



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 5, 2018 – 02:06 PM EST

PDB ID : 6FEC
EMDB ID: : EMD-4242
Title : Human cap-dependent 48S pre-initiation complex
Authors : Schaffitzel, C.; Schaffitzel, C.
Deposited on : 2017-12-31
Resolution : 6.30 Å(reported)

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

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

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

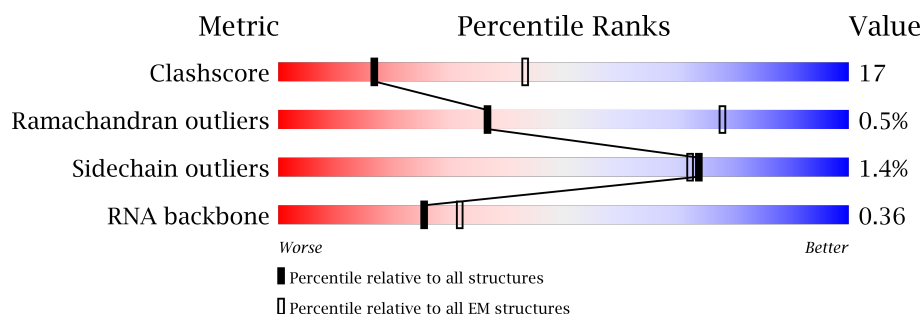
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.30 Å.

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






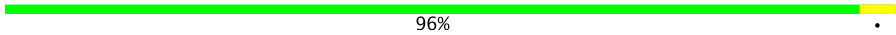
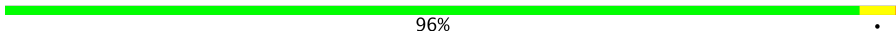
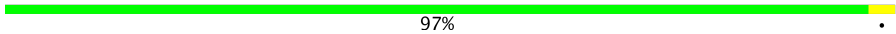
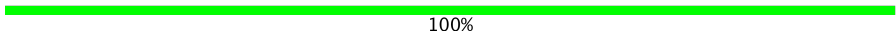
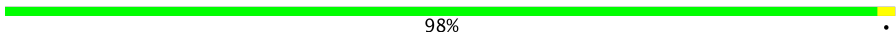
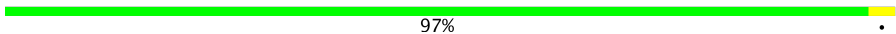







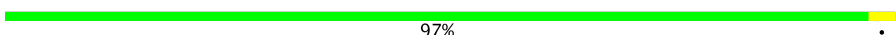
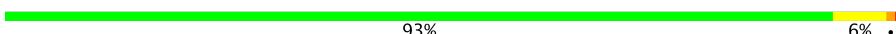
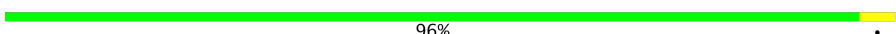
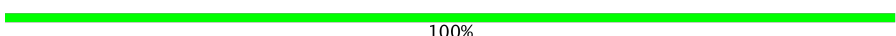
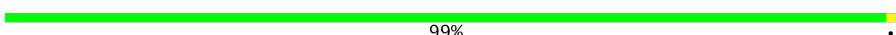
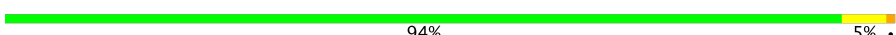
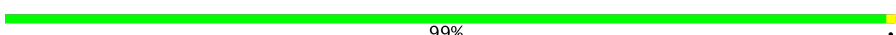
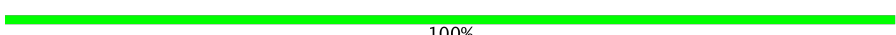

| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Clashscore | 125131 | 1336 |
| Ramachandran outliers | 121729 | 1120 |
| Sidechain outliers | 121581 | 1026 |
| RNA backbone | 3398 | 335 |

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | 1 | 1362 | 23% 20% . 56% |
| 2 | 2 | 843 | 40% 25% . 34% |
| 3 | 3 | 445 | 54% 38% . 6% |
| 4 | 4 | 364 | 39% 34% . 25% |
| 5 | 5 | 352 | 56% 34% . 8% |
| 6 | 6 | 218 | 59% 40% . |
| 7 | 7 | 564 | 44% 22% . 34% |
| 8 | 8 | 374 | 53% 43% .. |

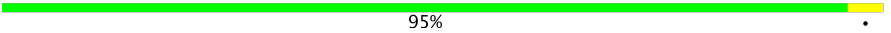
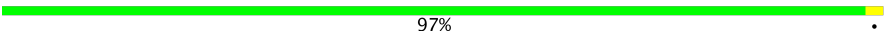

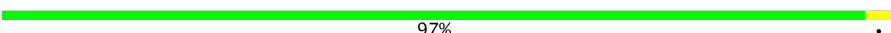
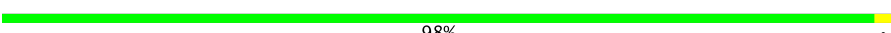
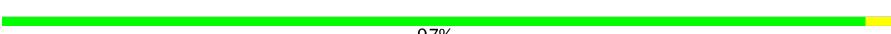
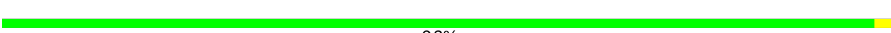








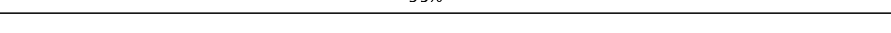

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 9 | 9 | 368 |  |
| 10 | A | 1776 |  |
| 11 | F | 26 |  |
| 12 | G | 158 |  |
| 13 | H | 141 |  |
| 14 | I | 263 |  |
| 15 | J | 53 |  |
| 16 | K | 182 |  |
| 17 | L | 137 |  |
| 18 | N | 75 |  |
| 19 | P | 266 |  |
| 20 | Q | 142 |  |
| 21 | R | 141 |  |
| 22 | S | 422 |  |
| 23 | U | 191 |  |
| 24 | V | 59 |  |
| 25 | W | 75 |  |
| 26 | X | 190 |  |
| 27 | Y | 84 |  |
| 28 | Z | 150 |  |
| 29 | a | 129 |  |
| 30 | b | 82 |  |
| 31 | c | 226 |  |
| 32 | d | 17 |  |
| 33 | e | 126 |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 34 | f | 208 |  95% . |
| 35 | g | 227 |  97% . |
| 36 | h | 104 |  98% . |
| 37 | i | 215 |  97% . |
| 38 | j | 136 |  98% . |
| 39 | k | 99 |  97% . |
| 40 | l | 64 |  98% . |
| 41 | m | 313 |  98% . |
| 42 | n | 127 |  93% 6% . |
| 43 | o | 206 |  97% . |
| 44 | p | 71 |  90% 10% . |
| 45 | q | 237 |  97% . |
| 46 | r | 124 |  96% . . |
| 47 | s | 131 |  98% . |
| 48 | t | 98 |  95% . . |
| 49 | u | 636 |  11% . 88% |
| 50 | w | 1121 |  36% 64% |

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 117189 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 Eukaryotic translation initiation factor 3 subunit A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 1 | 1 | 600 | Total | C | N | O | S | 0 | 1 |
| | | | 4935 | 3107 | 893 | 914 | 21 | | |

- Molecule 2 is a protein called Eukaryotic translation initiation factor 3 subunit C.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 2 | 2 | 558 | Total | C | N | O | S | 0 | 1 |
| | | | 4529 | 2842 | 805 | 849 | 33 | | |

- Molecule 3 is a protein called Eukaryotic translation initiation factor 3 subunit E.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 3 | 3 | 420 | Total | C | N | O | S | 0 | 1 |
| | | | 3466 | 2220 | 587 | 639 | 20 | | |

- Molecule 4 is a protein called Eukaryotic translation initiation factor 3 subunit F.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 4 | 4 | 272 | Total | C | N | O | S | 0 | 0 |
| | | | 2111 | 1330 | 359 | 410 | 12 | | |

- Molecule 5 is a protein called Eukaryotic translation initiation factor 3 subunit H.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 5 | 5 | 324 | Total | C | N | O | S | 0 | 0 |
| | | | 2624 | 1654 | 452 | 503 | 15 | | |

- Molecule 6 is a protein called Eukaryotic translation initiation factor 3 subunit K.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 6 | 6 | 216 | Total | C | N | O | S | 0 | 1 |
| | | | 1738 | 1109 | 286 | 330 | 13 | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| 6 | 166 | THR | SER | conflict | UNP Q9UBQ5 |
| 6 | 172 | MET | VAL | conflict | UNP Q9UBQ5 |

- Molecule 7 is a protein called Eukaryotic translation initiation factor 3 subunit L.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 7 | 7 | 373 | Total | C | N | O | S | 0 | 1 |
| | | | 3110 | 2010 | 520 | 563 | 17 | | |

There are 5 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| 7 | 13 | VAL | ALA | conflict | UNP Q9Y262 |
| 7 | 53 | ARG | LYS | conflict | UNP Q9Y262 |
| 7 | 117 | THR | ALA | conflict | UNP Q9Y262 |
| 7 | 151 | ALA | GLU | conflict | UNP Q9Y262 |
| 7 | 430 | SER | ASN | conflict | UNP Q9Y262 |

- Molecule 8 is a protein called Eukaryotic translation initiation factor 3 subunit M.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 8 | 8 | 366 | Total | C | N | O | S | 0 | 1 |
| | | | 2919 | 1850 | 494 | 558 | 17 | | |

- Molecule 9 is a protein called EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT D.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 9 | 9 | 356 | Total | C | N | O | S | 0 | 0 |
| | | | 2867 | 1804 | 500 | 548 | 15 | | |

- Molecule 10 is a RNA chain called 18S ribosomal RNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 10 | A | 1776 | Total | C | N | O | P | 0 | 0 |
| | | | 37881 | 16910 | 6782 | 12414 | 1775 | | |

- Molecule 11 is a RNA chain called Messenger RNA (26-MER).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|----|---------|-------|
| 11 | F | 26 | Total | C | N | O | P | 0 | 0 |
| | | | 544 | 245 | 95 | 179 | 25 | | |

- Molecule 12 is a protein called 40S ribosomal protein S11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12 | G | 158 | Total | C | N | O | S | 0 | 0 |
| | | | 1296 | 827 | 241 | 221 | 7 | | |

- Molecule 13 is a protein called 40S ribosomal protein S16.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 13 | H | 141 | Total | C | N | O | S | 0 | 0 |
| | | | 1124 | 715 | 212 | 194 | 3 | | |

- Molecule 14 is a protein called 40S ribosomal protein S4, X isoform.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 14 | I | 263 | Total | C | N | O | S | 0 | 0 |
| | | | 2083 | 1329 | 385 | 359 | 10 | | |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| I | 25 | SER | GLY | conflict | UNP P62701 |
| I | 51 | LYS | ARG | conflict | UNP P62701 |
| I | 78 | ALA | THR | conflict | UNP P62701 |
| I | 156 | MET | VAL | conflict | UNP P62701 |

- Molecule 15 is a protein called 40S ribosomal protein S29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 15 | J | 53 | Total | C | N | O | S | 0 | 0 |
| | | | 445 | 278 | 90 | 72 | 5 | | |

- Molecule 16 is a protein called 40S ribosomal protein S9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16 | K | 182 | Total | C | N | O | S | 0 | 0 |
| | | | 1499 | 952 | 300 | 245 | 2 | | |

- Molecule 17 is a protein called 40S ribosomal protein S18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17 | L | 137 | Total | C | N | O | S | 0 | 0 |
| | | | 1140 | 714 | 231 | 194 | 1 | | |

- Molecule 18 is a RNA chain called Transfer RNA (75-MER).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 18 | N | 75 | Total | C | N | O | P | 0 | 0 |
| | | | 1604 | 717 | 298 | 515 | 74 | | |

- Molecule 19 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 19 | P | 266 | Total | C | N | O | S | 0 | 0 |
| | | | 2147 | 1354 | 376 | 406 | 11 | | |

- Molecule 20 is a protein called 40S ribosomal protein S23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20 | Q | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1107 | 698 | 220 | 185 | 4 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21 | R | 141 | Total | C | N | O | S | 0 | 0 |
| | | | 1113 | 701 | 213 | 196 | 3 | | |

- Molecule 22 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 22 | S | 422 | Total | C | N | O | S | 0 | 0 |
| | | | 3214 | 2044 | 561 | 592 | 17 | | |

- Molecule 23 is a protein called 40S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23 | U | 191 | Total | C | N | O | S | 0 | 0 |
| | | | 1509 | 943 | 286 | 273 | 7 | | |

- Molecule 24 is a protein called 40S ribosomal protein S30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 24 | V | 59 | Total | C | N | O | S | 0 | 0 |
| | | | 473 | 293 | 104 | 75 | 1 | | |

There are 3 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| V | 83 | VAL | ALA | conflict | UNP P62861 |
| V | 91 | LEU | PRO | conflict | UNP P62861 |
| V | 102 | ARG | LYS | conflict | UNP P62861 |

- Molecule 25 is a protein called 40S ribosomal protein S25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25 | W | 75 | Total | C | N | O | S | 0 | 0 |
| | | | 599 | 382 | 111 | 105 | 1 | | |

- Molecule 26 is a protein called 40S ribosomal protein S7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 26 | X | 190 | Total | C | N | O | S | 0 | 0 |
| | | | 1530 | 975 | 281 | 273 | 1 | | |

- Molecule 27 is a protein called 40S ribosomal protein S27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27 | Y | 84 | Total | C | N | O | S | 0 | 0 |
| | | | 659 | 413 | 122 | 116 | 8 | | |

- Molecule 28 is a protein called 40S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 28 | Z | 150 | Total | C | N | O | S | 0 | 0 |
| | | | 1208 | 773 | 229 | 205 | 1 | | |

- Molecule 29 is a protein called 40S ribosomal protein S15a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29 | a | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1034 | 659 | 193 | 176 | 6 | | |

- Molecule 30 is a protein called 40S ribosomal protein S21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 30 | b | 82 | Total | C | N | O | S | 0 | 0 |
| | | | 620 | 378 | 117 | 120 | 5 | | |

- Molecule 31 is a protein called 40S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 31 | c | 226 | Total | C | N | O | S | 0 | 0 |
| | | | 1743 | 1127 | 300 | 307 | 9 | | |

- Molecule 32 is a protein called EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (eIF2-Beta).

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---|---------|-------|
| 32 | d | 17 | Total | C | N | O | S | 0 | 0 |
| | | | 147 | 94 | 22 | 30 | 1 | | |

- Molecule 33 is a protein called 40S ribosomal protein S17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33 | e | 126 | Total | C | N | O | S | 0 | 0 |
| | | | 1020 | 639 | 188 | 188 | 5 | | |

- Molecule 34 is a protein called 40S ribosomal protein SA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 34 | f | 208 | Total | C | N | O | S | 0 | 0 |
| | | | 1643 | 1045 | 289 | 301 | 8 | | |

- Molecule 35 is a protein called 40S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 35 | g | 227 | Total | C | N | O | S | 0 | 0 |
| | | | 1765 | 1124 | 317 | 316 | 8 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| g | 195 | SER | THR | conflict | UNP P23396 |

- Molecule 36 is a protein called 40S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 36 | h | 104 | Total | C | N | O | S | 0 | 0 |
| | | | 822 | 514 | 156 | 148 | 4 | | |

- Molecule 37 is a protein called 40S ribosomal protein S3a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 37 | i | 215 | Total | C | N | O | S | 0 | 0 |
| | | | 1742 | 1107 | 309 | 311 | 15 | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| i | 136 | HIS | ARG | conflict | UNP P61247 |
| i | 146 | CYS | ARG | conflict | UNP P61247 |

- Molecule 38 is a protein called 40S ribosomal protein S14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 38 | j | 136 | Total | C | N | O | S | 0 | 0 |
| | | | 1016 | 621 | 199 | 190 | 6 | | |

- Molecule 39 is a protein called 40S ribosomal protein S26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 39 | k | 99 | Total | C | N | O | S | 0 | 0 |
| | | | 790 | 491 | 162 | 131 | 6 | | |

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

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 40 | l | 64 | Total | C | N | O | S | 0 | 0 |
| | | | 507 | 308 | 102 | 95 | 2 | | |

- Molecule 41 is a protein called Receptor of activated protein C kinase 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 41 | m | 313 | Total | C | N | O | S | 0 | 0 |
| | | | 2437 | 1535 | 424 | 466 | 12 | | |

- Molecule 42 is a protein called 40S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42 | n | 127 | Total | C | N | O | S | 0 | 0 |
| | | | 1061 | 673 | 201 | 180 | 7 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| n | 46 | SER | ASN | conflict | UNP P62841 |

- Molecule 43 is a protein called 40S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 43 | o | 206 | Total | C | N | O | S | 0 | 0 |
| | | | 1680 | 1054 | 329 | 292 | 5 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| o | 47 | GLY | ARG | conflict | UNP P62241 |

- Molecule 44 is a protein called Ubiquitin-40S ribosomal protein S27a.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 44 | p | 71 | Total | C | N | O | S | 0 | 0 |
| | | | 582 | 367 | 109 | 99 | 7 | | |

- Molecule 45 is a protein called 40S ribosomal protein S6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 45 | q | 237 | Total | C | N | O | S | 0 | 0 |
| | | | 1924 | 1200 | 387 | 330 | 7 | | |

- Molecule 46 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 46 | r | 124 | Total | C | N | O | S | 0 | 0 |
| | | | 958 | 600 | 170 | 179 | 9 | | |

- Molecule 47 is a protein called 40S ribosomal protein S24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 47 | s | 131 | Total | C | N | O | S | 0 | 0 |
| | | | 1065 | 673 | 206 | 181 | 5 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| s | 41 | GLN | ARG | conflict | UNP P62847 |

- Molecule 48 is a protein called 40S ribosomal protein S10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 48 | t | 98 | Total | C | N | O | S | 0 | 0 |
| | | | 828 | 539 | 148 | 135 | 6 | | |

- Molecule 49 is a protein called Eukaryotic translation initiation factor 4B.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 49 | u | 76 | Total | C | N | O | 0 | 0 |
| | | | 608 | 385 | 104 | 119 | | |

There are 25 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------------------|------------|
| u | -119 | MET | - | initiating methionine | UNP P23588 |
| u | -118 | SER | - | expression tag | UNP P23588 |
| u | -117 | TYR | - | expression tag | UNP P23588 |
| u | -116 | TYR | - | expression tag | UNP P23588 |
| u | -115 | HIS | - | expression tag | UNP P23588 |
| u | -114 | HIS | - | expression tag | UNP P23588 |
| u | -113 | HIS | - | expression tag | UNP P23588 |
| u | -112 | HIS | - | expression tag | UNP P23588 |
| u | -111 | HIS | - | expression tag | UNP P23588 |
| u | -110 | HIS | - | expression tag | UNP P23588 |
| u | -109 | ASP | - | expression tag | UNP P23588 |
| u | -108 | TYR | - | expression tag | UNP P23588 |
| u | -107 | ASP | - | expression tag | UNP P23588 |
| u | -106 | ILE | - | expression tag | UNP P23588 |
| u | -105 | PRO | - | expression tag | UNP P23588 |
| u | -104 | THR | - | expression tag | UNP P23588 |
| u | -103 | THR | - | expression tag | UNP P23588 |
| u | -102 | GLU | - | expression tag | UNP P23588 |
| u | -101 | ASN | - | expression tag | UNP P23588 |
| u | -100 | LEU | - | expression tag | UNP P23588 |
| u | -99 | TYR | - | expression tag | UNP P23588 |
| u | -98 | PRO | - | expression tag | UNP P23588 |
| u | -97 | GLN | - | expression tag | UNP P23588 |
| u | -96 | GLY | - | expression tag | UNP P23588 |

Continued on next page...

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| u | -95 | ALA | - | expression tag | UNP P23588 |

- Molecule 50 is a protein called Eukaryotic translation initiation factor 3 subunit B.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 50 | w | 403 | Total | C | N | O | S | 0 | 0 |
| | | | 3308 | 2132 | 573 | 587 | 16 | | |

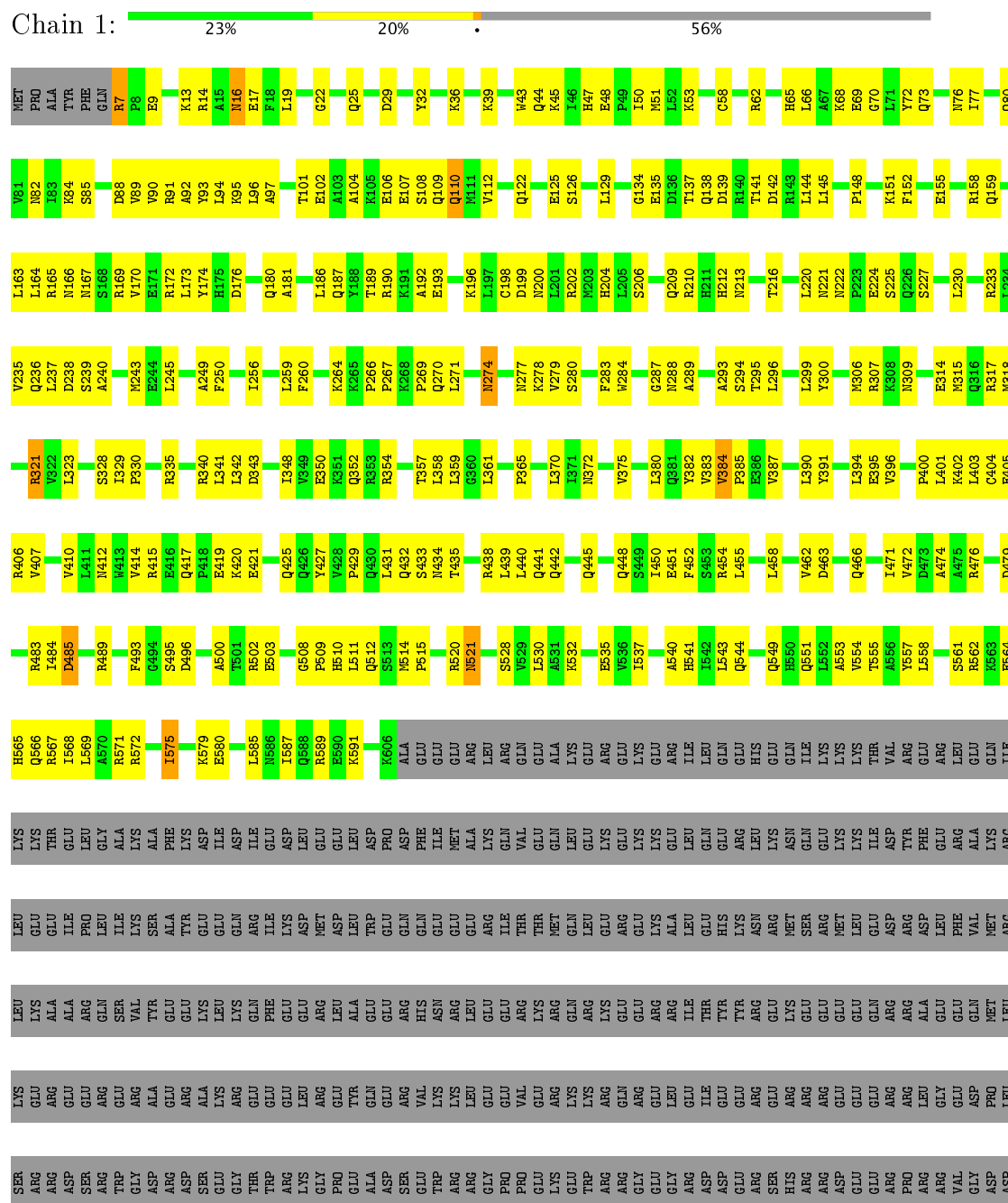
- Molecule 51 is water.

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|-----|---------|
| 51 | 1 | 1 | Total | O | 0 |
| | | | 1 | 1 | |
| 51 | 9 | 376 | Total | O | 0 |
| | | | 376 | 376 | |
| 51 | A | 6 | Total | O | 0 |
| | | | 6 | 6 | |
| 51 | H | 5 | Total | O | 0 |
| | | | 5 | 5 | |
| 51 | U | 13 | Total | O | 0 |
| | | | 13 | 13 | |
| 51 | j | 1 | Total | O | 0 |
| | | | 1 | 1 | |
| 51 | l | 8 | Total | O | 0 |
| | | | 8 | 8 | |
| 51 | m | 5 | Total | O | 0 |
| | | | 5 | 5 | |

3 Residue-property plots

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

- Molecule 1: Eukaryotic translation initiation factor 3 subunit A

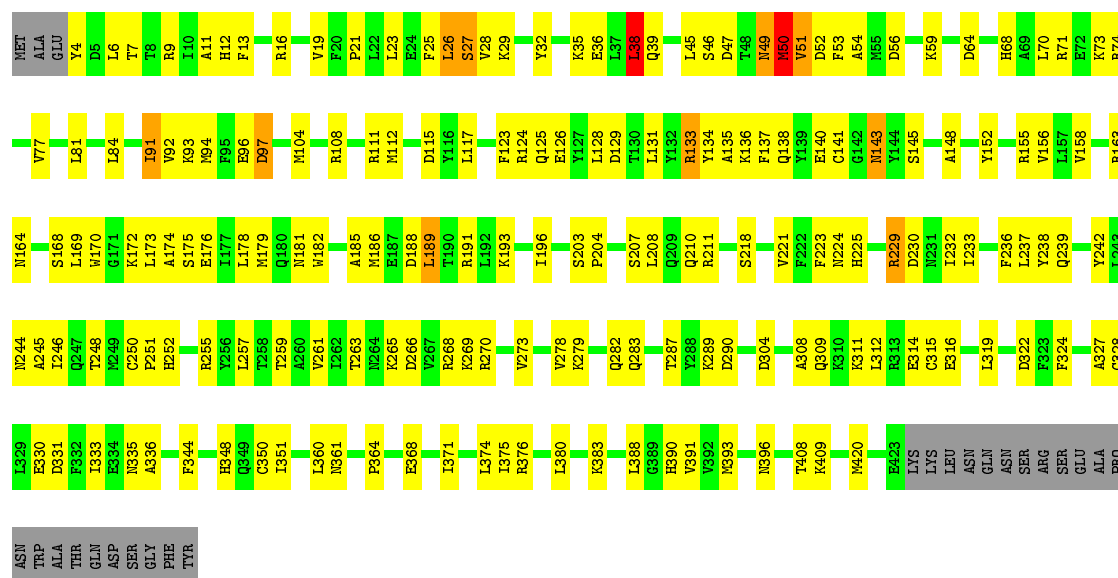




| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TYR | PHE | ARG | ASP | GLN | LYS | ASP | GLY | TYR | ARG | LYS | ASN | GLU | GLY | TYR | MET | ARG | ARG | GLY | GLY | TYR | ARG | GLN | GLN | GLN | SER | SER | GLN | THR | ALA | TYR |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

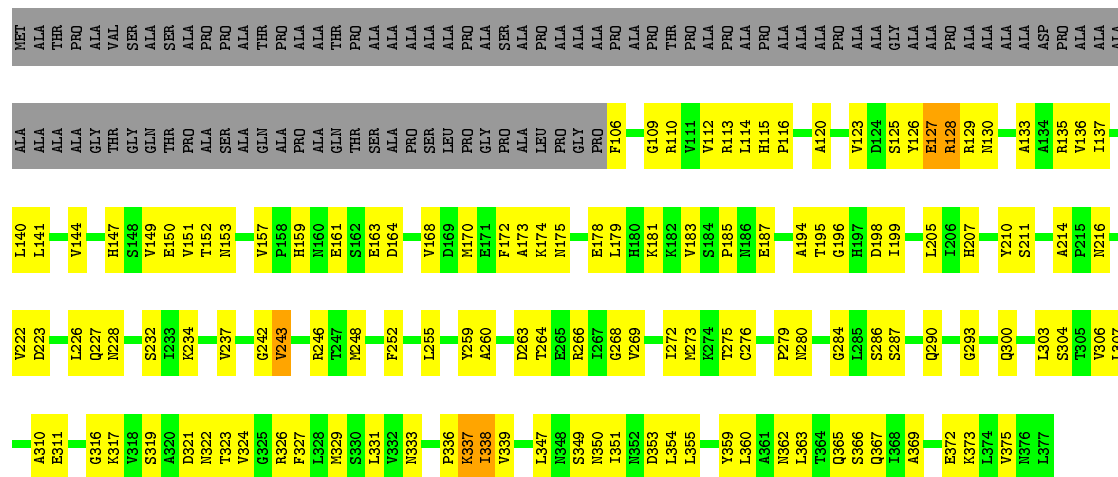
- Molecule 3: Eukaryotic translation initiation factor 3 subunit E

Chain 3: 54% 38% • 6%



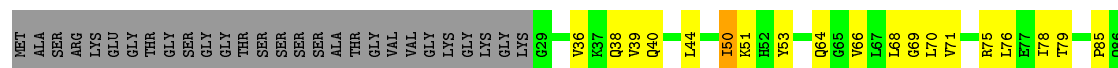
- Molecule 4: Eukaryotic translation initiation factor 3 subunit F

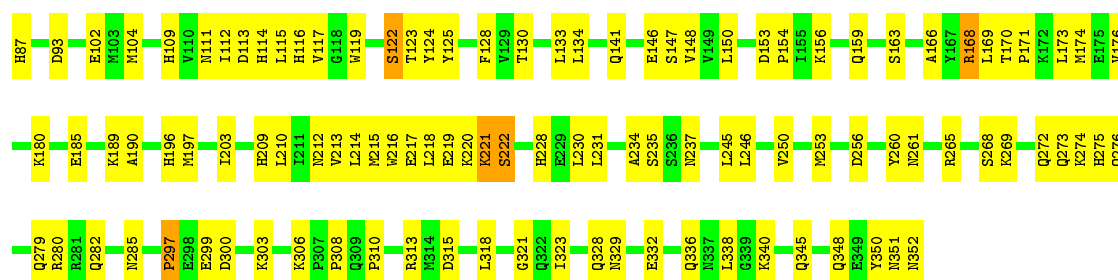
Chain 4: 39% 34% . 25%



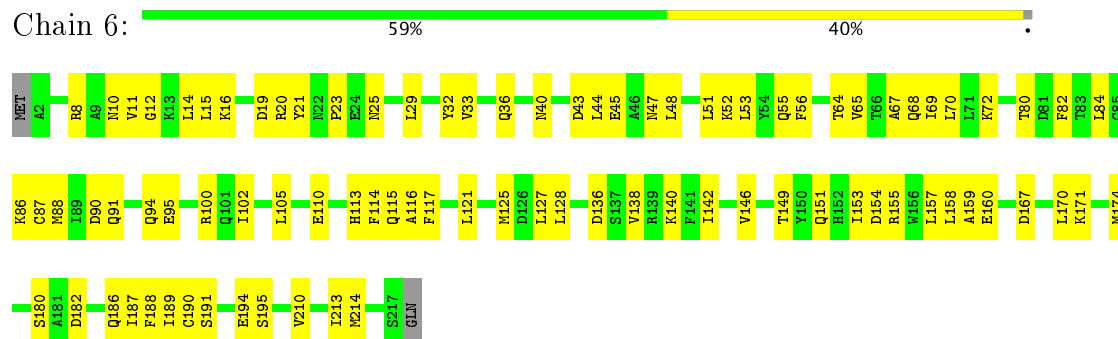
- Molecule 5: Eukaryotic translation initiation factor 3 subunit H

Chain 5:  56% 34% 8%

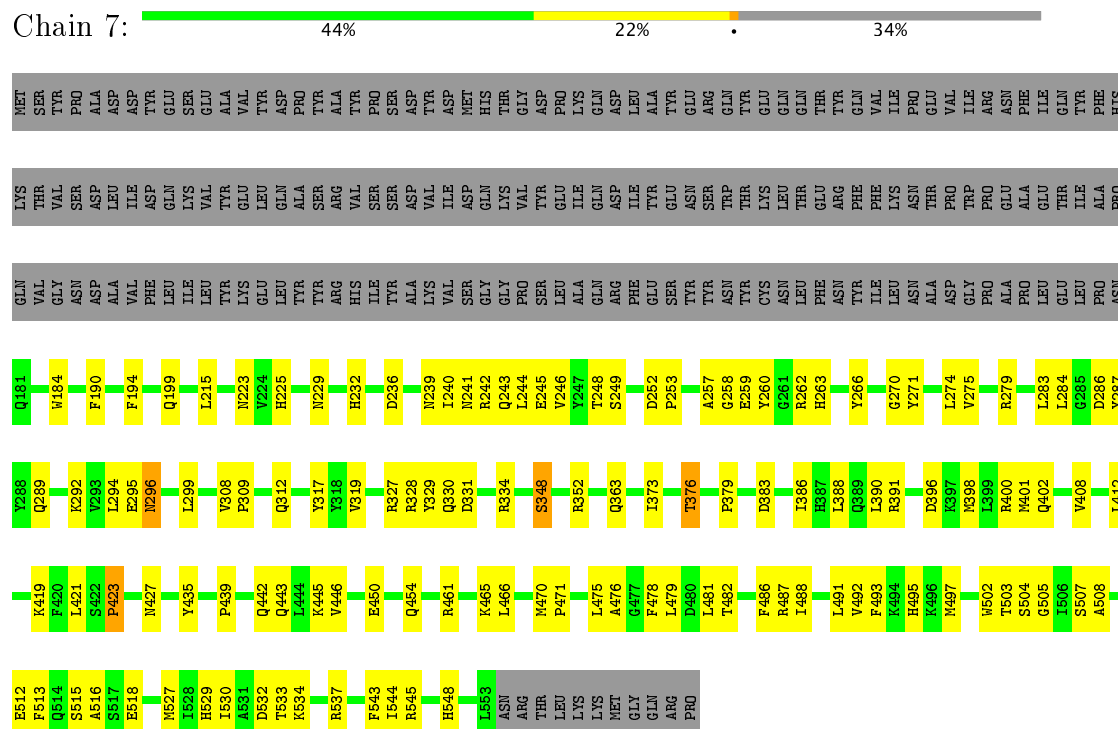




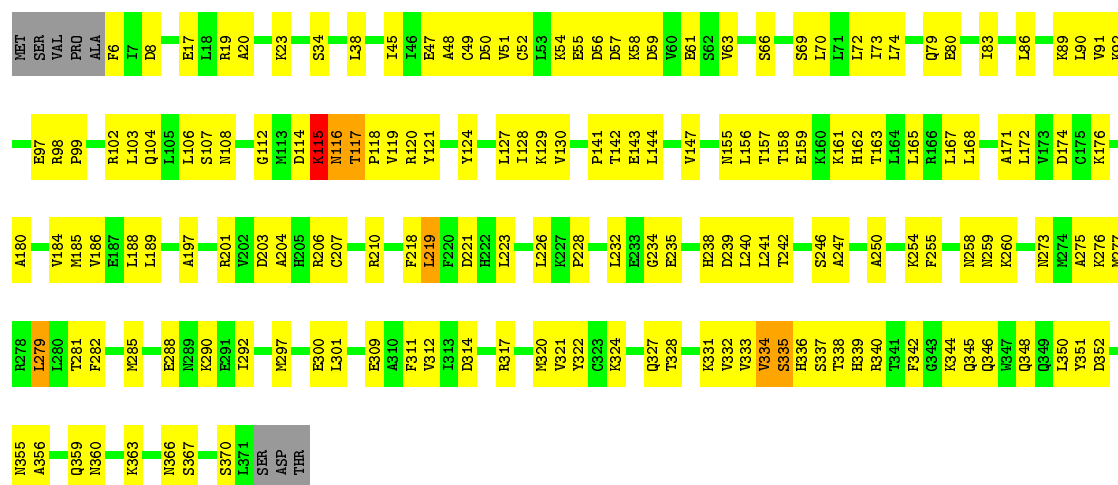
- Molecule 6: Eukaryotic translation initiation factor 3 subunit K



- Molecule 7: Eukaryotic translation initiation factor 3 subunit L

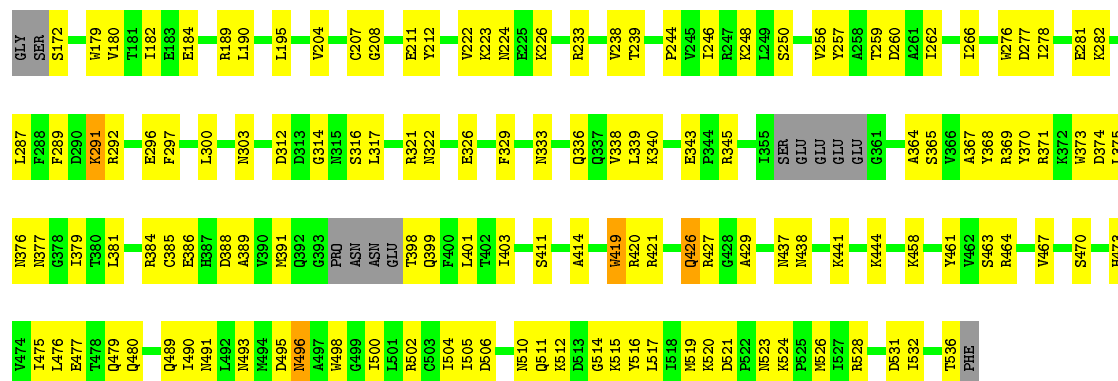


- Molecule 8: Eukaryotic translation initiation factor 3 subunit M



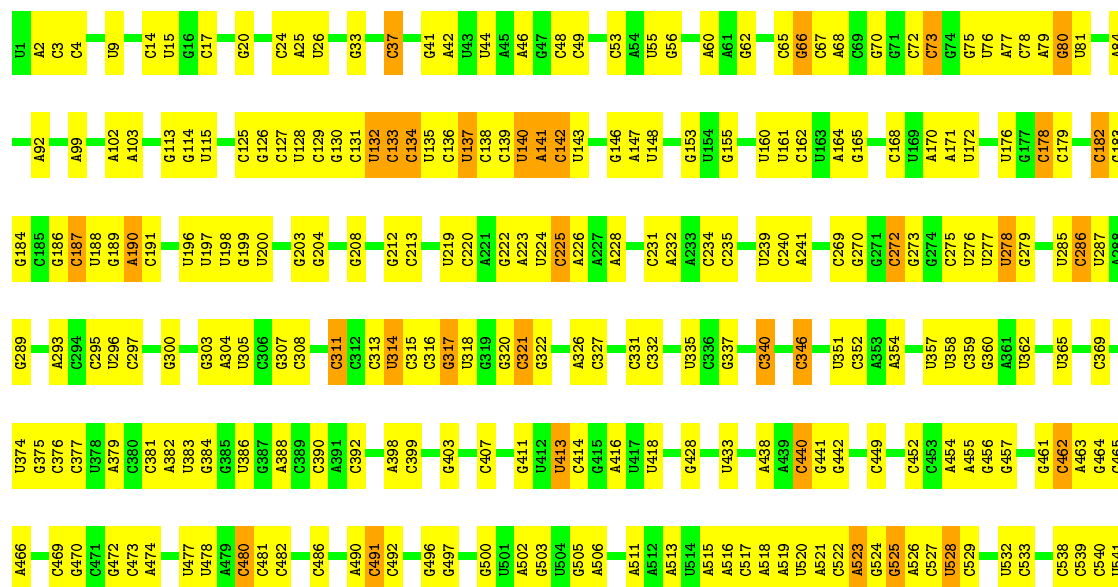
• Molecule 9: EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT D

Chain 9: 60% 36%



• Molecule 10: 18S ribosomal RNA

Chain A: 54% 39% 7%



| | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|------|------|------|------|
| A1794 | U1709 | C1527 | U1437 | U1354 | A1249 | G1136 | U1042 | C946 | A866 | G784 | U620 | G542 |
| A1795 | A1710 | A1528 | A1442 | U1360 | C1250 | A1139 | C1043 | C947 | U867 | G785 | U621 | U543 |
| C1796 | C1711 | U1530 | A1452 | U1366 | G1251 | A1139 | G1044 | G948 | A868 | C786 | C622 | A544 |
| U1797 | C1712 | U1531 | G1445 | A1365 | G1252 | A1142 | A1045 | C949 | G869 | C787 | C623 | A545 |
| U1798 | U1716 | A1532 | G1446 | A1366 | G1253 | C1142 | U1046 | G870 | A871 | G788 | A624 | U546 |
| G1800 | G1717 | C1533 | A1448 | A1367 | A1255 | C1143 | G1047 | G871 | G872 | G789 | G625 | U547 |
| A1801 | U1617 | U1534 | C1449 | U1368 | A1256 | A1144 | U1048 | G873 | C874 | A790 | C626 | C548 |
| U1802 | A1618 | G1535 | C1450 | C1369 | C1258 | G1147 | C1049 | G874 | G875 | A791 | U627 | G549 |
| A1803 | U1619 | G1536 | A1451 | A1374 | C1260 | C1148 | G1050 | G876 | G877 | C793 | A633 | A551 |
| U1804 | U1620 | C1537 | G1452 | A1374 | C1260 | C1149 | C1053 | G877 | G878 | G794 | G634 | U552 |
| G1621 | C1621 | U1538 | U1453 | G1377 | C1267 | U1150 | A1056 | A960 | U878 | U795 | A640 | G553 |
| C1624 | A1625 | C1539 | G1454 | A1378 | G1267 | U1151 | U1057 | G954 | C879 | U796 | U627 | A554 |
| G1632 | G1633 | G1543 | U1455 | A1378 | G1270 | G1155 | A1058 | C963 | U879 | U797 | A643 | C558 |
| G1633 | G1633 | G1544 | U1456 | A1382 | G1271 | U1156 | U1059 | U964 | C880 | C799 | A643 | A559 |
| A1636 | A1636 | G1545 | U1457 | G1383 | A1272 | U1157 | U1062 | U965 | U883 | A799 | G646 | C560 |
| U1637 | U1638 | U1546 | U1458 | A1384 | A1272 | U1157 | U1062 | G966 | U884 | G803 | G649 | U561 |
| U1638 | U1638 | U1546 | U1459 | C1385 | C1279 | A1166 | U1065 | A968 | U885 | A804 | U562 | U563 |
| G1643 | G1643 | G1547 | G1462 | U1386 | G1280 | G1175 | C1070 | C969 | U886 | A807 | C653 | A566 |
| G1649 | G1649 | C1552 | A1473 | C1390 | G1281 | A1179 | C1074 | G971 | U894 | A808 | A658 | A566 |
| C1655 | C1655 | C1553 | A1476 | G1391 | A1295 | C1187 | A1075 | C973 | G897 | U811 | A659 | U572 |
| C1655 | C1655 | C1555 | A1476 | C1391 | A1296 | A1190 | A1079 | A977 | U902 | U818 | A660 | C575 |
| A1659 | A1659 | G1562 | C1484 | A1397 | U1296 | A1190 | A1080 | U999 | U914 | U819 | A662 | C576 |
| G1660 | G1660 | C1563 | A1485 | A1398 | A1297 | G1194 | C1081 | A916 | C926 | G666 | G663 | A577 |
| C1661 | C1661 | A1564 | G1487 | U1400 | C1298 | G1199 | G1082 | G917 | C927 | A822 | C666 | A578 |
| C1665 | C1665 | U1565 | U1488 | A1403 | U1300 | A1200 | A1083 | G905 | G905 | A826 | C677 | A579 |
| C1666 | C1666 | G1566 | U1489 | A1402 | C1301 | A1200 | U1084 | C906 | C907 | A826 | C677 | A580 |
| A1670 | A1670 | G1567 | U1490 | C1406 | U1302 | G1202 | G1092 | C908 | C908 | G827 | U678 | U581 |
| A1674 | A1674 | A1574 | G1491 | C1407 | U1303 | A1205 | G1093 | A909 | C909 | G828 | U679 | C582 |
| C1683 | C1683 | C1576 | U1492 | G1408 | C1304 | A1205 | G1093 | U998 | U910 | C830 | C730 | C583 |
| C1684 | C1684 | C1576 | U1493 | G1409 | U1305 | G1208 | G1100 | U999 | U913 | C833 | C731 | A584 |
| U1685 | U1685 | U1580 | A1502 | A1410 | U1306 | C1208 | C1105 | U999 | U914 | A833 | C734 | G590 |
| U1686 | U1686 | U1581 | G1503 | C1411 | C1307 | C1211 | G1106 | C1002 | A915 | G834 | C735 | A594 |
| A1690 | A1690 | A1582 | A1504 | C1412 | G1308 | C1212 | U1107 | C1006 | C916 | C835 | C736 | A595 |
| C1691 | C1691 | A1583 | U1505 | C1413 | A1309 | A1213 | U1108 | G1006 | G917 | C837 | C744 | A596 |
| A1694 | A1694 | C1587 | G1506 | C1423 | U1310 | C1214 | A1109 | U1012 | G924 | G841 | U745 | U597 |
| C1695 | C1695 | U1587 | U1507 | G1424 | G1326 | G1225 | U1110 | U1013 | G925 | G842 | C746 | C598 |
| C1696 | C1696 | U1590 | U1508 | G1425 | C1327 | G1225 | U1111 | U1013 | G926 | G843 | C749 | U599 |
| C1697 | C1697 | U1591 | G1509 | C1426 | A1328 | G1220 | C1112 | A1016 | C927 | U844 | C749 | U602 |
| C1698 | C1698 | U1591 | G1512 | U1427 | G1330 | U1221 | C1113 | U1017 | G928 | C845 | C755 | C603 |
| C1699 | C1699 | U1594 | C1513 | U1428 | G1330 | U1221 | C1114 | U1018 | G929 | C846 | C756 | G604 |
| C1700 | C1700 | U1595 | U1514 | C1431 | U1339 | G1233 | A1115 | U1019 | C933 | C847 | C757 | C607 |
| C1705 | C1705 | A1596 | G1515 | C1432 | U1343 | A1236 | U1116 | A1027 | A934 | C848 | A758 | C608 |
| C1705 | C1705 | U1597 | G1516 | C1432 | U1343 | A1236 | U1116 | C1028 | U935 | C849 | A759 | A609 |
| C1708 | C1708 | G1599 | A1526 | A1434 | A1353 | U1239 | U1125 | U1034 | U939 | C852 | U776 | G613 |
| | | | | A1434 | A1353 | U1239 | G1126 | C1035 | A940 | U853 | C777 | G613 |
| | | | | A1434 | A1353 | U1239 | G1127 | C1035 | U941 | A857 | G780 | G616 |
| | | | | A1434 | A1353 | U1239 | U1133 | A1039 | C944 | C864 | C781 | U617 |
| | | | | A1434 | A1353 | U1239 | C1134 | A1039 | C944 | C864 | C781 | U617 |
| | | | | A1434 | A1353 | U1239 | C1135 | A1039 | C944 | C864 | C781 | U617 |
| | | | | A1434 | A1353 | U1239 | C1135 | A1039 | C944 | C864 | C781 | U617 |

• Molecule 11: Messenger RNA (26-MER)

Chain F:  46% 54%

| | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| C3 | C4 | C5 | C6 | C7 | C8 | C9 | C10 | C11 | C12 | C13 | C14 | C15 | C16 | C17 | C18 | C19 | C20 | C21 | C22 | C23 | C24 | C25 | C26 | C27 | C28 |
|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- Molecule 12: 40S ribosomal protein S11

Chain G:  96% .



- Molecule 13: 40S ribosomal protein S16

Chain H:  96% . .



- Molecule 14: 40S ribosomal protein S4, X isoform

Chain I:  97% .



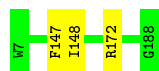
- Molecule 15: 40S ribosomal protein S29

Chain J:  100%

There are no outlier residues recorded for this chain.

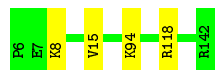
- Molecule 16: 40S ribosomal protein S9

Chain K:  98% .



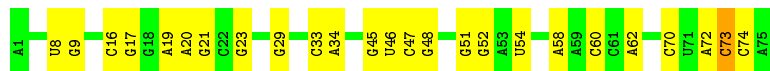
- Molecule 17: 40S ribosomal protein S18

Chain L:  97% .



- Molecule 18: Transfer RNA (75-MER)

Chain N:  67%  32% .



- Molecule 19: Eukaryotic translation initiation factor 2 subunit 1

Chain P:  92%  8%



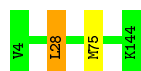
- Molecule 20: 40S ribosomal protein S23

Chain Q: 99% .



- Molecule 21: 40S ribosomal protein S19

Chain R: 99% ..



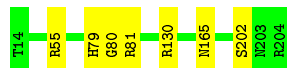
- Molecule 22: Eukaryotic translation initiation factor 2 subunit 3

Chain S: 98% .



- Molecule 23: 40S ribosomal protein S5

Chain U: 96% .



- Molecule 24: 40S ribosomal protein S30

Chain V: 97% .



- Molecule 25: 40S ribosomal protein S25

Chain W: 97% .



- Molecule 26: 40S ribosomal protein S7

Chain X: 93% 6% ..



- Molecule 27: 40S ribosomal protein S27

Chain Y:  96% .



- Molecule 28: 40S ribosomal protein S13

Chain Z:  100%

There are no outlier residues recorded for this chain.

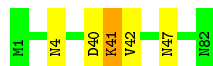
- Molecule 29: 40S ribosomal protein S15a

Chain a:  99% .



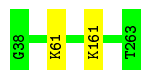
- Molecule 30: 40S ribosomal protein S21

Chain b:  94% 5% .



- Molecule 31: 40S ribosomal protein S2

Chain c:  99% .



- Molecule 32: EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (eIF2-Beta)

Chain d:  100%

There are no outlier residues recorded for this chain.

- Molecule 33: 40S ribosomal protein S17

Chain e:  97% .



- Molecule 34: 40S ribosomal protein SA

Chain f:  95% .



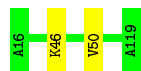
- Molecule 35: 40S ribosomal protein S3

Chain g: 97%



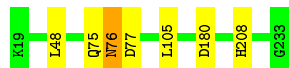
- Molecule 36: 40S ribosomal protein S20

Chain h: 98%



- Molecule 37: 40S ribosomal protein S3a

Chain i: 97%



- Molecule 38: 40S ribosomal protein S14

Chain j: 98%



- Molecule 39: 40S ribosomal protein S26

Chain k: 97%



- Molecule 40: 40S ribosomal protein S28

Chain l: 98%



- Molecule 41: Receptor of activated protein C kinase 1

Chain m: 98%



- Molecule 42: 40S ribosomal protein S15

Chain n:  93% 6% .




- Molecule 43: 40S ribosomal protein S8

Chain o:  97% .



- Molecule 44: Ubiquitin-40S ribosomal protein S27a

Chain p:  90% 10%



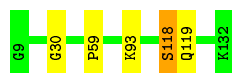
- Molecule 45: 40S ribosomal protein S6

Chain q:  97% .



- Molecule 46: 40S ribosomal protein S12

Chain r:  96% . .



- Molecule 47: 40S ribosomal protein S24

Chain s:  98% .



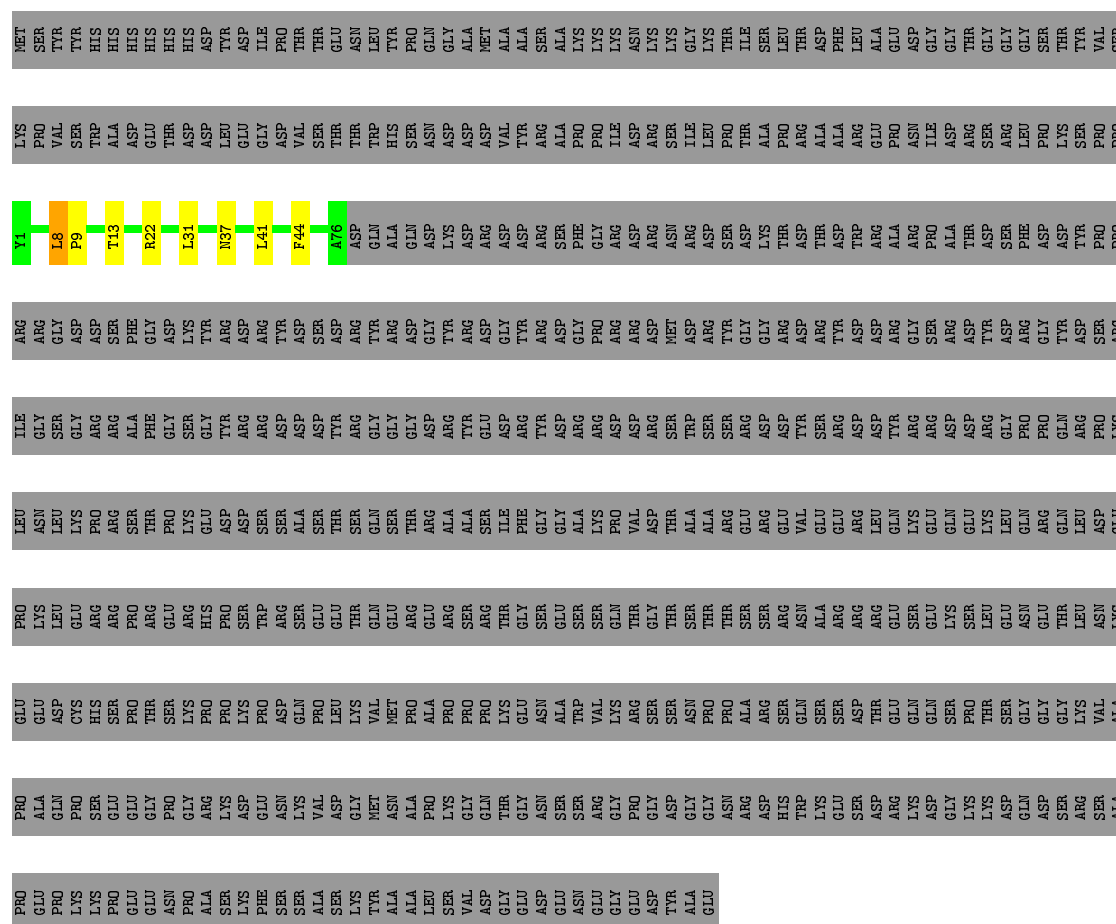
- Molecule 48: 40S ribosomal protein S10

Chain t:  95% . .



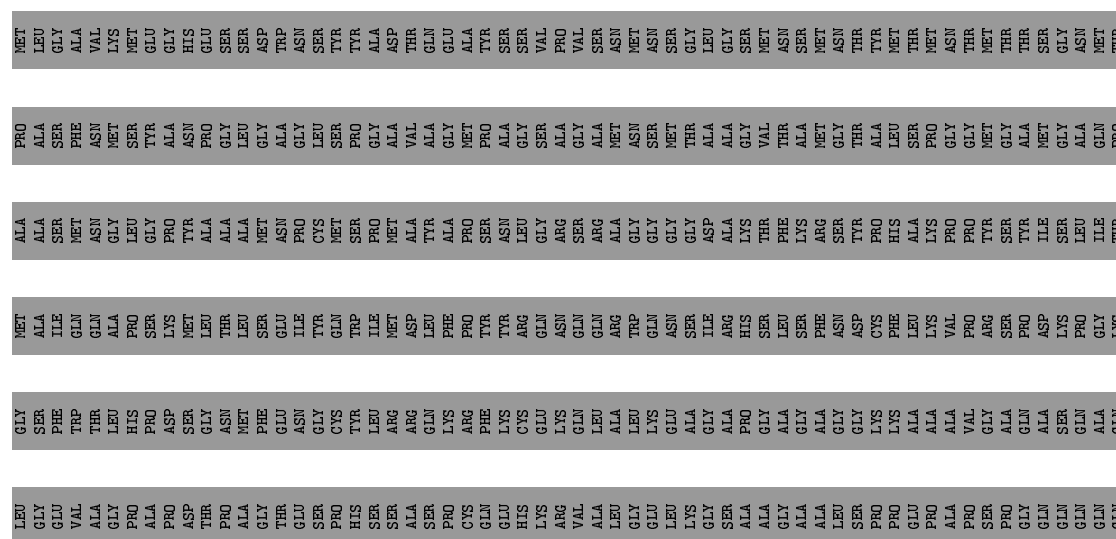
- Molecule 49: Eukaryotic translation initiation factor 4B

Chain u: 11% . 88%



- Molecule 50: Eukaryotic translation initiation factor 3 subunit B

Chain w: 36% 64%



[illegible]

4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| Reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, C1 | Depositor |
| Number of particles used | 50604 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 30 | Depositor |
| Minimum defocus (nm) | 1500 | Depositor |
| Maximum defocus (nm) | 4000 | Depositor |
| Magnification | 112000 | Depositor |
| Image detector | FEI FALCON II (4k x 4k) | Depositor |

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|----------------|-------------|------------------|
| | | RMSZ | # $ Z > 2$ | RMSZ | # $ Z > 2$ |
| 1 | 1 | 0.35 | 0/5021 | 0.63 | 1/6781 (0.0%) |
| 10 | A | 0.56 | 1/42353 (0.0%) | 1.31 | 441/66010 (0.7%) |
| 11 | F | 0.31 | 0/606 | 0.95 | 0/941 |
| 12 | G | 0.36 | 0/1319 | 0.65 | 0/1761 |
| 13 | H | 0.32 | 0/1142 | 0.63 | 0/1528 |
| 14 | I | 0.33 | 0/2125 | 0.64 | 1/2856 (0.0%) |
| 15 | J | 0.35 | 0/455 | 0.58 | 0/603 |
| 16 | K | 0.32 | 0/1523 | 0.60 | 0/2031 |
| 17 | L | 0.33 | 0/1158 | 0.63 | 0/1548 |
| 18 | N | 0.46 | 0/1795 | 1.13 | 6/2798 (0.2%) |
| 19 | P | 0.33 | 0/2178 | 0.68 | 0/2935 |
| 2 | 2 | 0.34 | 0/4608 | 0.57 | 1/6219 (0.0%) |
| 20 | Q | 0.32 | 0/1125 | 0.60 | 1/1500 (0.1%) |
| 21 | R | 0.35 | 0/1133 | 0.59 | 1/1517 (0.1%) |
| 22 | S | 0.30 | 0/3267 | 0.60 | 1/4415 (0.0%) |
| 23 | U | 0.31 | 0/1531 | 0.56 | 0/2059 |
| 24 | V | 0.30 | 0/478 | 0.69 | 0/628 |
| 25 | W | 0.36 | 0/605 | 0.67 | 0/810 |
| 26 | X | 0.35 | 0/1553 | 0.74 | 4/2079 (0.2%) |
| 27 | Y | 0.35 | 0/673 | 0.65 | 1/902 (0.1%) |
| 28 | Z | 0.31 | 0/1232 | 0.54 | 0/1656 |
| 29 | a | 0.28 | 0/1051 | 0.55 | 0/1406 |
| 3 | 3 | 0.35 | 0/3539 | 0.70 | 8/4788 (0.2%) |
| 30 | b | 0.32 | 0/627 | 0.64 | 0/839 |
| 31 | c | 0.34 | 0/1779 | 0.57 | 0/2399 |
| 32 | d | 0.24 | 0/149 | 0.49 | 0/197 |
| 33 | e | 0.32 | 0/1032 | 0.60 | 0/1383 |
| 34 | f | 0.36 | 0/1680 | 0.68 | 1/2283 (0.0%) |
| 35 | g | 0.32 | 0/1793 | 0.60 | 1/2412 (0.0%) |
| 36 | h | 0.29 | 0/832 | 0.59 | 0/1117 |
| 37 | i | 0.35 | 0/1770 | 0.65 | 1/2367 (0.0%) |
| 38 | j | 0.31 | 0/1029 | 0.65 | 0/1380 |
| 39 | k | 0.30 | 0/803 | 0.58 | 0/1076 |
| 4 | 4 | 0.33 | 0/2149 | 0.66 | 0/2920 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-----------------|-------------|-------------------|
| | | RMSZ | # Z >2 | RMSZ | # Z >2 |
| 40 | l | 0.35 | 0/509 | 0.60 | 0/680 |
| 41 | m | 0.38 | 0/2494 | 0.68 | 1/3394 (0.0%) |
| 42 | n | 0.36 | 0/1080 | 0.68 | 0/1437 |
| 43 | o | 0.40 | 0/1709 | 0.70 | 1/2278 (0.0%) |
| 44 | p | 0.44 | 0/594 | 0.78 | 1/786 (0.1%) |
| 45 | q | 0.35 | 0/1947 | 0.64 | 0/2590 |
| 46 | r | 0.36 | 0/968 | 0.66 | 0/1296 |
| 47 | s | 0.37 | 0/1083 | 0.66 | 1/1437 (0.1%) |
| 48 | t | 0.34 | 0/852 | 0.73 | 2/1147 (0.2%) |
| 49 | u | 0.35 | 0/619 | 0.83 | 2/836 (0.2%) |
| 5 | 5 | 0.33 | 0/2675 | 0.65 | 2/3609 (0.1%) |
| 50 | w | 0.27 | 0/3407 | 0.59 | 1/4620 (0.0%) |
| 6 | 6 | 0.33 | 0/1773 | 0.60 | 0/2398 |
| 7 | 7 | 0.31 | 0/3186 | 0.63 | 3/4298 (0.1%) |
| 8 | 8 | 0.32 | 0/2964 | 0.71 | 5/4000 (0.1%) |
| 9 | 9 | 0.29 | 0/2921 | 0.54 | 0/3957 |
| All | All | 0.43 | 1/122894 (0.0%) | 0.96 | 488/174907 (0.3%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1 | 1 | 0 | 6 |
| 12 | G | 0 | 1 |
| 13 | H | 0 | 2 |
| 14 | I | 0 | 2 |
| 16 | K | 0 | 1 |
| 17 | L | 0 | 3 |
| 19 | P | 0 | 11 |
| 2 | 2 | 0 | 8 |
| 22 | S | 0 | 1 |
| 23 | U | 0 | 2 |
| 24 | V | 0 | 1 |
| 25 | W | 0 | 2 |
| 26 | X | 0 | 5 |
| 27 | Y | 0 | 1 |
| 3 | 3 | 0 | 12 |
| 30 | b | 0 | 2 |
| 31 | c | 0 | 1 |
| 33 | e | 0 | 1 |

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| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 34 | f | 0 | 4 |
| 35 | g | 0 | 2 |
| 36 | h | 0 | 2 |
| 37 | i | 0 | 6 |
| 38 | j | 0 | 1 |
| 4 | 4 | 0 | 8 |
| 41 | m | 0 | 3 |
| 42 | n | 0 | 4 |
| 43 | o | 0 | 2 |
| 44 | p | 0 | 6 |
| 45 | q | 0 | 4 |
| 46 | r | 0 | 4 |
| 48 | t | 0 | 3 |
| 49 | u | 0 | 1 |
| 5 | 5 | 0 | 4 |
| 50 | w | 0 | 1 |
| 7 | 7 | 0 | 4 |
| 8 | 8 | 0 | 8 |
| 9 | 9 | 0 | 3 |
| All | All | 0 | 132 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|-------|-------------|----------|
| 10 | A | 1311 | U | N3-C4 | -5.60 | 1.33 | 1.38 |

The worst 5 of 488 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|----------|--------|-------------|----------|
| 10 | A | 1311 | U | N3-C2-O2 | -13.33 | 112.87 | 122.20 |
| 10 | A | 835 | C | N1-C2-O2 | 11.55 | 125.83 | 118.90 |
| 10 | A | 1549 | C | N1-C2-O2 | 11.46 | 125.77 | 118.90 |
| 10 | A | 1311 | U | N1-C2-O2 | 11.31 | 130.72 | 122.80 |
| 10 | A | 491 | C | N1-C2-O2 | 11.29 | 125.67 | 118.90 |

There are no chirality outliers.

5 of 132 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 1 | 1 | 264 | LYS | Peptide |
| 1 | 1 | 330 | PRO | Peptide |

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| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 1 | 1 | 384 | VAL | Peptide |
| 1 | 1 | 417 | GLN | Peptide |
| 1 | 1 | 7 | ARG | Peptide |

5.2 Too-close contacts

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | 1 | 4935 | 0 | 5017 | 227 | 0 |
| 2 | 2 | 4529 | 0 | 4533 | 158 | 0 |
| 3 | 3 | 3466 | 0 | 3446 | 121 | 0 |
| 4 | 4 | 2111 | 0 | 2105 | 116 | 0 |
| 5 | 5 | 2624 | 0 | 2592 | 104 | 0 |
| 6 | 6 | 1738 | 0 | 1706 | 81 | 0 |
| 7 | 7 | 3110 | 0 | 3084 | 101 | 0 |
| 8 | 8 | 2919 | 0 | 2950 | 137 | 0 |
| 9 | 9 | 2867 | 0 | 2838 | 108 | 0 |
| 10 | A | 37881 | 0 | 19144 | 0 | 0 |
| 11 | F | 544 | 0 | 283 | 0 | 0 |
| 12 | G | 1296 | 0 | 1374 | 0 | 0 |
| 13 | H | 1124 | 0 | 1193 | 0 | 0 |
| 14 | I | 2083 | 0 | 2189 | 0 | 0 |
| 15 | J | 445 | 0 | 442 | 0 | 0 |
| 16 | K | 1499 | 0 | 1608 | 0 | 0 |
| 17 | L | 1140 | 0 | 1191 | 0 | 0 |
| 18 | N | 1604 | 0 | 816 | 0 | 0 |
| 19 | P | 2147 | 0 | 2191 | 0 | 0 |
| 20 | Q | 1107 | 0 | 1179 | 0 | 0 |
| 21 | R | 1113 | 0 | 1149 | 0 | 0 |
| 22 | S | 3214 | 0 | 3354 | 0 | 0 |
| 23 | U | 1509 | 0 | 1563 | 0 | 0 |
| 24 | V | 473 | 0 | 524 | 0 | 0 |
| 25 | W | 599 | 0 | 656 | 0 | 0 |
| 26 | X | 1530 | 0 | 1627 | 0 | 0 |
| 27 | Y | 659 | 0 | 683 | 0 | 0 |
| 28 | Z | 1208 | 0 | 1294 | 0 | 0 |
| 29 | a | 1034 | 0 | 1080 | 0 | 0 |
| 30 | b | 620 | 0 | 622 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 31 | c | 1743 | 0 | 1836 | 0 | 0 |
| 32 | d | 147 | 0 | 146 | 0 | 0 |
| 33 | e | 1020 | 0 | 1075 | 0 | 0 |
| 34 | f | 1643 | 0 | 1646 | 0 | 0 |
| 35 | g | 1765 | 0 | 1863 | 0 | 0 |
| 36 | h | 822 | 0 | 887 | 0 | 0 |
| 37 | i | 1742 | 0 | 1815 | 0 | 0 |
| 38 | j | 1016 | 0 | 1039 | 0 | 0 |
| 39 | k | 790 | 0 | 839 | 0 | 0 |
| 40 | l | 507 | 0 | 536 | 0 | 0 |
| 41 | m | 2437 | 0 | 2393 | 0 | 0 |
| 42 | n | 1061 | 0 | 1120 | 0 | 0 |
| 43 | o | 1680 | 0 | 1762 | 0 | 0 |
| 44 | p | 582 | 0 | 599 | 0 | 0 |
| 45 | q | 1924 | 0 | 2089 | 0 | 0 |
| 46 | r | 958 | 0 | 993 | 0 | 0 |
| 47 | s | 1065 | 0 | 1137 | 0 | 0 |
| 48 | t | 828 | 0 | 854 | 0 | 0 |
| 49 | u | 608 | 0 | 598 | 0 | 0 |
| 50 | w | 3308 | 0 | 3235 | 0 | 0 |
| 51 | 1 | 1 | 0 | 0 | 0 | 0 |
| 51 | 9 | 376 | 0 | 0 | 27 | 0 |
| 51 | A | 6 | 0 | 0 | 1 | 0 |
| 51 | H | 5 | 0 | 0 | 0 | 0 |
| 51 | U | 13 | 0 | 0 | 1 | 0 |
| 51 | j | 1 | 0 | 0 | 0 | 0 |
| 51 | l | 8 | 0 | 0 | 0 | 0 |
| 51 | m | 5 | 0 | 0 | 0 | 0 |
| All | All | 117189 | 0 | 98895 | 1032 | 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 17.

The worst 5 of 1032 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) |
|-----------------|------------------|--------------------------|-------------------|
| 7:7:396:ASP:OD2 | 7:7:400:ARG:NH1 | 1.86 | 1.08 |
| 6:6:20:ARG:NH1 | 6:6:45:GLU:OE2 | 1.90 | 1.05 |
| 3:3:136:LYS:NZ | 3:3:140:GLU:OE2 | 1.89 | 1.04 |
| 5:5:36:VAL:HG11 | 5:5:168:ARG:HH12 | 1.29 | 0.94 |
| 3:3:266:ASP:OD1 | 3:3:269:LYS:NZ | 2.03 | 0.91 |

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|----------|-------------|-----|
| 1 | 1 | 598/1362 (44%) | 530 (89%) | 67 (11%) | 1 (0%) | 51 | 84 |
| 2 | 2 | 556/843 (66%) | 507 (91%) | 48 (9%) | 1 (0%) | 51 | 84 |
| 3 | 3 | 418/445 (94%) | 348 (83%) | 64 (15%) | 6 (1%) | 13 | 53 |
| 4 | 4 | 270/364 (74%) | 230 (85%) | 40 (15%) | 0 | 100 | 100 |
| 5 | 5 | 322/352 (92%) | 272 (84%) | 50 (16%) | 0 | 100 | 100 |
| 6 | 6 | 214/218 (98%) | 193 (90%) | 21 (10%) | 0 | 100 | 100 |
| 7 | 7 | 371/564 (66%) | 329 (89%) | 41 (11%) | 1 (0%) | 44 | 81 |
| 8 | 8 | 364/374 (97%) | 301 (83%) | 63 (17%) | 0 | 100 | 100 |
| 9 | 9 | 350/368 (95%) | 325 (93%) | 23 (7%) | 2 (1%) | 28 | 71 |
| 12 | G | 156/158 (99%) | 139 (89%) | 17 (11%) | 0 | 100 | 100 |
| 13 | H | 139/141 (99%) | 126 (91%) | 11 (8%) | 2 (1%) | 13 | 53 |
| 14 | I | 261/263 (99%) | 227 (87%) | 31 (12%) | 3 (1%) | 17 | 59 |
| 15 | J | 51/53 (96%) | 46 (90%) | 5 (10%) | 0 | 100 | 100 |
| 16 | K | 180/182 (99%) | 165 (92%) | 14 (8%) | 1 (1%) | 28 | 71 |
| 17 | L | 135/137 (98%) | 114 (84%) | 21 (16%) | 0 | 100 | 100 |
| 19 | P | 264/266 (99%) | 212 (80%) | 48 (18%) | 4 (2%) | 12 | 53 |
| 20 | Q | 140/142 (99%) | 124 (89%) | 16 (11%) | 0 | 100 | 100 |
| 21 | R | 139/141 (99%) | 125 (90%) | 14 (10%) | 0 | 100 | 100 |
| 22 | S | 420/422 (100%) | 366 (87%) | 54 (13%) | 0 | 100 | 100 |
| 23 | U | 189/191 (99%) | 173 (92%) | 15 (8%) | 1 (0%) | 32 | 74 |
| 24 | V | 57/59 (97%) | 49 (86%) | 8 (14%) | 0 | 100 | 100 |
| 25 | W | 73/75 (97%) | 65 (89%) | 8 (11%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|------------------|------------|------------|----------|-------------|-----|
| 26 | X | 188/190 (99%) | 166 (88%) | 17 (9%) | 5 (3%) | 6 | 39 |
| 27 | Y | 82/84 (98%) | 74 (90%) | 8 (10%) | 0 | 100 | 100 |
| 28 | Z | 148/150 (99%) | 143 (97%) | 5 (3%) | 0 | 100 | 100 |
| 29 | a | 127/129 (98%) | 120 (94%) | 7 (6%) | 0 | 100 | 100 |
| 30 | b | 80/82 (98%) | 69 (86%) | 9 (11%) | 2 (2%) | 6 | 40 |
| 31 | c | 224/226 (99%) | 205 (92%) | 19 (8%) | 0 | 100 | 100 |
| 32 | d | 15/17 (88%) | 15 (100%) | 0 | 0 | 100 | 100 |
| 33 | e | 124/126 (98%) | 111 (90%) | 12 (10%) | 1 (1%) | 22 | 66 |
| 34 | f | 206/208 (99%) | 177 (86%) | 27 (13%) | 2 (1%) | 18 | 61 |
| 35 | g | 225/227 (99%) | 203 (90%) | 20 (9%) | 2 (1%) | 20 | 63 |
| 36 | h | 102/104 (98%) | 94 (92%) | 8 (8%) | 0 | 100 | 100 |
| 37 | i | 213/215 (99%) | 188 (88%) | 25 (12%) | 0 | 100 | 100 |
| 38 | j | 134/136 (98%) | 117 (87%) | 16 (12%) | 1 (1%) | 25 | 68 |
| 39 | k | 97/99 (98%) | 92 (95%) | 5 (5%) | 0 | 100 | 100 |
| 40 | l | 62/64 (97%) | 58 (94%) | 4 (6%) | 0 | 100 | 100 |
| 41 | m | 311/313 (99%) | 271 (87%) | 40 (13%) | 0 | 100 | 100 |
| 42 | n | 125/127 (98%) | 106 (85%) | 17 (14%) | 2 (2%) | 11 | 51 |
| 43 | o | 204/206 (99%) | 173 (85%) | 29 (14%) | 2 (1%) | 18 | 61 |
| 44 | p | 69/71 (97%) | 48 (70%) | 21 (30%) | 0 | 100 | 100 |
| 45 | q | 235/237 (99%) | 211 (90%) | 22 (9%) | 2 (1%) | 20 | 63 |
| 46 | r | 122/124 (98%) | 97 (80%) | 23 (19%) | 2 (2%) | 11 | 51 |
| 47 | s | 129/131 (98%) | 110 (85%) | 18 (14%) | 1 (1%) | 22 | 66 |
| 48 | t | 96/98 (98%) | 76 (79%) | 19 (20%) | 1 (1%) | 18 | 61 |
| 49 | u | 74/636 (12%) | 61 (82%) | 12 (16%) | 1 (1%) | 13 | 53 |
| 50 | w | 401/1121 (36%) | 335 (84%) | 66 (16%) | 0 | 100 | 100 |
| All | All | 9460/12241 (77%) | 8286 (88%) | 1128 (12%) | 46 (0%) | 37 | 74 |

5 of 46 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 3 | 3 | 51 | VAL |
| 13 | H | 42 | ILE |
| 14 | I | 12 | VAL |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 26 | X | 17 | ASP |
| 30 | b | 42 | VAL |

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 | 1 | 551/1245 (44%) | 542 (98%) | 9 (2%) | 68 | 85 |
| 2 | 2 | 503/750 (67%) | 497 (99%) | 6 (1%) | 75 | 88 |
| 3 | 3 | 384/406 (95%) | 371 (97%) | 13 (3%) | 42 | 69 |
| 4 | 4 | 239/282 (85%) | 234 (98%) | 5 (2%) | 59 | 80 |
| 5 | 5 | 293/311 (94%) | 287 (98%) | 6 (2%) | 60 | 82 |
| 6 | 6 | 190/193 (98%) | 189 (100%) | 1 (0%) | 91 | 95 |
| 7 | 7 | 342/516 (66%) | 340 (99%) | 2 (1%) | 89 | 94 |
| 8 | 8 | 327/335 (98%) | 327 (100%) | 0 | 100 | 100 |
| 9 | 9 | 320/331 (97%) | 317 (99%) | 3 (1%) | 82 | 91 |
| 12 | G | 142/142 (100%) | 137 (96%) | 5 (4%) | 41 | 69 |
| 13 | H | 117/117 (100%) | 114 (97%) | 3 (3%) | 51 | 75 |
| 14 | I | 225/225 (100%) | 222 (99%) | 3 (1%) | 73 | 87 |
| 15 | J | 47/47 (100%) | 47 (100%) | 0 | 100 | 100 |
| 16 | K | 157/157 (100%) | 156 (99%) | 1 (1%) | 89 | 94 |
| 17 | L | 119/119 (100%) | 118 (99%) | 1 (1%) | 85 | 92 |
| 19 | P | 238/238 (100%) | 231 (97%) | 7 (3%) | 48 | 73 |
| 20 | Q | 114/114 (100%) | 113 (99%) | 1 (1%) | 82 | 91 |
| 21 | R | 113/113 (100%) | 111 (98%) | 2 (2%) | 64 | 84 |
| 22 | S | 354/354 (100%) | 349 (99%) | 5 (1%) | 71 | 86 |
| 23 | U | 161/161 (100%) | 157 (98%) | 4 (2%) | 53 | 77 |
| 24 | V | 49/49 (100%) | 48 (98%) | 1 (2%) | 60 | 82 |
| 25 | W | 66/66 (100%) | 66 (100%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|------------------|------------|----------|-------------|-----|
| 26 | X | 170/170 (100%) | 168 (99%) | 2 (1%) | 75 | 88 |
| 27 | Y | 76/76 (100%) | 75 (99%) | 1 (1%) | 73 | 87 |
| 28 | Z | 130/130 (100%) | 130 (100%) | 0 | 100 | 100 |
| 29 | a | 112/112 (100%) | 111 (99%) | 1 (1%) | 82 | 91 |
| 30 | b | 67/67 (100%) | 65 (97%) | 2 (3%) | 46 | 72 |
| 31 | c | 187/187 (100%) | 186 (100%) | 1 (0%) | 91 | 95 |
| 32 | d | 17/17 (100%) | 17 (100%) | 0 | 100 | 100 |
| 33 | e | 114/114 (100%) | 112 (98%) | 2 (2%) | 64 | 84 |
| 34 | f | 174/174 (100%) | 170 (98%) | 4 (2%) | 56 | 78 |
| 35 | g | 190/190 (100%) | 188 (99%) | 2 (1%) | 78 | 89 |
| 36 | h | 94/94 (100%) | 94 (100%) | 0 | 100 | 100 |
| 37 | i | 196/196 (100%) | 195 (100%) | 1 (0%) | 91 | 95 |
| 38 | j | 106/106 (100%) | 105 (99%) | 1 (1%) | 82 | 91 |
| 39 | k | 87/87 (100%) | 84 (97%) | 3 (3%) | 42 | 69 |
| 40 | l | 57/57 (100%) | 56 (98%) | 1 (2%) | 64 | 84 |
| 41 | m | 272/272 (100%) | 270 (99%) | 2 (1%) | 87 | 93 |
| 42 | n | 116/116 (100%) | 112 (97%) | 4 (3%) | 42 | 69 |
| 43 | o | 177/177 (100%) | 174 (98%) | 3 (2%) | 66 | 84 |
| 44 | p | 64/64 (100%) | 64 (100%) | 0 | 100 | 100 |
| 45 | q | 207/207 (100%) | 205 (99%) | 2 (1%) | 80 | 90 |
| 46 | r | 104/104 (100%) | 104 (100%) | 0 | 100 | 100 |
| 47 | s | 113/113 (100%) | 112 (99%) | 1 (1%) | 82 | 91 |
| 48 | t | 89/89 (100%) | 88 (99%) | 1 (1%) | 78 | 89 |
| 49 | u | 66/548 (12%) | 61 (92%) | 5 (8%) | 15 | 47 |
| 50 | w | 360/928 (39%) | 358 (99%) | 2 (1%) | 89 | 94 |
| All | All | 8396/10666 (79%) | 8277 (99%) | 119 (1%) | 74 | 86 |

5 of 119 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 14 | I | 49 | ARG |
| 21 | R | 28 | LEU |
| 45 | q | 131 | ARG |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 14 | I | 216 | ASN |
| 19 | P | 30 | MET |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 3 | 3 | 231 | ASN |
| 4 | 4 | 333 | ASN |
| 9 | 9 | 303 | ASN |
| 3 | 3 | 302 | ASN |
| 3 | 3 | 361 | ASN |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 10 | A | 1771/1776 (99%) | 707 (39%) | 51 (2%) |
| 11 | F | 25/26 (96%) | 14 (56%) | 1 (4%) |
| 18 | N | 74/75 (98%) | 21 (28%) | 2 (2%) |
| All | All | 1870/1877 (99%) | 742 (39%) | 54 (2%) |

5 of 742 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 10 | A | 3 | C |
| 10 | A | 4 | C |
| 10 | A | 9 | U |
| 10 | A | 17 | C |
| 10 | A | 20 | G |

5 of 54 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 10 | A | 619 | A |
| 10 | A | 1133 | U |
| 10 | A | 1819 | A |
| 10 | A | 730 | C |
| 10 | A | 829 | C |

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 10 | A | 5 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | A | 736:C | O3' | 744:C | P | 27.46 |
| 1 | A | 761:G | O3' | 774:U | P | 18.00 |
| 1 | A | 679:U | O3' | 683:G | P | 15.42 |
| 1 | A | 687:G | O3' | 730:C | P | 13.04 |
| 1 | A | 243:C | O3' | 267:G | P | 13.01 |