 1.26 | 1.41 |
| 48 | 5 | 935 | A | C6-N1 | -12.18 | 1.27 | 1.35 |
| 48 | 5 | 935 | A | C2-N3 | 10.23 | 1.42 | 1.33 |
| 48 | 5 | 481 | G | N1-C2 | -9.91 | 1.29 | 1.37 |
| 48 | 5 | 922(A) | G | O3'-P | 9.08 | 1.72 | 1.61 |

The worst 5 of 78 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|--------|-------------|----------|
| 48 | 5 | 481 | G | N1-C2-N2 | -52.63 | 68.83 | 116.20 |
| 48 | 5 | 935 | A | C5-C6-N6 | -48.73 | 84.72 | 123.70 |
| 48 | 5 | 935 | A | N1-C6-N6 | -35.80 | 97.12 | 118.60 |
| 48 | 5 | 935 | A | C6-N1-C2 | -31.95 | 99.43 | 118.60 |
| 48 | 5 | 481 | G | N3-C2-N2 | -29.88 | 98.98 | 119.90 |

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 2 | B | 16 | PHE | Peptide |
| 2 | B | 257 | TRP | Peptide |
| 3 | C | 90 | GLY | Peptide |
| 11 | L | 71 | ARG | Peptide |
| 13 | N | 184 | ILE | Peptide |

5.2 Too-close contacts [i](#)

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 | A | 1898 | 0 | 1993 | 23 | 0 |
| 2 | B | 3172 | 0 | 3310 | 29 | 0 |
| 3 | C | 2883 | 0 | 3053 | 34 | 0 |
| 4 | D | 2391 | 0 | 2424 | 16 | 0 |
| 5 | E | 1729 | 0 | 1887 | 8 | 0 |
| 6 | F | 1875 | 0 | 1995 | 16 | 0 |
| 7 | G | 1879 | 0 | 2027 | 14 | 0 |
| 8 | H | 1516 | 0 | 1597 | 19 | 0 |
| 9 | I | 1664 | 0 | 1712 | 9 | 0 |
| 10 | J | 1362 | 0 | 1399 | 10 | 0 |
| 11 | L | 1702 | 0 | 1820 | 4 | 0 |
| 12 | M | 1137 | 0 | 1211 | 13 | 0 |
| 13 | N | 1701 | 0 | 1749 | 16 | 0 |
| 14 | O | 1630 | 0 | 1778 | 23 | 0 |
| 15 | P | 1242 | 0 | 1274 | 8 | 0 |
| 16 | Q | 1515 | 0 | 1634 | 12 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 17 | R | 1508 | 0 | 1664 | 10 | 0 |
| 18 | S | 1462 | 0 | 1508 | 19 | 0 |
| 19 | T | 1298 | 0 | 1366 | 11 | 0 |
| 20 | U | 809 | 0 | 833 | 7 | 0 |
| 21 | V | 979 | 0 | 1039 | 7 | 0 |
| 22 | W | 860 | 0 | 903 | 9 | 0 |
| 23 | X | 967 | 0 | 1040 | 2 | 0 |
| 24 | Y | 1115 | 0 | 1205 | 5 | 0 |
| 25 | Z | 1107 | 0 | 1182 | 9 | 0 |
| 26 | a | 1162 | 0 | 1209 | 0 | 0 |
| 27 | b | 848 | 0 | 920 | 0 | 0 |
| 28 | c | 761 | 0 | 794 | 0 | 0 |
| 29 | d | 888 | 0 | 930 | 0 | 0 |
| 30 | e | 1053 | 0 | 1147 | 0 | 0 |
| 31 | f | 876 | 0 | 912 | 0 | 0 |
| 32 | g | 906 | 0 | 1002 | 0 | 0 |
| 33 | h | 1013 | 0 | 1147 | 0 | 0 |
| 34 | i | 830 | 0 | 916 | 0 | 0 |
| 35 | j | 705 | 0 | 738 | 0 | 0 |
| 36 | k | 569 | 0 | 637 | 0 | 0 |
| 37 | l | 447 | 0 | 480 | 0 | 0 |
| 38 | m | 429 | 0 | 466 | 0 | 0 |
| 39 | n | 239 | 0 | 289 | 0 | 0 |
| 40 | o | 851 | 0 | 920 | 0 | 0 |
| 41 | p | 708 | 0 | 756 | 0 | 0 |
| 42 | r | 994 | 0 | 1051 | 0 | 0 |
| 43 | s | 1507 | 0 | 1564 | 0 | 0 |
| 44 | t | 1160 | 0 | 1218 | 0 | 0 |
| 45 | 1 | 49 | 0 | 51 | 0 | 0 |
| 46 | 2 | 1616 | 0 | 824 | 2 | 0 |
| 47 | 3 | 1593 | 0 | 811 | 3 | 0 |
| 48 | 5 | 75972 | 0 | 38398 | 321 | 0 |
| 49 | 7 | 2558 | 0 | 1296 | 7 | 0 |
| 50 | 8 | 3208 | 0 | 1629 | 14 | 0 |
| 51 | 9 | 36249 | 0 | 18317 | 197 | 0 |
| 52 | AA | 1710 | 0 | 1708 | 18 | 0 |
| 53 | BB | 1729 | 0 | 1803 | 14 | 0 |
| 54 | CC | 1716 | 0 | 1806 | 11 | 0 |
| 55 | DD | 1768 | 0 | 1866 | 9 | 0 |
| 56 | EE | 2076 | 0 | 2177 | 13 | 0 |
| 57 | FF | 1471 | 0 | 1522 | 7 | 0 |
| 58 | GG | 1923 | 0 | 2089 | 12 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 59 | HH | 1488 | 0 | 1582 | 15 | 0 |
| 60 | II | 1686 | 0 | 1772 | 14 | 0 |
| 61 | JJ | 1525 | 0 | 1640 | 10 | 0 |
| 62 | KK | 810 | 0 | 836 | 7 | 0 |
| 63 | LL | 1175 | 0 | 1249 | 8 | 0 |
| 64 | MM | 908 | 0 | 939 | 16 | 0 |
| 65 | NN | 1202 | 0 | 1289 | 11 | 0 |
| 66 | OO | 1016 | 0 | 1039 | 11 | 0 |
| 67 | PP | 997 | 0 | 1045 | 19 | 0 |
| 68 | QQ | 1128 | 0 | 1195 | 8 | 0 |
| 69 | RR | 1068 | 0 | 1121 | 7 | 0 |
| 70 | SS | 1190 | 0 | 1249 | 22 | 0 |
| 71 | TT | 1097 | 0 | 1132 | 3 | 0 |
| 72 | UU | 795 | 0 | 862 | 4 | 0 |
| 73 | VV | 636 | 0 | 637 | 5 | 0 |
| 74 | WW | 1034 | 0 | 1080 | 13 | 0 |
| 75 | XX | 1098 | 0 | 1167 | 13 | 0 |
| 76 | YY | 1011 | 0 | 1083 | 3 | 0 |
| 77 | ZZ | 598 | 0 | 656 | 3 | 0 |
| 78 | aa | 814 | 0 | 863 | 0 | 0 |
| 79 | bb | 651 | 0 | 672 | 0 | 0 |
| 80 | cc | 488 | 0 | 514 | 0 | 0 |
| 81 | dd | 459 | 0 | 449 | 0 | 0 |
| 82 | ee | 443 | 0 | 492 | 0 | 0 |
| 83 | ff | 555 | 0 | 565 | 0 | 0 |
| 84 | gg | 2436 | 0 | 2393 | 0 | 0 |
| 85 | hh | 169 | 0 | 86 | 0 | 0 |
| 86 | ii | 2947 | 0 | 2957 | 0 | 0 |
| 87 | jj | 3292 | 0 | 3371 | 0 | 0 |
| 88 | 5 | 178 | 0 | 0 | 0 | 0 |
| 88 | 7 | 5 | 0 | 0 | 0 | 0 |
| 88 | 8 | 5 | 0 | 0 | 0 | 0 |
| 88 | 9 | 66 | 0 | 0 | 0 | 0 |
| 88 | B | 1 | 0 | 0 | 0 | 0 |
| 88 | I | 1 | 0 | 0 | 0 | 0 |
| 88 | L | 1 | 0 | 0 | 0 | 0 |
| 88 | P | 1 | 0 | 0 | 0 | 0 |
| 88 | V | 1 | 0 | 0 | 0 | 0 |
| 88 | a | 1 | 0 | 0 | 0 | 0 |
| 88 | e | 1 | 0 | 0 | 0 | 0 |
| 88 | g | 1 | 0 | 0 | 0 | 0 |
| 88 | j | 1 | 0 | 0 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 88 | jj | 1 | 0 | 0 | 0 | 0 |
| 89 | aa | 1 | 0 | 0 | 0 | 0 |
| 89 | dd | 1 | 0 | 0 | 0 | 0 |
| 89 | ff | 1 | 0 | 0 | 0 | 0 |
| 89 | g | 1 | 0 | 0 | 0 | 0 |
| 89 | j | 1 | 0 | 0 | 0 | 0 |
| 89 | m | 1 | 0 | 0 | 0 | 0 |
| 89 | o | 1 | 0 | 0 | 0 | 0 |
| 89 | p | 1 | 0 | 0 | 0 | 0 |
| 90 | jj | 32 | 0 | 14 | 0 | 0 |
| All | All | 222005 | 0 | 166945 | 993 | 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 3.

The worst 5 of 993 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) |
|-----------------|--------------------|--------------------------|-------------------|
| 48:5:3914:U:O4 | 48:5:4378:A:N1 | 1.58 | 1.35 |
| 48:5:922:C:C5' | 48:5:922(A):G:H3' | 1.59 | 1.31 |
| 48:5:922:C:H5'' | 48:5:922(B):C:O5' | 1.38 | 1.23 |
| 51:9:1283:C:N4 | 64:MM:102:LYS:HE3 | 1.52 | 1.21 |
| 48:5:1411:C:H4' | 48:5:1411(C):C:O4' | 1.41 | 1.16 |

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 | A | 246/257 (96%) | 220 (89%) | 24 (10%) | 2 (1%) | 24 | 69 |
| 2 | B | 392/403 (97%) | 355 (91%) | 35 (9%) | 2 (0%) | 34 | 77 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 3 | C | 360/425 (85%) | 332 (92%) | 23 (6%) | 5 (1%) | 14 | 57 |
| 4 | D | 291/297 (98%) | 278 (96%) | 10 (3%) | 3 (1%) | 19 | 65 |
| 5 | E | 208/291 (72%) | 189 (91%) | 19 (9%) | 0 | 100 | 100 |
| 6 | F | 223/247 (90%) | 204 (92%) | 16 (7%) | 3 (1%) | 15 | 59 |
| 7 | G | 229/319 (72%) | 216 (94%) | 11 (5%) | 2 (1%) | 21 | 67 |
| 8 | H | 188/192 (98%) | 172 (92%) | 16 (8%) | 0 | 100 | 100 |
| 9 | I | 201/214 (94%) | 177 (88%) | 23 (11%) | 1 (0%) | 34 | 77 |
| 10 | J | 168/178 (94%) | 157 (94%) | 9 (5%) | 2 (1%) | 16 | 61 |
| 11 | L | 208/211 (99%) | 193 (93%) | 14 (7%) | 1 (0%) | 34 | 77 |
| 12 | M | 136/218 (62%) | 125 (92%) | 11 (8%) | 0 | 100 | 100 |
| 13 | N | 201/204 (98%) | 181 (90%) | 19 (10%) | 1 (0%) | 34 | 77 |
| 14 | O | 197/203 (97%) | 183 (93%) | 13 (7%) | 1 (0%) | 34 | 77 |
| 15 | P | 151/184 (82%) | 140 (93%) | 9 (6%) | 2 (1%) | 15 | 59 |
| 16 | Q | 185/188 (98%) | 168 (91%) | 16 (9%) | 1 (0%) | 34 | 77 |
| 17 | R | 178/196 (91%) | 171 (96%) | 6 (3%) | 1 (1%) | 30 | 74 |
| 18 | S | 174/176 (99%) | 159 (91%) | 12 (7%) | 3 (2%) | 11 | 53 |
| 19 | T | 157/160 (98%) | 142 (90%) | 15 (10%) | 0 | 100 | 100 |
| 20 | U | 97/128 (76%) | 86 (89%) | 9 (9%) | 2 (2%) | 9 | 49 |
| 21 | V | 129/140 (92%) | 113 (88%) | 16 (12%) | 0 | 100 | 100 |
| 22 | W | 102/157 (65%) | 93 (91%) | 8 (8%) | 1 (1%) | 19 | 65 |
| 23 | X | 116/156 (74%) | 109 (94%) | 6 (5%) | 1 (1%) | 21 | 67 |
| 24 | Y | 132/145 (91%) | 126 (96%) | 5 (4%) | 1 (1%) | 24 | 69 |
| 25 | Z | 133/136 (98%) | 123 (92%) | 8 (6%) | 2 (2%) | 13 | 56 |
| 26 | a | 145/148 (98%) | 135 (93%) | 10 (7%) | 0 | 100 | 100 |
| 27 | b | 100/245 (41%) | 93 (93%) | 6 (6%) | 1 (1%) | 19 | 65 |
| 28 | c | 96/115 (84%) | 89 (93%) | 7 (7%) | 0 | 100 | 100 |
| 29 | d | 105/125 (84%) | 94 (90%) | 10 (10%) | 1 (1%) | 19 | 65 |
| 30 | e | 126/135 (93%) | 121 (96%) | 5 (4%) | 0 | 100 | 100 |
| 31 | f | 107/110 (97%) | 97 (91%) | 8 (8%) | 2 (2%) | 10 | 51 |
| 32 | g | 112/117 (96%) | 103 (92%) | 8 (7%) | 1 (1%) | 21 | 67 |
| 33 | h | 120/123 (98%) | 116 (97%) | 3 (2%) | 1 (1%) | 24 | 69 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 34 | i | 100/105 (95%) | 92 (92%) | 8 (8%) | 0 | 100 | 100 |
| 35 | j | 84/97 (87%) | 74 (88%) | 9 (11%) | 1 (1%) | 16 | 61 |
| 36 | k | 67/70 (96%) | 63 (94%) | 3 (4%) | 1 (2%) | 13 | 56 |
| 37 | l | 48/51 (94%) | 41 (85%) | 7 (15%) | 0 | 100 | 100 |
| 38 | m | 50/102 (49%) | 46 (92%) | 4 (8%) | 0 | 100 | 100 |
| 39 | n | 23/25 (92%) | 22 (96%) | 1 (4%) | 0 | 100 | 100 |
| 40 | o | 102/106 (96%) | 92 (90%) | 9 (9%) | 1 (1%) | 19 | 65 |
| 41 | p | 89/92 (97%) | 81 (91%) | 7 (8%) | 1 (1%) | 17 | 63 |
| 42 | r | 122/137 (89%) | 104 (85%) | 14 (12%) | 4 (3%) | 5 | 39 |
| 43 | s | 194/318 (61%) | 174 (90%) | 18 (9%) | 2 (1%) | 19 | 65 |
| 44 | t | 151/165 (92%) | 134 (89%) | 15 (10%) | 2 (1%) | 15 | 59 |
| 45 | 1 | 5/7 (71%) | 2 (40%) | 3 (60%) | 0 | 100 | 100 |
| 52 | AA | 215/295 (73%) | 195 (91%) | 19 (9%) | 1 (0%) | 34 | 77 |
| 53 | BB | 211/264 (80%) | 199 (94%) | 12 (6%) | 0 | 100 | 100 |
| 54 | CC | 219/293 (75%) | 202 (92%) | 16 (7%) | 1 (0%) | 34 | 77 |
| 55 | DD | 226/243 (93%) | 206 (91%) | 18 (8%) | 2 (1%) | 21 | 67 |
| 56 | EE | 260/263 (99%) | 242 (93%) | 18 (7%) | 0 | 100 | 100 |
| 57 | FF | 181/204 (89%) | 168 (93%) | 10 (6%) | 3 (2%) | 11 | 53 |
| 58 | GG | 235/249 (94%) | 217 (92%) | 17 (7%) | 1 (0%) | 39 | 80 |
| 59 | HH | 181/194 (93%) | 168 (93%) | 13 (7%) | 0 | 100 | 100 |
| 60 | II | 204/208 (98%) | 191 (94%) | 11 (5%) | 2 (1%) | 19 | 65 |
| 61 | JJ | 183/194 (94%) | 175 (96%) | 8 (4%) | 0 | 100 | 100 |
| 62 | KK | 94/165 (57%) | 85 (90%) | 6 (6%) | 3 (3%) | 5 | 40 |
| 63 | LL | 139/158 (88%) | 124 (89%) | 14 (10%) | 1 (1%) | 26 | 72 |
| 64 | MM | 115/132 (87%) | 99 (86%) | 16 (14%) | 0 | 100 | 100 |
| 65 | NN | 147/151 (97%) | 134 (91%) | 13 (9%) | 0 | 100 | 100 |
| 66 | OO | 134/168 (80%) | 120 (90%) | 13 (10%) | 1 (1%) | 26 | 72 |
| 67 | PP | 118/145 (81%) | 103 (87%) | 14 (12%) | 1 (1%) | 24 | 69 |
| 68 | QQ | 140/146 (96%) | 132 (94%) | 8 (6%) | 0 | 100 | 100 |
| 69 | RR | 130/135 (96%) | 115 (88%) | 14 (11%) | 1 (1%) | 24 | 69 |
| 70 | SS | 142/152 (93%) | 134 (94%) | 8 (6%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 71 | TT | 139/145 (96%) | 131 (94%) | 7 (5%) | 1 (1%) | 26 | 72 |
| 72 | UU | 98/119 (82%) | 92 (94%) | 6 (6%) | 0 | 100 | 100 |
| 73 | VV | 81/83 (98%) | 76 (94%) | 5 (6%) | 0 | 100 | 100 |
| 74 | WW | 127/130 (98%) | 116 (91%) | 9 (7%) | 2 (2%) | 12 | 54 |
| 75 | XX | 139/143 (97%) | 124 (89%) | 12 (9%) | 3 (2%) | 8 | 48 |
| 76 | YY | 122/130 (94%) | 116 (95%) | 6 (5%) | 0 | 100 | 100 |
| 77 | ZZ | 73/125 (58%) | 71 (97%) | 2 (3%) | 0 | 100 | 100 |
| 78 | aa | 99/115 (86%) | 88 (89%) | 9 (9%) | 2 (2%) | 9 | 50 |
| 79 | bb | 81/84 (96%) | 73 (90%) | 7 (9%) | 1 (1%) | 16 | 61 |
| 80 | cc | 60/69 (87%) | 55 (92%) | 3 (5%) | 2 (3%) | 5 | 39 |
| 81 | dd | 53/56 (95%) | 48 (91%) | 5 (9%) | 0 | 100 | 100 |
| 82 | ee | 53/133 (40%) | 50 (94%) | 3 (6%) | 0 | 100 | 100 |
| 83 | ff | 66/156 (42%) | 60 (91%) | 5 (8%) | 1 (2%) | 13 | 56 |
| 84 | gg | 311/317 (98%) | 284 (91%) | 24 (8%) | 3 (1%) | 19 | 65 |
| 86 | ii | 370/403 (92%) | 343 (93%) | 26 (7%) | 1 (0%) | 46 | 83 |
| 87 | jj | 423/710 (60%) | 381 (90%) | 38 (9%) | 4 (1%) | 21 | 67 |
| All | All | 12317/14495 (85%) | 11302 (92%) | 923 (8%) | 92 (1%) | 31 | 72 |

5 of 92 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 6 | F | 236 | GLU |
| 18 | S | 155 | PRO |
| 31 | f | 107 | PRO |
| 75 | XX | 62 | PRO |
| 87 | jj | 605 | GLN |

5.3.2 Protein sidechains ⓘ

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

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 1 | A | 190/199 (96%) | 176 (93%) | 14 (7%) | 17 | 56 |
| 2 | B | 342/348 (98%) | 312 (91%) | 30 (9%) | 12 | 48 |
| 3 | C | 302/347 (87%) | 278 (92%) | 24 (8%) | 15 | 53 |
| 4 | D | 247/250 (99%) | 236 (96%) | 11 (4%) | 34 | 73 |
| 5 | E | 190/251 (76%) | 179 (94%) | 11 (6%) | 25 | 65 |
| 6 | F | 196/215 (91%) | 177 (90%) | 19 (10%) | 10 | 42 |
| 7 | G | 200/272 (74%) | 186 (93%) | 14 (7%) | 19 | 59 |
| 8 | H | 169/171 (99%) | 155 (92%) | 14 (8%) | 14 | 50 |
| 9 | I | 175/181 (97%) | 161 (92%) | 14 (8%) | 15 | 52 |
| 10 | J | 143/149 (96%) | 134 (94%) | 9 (6%) | 22 | 63 |
| 11 | L | 175/176 (99%) | 165 (94%) | 10 (6%) | 25 | 66 |
| 12 | M | 117/161 (73%) | 109 (93%) | 8 (7%) | 20 | 60 |
| 13 | N | 171/172 (99%) | 161 (94%) | 10 (6%) | 25 | 65 |
| 14 | O | 171/173 (99%) | 156 (91%) | 15 (9%) | 12 | 48 |
| 15 | P | 134/163 (82%) | 124 (92%) | 10 (8%) | 17 | 55 |
| 16 | Q | 164/165 (99%) | 149 (91%) | 15 (9%) | 12 | 46 |
| 17 | R | 159/175 (91%) | 143 (90%) | 16 (10%) | 9 | 41 |
| 18 | S | 157/157 (100%) | 145 (92%) | 12 (8%) | 16 | 55 |
| 19 | T | 139/140 (99%) | 126 (91%) | 13 (9%) | 11 | 44 |
| 20 | U | 89/114 (78%) | 87 (98%) | 2 (2%) | 60 | 85 |
| 21 | V | 101/107 (94%) | 90 (89%) | 11 (11%) | 8 | 36 |
| 22 | W | 86/126 (68%) | 85 (99%) | 1 (1%) | 78 | 91 |
| 23 | X | 106/134 (79%) | 101 (95%) | 5 (5%) | 32 | 72 |
| 24 | Y | 124/135 (92%) | 116 (94%) | 8 (6%) | 21 | 62 |
| 25 | Z | 117/118 (99%) | 112 (96%) | 5 (4%) | 35 | 74 |
| 26 | a | 119/120 (99%) | 115 (97%) | 4 (3%) | 44 | 79 |
| 27 | b | 84/184 (46%) | 80 (95%) | 4 (5%) | 31 | 71 |
| 28 | c | 84/98 (86%) | 77 (92%) | 7 (8%) | 14 | 50 |
| 29 | d | 98/110 (89%) | 85 (87%) | 13 (13%) | 5 | 26 |
| 30 | e | 114/121 (94%) | 106 (93%) | 8 (7%) | 19 | 59 |
| 31 | f | 88/89 (99%) | 81 (92%) | 7 (8%) | 15 | 52 |
| 32 | g | 98/100 (98%) | 92 (94%) | 6 (6%) | 23 | 63 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|-----|
| 33 | h | 109/110 (99%) | 104 (95%) | 5 (5%) | 33 | 72 |
| 34 | i | 86/89 (97%) | 82 (95%) | 4 (5%) | 32 | 72 |
| 35 | j | 73/80 (91%) | 68 (93%) | 5 (7%) | 20 | 60 |
| 36 | k | 64/65 (98%) | 61 (95%) | 3 (5%) | 32 | 72 |
| 37 | l | 47/48 (98%) | 45 (96%) | 2 (4%) | 35 | 74 |
| 38 | m | 48/90 (53%) | 44 (92%) | 4 (8%) | 14 | 50 |
| 39 | n | 24/24 (100%) | 22 (92%) | 2 (8%) | 14 | 50 |
| 40 | o | 92/94 (98%) | 89 (97%) | 3 (3%) | 45 | 79 |
| 41 | p | 74/75 (99%) | 69 (93%) | 5 (7%) | 20 | 60 |
| 42 | r | 108/121 (89%) | 97 (90%) | 11 (10%) | 9 | 40 |
| 43 | s | 164/258 (64%) | 158 (96%) | 6 (4%) | 41 | 76 |
| 44 | t | 126/137 (92%) | 122 (97%) | 4 (3%) | 46 | 80 |
| 45 | l | 6/6 (100%) | 6 (100%) | 0 | 100 | 100 |
| 52 | AA | 180/245 (74%) | 161 (89%) | 19 (11%) | 8 | 38 |
| 53 | BB | 194/231 (84%) | 176 (91%) | 18 (9%) | 11 | 45 |
| 54 | CC | 187/225 (83%) | 170 (91%) | 17 (9%) | 12 | 46 |
| 55 | DD | 190/202 (94%) | 173 (91%) | 17 (9%) | 12 | 47 |
| 56 | EE | 224/225 (100%) | 204 (91%) | 20 (9%) | 12 | 47 |
| 57 | FF | 158/170 (93%) | 147 (93%) | 11 (7%) | 19 | 59 |
| 58 | GG | 207/218 (95%) | 185 (89%) | 22 (11%) | 8 | 38 |
| 59 | HH | 165/174 (95%) | 152 (92%) | 13 (8%) | 15 | 53 |
| 60 | II | 178/180 (99%) | 167 (94%) | 11 (6%) | 23 | 63 |
| 61 | JJ | 161/168 (96%) | 142 (88%) | 19 (12%) | 6 | 31 |
| 62 | KK | 87/136 (64%) | 81 (93%) | 6 (7%) | 19 | 59 |
| 63 | LL | 130/142 (92%) | 114 (88%) | 16 (12%) | 6 | 29 |
| 64 | MM | 99/108 (92%) | 86 (87%) | 13 (13%) | 5 | 26 |
| 65 | NN | 130/131 (99%) | 114 (88%) | 16 (12%) | 6 | 29 |
| 66 | OO | 106/130 (82%) | 97 (92%) | 9 (8%) | 13 | 49 |
| 67 | PP | 109/130 (84%) | 97 (89%) | 12 (11%) | 8 | 36 |
| 68 | QQ | 117/121 (97%) | 110 (94%) | 7 (6%) | 24 | 64 |
| 69 | RR | 119/121 (98%) | 109 (92%) | 10 (8%) | 14 | 50 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-------------------|------------|----------|-------------|----|
| 70 | SS | 125/132 (95%) | 107 (86%) | 18 (14%) | 4 | 22 |
| 71 | TT | 111/115 (96%) | 102 (92%) | 9 (8%) | 15 | 52 |
| 72 | UU | 92/107 (86%) | 83 (90%) | 9 (10%) | 10 | 42 |
| 73 | VV | 67/67 (100%) | 63 (94%) | 4 (6%) | 24 | 64 |
| 74 | WW | 112/113 (99%) | 103 (92%) | 9 (8%) | 15 | 52 |
| 75 | XX | 113/115 (98%) | 105 (93%) | 8 (7%) | 18 | 58 |
| 76 | YY | 107/112 (96%) | 92 (86%) | 15 (14%) | 4 | 24 |
| 77 | ZZ | 66/103 (64%) | 59 (89%) | 7 (11%) | 8 | 38 |
| 78 | aa | 88/98 (90%) | 75 (85%) | 13 (15%) | 4 | 21 |
| 79 | bb | 75/76 (99%) | 66 (88%) | 9 (12%) | 6 | 30 |
| 80 | cc | 55/62 (89%) | 47 (86%) | 8 (14%) | 4 | 22 |
| 81 | dd | 48/49 (98%) | 44 (92%) | 4 (8%) | 14 | 50 |
| 82 | ee | 46/106 (43%) | 39 (85%) | 7 (15%) | 3 | 20 |
| 83 | ff | 61/140 (44%) | 58 (95%) | 3 (5%) | 31 | 70 |
| 84 | gg | 272/275 (99%) | 257 (94%) | 15 (6%) | 27 | 67 |
| 86 | ii | 326/353 (92%) | 310 (95%) | 16 (5%) | 31 | 70 |
| 87 | jj | 358/608 (59%) | 331 (92%) | 27 (8%) | 17 | 55 |
| All | All | 10733/12306 (87%) | 9892 (92%) | 841 (8%) | 20 | 53 |

5 of 841 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 41 | p | 47 | MET |
| 55 | DD | 190 | LEU |
| 82 | ee | 109 | MET |
| 42 | r | 67 | ARG |
| 53 | BB | 82 | ARG |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 43 | s | 34 | ASN |
| 56 | EE | 98 | ASN |
| 86 | ii | 109 | GLN |
| 54 | CC | 235 | ASN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 57 | FF | 118 | ASN |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 46 | 2 | 74/76 (97%) | 15 (20%) | 0 |
| 47 | 3 | 72/75 (96%) | 21 (29%) | 1 (1%) |
| 48 | 5 | 3506/3543 (98%) | 881 (25%) | 182 (5%) |
| 49 | 7 | 119/120 (99%) | 13 (10%) | 1 (0%) |
| 50 | 8 | 149/156 (95%) | 38 (25%) | 6 (4%) |
| 51 | 9 | 1680/1869 (89%) | 435 (25%) | 85 (5%) |
| 85 | hh | 7/8 (87%) | 4 (57%) | 0 |
| All | All | 5607/5847 (95%) | 1407 (25%) | 275 (4%) |

5 of 1407 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 46 | 2 | 9 | A |
| 46 | 2 | 13 | U |
| 46 | 2 | 14 | A |
| 46 | 2 | 16 | C |
| 46 | 2 | 19 | G |

5 of 275 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 48 | 5 | 2754 | G |
| 48 | 5 | 4221 | C |
| 51 | 9 | 1438 | A |
| 48 | 5 | 2874 | U |
| 48 | 5 | 3809 | G |

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 273 ligands modelled in this entry, 272 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
| | | | | | Counts | RMSZ | # Z > 2 | Counts | RMSZ | # Z > 2 |
| 90 | GCP | jj | 700 | 88 | 29,34,34 | 2.56 | 9 (31%) | 31,54,54 | 1.05 | 2 (6%) |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|-----|------|---------|------------|---------|
| 90 | GCP | jj | 700 | 88 | - | 0/18/38/38 | 0/3/3/3 |

The worst 5 of 9 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|--------|--------|-------------|----------|
| 90 | jj | 700 | GCP | C4-N9 | -10.51 | 1.33 | 1.47 |
| 90 | jj | 700 | GCP | C8-N9 | -3.81 | 1.35 | 1.47 |
| 90 | jj | 700 | GCP | C5-C6 | -2.26 | 1.48 | 1.53 |
| 90 | jj | 700 | GCP | PB-C3B | 2.25 | 1.82 | 1.80 |
| 90 | jj | 700 | GCP | PB-O2B | 2.29 | 1.61 | 1.56 |

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|------|-------------|----------|
| 90 | jj | 700 | GCP | C4-C5-N7 | 2.37 | 106.37 | 102.67 |
| 90 | jj | 700 | GCP | C8-N9-C4 | 3.10 | 108.31 | 104.78 |

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 48 | 5 | 42 |
| 51 | 9 | 8 |
| 47 | 3 | 2 |
| 46 | 2 | 1 |

The worst 5 of 53 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | 5 | 2113:G | O3' | 2258:C | P | 40.91 |
| 1 | 5 | 1252:C | O3' | 1271:G | P | 36.05 |
| 1 | 5 | 1405:C | O3' | 1406:G | P | 23.79 |
| 1 | 5 | 1219:G | O3' | 1233:G | P | 22.30 |
| 1 | 5 | 1406:G | O3' | 1406(A):G | P | 20.51 |