



## wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:53 PM UTC

PDB ID : 7PZY / pdb\_00007pzy  
EMDB ID : EMD-13737  
Title : Structure of the vacant *Candida albicans* 80S ribosome  
Authors : Zgadzay, Y.; Kolosova, O.; Stetsenko, A.; Jenner, L.; Guskov, A.; Yusupova, G.; Yusupov, M.  
Deposited on : 2021-10-13  
Resolution : 2.32 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

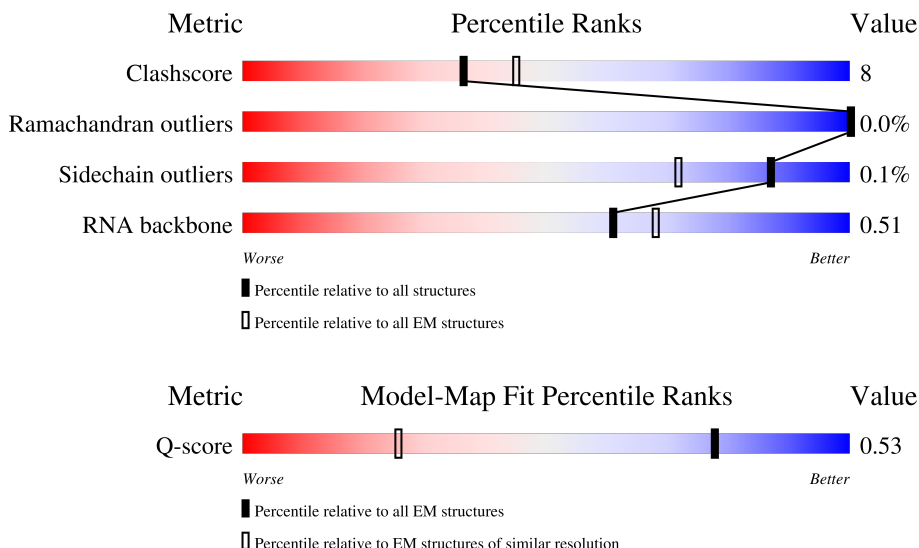
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.32 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<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore            | 229148                      | 23984                       | -                                                        |
| Ramachandran outliers | 224038                      | 23583                       | -                                                        |
| Sidechain outliers    | 223484                      | 23102                       | -                                                        |
| RNA backbone          | 8273                        | 3508                        | -                                                        |
| Q-score               | -                           | 25397                       | 4359 ( 1.82 - 2.82 )                                     |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1   | 1     | 3359   |                  |
| 2   | 3     | 121    |                  |
| 3   | 4     | 158    |                  |

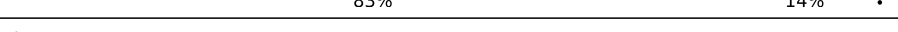
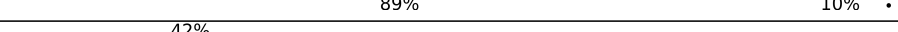
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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 4   | 10    | 76     |                  |
| 5   | j     | 254    |                  |
| 6   | k     | 389    |                  |
| 7   | l     | 363    |                  |
| 8   | m     | 298    |                  |
| 9   | n     | 176    |                  |
| 10  | o     | 241    |                  |
| 11  | p     | 262    |                  |
| 12  | q     | 191    |                  |
| 13  | r     | 220    |                  |
| 14  | s     | 174    |                  |
| 15  | t     | 202    |                  |
| 16  | u     | 131    |                  |
| 17  | v     | 204    |                  |
| 18  | w     | 200    |                  |
| 19  | x     | 185    |                  |
| 20  | y     | 186    |                  |
| 21  | z     | 190    |                  |
| 22  | 0     | 172    |                  |
| 23  | 2     | 160    |                  |
| 24  | 5     | 124    |                  |
| 25  | 6     | 137    |                  |
| 26  | 7     | 155    |                  |
| 27  | 8     | 142    |                  |
| 28  | 9     | 127    |                  |

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| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 29  | AA    | 136    |    |
| 30  | AB    | 149    |    |
| 31  | AC    | 63     |    |
| 32  | AD    | 106    |    |
| 33  | AE    | 112    |    |
| 34  | AF    | 131    |    |
| 35  | AG    | 107    |    |
| 36  | AH    | 122    |    |
| 37  | AI    | 120    |    |
| 38  | AJ    | 99     |    |
| 39  | AK    | 90     |    |
| 40  | AL    | 78     |    |
| 41  | AM    | 51     |  |
| 42  | AN    | 52     |  |
| 43  | AO    | 25     |  |
| 44  | AP    | 106    |  |
| 45  | AQ    | 92     |  |
| 46  | i     | 267    |  |
| 47  | A     | 1787   |  |
| 48  | B     | 261    |  |
| 49  | C     | 256    |  |
| 50  | D     | 249    |  |
| 51  | E     | 251    |  |
| 52  | F     | 262    |  |
| 53  | G     | 225    |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 54  | H     | 236    |                  |
| 55  | I     | 186    |                  |
| 56  | J     | 206    |                  |
| 57  | K     | 189    |                  |
| 58  | L     | 118    |                  |
| 59  | M     | 155    |                  |
| 60  | N     | 143    |                  |
| 61  | O     | 151    |                  |
| 62  | P     | 132    |                  |
| 63  | Q     | 142    |                  |
| 64  | R     | 142    |                  |
| 65  | S     | 137    |                  |
| 66  | T     | 145    |                  |
| 67  | U     | 145    |                  |
| 68  | V     | 119    |                  |
| 69  | W     | 87     |                  |
| 70  | X     | 130    |                  |
| 71  | Y     | 145    |                  |
| 72  | Z     | 135    |                  |
| 73  | a     | 105    |                  |
| 74  | b     | 119    |                  |
| 75  | c     | 82     |                  |
| 76  | d     | 67     |                  |
| 77  | e     | 56     |                  |
| 78  | f     | 63     |                  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 79  | g     | 193    |                  |
| 80  | h     | 317    |                  |

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

| Mol | Type | Chain | Res  | Chirality | Geometry | Clashes | Electron density |
|-----|------|-------|------|-----------|----------|---------|------------------|
| 81  | SPD  | 1     | 3404 | -         | -        | X       | -                |
| 81  | SPD  | 1     | 3405 | -         | -        | X       | -                |
| 81  | SPD  | 1     | 3406 | -         | -        | X       | -                |
| 81  | SPD  | 1     | 3407 | -         | -        | X       | -                |
| 81  | SPD  | 1     | 3408 | -         | -        | X       | -                |
| 81  | SPD  | 1     | 3409 | -         | -        | X       | -                |
| 81  | SPD  | 1     | 3410 | -         | -        | X       | -                |
| 81  | SPD  | 1     | 3411 | -         | -        | X       | -                |
| 82  | PUT  | 1     | 3403 | -         | -        | X       | -                |
| 82  | PUT  | 4     | 201  | -         | -        | X       | -                |

## 2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 201513 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S ribosomal RNA.

| Mol | Chain | Residues | Atoms |       |       |       |      | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 1   | 1     | 3209     | Total | C     | N     | O     | P    | 0       | 0     |
|     |       |          | 68595 | 30642 | 12317 | 22427 | 3209 |         |       |

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

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 2   | 3     | 121      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 2579  | 1153 | 463 | 842 | 121 |         |       |

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

| Mol | Chain | Residues | Atoms |      |     |      |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|---------|-------|
| 3   | 4     | 158      | Total | C    | N   | O    | P   | 0       | 0     |
|     |       |          | 3353  | 1500 | 585 | 1110 | 158 |         |       |

- Molecule 4 is a RNA chain called Mixture of endogenous E-tRNAs.

| Mol | Chain | Residues | Atoms |     |    |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|-----|----|---------|-------|
| 4   | 10    | 16       | Total | C   | N  | O   | P  | 0       | 0     |
|     |       |          | 338   | 151 | 59 | 112 | 16 |         |       |

- Molecule 5 is a protein called Ribosomal 60S subunit protein L2A.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 5   | j     | 249      | Total | C    | N   | O   | S | 1       | 0     |
|     |       |          | 1894  | 1185 | 377 | 330 | 2 |         |       |

- Molecule 6 is a protein called 60S ribosomal protein L3.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 6   | k     | 386      | Total | C    | N   | O   | S | 1       | 0     |
|     |       |          | 3084  | 1955 | 584 | 538 | 7 |         |       |

- Molecule 7 is a protein called Ribosomal 60S subunit protein L4B.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 7   | l     | 361      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2751  | 1729 | 529 | 490 | 3 |         |       |

- Molecule 8 is a protein called Ribosomal 60S subunit protein L5.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 8   | m     | 292      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2394  | 1526 | 416 | 450 | 2 |         |       |

- Molecule 9 is a protein called 60S ribosomal protein L6.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 9   | n     | 155      | Total | C   | N   | O   |  | 1       | 0     |
|     |       |          | 1237  | 794 | 226 | 217 |  |         |       |

- Molecule 10 is a protein called Ribosomal 60S subunit protein L7A.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 10  | o     | 234      | Total | C    | N   | O   | S | 1       | 0     |
|     |       |          | 1893  | 1213 | 348 | 331 | 1 |         |       |

- Molecule 11 is a protein called 60S ribosomal protein L8.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 11  | p     | 238      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1839  | 1175 | 327 | 334 | 3 |         |       |

- Molecule 12 is a protein called Ribosomal 60S subunit protein L9B.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12  | q     | 190      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1519  | 958 | 276 | 281 | 4 |         |       |

- Molecule 13 is a protein called Ribosomal 60S subunit protein L10.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 13  | r     | 208      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1689  | 1069 | 322 | 291 | 7 |         |       |

- Molecule 14 is a protein called Ribosomal 60S subunit protein L11B.



| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 14  | s     | 172      | Total | C   | N   | O   | S | 1       | 0     |
|     |       |          | 1385  | 864 | 262 | 255 | 4 |         |       |

- Molecule 15 is a protein called 60S ribosomal protein L13.

| Mol | Chain | Residues | Atoms |      |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|--|---------|-------|
| 15  | t     | 200      | Total | C    | N   | O   |  | 0       | 0     |
|     |       |          | 1610  | 1009 | 318 | 283 |  |         |       |

- Molecule 16 is a protein called Ribosomal 60S subunit protein L14B.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16  | u     | 130      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1029  | 660 | 193 | 175 | 1 |         |       |

- Molecule 17 is a protein called Ribosomal protein L15.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 17  | v     | 203      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1713  | 1075 | 356 | 280 | 2 |         |       |

- Molecule 18 is a protein called Ribosomal 60S subunit protein L16A.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 18  | w     | 199      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1590  | 1025 | 294 | 269 | 2 |         |       |

- Molecule 19 is a protein called Ribosomal 60S subunit protein L17B.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 19  | x     | 172      | Total | C   | N   | O   |  | 0       | 0     |
|     |       |          | 1375  | 850 | 279 | 246 |  |         |       |

- Molecule 20 is a protein called Ribosomal 60S subunit protein L18A.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 20  | y     | 185      | Total | C   | N   | O   |  | 3       | 0     |
|     |       |          | 1478  | 930 | 302 | 246 |  |         |       |

- Molecule 21 is a protein called Ribosomal protein L19.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21  | z     | 179      | Total | C   | N   | O   | S | 1       | 0     |
|     |       |          | 1462  | 904 | 311 | 244 | 3 |         |       |

- Molecule 22 is a protein called 60S ribosomal protein L20.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 22  | 0     | 171      | Total | C   | N   | O   | S | 2       | 0     |
|     |       |          | 1442  | 933 | 262 | 244 | 3 |         |       |

- Molecule 23 is a protein called Ribosomal 60S subunit protein L21A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23  | 2     | 159      | Total | C   | N   | O   | S | 2       | 0     |
|     |       |          | 1276  | 807 | 244 | 223 | 2 |         |       |

- Molecule 24 is a protein called Ribosomal 60S subunit protein L22B.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 24  | 5     | 103      | Total | C   | N   | O   |  | 2       | 0     |
|     |       |          | 848   | 553 | 139 | 156 |  |         |       |

- Molecule 25 is a protein called Ribosomal 60S subunit protein L23B.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25  | 6     | 131      | Total | C   | N   | O   | S | 1       | 0     |
|     |       |          | 986   | 621 | 186 | 171 | 8 |         |       |

- Molecule 26 is a protein called Ribosomal 60S subunit protein L24A.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 26  | 7     | 63       | Total | C   | N   | O  | S | 0       | 0     |
|     |       |          | 524   | 334 | 103 | 86 | 1 |         |       |

- Molecule 27 is a protein called Ribosomal 60S subunit protein L25.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27  | 8     | 121      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 974   | 622 | 175 | 176 | 1 |         |       |

- Molecule 28 is a protein called Ribosomal 60S subunit protein L26B.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 28  | 9     | 126      | Total | C   | N   | O   |         |       |
|     |       |          | 989   | 618 | 190 | 181 | 0       | 0     |

- Molecule 29 is a protein called 60S ribosomal protein L27.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29  | AA    | 135      | Total | C   | N   | O   | S |         |       |
|     |       |          | 1087  | 705 | 197 | 183 | 2 | 0       | 0     |

- Molecule 30 is a protein called Ribosomal 60S subunit protein L28.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 30  | AB    | 148      | Total | C   | N   | O   | S |         |       |
|     |       |          | 1170  | 741 | 231 | 197 | 1 | 0       | 0     |

- Molecule 31 is a protein called 60S ribosomal protein L29.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 31  | AC    | 63       | Total | C   | N   | O  | S |         |       |
|     |       |          | 509   | 317 | 109 | 82 | 1 | 1       | 0     |

- Molecule 32 is a protein called Ribosomal 60S subunit protein L30.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32  | AD    | 96       | Total | C   | N   | O   | S |         |       |
|     |       |          | 729   | 469 | 121 | 137 | 2 | 0       | 0     |

- Molecule 33 is a protein called Ribosomal 60S subunit protein L31B.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33  | AE    | 109      | Total | C   | N   | O   | S |         |       |
|     |       |          | 889   | 562 | 167 | 158 | 2 | 0       | 0     |

- Molecule 34 is a protein called Ribosomal 60S subunit protein L32.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 34  | AF    | 125      | Total | C   | N   | O   | S |         |       |
|     |       |          | 1015  | 649 | 197 | 168 | 1 | 1       | 0     |

- Molecule 35 is a protein called Ribosomal 60S subunit protein L33A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 35  | AG    | 106      | Total | C   | N   | O   | S | 3       | 0     |
|     |       |          | 867   | 558 | 166 | 142 | 1 |         |       |

- Molecule 36 is a protein called Ribosomal 60S subunit protein L34B.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 36  | AH    | 112      | Total | C   | N   | O   | S | 4       | 0     |
|     |       |          | 913   | 567 | 188 | 154 | 4 |         |       |

- Molecule 37 is a protein called Ribosomal 60S subunit protein L35A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 37  | AI    | 119      | Total | C   | N   | O   | S | 1       | 0     |
|     |       |          | 990   | 629 | 195 | 166 |   |         |       |

- Molecule 38 is a protein called 60S ribosomal protein L36.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 38  | AJ    | 98       | Total | C   | N   | O   | S | 1       | 0     |
|     |       |          | 772   | 481 | 158 | 131 | 2 |         |       |

- Molecule 39 is a protein called Ribosomal protein L37.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 39  | AK    | 86       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 677   | 413 | 148 | 110 | 6 |         |       |

- Molecule 40 is a protein called Ribosomal 60S subunit protein L38.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 40  | AL    | 77       | Total | C   | N   | O   | S | 1       | 0     |
|     |       |          | 623   | 398 | 116 | 109 |   |         |       |

- Molecule 41 is a protein called 60S ribosomal protein L39.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 41  | AM    | 50       | Total | C   | N   | O  | S | 1       | 0     |
|     |       |          | 446   | 280 | 100 | 66 |   |         |       |

- Molecule 42 is a protein called Rpl40bp.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 42  | AN    | 52       | Total | C   | N  | O  | S | 1       | 0     |
|     |       |          | 427   | 265 | 89 | 67 | 6 |         |       |

- Molecule 43 is a protein called 60S ribosomal protein L41.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 43  | AO    | 25       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 236   | 144 | 63 | 28 | 1 |         |       |

- Molecule 44 is a protein called Ribosomal 60S subunit protein L42A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 44  | AP    | 103      | Total | C   | N   | O   | S | 2       | 0     |
|     |       |          | 843   | 533 | 168 | 137 | 5 |         |       |

- Molecule 45 is a protein called Ribosomal 60S subunit protein L43A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 45  | AQ    | 91       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 698   | 430 | 140 | 124 | 4 |         |       |

- Molecule 46 is a protein called HABP4\_PAI-RBP1 domain-containing protein.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 46  | i     | 113      | Total | C   | N   | O   |  | 0       | 0     |
|     |       |          | 853   | 512 | 155 | 186 |  |         |       |

- Molecule 47 is a RNA chain called 18S ribosomal RNA.

| Mol | Chain | Residues | Atoms |       |      |       |      | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 47  | A     | 1692     | Total | C     | N    | O     | P    | 0       | 0     |
|     |       |          | 36083 | 16130 | 6412 | 11849 | 1692 |         |       |

- Molecule 48 is a protein called 40S ribosomal protein S0.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 48  | B     | 208      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1627  | 1041 | 284 | 297 | 5 |         |       |

- Molecule 49 is a protein called 40S ribosomal protein S1.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 49  | C     | 214      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1724  | 1094 | 313 | 313 | 4 |         |       |

- Molecule 50 is a protein called Ribosomal 40S subunit protein S2.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 50  | D     | 216      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1620  | 1033 | 287 | 295 | 5 |         |       |

- Molecule 51 is a protein called Ribosomal 40S subunit protein S3.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 51  | E     | 223      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1707  | 1087 | 311 | 305 | 4 |         |       |

- Molecule 52 is a protein called 40S ribosomal protein S4.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 52  | F     | 260      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2055  | 1306 | 386 | 358 | 5 |         |       |

- Molecule 53 is a protein called Ribosomal 40S subunit protein S5.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 53  | G     | 206      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1614  | 1008 | 301 | 301 | 4 |         |       |

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

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 54  | H     | 226      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1820  | 1133 | 351 | 330 | 6 |         |       |

- Molecule 55 is a protein called 40S ribosomal protein S7.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 55  | I     | 182      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 1466  | 939 | 264 | 263 |         |       |

- Molecule 56 is a protein called 40S ribosomal protein S8.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 56  | J     | 203      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1579  | 973 | 322 | 283 | 1 |         |       |

- Molecule 57 is a protein called Ribosomal 40S subunit protein S9B.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 57  | K     | 178      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1453  | 918 | 286 | 248 | 1 |         |       |

- Molecule 58 is a protein called Ribosomal 40S subunit protein S10A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 58  | L     | 93       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 783   | 511 | 129 | 142 | 1 |         |       |

- Molecule 59 is a protein called Ribosomal 40S subunit protein S11A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 59  | M     | 141      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1129  | 722 | 212 | 192 | 3 |         |       |

- Molecule 60 is a protein called 40S ribosomal protein S12.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 60  | N     | 116      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 885   | 550 | 158 | 172 | 5 |         |       |

- Molecule 61 is a protein called Ribosomal 40S subunit protein S13.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 61  | O     | 150      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1187  | 757 | 219 | 210 | 1 |         |       |

- Molecule 62 is a protein called Ribosomal 40S subunit protein S14B.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 62  | P     | 127      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 942   | 579 | 186 | 174 | 3 |         |       |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference      |
|-------|---------|----------|--------|----------|----------------|
| P     | 119     | IAS      | ASP    | conflict | UNP A0A1D8PDT3 |

- Molecule 63 is a protein called Ribosomal 40S subunit protein S15.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 63  | Q     | 118      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 935   | 598 | 169 | 162 | 6 |         |       |

- Molecule 64 is a protein called Ribosomal 40S subunit protein S16A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 64  | R     | 140      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1091  | 700 | 198 | 192 | 1 |         |       |

- Molecule 65 is a protein called Ribosomal 40S subunit protein S17B.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 65  | S     | 125      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1002  | 631 | 184 | 186 | 1 |         |       |

- Molecule 66 is a protein called Ribosomal 40S subunit protein S18B.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 66  | T     | 142      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1169  | 733 | 228 | 205 | 3 |         |       |

- Molecule 67 is a protein called Ribosomal 40S subunit protein S19A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 67  | U     | 141      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1100  | 689 | 210 | 200 | 1 |         |       |

- Molecule 68 is a protein called Ribosomal 40S subunit protein S20.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 68  | V     | 100      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 790   | 499 | 146 | 143 | 2 |         |       |

- Molecule 69 is a protein called 40S ribosomal protein S21.



| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 69  | W     | 87       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 676   | 415 | 126 | 133 | 2 |         |       |

- Molecule 70 is a protein called 40S ribosomal protein S22-A.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 70  | X     | 129      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1032  | 655 | 191 | 183 | 3 |         |       |

- Molecule 71 is a protein called Ribosomal 40S subunit protein S23B.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 71  | Y     | 143      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1110  | 701 | 219 | 188 | 2 |         |       |

- Molecule 72 is a protein called 40S ribosomal protein S24.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 72  | Z     | 132      | Total | C   | N   | O   |  | 0       | 0     |
|     |       |          | 1072  | 670 | 216 | 186 |  |         |       |

- Molecule 73 is a protein called 40S ribosomal protein S25.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 73  | a     | 72       | Total | C   | N   | O   |  | 0       | 0     |
|     |       |          | 578   | 369 | 103 | 106 |  |         |       |

- Molecule 74 is a protein called 40S ribosomal protein S26.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 74  | b     | 100      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 799   | 494 | 169 | 130 | 6 |         |       |

- Molecule 75 is a protein called 40S ribosomal protein S27.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 75  | c     | 81       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 614   | 383 | 110 | 114 | 7 |         |       |

- Molecule 76 is a protein called Ribosomal 40S subunit protein S28B.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 76  | d     | 62       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 487   | 299 | 98 | 88 | 2 |         |       |

- Molecule 77 is a protein called Ribosomal 40S subunit protein S29A.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 77  | e     | 55       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 454   | 281 | 94 | 75 | 4 |         |       |

- Molecule 78 is a protein called 40S ribosomal protein S30.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 78  | f     | 56       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 444   | 278 | 89 | 75 | 2 |         |       |

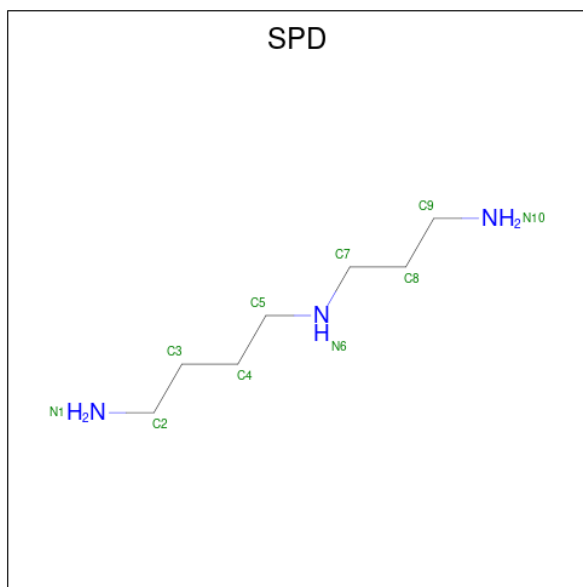
- Molecule 79 is a protein called Ubiquitin-ribosomal 40S subunit protein S31 fusion protein.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 79  | g     | 70       | Total | C   | N   | O  | S | 0       | 0     |
|     |       |          | 574   | 362 | 113 | 93 | 6 |         |       |

- Molecule 80 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

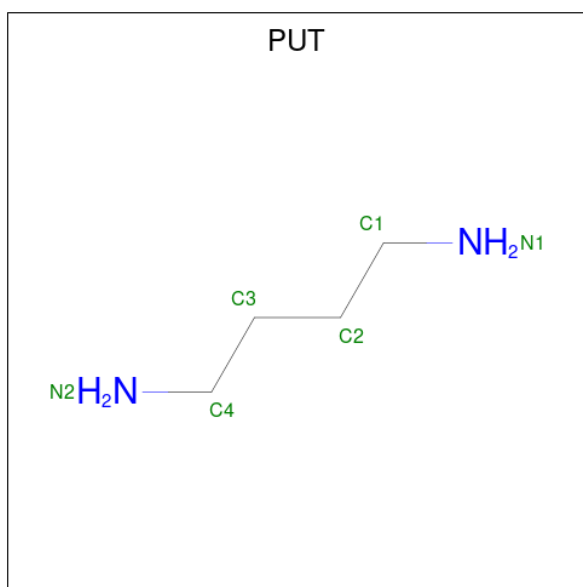
| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 80  | h     | 311      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2398  | 1519 | 412 | 462 | 5 |         |       |

- Molecule 81 is SPERMIDINE (CCD ID: SPD) (formula: C<sub>7</sub>H<sub>19</sub>N<sub>3</sub>).



| Mol | Chain | Residues | Atoms |   |   | AltConf |
|-----|-------|----------|-------|---|---|---------|
| 81  | 1     | 1        | Total | C | N | 0       |
|     |       |          | 10    | 7 | 3 |         |
| 81  | 1     | 1        | Total | C | N | 0       |
|     |       |          | 10    | 7 | 3 |         |
| 81  | 1     | 1        | Total | C | N | 0       |
|     |       |          | 10    | 7 | 3 |         |
| 81  | 1     | 1        | Total | C | N | 0       |
|     |       |          | 10    | 7 | 3 |         |
| 81  | 1     | 1        | Total | C | N | 0       |
|     |       |          | 10    | 7 | 3 |         |
| 81  | 1     | 1        | Total | C | N | 0       |
|     |       |          | 10    | 7 | 3 |         |
| 81  | 1     | 1        | Total | C | N | 0       |
|     |       |          | 10    | 7 | 3 |         |
| 81  | 1     | 1        | Total | C | N | 0       |
|     |       |          | 10    | 7 | 3 |         |

- Molecule 82 is 1,4-DIAMINOBUTANE (CCD ID: PUT) (formula:  $C_4H_{12}N_2$ ).



| Mol | Chain | Residues | Atoms |   |   | AltConf |
|-----|-------|----------|-------|---|---|---------|
| 82  | 1     | 1        | Total | C | N | 0       |
|     |       |          | 6     | 4 | 2 |         |
| 82  | 4     | 1        | Total | C | N | 0       |
|     |       |          | 6     | 4 | 2 |         |

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms |     | AltConf |
|-----|-------|----------|-------|-----|---------|
| 83  | 1     | 296      | Total | Mg  | 0       |
|     |       |          | 296   | 296 |         |
| 83  | 4     | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 83  | j     | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 83  | k     | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 83  | o     | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 83  | r     | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 83  | x     | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 83  | 2     | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 83  | AC    | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |
| 83  | AF    | 1        | Total | Mg  | 0       |
|     |       |          | 1     | 1   |         |

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| Mol | Chain | Residues | Atoms        |           | AltConf |
|-----|-------|----------|--------------|-----------|---------|
| 83  | AH    | 1        | Total<br>1   | Mg<br>1   | 0       |
| 83  | AK    | 1        | Total<br>1   | Mg<br>1   | 0       |
| 83  | AP    | 1        | Total<br>1   | Mg<br>1   | 0       |
| 83  | A     | 133      | Total<br>133 | Mg<br>133 | 0       |
| 83  | F     | 1        | Total<br>1   | Mg<br>1   | 0       |
| 83  | U     | 1        | Total<br>1   | Mg<br>1   | 0       |

- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms      |         | AltConf |
|-----|-------|----------|------------|---------|---------|
| 84  | AK    | 1        | Total<br>1 | Zn<br>1 | 0       |
| 84  | AN    | 1        | Total<br>1 | Zn<br>1 | 0       |
| 84  | AP    | 1        | Total<br>1 | Zn<br>1 | 0       |
| 84  | AQ    | 1        | Total<br>1 | Zn<br>1 | 0       |
| 84  | b     | 1        | Total<br>1 | Zn<br>1 | 0       |
| 84  | c     | 1        | Total<br>1 | Zn<br>1 | 0       |
| 84  | e     | 1        | Total<br>1 | Zn<br>1 | 0       |
| 84  | g     | 1        | Total<br>1 | Zn<br>1 | 0       |

- Molecule 85 is water.

| Mol | Chain | Residues | Atoms         |           | AltConf |
|-----|-------|----------|---------------|-----------|---------|
| 85  | 1     | 1019     | Total<br>1019 | O<br>1019 | 0       |
| 85  | 3     | 8        | Total<br>8    | O<br>8    | 0       |
| 85  | 4     | 39       | Total<br>39   | O<br>39   | 0       |

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| Mol | Chain | Residues | Atoms       |         | AltConf |
|-----|-------|----------|-------------|---------|---------|
| 85  | j     | 16       | Total<br>16 | O<br>16 | 0       |
| 85  | k     | 38       | Total<br>38 | O<br>38 | 0       |
| 85  | l     | 20       | Total<br>20 | O<br>20 | 0       |
| 85  | m     | 1        | Total<br>1  | O<br>1  | 0       |
| 85  | n     | 1        | Total<br>1  | O<br>1  | 0       |
| 85  | o     | 11       | Total<br>11 | O<br>11 | 0       |
| 85  | p     | 1        | Total<br>1  | O<br>1  | 0       |
| 85  | r     | 1        | Total<br>1  | O<br>1  | 0       |
| 85  | t     | 7        | Total<br>7  | O<br>7  | 0       |
| 85  | v     | 24       | Total<br>24 | O<br>24 | 0       |
| 85  | w     | 10       | Total<br>10 | O<br>10 | 0       |
| 85  | x     | 14       | Total<br>14 | O<br>14 | 0       |
| 85  | y     | 6        | Total<br>6  | O<br>6  | 0       |
| 85  | z     | 3        | Total<br>3  | O<br>3  | 0       |
| 85  | 0     | 4        | Total<br>4  | O<br>4  | 0       |
| 85  | 2     | 1        | Total<br>1  | O<br>1  | 0       |
| 85  | 6     | 3        | Total<br>3  | O<br>3  | 0       |
| 85  | 7     | 3        | Total<br>3  | O<br>3  | 0       |
| 85  | 8     | 4        | Total<br>4  | O<br>4  | 0       |
| 85  | AA    | 1        | Total<br>1  | O<br>1  | 0       |
| 85  | AB    | 12       | Total<br>12 | O<br>12 | 0       |

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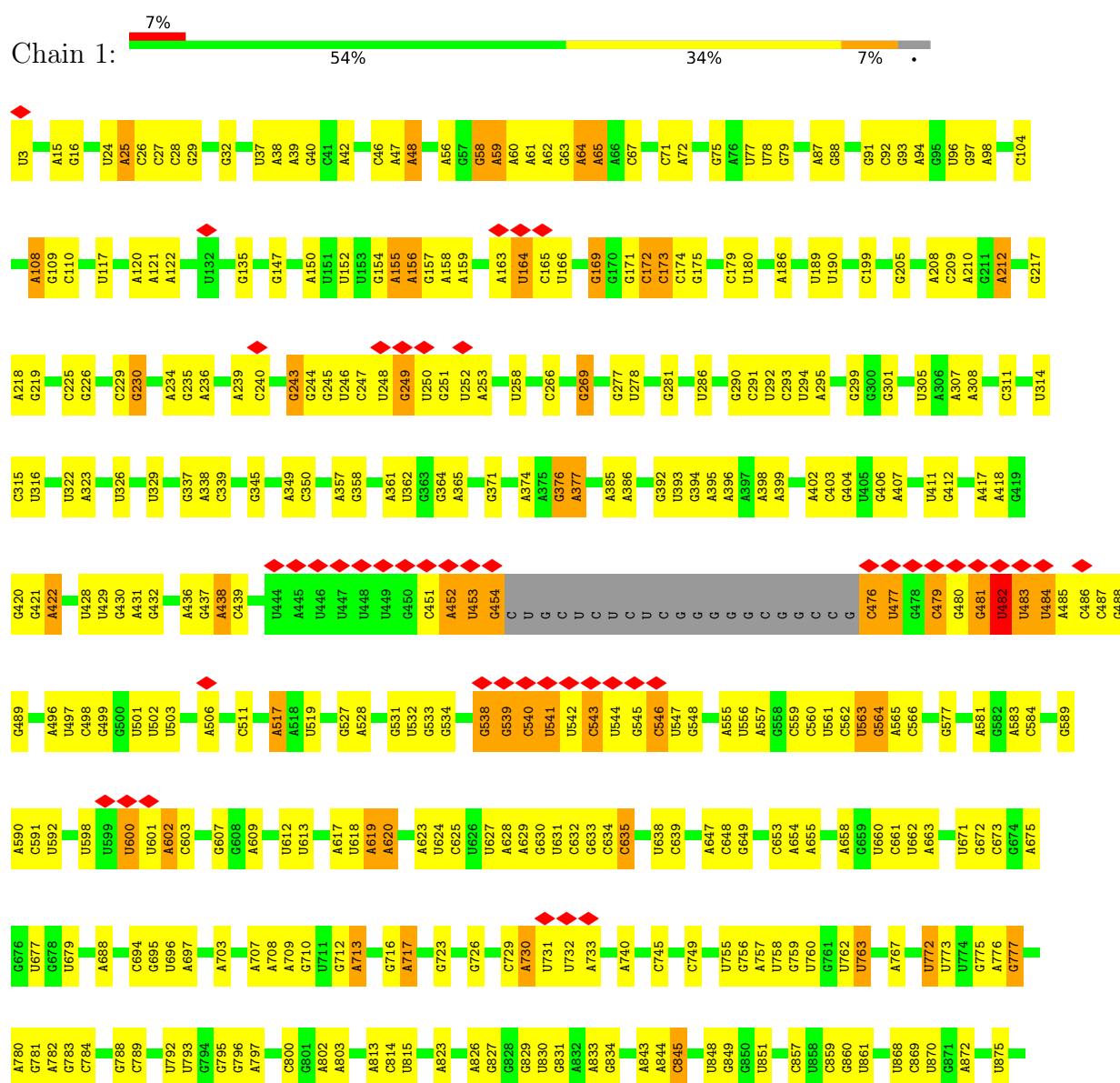
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| Mol | Chain | Residues | Atoms       |         | AltConf |
|-----|-------|----------|-------------|---------|---------|
| 85  | AC    | 6        | Total<br>6  | O<br>6  | 0       |
| 85  | AE    | 3        | Total<br>3  | O<br>3  | 0       |
| 85  | AF    | 16       | Total<br>16 | O<br>16 | 0       |
| 85  | AG    | 10       | Total<br>10 | O<br>10 | 0       |
| 85  | AH    | 11       | Total<br>11 | O<br>11 | 0       |
| 85  | AI    | 4        | Total<br>4  | O<br>4  | 0       |
| 85  | AK    | 16       | Total<br>16 | O<br>16 | 0       |
| 85  | AM    | 3        | Total<br>3  | O<br>3  | 0       |
| 85  | AP    | 2        | Total<br>2  | O<br>2  | 0       |
| 85  | AQ    | 3        | Total<br>3  | O<br>3  | 0       |
| 85  | A     | 38       | Total<br>38 | O<br>38 | 0       |
| 85  | G     | 1        | Total<br>1  | O<br>1  | 0       |
| 85  | O     | 1        | Total<br>1  | O<br>1  | 0       |

### 3 Residue-property plots

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

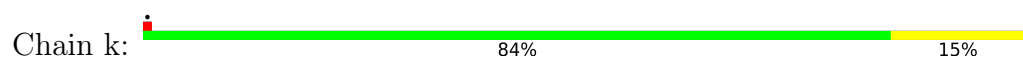
#### • Molecule 1: 25S ribosomal RNA

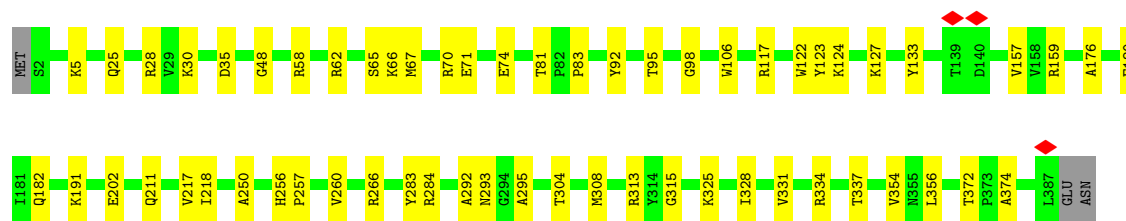




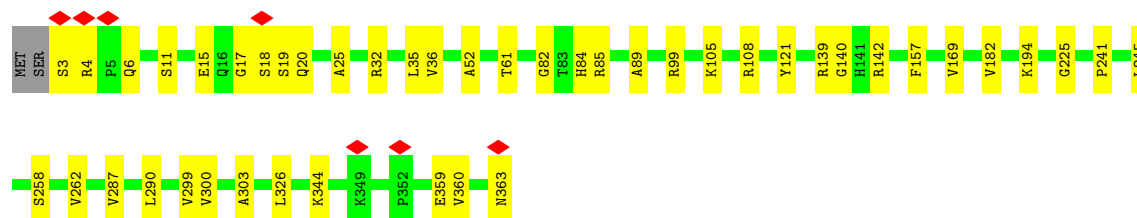
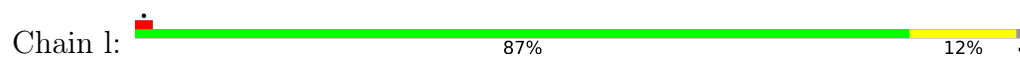


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|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| U3216 | G3217 | U3218 | G3219 | G3220 | G3221 | U3224 | G3228 | A3233 | U3234 | A3235 | U3240 | G3241 | A3244 | A3245 | G3246 | A3247 | U3248 | A3249 | A3250 | A3251 | A3252 | A3253 | A3254 | A3255 | A3256 | A3257 | A3258 | A3259 | A3260 | A3261 | A3262 | A3263 | A3264 | A3265 | A3266 | A3267 | A3268 | A3269 | A3270 | A3271 | A3272 | A3273 | A3274 | A3275 | A3276 | A3277 | A3278 | A3279 | A3280 | A3281 | A3282 | A3283 | A3284 | A3285 | A3286 | A3287 | A3288 | U3289 | U3290 | U3291 | U3292 | U3293 | U3294 | U3295 | U3296 | U3297 | U3298 | U3299 | U3300 | A3301 |
| A3135 | C3136 | U3137 | U3138 | U3139 | G3143 | A3144 | U3145 | U3146 | U3147 | U3148 | U3149 | A3150 | A3151 | A3152 | A3153 | A3154 | A3157 | C3158 | A3159 | C3160 | U3161 | U3162 | U3163 | U3164 | A3165 | A3166 | G3167 | U3079 | G3080 | G3081 | C3082 | U3083 | G3084 | C3090 | U3091 | C3092 | U3093 | A3094 | A3101 | C3103 | U3103 | C3104 | C3105 | U3106 | C3197 | C3198 | G3199 | G3207 | A3208 | A3209 | A3210 | G3211 | U3299 | G3298 | U3299 | A3300 | A3301 |       |       |       |       |       |       |       |       |       |       |       |       |       |
| U3028 | U3029 | U3030 | G3031 | U3038 | G3039 | U3040 | G3041 | A3042 | U3043 | A3044 | A3045 | A3050 | C3051 | G3052 | A3058 | A3059 | C3060 | C3061 | U3062 | A3063 | C3064 | C3065 | A3066 | U3076 | U3079 | G3080 | G3081 | C3082 | U3083 | G3084 | C3090 | U3091 | C3092 | U3093 | A3094 | A3101 | C3103 | U3103 | C3104 | C3105 | U3110 | A3111 | G3112 | A3113 | A3114 | C3115 | U3127 | G3133 | A3134 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| U2926 | U2927 | C2931 | G2932 | G2933 | U2934 | A2941 | C2942 | A2943 | A2944 | U2945 | U2946 | U2947 | C2955 | U2958 | A2959 | C2960 | U2961 | G2962 | A2967 | U2968 | G2969 | C2974 | A2978 | U2979 | A2984 | U2985 | U2986 | G2987 | A2988 | A2989 | A2996 | G3000 | A3001 | A3005 | C3006 | U3010 | U3013 | U3014 | U3019 | A3020 | A3021 | U3022 | G3025 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| U2847 | G2850 | A2851 | U2852 | C2853 | U2854 | U2855 | C2856 | C2857 | U2858 | A2859 | U2860 | C2861 | A2862 | C2866 | C2867 | A2868 | C2869 | C2870 | C2871 | A2872 | C2873 | U2876 | U2877 | A2883 | C2884 | C2885 | C2886 | U2887 | U2888 | U2895 | A2902 | C2903 | U2904 | A2905 | A2906 | U2907 | A2908 | G2911 | A2912 | C2914 | G2915 | U2916 | G2917 | A2918 | G2919 | C2920 | G2923 | G2924 | U2925 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| U2729 | A2734 | U2735 | C2736 | C2737 | U2738 | U2739 | U2740 | A2741 | C2745 | G2749 | A2750 | G2755 | G2765 | C2768 | A2771 | G2772 | A2773 | A2774 | C2782 | A2785 | G2786 | A2789 | U2790 | G2796 | C2797 | U2807 | C2808 | A2809 | A2810 | U2814 | U2815 | C2816 | A2817 | C2824 | C2829 | U2833 | A2836 | U2837 | U2838 | C2839 | G2843 | A2844 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| C2521 | U2522 | C2523 | U2524 | A2525 | C2526 | U2529 | C2530 | G2533 | C2534 | A2535 | U2536 | U2537 | A2538 | U2544 | C2545 | U2546 | G2547 | C2554 | G2567 | A2568 | C2569 | G2578 | G2579 | U2583 | U2584 | U2585 | G2586 | G2587 | C2588 | A2598 | U2603 | U2605 | A2609 | G2623 | U2624 | U2627 | A2628 | G2632 | G2633 | G2634 | A2635 | G2644 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| A2645 | A2646 | C2647 | A2648 | A2649 | A2650 | U2653 | C2654 | U2655 | C2656 | C2657 | A2658 | C2659 | U2660 | A2661 | C2662 | A2663 | A2666 | A2667 | A2668 | A2669 | C2670 | A2671 | C2672 | A2676 | A2677 | C2678 | C2683 | G2686 | U2691 | U2694 | U2695 | U2696 | U2697 | U2701 | C2709 | C2713 | U2716 | G2717 | A2718 | A2719 | A2720 | G2721 | U2722 | G2723 | U2724 | A2725 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
| U2484 | U2485 | U2486 | A2489 | U2492 | U2493 | A2498 | U2499 | G2500 | C2504 | G2511 | G2512 | A2513 | G2514 | G2515 | U2516 | G2517 | A2518 | A2519 | A2520 |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |

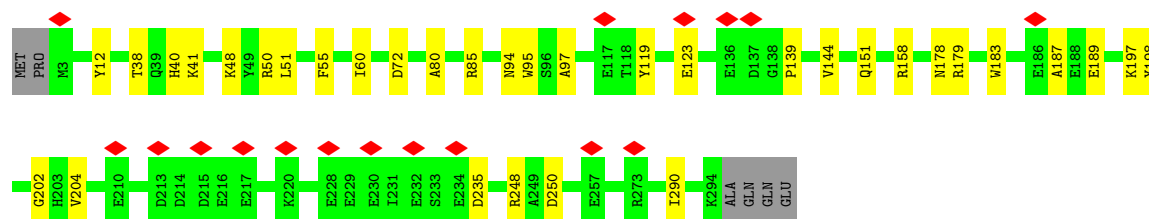
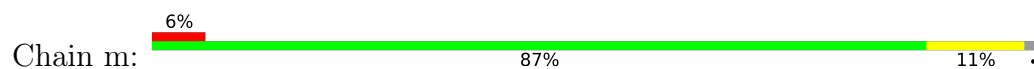




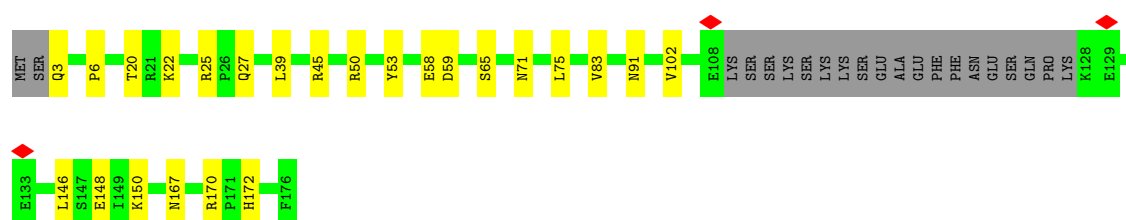
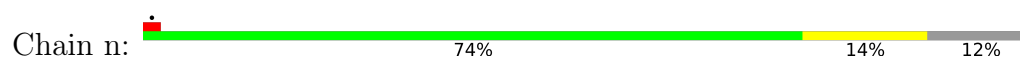
• Molecule 7: Ribosomal 60S subunit protein L4B



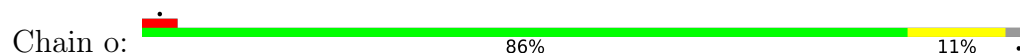
• Molecule 8: Ribosomal 60S subunit protein L5



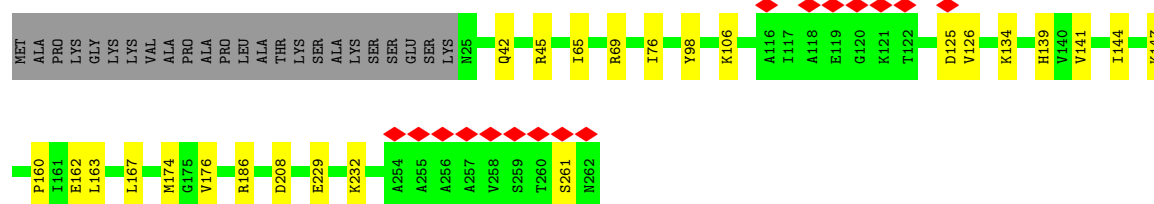
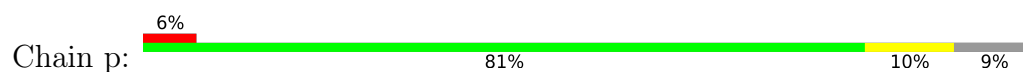
• Molecule 9: 60S ribosomal protein L6



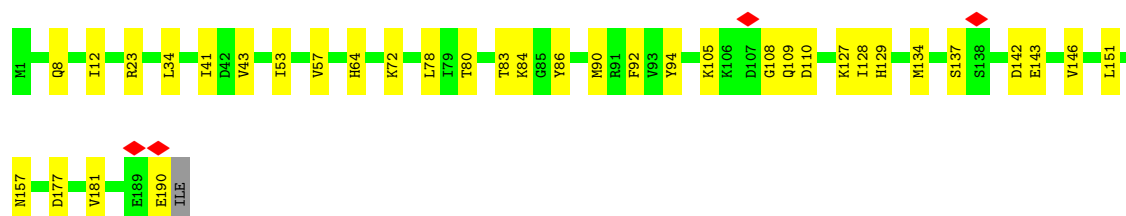
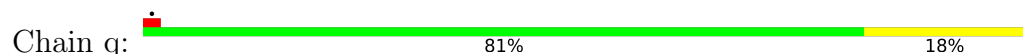
• Molecule 10: Ribosomal 60S subunit protein L7A



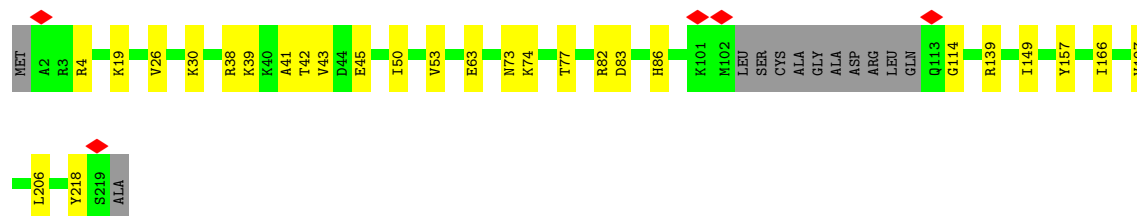
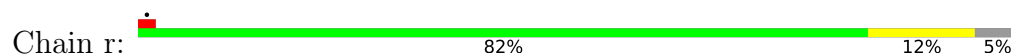
• Molecule 11: 60S ribosomal protein L8



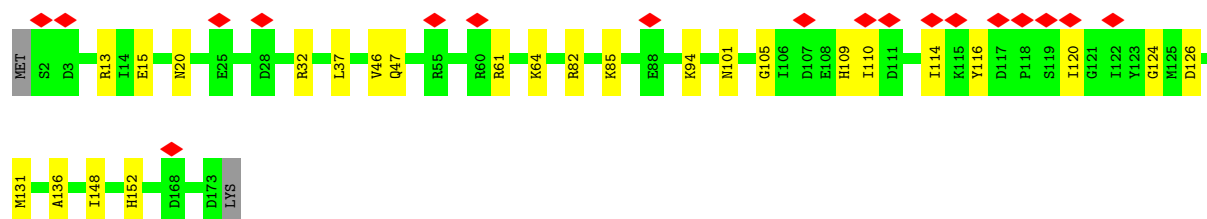
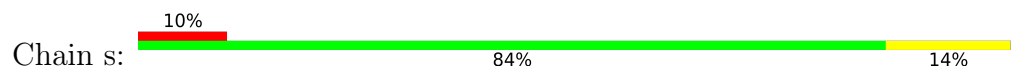
• Molecule 12: Ribosomal 60S subunit protein L9B



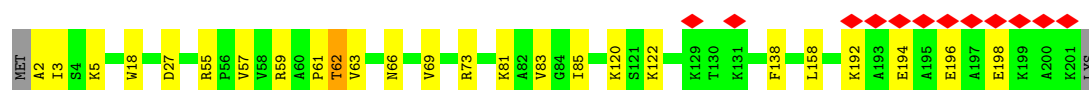
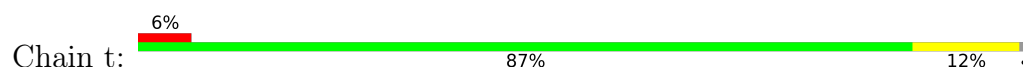
• Molecule 13: Ribosomal 60S subunit protein L10



• Molecule 14: Ribosomal 60S subunit protein L11B

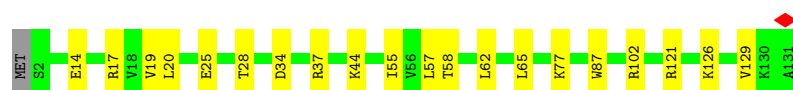


• Molecule 15: 60S ribosomal protein L13



- Molecule 16: Ribosomal 60S subunit protein L14B

Chain u:  84% 15%



- Molecule 17: Ribosomal protein L15

Chain v:  76% 23%



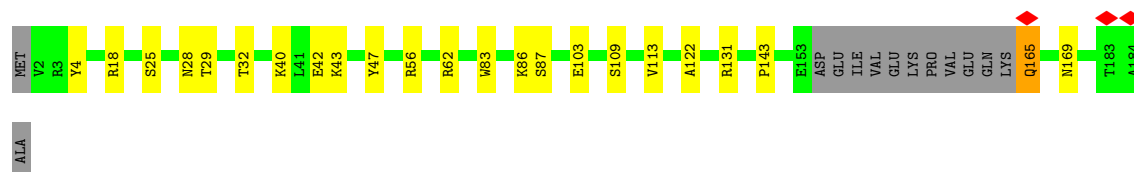
- Molecule 18: Ribosomal 60S subunit protein L16A

Chain w:  86% 14%



- Molecule 19: Ribosomal 60S subunit protein L17B

Chain x:  81% 12% 7%



- Molecule 20: Ribosomal 60S subunit protein L18A

Chain y:  83% 16%



- Molecule 21: Ribosomal protein L19

Chain z:  14% 82% 13% 6%





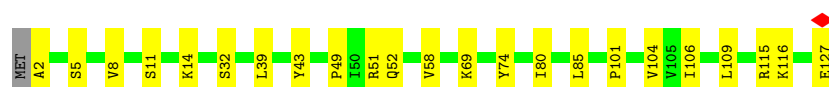
- Molecule 27: Ribosomal 60S subunit protein L25

Chain 8:  71% 14% 15%



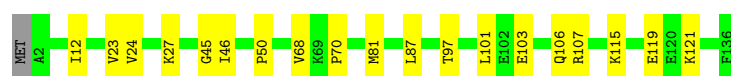
- Molecule 28: Ribosomal 60S subunit protein L26B

Chain 9:  81% 18% .



- Molecule 29: 60S ribosomal protein L27

Chain AA:  85% 14% .



- Molecule 30: Ribosomal 60S subunit protein L28

Chain AB:  83% 16% .



- Molecule 31: 60S ribosomal protein L29

Chain AC:  11% 84% 16%



- Molecule 32: Ribosomal 60S subunit protein L30

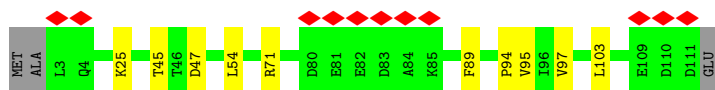
Chain AD:  73% 18% 9%



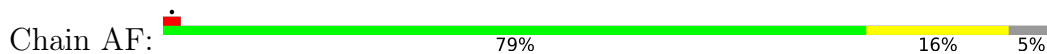
- Molecule 33: Ribosomal 60S subunit protein L31B

Chain AE:  10% 88% 9% .

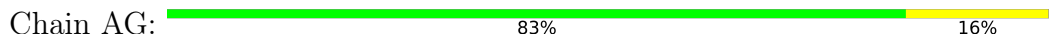




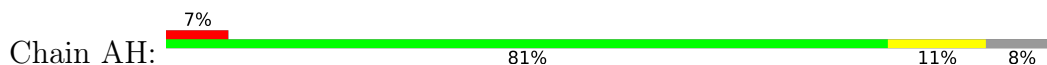
- Molecule 34: Ribosomal 60S subunit protein L32



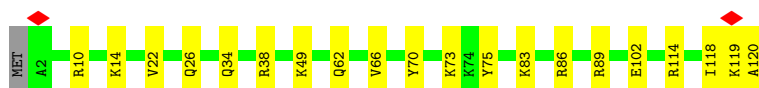
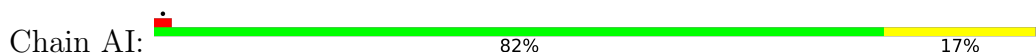
- Molecule 35: Ribosomal 60S subunit protein L33A



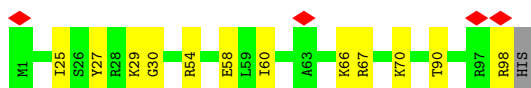
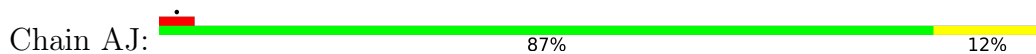
- Molecule 36: Ribosomal 60S subunit protein L34B



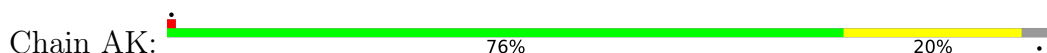
- Molecule 37: Ribosomal 60S subunit protein L35A



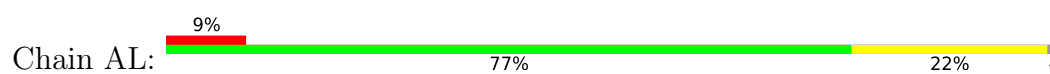
- Molecule 38: 60S ribosomal protein L36



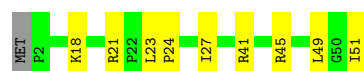
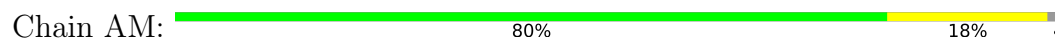
- Molecule 39: Ribosomal protein L37



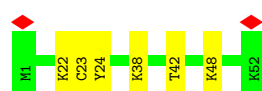
- Molecule 40: Ribosomal 60S subunit protein L38



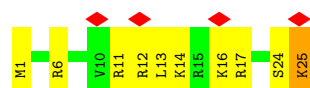
- Molecule 41: 60S ribosomal protein L39



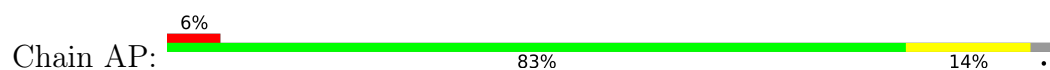
- Molecule 42: Rpl40bp



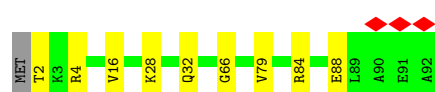
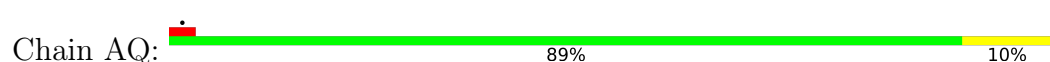
- Molecule 43: 60S ribosomal protein L41



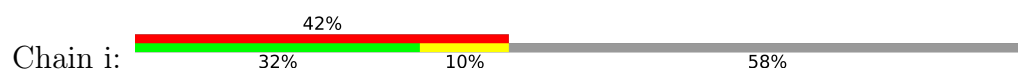
- Molecule 44: Ribosomal 60S subunit protein L42A

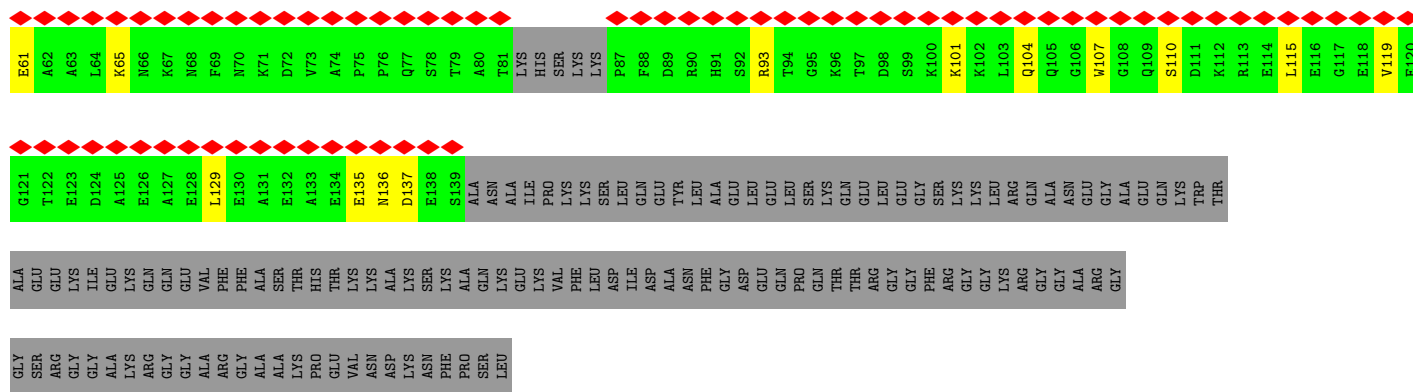


- Molecule 45: Ribosomal 60S subunit protein L43A

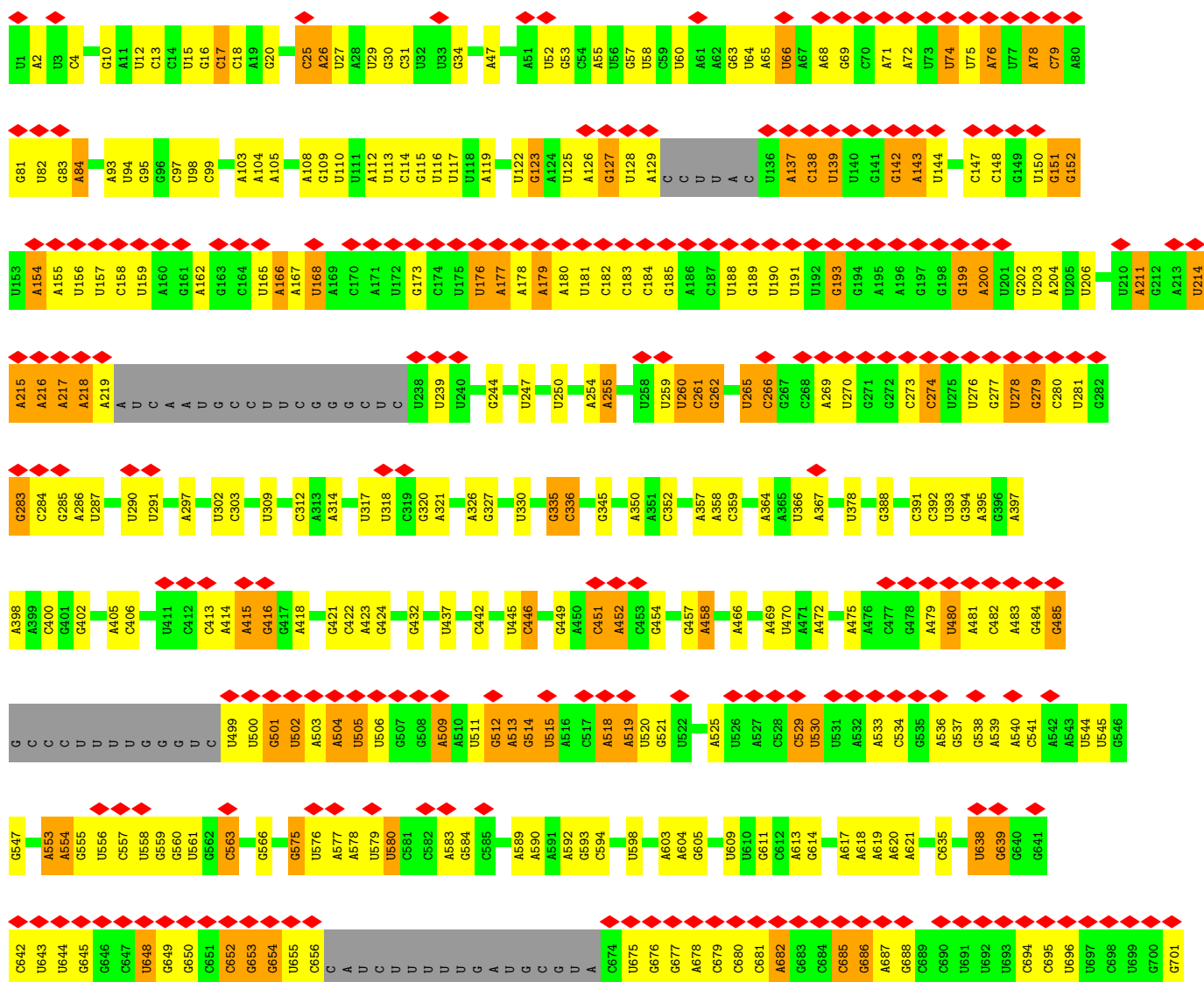
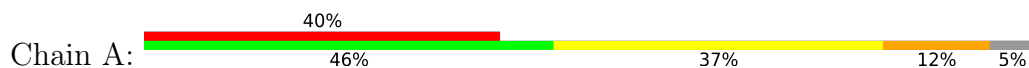


- Molecule 46: HABP4\_PAI-RBP1 domain-containing protein

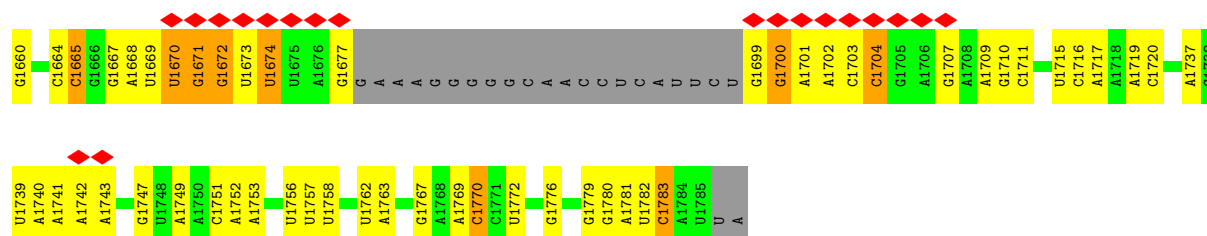




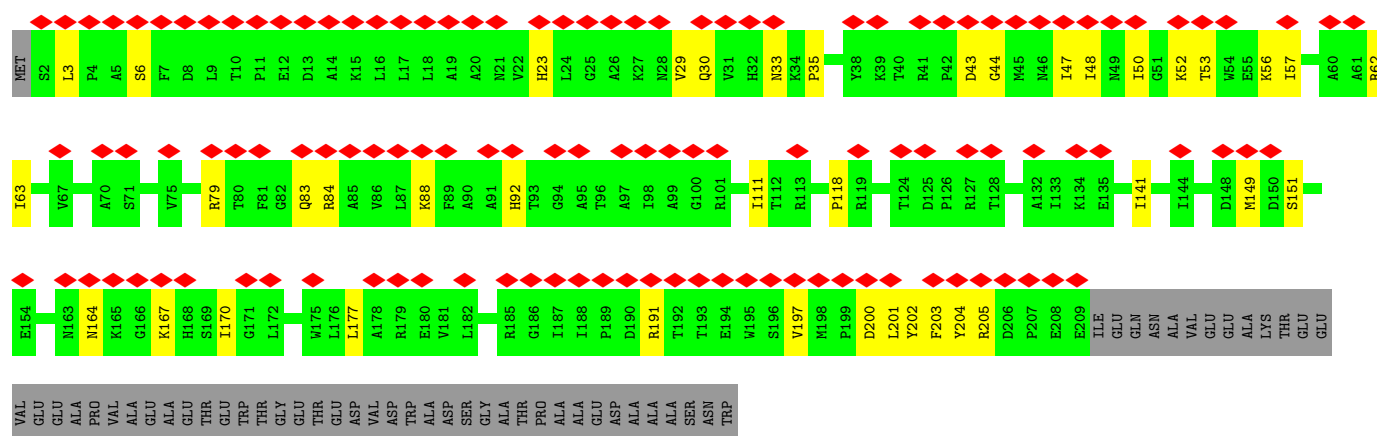
# Molecule 47: 18S ribosomal RNA



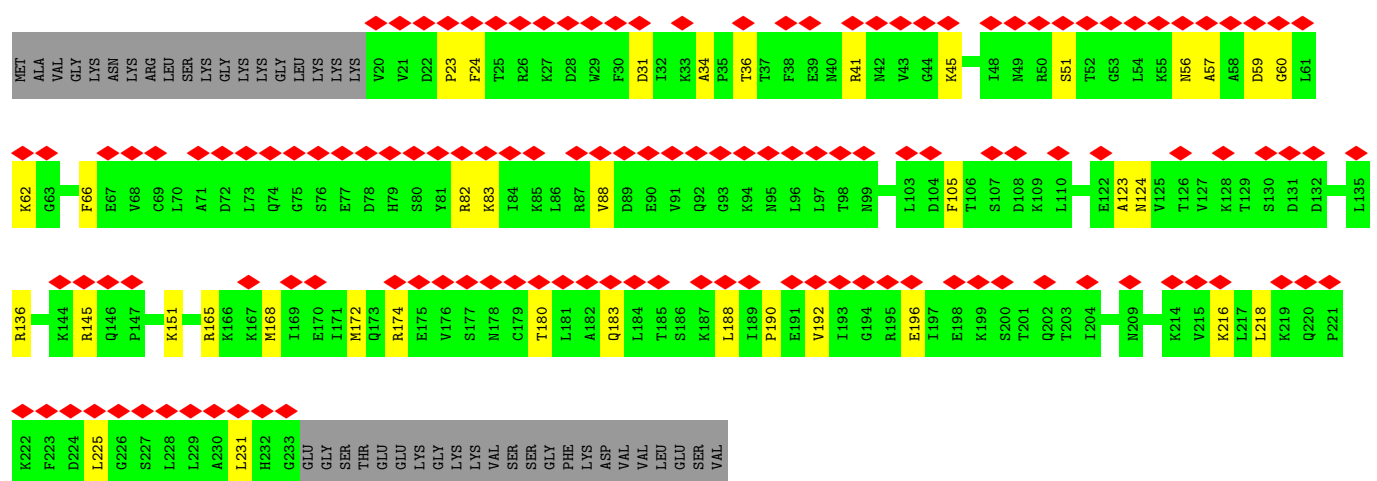




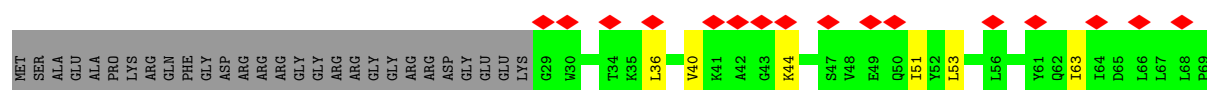
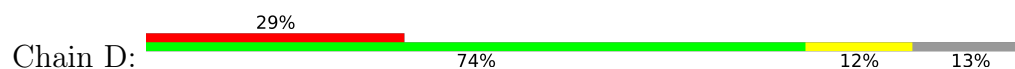
• Molecule 48: 40S ribosomal protein S0

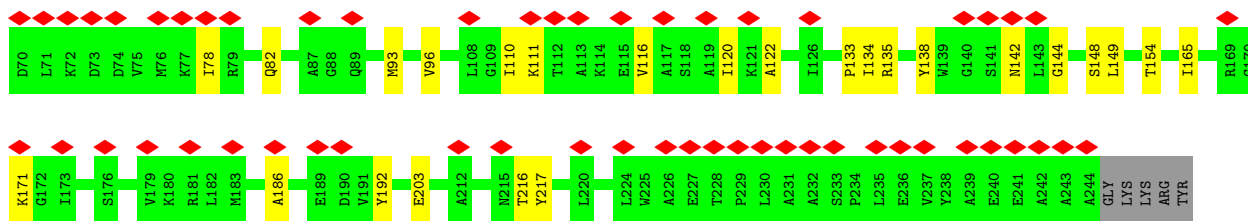


• Molecule 49: 40S ribosomal protein S1

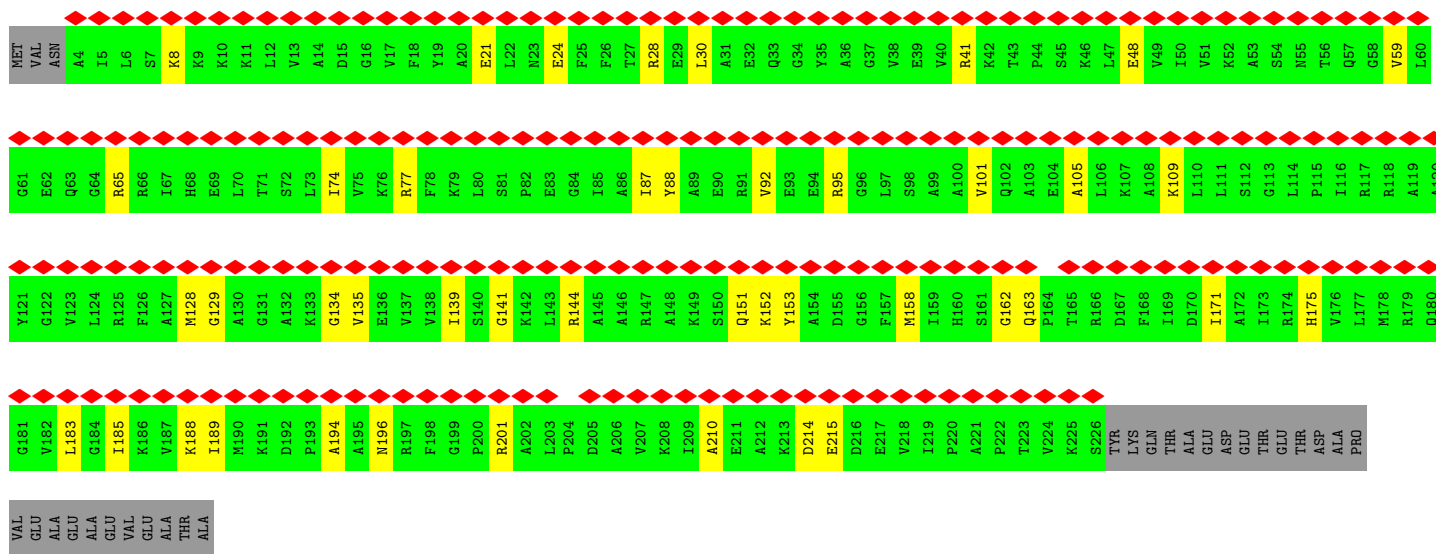
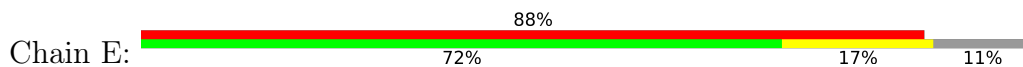


• Molecule 50: Ribosomal 40S subunit protein S2

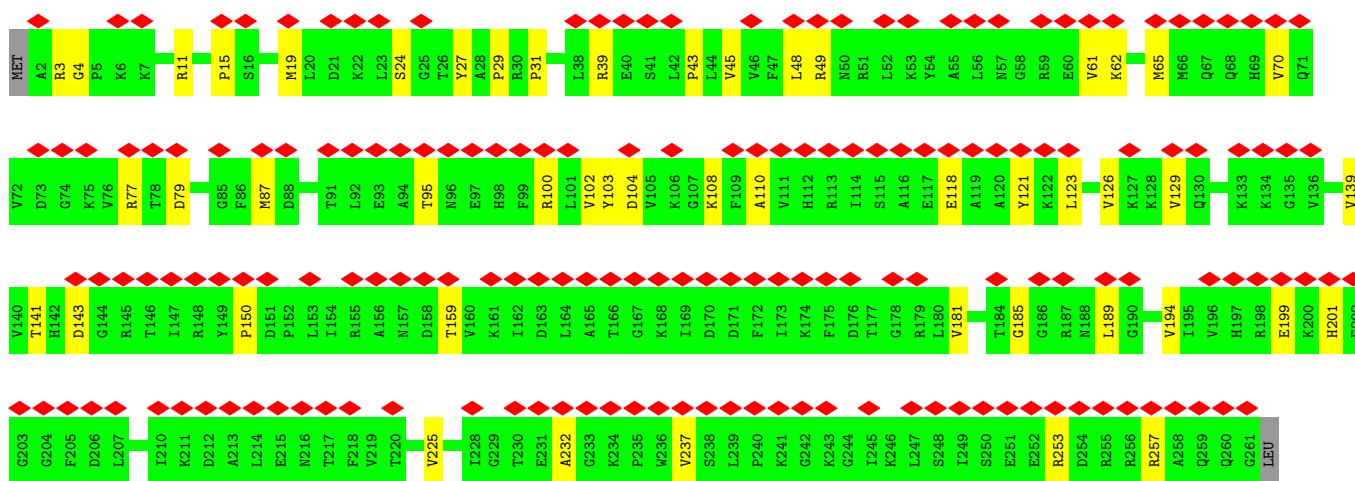
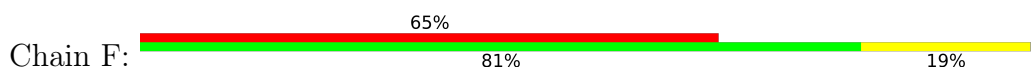




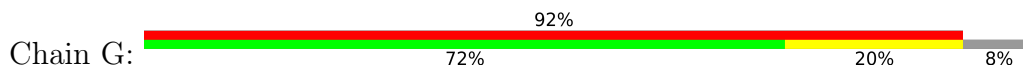
• Molecule 51: Ribosomal 40S subunit protein S3

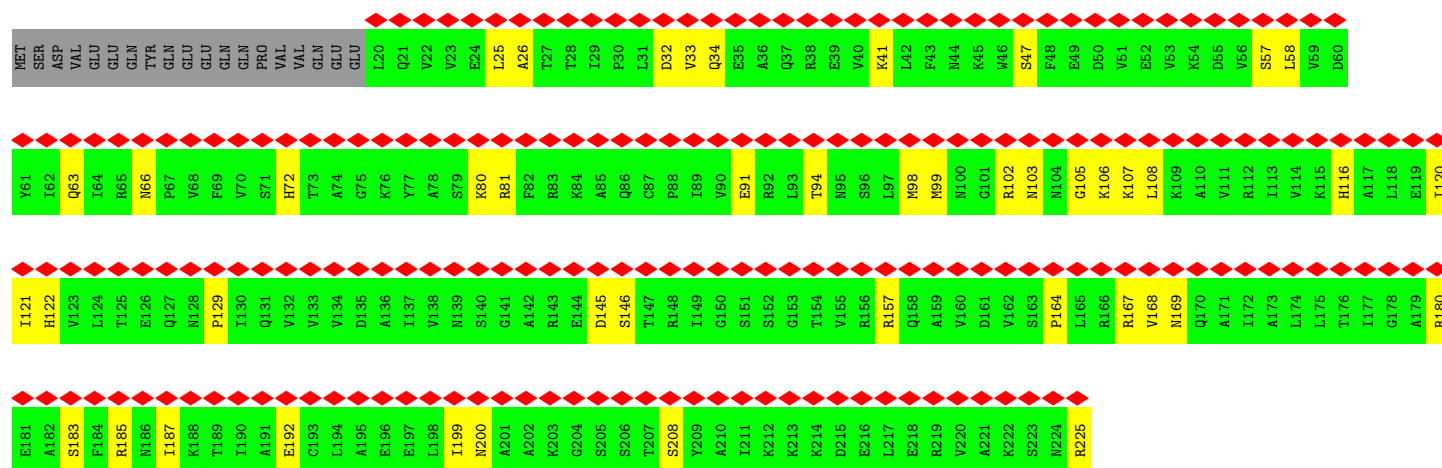


• Molecule 52: 40S ribosomal protein S4

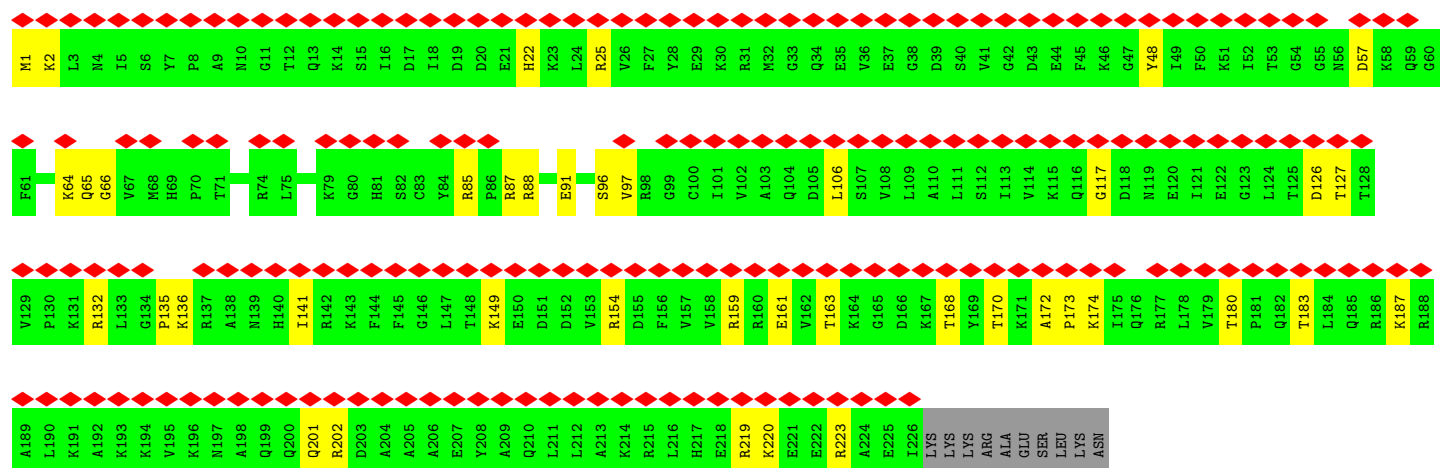
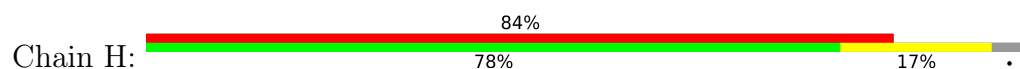


• Molecule 53: Ribosomal 40S subunit protein S5

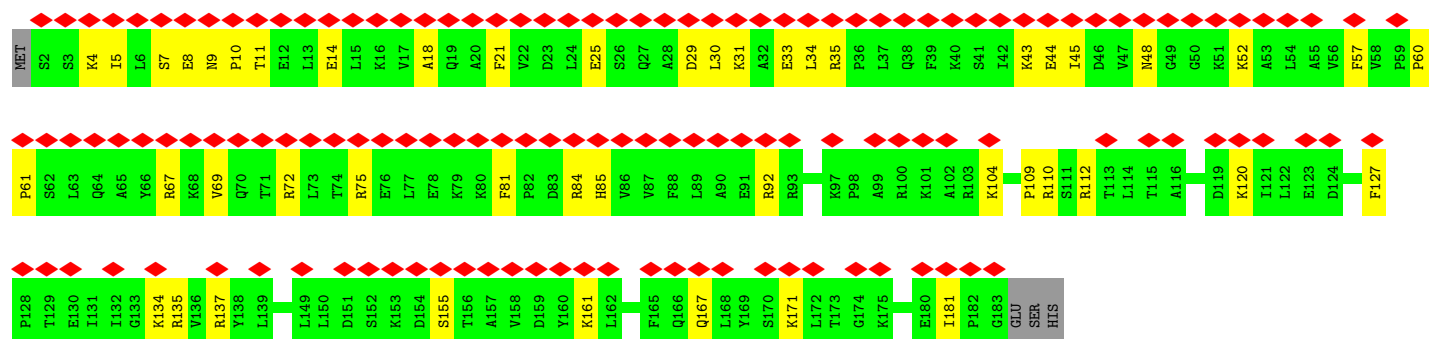




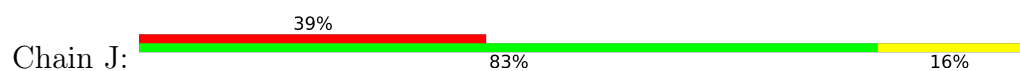
• Molecule 54: 40S ribosomal protein S6

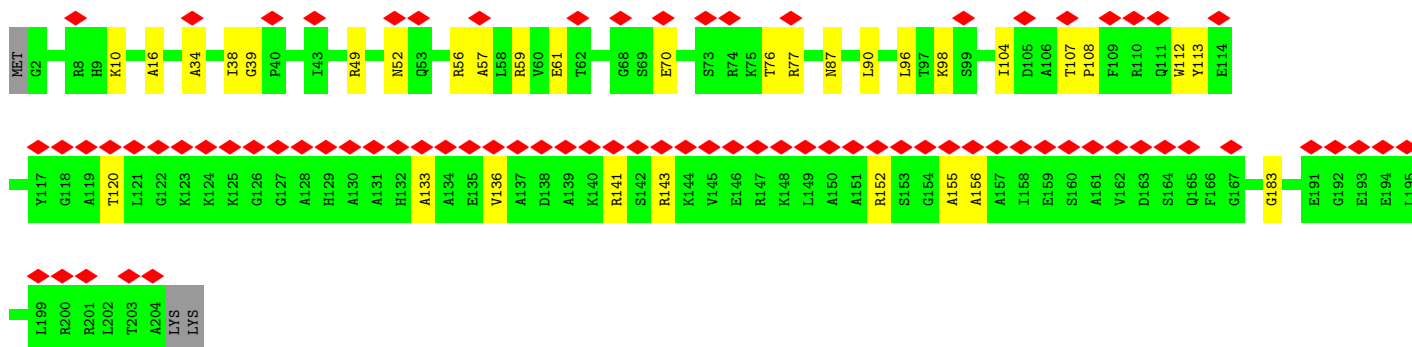


• Molecule 55: 40S ribosomal protein S7

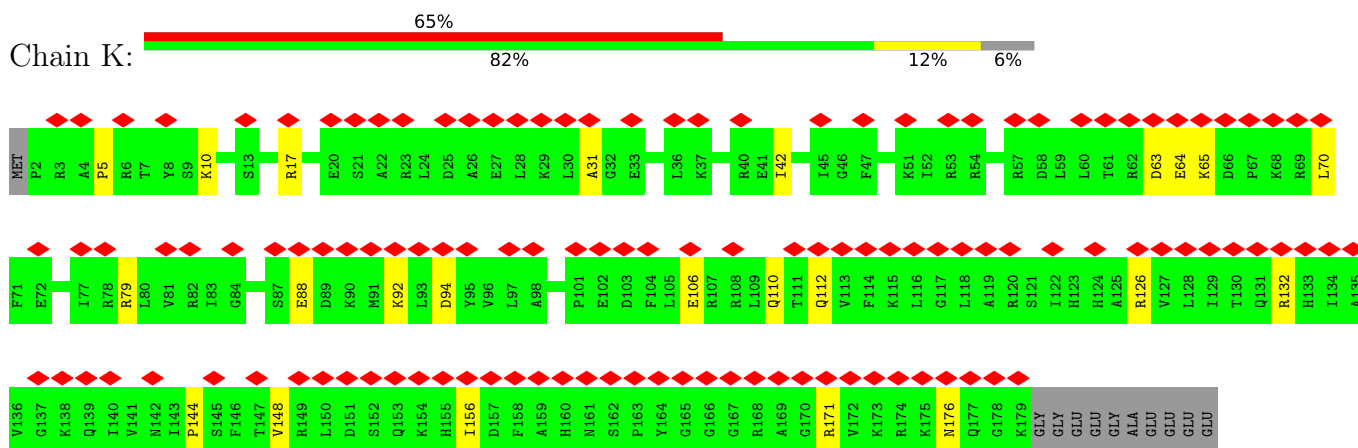


• Molecule 56: 40S ribosomal protein S8

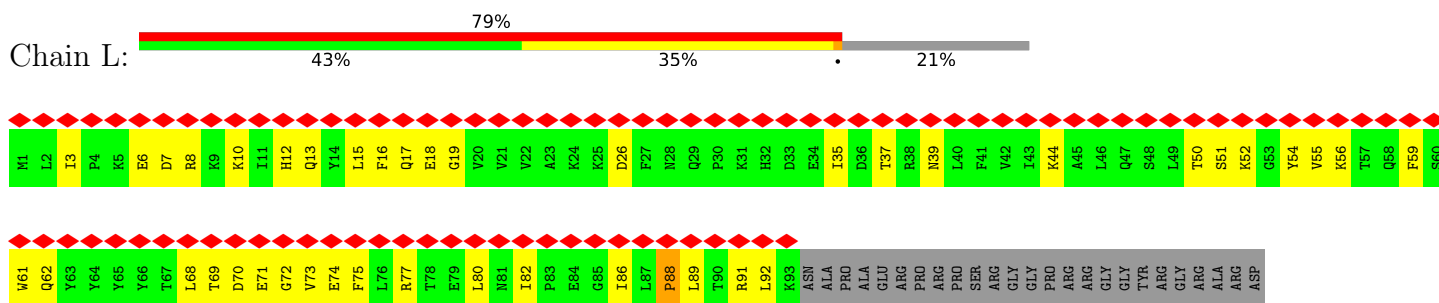




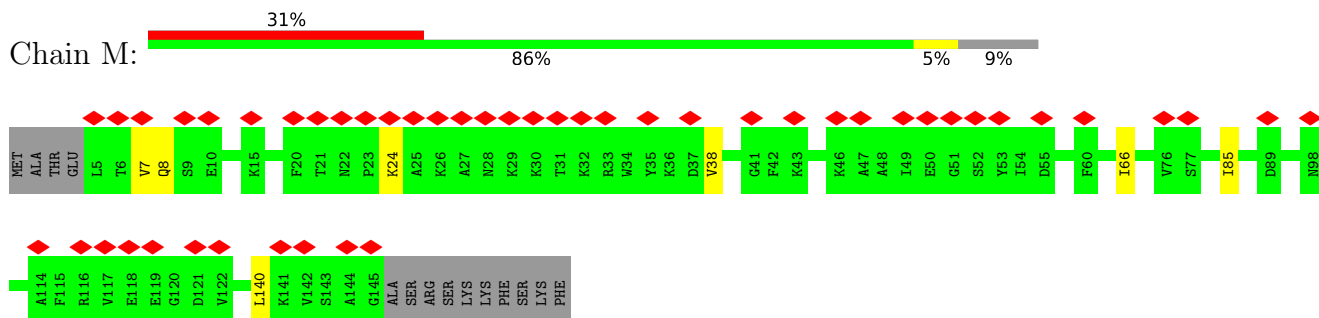
- Molecule 57: Ribosomal 40S subunit protein S9B



- Molecule 58: Ribosomal 40S subunit protein S10A

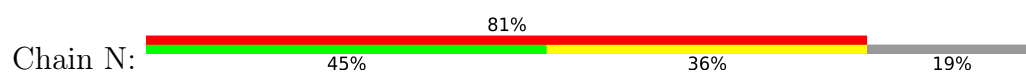


- Molecule 59: Ribosomal 40S subunit protein S11A

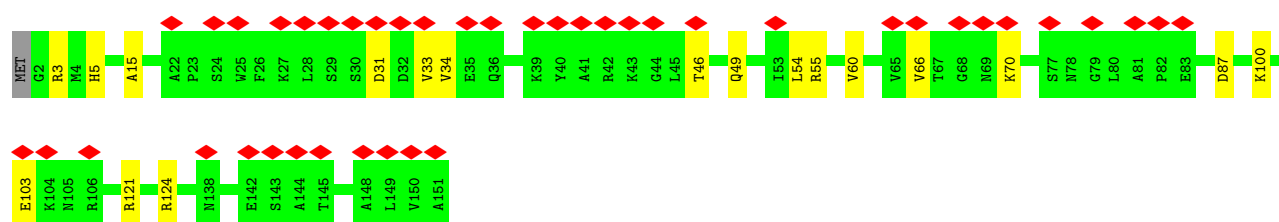
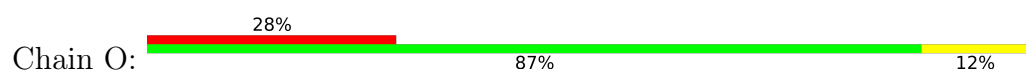


- Molecule 60: 40S ribosomal protein S12

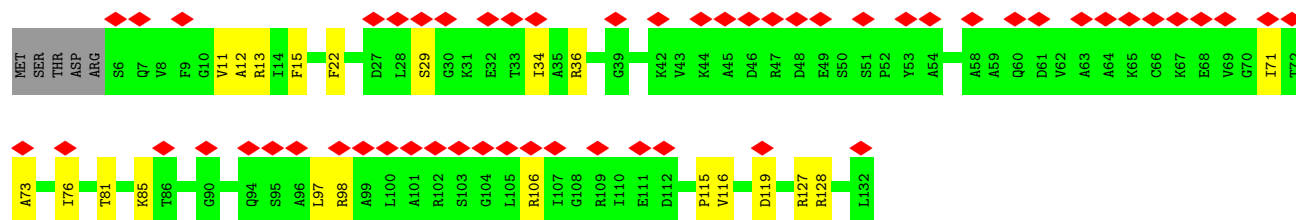
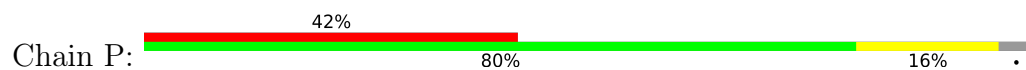




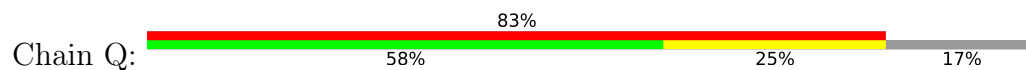
• Molecule 61: Ribosomal 40S subunit protein S13



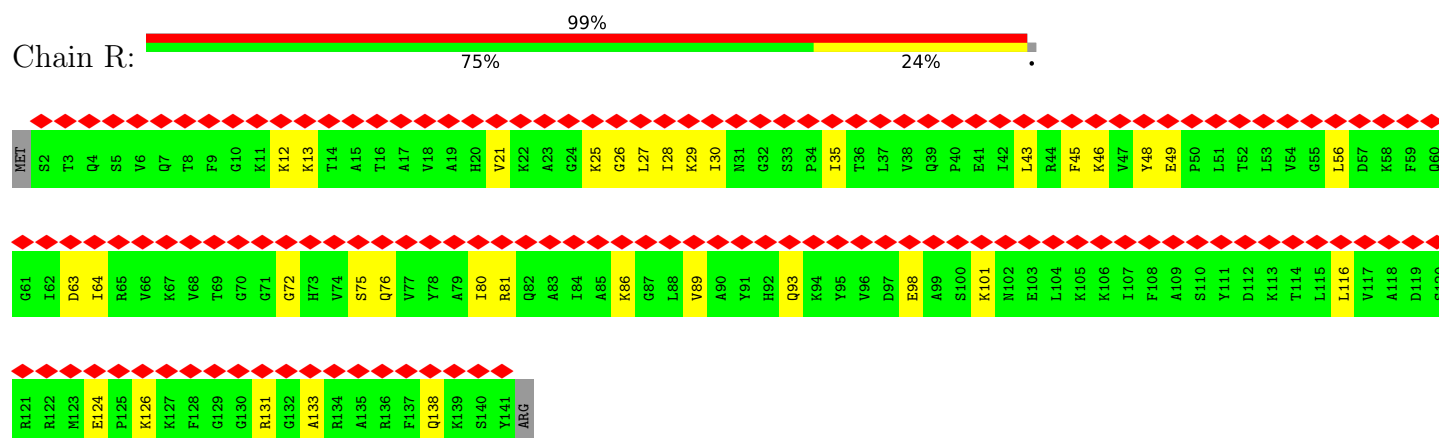
• Molecule 62: Ribosomal 40S subunit protein S14B



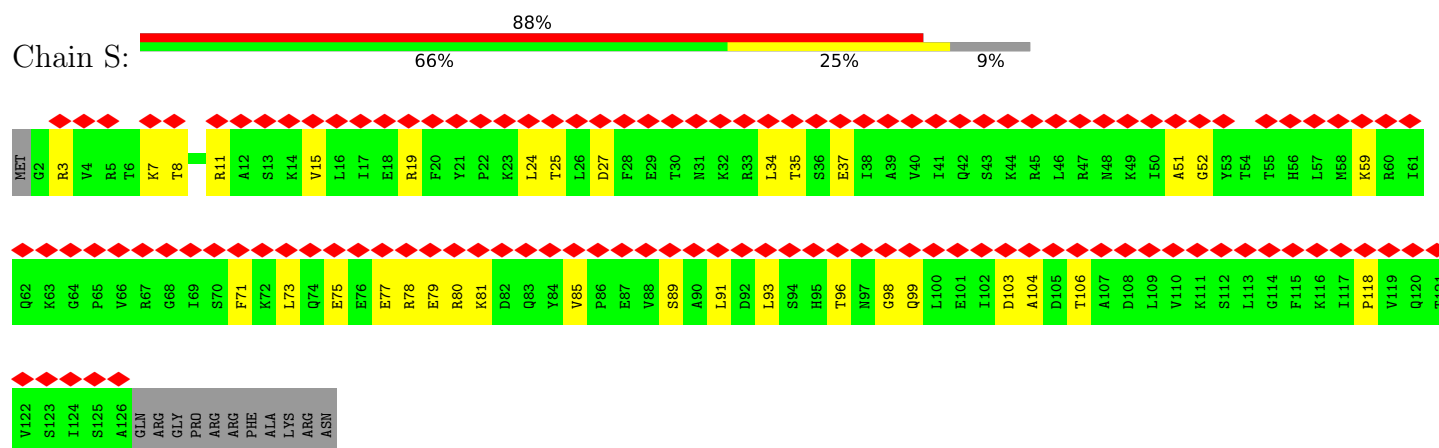
• Molecule 63: Ribosomal 40S subunit protein S15



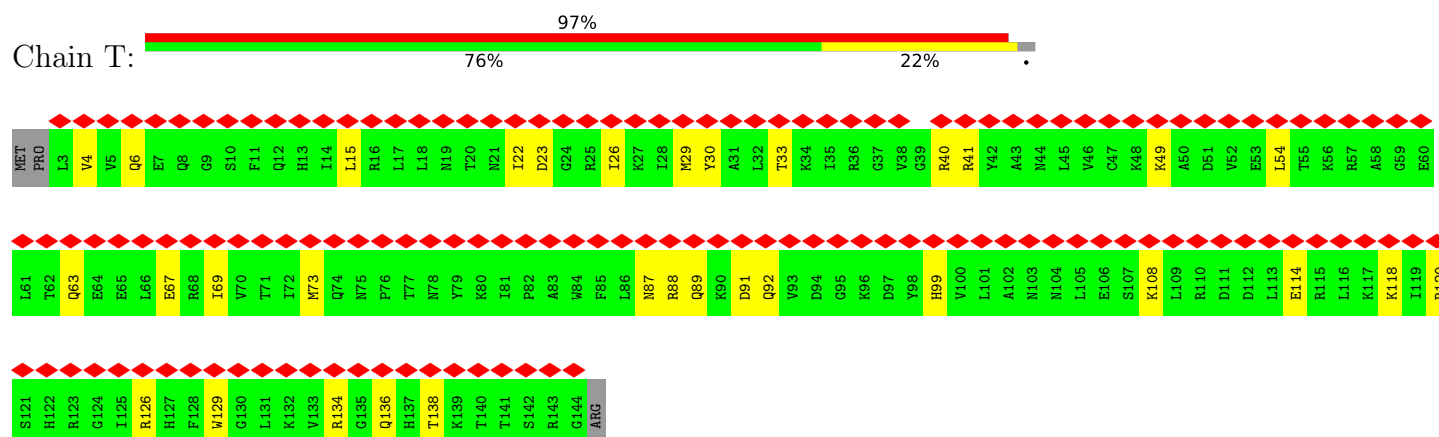
- Molecule 64: Ribosomal 40S subunit protein S16A



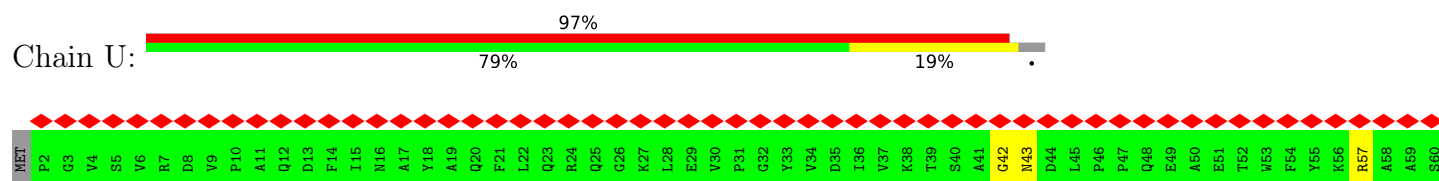
- Molecule 65: Ribosomal 40S subunit protein S17B

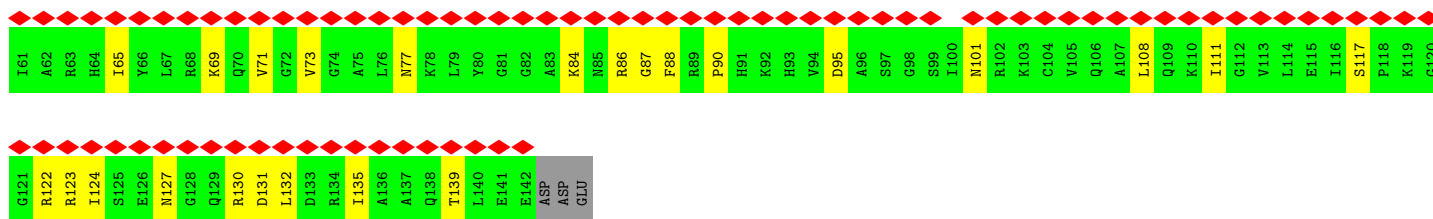


- Molecule 66: Ribosomal 40S subunit protein S18B

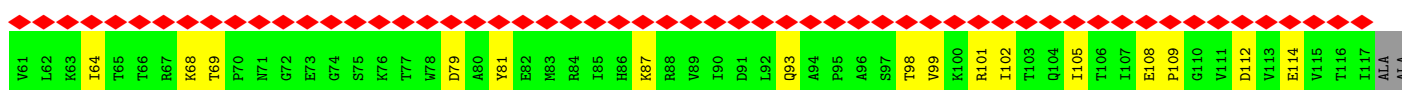
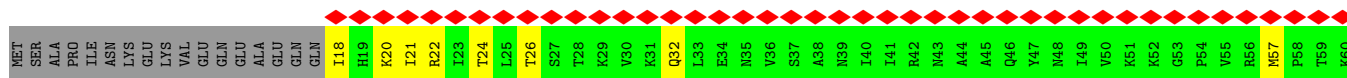
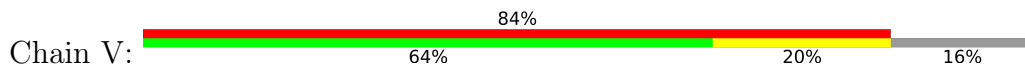


- Molecule 67: Ribosomal 40S subunit protein S19A

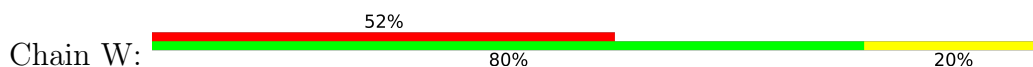




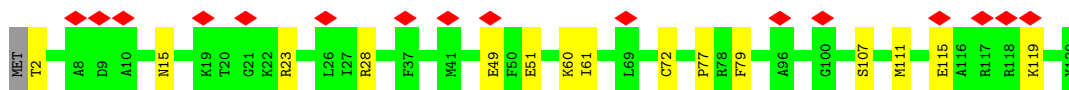
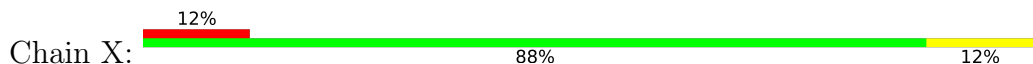
• Molecule 68: Ribosomal 40S subunit protein S20



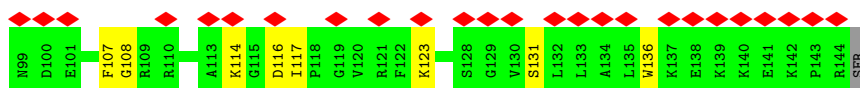
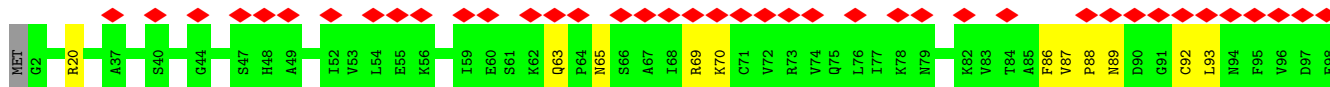
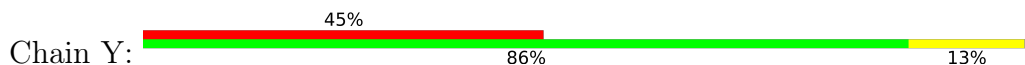
• Molecule 69: 40S ribosomal protein S21



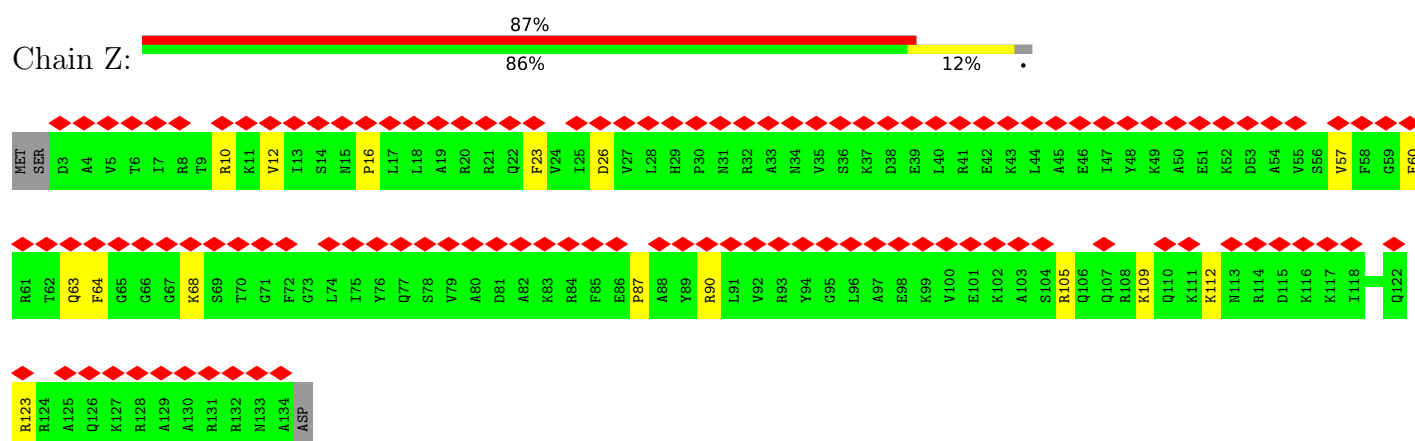
• Molecule 70: 40S ribosomal protein S22-A



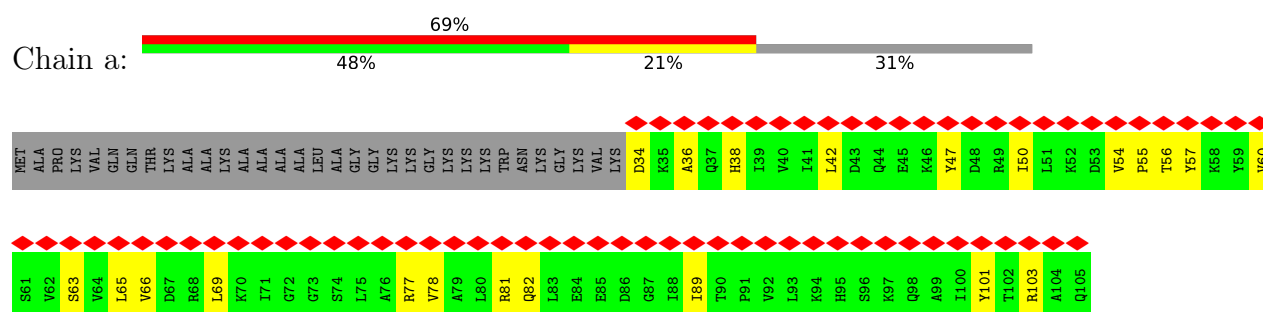
• Molecule 71: Ribosomal 40S subunit protein S23B



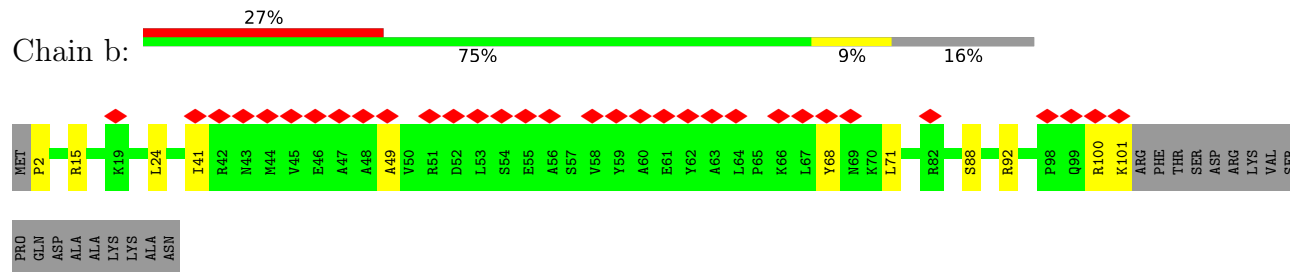
• Molecule 72: 40S ribosomal protein S24



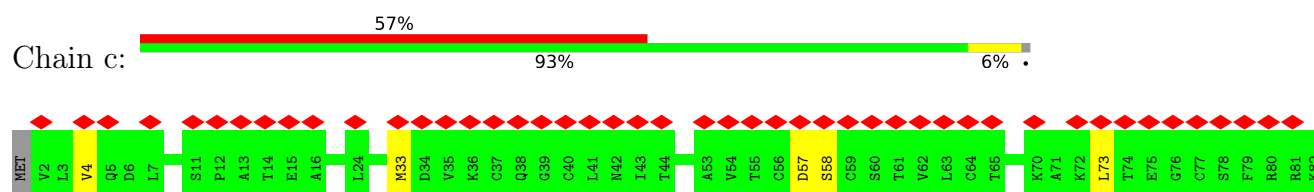
• Molecule 73: 40S ribosomal protein S25



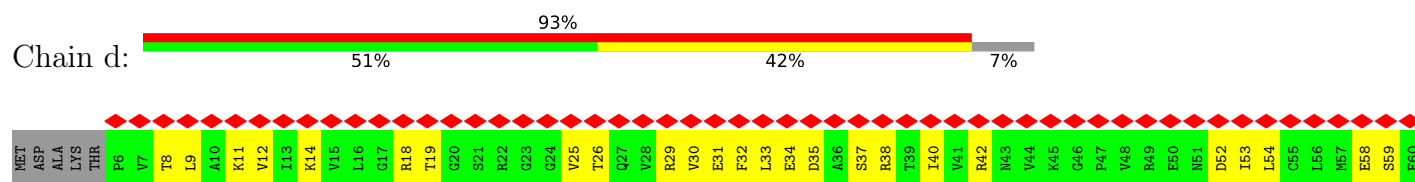
• Molecule 74: 40S ribosomal protein S26



• Molecule 75: 40S ribosomal protein S27

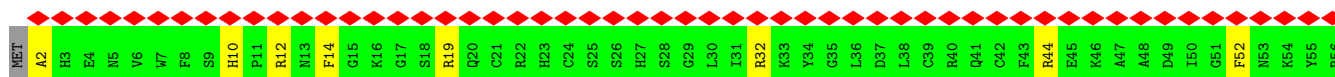
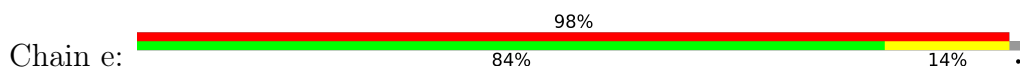


• Molecule 76: Ribosomal 40S subunit protein S28B

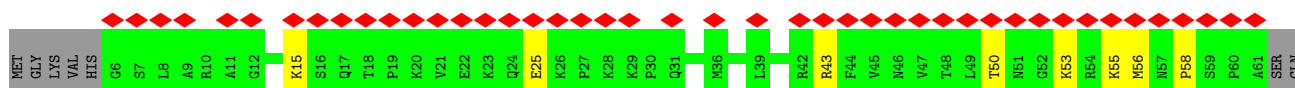
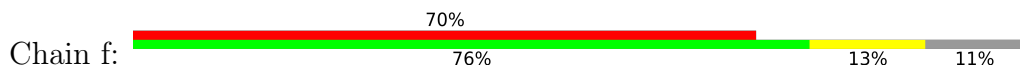




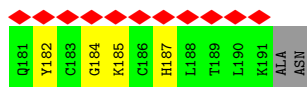
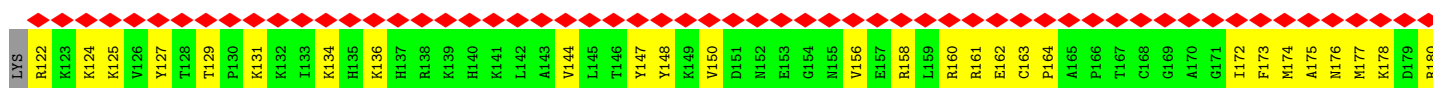
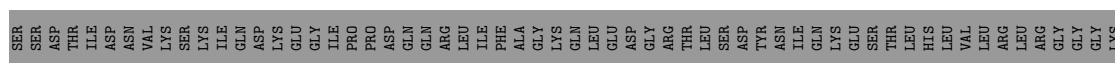
- Molecule 77: Ribosomal 40S subunit protein S29A



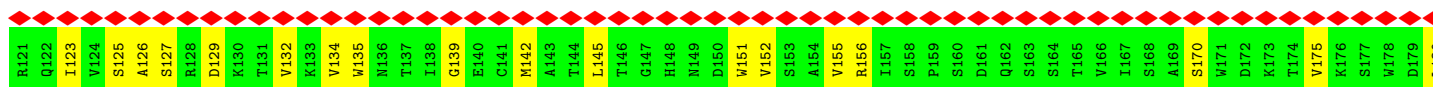
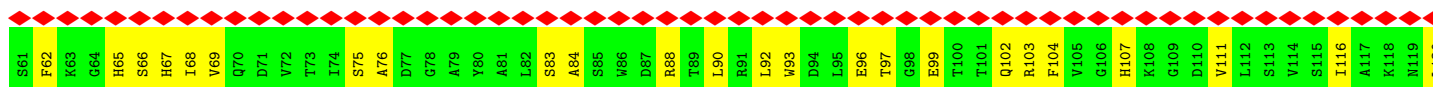
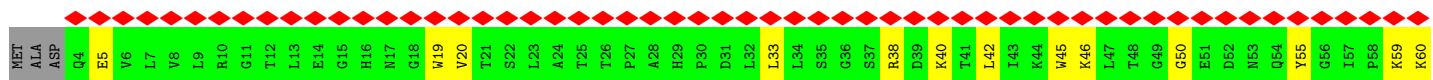
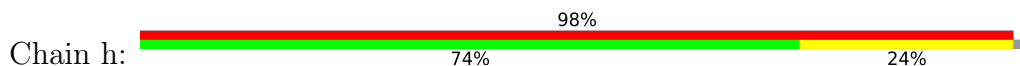
- Molecule 78: 40S ribosomal protein S30



- Molecule 79: Ubiquitin-ribosomal 40S subunit protein S31 fusion protein



- Molecule 80: Guanine nucleotide-binding protein subunit beta-like protein



|                   |                                                                                                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
|-------------------|--------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| PRO<br>SER<br>ALA | G301<br>Y302<br>T303<br>D304<br>N305<br>V306<br>I307<br>R308<br>V309<br>W310<br>Q311<br>V312<br>M313<br>T314 | A241<br>F242<br>S243<br>P244<br>N245<br>R246<br>T247<br>W248<br>L249<br>A250<br>A251<br>A252<br>T253<br>T254<br>S255<br>G256<br>T257<br>K258<br>T259<br>F260<br>K261<br>L262<br>Q263<br>E264<br>R265<br>S266<br>T267<br>L268<br>D269<br>E270<br>L271<br>K272<br>P273<br>E274<br>F275<br>A276<br>T277<br>G278<br>A279<br>T280<br>A281<br>K282<br>D283<br>P284<br>E285<br>A286<br>T287<br>S288<br>L289<br>A290<br>W291<br>S292<br>A293<br>D294<br>G295<br>Q296<br>N297<br>L298<br>F299<br>A300 | A181 | D182 | Y183 | S184 | N185 | M186 | A187 | D188 | F189 | I190 | G191 | H192 | T193 | G194 | Y195 | I196 | S197 | C198 | I199 | T200 | L201 | S202 | P203 | D204 | G205 | S206 | L207 | C208 | A209 | S210 | A211 | G212 | K213 | D214 | G215 | V216 | L217 | I218 | L219 | W220 | D221 | L222 | N223 | K224 | N225 | K226 | T227 | L228 | Y229 | T230 | L231 | E232 | A233 | K234 | A235 | E236 | V237 | H238 | A239 | L240 |
|-------------------|--------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|

## 4 Experimental information

| Property                             | Value                           | Source    |
|--------------------------------------|---------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                 | Depositor |
| Imposed symmetry                     | POINT, Not provided             |           |
| Number of particles used             | 243386                          | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF               | Depositor |
| CTF correction method                | NONE                            | Depositor |
| Microscope                           | FEI TITAN KRIOS                 | Depositor |
| Voltage (kV)                         | 300                             | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 60                              | Depositor |
| Minimum defocus (nm)                 | 900                             | Depositor |
| Maximum defocus (nm)                 | 2400                            | Depositor |
| Magnification                        | Not provided                    |           |
| Image detector                       | GATAN K3 (6k x 4k)              | Depositor |
| Maximum map value                    | 2.113                           | Depositor |
| Minimum map value                    | -0.967                          | Depositor |
| Average map value                    | 0.007                           | Depositor |
| Map value standard deviation         | 0.063                           | Depositor |
| Recommended contour level            | 0.226                           | Depositor |
| Map size ( $\text{\AA}$ )            | 426.36002, 426.36002, 426.36002 | wwPDB     |
| Map dimensions                       | 510, 510, 510                   | wwPDB     |
| Map angles ( $^\circ$ )              | 90.0, 90.0, 90.0                | wwPDB     |
| Pixel spacing ( $\text{\AA}$ )       | 0.836, 0.836, 0.836             | Depositor |

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SPD, IAS, PUT, MG, OMC, ZN, OMG, MLZ

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

| Mol | Chain | Bond lengths |                 | Bond angles |                 |
|-----|-------|--------------|-----------------|-------------|-----------------|
|     |       | RMSZ         | $\# Z  > 5$     | RMSZ        | $\# Z  > 5$     |
| 1   | 1     | 0.23         | 10/76718 (0.0%) | 0.33        | 1/119600 (0.0%) |
| 2   | 3     | 0.18         | 0/2884          | 0.25        | 0/4492          |
| 3   | 4     | 0.21         | 0/3746          | 0.29        | 0/5832          |
| 4   | 10    | 0.33         | 1/375 (0.3%)    | 0.21        | 0/579           |
| 5   | j     | 0.20         | 0/1931          | 0.33        | 0/2592          |
| 6   | k     | 0.20         | 0/3156          | 0.35        | 0/4246          |
| 7   | l     | 0.17         | 0/2799          | 0.35        | 0/3777          |
| 8   | m     | 0.15         | 0/2447          | 0.31        | 0/3294          |
| 9   | n     | 0.16         | 0/1258          | 0.30        | 0/1696          |
| 10  | o     | 0.18         | 0/1929          | 0.36        | 0/2589          |
| 11  | p     | 0.15         | 0/1869          | 0.30        | 0/2519          |
| 12  | q     | 0.16         | 0/1537          | 0.29        | 0/2067          |
| 13  | r     | 0.16         | 0/1724          | 0.29        | 0/2314          |
| 14  | s     | 0.14         | 0/1404          | 0.29        | 0/1880          |
| 15  | t     | 0.62         | 5/1637 (0.3%)   | 0.50        | 1/2195 (0.0%)   |
| 16  | u     | 0.17         | 0/1044          | 0.33        | 0/1407          |
| 17  | v     | 0.20         | 0/1753          | 0.35        | 0/2347          |
| 18  | w     | 0.18         | 0/1620          | 0.32        | 0/2167          |
| 19  | x     | 0.18         | 0/1398          | 0.33        | 0/1879          |
| 20  | y     | 0.18         | 0/1511          | 0.34        | 0/2022          |
| 21  | z     | 0.16         | 0/1483          | 0.27        | 0/1972          |
| 22  | 0     | 0.19         | 0/1483          | 0.32        | 0/1997          |
| 23  | 2     | 0.17         | 0/1305          | 0.29        | 0/1749          |
| 24  | 5     | 0.14         | 0/871           | 0.37        | 0/1175          |
| 25  | 6     | 0.17         | 0/994           | 0.36        | 0/1339          |
| 26  | 7     | 0.17         | 0/536           | 0.29        | 0/712           |
| 27  | 8     | 0.18         | 0/990           | 0.32        | 0/1337          |
| 28  | 9     | 0.17         | 0/999           | 0.35        | 0/1334          |
| 29  | AA    | 0.16         | 0/1112          | 0.26        | 0/1488          |
| 30  | AB    | 0.19         | 0/1199          | 0.32        | 0/1607          |
| 31  | AC    | 0.15         | 0/522           | 0.27        | 0/692           |
| 32  | AD    | 0.16         | 0/738           | 0.25        | 0/994           |



| Mol | Chain | Bond lengths |                | Bond angles |                |
|-----|-------|--------------|----------------|-------------|----------------|
|     |       | RMSZ         | # Z  >5        | RMSZ        | # Z  >5        |
| 33  | AE    | 0.17         | 0/902          | 0.31        | 0/1212         |
| 34  | AF    | 0.18         | 0/1039         | 0.35        | 0/1390         |
| 35  | AG    | 0.20         | 0/895          | 0.31        | 0/1201         |
| 36  | AH    | 0.17         | 0/934          | 0.34        | 0/1242         |
| 37  | AI    | 0.16         | 0/1004         | 0.38        | 0/1337         |
| 38  | AJ    | 0.14         | 0/780          | 0.27        | 0/1033         |
| 39  | AK    | 0.22         | 0/690          | 0.41        | 0/916          |
| 40  | AL    | 0.18         | 0/632          | 0.33        | 0/842          |
| 41  | AM    | 0.17         | 0/458          | 0.27        | 0/609          |
| 42  | AN    | 0.15         | 0/436          | 0.31        | 0/577          |
| 43  | AO    | 0.49         | 0/237          | 0.80        | 0/304          |
| 44  | AP    | 0.16         | 0/840          | 0.29        | 0/1108         |
| 45  | AQ    | 0.18         | 0/705          | 0.33        | 0/940          |
| 46  | i     | 0.12         | 0/864          | 0.35        | 0/1156         |
| 47  | A     | 0.20         | 1/40362 (0.0%) | 0.33        | 1/62888 (0.0%) |
| 48  | B     | 0.16         | 0/1666         | 0.29        | 0/2273         |
| 49  | C     | 0.15         | 0/1750         | 0.27        | 0/2354         |
| 50  | D     | 0.17         | 0/1648         | 0.28        | 0/2237         |
| 51  | E     | 0.14         | 0/1731         | 0.32        | 0/2324         |
| 52  | F     | 0.17         | 0/2096         | 0.30        | 0/2822         |
| 53  | G     | 0.14         | 0/1631         | 0.32        | 0/2199         |
| 54  | H     | 0.14         | 0/1845         | 0.27        | 0/2464         |
| 55  | I     | 0.16         | 0/1490         | 0.31        | 0/2004         |
| 56  | J     | 0.16         | 0/1606         | 0.28        | 0/2150         |
| 57  | K     | 0.16         | 0/1478         | 0.25        | 0/1978         |
| 58  | L     | 0.17         | 0/801          | 0.52        | 0/1081         |
| 59  | M     | 0.18         | 0/1154         | 0.28        | 0/1553         |
| 60  | N     | 0.14         | 0/892          | 0.49        | 0/1203         |
| 61  | O     | 0.15         | 0/1210         | 0.26        | 0/1631         |
| 62  | P     | 0.15         | 0/944          | 0.28        | 0/1265         |
| 63  | Q     | 0.15         | 0/954          | 0.41        | 0/1282         |
| 64  | R     | 0.15         | 0/1109         | 0.35        | 0/1486         |
| 65  | S     | 0.13         | 0/1014         | 0.32        | 0/1361         |
| 66  | T     | 0.12         | 0/1186         | 0.28        | 0/1590         |
| 67  | U     | 0.15         | 0/1120         | 0.33        | 0/1508         |
| 68  | V     | 0.14         | 0/800          | 0.29        | 0/1082         |
| 69  | W     | 0.17         | 0/683          | 0.37        | 0/918          |
| 70  | X     | 0.19         | 0/1049         | 0.27        | 0/1412         |
| 71  | Y     | 0.48         | 4/1128 (0.4%)  | 0.45        | 0/1505         |
| 72  | Z     | 0.16         | 0/1086         | 0.24        | 0/1447         |
| 73  | a     | 0.14         | 0/585          | 0.30        | 0/789          |
| 74  | b     | 0.16         | 0/811          | 0.30        | 0/1085         |
| 75  | c     | 0.17         | 0/624          | 0.30        | 0/843          |

| Mol | Chain | Bond lengths |                  | Bond angles |                 |
|-----|-------|--------------|------------------|-------------|-----------------|
|     |       | RMSZ         | # Z  >5          | RMSZ        | # Z  >5         |
| 76  | d     | 0.15         | 0/489            | 0.39        | 0/654           |
| 77  | e     | 0.14         | 0/466            | 0.31        | 0/620           |
| 78  | f     | 0.15         | 0/451            | 0.31        | 0/601           |
| 79  | g     | 0.13         | 0/585            | 0.41        | 0/778           |
| 80  | h     | 0.14         | 0/2451           | 0.33        | 0/3337          |
| All | All   | 0.21         | 21/214283 (0.0%) | 0.33        | 3/314481 (0.0%) |

The worst 5 of 21 bond length outliers are listed below:

| Mol | Chain | Res  | Type | Atoms | Z      | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|--------|-------------|----------|
| 15  | t     | 3    | ILE  | C-O   | -11.15 | 1.11        | 1.24     |
| 15  | t     | 62   | THR  | C-O   | -10.39 | 1.10        | 1.24     |
| 1   | 1     | 1738 | U    | O3'-P | -8.78  | 1.48        | 1.61     |
| 71  | Y     | 88   | PRO  | C-O   | -8.34  | 1.14        | 1.23     |
| 15  | t     | 59   | ARG  | C-O   | -7.21  | 1.15        | 1.23     |

All (3) bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms       | Z     | Observed(°) | Ideal(°) |
|-----|-------|------|------|-------------|-------|-------------|----------|
| 1   | 1     | 1738 | U    | C1'-C2'-O2' | -6.81 | 98.19       | 108.40   |
| 47  | A     | 1364 | U    | C4'-C3'-O3' | -6.28 | 103.58      | 113.00   |
| 15  | t     | 59   | ARG  | CG-CD-NE    | -5.83 | 99.16       | 112.00   |

There are no chirality outliers.

There are no planarity outliers.

## 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   | 1     | 68595 | 0        | 34478    | 905     | 0            |
| 2   | 3     | 2579  | 0        | 1304     | 17      | 0            |
| 3   | 4     | 3353  | 0        | 1694     | 54      | 0            |
| 4   | 10    | 338   | 0        | 175      | 5       | 0            |
| 5   | j     | 1894  | 0        | 1975     | 35      | 0            |
| 6   | k     | 3084  | 0        | 3173     | 48      | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 7   | l     | 2751  | 0        | 2879     | 39      | 0            |
| 8   | m     | 2394  | 0        | 2362     | 25      | 0            |
| 9   | n     | 1237  | 0        | 1316     | 18      | 0            |
| 10  | o     | 1893  | 0        | 1990     | 16      | 0            |
| 11  | p     | 1839  | 0        | 1957     | 18      | 0            |
| 12  | q     | 1519  | 0        | 1588     | 18      | 0            |
| 13  | r     | 1689  | 0        | 1731     | 20      | 0            |
| 14  | s     | 1385  | 0        | 1418     | 19      | 0            |
| 15  | t     | 1610  | 0        | 1686     | 18      | 0            |
| 16  | u     | 1029  | 0        | 1116     | 16      | 0            |
| 17  | v     | 1713  | 0        | 1764     | 44      | 0            |
| 18  | w     | 1590  | 0        | 1705     | 19      | 0            |
| 19  | x     | 1375  | 0        | 1403     | 22      | 0            |
| 20  | y     | 1478  | 0        | 1590     | 27      | 0            |
| 21  | z     | 1462  | 0        | 1570     | 29      | 0            |
| 22  | 0     | 1442  | 0        | 1500     | 33      | 0            |
| 23  | 2     | 1276  | 0        | 1333     | 16      | 0            |
| 24  | 5     | 848   | 0        | 864      | 19      | 0            |
| 25  | 6     | 986   | 0        | 1040     | 17      | 0            |
| 26  | 7     | 524   | 0        | 545      | 7       | 0            |
| 27  | 8     | 974   | 0        | 1032     | 15      | 0            |
| 28  | 9     | 989   | 0        | 1064     | 15      | 0            |
| 29  | AA    | 1087  | 0        | 1154     | 12      | 0            |
| 30  | AB    | 1170  | 0        | 1203     | 22      | 0            |
| 31  | AC    | 509   | 0        | 545      | 17      | 0            |
| 32  | AD    | 729   | 0        | 775      | 12      | 0            |
| 33  | AE    | 889   | 0        | 936      | 8       | 0            |
| 34  | AF    | 1015  | 0        | 1095     | 15      | 0            |
| 35  | AG    | 867   | 0        | 932      | 14      | 0            |
| 36  | AH    | 913   | 0        | 1002     | 11      | 0            |
| 37  | AI    | 990   | 0        | 1094     | 17      | 0            |
| 38  | AJ    | 772   | 0        | 863      | 9       | 0            |
| 39  | AK    | 677   | 0        | 695      | 15      | 0            |
| 40  | AL    | 623   | 0        | 688      | 11      | 0            |
| 41  | AM    | 446   | 0        | 488      | 9       | 0            |
| 42  | AN    | 427   | 0        | 473      | 4       | 0            |
| 43  | AO    | 236   | 0        | 285      | 7       | 0            |
| 44  | AP    | 843   | 0        | 914      | 9       | 0            |
| 45  | AQ    | 698   | 0        | 734      | 11      | 0            |
| 46  | i     | 853   | 0        | 830      | 23      | 0            |
| 47  | A     | 36083 | 0        | 18151    | 600     | 0            |
| 48  | B     | 1627  | 0        | 1644     | 32      | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 49  | C     | 1724  | 0        | 1805     | 24      | 0            |
| 50  | D     | 1620  | 0        | 1715     | 20      | 0            |
| 51  | E     | 1707  | 0        | 1807     | 35      | 0            |
| 52  | F     | 2055  | 0        | 2137     | 32      | 0            |
| 53  | G     | 1614  | 0        | 1688     | 37      | 0            |
| 54  | H     | 1820  | 0        | 1896     | 34      | 0            |
| 55  | I     | 1466  | 0        | 1561     | 35      | 0            |
| 56  | J     | 1579  | 0        | 1602     | 23      | 0            |
| 57  | K     | 1453  | 0        | 1532     | 16      | 0            |
| 58  | L     | 783   | 0        | 799      | 33      | 0            |
| 59  | M     | 1129  | 0        | 1183     | 6       | 0            |
| 60  | N     | 885   | 0        | 915      | 33      | 0            |
| 61  | O     | 1187  | 0        | 1249     | 12      | 0            |
| 62  | P     | 942   | 0        | 980      | 16      | 0            |
| 63  | Q     | 935   | 0        | 970      | 29      | 0            |
| 64  | R     | 1091  | 0        | 1155     | 26      | 0            |
| 65  | S     | 1002  | 0        | 1058     | 32      | 0            |
| 66  | T     | 1169  | 0        | 1216     | 24      | 0            |
| 67  | U     | 1100  | 0        | 1114     | 19      | 0            |
| 68  | V     | 790   | 0        | 855      | 19      | 0            |
| 69  | W     | 676   | 0        | 677      | 14      | 0            |
| 70  | X     | 1032  | 0        | 1066     | 13      | 0            |
| 71  | Y     | 1110  | 0        | 1182     | 11      | 0            |
| 72  | Z     | 1072  | 0        | 1123     | 13      | 0            |
| 73  | a     | 578   | 0        | 613      | 18      | 0            |
| 74  | b     | 799   | 0        | 860      | 8       | 0            |
| 75  | c     | 614   | 0        | 627      | 3       | 0            |
| 76  | d     | 487   | 0        | 523      | 20      | 0            |
| 77  | e     | 454   | 0        | 431      | 9       | 0            |
| 78  | f     | 444   | 0        | 483      | 7       | 0            |
| 79  | g     | 574   | 0        | 606      | 29      | 0            |
| 80  | h     | 2398  | 0        | 2374     | 55      | 0            |
| 81  | 1     | 100   | 0        | 190      | 118     | 0            |
| 82  | 1     | 6     | 0        | 12       | 11      | 0            |
| 82  | 4     | 6     | 0        | 12       | 8       | 0            |
| 83  | 1     | 296   | 0        | 0        | 0       | 0            |
| 83  | 2     | 1     | 0        | 0        | 0       | 0            |
| 83  | 4     | 1     | 0        | 0        | 0       | 0            |
| 83  | A     | 133   | 0        | 0        | 0       | 0            |
| 83  | AC    | 1     | 0        | 0        | 0       | 0            |
| 83  | AF    | 1     | 0        | 0        | 0       | 0            |
| 83  | AH    | 1     | 0        | 0        | 0       | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 83  | AK    | 1     | 0        | 0        | 0       | 0            |
| 83  | AP    | 1     | 0        | 0        | 0       | 0            |
| 83  | F     | 1     | 0        | 0        | 0       | 0            |
| 83  | U     | 1     | 0        | 0        | 0       | 0            |
| 83  | j     | 1     | 0        | 0        | 0       | 0            |
| 83  | k     | 1     | 0        | 0        | 0       | 0            |
| 83  | o     | 1     | 0        | 0        | 0       | 0            |
| 83  | r     | 1     | 0        | 0        | 0       | 0            |
| 83  | x     | 1     | 0        | 0        | 0       | 0            |
| 84  | AK    | 1     | 0        | 0        | 0       | 0            |
| 84  | AN    | 1     | 0        | 0        | 0       | 0            |
| 84  | AP    | 1     | 0        | 0        | 0       | 0            |
| 84  | AQ    | 1     | 0        | 0        | 0       | 0            |
| 84  | b     | 1     | 0        | 0        | 0       | 0            |
| 84  | c     | 1     | 0        | 0        | 0       | 0            |
| 84  | e     | 1     | 0        | 0        | 0       | 0            |
| 84  | g     | 1     | 0        | 0        | 0       | 0            |
| 85  | 0     | 4     | 0        | 0        | 2       | 0            |
| 85  | 1     | 1019  | 0        | 0        | 33      | 0            |
| 85  | 2     | 1     | 0        | 0        | 0       | 0            |
| 85  | 3     | 8     | 0        | 0        | 1       | 0            |
| 85  | 4     | 39    | 0        | 0        | 1       | 0            |
| 85  | 6     | 3     | 0        | 0        | 1       | 0            |
| 85  | 7     | 3     | 0        | 0        | 0       | 0            |
| 85  | 8     | 4     | 0        | 0        | 0       | 0            |
| 85  | A     | 38    | 0        | 0        | 4       | 0            |
| 85  | AA    | 1     | 0        | 0        | 0       | 0            |
| 85  | AB    | 12    | 0        | 0        | 2       | 0            |
| 85  | AC    | 6     | 0        | 0        | 0       | 0            |
| 85  | AE    | 3     | 0        | 0        | 0       | 0            |
| 85  | AF    | 16    | 0        | 0        | 1       | 0            |
| 85  | AG    | 10    | 0        | 0        | 0       | 0            |
| 85  | AH    | 11    | 0        | 0        | 2       | 0            |
| 85  | AI    | 4     | 0        | 0        | 1       | 0            |
| 85  | AK    | 16    | 0        | 0        | 0       | 0            |
| 85  | AM    | 3     | 0        | 0        | 0       | 0            |
| 85  | AP    | 2     | 0        | 0        | 0       | 0            |
| 85  | AQ    | 3     | 0        | 0        | 1       | 0            |
| 85  | G     | 1     | 0        | 0        | 0       | 0            |
| 85  | O     | 1     | 0        | 0        | 0       | 0            |
| 85  | j     | 16    | 0        | 0        | 1       | 0            |
| 85  | k     | 38    | 0        | 0        | 0       | 0            |

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| Mol | Chain | Non-H  | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 85  | l     | 20     | 0        | 0        | 1       | 0            |
| 85  | m     | 1      | 0        | 0        | 0       | 0            |
| 85  | n     | 1      | 0        | 0        | 1       | 0            |
| 85  | o     | 11     | 0        | 0        | 0       | 0            |
| 85  | p     | 1      | 0        | 0        | 0       | 0            |
| 85  | r     | 1      | 0        | 0        | 0       | 0            |
| 85  | t     | 7      | 0        | 0        | 0       | 0            |
| 85  | v     | 24     | 0        | 0        | 1       | 0            |
| 85  | w     | 10     | 0        | 0        | 1       | 0            |
| 85  | x     | 14     | 0        | 0        | 1       | 0            |
| 85  | y     | 6      | 0        | 0        | 1       | 0            |
| 85  | z     | 3      | 0        | 0        | 0       | 0            |
| All | All   | 201513 | 0        | 148769   | 2646    | 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 8.

The worst 5 of 2646 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) |
|-------------------|----------------------|--------------------------|-------------------|
| 78:f:50:THR:OG1   | 78:f:53:LYS:HB2      | 1.28                     | 1.33              |
| 1:1:909:A:OP2     | 81:1:3411:SPD:H82    | 1.27                     | 1.25              |
| 81:1:3406:SPD:C3  | 31:AC:14[B]:ARG:HH12 | 1.50                     | 1.25              |
| 81:1:3406:SPD:H32 | 31:AC:14[B]:ARG:NH1  | 1.51                     | 1.25              |
| 1:1:634:C:H5"     | 81:1:3405:SPD:H51    | 1.21                     | 1.17              |

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 |     |
|-----|-------|----------------|-----------|---------|----------|-------------|-----|
| 5   | j     | 248/254 (98%)  | 240 (97%) | 8 (3%)  | 0        | 100         | 100 |
| 6   | k     | 385/389 (99%)  | 373 (97%) | 12 (3%) | 0        | 100         | 100 |
| 7   | l     | 359/363 (99%)  | 349 (97%) | 10 (3%) | 0        | 100         | 100 |
| 8   | m     | 290/298 (97%)  | 279 (96%) | 11 (4%) | 0        | 100         | 100 |
| 9   | n     | 152/176 (86%)  | 150 (99%) | 2 (1%)  | 0        | 100         | 100 |
| 10  | o     | 233/241 (97%)  | 226 (97%) | 7 (3%)  | 0        | 100         | 100 |
| 11  | p     | 236/262 (90%)  | 231 (98%) | 5 (2%)  | 0        | 100         | 100 |
| 12  | q     | 188/191 (98%)  | 183 (97%) | 5 (3%)  | 0        | 100         | 100 |
| 13  | r     | 204/220 (93%)  | 201 (98%) | 3 (2%)  | 0        | 100         | 100 |
| 14  | s     | 171/174 (98%)  | 166 (97%) | 5 (3%)  | 0        | 100         | 100 |
| 15  | t     | 198/202 (98%)  | 196 (99%) | 2 (1%)  | 0        | 100         | 100 |
| 16  | u     | 128/131 (98%)  | 125 (98%) | 3 (2%)  | 0        | 100         | 100 |
| 17  | v     | 201/204 (98%)  | 198 (98%) | 3 (2%)  | 0        | 100         | 100 |
| 18  | w     | 197/200 (98%)  | 195 (99%) | 2 (1%)  | 0        | 100         | 100 |
| 19  | x     | 168/185 (91%)  | 165 (98%) | 3 (2%)  | 0        | 100         | 100 |
| 20  | y     | 186/186 (100%) | 182 (98%) | 4 (2%)  | 0        | 100         | 100 |
| 21  | z     | 178/190 (94%)  | 175 (98%) | 3 (2%)  | 0        | 100         | 100 |
| 22  | 0     | 171/172 (99%)  | 170 (99%) | 1 (1%)  | 0        | 100         | 100 |
| 23  | 2     | 159/160 (99%)  | 157 (99%) | 2 (1%)  | 0        | 100         | 100 |
| 24  | 5     | 103/124 (83%)  | 97 (94%)  | 5 (5%)  | 1 (1%)   | 12          | 14  |
| 25  | 6     | 129/137 (94%)  | 126 (98%) | 3 (2%)  | 0        | 100         | 100 |
| 26  | 7     | 61/155 (39%)   | 61 (100%) | 0       | 0        | 100         | 100 |
| 27  | 8     | 119/142 (84%)  | 118 (99%) | 1 (1%)  | 0        | 100         | 100 |
| 28  | 9     | 124/127 (98%)  | 123 (99%) | 1 (1%)  | 0        | 100         | 100 |
| 29  | AA    | 133/136 (98%)  | 132 (99%) | 1 (1%)  | 0        | 100         | 100 |
| 30  | AB    | 146/149 (98%)  | 138 (94%) | 8 (6%)  | 0        | 100         | 100 |
| 31  | AC    | 62/63 (98%)    | 61 (98%)  | 1 (2%)  | 0        | 100         | 100 |
| 32  | AD    | 94/106 (89%)   | 93 (99%)  | 1 (1%)  | 0        | 100         | 100 |
| 33  | AE    | 107/112 (96%)  | 106 (99%) | 1 (1%)  | 0        | 100         | 100 |
| 34  | AF    | 124/131 (95%)  | 123 (99%) | 1 (1%)  | 0        | 100         | 100 |
| 35  | AG    | 107/107 (100%) | 104 (97%) | 3 (3%)  | 0        | 100         | 100 |
| 36  | AH    | 114/122 (93%)  | 112 (98%) | 2 (2%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Favoured   | Allowed  | Outliers | Percentiles |     |
|-----|-------|---------------|------------|----------|----------|-------------|-----|
| 37  | AI    | 118/120 (98%) | 114 (97%)  | 4 (3%)   | 0        | 100         | 100 |
| 38  | AJ    | 97/99 (98%)   | 96 (99%)   | 1 (1%)   | 0        | 100         | 100 |
| 39  | AK    | 84/90 (93%)   | 81 (96%)   | 3 (4%)   | 0        | 100         | 100 |
| 40  | AL    | 76/78 (97%)   | 73 (96%)   | 3 (4%)   | 0        | 100         | 100 |
| 41  | AM    | 49/51 (96%)   | 48 (98%)   | 1 (2%)   | 0        | 100         | 100 |
| 42  | AN    | 51/52 (98%)   | 51 (100%)  | 0        | 0        | 100         | 100 |
| 43  | AO    | 23/25 (92%)   | 23 (100%)  | 0        | 0        | 100         | 100 |
| 44  | AP    | 101/106 (95%) | 100 (99%)  | 1 (1%)   | 0        | 100         | 100 |
| 45  | AQ    | 89/92 (97%)   | 85 (96%)   | 4 (4%)   | 0        | 100         | 100 |
| 46  | i     | 109/267 (41%) | 102 (94%)  | 7 (6%)   | 0        | 100         | 100 |
| 48  | B     | 206/261 (79%) | 201 (98%)  | 5 (2%)   | 0        | 100         | 100 |
| 49  | C     | 212/256 (83%) | 207 (98%)  | 5 (2%)   | 0        | 100         | 100 |
| 50  | D     | 214/249 (86%) | 209 (98%)  | 5 (2%)   | 0        | 100         | 100 |
| 51  | E     | 221/251 (88%) | 214 (97%)  | 7 (3%)   | 0        | 100         | 100 |
| 52  | F     | 258/262 (98%) | 254 (98%)  | 4 (2%)   | 0        | 100         | 100 |
| 53  | G     | 204/225 (91%) | 197 (97%)  | 7 (3%)   | 0        | 100         | 100 |
| 54  | H     | 224/236 (95%) | 221 (99%)  | 3 (1%)   | 0        | 100         | 100 |
| 55  | I     | 180/186 (97%) | 174 (97%)  | 6 (3%)   | 0        | 100         | 100 |
| 56  | J     | 201/206 (98%) | 200 (100%) | 1 (0%)   | 0        | 100         | 100 |
| 57  | K     | 176/189 (93%) | 175 (99%)  | 1 (1%)   | 0        | 100         | 100 |
| 58  | L     | 91/118 (77%)  | 84 (92%)   | 6 (7%)   | 1 (1%)   | 11          | 12  |
| 59  | M     | 139/155 (90%) | 136 (98%)  | 3 (2%)   | 0        | 100         | 100 |
| 60  | N     | 114/143 (80%) | 96 (84%)   | 18 (16%) | 0        | 100         | 100 |
| 61  | O     | 148/151 (98%) | 145 (98%)  | 3 (2%)   | 0        | 100         | 100 |
| 62  | P     | 123/132 (93%) | 119 (97%)  | 4 (3%)   | 0        | 100         | 100 |
| 63  | Q     | 116/142 (82%) | 107 (92%)  | 9 (8%)   | 0        | 100         | 100 |
| 64  | R     | 138/142 (97%) | 134 (97%)  | 4 (3%)   | 0        | 100         | 100 |
| 65  | S     | 123/137 (90%) | 120 (98%)  | 3 (2%)   | 0        | 100         | 100 |
| 66  | T     | 140/145 (97%) | 136 (97%)  | 4 (3%)   | 0        | 100         | 100 |
| 67  | U     | 139/145 (96%) | 136 (98%)  | 3 (2%)   | 0        | 100         | 100 |
| 68  | V     | 98/119 (82%)  | 96 (98%)   | 2 (2%)   | 0        | 100         | 100 |

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| Mol | Chain | Analysed          | Favoured    | Allowed  | Outliers | Percentiles |     |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 69  | W     | 85/87 (98%)       | 83 (98%)    | 2 (2%)   | 0        | 100         | 100 |
| 70  | X     | 127/130 (98%)     | 125 (98%)   | 2 (2%)   | 0        | 100         | 100 |
| 71  | Y     | 141/145 (97%)     | 139 (99%)   | 2 (1%)   | 0        | 100         | 100 |
| 72  | Z     | 130/135 (96%)     | 130 (100%)  | 0        | 0        | 100         | 100 |
| 73  | a     | 70/105 (67%)      | 69 (99%)    | 1 (1%)   | 0        | 100         | 100 |
| 74  | b     | 98/119 (82%)      | 96 (98%)    | 2 (2%)   | 0        | 100         | 100 |
| 75  | c     | 79/82 (96%)       | 75 (95%)    | 4 (5%)   | 0        | 100         | 100 |
| 76  | d     | 60/67 (90%)       | 55 (92%)    | 5 (8%)   | 0        | 100         | 100 |
| 77  | e     | 53/56 (95%)       | 51 (96%)    | 2 (4%)   | 0        | 100         | 100 |
| 78  | f     | 54/63 (86%)       | 52 (96%)    | 2 (4%)   | 0        | 100         | 100 |
| 79  | g     | 68/193 (35%)      | 61 (90%)    | 7 (10%)  | 0        | 100         | 100 |
| 80  | h     | 309/317 (98%)     | 291 (94%)   | 18 (6%)  | 0        | 100         | 100 |
| All | All   | 11011/12138 (91%) | 10716 (97%) | 293 (3%) | 2 (0%)   | 100         | 100 |

All (2) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 58  | L     | 88  | PRO  |
| 24  | 5     | 20  | ALA  |

### 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 |     |
|-----|-------|---------------|------------|----------|-------------|-----|
| 5   | j     | 191/194 (98%) | 191 (100%) | 0        | 100         | 100 |
| 6   | k     | 326/328 (99%) | 326 (100%) | 0        | 100         | 100 |
| 7   | l     | 290/292 (99%) | 290 (100%) | 0        | 100         | 100 |
| 8   | m     | 247/252 (98%) | 247 (100%) | 0        | 100         | 100 |
| 9   | n     | 135/154 (88%) | 135 (100%) | 0        | 100         | 100 |
| 10  | o     | 199/204 (98%) | 199 (100%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed       | Rotameric  | Outliers | Percentiles |     |
|-----|-------|----------------|------------|----------|-------------|-----|
| 11  | p     | 198/216 (92%)  | 198 (100%) | 0        | 100         | 100 |
| 12  | q     | 169/170 (99%)  | 169 (100%) | 0        | 100         | 100 |
| 13  | r     | 178/186 (96%)  | 178 (100%) | 0        | 100         | 100 |
| 14  | s     | 148/149 (99%)  | 148 (100%) | 0        | 100         | 100 |
| 15  | t     | 166/168 (99%)  | 165 (99%)  | 1 (1%)   | 78          | 88  |
| 16  | u     | 108/109 (99%)  | 108 (100%) | 0        | 100         | 100 |
| 17  | v     | 177/178 (99%)  | 177 (100%) | 0        | 100         | 100 |
| 18  | w     | 166/167 (99%)  | 166 (100%) | 0        | 100         | 100 |
| 19  | x     | 142/154 (92%)  | 141 (99%)  | 1 (1%)   | 76          | 86  |
| 20  | y     | 156/154 (101%) | 156 (100%) | 0        | 100         | 100 |
| 21  | z     | 147/153 (96%)  | 147 (100%) | 0        | 100         | 100 |
| 22  | 0     | 158/157 (101%) | 158 (100%) | 0        | 100         | 100 |
| 23  | 2     | 135/134 (101%) | 135 (100%) | 0        | 100         | 100 |
| 24  | 5     | 95/112 (85%)   | 93 (98%)   | 2 (2%)   | 47          | 65  |
| 25  | 6     | 101/103 (98%)  | 101 (100%) | 0        | 100         | 100 |
| 26  | 7     | 57/127 (45%)   | 57 (100%)  | 0        | 100         | 100 |
| 27  | 8     | 108/121 (89%)  | 108 (100%) | 0        | 100         | 100 |
| 28  | 9     | 111/112 (99%)  | 111 (100%) | 0        | 100         | 100 |
| 29  | AA    | 117/118 (99%)  | 117 (100%) | 0        | 100         | 100 |
| 30  | AB    | 120/121 (99%)  | 120 (100%) | 0        | 100         | 100 |
| 31  | AC    | 50/49 (102%)   | 50 (100%)  | 0        | 100         | 100 |
| 32  | AD    | 81/90 (90%)    | 81 (100%)  | 0        | 100         | 100 |
| 33  | AE    | 98/100 (98%)   | 98 (100%)  | 0        | 100         | 100 |
| 34  | AF    | 111/115 (96%)  | 111 (100%) | 0        | 100         | 100 |
| 35  | AG    | 94/92 (102%)   | 94 (100%)  | 0        | 100         | 100 |
| 36  | AH    | 99/102 (97%)   | 99 (100%)  | 0        | 100         | 100 |
| 37  | AI    | 106/106 (100%) | 106 (100%) | 0        | 100         | 100 |
| 38  | AJ    | 79/79 (100%)   | 79 (100%)  | 0        | 100         | 100 |
| 39  | AK    | 70/73 (96%)    | 70 (100%)  | 0        | 100         | 100 |
| 40  | AL    | 69/69 (100%)   | 69 (100%)  | 0        | 100         | 100 |
| 41  | AM    | 47/47 (100%)   | 47 (100%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Rotameric  | Outliers | Percentiles |     |
|-----|-------|---------------|------------|----------|-------------|-----|
| 42  | AN    | 48/47 (102%)  | 48 (100%)  | 0        | 100         | 100 |
| 43  | AO    | 24/24 (100%)  | 20 (83%)   | 4 (17%)  | 2           | 2   |
| 44  | AP    | 88/89 (99%)   | 88 (100%)  | 0        | 100         | 100 |
| 45  | AQ    | 72/73 (99%)   | 72 (100%)  | 0        | 100         | 100 |
| 46  | i     | 92/212 (43%)  | 92 (100%)  | 0        | 100         | 100 |
| 48  | B     | 176/215 (82%) | 176 (100%) | 0        | 100         | 100 |
| 49  | C     | 194/229 (85%) | 194 (100%) | 0        | 100         | 100 |
| 50  | D     | 174/198 (88%) | 174 (100%) | 0        | 100         | 100 |
| 51  | E     | 174/196 (89%) | 174 (100%) | 0        | 100         | 100 |
| 52  | F     | 218/220 (99%) | 218 (100%) | 0        | 100         | 100 |
| 53  | G     | 178/197 (90%) | 178 (100%) | 0        | 100         | 100 |
| 54  | H     | 195/204 (96%) | 195 (100%) | 0        | 100         | 100 |
| 55  | I     | 163/167 (98%) | 163 (100%) | 0        | 100         | 100 |
| 56  | J     | 157/160 (98%) | 157 (100%) | 0        | 100         | 100 |
| 57  | K     | 153/160 (96%) | 153 (100%) | 0        | 100         | 100 |
| 58  | L     | 87/104 (84%)  | 87 (100%)  | 0        | 100         | 100 |
| 59  | M     | 122/134 (91%) | 122 (100%) | 0        | 100         | 100 |
| 60  | N     | 98/123 (80%)  | 98 (100%)  | 0        | 100         | 100 |
| 61  | O     | 129/130 (99%) | 129 (100%) | 0        | 100         | 100 |
| 62  | P     | 96/101 (95%)  | 96 (100%)  | 0        | 100         | 100 |
| 63  | Q     | 102/121 (84%) | 102 (100%) | 0        | 100         | 100 |
| 64  | R     | 114/116 (98%) | 114 (100%) | 0        | 100         | 100 |
| 65  | S     | 112/122 (92%) | 112 (100%) | 0        | 100         | 100 |
| 66  | T     | 126/129 (98%) | 126 (100%) | 0        | 100         | 100 |
| 67  | U     | 113/117 (97%) | 113 (100%) | 0        | 100         | 100 |
| 68  | V     | 90/105 (86%)  | 90 (100%)  | 0        | 100         | 100 |
| 69  | W     | 71/71 (100%)  | 71 (100%)  | 0        | 100         | 100 |
| 70  | X     | 112/113 (99%) | 112 (100%) | 0        | 100         | 100 |
| 71  | Y     | 116/118 (98%) | 116 (100%) | 0        | 100         | 100 |
| 72  | Z     | 109/112 (97%) | 109 (100%) | 0        | 100         | 100 |
| 73  | a     | 64/85 (75%)   | 64 (100%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed         | Rotameric   | Outliers | Percentiles |     |
|-----|-------|------------------|-------------|----------|-------------|-----|
| 74  | b     | 86/102 (84%)     | 86 (100%)   | 0        | 100         | 100 |
| 75  | c     | 72/73 (99%)      | 72 (100%)   | 0        | 100         | 100 |
| 76  | d     | 54/58 (93%)      | 54 (100%)   | 0        | 100         | 100 |
| 77  | e     | 47/48 (98%)      | 47 (100%)   | 0        | 100         | 100 |
| 78  | f     | 48/54 (89%)      | 48 (100%)   | 0        | 100         | 100 |
| 79  | g     | 62/175 (35%)     | 62 (100%)   | 0        | 100         | 100 |
| 80  | h     | 259/263 (98%)    | 259 (100%)  | 0        | 100         | 100 |
| All | All   | 9444/10220 (92%) | 9436 (100%) | 8 (0%)   | 87          | 94  |

5 of 8 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res   | Type |
|-----|-------|-------|------|
| 43  | AO    | 25    | LYS  |
| 43  | AO    | 24    | SER  |
| 43  | AO    | 6     | ARG  |
| 24  | 5     | 31[B] | GLU  |
| 43  | AO    | 12    | ARG  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 70 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 58  | L     | 62  | GLN  |
| 59  | M     | 127 | GLN  |
| 66  | T     | 89  | GLN  |
| 21  | z     | 134 | HIS  |
| 19  | x     | 50  | GLN  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 1   | 1     | 3205/3359 (95%) | 560 (17%)         | 36 (1%)         |
| 2   | 3     | 120/121 (99%)   | 9 (7%)            | 0               |
| 3   | 4     | 157/158 (99%)   | 24 (15%)          | 3 (1%)          |
| 4   | 10    | 14/76 (18%)     | 3 (21%)           | 0               |
| 47  | A     | 1685/1787 (94%) | 390 (23%)         | 47 (2%)         |
| All | All   | 5181/5501 (94%) | 986 (19%)         | 86 (1%)         |

5 of 986 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 1     | 24  | U    |
| 1   | 1     | 25  | A    |
| 1   | 1     | 29  | G    |
| 1   | 1     | 39  | A    |
| 1   | 1     | 42  | A    |

5 of 86 RNA pucker outliers are listed below:

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 47  | A     | 553  | A    |
| 47  | A     | 1335 | U    |
| 47  | A     | 638  | U    |
| 47  | A     | 820  | U    |
| 47  | A     | 1396 | A    |

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

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 | $\# Z  > 2$ |
| 44  | MLZ  | AP    | 40   | 44   | 8,9,10       | 0.72 | 0           | 4,9,11      | 0.94 | 0           |
| 1   | OMC  | 1     | 2808 | 1    | 19,22,23     | 2.97 | 8 (42%)     | 25,31,34    | 1.21 | 3 (12%)     |
| 1   | OMG  | 1     | 2765 | 1    | 23,26,27     | 2.35 | 9 (39%)     | 32,38,41    | 1.86 | 9 (28%)     |
| 62  | IAS  | P     | 119  | 62   | 6,7,8        | 1.05 | 0           | 3,8,10      | 1.66 | 0           |
| 44  | MLZ  | AP    | 55   | 44   | 8,9,10       | 0.68 | 0           | 4,9,11      | 0.81 | 0           |
| 25  | MLZ  | 6     | 110  | 25   | 8,9,10       | 0.73 | 0           | 4,9,11      | 0.90 | 0           |

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 |
|-----|------|-------|-----|------|---------|----------|-------|
| 44  | MLZ  | AP    | 40  | 44   | -       | 0/7/8/10 | -     |

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| Mol | Type | Chain | Res  | Link | Chirals | Torsions  | Rings   |
|-----|------|-------|------|------|---------|-----------|---------|
| 1   | OMC  | 1     | 2808 | 1    | -       | 3/9/27/28 | 0/2/2/2 |
| 1   | OMG  | 1     | 2765 | 1    | -       | 0/9/27/28 | 0/3/3/3 |
| 62  | IAS  | P     | 119  | 62   | -       | 1/7/7/8   | -       |
| 44  | MLZ  | AP    | 55   | 44   | -       | 3/7/8/10  | -       |
| 25  | MLZ  | 6     | 110  | 25   | -       | 3/7/8/10  | -       |

The worst 5 of 17 bond length outliers are listed below:

| Mol | Chain | Res  | Type | Atoms | Z    | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|------|-------------|----------|
| 1   | 1     | 2808 | OMC  | C2-N3 | 6.33 | 1.48        | 1.36     |
| 1   | 1     | 2765 | OMG  | C4-N3 | 6.29 | 1.48        | 1.34     |
| 1   | 1     | 2808 | OMC  | C6-C5 | 5.80 | 1.48        | 1.35     |
| 1   | 1     | 2765 | OMG  | C2-N3 | 5.34 | 1.46        | 1.33     |
| 1   | 1     | 2808 | OMC  | C2-N1 | 4.86 | 1.50        | 1.40     |

The worst 5 of 12 bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms    | Z     | Observed(°) | Ideal(°) |
|-----|-------|------|------|----------|-------|-------------|----------|
| 1   | 1     | 2765 | OMG  | C5-C4-N3 | -4.68 | 120.94      | 128.39   |
| 1   | 1     | 2765 | OMG  | C2-N3-C4 | 4.58  | 120.19      | 112.30   |
| 1   | 1     | 2765 | OMG  | N9-C8-N7 | -3.24 | 107.39      | 113.40   |
| 1   | 1     | 2808 | OMC  | O2-C2-N3 | -3.17 | 117.34      | 122.33   |
| 1   | 1     | 2765 | OMG  | C2-N1-C6 | -2.89 | 119.87      | 125.11   |

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

| Mol | Chain | Res  | Type | Atoms         |
|-----|-------|------|------|---------------|
| 1   | 1     | 2808 | OMC  | O4'-C1'-N1-C2 |
| 1   | 1     | 2808 | OMC  | O4'-C1'-N1-C6 |
| 25  | 6     | 110  | MLZ  | N-CA-CB-CG    |
| 25  | 6     | 110  | MLZ  | C-CA-CB-CG    |
| 25  | 6     | 110  | MLZ  | CD-CE-NZ-CM   |

There are no ring outliers.

2 monomers are involved in 4 short contacts:

| Mol | Chain | Res  | Type | Clashes | Symm-Clashes |
|-----|-------|------|------|---------|--------------|
| 1   | 1     | 2808 | OMC  | 3       | 0            |
| 62  | P     | 119  | IAS  | 1       | 0            |

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 463 ligands modelled in this entry, 451 are monoatomic - leaving 12 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 | $\# Z  > 2$ |
| 81  | SPD  | 1     | 3402 | -    | 9,9,9        | 0.16 | 0           | 8,8,8       | 0.20 | 0           |
| 81  | SPD  | 1     | 3405 | -    | 9,9,9        | 0.60 | 0           | 8,8,8       | 1.48 | 2 (25%)     |
| 81  | SPD  | 1     | 3408 | -    | 9,9,9        | 0.15 | 0           | 8,8,8       | 0.22 | 0           |
| 81  | SPD  | 1     | 3411 | -    | 9,9,9        | 0.52 | 0           | 8,8,8       | 0.63 | 0           |
| 81  | SPD  | 1     | 3410 | -    | 9,9,9        | 0.34 | 0           | 8,8,8       | 0.61 | 0           |
| 81  | SPD  | 1     | 3406 | -    | 9,9,9        | 0.15 | 0           | 8,8,8       | 0.25 | 0           |
| 81  | SPD  | 1     | 3401 | -    | 9,9,9        | 0.31 | 0           | 8,8,8       | 0.83 | 0           |
| 81  | SPD  | 1     | 3407 | -    | 9,9,9        | 0.27 | 0           | 8,8,8       | 0.46 | 0           |
| 81  | SPD  | 1     | 3404 | -    | 9,9,9        | 0.14 | 0           | 8,8,8       | 0.18 | 0           |
| 82  | PUT  | 4     | 201  | -    | 5,5,5        | 0.23 | 0           | 4,4,4       | 0.19 | 0           |
| 82  | PUT  | 1     | 3403 | -    | 5,5,5        | 0.13 | 0           | 4,4,4       | 0.21 | 0           |
| 81  | SPD  | 1     | 3409 | -    | 9,9,9        | 0.16 | 0           | 8,8,8       | 0.18 | 0           |

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 |
|-----|------|-------|------|------|---------|----------|-------|
| 81  | SPD  | 1     | 3402 | -    | -       | 4/7/7/7  | -     |
| 81  | SPD  | 1     | 3405 | -    | -       | 4/7/7/7  | -     |
| 81  | SPD  | 1     | 3408 | -    | -       | 6/7/7/7  | -     |
| 81  | SPD  | 1     | 3411 | -    | -       | 5/7/7/7  | -     |
| 81  | SPD  | 1     | 3410 | -    | -       | 4/7/7/7  | -     |
| 81  | SPD  | 1     | 3406 | -    | -       | 3/7/7/7  | -     |

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| Mol | Type | Chain | Res  | Link | Chirals | Torsions | Rings |
|-----|------|-------|------|------|---------|----------|-------|
| 81  | SPD  | 1     | 3401 | -    | -       | 1/7/7/7  | -     |
| 81  | SPD  | 1     | 3407 | -    | -       | 4/7/7/7  | -     |
| 81  | SPD  | 1     | 3404 | -    | -       | 5/7/7/7  | -     |
| 82  | PUT  | 4     | 201  | -    | -       | 2/3/3/3  | -     |
| 82  | PUT  | 1     | 3403 | -    | -       | 0/3/3/3  | -     |
| 81  | SPD  | 1     | 3409 | -    | -       | 4/7/7/7  | -     |

There are no bond length outliers.

All (2) bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms    | Z     | Observed(°) | Ideal(°) |
|-----|-------|------|------|----------|-------|-------------|----------|
| 81  | 1     | 3405 | SPD  | C7-N6-C5 | -3.09 | 98.78       | 113.40   |
| 81  | 1     | 3405 | SPD  | C4-C5-N6 | 2.07  | 117.64      | 112.07   |

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

| Mol | Chain | Res  | Type | Atoms       |
|-----|-------|------|------|-------------|
| 81  | 1     | 3409 | SPD  | C4-C5-N6-C7 |
| 81  | 1     | 3411 | SPD  | N6-C7-C8-C9 |
| 81  | 1     | 3404 | SPD  | N6-C7-C8-C9 |
| 81  | 1     | 3405 | SPD  | C3-C4-C5-N6 |
| 81  | 1     | 3410 | SPD  | C3-C4-C5-N6 |

There are no ring outliers.

11 monomers are involved in 137 short contacts:

| Mol | Chain | Res  | Type | Clashes | Symm-Clashes |
|-----|-------|------|------|---------|--------------|
| 81  | 1     | 3405 | SPD  | 16      | 0            |
| 81  | 1     | 3408 | SPD  | 16      | 0            |
| 81  | 1     | 3411 | SPD  | 14      | 0            |
| 81  | 1     | 3410 | SPD  | 8       | 0            |
| 81  | 1     | 3406 | SPD  | 19      | 0            |
| 81  | 1     | 3401 | SPD  | 1       | 0            |
| 81  | 1     | 3407 | SPD  | 14      | 0            |
| 81  | 1     | 3404 | SPD  | 16      | 0            |
| 82  | 4     | 201  | PUT  | 8       | 0            |
| 82  | 1     | 3403 | PUT  | 11      | 0            |
| 81  | 1     | 3409 | SPD  | 14      | 0            |



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

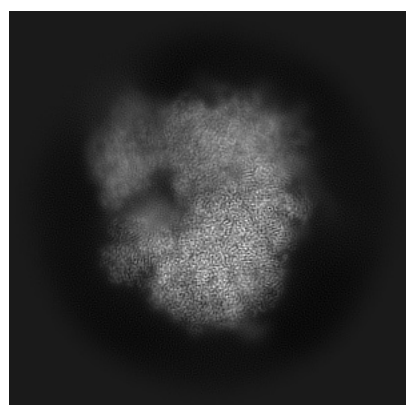
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13737. These allow visual inspection of the internal detail of the map and identification of artifacts.

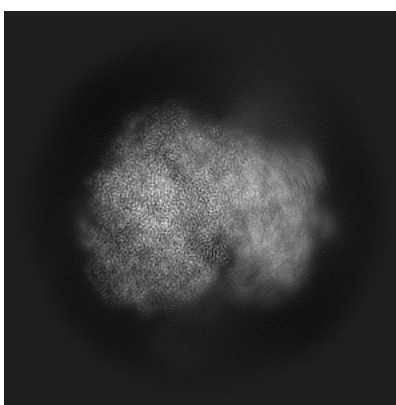
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

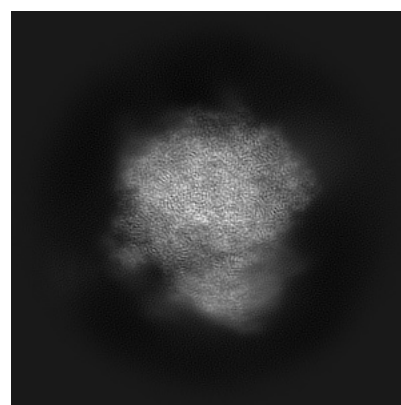
#### 6.1.1 Primary map



X



Y

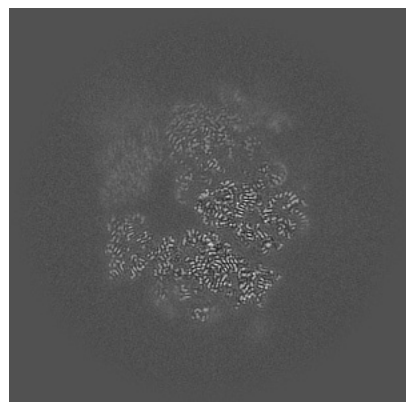


Z

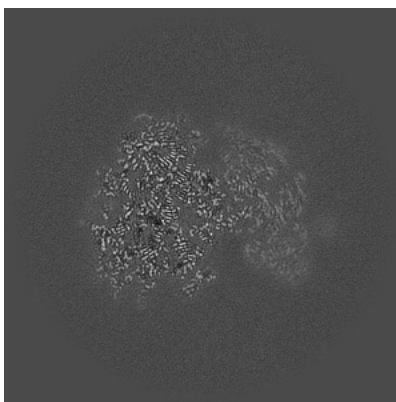
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

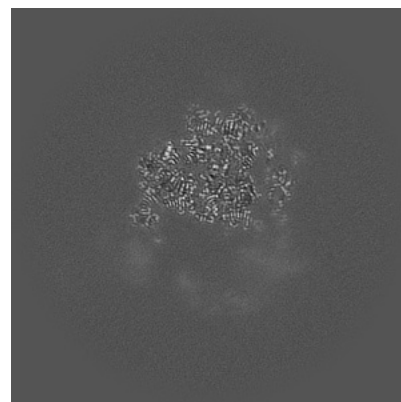
#### 6.2.1 Primary map



X Index: 255



Y Index: 255

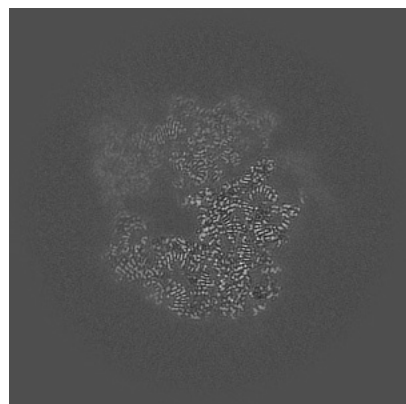


Z Index: 255

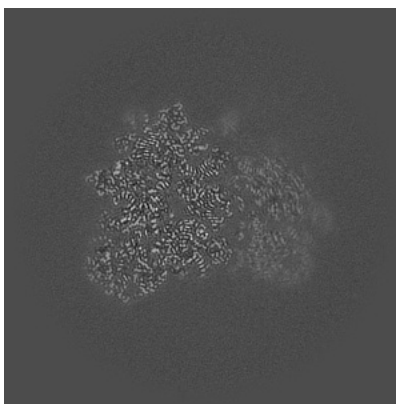
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

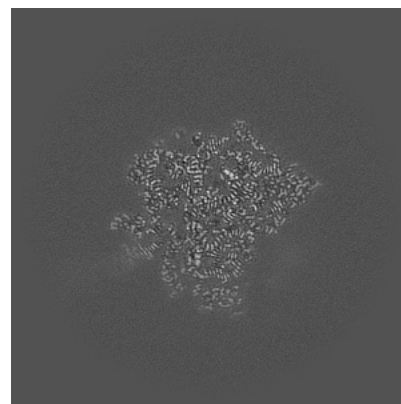
### 6.3.1 Primary map



X Index: 274



Y Index: 273

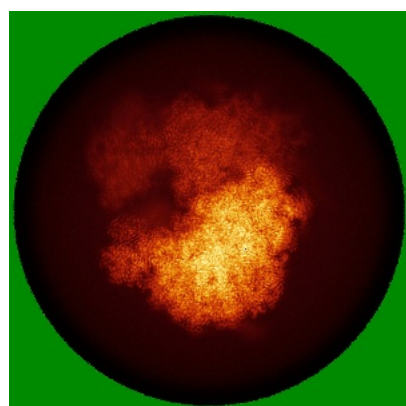


Z Index: 206

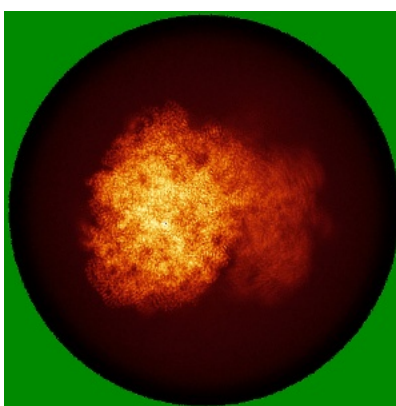
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

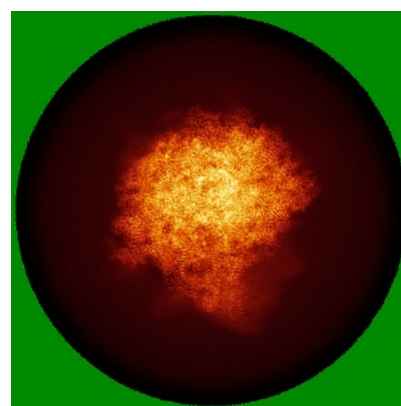
### 6.4.1 Primary map



X



Y

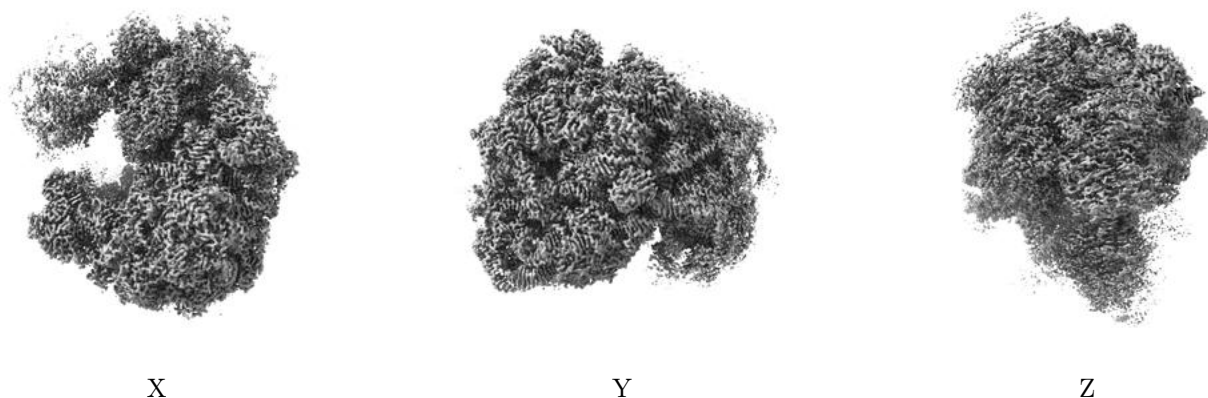


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.226. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

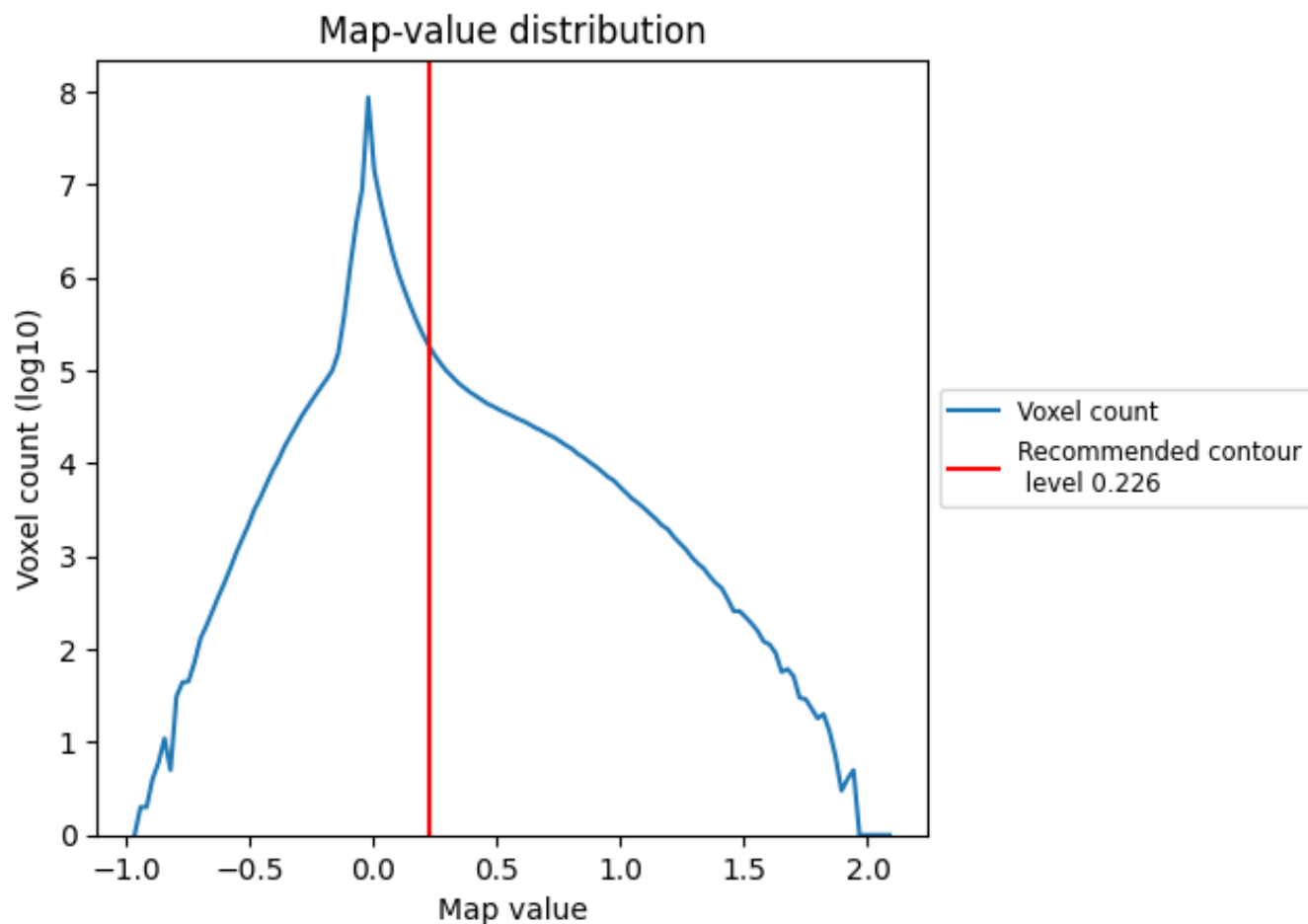
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

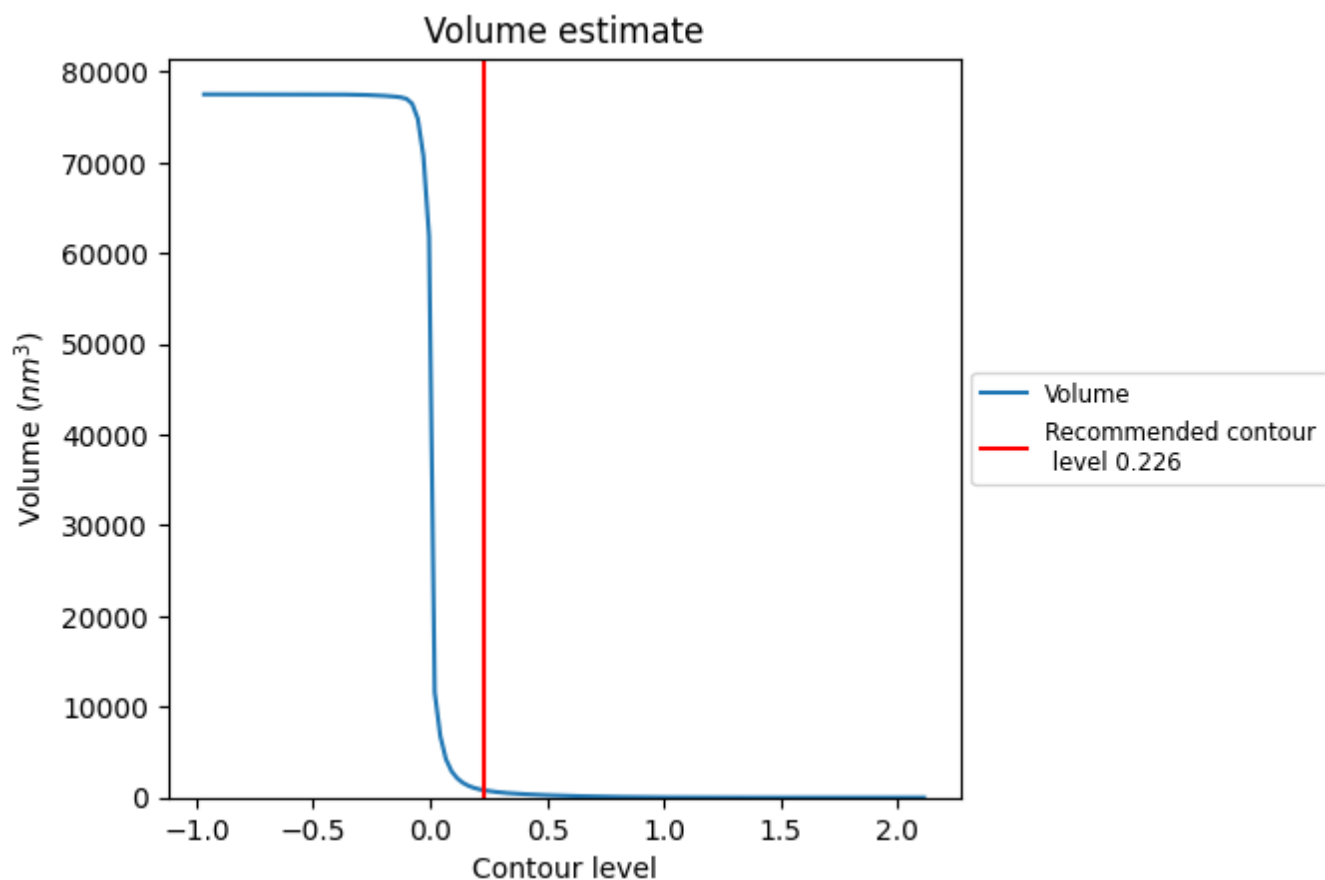
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

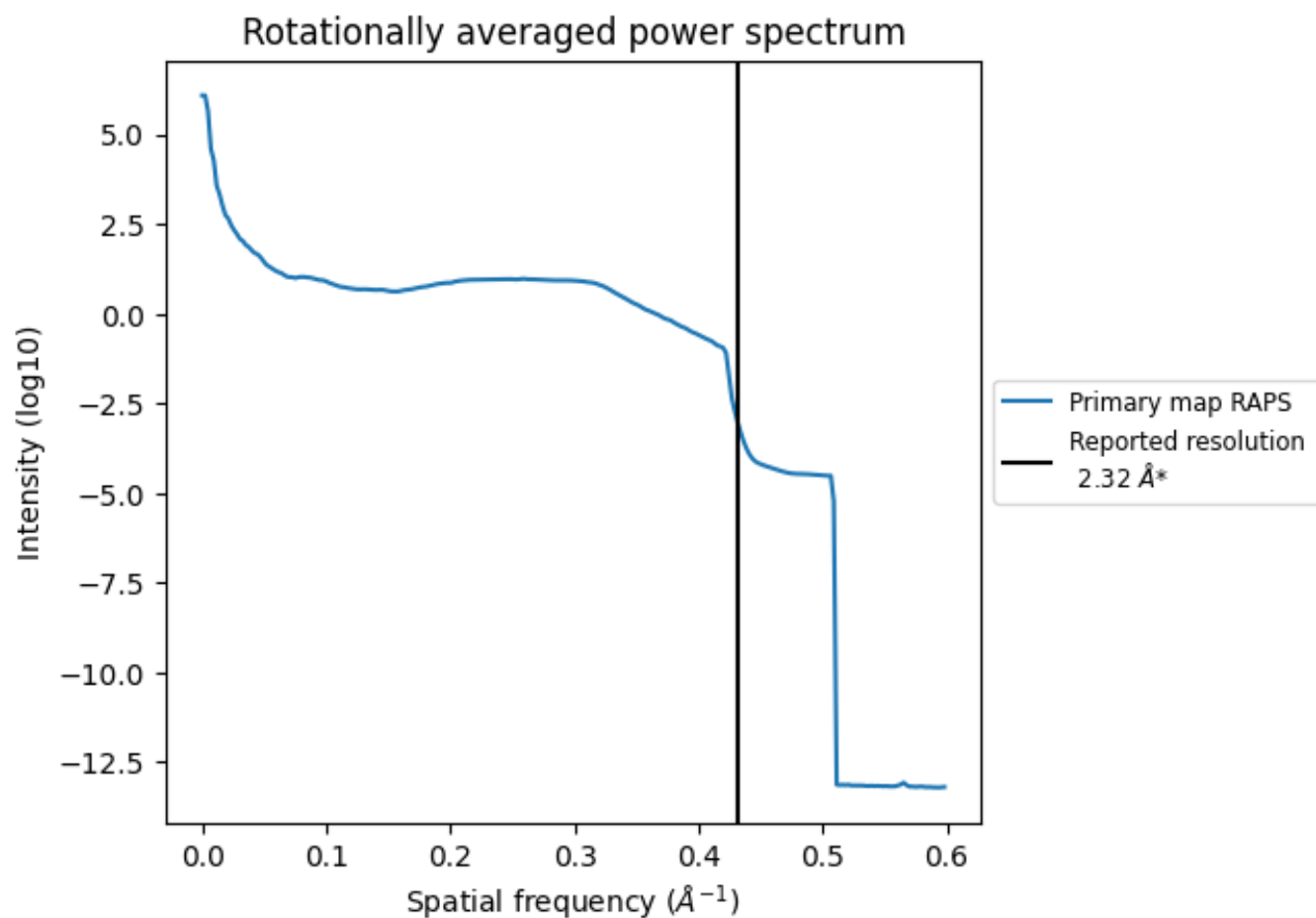
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 830 nm<sup>3</sup>; this corresponds to an approximate mass of 750 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ

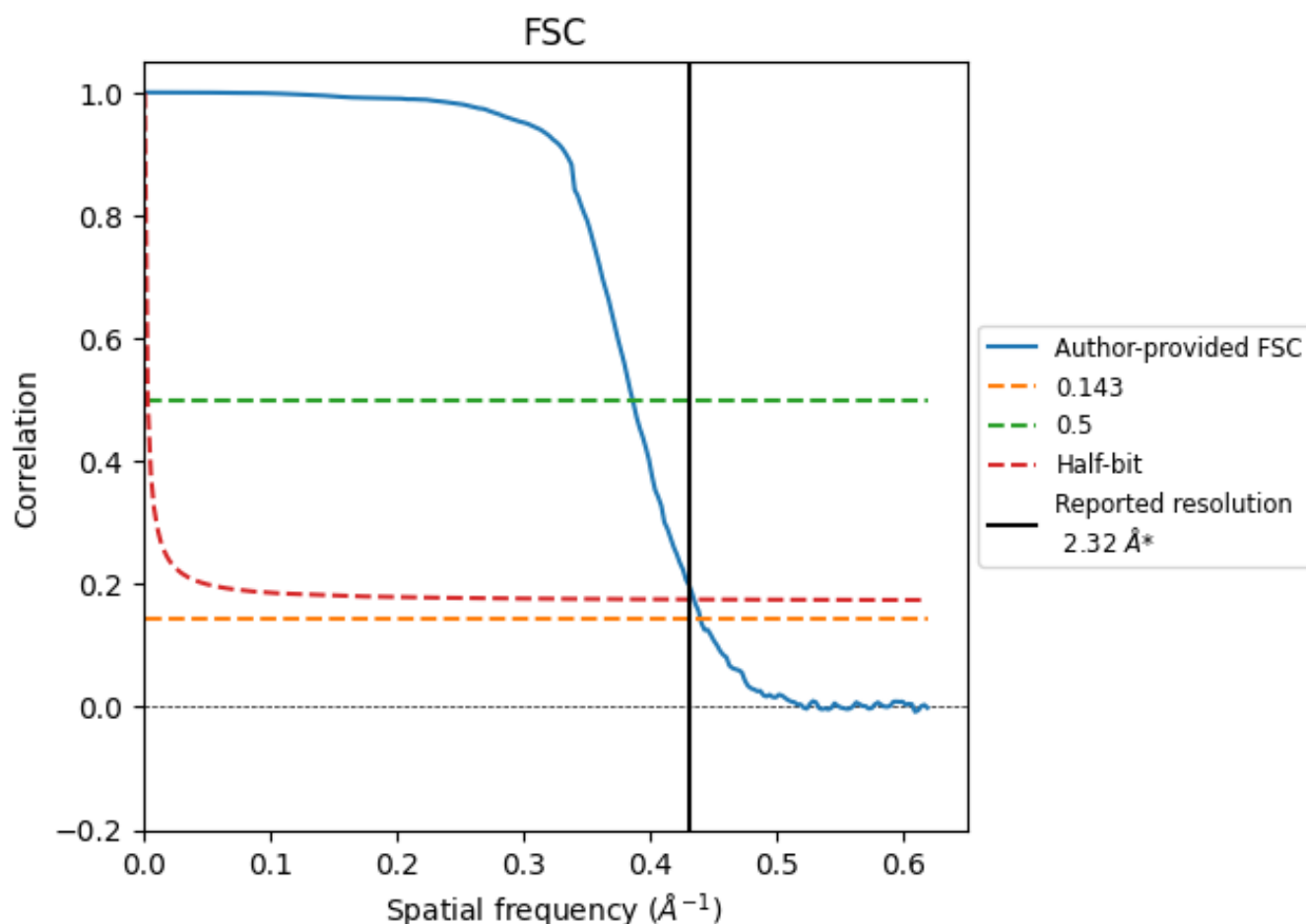


\*Reported resolution corresponds to spatial frequency of 0.431 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.431 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

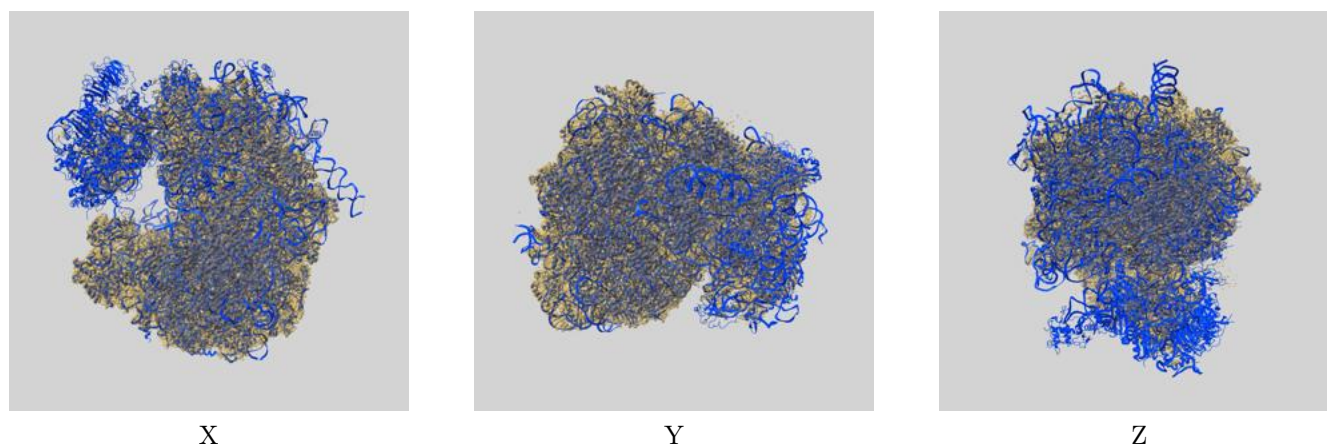
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 2.32                               | -    | -        |
| Author-provided FSC curve | 2.27                               | 2.59 | 2.30     |
| Unmasked-calculated*      | -                                  | -    | -        |

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

## 9 Map-model fit [i](#)

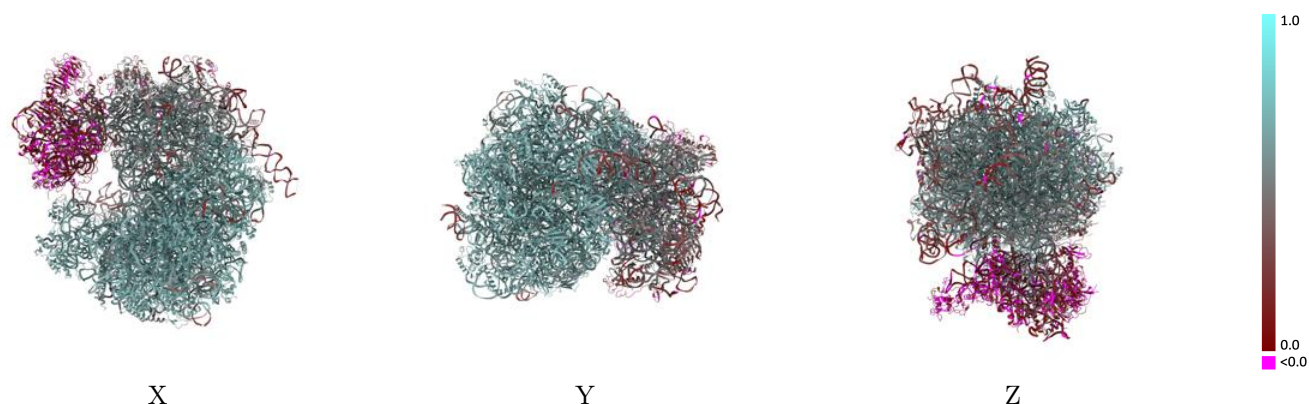
This section contains information regarding the fit between EMDB map EMD-13737 and PDB model 7PZY. Per-residue inclusion information can be found in [section 3](#) on [page 24](#).

### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.226 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

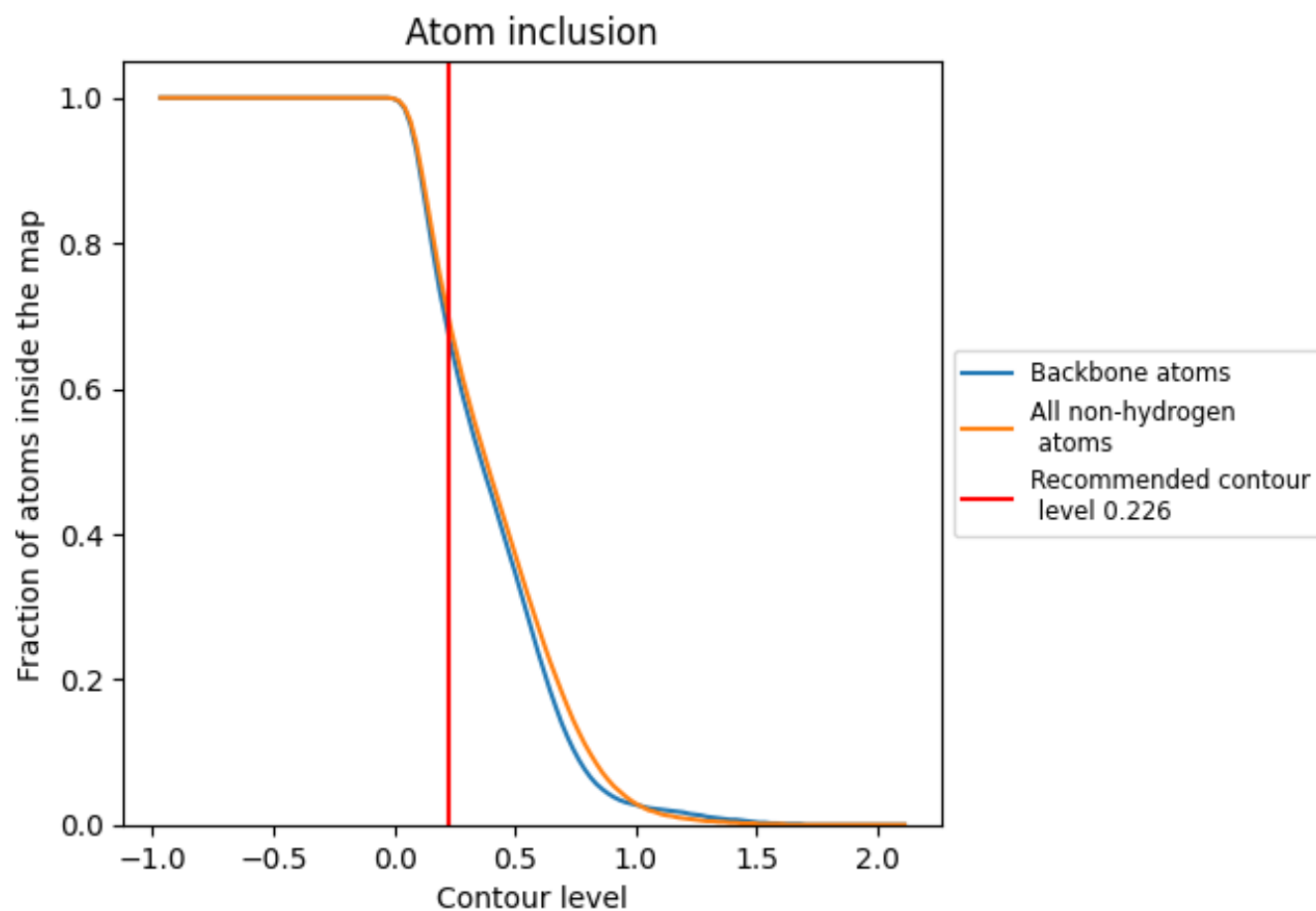


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.226) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| All   |  0.6960   |  0.5300   |
| 0     |  0.9420   |  0.6670   |
| 1     |  0.9000   |  0.6260   |
| 10    |  0.2160   |  0.4920   |
| 2     |  0.9090   |  0.6550   |
| 3     |  0.9730   |  0.6480   |
| 4     |  0.9590   |  0.6500   |
| 5     |  0.6940   |  0.5950   |
| 6     |  0.9480   |  0.6720   |
| 7     |  0.9330   |  0.6690   |
| 8     |  0.9250   |  0.6630   |
| 9     |  0.9200   |  0.6570   |
| A     |  0.4920   |  0.3990   |
| AA    |  0.8720   |  0.6520   |
| AB    |  0.9490  |  0.6740  |
| AC    |  0.8320 |  0.6250 |
| AD    |  0.8930 |  0.6520 |
| AE    |  0.8700 |  0.6570 |
| AF    |  0.9490 |  0.6710 |
| AG    |  0.9760 |  0.6840 |
| AH    |  0.8950 |  0.6570 |
| AI    |  0.9150 |  0.6460 |
| AJ    |  0.8430 |  0.6330 |
| AK    |  0.9660 |  0.6790 |
| AL    |  0.7800 |  0.6190 |
| AM    |  0.9620 |  0.6660 |
| AN    |  0.9190 |  0.6680 |
| AO    |  0.6740 |  0.6110 |
| AP    |  0.8810 |  0.6580 |
| AQ    |  0.9180 |  0.6640 |
| B     |  0.3290 |  0.4290 |
| C     |  0.3460 |  0.4950 |
| D     |  0.5160 |  0.5000 |
| E     |  0.0350 |  0.1030 |
| F     |  0.3100 |  0.4590 |



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| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| G     |  0.0080   |  0.0660   |
| H     |  0.1470   |  0.3320   |
| I     |  0.2290   |  0.4000   |
| J     |  0.4730   |  0.4890   |
| K     |  0.2910   |  0.4210   |
| L     |  0.0010   |  0.0160   |
| M     |  0.5210   |  0.5020   |
| N     |  0.0000   |  0.0050   |
| O     |  0.5910   |  0.5440   |
| P     |  0.4430   |  0.5100   |
| Q     |  0.0100   |  0.0580   |
| R     |  0.0300   |  0.1590   |
| S     |  0.0740   |  0.2740   |
| T     |  0.0130   |  0.0680   |
| U     |  0.0160   |  0.0980   |
| V     |  0.0350   |  0.1150   |
| W     |  0.3960   |  0.4560   |
| X     |  0.6400   |  0.5530   |
| Y     |  0.4610   |  0.4620   |
| Z     |  0.1400   |  0.3380   |
| a     |  0.0020  |  -0.0030 |
| b     |  0.5690 |  0.5030 |
| c     |  0.3970 |  0.4550 |
| d     |  0.0110 |  0.0840 |
| e     |  0.0500 |  0.0860 |
| f     |  0.1980 |  0.3090 |
| g     |  0.0000 |  0.0270 |
| h     |  0.0020 |  0.0980 |
| i     |  0.0060 |  0.2070 |
| j     |  0.9700 |  0.6820 |
| k     |  0.9510 |  0.6730 |
| l     |  0.9230 |  0.6590 |
| m     |  0.8290 |  0.6250 |
| n     |  0.8790 |  0.6460 |
| o     |  0.9050 |  0.6560 |
| p     |  0.8320 |  0.6330 |
| q     |  0.8790 |  0.6480 |
| r     |  0.9020 |  0.6560 |
| s     |  0.7180 |  0.5940 |
| t     |  0.8740 |  0.6470 |
| u     |  0.9040 |  0.6540 |
| v     |  0.9830 |  0.6820 |

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| Chain | Atom inclusion                                                                           | Q-score                                                                                  |
|-------|------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------|
| w     |  0.9460 |  0.6710 |
| x     |  0.9340 |  0.6710 |
| y     |  0.9580 |  0.6680 |
| z     |  0.8190 |  0.6330 |